"Absence of non-tuberculous mycobacteria recovery in sputum of cystic fibrosis patients despite adequate decontamination: a possible role of specific antimicrobial therapy used in our centre"

André, Emmanuel ; Degraux, Josiane ; Simon, Anne ; Huang, Te-Din

Abstract
Objectives: Non-tuberculous mycobacteria (NTM) were pathogens of growing importance in non-paediatric cystic fibrosis (CF) patients. In our centre, the prevalence of NTM in these patients observed (0.5%) during the last decade was markedly inferior to those reported in the literature ranging from 6.5% to 24%. The aim of this study was to screen for NTM in adult patients in our centre with 3 different decontamination methods for mycobacterial cultures in order to determine whether the choice of the decontamination technique of samples may have an impact on their recovery in our centre.
Methods: Between January and June 2009, consecutive sputum samples from adult patients with clinical suspicion of NTM infection (respiratory function degradation without other microbiologic explanation) were included in this study. 3 different decontamination protocols were used: N-acetyl-l-cysteine (NALC)-NaOH (DCT1), NALC-NaOH-oxalic acid 5% (DCT2) and DTT-Chlorhexidine 1% (DCT3). Decontaminated speci...

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New aspects of emerging *Clostridium difficile* infections (CDI)

**S4** Emerging community-acquired CDI in North America and Europe

S. Dial* (Montreal, CA)

*Clostridium difficile* has long been recognised as an important cause of antibiotic associated diarrhoea in hospitalised patients. Although community associated disease has been described in the 80’s, it is only in this decade that it has been recognised as an important cause of infectious diarrhoea in patients in the community. As *C. difficile* was mostly recognised as a nosocomial pathogen, the majority of studies of clinical *C. difficile* infections (CDI) have been conducted in acute care hospitals, and many have been performed during outbreak situations. The hospital environment has very specific characteristics which are likely to be important determinants of infectious disease occurrence and transmission, such as clustering of susceptible hosts, increased possibility of environmental contamination, physical proximity and multiple person to person contacts. Similarly, the demographics of hospitalized patients population also differ significantly from that of the community. In hospitals, the prevalence of antibiotic use is very high, and highly correlated with many other factors which could be important in the expression of CDI. Until recently antibiotics were believed to be a prerequisite for the development of CDI but studies of community acquired disease are consistently describing disease occurring in a high proportion of patients who have no such exposure. This has lead to research examining other risk factors.

CDI appears to be increasing in the community especially in the elderly, but also in the pediatric population. As up to 50% of CDI in the community may not be preceded by recent antibiotic exposure particularly in patients without a recent hospitalization, many of the recommended diarrhea testing algorithms will result in this diagnosis being missed or delayed. This could have important implications for patient care and control of outbreaks. Well designed studies of *C. difficile* in the community could improve our understanding of this disease and improve the ability to explore other risk factors and where antibiotic exposure maybe less confounded.

Presentation of International Sepsis Forum Award

**SS** Genetic analysis of pattern recognition receptors links a functional polymorphism in the gene for CD14 to susceptibility for meningococcal septic shock

T. Sprong*†, M. Emonts, R. Rossau, E. de Meester, M. van Thiel, M.G. Netea, C. Neeleman, J. Klauw, R. de Groot, J.A. Hazeltz, J van der Meer, J. Drenth, M. van Deuren (Nijmegen, Rotterdam, NL; Ghent, BE)

**Objectives**: Contact with, and colonization by, pathogenic meningococci occurs rather often. Still, only a limited number of individuals develop invasive disease, most often within a few days after acquisition of a new meningococcal strain. Thus, it can be assumed that disease develops because of defects in the early innate defense. We hypothesized that polymorphisms in Pattern Recognition Receptors (PRRs) influence susceptibility to meningococcal disease or alter disease severity.

**Methods**: 73 different single-nucleotide polymorphisms (SNPs) in 21 genes encoding PRRs and related molecules of the innate immune system were investigated using a research prototype of a line-probe assay (INNO-LIPA, Innogenetics). We performed a three-stage approach. First (stage 1) we performed a case-parent study in subjects with meningococcal disease admitted to the intensive care unit (ICU) (n=118). Second (stage 2), we performed a case–control study in an

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**S3** New treatment aspects of CDI

M. Wilcox* (Leeds, UK)

The need for new therapeutic alternatives in CDI is clear. Current recurrence rates are unacceptable high. The optimal treatment of severe CDI, infection caused by strains associated with poor outcome (e.g. *C. difficile* ribotype 027), and multiple recurrences is unclear. There are several potentially promising new CDI treatment approaches under investigation, including antibiotic, anti-toxin and bacterial interference options. Probiotic therapy remains of unproven benefit. As new options become available, prognostic data will be needed to guide on the most appropriate therapeutic choices.

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**S2** Pros and cons of molecular fingerprinting for *Clostridium difficile* infections

E.J. Kuijper* (Leiden, NL)

Since the 1980s the epidemiology of *Clostridium difficile* infection (CDI) has been investigated by the application of many different typing or fingerprinting methods. To study the epidemiology of CDI, a typing method with a high discriminatory power, typeability, stability, power, reproducibility and epidemiological concordance is required. It should also have technical advantages, such as ease of performance, relative low cost, and high throughput. A growing number of molecular methods have been applied to *C. difficile*. For the early and rapid detection of outbreak situations, methods such as restriction enzyme analysis, arbitrary primed polymerase chain reaction (PCR), pulsed-field gel electrophoresis, and PCR ribotyping are commonly used. For long-term epidemiology, multilocus sequence typing, multilocus variable number of tandem repeats analysis (MLVA), and amplified fragment length polymorphism are of interest. Currently, the PCR-ribotyping method and the library of PCR ribotypes in Cardiff are the benchmarks to which most typing studies around the world are compared. Conventional agarose gel-based PCR ribotyping is easy to use and relatively cheap, but analysis of fragment lengths is hampered by poor resolution. Recently, a capillary gel electrophoresis-based PCR ribotyping assay has been developed that significantly reduces the hands-on time required for *C. difficile* PCR ribotyping. The results were highly reproducible, independent of reagent batches or brands used and allows inter-laboratory comparisons of typing results. The analysis of the sequenced *C. difficile* genome revealed a high percentage of DNA that consisted of a variable number of tandem repeats (VNTR). Recently, a new MLVA method was developed using small short tandem repeats (2–9 bp) to facilitate automated fragment analysis with multicoloured capillary electrophoresis instead of sequencing. In a study using isolates from laboratories in Canada, the Netherlands, the United Kingdom, and the United States, seven *C. difficile* typing techniques were compared, but only REA and MLVA showed sufficient discrimination to distinguish strains from different outbreaks. MLVA has also been applied to study local outbreaks of *C. difficile* PCR ribotype 027 strains. MLVA is currently the most discriminative typing method and will contribute significantly to our understanding of the epidemiology of *C. difficile*.

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**S1** Oral presentations

New aspects of emerging *Clostridium difficile* infections (CDI)

Oralpresentations

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Presentation of International Sepsis Forum Award

**SS** Genetic analysis of pattern recognition receptors links a functional polymorphism in the gene for CD14 to susceptibility for meningococcal septic shock

T. Sprong*†, M. Emonts, R. Rossau, E. de Meester, M. van Thiel, M.G. Netea, C. Neeleman, J. Klauw, R. de Groot, J.A. Hazeltz, J van der Meer, J. Drenth, M. van Deuren (Nijmegen, Rotterdam, NL; Ghent, BE)

**Objectives**: Contact with, and colonization by, pathogenic meningococci occurs rather often. Still, only a limited number of individuals develop invasive disease, most often within a few days after acquisition of a new meningococcal strain. Thus, it can be assumed that disease develops because of defects in the early innate defense. We hypothesized that polymorphisms in Pattern Recognition Receptors (PRRs) influence susceptibility to meningococcal disease or alter disease severity.

**Methods**: 73 different single-nucleotide polymorphisms (SNPs) in 21 genes encoding PRRs and related molecules of the innate immune system were investigated using a research prototype of a line-probe assay (INNO-LIPA, Innogenetics). We performed a three-stage approach. First (stage 1) we performed a case-parent study in subjects with meningococcal disease admitted to the intensive care unit (ICU) (n=118). Second (stage 2), we performed a case–control study in an
extended cohort (n = 147). Finally (stage 3), the observed associations were tested for replication in an independent case-control study (n = 146).

**Results:** In stage 1, we found SNPs in the genes for MASp2, CD14, LBP and TLR6 to be associated with increased susceptibility to meningococcal disease. For the rs2563298 SNP in CD14 this was replicated in the case control study (stage 2; OR 1.65, 95% CI 1.17–2.31) and in the separate replication study with the independent (confirmatory) cohort (Stage 3; OR 1.44, 95% CI 1.02–2.04). Subgroup analysis showed that the CD14 SNP conferred increased risk only in shock patients (OR 1.99, 95% CI 1.28–3.08). This CD14 SNP is functional and leads to decreased IL-10 and IL-12 production in a whole blood model of meningococcal sepsis.

**Conclusions:** In conclusion, we identified a functional SNP in CD14 that is associated with an increased risk for meningococcal septic shock. Possible other SNPs associated with increased risk for meningococcal disease were in MASp2, LBP and TLR6.

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**Histones in sepsis**

**T. Roger**  (Lausanne, CH)

Chromatin is made-up of DNA, histones and non-histones proteins. Covalent modifications of histones through acetylation at Lysine residues strongly influence the structure and the function of the chromatin. Whereas acetylation of histones results in a relaxed chromatin structure that is associated with active transcription, de-acetylation of histones results in a compacted chromatin structure associated with repressed transcription. Global histone acetylation is regulated by the opposing actions of histone acetyltransferases (HATs) and histone deacetylases (HDACs). Beside histones, non histones proteins are modified by reversible acetylation, among which α-tubulin, HSP90 and transcription regulators. Therefore, HDACs impact on many biological functions, primarily cell differentiation, growth and survival. HDAC inhibitors (HDIs) were originally developed for their powerful anti-cancer activity. Yet, recent preclinical studies suggest that HDIs possess anti-inflammatory activity. Based on these observations, we postulated that HDIs could impact on innate immune response to microbial infection. Here we will discuss the results from our studies on the effect of HDIs on the innate immune system. We first performed genome-wide gene expression analyses to have a global view of the impact of HDIs on the transcriptome of resting and microbial product-stimulated primary macrophages. We then studied the influence of HDIs on key parameters (activation of the intracellular signal transduction pathways, production of cytokines and chemokines, expression of co-stimulatory and chemokine receptors.) of macrophages, dendritic cells and whole blood activated by a broad range of microbial products. Finally, we analyzed the impact of HDIs in preclinical models of non-severe bacterial and fungal infections, toxic shock and severe sepsis. Overall, these studies demonstrate that HDIs are powerful anti-inflammatory and immunosuppressive drugs that impair innate immune responses to microbial infections in vitro and in vivo. While the results suggest that HDIs may represent attractive adjunctive therapies to treat pathological situations characterized by dysregulated inflammatory responses such as autoimmune diseases and severe sepsis, they also warn that HDIs may increase the risk of developing opportunistic infections and sepsis, especially in immunocompromised cancer patients.

**Latest trends from the molecular laboratory for studying fungal pathogens and invasive fungal infections**

**S14 Diagnostic PCR for IFL. Does it really work?**

*M. Cuenca-Estrella*  (Majadahonda, ES)

Invasive aspergillosis (IA) continues to have high mortality, partly as a consequence of the difficulties of early diagnosis and also due to therapeutic limitations. Nowadays IA diagnosis is based on extensive use of galactomannan (GM) and high-resolution chest tomography (HRCT). Despite the fact positive GM has prompted an earlier treatment of IA, mortality is still high in this population showing that other diagnostic approaches should be taken into account. Detection of nucleic acids, PCR-based methods mainly, appears to be an option to assess although to date there are many doubts as to the profitability of this type of methods.

Diagnostic PCR must be considered an additional test that is being developed and that is used in some reference laboratories. Its lack of standardization should be stressed, since different laboratories use different approaches in terms of extraction, probes, primers, PCR conditions, and measurement. Furthermore the benefit of detecting DNA of *Aspergillus fumigatus* depends on the clinical sample used. PCR techniques have shown high diagnostic reliability in tissue biopsies and respiratory samples with high negative predictive values and discreet positive predictive values, but lower diagnostic reliability has been obtained in blood samples. Those high negative predictive values could be useful to rule out the presence of infection.

Newer approaches such as serial determinations of *Aspergillus* DNA in serum or blood, and detection of fungal DNA in higher volumes of blood is shown a greater diagnostic applicability, which increases when combined with GM quantification and high-resolution chest tomography. Those approaches have had higher rates of both sensitivity and specificity and improved the early diagnosis of aspergillosis. Fewer data are available for other mycoses. PCR methods have been developed to detect *Candida*, endemic mycosis and emerging pathogens but more data are needed and reliable conclusions should not be drawn.

**S16 Clinically relevant novel fungal taxa from old species complexes**

*T. Boekhout*, F. Hugen, B. Theelen, K. Khayhan, C. Klausen, J. Meis (Utrecht, Nijmegen, NL)

Our understanding of causative agents of fungal diseases has changed considerably during recent years. This is mainly due to the large scale introduction of molecular studies, in which one or more stretches of DNA are compared across a wide range of fungi, including human and animal pathogens. One of the most striking discoveries was the recognition of *Pneumocystis* as a fungus, as this organism was considered previously to belong to the parasites. In many cases traditional ‘species’ turned out to represent species complexes and many of the newly recognized clinically relevant species may differ in the susceptibility to commonly used antifungals. Therefore, correct identification of these new pathogens is important for proper patient management.

A brief overview will be presented of these developments in fungal taxonomy and their implications for the clinical practice. Examples will be given from the main lineages of the fungal kingdom, namely *Zygomycetes*, *Ascomycetes* (*Aspergillus*, *Fusarium*, and *Candida spp.*) and *Bassidiomycetes* (*Malassezia*, *Trichosporon* and *Cryptococcus spp.*). Due to our own experience with the basidiomycetous yeasts we will give more in depth information on these fungi. The number of recognized species is rapidly increasing due to the application of molecular systematics and the availability of a large database of ribosomal DNA (rDNA) sequences, most notable the D1/D2 domains of the LSU rDNA and the ITS 1 and 2 regions. Only a few species are generally recognized as important pathogens for humans and animals, including *Cryptococcus neoformans* and *Cr. gattii*, several Trichosporon species and *Malassezia* spp. However, several non-conventional basidiomycetous yeast species can cause infection or are otherwise involved in health problems, such as hypersensitivity pneumonitis. We will present data on the involvement of these emerging basidiomycetous species, such as *C. adeliensis*, *C. difficiens*, *C. fluaxescens* and *C. laurentii* in human diseases. Emphasis will be on the *Cr. neoformans-Cr. gattii* and *Malassezia* species complexes, especially the role of the newly recognized species in disease, virulence, and susceptibility to antifungals.
**DNA-based methods to detect MRSA**

**S17** Is molecular subtyping a clinical tool?

*S. Breitagne*° (Créteil, FR)

The main application of genotyping is for the investigation of epidemics or tracking routes of contamination. Several molecular typing techniques have been developed for fungi. Ideally, typing results should be accurate, reproducible, and easy to interpret. Importantly, methods should be transferable to other settings. Many typing methods such as randomly amplified polymorphic DNA; restriction fragment length polymorphism, single-strand conformation polymorphism analysis, and amplified fragment length polymorphism yield fingerprint profiles that are difficult to reproduce in different settings. In contrast, two methods have emerged for clinical applications as providing reliable, portable and easy to obtain data: microsatellite markers and Multi Locus Sequence Typing (MLST).

Microsatellites, or short tandem repeats, are defined as tandemly repetitive stretches of two to five nucleotides. After amplification, PCR products are analyzed based on ampiclon length. The present limitation of microsatellite typing is transferability. A straightforward and universally applicable method to achieve such a calibration is through the use of allelic ladders. MLST is based on sequencing several housekeeping genes. Active MLST schemes are publicly available [http://www.mlst.net/](http://www.mlst.net/) for yeasts. The main advantage of MLST is the ability to provide indisputable data based on sequencing. However, MLST is laborious, based on the quality of the sequences, has a long turn-around time and is associated with significant costs.

The nosocomial acquisition of invasive infections has been investigated. The conclusion are disappointing for invasive aspergillosis but unambiguous for invasive candidiasis. However, genotyping itself is not sufficient. Sampling, collection of clinical and epidemiological data are compulsory to reach a meaningful conclusion. Another interesting point is the propagation of a given clone with a resistant phenotype. This has already been investigated for *Aspergillus fumigatus* and *Candida tropicalis*.

Getting more and more pieces of information on the genome of each microorganism will probably be part of the future routine laboratories. The current trend towards mass sequencing creates such opportunities. This technology might lead to several modifications in the way we identify a species or characterize an isolate.

**Pulmonary hypertension and infectious diseases**

**S19** Pulmonary arterial hypertension related to HIV: update on diagnosis and treatment

*N. Petrosillo*° (Rome, IT)

The introduction of the highly active antiretroviral therapy (HAART) has profoundly influenced the course of HIV infection, improving the survival of HIV infected patients and reducing HIV-associated opportunistic infections. Nevertheless, long-term outcomes secondary to HIV infection are now serious concerns, like non-infectious cardiovascular complications including cardiomegaly, pericarditis, myocarditis and pulmonary arterial hypertension.

The lung is the most frequent target organ for disorders associated with HIV infection, and the cardiopulmonary vascular system can be sometimes involved; indeed, HIV-related pulmonary arterial hypertension (HRPAH) affects more HIV-infected individuals (i.e. 0.5%) than uninfected (i.e., 1 to 2 cases per million people).

The average age of HRPAH patients is 33 years, although the range can span from infancy to old age. There is no trend between HRPAH and HIV viral loads or CD4+ T cell counts but is more severe in AIDS patients. Shortness of breath is the most common symptom, and a clinical, cardiological, radiological work up is required for diagnosis. Cardiac catheterisation is the gold standard for the final diagnosis, and is mandatory to characterize the disease and exclude secondary causes.

There is no definitive evidence of HIV as a causal agent for HRPAH. However, viral proteins and its interactions with molecular partners in the infected host are strong candidates for cause-effect relationships because they may promote apoptosis, growth and proliferation. At least three of the HIV proteins are implicated in the pathology of PAH: the HIV envelope glycoprotein-120 (Env), the HIV protein Tat and HIV Nef (negative factor). Nef impairs vasomotor functions in pulmonary artery cells, decreases the expression of endothelial nitric oxide synthase and increases oxidative stress, suggesting a strong role in the formation of miform lesions in the lung vasculature.

The role of antiretroviral therapy (ART) in HRPAH is still debated. From a literature review, survival rates are 69% and 38% among patients treated or not with ART and specific therapy for PAH, respectively (p<0.02), thus suggesting that specific therapy for pulmonary arterial hypertension should be strongly recommended in these patients. The role of the combination treatment with antiretrovirals in influencing the outcome of HRPAH is controversial, even if some evidences seem to indicate a beneficial effect in the clinical course of the disease.

**DNA-based methods to detect MRSA**

**[Q22]** Comparison of different bacterial DNA isolation methods to accelerate differentiation of *Staphylococcus aureus* from coagulase negative staphylococci from blood culture material

A. Loomen*, W. Hansen, A. Janus, H. Kreeftenberg, C.A. Bruggeman, P. Wolfs, A. van den Brule (Veldhoven, Maastricht, Eindhoven, NL)

**Objectives:** This study aims to compare 6 different DNA extraction methods from 2 commonly used blood culture materials, BACTEC (BD) and Bact/ALERT (Biomerieux), to accelerate differentiation between *S. aureus* and Coagulase Negative Staphylococci (CNS).

**Methods:** Two fast real-time PCR duplex assays, targeting the Tuf gene, to differentiate *S. aureus* from CNS, were developed in order to select the most sensitive one. This Tuf RT-PCR was used to compare 6 different DNA isolation protocols on two different blood culture systems. Negative blood culture material was spiked with *S. aureus*; bacterial DNA was isolated with: automated extractor EasyMAG by using 3 different protocols (Biomerieux), automated extractor MagNA Pure (Roche), a manual kit MolYsis Plus (MolZyme), and a combination between MolYsis Plus and the EasyMAG. The most optimal isolation method was used to evaluate the possibility of reduced bacterial culture times.

**Results:** Approximately 160 positive blood cultures containing Gram-positive cocci in clusters were tested in the Tuf RT-PCR and all were identified correctly. Bacterial DNA isolation, from spiked blood culture material, with the MolYsis Plus kit in combination with the EasyMAG showed the highest analytical performance, with a detection limit of 10 CFU/ml in Bact/ALERT, whereas using BACTEC resulted in a detection limit of 100 CFU/ml. With this sensitive bacterial DNA isolation method 1 CFU/ml *S. aureus* in Bact/ALERT material was detected after a 5 hour pre-culture step in the Bact/ALERT3D.

**Conclusions:** A sensitive RT-PCR was developed for detection and differentiation of *S. aureus* versus CNS. Bacterial DNA isolation with the MolYsis Plus kit in combination with the EasyMAG resulted in the most sensitive detection of *S. aureus*, with a detection limit of 10 CFU/ml, in Bact/ALERT material. An initial *S. aureus* load of 1 CFU/ml can be detected after 5 hours incubation in Bact/ALERT3D by usage of the TUF test.

**[Q23]** Comparison of MRSA detection by Xpert MRSA test, Xpert MRSA/SA nasal test and culture

N.P. Brenwald*, B. Walker, K. Chana, M. Parsons, R. Fleming, B. Oppenheim (Birmingham, UK)

**Objectives:** PCR based tests are increasingly being used to screen patients for MRSA carriage. Most commercially available tests use the SCCmec / orX junction as one of the main targets for amplification. However, false positive MRSA results have been described due to
the presence of incomplete SCCmec cassettes in meticillin sensitive
S. aureus (MSSA). Recently, PCR tests have been developed that detect
targets, in addition to SCCmec, to overcome the problems of associated
with partial SCCmec. Our study compares the detection of MRSA
by the Xpert MRSA test (single target) with the Xpert MRSA/SA nasal test
(multiple targets) and a sensitive enrichment culture method.

Methods: Nasal samples were collected with double-headed swabs from
patients admitted to the Sandwell and West Birmingham Hospitals NHS
Trust. Swabs were tested for MRSA using the Xpert MRSA/SA nasal test
and the Xpert MRSA test (Cepheid Europe) run on the Cepheid
GeneXpert system. All samples were also cultured for MRSA and MSSA
using 2.5% NaCl broth and sub-cultured onto chromogenic MRSA agar
and non-selective blood agar.

Results: 304 nasal swabs were included in the study (189 Xpert MRSA
positive; 115 Xpert MRSA negative). MRSA was cultured from 92/304
(30.3%) of the samples. The Xpert MRSA SA nasal test versus Xpert
culture showed a sensitivity, specificity, PPV and NPV of 84.9, 91.0,
80.4 and 93.2, respectively. 23/48 MSSA (so far analysed) isolated from
nasal swabs testing PCR positive, but culture negative were identified as
presumptive SCCmec mutants (SCCmec/chromosome junction positive;
meA negative). All 23 isolates were positive by the Xpert MRSA test
whilst only 6/23 isolates were MRSA positive by the Xpert MRSA/SA
nasal test.

Conclusion: Both the Xpert MRSA and MRSA/SA nasal tests showed
high NPVs compared with MRSA culture making them useful as
screening tests for MRSA. However, the benefit of detecting multiple
targets (SCCmec/orfX, mecA, spa) by the Xpert MRSA/SA nasal test
compared with only SCCmec/orfX by the Xpert MRSA test was reflected
in the reduced number of false positives reported using the Xpert
MRSA/SA nasal test. Our sample group was skewed to contain large
numbers of PCR positive samples to increase to likelihood of detecting
false positives. In a normal sample population, false positive results
would only constitute a very small proportion of the overall results.

O25 Performance of the novel NucliSens EasyQ® MRSA assay
with a diverse selection of clonal complexes from a low
prevalence country

M. Mølgaard° (Aalborg, DK)

Objectives: Several assay have been developed for the rapid
detection of MRSA colonization directly from nasal swabs, but genetic
variations within the SCCmec cassette poses a constant challenge in
the primer design. Another pitfall is the sharing of the SCCmec cassette
among S. aureus and coagulase-negative staphylococci. NuclISENS
EasyQ® MRSA (bioMérieux) is a novel test which simultaneous
detects both the meA gene and a specific cassette junction confirming
the presence of the SCCmec cassette integrated in the S. aureus
chromosome. The objective is to evaluate the performance of the assay
with a collection of community-acquired MRSA strains from a low
prevalence country.

Method: MRSA isolates were obtained from residents in North Jutland,
Denmark and were characterized genetically by spa typing and clustered
into spa clonal complex (CC) groups (www.ridom.de) as part of the
Danish national surveillance program maintained by Statens Serum
Institut. Cultures of MRSA strains were processed according to the
manufacturer’s guidelines for positive controls and analysed on the
EasyQ instrument, a NASBA based platform.

Results: The study comprised 15 MRSA strains representing 10 different
clonal complexes [number in brackets]: CC1 [1], 5 [3], 8 [1], 22 [2],
30 [1], 59 [1], 72 [1], 88 [3], 97 [1], 398 [1]). Eleven were reported to
be MRSA whereas 4 were found MRSA negative (CC5 [1], CC59 [1],
CC97 [1], CC398 [1]). The meA gene was reported for all 15 strains,
however both genes have to be present before denoted MRSA and the
4 cases of a negative test result were due to failure in detection of the
SCCmec cassette junction.

Conclusion: A very rapid test (<3 hours) and easy to perform. The
sequence targeted at the junction of the SCCmec cassette serves to ensure
the S. aureus diagnosis and is a safeguard against false positive results.
However, the current results raise the question whether genetic variation
in the junction area reduces the sensitivity of the test. This study will be
extended to a larger and more diverse collection of MRSA strains and
patient swabs.

O24 Rapid detection of MRSA in screening specimens during a
hospital outbreak

D.S. Blanc°, I. Nahimana Tessemo, K. Jaton-Oguy, G. Zanetti
(Lausanne, CH)

Objectives: To compare the results of rapid PCR screening for MRSA
using the GeneXpert system with those of cultures in an outbreak setting.

Methods: GeneXpert was used for screening MRSA in nose, throat,
groin, and other clinical samples during a 6-month period. Samples were
performed using a double-swab transystem. When >1 sample was found
positive in a screening set, all second swabs of the set were analysed by
culture.

Results: From June to October 2009, 7568 rapid tests were performed,
among which 432 (5.7%) were positive (nose: 149/2090, 7.1%; throat:
98/2078, 4.7%; groin: 152/2080, 7.3%; urine: 14/1090, 1.3%; wounds:
18/150, 12%; and others:1/27, 3.7%), and 84 (1.1%) were invalid. A
total of 1517 samples were analyzed by both rapid PCR and culture.

Conclusions: The Xpert MRSA/SA nasal test is a sensitive, specific,
and non-selective blood agar.

O26 Multicentre evaluation of laboratory work time and cost
for real-time PCR tests for methicillin-resistant Staphylococcus
aureus compared to microbiological culture

L. Peterson°, C.W. Woods, S. Allen, D. Pombo, A. Onderdonk,
O. Liesenfeld (Evanston, Durham, Indianapolis, Murray, Boston,
Pleasanton, US)

Objectives: MRSA continues to increase globally. Rapid detection
of MRSA colonization followed by appropriate isolation can reduce
transmission and infection in healthcare settings (Ann Int Med 148:409–
418, 2008). A concern raised is the cost of molecular assays plus the
personnel time to perform this testing compared to culture. The BD
GeneOhm™ MRSA (BD) test is a FDA cleared diagnostic assay for
rapid detection of MRSA. Our objective was to compare personnel
work time and cost needed for this assay and the LightCycler®
MRSA Advanced test (Roche) to culture.

Methods: Double headed swabs were used to collect anterior nasal
specimens from each subject. For the BD test, one swab was broken off
in sample buffer tube, DNA was extracted and rt-PCR performed according
to package insert. For the Roche test, DNA was extracted and rt-PCR
performed according to proposed package insert. For culture, one swab
was plated directly to CHROMagar™ as well as an enrichment broth
that was subsequently plated to CHROMagar™. Colonies resembling
Staphylococcus species were confirmed as MRSA by standard methods.

Results: Total hands-on technologist processing time for an average
of 25 specimens was 75.4 min for the BD test (N = 263 runs) and 41
min for the Roche assay (N = 435 runs). The amplification and detection
time
was 61.8 and 77.6 min, respectively. Hands on time for enriched culture processing of 25 specimens is estimated at 63 min (AUPC 131:532–9, 2009). Potential reporting time for a final result was <2 hours for the rt-PCR tests and 48.7 hours for enriched culture. The reagent cost for culture, including or excluding broth enrichment, is somewhat lower (8–10 Euro) than the rt-PCR tests from BD and Roche; costs of rt-PCR tests are comparable between these two suppliers. New rt-PCR methods have a comparable time of processing and cost of materials, but offer potentially much faster reporting time than does culture. The hands on time for the Roche assay was 1.8 min on average compared to 3 min with the BD assay and 2.5 min/test for culture.

Conclusion: The Roche and BD tests had little difference in overall time to result. With respect to resource utilization, hands-on time for the Roche assay was lower than BD and culture; the cost per test is comparable for both PCR assays. Molecular assays are able to report results more rapidly compared to culture with comparable resource utilization.

A novel multiplex PCR identifies 7 staphylococcal species and mecA gene directly from blood cultures

K.S. Chatzigeorgiou*, N. Siafakas, A. Tarpatsi, E. Petinati, L. Zerva (Chaidari, Athens, Larisa, Greece, GR)

Objectives: Besides the well-established pathogenic potential of Staphylococcus aureus, coagulase negative species virulence is increasingly being appreciated. The aim of the present report was to describe a multiplex PCR assay suitable for the identification of 7 staphylococcal species and the detection of the methicillin resistance determinant mecA.

Methods: Eight different primer pairs targeting femA (for S. aureus, Staphylococcus hominis and Staphylococcus saprophyticus), sodA (for Staphylococcus haemolyticus and Staphylococcus capitis), fbl (for Staphylococcus epidermidis), a gene of unknown function (for Staphylococcus epidermidis) and mecA, were used for the optimization of the multiplex PCR protocol. The assay was tested on DNA extracted from solid cultures of 213 isolates belonging to 12 staphylococcal and 17 non-staphylococcal species (6 Gram-positive and 11 Gram-negative). RFLP analysis of the tuf gene was used as a reference method for species of 196 staphylococcal isolates, whereas the presence of mecA gene was assayed by a uniplex PCR. The 17 non-staphylococcal strains were speciated by Phoenix System (Becton Dickinson, BD). The assay was also tested on DNA extracted directly from 21 blood culture broths (Aerobic/F, Anaerobic/F, BD), spiked with isolates previously assigned to the staphylococcal 7 species (one reference strain and two clinical from each species) included in the multiplex protocol. An organic extraction protocol using benzyl alcohol was optimized for DNA extraction from the blood culture broths.

Results: The new method identified correctly 67 strains as S. aureus, 64 as S. epidermidis, 18 as S. lugdunensis, 16 as S. haemolyticus, 10 as S. hominis, 6 as S. saprophyticus and 4 as S. capitis. No amplification products were recorded for the remaining staphylococcal species and genera. In accordance with the uniplex mecA PCR, 61 methicillin resistant staphylococci were detected by the multiplex protocol. Application of the protocol on DNA extracted directly from spiked blood bottles produced the expected results in all cases within 6–8 hours.

Conclusion: The newly developed multiplex PCR assay specifically discriminates the 7 most commonly encountered staphylococcal species and concurrently determines their resistance towards methicillin. Its application on positive blood cultures is expected to reduce significantly the turnaround time and reliable identification and susceptibility results.

Different PVL encoding phages insert into the same chromosomal locus in distinct lineages of MRSA in England and Wales

E. Boakes*, A.M. Kearns, R. Hill, M.J. Ellington (London, UK)

Objectives: To date, six Panton-Valentine Leukocidin (PVL) encoding phages (phiPVL, phiSLT, phiSa2maw, phi108PVL, phiSa2USA and phiSa2958) have been reported in PVL positive MRSA (PVL-MRSA). We sought to detect and analyse the DNA sequence of the chromosomal insertion site(s) of lysogenised PVL-phages amongst diverse PVL-MRSA clones found in England and Wales.

Methods: PCRs differentiated the lysogenised PVL-encoding phage present in PVL-MRSA strains of MLST Clonal Complexes (CCs) 1 (n = 11), 5 (n = 9), 59 (n = 3), 88 (n = 5) and ST93 (Queensland clone) (n = 11) as well as CC8 (USA300; n = 12) and CC30 (European clone; n = 7). Additional PCRs spanning the proximal and distal junctions of the phage / chromosome DNA were designed to detect the insertion site of the six known PVL phages and resultant DNA amplicons were sequenced on both strands.

Results: PCR and DNA sequence data indicated different PVL phages integrated at the same chromosomal locus in isolates of different lineages of PVL-MRSA. Lineage specific sequence polymorphisms in the chromosomal insertion site surrounding the PVL phage sequence occurred in isolates of CC 59 (SNPs = 8), 93 (SNPs = 5) and 5 (SNP = 1). By contrast, in CC1 and CC8 the insertion site sequence was identical to the USA300 genome. The PVL encoding phage was consistent within the lineage for: CC8 (phiSa2USA); CC80 (phiSa2MW); CC88 (Unknown Elongated Phage) and ST93 (phiSa2USA). Conversely, different PVL phages were identified within the same lineage for CCs 1, 5 and 59. Polymorphisms in both ends of the phage genomes were detected and in most cases SNPs correlated with the identity of the PVL encoding phage. However, in some lineages the same SNPs occurred in apparently variant phages; in CC1 the same SNPs were identified in three different phages; phiSa2USA (n = 7) and phiSa2MW (n = 3) and unknown PVL phage (n = 1), whilst in CC5 a single SNP occurred at the 5′ end of either phiSa2USA (n = 7) or an unknown variant phage(s) (n = 2).

Conclusion: Amongst genetically diverse UK PVL-MRSA different PVL phages integrated at the same chromosomal locus. In some lineages virulent strains is frequently associated with the acquisition of genes encoding diverse virulence factors. As such, the recent spread of CA-MRSA was found associated with the presence of Panton Valentine (PVL) toxin. However, the exotoxin profile of PVL-positive MRSA versus MSSA is not known.

Methods: We analyzed a collection of 79 clinical isolates of PVL-positive MRSA and MSSA for the presence of genes encoding 22 exotoxins, including enterotoxins (ET) (sea-see, seg-ser, seu), toxic shock syndrome toxin (TSST)-1 (tst), exfoliative toxins (EF) (eta, etb) and hemolysines (HL) (tha) using PCR. Furthermore, MRSA genes (mecA, SCCmec) and agr-locus were investigated by PCR.

Results: In total we studied 61 MRSA and 18 MSSA strains. More than 90% of mecA positive MRSA harboured the SCCmec cassette SCCmec IV (71%) and 21% SCCmec V (21%), indicating the high incidence of CA-MRSA in the investigated collection. While agr3 was present in most MRSA and MSSA altogether (52%), agr4 was surprisingly only found in MSSA (56% of MSSA). Overall, MRSA harboured significantly fewer toxin genes as compared to MSSA. This holds true for enterotoxins, among which the genes for seg, sei, sen, seo, and seu (= enterotoxin gene cluster eeg) were the most prevalent ones (on average 30% of MRSA and 95% of MSSA tested positive for respective genes). Rather surprising, and in contrast to published studies from PVL-positive MRSA, we only discovered 12% of PVL-positive MRSA to express enterotoxin a (Sea).
the DNA sequence at the phage insertion locus was specific to the PVL-MRSA lineage, we also detected SNPs in the extremities of the genomes of the lysogenised PVL phages. Together with MLST CC and SCCmec, these data suggest hitherto unidentified variance in lysogenised phages and suggests that lineages of PVL-MRSA have evolved on multiple occasions.

**O30** Kinetics of bacterial DNA in blood during endovascular infections with *Staphylococcus aureus*

W Rozemeijer*, R.P Peters, J Khutynans, P Saavelkoul, R.P Schade (Amsterdam, NL)

**Objectives:** Endovascular infection with *Staphylococcus aureus* is a serious infection that requires rapid and adequate treatment to minimize the risk of metastatic foci. Currently there are no effective tools to monitor response to therapy. Sensitivity of blood cultures significantly decreases after initiation of antimicrobial therapy and other laboratory parameters such as C-reactive protein lack specificity. Measurement of bacterial DNA load (BDL) is not influenced by the use of antibiotics and has been shown to have a good correlation with severity of infection. To understand the kinetics of this parameter and to investigate its possible usefulness in guiding clinical management, we have prospectively determined the sequential BDL in patients with *S. aureus* endovascular infections.

**Methods:** Whole blood samples were collected from patients with culture proven *S. aureus* bacteremia at several time points over a 2 week period. BDL was determined in 44 sequential samples from 8 patients with endovascular infection. We studied 4 severe endovascular infections (endocarditis and/or other intravascular foci) requiring more than 2 weeks of therapy, and 4 non-severe endovascular infections (phlebitis) requiring a maximum of 14 days of therapy. Quantification of *S. aureus* specific DNA was performed by real time PCR on DNA extracted from 200ul of blood.

**Results:** The *S. aureus* specific BDL was above the cut-off (5 cfu/ml) in 4 of 6 available samples taken within 24 hours after the first positive blood culture. Median BDL was 28 cfu/ml (range: 11–664). In all five patients who had detectable BDL levels during treatment, the load decreased significantly in the first days after treatment. In patients with non-severe infections, the BDL decreased below the detection limit within 4 days. In contrast, in patients with severe infections, the load remained detectable during the first 7 days. CRP measurements showed no correlation with disease severity.

**Conclusion:** We present the first description of kinetics of BDL in blood from patients with *S. aureus* endovascular infections. The results indicate that severe infections are characterized by prolonged presence of detectable BDL. These results provide new insights and suggest that BDL measurement has the potential to be used for monitoring treatment response.

**O31** External quality assessment of molecular diagnostics of methicillin-resistant *Staphylococcus aureus*

R. te Witt*, A. van Belkum, W MacKay, P Wallace, W van Leeuwen (Rotterdam, NL; Glasgow, UK)

**Background:** This external quality assessment study determines the performance of molecular diagnostics for methicillin-resistant *Staphylococcus aureus* (MRSA) in the participating laboratories and was organised by Quality Control for Molecular Diagnostics (QCMD) (www.qcmd.org).

**Methods:** Eleven samples containing various concentrations of inactive cells of MRSA, metillin-susceptible *S. aureus* (MSSA), methicillin-resistant coagulase-negative staphylococci (MRCoNS) and *Escherichia coli* were distributed to 80 laboratories in August 2009.

**Results:** Out of the 80 participants, 68 (85%) responded. Samples containing 102 or 103 MRSA cells were correctly detected in only 16% and 46% of the datasets returned, respectively. Two MSSA panel strains contained a SCCmec cassette lacking the mecA gene. Only 12% of the datasets generated using commercial PCR kits, reported correct results for these two MSSA strains, which is a marked difference compared to the MSSA strain lacking the SCCmec cassette (89% correct results). The MRCoNS sample was correctly reported as negative in 89% of datasets generated using commercial tests used and by 70% of in-house assays. The *E. coli* sample was correctly reported as negative in 89% of datasets.

**Discussion:** In this EQA study on molecular diagnostics for the detection of MRSA, we conclude that the detection of MRSA by using samples with high CFU counts is reliable, which can and has been implemented in the laboratory setting with confidence. Pre-enrichment of clinical samples leads to concentrations of MRSA exceeding 109 CFU/ml, but also reduces one of the major improvements offered by NAAT, namely more rapid diagnosis. This year, two MSSA samples harbouring a SCCmec cassette, but lacking the mecA gene, were included. The high percentages of incorrect results for commercial PCR underscore the need for improved specificity of these MRSA tests and therefore positive results should always be confirmed by a culture method or a second molecular test.

Performance in 2009 shows no significant changes since our first EQA in 2006. Major diagnostic performance discrepancies still exist between diagnostic microbiology laboratories.

In conclusion, the quality of molecular diagnostic MRSA tests still needs improvement. Programme expansion is required and regular quality control and international standardisation for MRSA diagnostics should be mandatory for the years to come.

**Drugs and combinations for difficult-to-treat *S. aureus* infections**

**O32** A novel approach to identify antimicrobial synergy against methicillin-resistant *Staphylococcus aureus*

S.M. Garonzik*, A. Forrest, W Wisniewski, B. Tsuji (Buffalo, US)

The increasing occurrence of vancomycin (V) resistance among methicillin-resistant *Staphylococcus aureus* (MRSA) represents a serious therapeutic problem. Proposed empiric approaches to combination therapy have been based on little evidence.

**Objectives:** 1) To examine the pharmacodynamics (PD) of V paired with several antibiotics. 2) To identify synergistic combinations. 3) To develop better approaches to describe PD drug interactions.

**Methods:** Two MRSA strains Mu50 VISA and USA300 heteroresistant-VISA (USA300 hVISA) were used. MICs were completed as per CLSI. Time kill experiments were performed for V at 0, 0.5, 1, 2, 4, 8, 16, 32, 64, 128 & 256 mg/L vs. each strain in log phase growth at two initial inocula: 10^6 & 10^7 CFU/mL. To accommodate the study of multiple antimicrobials a previously unexploited screening method was used employing the maximal effect (Emax) concentrations (guided by highest clinically achievable conc.) vs. two initial initial inocula for 6 pairs of antibiotics: V 128 mg/L + gentamicin (G), ciprofloxacin, TMP/SMX, cefazidime, tetracycline and linezolid. Combinations that demonstrated activity at screening were studied at 9 combinations for the same two drugs with combinations ranging from low to Emax of each drug. PD analysis was performed by integrated area approach for reduction in area under the CFU vs. time curves, which were fit to 2-D or 3-D Hill-type PD models. We developed a new PD model which adheres to Loewe additivity and an interaction index (AFa index).

**Results:** Maximal bacterial reductions for V vs. 10^6 CFU/mL were ~2.91 (~1.97) and ~3.04 (~1.42) for Mu50 and USA300 hVISA at 48 h (24h). For USA300 hVISA V-G was synergistic against 10^6 CFU/mL with max reductions of ~7.85 (~7.85) at 48h (24h). 48h log reductions for were: V32 (~2.91) + G (0.5+(1.4) ~3.28, V32 + G (~1.58) ~6.45, V32 + G (6(1.64) ~7.84, V128 (~3.03) +G10.5 ~6.26, V128 + G =7-6.70, V128 + G4 ~7.85. AUC based PD parameters for V at 48h/24h/8h were H=4.603.5/7.68, Emax =1.48/1.05/0.538, EC50 = 18/14.07/9.13, R^2 = 0.998/0.994/0.992. The same parameters for G at 8h were H=1.67, Emax =1.51, EC50 = 3.55, R^2 = 0.996. Per the AFA index all V+G combinations studied for V ~1 mg/L demonstrate activity 400-500 fold greater than additivity (see fig. 1).
Conclusion: MRSA hVISA represents a therapeutic challenge with few alternatives. This study may have implications for optimal therapy of difficult to treat MRSA infections to preserve the usefulness of V if combined with other drugs.

Figure 1. PD interaction surface analysis: vancomycin & gentamicin departures from additivity.

**033** Telavancin pharmacokinetics and pharmacodynamics in patients with complicated skin and skin structure infections with varying degrees of renal function


**Objectives:** Telavancin is a lipoglycopeptide approved in the US and Canada for complicated skin and skin structure infections (cSSSI) due to Gram-positive bacteria, including MRSA. The objectives were to (1) simulate telavancin plasma concentration-time profiles in cSSSI patients with varying degrees of renal function and (2) evaluate the percentage of subjects with AUC/MIC ratios greater than the pharmacodynamic target of 219.

**Methods:** Data from 513 patients from telavancin phase 2–3 cSSSI clinical trials were used to perform the analysis. Individual concentration-time profiles were simulated for 10260 subjects (NONMEM VI, Icon, Elliot City, MD) using a previously described population two-compartment model, with a combined additive and proportional residual error model. The structural model was parameterized on clearance (CL), volume of the central compartment (V1), intercompartment clearance (Q), and volume of the peripheral compartment (V2). Distributions of body weight and creatinine clearance of the 513 patients were used to simulate body weight and creatinine clearance values for 10260 subjects in Matlab R2006a (Mathworks, Natick, MA). Telavancin dosing regimens simulated were 10 mg/kg Q24H for creatinine clearance (CrCl) > 50 mL/min, 7.5 mg/kg Q24H for CrCl 30–50 mL/min and 10 mg/kg Q48H for CrCl < 30 mL/min. AUC under one dosing interval (AUC(tau)) was computed as dose/CL. The number of subjects achieving an AUC(tau)/MIC ratio of 219 or greater was evaluated separately in subjects with mild renal impairment to normal renal function (CrCl > 50 mL/min), moderate renal impairment (CrCl between 30–50 mL/min), and severe renal impairment (CrCl < 30 mL/min), using MIC values of 0.5, 1, and 2 mg/L.

**Results:** Summary statistics of AUC(tau) values of subjects with varying degrees of renal function are provided in the table. Using the 3 dosing regimens, AUC(tau) values were similar across the renal function groups. More than 90% of the simulated subjects achieved an AUC(tau)/MIC ratio of 219 or greater, assuming an MIC of 0.5, 1 or 2 mg/L (targeting 2 × and 4 × the MRSA MIC90 of 0.5 mg/L).

**Conclusion:** Using the three dosing regimens, AUC(tau) were similar across the different renal function groups, indicating that the dose adjustments employed in the phase 3 cSSSI trials were appropriate.

All proposed telavancin dosing regimens are expected to provide an AUC(tau)/MIC ratio of 219 or greater in at least 90% of the population, for organisms with an MIC of 2 mg/L or less.

Simulated AUC(tau) and the AUC(tau)/MIC ratio in subjects with various degrees of renal function

<table>
<thead>
<tr>
<th>Parameter</th>
<th>CrCl (mL/min)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>&lt;30°</td>
</tr>
<tr>
<td>AUC(tau), (mean±SD, mg·h/L)</td>
<td>1058±316</td>
</tr>
<tr>
<td>AUC(tau) range (min, max, mg·h/L)</td>
<td>(466, 2071)</td>
</tr>
<tr>
<td>Percentage of population with AUC/MIC &gt; 219</td>
<td></td>
</tr>
<tr>
<td>MIC=0.5</td>
<td>100%</td>
</tr>
<tr>
<td>MIC=1</td>
<td>100%</td>
</tr>
<tr>
<td>MIC=2</td>
<td>98.6%</td>
</tr>
</tbody>
</table>

1Based on 140 simulated profiles; †based on 480 simulated profiles; ‡based on 9640 simulated profiles.

**034** Biphasic killing of levofloxacin against *Staphylococcus aureus*: modelling bacterial response to drug-selective pressures


**Objective:** We have previously developed a mathematical model predicting the response of *P. aeruginosa* to levofloxacin (LEV) (Ann Biomed Eng 07). However, the applicability of the model to other pathogens is unknown. We extended our model to predict the effect of various fluctuating LEV exposures on *Staphylococcus aureus* (SA), a bacterium commonly associated with nosocomial bloodstream and surgical site infections.

**Methods:** Time-kill studies (TKS) with 10° CFU/ml of SA ATCC 29213 at baseline were performed in duplicate. LEV at 0–16 mg/L was used for 24 h (MIC = 0.25 mg/L). The experimental data were used to derive estimates of the best-fit model parameters, and SA response (resistance development or suppression) to various LEV exposures was predicted via a 3-dimensional response surface. The computer model predictions were subsequently validated using an in vitro hollow fiber infection model (HFIM); LEV profiles (t1/2 = 7 h) corresponding to different daily doses (given every 12 or 24 h) were investigated over 120 h.

**Results:** In contrast to the anticipated concentration-dependent killing, LEV exhibited a biphasic killing profile in TKS. The data could only be satisfactorily captured by a modified mathematical model (r² = 0.977).

**Conclusions:** The modified mathematical model was reasonable in predicting extended SA response to various fluctuating LEV exposures qualitatively, based on limited input data from TKS. In view of its robustness and efficiency, our mathematical modeling approach could be used as a decision-support tool for dosing regimen selection in antimicrobial (pre)-clinical development.

**035** Penetration of daptomycin in serum and bradytroph tissues of patients undergoing orthopaedic surgery

*D. Maier-Lenz*, A. König, U. Frank (Freiburg i.Br., DE)

**Objective:** To investigate the serum and tissue concentrations of daptomycin in patients undergoing orthopaedic surgery.

**Methods:** A total of 18 patients received 350 mg of daptomycin in a short intravenous bolus infusion. Three groups of six patients each received the drug prior to hip- or knee replacement surgery, i.e. between 1–1.5 h (Group I), between 1.5–2.5 h (Group II) and between 2.5–3.5 h (Group III) before intra-operative sampling of serum and tissue, i.e. bone, cartilage, muscle, fat, was performed.
Results: Daptomycin serum concentrations showed a mean of 62.5 [μg/ml] in group I, 45.2 [μg/ml] in group II and 31.9 [μg/ml] in group III. In bone a mean of 5.3 [μg/g] in group I, 4.5 [μg/g] in group II and 4.5 [μg/g] in group III was found. Cartilage showed a mean of 1.9 [μg/g] in group I, 2.0 [μg/g] in group II and 1.7 [μg/g] in group III. Muscle revealed a mean of 4.0 [μg/g] in group I, 2.3 [μg/g] in group II (for 5 patients) and 2.6 [μg/g] in group III. In fat only a few samples could be successfully analysed. These showed a mean of 6.0 [μg/g] in group I (evaluable samples only for two patients), a mean of 1.9 [μg/g] in group II (evaluable samples only for three patients); for group III the samples of all six patients were below the detection limit.

A linear regression analysis of the decrease of serum daptomycin concentration per minute was estimated as −0.230, 95% confidence interval (CI) [−0.347, −0.112], p = 0.0008. For bone concentrations the decrease was −0.0078, 95% CI [−0.0247, 0.0092], p = 0.35) including all 18 patients, and −0.012, 95% CI [−0.024, −0.0053], p = 0.042) excluding one single patient with an extraordinary high value. For cartilage, muscle and fat, no decrease over time was shown. However, for serum, bone, cartilage, muscle and fat the daptomycin concentrations were clearly above the MIC values for staphlococci (<0.1 μg/ml).

Conclusions: Daptomycin concentrations in serum showed a slow decrease and the drug concentrations measured in both serum and bradytroph tissues remained clearly above the MICs for staphylococci for up to 3.5 hours. Within the postoperative observational period of one week, no postoperative wound infection occurred. The application of daptomycin was well tolerated without any adverse effects.

O36 Vancomycin serum trough levels and outcomes in patients with hospital-acquired pneumonia due to Staphylococcus aureus: the ATTAIN study
M. Stryjewski, G.R. Corey, S. Barriere*, F.C. Genter, E. Rubinstein on behalf of the ATTAIN study group

Objectives: Higher vancomycin (VAN) serum trough levels (STL) have been recommended when MRSA HAP is suspected. However, the correlation between VAN STL and clinical outcomes and safety is still poorly understood.

Methods: ATTAIN 1 and 2 were randomized, methodologically identical, double-blind, phase 3, clinical trials in patients with hospital-acquired pneumonia (HAP). We analyzed baseline characteristics and outcomes from patients with S. aureus (SA) randomized to VAN (1 g IV q12h, 7 to 21 days) as a function of median VAN STL. VAN could be adjusted for renal function and/or institutional policies. The all-treated (AT) population included randomized patients who received ≥1 dose of study medication. This analysis was limited to the subset of SA-infected patients with VAN STL.

Results: 98 VAN AT patients with S aureus had STL (Table).

Conclusions: Patients in whom higher VAN STL were achieved had poorer outcomes; and were more likely to experience renal adverse events than patients with lower VAN STL.

[O37] Combination therapy with cefotixin and β-lactams is synergistic against community-associated but not hospital-acquired methicillin-resistant Staphylococcus aureus strains in vitro

Objective: There is an urgent need for strategies to treat community-associated methicillin-resistant Staphylococcus aureus (CA-MRSA) infections. Preliminary in vitro studies demonstrate that nafcillin minimal inhibitory concentrations (MICs) for USA300 and USA400 strains decrease in the presence of subinhibitory concentrations of cefoxitin. The aim of this study was to characterize the in vitro antimicrobial activity of cefotixin and several anti-staphylococcal β-lactams alone and together against MRSA isolates using MICs and time kill assays.

Methods: MICs and time kill assays were performed using standard methods with the following strains: ATCC29213 (control strain), USA300 and USA400 (CA-MRSA strains), N315 and COLn [hospital-acquired (HA) MRSA strains]. Time kill assays were performed with a starting inoculum of 5.5 to 6.5 log10 CFU/ml and quantitative cultures performed at 0, 6 and 24 h.

Results: The MICs of nafcillin, cefazolin, cefoxatine, ceftriaxone and cefotaxime decreased in the presence of 10 μg/ml cefotaxin to a greater extent for CA- than HA-MRSA strains (see table). In triplicate time kill assays, cefotixin (10 μg/ml) combined with either nafcillin (4 μg/ml) or cefazolin (16 μg/ml) displayed synergy against CA- but not HA-MRSA strains. Compared to nafcillin alone, nafcillin plus cefotixin showed a log10 CFU/ml reduction ranging from 0.8 to 2.1 for USA300 and 1.5 to 2.1 for USA400. Compared to cefazolin alone, cefazolin plus cefotixin showed a log10 CFU/ml reduction ranging from 2.8 to 2.9 for USA300 and 2.9 to 4.7 for USA400. Overall, cefazolin plus cefotixin caused a log10 CFU/ml reduction of the initial inoculum at 24 h ranging from 0.8 to 1.2 for USA 300 and 1.6 to 3.1 for USA400. The activity of cefazolin combined with cefotixin was superior to that of clindamycin (8 μg/ml) alone but inferior to that of vancomycin (16 μg/ml) alone for USA300 and USA400.

Conclusion: Cefotixin combined with a variety of β-lactams enhanced their activity against CA-MRSA strains in vitro. Cefotixin synergy was greater with cefazolin than with nafcillin. Combination β-lactam therapy for CA-MRSA deserves further study.

O38 Evaluation of vancomycin and oxacillin combination against mecA positive vancomycin-intermediate Staphylococcus aureus (VISA) and heterogeneous VISA with varying oxacillin susceptibility
C. Vidaillac*, K. Murray, M. Rybak (Detroit, US)

Objectives: S. aureus with reduced susceptibility to vancomycin (VAN) currently represents a serious clinical dilemma given the limited availability of alternative treatments. The VAN intermediate-type of resistance in S. aureus (VISA) has been previously reported to result in cell wall remodeling and antimicrobial susceptibility changes in favor of β-lactam activity. We evaluated the activity of VAN, oxacillin (OKA) and cefoxitin (CFX) and the potential for synergy of the combination of VAN+OKA against a collection of clinical heterogeneous VISA (bVISA) and VISA strains.
Methods: 60 VISA and 93 hVISA isolates carrying the mecA genes were selected from the Anti-Infective Research Laboratory collection. VAN, OXA and CFX MICs were determined in duplicate by broth microdilution according to CLSI guidelines. Pearson’s rank correlation coefficient test was used to assess the association between VAN and OXA or CFX MICs. Eight VISA and hVISA strains were selected on the basis of their OXA MIC to be evaluated by time kill curves (TK) against VAN and OXA alone or in combination at 0.5 and 0.25 × MIC in presence of 50% human serum. Synergy (S) was defined as ≥2 log kill compared to the most efficient drug alone.

Results: MIC distribution is reported in Table 1. Of interest, 23% and 10% of the VISA strains were susceptible to OXA and CFX, respectively. A significant inverse correlation was found between the MICs of VAN and OXA (P = 0.003), and VAN and CFX (P = 0.001). Considering the subpopulation with the highest VAN MIC for each hVISA strain, 36% displayed a 2−8× decrease in the OXA MIC compared to the overall population. In contrast, 41% had a 2−16× increase in OXA MIC. Isolates performed in TK exhibited a MIC range of 2−8 mg/L and 0.5−512 mg/L for VAN and OXA, respectively. In TK, S was observed with the combination of VAN+OXA at 0.5 × MIC against all VISA and hVISA isolates, except 1 VISA strain resistant to OXA and 1 hVISA exhibiting a decreased OXA MIC in the population with the highest VAN MIC. Combination of VAN+OXA at 0.25 × MIC did not demonstrate S against any tested isolates.

Conclusions: We confirmed susceptibility changes in favor of b-lactam activity in the VISA collection. Further in vitro and in vivo experiments are now warranted to determine if the potentially synergistic combination of VAN+OXA would be useful to treat patients with infections caused by MRSA, in order to eradicate the infection and/or prevent emergence of VAN intermediate resistance.

Table 1. MICs distribution of 93 hVISA and 60 VISA isolates.

<table>
<thead>
<tr>
<th>Species</th>
<th>Percent of isolates</th>
</tr>
</thead>
<tbody>
<tr>
<td>VISA (n = 93)</td>
<td>66 30 0</td>
</tr>
<tr>
<td>VISA (n = 60)</td>
<td>0 0 100 23 25 52 10 48 42</td>
</tr>
</tbody>
</table>

**O39 In vitro synergism between cefobiprole and vancomycin against methicillin-resistant and glycopeptide-intermediate Staphylococcus aureus**

J.M. Entenza*, J. Voulamoz, A. Bizzini, M. Girdey, J. Bille, P. Moreillon (Lausanne, CH)

Objective: Several studies have reported synergy in vitro between b-lactams and vancomycin (VAN) in their activity against methicillin-resistant S. aureus (MRSA) and glycopeptide-intermediate S. aureus (GISA) isolates. Nevertheless, attempts to use such combinations against GISA in animal infection models yielded conflicting results. This was probably due to the fact that the b-lactams used (e.g., cloxacillin and nafcillin) had weak affinity for penicillin-binding protein 2A (PBP2A), the major determinant of methicillin resistance in MRSA and GISA. Cefobiprole (BPR) is a novel cephalosporin with improved affinity for PBP2A, and enhanced in vitro activity against MRSA and GISA. Here we tested the potential for synergy between BPR and VAN against both MRSA and GISA in vitro.

Methods: Three GISA clinical isolates (Mu50, PC3 and 1092, a human isolate from Switzerland) were tested. One VAN-susceptible MRSA (COL) and one VAN-susceptible methicillin-resistant S. aureus (MSSA 1112) were used as controls. The interaction of BPR with VAN was determined by applying BPR or VAN Etest strips to inoculated (0.5 McFarland) BHI agar plates with the partner drug incorporated into the agar at 0, 0.25 × and 0.5 × MIC for each strain. The time-kill assay was used to test for BPR and VAN synergy using antibiotic concentrations of 0.25 × to 1 × the MIC.

Results: MICs of BPR were 1–2mg/L for GISA, 1mg/L for MRSA, and 0.12mg/L for MSSA. MICs of VAN were 4–8mg/L for GISA, and 2mg/L for both MSSA and MRSA. Subinhibitory concentrations of VAN added to the agar medium caused 2- to 4-fold decreases in BPR MICs for GISA and 4-fold for MRSA. The GISA and MRSA isolates showed corresponding 4- to 8-fold decrease in VAN MIC in the presence of subinhibitory levels of BPR. In time-kill curves, combinations of BPR and VAN displayed synergy (defined by a decrease of ≥2log10 CFU/ml at 24h compared with the single most active agent and with the starting inoculum) for all GISA and MRSA strains. For MSSA, the combination was indifferrent by both Etest and time-kill methods.

Conclusions: In vitro, BPR and VAN were synergetic against GISA and MRSA. An indifferent effect was noted against MSSA. Assessment of BPR plus VAN for the therapy of GISA in an experimental animal model of infection (experimental endocarditis) is currently in progress to assess the potential clinical therapeutic benefit of this combination.

**O40 Comparative in vitro activity of torezolid and linezolid against Staphylococcus and Enterococcus isolates**


Objective: Torezolid is a new oxazolidinone with in vitro and in vivo efficacy against several Gram-positive species. The aim of our study was (i) to determine Linezolid (LZ) MICs against 104 French isolates of Staphylococcus and Enterococcus (ii) to characterize LZ resistance mechanisms for the strains with a LZ MIC >2mg/L (iii) to compare the in vitro activity of Torezolid with LZ.

Methods: A total of 104 French isolates of animal and clinical origin resistant to chloramphenicol were studied including 38 Staphylococcus strains and 66 Enterococcus strains. MICs of LZ and Torezolid were determined using the Mueller Hinton agar dilution method according to CLSI guidelines. 23s rRNA target mutations and cfr genes were detected by PCR and sequencing.

Results: For all 104 strains, MICs of LZ were 0.5−64mg/L (geom. mean MIC 7.3mg/L). MIC of LZ was >2mg/L for 23 strains: 6 S. aureus isolates and 17 Enterococcus isolates (12 E. faecalis and 5 E. faecium), all of clinical origin. All S. aureus isolates resistant to linezolid harbored a G2567T mutation in rrl gene. Enterococcus isolates harbored either G2447T (n = 4), G2505A (n = 3) or G2576T (n = 10), No strains whatever their susceptibility to LZ harbored cfr gene.

For all 104 strains, MICs of Torezolid were <0.5−8mg/L (mean MIC 1mg/L). MICs of LZ were <0.5−8mg/L. MICs of Torezolid were <0.5−1mg/L vs. 0.5−2mg/L for LZ-susceptible staphylococci (n = 32) irrespective of species and methicillin resistance. Against linezolid susceptible Enterococcus of animal origin (n = 34) and clinical origin (n = 15), MICs of Torezolid were 0.5−1mg/L vs. 2mg/L. LZ MICs of Torezolid for LZ-resistant Enterococcus isolates were 1–8mg/L vs. 4–64mg/L LZ.

Conclusion: No cfr genes were found in French chloramphenicol-resistant Staphylococcus and Enterococcus isolates of human or animal origin. Torezolid was 4 to 8 fold more active than Linezolid against LZ-susceptible strains and LZ-resistant Staphylococcus and Enterococcus isolates with G2576T, G2505A or G2447T mutations.

**O41 In vitro evaluation of the bactericidal activities of MRSA active antibiotics in four different peritoneal dialyses fluids**

S. Toubal*, W. Püppi, C. Kratzer, W. Graninger, H. Burgmann (Vienna, AT)

Objectives: Continuous ambulatory peritoneal dialysis used in the treatment of patients with end-stage renal failure is often complicated by peritonitis. Staphylococcus aureus peritonitis is associated with severe peritonitis, particularly if caused by methicillin resistant strain (MRSA). The intraperitoneal administration (IP) of drugs for peritonitis is preferable to intravenous or oral administration because of the resulting higher local antibiotic concentrations. Peritoneal dialyses fluids (PDFs) affect bacteriostatic, which may compromise the effectiveness of antibiotics. Therefore, it is important that prescribed antibiotics are compatible
with PDfs. The purpose of this study was to investigate in vitro the bactericidal effectiveness of for MRSA infections appropriated antibiotic in diverse PDfs.

Methods: Against MRSA the bactericidal activities of vancomycin (VAN), teicoplanin (TEI), daptomycin (DAP), linezolid (LIN), cefotibiprole (CEF) and tigecycline (TIG) in different PDfs: Dianal PD4 Glucose 1.36%; Physioneal 40 Glucose 1.36%; Extraneal 7.5% Icodextrin, and Nutrineal PD4 1.1% amino acid were proved. Cation-adjusted Mueller-Hinton Broth. (CAMHB) was used as a control broth. Ten milliliters of diverse PDfs and CAMHB containing bacteria inoculum of approximately 100 CFU/ml was incubated for 2 h at 37°C. Following incubation, the antibodies at concentrations: 1× MIC, 4× MIC, 8× MIC were added. Additionally, the bactericidal concentration at clinical used concentration: VAN 50 μg/ml, TEI 20 μg/ml, DAP 60 μg/ml, CEF 30 μg/ml, LIN 32 μg/ml, TIG 50 mg/ml was tested. Samples were taken at 2, 4, 6, 8 and 24 h and the number of CFU/ml was determined. To stimulate in vivo conditions human serum albumin at 2 g/l was added. Control experiments with bacteria and no antibiotics in PDfs and CAMHB were run.

Results: All antibodies showed concentration- and time-dependent bactericidal activities, but the reduction of CFU/ml in diverse PDfs differed considerably. All tested antibiotics showed significantly higher bactericidal activity in Extraneal 7.5% Icodextrin, and Nutrineal PD4 1.1% amino acid than in Dianal PD4 Glucose 1.36% and Physioneal 40 Glucose 1.36% (p < 0.05). The highest decrease in CFU/ml attained in Extraneal 7.5% Icodextrin, and Nutrineal PD4 1.1% amino acid showed DAP and VAN.

Conclusion: Based on these in vitro data, we conclude that the choice of PDfs used for IP administration is not trivial and could be crucial for therapy outcome.

Imported infections: tropical and travel medicine

[042] Investigation of molecular diagnostic assays for the detection of Trypanosoma cruzi DNA in blood


Objectives: Chagas disease, caused by Trypanosoma cruzi, is endemic to Latin America, and of emerging importance in non-endemic countries because of migration of people infected with T. cruzi. The majority of patients diagnosed in non-endemic settings are in the indeterminate or chronic phases. However, acute cases may be seen in congenitally-infected infants and in people receiving blood products or organs from infected donors. Molecular diagnostic assays needed to be standardized to diagnose and monitor congenital infection, aid serological diagnosis in expatriate travellers and migrants from Latin America, and monitor infection in known cases of Chagas Disease.

Methods: Two molecular assays for the diagnosis of T. cruzi infection were investigated, a SYBR green real-time PCR targeting nuclear DNA and a hotstart PCR targeting kinetoplast DNA (kDNA). One hundred and eighty PCR controls and 180 blood-simulated specimens prepared from cultures of T. cruzi strains of lineages TcI, TcIIb and TcIIe were evaluated. Samples for DNA were prepared from the specimens using 3 lysis methods (Qiagen (Q), Guanidine-EDTA (GE) and GE-boiling (GEB)). DNA extraction after lysis was carried out using silica-membrane technology. Ten-fold serial dilutions were prepared. Statistical analysis was performed by SPSS v15, Chicago IL.

Results: The sensitivity of the real-time PCR assay was calculated by PROBIT analysis with 12 replicates of 8-fold serial dilutions of the DNA from culture of TcIIb extracted by Qiagen. The 95% and 50% positive hit rates were 0.8 parasites/ml (95% IC: 0.41–1.53) and 0.2 parasites/ml (95% IC: 0.82–0.99), respectively. The assay showed a specificity of 100%. More consistent results were found for all lineages and types of samples when DNA was extracted by the Qiagen method. A higher detection limit was found in lineage TcI (p < 0.01). Lineage TcIIb showed statistically better results in controls and simulated specimens, than the other two lineages (p < 0.01). The kDNA assay was performed in simulated specimens from the three lineages, and it gave better results using Q and GEB methods on low concentration samples, although not statistically significant (p = 0.08).

Conclusions: Molecular assays are very promising in the diagnosis of T. cruzi infection and have applications where serological assays are not of use. Further work should be done to standardize the methods.

[043] Congenital transmission of Chagas’ disease in Latin American immigrants in a health department of Valencia, Spain


Objective: To describe congenital transmission of Chagas disease in Latin American immigrants in our Health Department 07-La Fe, in Valencia (Spain).

Methods: We collected sera from pregnant women from Latin America who attended our hospital between June 2007 and October 2009. The samples were tested for anti-Trypanosoma cruzi antibodies (IgG) using 2 different enzyme-linked immunosorbent assays (ELISA) and a particle gel immuno assay. Positive sera were then confirmed with an immunofluorescent assay (IFA). Total blood from infected patients was sent to Carlos III Health Institute (Madrid) in order to perform a polymerase chain reaction (PCR) study. Newborns’ sera and umbilical cord blood from infected mothers were tested for anti-T. cruzi antibodies and blood microscopic examination, microhematocrit concentration technique and PCR, respectively, at birth, at 1–6 months old. Infected children, considering 2 positive PCR and/or positive parasitological examination for diagnosis, were treated with a 60-day course of benznidazol (3.5–7 mg/kg/day).

Results: Out of 574 pregnant women sera, 35 (6.1%) were positive for T. cruzi serology and gave birth at our hospital. Their mean age was 29.1 years old; All of them were from Bolivia, mainly from Santa Cruz (39.3%) and Cochabamba (28.6%) departments, except one from Argentina. 12 pregnant women PCR were positive, but none of them was symptomatic for Chagas disease. 2 newborns had two positive PCR along the first 6 months and 1 newborn had positive blood examination also. Two of them were born from positive PCR women and the other is unknown. Only one of the babies had symptoms at birth (dilated cardiomyopathy and a neuroblastoma). Benznidazol treatment was well tolerated by all babies.

Conclusions:

1. Although we have not documented any congenital transmission in newborns from negative PCR mothers, we cannot consider yet that positive PCR is a predictor factor for T. cruzi infection transmission.
2. Positive PCR results at birth allows us to initiate an early treatment in infected newborns, which has been demonstrated as the most effective treatment.
3. Benznidazol has been well tolerated by newborns with no side effects.
4. It is really important to follow-up seropositive children at least during one year with serology tests. Negative PCR blood from newborns only can be confirmed as non-infected patients when T. cruzi antibodies desappear along the first year.

[044] Paediatric drug formulations of artemisinin combination therapies: is there evidence for improvement of patient management in the treatment of children suffering from malaria? A systematic review and meta-analysis

M. Rambarter*, P. Kremser (Vienna, AT; Tuebingen, DE)

Objectives: Artemisinin combination therapy (ACT) is the mainstay of antimalarial treatment with high efficacy, good tolerability, and a reduced risk for resistance selection. However, conventional fixed dose ACTs are inadequate for the treatment of young children – the most important target population – due to difficulties in drug administration of tablets. Recently, a number of ACTs with paediatric
is benign tertian malaria actually benign?

Methods: We performed a systematic review and meta-analysis of controlled clinical trials evaluating paediatric artemisinin combination therapies compared to tablet drug formulations. Outcome parameters were efficacy, safety, tolerability, and tolerability of drug administration.

Results: Out of 667 potentially relevant publication, seven studies met the predefined inclusion criteria. Meta-analysis of 2515 children was performed evaluating paediatric drug formulations of the following ACTs: artesunate-mefloquine, arteether-lumefantrine, and pyronaridine-artesunate. Per protocol and intention to treat analysis of efficacy, safety, and tolerability of drug administration were comparable between groups. However, the tolerability of drug administration evaluated by the number of drug related adverse events (RR: 0.79, 95% CI: 0.64–0.96), drug related vomiting (RR: 0.77, 95% CI: 0.61–0.99), and drug related gastrointestinal disorders (RR: 0.34, 95% CI: 0.15–0.80) was considerably improved for paediatric drug formulations.

Conclusion: Data of this meta-analysis show for the first time objective evidence of an improved tolerability of drug administration by paediatric ACTs compared to tablet ACTs. To our knowledge this is the first evidence for an improvement in patient management by paediatric drug formulations in any indication. Therefore paediatric ACTs should be considered in international recommendations for the treatment of malaria in young children.

Is benign tertian malaria actually benign?

A. Gogia", A. Kakar, S. Byotra (New Delhi, IN)

Objective: This retrospective study was conducted to determine the incidence of various complications of Plasmodium vivax malaria based on review of case records in a tertiary care hospital, New Delhi, India.

Methods: The case records of all confirmed cases of malaria over the period of one year (September 2008-August 2009) were studied. Complete blood count, peripheral blood findings, liver and kidney functions were reviewed. The results of rapid diagnostic test for malaria (OptiMAL test, DiaMed AG, Switzerland) were correlated with the peripheral blood smear findings in the patients in whom it was requested. All abnormal results like a positive direct Coomb's test were noted. Findings were clinically correlated.

Results: There were 165 confirmed cases by peripheral blood examination. Of these 121 were due to Plasmodium vivax and 42 due to P. falciparum. Two cases had mixed infection. The peak incidence of malaria was seen in September 2008 and July 2009. The complications in P. vivax were thrombocytopenia, biochemical evidence of hepatic dysfunction, renal damage, positive DCT and death due to ARDS. Thrombocytopenia was seen in 113 patients with count < 20 x 10^3 microl in 43 patients. Fifteen patients had serum bilirubin > 3 mg/dl with normal liver enzymes. Liver enzymes were elevated in 55 patients with twelve patients showing liver enzymes level, three times the normal. Renal dysfunction was seen in 21 patients with serum creatinine ranging from 1.3–10.65 mg/dl. There were three deaths due to ARDS.

Conclusion: This paper is presented to highlight that P. vivax malaria though considered to be a benign entity can also have a severe and complicated course which is usually associated with P. falciparum malaria.

Incidence of influenza, dengue and Japanese encephalitis in Australian travellers visiting South and south-eastern Asia


Objective: To estimate the incidence density of influenza, dengue and Japanese encephalitis (JE) in Australian travellers to Asia.

Methods: Prospective cohort study of Australian travellers to South and South East Asia over a 2 year period. Travellers ≥16 years of age were recruited from 3 travel clinics, completed validated questionnaires and provided pre and post-travel blood samples for serological testing. Demographic data, destinations and travel patterns, vaccination details and history of flavivirus infection were obtained. Serological testing for dengue IgG by ELISA (Pan-Bio assay), Influenza A and B (complement fixation antibody) and JE (In-house indirect fluorescence antibody) was performed.

Results: Among 450 travellers enrolled, 345 have returned for follow-up, 53 (11.7%) have been lost to follow-up and paired sera have been tested for 324 travellers; 58% were female, median age was 32 years and 24% were born overseas. 72% were short term travellers (<30 days) and main traveller types were vacation/holiday goers (69%) and business travellers (16%). 76% reported prior travel to Asia and 10.8% and 54% had received the JE and influenza vaccines respectively. Dengue sero-prevalence: Acute seroconversion for dengue virus infection was demonstrated in 4/324 (1.2%) of travellers tested. This translates to an incidence of 4.17 dengue virus infections per 10,000 days of travel (95% CI 1.7–10.7). A further 13 travellers (4%) were positive for dengue IgG prior to travel indicating past exposure. Travellers with acute dengue infection had travelled to China (n=2) India (n=1) and Thailand (n=1), and two of these travellers had received the JE vaccine. Influenza sero-prevalence: 4/324 (1.2%) had evidence of recent influenza infection. The incidence of influenza virus infections is 4.17 per 10,000 days of travel (95% CI 1.7–10.7). JE sero-prevalence: There was no acute JE seroconversion in this cohort.

Conclusion: To our knowledge, this is the largest prospective study estimating the incidence of both respiratory and arboviral infections in travellers. For travellers to Asia, the risk of acquiring dengue in an inter-epidemic period is low (incidence density 4.17 infections per 10,000 days of travel). The risk of acquiring influenza in this well vaccinated cohort was equally as low and no JE infections were observed. These findings have important implications for practitioners advising prospective travellers.

Genetic diversity of intestinal protists: the implication for PCR-based diagnostic assays

C.R. Stensvold", M. Leebad (Copenhagen, DK; Solna, SE)

Objective: Diagnosis of intestinal protists by PCR is being employed more and more by diagnostic and research laboratories. Data from molecular characterisation of intestinal protists is the raw material for our current and future efforts to develop improved diagnostic PCRs. Apart from our ability to sample correctly and extract DNA from parasites directly from faeces, important issues include primer specificity and sensitivity, which have impact on predictive values of the diagnostic assays. Thus, it is important to be aware of the genetic diversity among these parasites. Extensive data from the molecular characterisation of intestinal protists are necessary if PCR-based diagnosis is to detect all genetic variants of intestinal parasites especially if the eventual aim is for it to substitute for morphology-based methods. Diagnostic PCRs are very often based on amplification of the Small Subunit (SSU) rRNA gene, partly due to the fact that this gene is present in a high-copy number. However, data from very few strains are currently available for the SSU rRNA gene of most intestinal parasites. Often one or two sequences are available in the Genbank database.

Methods and Results: We are in the process of collecting data from the genetic characterisation of protozoa such as Iodamoeba, Entamoeba coli,
Entamoeba hartmanni and Entamoeba polecki-like organisms isolated from clinical samples. Knowing the amount of diversity displayed among clinical isolates of these (and other) parasites will help us generate specific and sensitive primers that can be used in cases where a definitive diagnosis cannot be established on the basis of microscopy. Preliminary results show that the genetic diversity within Entamoeba coli is extensive, and that no less than four genetic subtypes of uninculcated amoebic cysts can be isolated from human faeces. We have also obtained genetic data from protozoan genera that have not been sequenced before.

**Conclusion:** If future platforms for the diagnosis of intestinal protists are to rely on PCR, comprehensive data from molecular characterisation of these organisms are needed to design, evaluate, validate and optimise PCR protocols.

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**O48 Synthesis and evaluation of 4-fluoro-amodiaquine a novel antimalarial drug against sensitive and resistant strains of Plasmodium falciparum**

E. Asadollahy, P. O’Neill* (Ilam, IR; Liverpool, UK)

**Objectives:** Resistance to chloroquine (CQ) in Plasmodium falciparum malaria has become a major health concern of the developing world. This resistance has prompted a re-examination of the pharmacology of alternative antimalarials that may be effective against resistant strains. Amodiaquine (AQ) is a 4-aminoquinoline antimalarial which is effective against many chloroquine-resistant strains of P. falciparum. However, clinical use of AQ has been severely restricted because of associations with hepatotoxicity and agranulocytosis. Based on a knowledge of the metabolic basis of amodiaquine toxicity, the aim of this study was to examine the effects of replacing the 4′OH function of amodiaquine with fluorine.

**Materials and Methods:** A successful four-step synthesis of a new series of 4′-fluoro analogues has been designed and applied to the synthesis of an array of 10 analogues. Malaria parasites were maintained in continuous culture using the method of Jensen and Trager. Antimalarial activity was assessed with an adaption of the 48-h sensitivity assay of Desjardins et al., using [3H]-hypoxanthine incorporation as an assessment of parasite growth.

**Results:** The chemistry in the 4′fluoro series provided the target compounds in higher overall yields. Initial testing on both series of analogues was carried out on a chloroquine sensitive (3D7) and resistant strains TM6, K1, TM4, V1S and J164 at the Liverpool School of Tropical. It is apparent that several analogues have potent antimalarial activity against sensitive 3D7 strain of the parasite. The data indicates that 6h is superior to the pyrroolidino analogue 6b against all of the strains examined. It is also clear that N-tert butyl analogue 6b is potent against chloroquine resistant strains, though it is not quite as active as amodiaquine (AQ) against both chloroquine sensitive and resistant parasites.

**Conclusion:** In summary, work conducted in this study has identified several potent back-up compounds to the clinical candidate. It is clear that the 4′fluoro series has several members with potent activity compared to amodiaquine. It has been shown that (6h) has is slightly less potent than amodiaquine, chloroquine and the clinical candidate (4b). Further studies on the metabolism and pharmacokinetics of 6h are necessary.

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**S55 Carbenem-resistant Acinetobacter: a study of class D b-lactamases**

R.A. Bonomo* (Cleveland, US)

Carbenem resistant Acinetobacter represent a major threat to our antibiotic armamentarium. In general, Class B and D b-lactamases form the basis for this phenotype. Class D b-lactamases are serine enzymes that are either monomers or dimers that possess unique structural motifs. By utilizing a carbamylated Lysine, a distinctive complex hydrogen-bonding network is created to fix the b-lactam in the substrate-binding pocket and assist in binding, acylation and deacylation. As a result of substitutions accelerated by b-lactam use, many class D enzymes emerged that possess functional and structural properties which confer a selective advantage to the bacterium housing the carbenem hydrolyzing b-lactamase. Important carbenemases in Acinetobacter include: blaOXA-23, bldOXA-24, bldOXA-48, bldOXA-58, bldOXA-65. With these notions in mind, our purpose will be to i) review the molecular epidemiology and genetics of the major class D serine carbenemases that are present in Acinetobacter spp; ii) analyze how amino acid changes have altered substrate specificity by using select examples; and iii) highlight changes in the expression of efflux pumps and outer membrane proteins in the amplification of carbenem resistance. The crystal structures of important class D enzymes will be reviewed and analyzed.

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**S58 Multidrug-resistant Pseudomonas aeruginosa**

N. Petrosillo* (Rome, IT)

In recent decades Pseudomonas aeruginosa has emerged as a major threat as a result of the significant mortality associated with pneumonia and bacteraemia, and the evolving resistance exhibited by the pathogen to numerous antibacterials. Since a timely and appropriate therapy is needed for severe P aeruginosa infections, clinicians should be aware of the risk factors associated with this pathogen and with multidrug resistance. There is still debate if a combination or a monotherapy should be instituted for Ps. aeruginosa infections.

The use of combination therapies for Ps. aeruginosa pneumonia has been a long-advocated practice, but the potential increased value of...
Combination therapy over monotherapy remains controversial. However, empirical combination therapy maximizes the chances of bacterial coverage, especially in severe infections, and likely exerts a lower resistance selection pressure.

Upon confirmation of *Ps. aeruginosa* infection, treatment should be given according to the site of infection, the pathophysiology of the patient, the pharmacokinetic/pharmacodynamic profile of the antimicrobials, and the antimicrobial susceptibility pattern, including the MIC values.

For strains that are resistant to all antimicrobials but colistin, this antimicrobial is advocated as the choice option either in mono- or in combination therapy. Indeed, since there are no novel antibiotics in the drug development pipeline for multidrug-resistant *Ps. aeruginosa*, old antibiotics, such as the polymyxins (ie, colistin, also known as polymyxin E and polymyxin B), have re-emerged as the last resort therapy. However, current clinical use of colistin is largely informed by inadequate and, in some cases inaccurate, pharmacokinetic and pharmacodynamic data.

Rifampin, sulbactam, carbapenems, fosfomycin are all possible options for combination treatment, due to their *in vitro* synergistic effect. Among carbapenems, doripenem seems to possess a lower potential for resistance selection and a more favourable pharmacokinetic profile. Newer anti-pseudomonal antibacterials are expected to be available in the near future. Among them, experimental polypeptides (ie. the anti-PerV immunoglobulin G antibody) may provide a new therapeutic approach.

**ESBL-producing enterobacteria beyond carbapenems**

J. Rodríguez-Baño* (Seville, ES)

Carbapenems are considered the drugs of choice for the treatment of serious infections caused by ESBL-producing enterobacteria. However, alternatives are needed because carbapenem-resistance due to carbapenemases and other mechanisms are increasing worldwide. For the treatment of uncomplicated cystitis due to ESBL producers, observational studies showed high cure rates with oral fosfomycin, nitrofurantoin, and amoxicillin–clavulatane when a susceptible isolate was involved. Metcillin, which is stable against ESBLs, is also a potential option. For patients with other types of infections including complicated urinary tract infections, the options are more limited. Some isolates may show low MIC to specific cephalosporins depending on the type of ESBL produced; PK/PD data suggest that these infections can be treated with these cephalosporins (particularly cefepime) using appropriate doses, but this practice is not recommended for empirical therapy because the MIC cannot be predicted. Adding an aminoglycoside to a standard regimen is a reasonable option for selected patients at low risk of renal toxicity in areas where prevalence of aminoglycoside resistance among ESBL-producers is low. The efficacy of combinations of cephalosporins with β-lactamase inhibitors (as cefoperazone-sulbactam, or as the combination of a cephalosporin and amoxicillin/clavulanate) and temocillin are to be studied in different clinical settings. However, the worldwide spread of the multi-drug resistant clones of *E. coli* and *K. pneumoniae* further reduce the therapeutic options, for which only carbapenems, tigecycline and colistin might be active. While older drugs, such as fosfomycin (probably in combination), merit being investigated in systemic infections, new drugs active against these organisms are clearly needed. The increasing prevalence of ESBL producing Enterobacteria in the community and hospital is not just a threat anymore but a real everyday problem.

**Carbapenemase-producing enterobacteria**

H. Giamarello+ (Athens, GR)

Resistance to carbapenems due to the production of metallo-β-lactamases (MBL) or KPC enzymes in Enterobacteriaceae is an increasing international public health problem. An MDR or even an PDR phenotype is associated with carbapenem resistance in Enterobacteriaceae, because these strains usually harbor mechanisms of resistance to aminoglycosides and quinolones, as well. Nevertheless, some of these strains often exhibit low-level resistance to carbapenems with MICs remaining in the susceptible range rendering the therapeutic role of carbapenems questionable.

The armamentarium against PDR Gram-negative microorganisms has almost been exhausted. The only options left are colistin, an antibiotic introduced in the 1950s, and tigecycline, a modified minocycline. Monotherapy or combination therapy with colistin is most often used but recently, the emergence of colistin-resistant strains of *Klebsiella pneumoniae* has limited our therapeutic options even further. There is accumulated evidence on the *in vivo* activity of tigecycline against MDR Enterobacteriaceae but the low levels of the drug achieved in blood indicate the necessity of a higher dose in case of bacteraemia. Some of the MBL or KPC producing Enterobacteriaceae are *in vitro* susceptible to fosfomycin. Clinical experience in the setting of serious infections by carbapenemase-producing bacteria is still limited. Finally, combination regimens have very often been used empirically in clinical practice although scientific evidence on the advantages of combinations is usually scarce with the exception of carbapenem-susceptible *K. pneumoniae*, for which clinical data suggest that the combination of meropenem and gentamicin could be active *in vivo*, in the case of meropenem MIC ≤ 2 μg/ml.

The emergence of carbapenemase-producing Enterobacteriaceae highlights the “end of antibiotics”. Concentrated efforts are needed to preserve and wisely use the few options available. In the meantime, intensified infection control measures may protect our hospitalized patients from these difficult to treat pathogens.

**Biomarkers for the diagnosis of sepsis: do they provide added value?**

B. Müller* (Aarau, CH)

The ambiguities of clinical signs and the limitations of current microbial techniques for the diagnosis of bacterial infections – and to grade their severity – are well known. The use of biomarkers provides a novel, complementary approach to diagnose infection, and to estimate treatment response and the outcome of patients. A plethora of proteins has been speculated to be “promising markers” in observational studies including c-reactive protein, various interleukins and chemokines and procalcitonin, among others. Unfortunately, in most infections including sepsis, a true “gold standard” for diagnosis does not exist. Thus, the true “added value” of a biomarker in clinical use can only be assessed in interventions studies, where the endpoints are safety and antibiotic use. In the hospital setting, this has only been shown for procalcitonin (PCT) in multiple randomized controlled intervention studies from several independent groups. With a similar outcome antibiotic exposure could be reduced from by 50 to 75%. For prognostic assessment, other biomarkers (e.g. adrenomedullin) have demonstrated high predictive potential to estimate the risk for mortality in the short and long term, and other adverse outcomes. A critical appraisal of the advantages and limitations of biomarkers in different clinical situations is mandatory. We discuss the current data on the use of PCT and other biomarkers for the diagnosis, treatment guidance, and prognostic assessment of bacterial infections, and their potential role in the overall assessment of patients with sepsis and respiratory tract infection as its most important precursor.

**Rapid detection of pathogens in sepsis: molecular techniques versus culture**

C. Vandenbroucke-Grauls* (Amsterdam, NL)

Molecular techniques are gaining more and more interest for rapid diagnosis of severe bacterial infections. DNA-hybridisation probes and PCR-based detection are used for rapid identification of bacteria after
the first signal of growth in conventional blood cultures. PCR-assays can also be used for direct detection of pathogens in blood. Such PCRs can be aimed at specific pathogens, or be more broad-range, in which case the PCR is followed by sequencing of the PCR product for identification. PCR can also be used for quantification of the amount of bacterial DNA in blood; several studies point to the value of the bacterial DNA load (BDL) in blood as a marker of severity of infection. This has been shown for pneumococci and meningococci in particular, and there is anecdotal evidence that BDL also correlates with severity of infection in staphylococcal infections. Interpretation of the results of PCR applied directly on blood samples needs further study, however, because several aspects of the kinetics of the presence of bacterial DNA in blood during infection are still unknown. In particular, we must be aware that it is difficult to define the best gold standard for bacteraemia, that PCR detects DNA, rather than living pathogens, that there is always a risk of contamination, and that little is known yet about background bacterial DNA in blood.

Significance of DNAemia in sepsis

K.P. Hunsfeld* (Frankfurt/M., DE)

Sepsis is associated with mortality rates ranging from 20% to 50% and represents the second leading cause of death in the non-coronary intensive care unit. Early diagnosis of sepsis followed by prompt appropriate treatment improves the prognosis of septic patients. It has been suggested that nucleic-acid-based technology such as PCR is more sensitive and can also shorten the time to result when compared with conventional blood culture techniques. To date, however, little is known about the kinetics and the clinical and therapeutic relevance of bacterial DNA present in the blood of patients with sepsis over time in the course of an invasive blood stream infection. The recent introduction of methods based on PCR-based diagnostic assays including tests that provide a more exact quantitative measurement of DNA, therefore, may open a window of opportunity for a better understanding of the kinetics and clinical significance of microbial DNA circulating in the blood of patients during a blood stream infection. In fact, the potential influence of bacterial DNA on the severity and outcome of blood stream infections is underlined by the findings of recent clinical and laboratory studies suggesting that procalcitonin plasma levels and SOFA scores were significantly higher, length of ICU and hospital stay were longer, and survival was clearly decreased in subgroups of septic patients revealing positive findings in both PCR testing and blood culture. Whether a better insight into the clinical significance of DNAemia will indeed contribute to more rapid initiation of better-tailored therapy and improved management of septic patients in conjunction with other laboratory markers, however, awaits further evaluation of in laboratory studies and interventional clinical trials. The present lecture will summarise what is known from recent studies on the diagnostic and clinical significance of DNAemia in patients with sepsis.

Diagnostic dilemmas – things that look like infections but aren’t

Non-infectious causes of fever in the critical-care unit

M. Skalvett* (Cleveland, US)

“Fever” is a common symptom in critically ill patients and often sets into play a series of investigations by health care providers to establish an etiology. Recent practice guidelines for the evaluation of fever in the ICU patient recognize that “knee-jerk” responses to this syndrome, in the absence of careful clinical evaluation, lead to increased costs and morbidity for patients. In addition, many diagnostic studies are uninformative. Nevertheless, non-infectious causes of fever are often diagnoses of exclusion; a balance between expensive and invasive investigations, and “old fashioned” clinical acumen needs to be applied to evaluate fever in the ICU. In this session, common non-infectious etiologies of fever will be discussed with illustrative case examples, e.g. gout, drug fever, vasculitis, etc. In addition the role of molecular tests that are used to assist in determining the infectious etiologies of fever (PCR methods and biomarkers such procalcitonin and 1,3-β-glucan) will be reviewed.

When are arthritis real infections?

M.A. Muninian* (Seville, ES)

Joint diseases may present as acute, chronic and at the same time as monarticular or polyarticular arthritis. Most of the aetiological agents who have been identified in monarticular infections may also cause polyarticular infections. Similarly, most of the polyarticular non infectious arthritis may appear as monarticular. In many clinical situations extra-articular manifestations may differentiate infectious from non infectious arthritis.

The recent development of new technology for culture and molecular biology has permitted to recognise virus or bacteria into the joints of degenerative, inflammatory and of course, infectious arthritis. Reactive arthritis (ReA) is the conceptual ground somewhere between septic arthritis and autoimmune diseases such as rheumatoid arthritis. The fact that some arthritis (Whipple, SAPHO etc) now have been recognised as infectious arthritis and may respond to antibiotic treatment, as prompted to treat a number of patients with arthritis of “unknown aetiology” with antimicrobials.

Form a practical point of view the answer to the question “When are arthritis real infections?” may be “When we can treat and cure the infection”. Three aetiologies are involved in most or the patients with acute monarticular arthritis; mechanical, infections and microcrystallines. Inflammatory arthritis may also present as monarticular arthritis. But besides that, more than 20 different non infectious diseases can produce acute arthritis (“pseudoinfective arthritis”). The tools for the diagnosis of arthritis are limited. As a matter of fact in Rheumatology the “pattern” of the disease is particularly important; what joints are involved, what is the sequence, the accompanying symptoms or even the duration of the disease. There are no definitive laboratory markers (except crystals and cultures in the synovial fluid). Biochemical and cytology values in synovial fluid permit to classified arthritis as mechanical, inflammatory or septic, but in a particular patient they have only a marginal value. In critical reviews for cytology in the synovial, fluid the evidence is mainly anecdotal and there are no reports of specificity, sensitivity and reliability.

In this topic as in many other, medical history, epidemiological investigation and clinical examination are the main stone for the diagnosis. Detailed history and physical examinations may raise the possibility of some initially unsuspected systemic or localized non infectious disease.

Autoimmunity and infection: a bidirectional relationship

R. Cervera* (Barcelona, ES)

The hypothesis of an infectious origin for autoimmune diseases has received great attention during the recent years. Microbial agents or viruses can induce autoimmune diseases by a variety of mechanisms. For example, proteins of certain infectious agents can act as polyclonal activators on unique lymphocyte subsets. Viruses can preferentially infect/destroy a particular T cell subset, leading to an imbalance in the immune response. In other instances, infectious agents can up-regulate Th1 cytokines, thereby increasing selective expression of molecules such as major histocompatibility complex (MHC) glycoproteins, as well as activation of costimulatory molecules. Several microbial agents have been found to encode superantigens that can selectively activate subsets of T cells. Microbes can also direct the release of cytokines and chemokines, which can act as growth, differentiation, or chemotactic factors for different Th populations and regulate expression of MHC class I and class II molecules.

On the other hand, the healthy immune system is tolerant to the molecules of which the body is composed of. However, one can find
that among the major antigens recognized during a wide variety of bacterial viral and parasitic diseases, many belong to conserved protein families, sharing extensive sequence identity or conformational fits, with host’s molecules, namely molecular mimicry. Antigenic similarity of either molecules’ linear amino-acid sequences or their conformational structure between antigens of infectious agents and host tissues might trigger an immune response against the shared determinant. As a result, the tolerance to autoantigens breaks down, and the pathogen-specific immune response that is generated cross-react with host structures to cause tissue damage and disease.

In this presentation, the cases of Sjögren’s syndrome, systemic lupus erythematosus and the antiphospholipid syndrome, among others, will be reviewed as clear examples of autoimmune diseases where an infectious origin is postulated.

**Pneumococcal infection: insights into pathogenesis and therapeutic potential**

*D.H. Dockrell* (Sheffield, UK)

Nasopharyngeal colonisation with pneumococci is frequent but in contrast pneumococcal pneumonia and invasive pneumococcal disease are comparatively infrequent events. This reflects the success of both innate and adaptive host responses to pneumococci. The presence of a variety of virulence factors including polysaccharide capsule and pneumolysin challenges the host response. Epithelial cells sense microbial products and release cytokines in response to pneumococci in the lower respiratory tract. Soluble factors, including complement factors, activated through both the classical and alternative pathway, play an important contribution to host defence in the lung. Alveolar macrophages play a critical role as the resident phagocytes in the lung clearing bacteria from the lung and orchestrating the inflammatory response. Once resident defence becomes compromised an inflammatory response including the recruitment of neutrophils becomes essential to microbial control but comes at the potential cost of compromising lung homeostasis. The regulation of this process also requires macrophage competence to ensure a limited inflammatory response which results in bacterial clearance but without lung injury. During the evolution of pulmonary infection a number of critical transition points occur when specific molecules and host responses are critical in determining how the infection evolves and what the outcome of infection will be. The infectious inoculum, the virulence of the pathogen and host susceptibility determines the position of these transitions and the relative role of key host defence strategies. There is increasing recognition of the role of T-cells, B-cells and dendritic cells in the pulmonary response to pneumococci. The integration of these various host responses to pneumococci, in most cases, represents a paradigm which provides a template for successful host responses to pathogenic pulmonary bacteria.

**Bacterial evolution in the face of immunological pressure**

*C. Donati*, A. Muzzi, A. Covacci, R. Rappuoli, V. Masignani, M. Barocchi (Siena, IT)

*S. pneumoniae* is part of the normal upper respiratory tract flora but it can become pathogenic causing a variety of diseases, which range from otitis media and sinusitis to pneumonia, septicaemia, and meningitis. Due to its intimate relationship with the human host, *S. pneumoniae* has evolved a series of strategies to vary its genetic repertoire to evade the host immune response. Using their ability to recombine DNA acquired from the environment, *S. pneumoniae* strains are able to renew their dispensable genome (i.e., those regions of the genome that are not shared by all isolates). Dispensable genes are frequently acquired and lost, causing a loss of correlation between the phylogenetic history of strains and the presence of genes encoding proteins with antigenic properties. As a consequence these organisms have access to a genetic repertoire—the pan-genome—that is larger than the genome of any component strain. At the species level the pan-genome of *S. pneumoniae* grows as the number of sequenced strains increases due to the influx of genetic material from closely related species, and the mode of this growth positions the pneumococcal species on the edge between open and closed pan-genome. A second strategy for antigenic variation is shown by the evolution of pili, long filamentous appendages involved in adhesion to host cells. Pili are encoded in the rrA islet, a 12 kb genomic region, that consists of the rrA transcriptional regulator, rrgA, rrgB and rrgC, coding for LPXTG proteins forming the structure of the pilus, and srtB, srtC and srtD, coding for sortase enzymes catalyzing the pilus polymerization reaction. Due to their exposure to the host immune response, rrgA and rrgB are under positive selection that causes an increased rate of fixation of new alleles, and exist in three distinct clades that correlate with the MLST designation of the strains. Instead the rrgC, srtB, srtC and srtD genes, coding for proteins not directly exposed to the host immune system, are not under positive selection. In the region containing these genes, there is evidence of homologous recombination, and 4 major recombination hotspots can be identified. Due to the homogenizing effect of recombination these genes, differently from the major structural components of the pilus, are well conserved at the sequence level. In addition, piloted strains of Pneumococcus have been associated with multi-drug resistance cassettes that may provide *S. pneumoniae* added fitness.

**Pneumococcal vaccination**

*D. Bogaren* (Utrecht, NL)

*Streptococcus pneumoniae* is worldwide a leading cause of morbidity and mortality due to respiratory and invasive diseases. WHO estimates that annually at least one million children under 5 years of age die of infections caused by this pathogen. The more than 90 different capsular serotypes make it difficult to design a preventive strategy with universal pneumococcal coverage. In 1983, a 23-valent polysaccharide vaccine was marketed, being effective against invasive pneumococcal bloodstream infections in adults. Unfortunately, this vaccine proved low immunogenic in children due to it’s T-cell independent type of immune-protection. In 2000, a new 7-valent conjugate vaccine (PCV7) was licensed in the USA, protecting very well against invasive pneumococcal diseases (IPD) caused by vaccine serotypes, also in infants and young children. However, within the years following implementation of PCV7, in addition to a serious drop in vaccine serotype diseases, a significant increase in IPD caused by non-vaccine serotypes was observed. The impact of this so called ‘replacement’ disease on the total incidence of IPD seems to vary by population and country. Recently, two extended pneumococcal conjugate vaccines have been approved for use in children and adults, covering most of the currently ‘emerging serotypes’.

In this presentation, the following topics will be addressed; What most likely causes ‘replacement’ disease: vaccine pressure, ‘unmasking’ of non-vaccine serotypes, secular trends or a combination of those? Do we expect the new extended conjugate vaccines to solve the issue of ‘replacement’ disease? Do we expect in addition to shifts within IPD causing serotypes also shifts in diseases caused by other respiratory bacteria? What are potential new vaccine candidates, and what do we expect of those vaccines with respect to impact on pneumococcal and non-pneumococcal diseases?

**Nosocomial infections in critical-care patients**

*S. Nseir* (Lille, FR)

Ventilator-associated tracheobronchitis (VAT) is an intermediate process between colonization of lower respiratory tract and ventilator-associated pneumonia (VAP). Postmortem studies showed a continuum between...
CMV and HSV in mechanically ventilated ICU patients. The progression from colonization to VAT, and in some cases to VAP depends on quantity and virulence of the bacterial pathogen, and host lung defenses. VAT is common in mechanically ventilated patients. Its incidence ranges from 3–10% of ICU patients. Definition of VAT is matter of debate. Our group defined VAT using all the following criteria: fever (>38°C) with no other recognizable cause, purulent sputum production, positive culture of respiratory specimen at significant threshold, and no radiographic signs of new pneumonia. Portable chest radiograph is inaccurate in diagnosing new infiltrates in mechanically ventilated patients. Therefore, differentiating VAT from VAP could be a difficult task in ICU patients. VAT is frequently caused by Gram-negative bacilli, especially Pseudomonas aeruginosa. Although several studies investigated risk factors for VAP, few have evaluated risk factors for VAT. However, risk factors for these infections appear to be similar. Age >60 years, COPD, prior antimicrobial treatment and surgery were identified as risk factors for VAT. Tracheobronchitis is characterized by lower respiratory tract inflammation and increased sputum production. These factors may generate weaning difficulties, resulting in longer duration of mechanical ventilation. In a large cohort of mechanically ventilated patients, VAT was significantly associated with longer duration of mechanical ventilation and ICU stay. Beneficial effects of antimicrobial therapy were recently reported in VAT patients. In a randomized blinded placebo-controlled trial, aerosolized antibiotics significantly reduced the incidence of subsequent VAP. Further, aerosolized antibiotics increased weaning from mechanical ventilation, reduced usage of systemic antibiotics and antibiotic resistance. The impact of systemic antibiotics on outcomes of VAT patients was evaluated in a randomized unblinded controlled study. Antibiotic treatment increased mechanical ventilation free days, and reduced the incidence of subsequent VAP and ICU-mortality. Future studies should confirm these promising results, and determine the best duration of antimicrobial therapy in VAT patients.

CMV and HSV in critical-care patients: pathogens or bystanders?

C. Linssen* (Maastricht, NL)

Cytomegalovirus (CMV) and human herpes simplex virus (HSV) belong to the family of Herpesviridae. Both CMV and HSV are highly prevalent and ubiquitously distributed. In the immunocompetent adult host CMV and HSV infections usually have a benign course. As is the case with other herpesviruses, the initial infection is followed by a lifelong latent infection from which reactivation can occur. In immunocompetent individuals, asymptomatic viral shedding may be detectable in respiratory materials such as saliva or sputum in case of both HSV and CMV and also in urine in case of CMV. This viral shedding in patients without active viral disease makes it difficult to diagnose active disease in patients, especially since the symptoms of CMV and HSV infection (excluding typical skin lesions) are often non-specific. In immunocompromised patients CMV can lead to severe disease varying from retinitis and pneumonitis to generalized CMV disease. Occasionally, HSV may cause pneumonia as a result of immunosuppression, with a high mortality. However, critically ill patients admitted to the intensive care unit (ICU) are considered immunocompetent. Studies performed in ICU patients have shown these patients to be at risk for severe infections with CMV and HSV. In case of CMV, results from previously conducted studies point towards reactivation from latency as the most likely explanation rather than primary infection in ICU patients. Recent studies suggest that active CMV infection is quite common in ICU patients, with a prevalence up to 35%, depending on the sub-group of patients studied. Furthermore, an association between the presence of a CMV infection and increased mortality in critically ill patients was found. In recent years, the interest in HSV as a causative micro-organism in ICU patients has increased, especially as a cause of pulmonary infection. Recent reports detected HSV-1 in respiratory samples from ICU patients not considered to be primarily immunocompromised. In all studies a significant adverse effect of HSV-1 shedding in the respiratory tract on clinical outcome was established. Two studies showed an association between a high load of HSV present in the respiratory tract and increased mortality. At this moment it is not clear whether the association of both CMV and HSV with increased mortality is due to the micro-organism itself or that it is just an indication of the deteriorating physical condition of the patients leading to reactivation of the virus.

The concept of clinical sepsis – when all cultures are negative in a “septic” patient

P. Eggimann* (Lausanne, CH)

Despite all attempts to prevent them, nosocomial infection (NI) may complicate the stay of up to one third of patients requiring ICU management and the development of a sepsis of any severity should be considered as a potential NI. Prompt initiation of broad-spectrum antibiotics and source control are key factors for favorable outcome. A majority of them are device-related and a systematic workshop should be performed to identify them. Documentation of the source of infection may then allow to more specific measures, such as abscess drainage or catheter removal. Guidelines nowadays also include recommendations for systematic periodic re-evaluation of the evolution in order to adapt antibiotics and other therapeutic measures. In the absence of positive cultures, combination of clinical evolution and some biological parameters may contribute to safe de-escalation strategy.

Bacterial pathogenesis

M. Miskinyte*, S. Magalhaes, I. Gordo (Oeiras, PT)

During millions of years “arms-race” shaped evolution not only between the species across the planet but also inside the human body. Innate immune system is constantly evolving different strategies to detect and destroy intrusive microbes, while microbes evolving herewith. What are the strategies that microbes can develop to avoid and circumvent immune recognition?

We study the evolution of the model organism Escherichia coli under the selective pressure of bacterial killing cells, the macrophages (cell line RAW 264.7), which form an important component of the innate immune system. In approximately 100 generations all bacterial lines, evolved in the presence of the macrophages, showed a remarkable polymorphism, which did not occur in the controls. The relative abundance of the new morphs fluctuated stochastically over time, exhibiting a mixture of local peaks and short periods of apparent stable frequency. The distinct genotypes are marked by morphological differences clearly seen in the E. coli forming colonies and in FACS measurements. Furthermore, the first observed morphs that persist better inside the macrophages because of the slow growth rate and deficiency in metabolism have the same characteristics as SCVs (small colony variants) sampled from patients with various recurrent and persistent infections. Other morphs became resistant to engulfment and possibly killing by phagocytes and showed mucoid phenotype.

Investigating the long-term consequences of biotic interactions is clearly an emerging field of research because has implications on applied biomedicine furthermore it will be able to generate predictions concerning the nature of adaptations of microorganisms to multiple infections and to the immune system.
Intracellular lifestyle of *Streptococcus pyogenes* in human macrophages: survival strategies, replication, egress and re-infection

E. Hertzén*, L. Johansson, M. Märgelin, R. Wallin, A. Norry-Östlund (Stockholm, Lund, SE)

**Objectives:** Our recent studies using tissue biopsies from patients suffering from sepsis, necrotising faciitis and toxic shock demonstrated that *S. pyogenes* survive intracellularly in macrophages and contributes to bacterial persistence during acute deep tissue infections. This study aimed to elucidate the mechanisms by which *S. pyogenes* enters and survives in macrophages during severe streptococcal infections.

**Methods:** Primary human monocyte-derived macrophages were infected in kinetic experiments with a clinical MIT1 *S. pyogenes* isolate expressing green fluorescent protein (GFP), or an isogenic mutant deficient in M1 protein. Viability of bacteria was assessed by GFP-expression and confirmed by use of a bacterial viability staining kit or viable counts. Uptake, intracellular trafficking, and egress were analysed using flow cytometry, confocal and electron microscopy (EM). Re-infection was assessed by co-culture with FarRed labelled cells.

**Results:** *S. pyogenes* are taken up by large pseudopod loops in an actin-dependent manner, after which they reside within membrane surrounded vesicles. In kinetic studies, transient co-localisation is seen with early endosomal marker (EEA-1), whereas no association is noted with the late endosomes/lysosomes (LAMP-1 and lysotracker stain). In contrast, infection with the M1 mutant results in fusion with vesicles and significantly reduced bacterial counts intracellularly, as compared to the wild type strain (p = 0.03). Moreover, EM-studies demonstrated that the bacteria replicate intracellularly, and that after 6−10 h the bacteria migrate out of the cells. This is an active process as fixed bacteria used in control experiments remains intracellularly. Lactate dehydrogenase (LDH)-release experiments indicate that the egress is associated with cell death.

**Conclusions:** The findings demonstrate that M1 protein is crucial for intracellular survival of *S. pyogenes* in macrophages. Survival seems to be associated with impaired fusion with the lysosomes. Subsequent intracellular bacterial replication and egress of the bacteria is followed by re-infection of surrounding cells. This is likely an important event for dissemination and progression of severe streptococcal infections.

Inhibition of the inflammasome is a considerable component of the phenomenon of immunoparalysis presented among patients with Gram-negative sepsis.

**Objectives:** Bacterial pathogenesis

E.J Giamarellos-Bourboulis*, F.L van de Veerdonk, M. Mouktaroudi, M. Ralfiogiani, A. Antonopoulos, M. Georgiatis, J. van der Meer, M.G. Netea (Athens, GR; Nijmegen, NL)

**Objective:** Immunoparalysis in sepsis is characterized by impairment of cytokine production by monocytes. Interleukin (IL)-1β to be produced requires cleavage of its pro-form that is mediated through the inflammasome. The function of inflammasome in sepsis was assessed.

**Methods:** Peripheral blood mononuclear cells (PBMCs) were isolated from 34 healthy volunteers and from 92 patients with sepsis (49 in adult, 43 in pediatric groups). PBMCs were isolated with AIM-V (medium without antibiotics). PBMCs were cultured with LPS and MSU in different concentrations (0, 0.01, 0.1, 1.0, 10.0 μg), and cytokine production was measured by tetramer and ELISA.

**Results:** Percentage of viable cells (as assessed by trypan blue exclusion) was similar in both groups. No significant differences were observed in cytokine production. However, there was a trend towards decreased cytokine production in septic patients (Figure 1).

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**O78**

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**O79**

Inhibition of the inflammasome is a component of the phenomenon of immunoparalysis in Gram-negative sepsis

E.J Giamarellos-Bourboulis*, F.L van de Veerdonk, M. Mouktaroudi, M. Ralfiogiani, A. Antonopoulos, M. Georgiatis, J. van der Meer, M.G. Netea (Athens, GR; Nijmegen, NL)

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**O80**

Fluoroquinolone-resistant *Salmonella Typhimurium* has decreased intracellular survival in macrophages

A. Dehn Lunn*, A. Fährega, J. Vila, R. Read (Sheffield, UK; Barcelona, ES)

**Objectives:** Previous studies have suggested that fluoroquinolone resistance may be associated with attenuated virulence, and this may be the reason for the low levels of fluoroquinolone resistance compared with nalidixic acid resistance in *Salmonella* clinical isolates. We compared the intracellular survival of wild-type (ciprofloxacin MIC: 0.012 μg ml−1), fluoroquinolone-resistant (ciprofloxacin MIC: 64 μg ml−1) and reverted (ciprofloxacin MIC: 1.5 μg ml−1) *S. Typhimurium* in murine macrophages.

**Methods:** The fluoroquinolone-resistant *S. Typhimurium* was obtained from passage of the fluoroquinolone-resistant strain on antibiotic-free media. 1774.2 macrophages were seeded at 2 × 10⁵ cells per well and left to adhere for 24 hours. Control wells were fixed with paraformaldehyde. Prior to infection, wells were blocked with BSA for 30 minutes. Bacterial cultures were grown to log phase and then diluted to infect the macrophages with an MOI of 100. A gentamicin protection assay was performed, with viable counts performed at 0, 1, 4 and 24 hours.

**Results:** Fluoroquinolone-resistant *S. Typhimurium* showed significantly decreased overall survival in comparison to wild-type (median area under the curve (AUC) of 1.49 × 10⁵ versus 1.43 × 10⁵, statistically significant at the 1% level). In most experiments, there was a log difference in bacterial concentration (cfu ml−1) between the wild-type and resistant strains at all timepoints. There was not a significant difference between the wild-type and reverted strains or between the reverted and fluoroquinolone-resistant strains. To determine whether there was a difference in intracellular replication, data were analysed as a percentage of the bacterial concentration at t = 0 (that is, 90 minutes after infection). There was not a statistically significant difference between groups (p = 0.96).

**Conclusions:** Fluoroquinolone-resistant *S. Typhimurium* showed decreased survival in murine macrophages. Further work is needed to identify the genes responsible for this change, since the mutants were not isogenic.
**Binding and activation of plasminogen on *Fusobacterium necrophorum***

P. Kaukela*, N. Friberg, H. Jarva, P. Mattila, R. Solyman, M. Baumann (Helsinki, FI)

**Objective:** Many bacteria have plasminogen (Plg) receptors (PlgR) on their surface. Binding to PlgR enhances activation of the bound Plg to active enzyme plasmin and leads to protection of surface-associated plasmin against physiological plasmin inhibitors. Surface-associated plasmin is thought to play a pathogenetic role in various infections. In this work we have studied Plg binding and activation on *Fusobacterium necrophorum* (Fnec), an important Gram-negative rod-shaped anaerobe causing Lemierre's syndrome characterized by sepsis and internal jugular vein thrombosis preceded by an oropharyngeal infection.

**Methods:** Plg binding was monitored by incubating bacteria isolated from clinical samples with 1125 Plg alone or in various combinations with lysine analog epilson-amino-caproyc acid (EACA), tissue-type plasminogen activator (tPA) and alpha2-antiplasmin (alpha2AP), the physiological plasmin inhibitor, followed by counting of the bound radioactivity or by analyzing the bound Plg with SDS-PAGE and autoradiography. Plg activation was recorded by following the breakdown of the chromogenic substrate S-2251 in various reagent combinations.

**Results:** Fnec (n=11) bound significantly better iodinated Plg than *F. nucleatum* (n=14). Binding was inhibited by EACA and lead to enhanced activation by tPA. Formed plasmin was protected against inhibition by alpha2AP. Additionally, SDS-PAGE analysis of the bound plasmin revealed trimming of the formed Glu-plasmin to a slightly shorter Lys-form of the enzyme. Lidag blotting/MALDI-ToF analyses revealed that alpha2-CoA dehydrogenase was a predominant Plg binder among the fusobacterial outer membrane proteins.

**Conclusions:** The present results show that Fnec has a much stronger capacity to bind Plg than *F. nucleatum*. Inhibition of binding by EACA indicates that lysine binding sites in the N-terminal portion of Plg are involved in the binding. Inability of alpha2AP to inhibit formed plasmin activity emphasizes the receptor association of plasmin. Trimming of the surface-associated Glu-plasmin into the Lys-form speaks for an increased affinity between plasmin and PlgR. Acyl-CoA dehydrogenase is a strong tentative PlgR on Fnec. The data indicate that formation of surface associated plasmin on Fnec may play an important role in tissue invasion and in escape from thrombi.

**Characterization of the *Klebsiella oxytoca* cytotoxin**

G. Schmeditz*, M.M. Joaing, C. Högenauer, E.L. Zechner (Graz, AT)

**Objectives:** *Klebsiella oxytoca* has been shown to be the causative agent for Antibiotic Associated Hemorrhagic colitis (AAHC). The disease occurs during medical treatment with penicillin and results in a sudden onset of bloody diarrhea and abdominal cramps. Pathological features are mucosal haemorrhage and mucosal oedema that affect the ascending colon and cecum. The histological features of the AAHC resemble toxin-induced colitis and a cytotoxic substance is found in conditioned (cell-free) medium of bacterial cultures.

We aim to identify genes involved in cytotoxin production and secretion. The identification of cytotoxicity related genes will allow the biochemical description of the toxin and should provide insights into the effects on the host cells.

**Methods:** A human epithelial Hep2 cell line is used to measure cytotoxicity of the *Klebsiella* product quantitatively and qualitatively via the MTT viability assay. A random miniTn5 transposon mutagenesis created a library of randomly inserted knock out mutants in an AAHC patient isolate of *K. oxytoca*. The mutant library was screened for loss of cytotoxicity. The transposon insertion sites of toxin negative mutants were identified through isolation of adjacent chromosomal DNA via a plasposon rescue protocol followed by DNA sequencing. Finally, specific deletion mutants of the identified genes were generated and complementation of the cytotoxic negative phenotype was performed. Structure and regulation of cytotoxin production genes and the cytotoxin's chemical nature are under investigation. Cytotoxin positive and -negative *K. oxytoca* strains will be screened furthermore for distribution of those genes.

**Results:** So far screening the mutant library revealed two toxin negative mutants. The insertion sites cluster in the same region, indicating an operon. Three functionally related putative genes could be identified: a non-ribosomal peptide synthase, a DAHP synthase and a Xaa proline amino peptidase. The genes are involved in the non-ribosomal peptide biosynthesis and are not conserved in other *Klebsiella* species.

**Conclusion:** The clustering of mutations leading to a cytotoxicity negative phenotype suggests that the non-ribosomal biosynthesis pathway is essential for cytotoxin production. The substance family known to be synthesized through that pathway in other organisms includes numerous fungal and bacterial effecter substances, including antibiotics, cytokstes and siderophores.

**Infrequent deletion of the chromosomal genes speB and speF in GAS clinical isolates**

A. Friaes*, C. Silva-Costa, J. Melo-Cristino, M. Ramirez (Lisbon, PT)

**Objectives:** The chromosomal genes speB and speF do not encode true exotoxins (SpeB is a cysteine protease and SpeF a mitogonic factor), but are commonly included in the exotoxin gene profiling of Group A Streptococci (GAS) and have both been implicated in virulence. The aim of the present work was to confirm the presence of these genes in all GAS isolates and to characterise in detail any putative genomic deletions.

**Methods:** The genes speA, speB, speC, speF, speH, and ssa were PCR-screened in a total of 724 GAS isolates (160 from invasive infections and 564 from pharyngitis). PCR-negative results for speB and speF were confirmed by Southern blot hybridization with probes specific for each gene. Long-range PCR with primers specific for the regions flanking the putative deletions was performed, and the exact deletion breakpoints were determined by sequencing.

**Results:** The absence of speB was detected in four isolates, one of which was also the only isolate negative for speF. The latter was an emm28/ST52 strain isolated from blood. Sequencing confirmed a deletion of 4933 bp by comparison with the published genome sequence of the emm28 strain MGA6180, between nucleotides 2463 and 7395 (GenBank NC007296). The other speB-negative isolates belonged to emm types 4, 11, and 13, and were all isolated from pharyngitis cases.

**Conclusion:** The presence of the speB and speF genes is a characteristic of GAS recovered from human infections. Still, four isolates (0.6%) were speB-negative and one (0.1%) was speF-negative. The speB–speF– isolate was apparently highly virulent, in spite of the 4933 bp deletion encompassing several genes encoding proteins recognized to be important for virulence, such as SpeB, SpeF, the transcriptional regulator Rgg, the glycerol dehydrogenase, as well as four ORFs of unidentified function.

**Lipocolin 2 is detrimental during murine pneumococcal pneumonia**

J. Warszawski*, O. Sharif, B. Doninger, I. Mesteri, K. Stich, S. Knapp (Vienna, AT)

**Objectives:** Lipocolin 2 (Lcn2) is an antibacterial protein, known to interfere with bacterial siderophore-dependent iron acquisition. Thus, Lcn2−/− mice are highly susceptible to infections with siderophore-dependent pathogens such as *E. coli* and mycobacteria. Although no siderophores have been detected in *Streptococcus pneumoniae*, infection with this bacterium induces tremendously elevated levels of Lcn2 – and the biological role of this finding remains elusive. We therefore attempted to investigate the role of Lcn2 during pneumococcal pneumonia.
Methods: Age- and sex-matched C57BL/6 and Lcn2−/− mice were inoculated intranasally with Streptococcus pneumoniae and sacrificed 6 or 48 hours after infection or monitored for survival. Lungs were homogenized and plated on agar plates for bacterial counts and cytokine detection or embedded in paraffin for histological analysis.

Results: We observed significantly more KC and IL-6 in the bronchoalveolar lavage of Lcn2−/− mice 6 hours after infection. This resulted in significantly increased neutrophil influx after 6 hours leading to improved bacterial clearance after 48 hours. Consistent with this observation we found decreased cytokine levels and reduced lung inflammation in Lcn2−/− mice at later time-points after infection. Finally, Lcn2KO mice displayed a significant survival advantage over wild type animals.

Conclusion: Lcn2 is detrimental during murine pneumococcal pneumonia. We postulate that Lipocalin 2 prevents the early induction of inflammation upon S. pneumoniae infection and thus impairs clearance of bacteria and survival.

Apolipoprotein E in brain injury

H. A. Cottrell, W. P. Cuellar, A. Y. Chiu, F. H. Miller, W. C. Davis (Baltimore, MD)

Background: Apolipoprotein E (ApoE) is expressed in brain parenchyma and has an essential role in neuronal and glial development. ApoE4 has been linked to increased incidence of neurodegenerative diseases.

Objective: To determine whether ApoE4 alters the response of neural progenitor cells to infectious stimuli.

Methods: Neural progenitor cells were isolated from embryonic rat brains and cultured in the presence of either no cytokines, or 10 ng/ml each of IL-4 or TNF-α. Neuronal progenitor cells were differentiated and apoptosis was assessed by detection of Annexin V and active caspase-3.

Results: ApoE4 altered the response of neural progenitor cells to inflammatory cytokines. IL-4, but not TNF-α, induced apoptosis in ApoE4 expressing cells but not in wild type mice. ApoE4 expression also altered the survival rate of neural progenitor cells after differentiation.

Conclusion: ApoE4 alters the response of neural progenitor cells to inflammatory cytokines and may contribute to the development of neurodegenerative diseases.

Brain Cell Biology

S. Kurz, M. A. Boyken, T. Tran, R. A. Zawistowski, A. J. Leslie, M. H. Winge (Berkeley, CA)

Background: The brain is a unique organ that is highly susceptible to structural and functional changes following injury.

Objective: To investigate the role of microglia in the brain following injury and to determine the effects of c-Jun N-terminal kinase (JNK) inhibition on microglia activation and subsequent neuronal cell death.

Methods: Microglia were isolated from the brain of adult mice and cultured with or without JNK inhibitor. Neuronal cells were co-cultured with microglia in the presence of bacterial lipopolysaccharide. The effects of JNK inhibition on microglia activation and neuronal cell death were assessed.

Results: JNK inhibition reduced microglia activation and neuronal cell death. These findings suggest that JNK inhibition may be a potential therapeutic strategy for treating brain injury.

Conclusion: JNK inhibition may be a potential therapeutic strategy for treating brain injury.

Streptococcus suis, an emerging zoonotic agent of meningitis, triggers different inflammatory signalling pathways by murine microglia

M.C. Dominguez Punaro°, M. Segura, I. Contreras, N. Fittipaldi, M.P. Lecours, M. Olieder, M. Gottschalk on behalf of the Centre de Recherche en Infectiologie Porcine (CRIP) and the Groupe de Recherche sur les Maladies Infectieuses du Porc (GREMIP)

Objective: Streptococcus suis type 2 is an important swine and human pathogen responsible for septicaemia and meningitis. We demonstrated that in the brain of infected mice with S. suis, microglia expressed increased levels of different pro-inflammatory genes. To expand our knowledge of the interactions between S. suis and microglia, we evaluated the signalling pathways underlying S. suis-induced pro-inflammatory events.

Methods: Mouse microglia line BV-2 was infected with a virulent wild type (WT) strain of S. suis or a panel of mutants altered at the capsule (CPS-mutant) or cell wall levels. Phagocytosis was quantified by an antibiotic protection assay. Cell supernatants were used to measure pro-inflammatory cytokines by ELISA and nitric oxide (NO) by the Griess reaction. Analysis from cell lysates, to evaluate inflammation-associated intracellular signalization pathways, was carried out by western blot using specific antibodies against NO production from microglia. The involvement of the inflammatory transcription factor NF-kB was monitored by EMSA.

Results: Phagocytosis and cytokine studies showed that the CPS was the only relevant virulence factor modulating bacterial interactions with microglia. The CPS helped bacteria to resist phagocytosis and regulate the inflammatory response as it hides pro-inflammatory components from the bacterial cell wall. S. suis induced iNOS expression and further NO production from microglia. Cells infected with the CPS-mutant showed stronger phosphorylation profiles for PKC, Tyr and MAPK. Likewise, pharmacologic inhibition of MAPK abrogated TNF-α and MCP-1 production from infected cells. Finally, S. suis-induced NF-kB translocation was faster for cells stimulated with the CPS-mutant, suggesting that bacterial cell wall components are potent inducers of NF-kB.

Conclusions: Our data help to better understand the mechanisms underlying S. suis induction of inflammation in the brain, that in turn would be useful to design more efficient anti-inflammatory strategies for meningitis.
Antimicrobial stewardship and antibiotic policies

**[O87]** Antimicrobial stewardship programs in Spanish hospitals: a nationwide survey

J.R. Paño-Pardo *, M.P. Romero-Gómez, J.M. Ortega-Gómez, A. Martín Quirós, M. Moro, A. Rico, J.P. Horcajada, B. Padilla, J. Rodríguez-Batillo on behalf of GEIH (Spanish Study Group on Hospital Acquired Infections), GEMARA, and GEIPC from SEIMC (Spanish Society of Infectious Diseases and Clinical Microbiology)

**Objectives:** 1) To describe the number, distribution and main features of antimicrobial stewardship programs (ASP) in Spanish hospitals. 2) To describe the Spanish Infectious Diseases (ID) community perceptions about antimicrobial (ABX) stewardship.

**Methods:** An online survey was designed. The link was distributed through the e-mailing lists of several working groups of the Spanish Clinical Microbiology and Infectious Diseases Society (SEIMC). The survey was anonymously submitted.

**Results:** Between Sept 15 2009 and Nov 15 2009, 110 surveys representing 76 hospitals were received from all over the country. 84 surveys were completely fulfilled (76%). Distribution of the replies per hospital size is described in table 1. Most of the respondents were either ID physicians (50%) or microbiologists (29%). 35/76 hospitals (41%) had an ongoing ASP. These programs were not homogenously distributed along the country but concentrated in 4 of the 17 Spanish Autonomous Communities, especially in Catalonia. 19/30 (63%) of the ASP were not limited to a specific clinical area of the hospital and could be considered “hospitalwide” programs. Most of these ASP (70%) have been working for more than 5 years. The most frequent principles of ABX stewardship implemented in these programs were: 1) ABX streamlining or de-escalation and 2) intravenous to P.O. switch, both present in 23/30 of the surveys.

**Conclusions:** A minority (41%) of the surveyed hospitals in Spain has an ongoing ASP and large geographical variations were observed. Few of the ASP (30%) have been implemented in the last 5 years. TAFB was perceived as the most useful intervention in the setting of ASP. The intervention model demonstrated that the restrictive antibiotic policy on the incidence of methicillin-resistant *Staphylococcus aureus* (MRSA) in the 18-bed general Intensive Care Unit (ICU) of an 850-bed tertiary care hospital in Italy.

**Methods:** Between January 2007 and December 2008, a multidisciplinary Antimicrobial Management Team (AMT) provided a two-phase intervention in our 21-bed Division of Neurosurgery (NSU). In the observational period (2007), clinical, microbiological and pharmaceutical data of the year were collected, and reviewed with the ward medical staff thereafter. In the interventional period (2008), the AMT provided antimicrobial recommendation prescription on a regular and on-call basis, together with formulary restrictions and encouraged appropriate prophylaxis or targeted therapy whenever indicated. Recommendations were driven by updated specific pathogen resistance patterns and clinical pharmacology parameters; pharmaceutical data analysis was performed through the ESGAP ABC 3.1 program.

**Results:** The total number of admissions was 797 (bed-occupancy index = 0.87) in 2007 and 761 (bed-occupancy index = 0.82) in 2008, accounting for 6686.55 and 6302.52 bed-days, respectively. Among antimicrobial drugs commonly used for prophylaxis, the defined daily doses/100 bed-days (DDD) decreased from 558.33 to 406 for cefazolin, and from 363.66 to 239 for amoxicillin/clavulanate between 2007 and 2008. Among therapeutically used antimicrobials, vancomycin decreased from 205.5 to 37, meropenem from 360 to 249.5, levofloxacin from 804 to 564, and linezolid from 275.5 to 199, whereas etrapenem slightly increased (from 17 to 30) because of few invasive infections caused by ESBL-producing Enterobacteriaceae. However, mean length of stay decreased from 9.29 days to 8.90 between the two years, and no patients died in NSU due to infection-related causes during 2008. The grand total of antimicrobial expenditures also decreased from Euros 88,787.94 to 60,584.34.

**Conclusion:** The interventional policy by an AMT, based on the development of agreed upon prophylactic and therapeutic antimicrobial regimens, regular educational activities and microbiological and pharmacoeconomic monitoring significantly improved not only the appropriateness of antimicrobial prescription in this high-risk setting, but also the economical costs of antimicrobial acquisition.

**Objectives:** To determine the efficacy and the efficiency of a restrictive antibiotic policy on the incidence of methicillin-resistant *Staphylococcus aureus* (MRSA) in an 850-bed tertiary care hospital in Italy.

**Methods:** Based on updated microbiological reports and clinical pharmacology parameters, the dedicated Antimicrobial Management Team pursued a more appropriate approach to antimicrobial prophylaxis and empirical therapy in ICU, either withdrawing ampicillin/sulbactam (AS) prophylaxis, or targeting vancomycin (VAN) therapy whenever indicated. Using an intervention time-series analysis, we first evaluated the efficacy of AS and VAN restrictions on their consumption, then combined this model with a transfer function model on use of other antibiotics and finally assessed the efficiency on the incidence of clinical isolates of MRSA from April 2004 to December 2007. The WHO ATC/DDD classification was used as reference normalized per 100 patient-days (PD).

**Results:** The intervention model demonstrated that the restrictive antibiotic policy yielded a statistical significant decrease of AS from 303 to 134 DDD/100 PD, and R2 was 64% in November 2003; six months later, VAN decreased from 36 to 11 DDD/100 PD (R2 of 46%). Five months after AS restriction, the MRSA incidence significantly decreased from 3.4 to 1.4 cases. The final model explained 42% of the incidence of MRSA over time, showing, conversely, that an increase of 1 DDD/100 PD of antibiotics increased the incidence of MRSA isolates from current level, i.e. 0.043 for ceftriaxone (significant impact at lag 2 and 3), and 0.012 for levofloxacin, at the same time.

**Conclusion:** This study shows that modelling antibiotic use can either drive a more appropriate empirical and targeted antimicrobial therapy, or inform policy makers about negative adverse effects of certain antibiotic

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**[O88]** Antimicrobial stewardship improves appropriateness of antimicrobial therapy prescription in a neurosurgical unit

L. Pagani *, N. Vernaz, R. Aschbacher, M. Falciani, P. Mian, P. Bonnabry, L. Pagani (Geneva, CH; Bolzano, IT)

**Objectives:** To assess the impact of an Antimicrobial Stewardship Program (ASP) on antimicrobial usage and consumption, and patients’ outcome in the neurosurgical setting of an Italian 850-bed tertiary hospital.

Methods: Between January 2007 and December 2008, a multidisciplinary Antimicrobial Management Team (AMT) provided a two-phase intervention in our 21-bed Division of Neurosurgery (NSU). In the observational period (2007), clinical, microbiological and pharmaceutical data of the year were collected, and reviewed with the ward medical staff thereafter. In the interventional period (2008), the AMT provided antimicrobial recommendation prescription on a regular and on-call basis, together with formulary restrictions and encouraged appropriate prophylaxis or targeted therapy whenever indicated. Recommendations were driven by updated specific pathogen resistance patterns and clinical pharmacology parameters; pharmaceutical data analysis was performed through the ESGAP ABC 3.1 program.

Results: The total number of admissions was 797 (bed-occupancy index = 0.87) in 2007 and 761 (bed-occupancy index = 0.82) in 2008, accounting for 6686.55 and 6302.52 bed-days, respectively. Among antimicrobial drugs commonly used for prophylaxis, the defined daily doses/100 bed-days (DDD) decreased from 558.33 to 406 for cefazolin, and from 363.66 to 239 for amoxicillin/clavulanate between 2007 and 2008. Among therapeutically used antimicrobials, vancomycin decreased from 205.5 to 37, meropenem from 360 to 249.5, levofloxacin from 804 to 564, and linezolid from 275.5 to 199, whereas etrapenem slightly increased (from 17 to 30) because of few invasive infections caused by ESBL-producing Enterobacteriaceae. However, mean length of stay decreased from 9.29 days to 8.90 between the two years, and no patients died in NSU due to infection-related causes during 2008. The grand total of antimicrobial expenditures also decreased from Euros 88,787.94 to 60,584.34.

Conclusion: The interventional policy by an AMT, based on the development of agreed upon prophylactic and therapeutic antimicrobial regimens, regular educational activities and microbiological and pharmaco-economic monitoring significantly improved not only the appropriateness of antimicrobial prescription in this high-risk setting, but also the economical costs of antimicrobial acquisition.
agents on selection of MRSA, and may ultimately control and prevent
the misuse of antimicrobials. Restriction of several broad-spectrum
antimicrobials might positively impact on MRSA, even if case-mix and
the huge homogeneity of patients in general ICU may negatively affect
the overall fitness of the model.

**Modelling the impact of antibiotic use on antibiotic-resistant
Escherichia coli using population-based data from a large hospital and its surrounding community**

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J. López-Lozano, J. Schrenzel, S. Harbarth (Geneva, CH; Alicante, ES)

**Objectives:** We determined the temporal relationship between antibiotic use and the incidence of antibiotic-resistant *Escherichia coli* both in the inpatient and outpatient setting of the Swiss canton of Geneva.

**Methods:** An observational time-series analysis was performed to evaluate the incidence of non-duplicate clinical isolates of *E. coli* resistant to ciprofloxacin, trimethoprim/sulfamethoxazole and cefepime from January 2000 through December 2007. The resistance data were combined with a transfer function model of aggregated data on antibiotic use in both settings obtained from the hospital’s pharmacy and outpatient billing offices.

**Results:** Ciprofloxacin resistance increased from 6% (2000) to 15.4% (2007; P < 0.0001) and ceftazidime resistance from 0.9% to 3.2% (P = 0.01). Trimethoprim/sulfamethoxazole resistance showed no trend (23.7%--28.8%). Total antibiotic use increased in both settings, while fluoroquinolone use increased significantly only among outpatients. A temporal effect between resistance in community isolates and outpatient use of ciprofloxacin (immediate and time lag, 1 month) and moxifloxacin (time lag 4 months) was observed, explaining 52% of the variance over time. The incidence of ceftazidime resistance in *E. coli*, as surrogate marker for ESBL, was correlated to ciprofloxacin use in the inpatient (lag 1 month) and outpatient (lag 4 months) settings and to the use of ceftriaxone (lag 0 months), piperacillin/tazobactam (lag 3 months) and cefepime (3 months) in the hospital (R2, 51%).

**Conclusions:** These results support efforts to reduce prescriptions of selected antimicrobial drug classes such as fluoroquinolones for reduction of resistant *E. coli* including ESBL and show the added value of time series analysis to better understand the interaction between community and hospital antibiotic prescribing.

**Table. Multivariate transfer function model of fluoroquinolone use in the inpatient and outpatient setting and temporal relation with the incidence of non-duplicate clinical isolates of *E. coli*-resistance per 100 patient-days to ciprofloxacin. University of Geneva Hospitals, January 2000 to December 2007.**

<table>
<thead>
<tr>
<th>Variable</th>
<th>CIP-R-CA, R2 = 0.52</th>
<th>Ciprofloxacin, R2 = 0.18</th>
</tr>
</thead>
<tbody>
<tr>
<td>Parameter</td>
<td>t-Statistic</td>
<td>p-Value</td>
</tr>
<tr>
<td>Constant</td>
<td>-3.54 (0.24)</td>
<td>0.0000</td>
</tr>
<tr>
<td>Ciprofloxacin, outpatient use</td>
<td>-1.51 (0.49)</td>
<td>0.0009</td>
</tr>
<tr>
<td>Moxifloxacin, outpatient use</td>
<td>-0.64 (0.16)</td>
<td>0.0001</td>
</tr>
<tr>
<td>Antimicrobial term a</td>
<td>0.31 (0.15)</td>
<td>0.24 (0.10)</td>
</tr>
<tr>
<td>Moving average term b</td>
<td>0.56 (0.11)</td>
<td>0.0017</td>
</tr>
</tbody>
</table>

**CIP-R-CA: Community-acquired ciprofloxacin-resistant *E. coli* isolates; CIP-R-DA: hospital-acquired ciprofloxacin-resistant *E. coli* isolates.

*Delay (months) necessary to observe the effect. bSize and direction of the effect. cThe autoregressive term represents the past value of the resistance. dThe moving average term represents disturbances or abrupt changes of resistance.**

**Reduction in ciprofloxacin use in a university hospital correlates with increased susceptibility to both quinolone and B-lactam antibiotics in Gram-negative organisms**

J. Troughhton*, G. Millar, E. Smyth, R. McMillan (Belfast, UK)

**Objectives:** An antibiotic policy revision was implemented at our institution, a university hospital in Belfast, in July 2008. Its purpose was to substitute ceftriaxone and ciprofloxacin, with B-lactam antibiotics.

The aim of this study was to investigate whether, following the policy change, there was a:

- change in usage of piperacillin–tazobactam (pip–tazo), aztreonam, ceftriaxone, ciprofloxacin and meropenem, based on defined daily doses (DDD) prescribed;
- shift in the proportion of Gram-negative organisms susceptible to these antibiotics;
- significant relationship between susceptibility and usage of these antibiotics.

**Methods:** The first isolate of all Gram-negative organisms recovered from blood cultures, sputum and urine of hospitalised adults, between January 2008 and August 2009, were included. The proportion of isolates reported susceptible, before and after the policy change, were compared by Z2 test; DDD before and after were compared using independent t-test. The association between DDD prescription and susceptibility was tested using Pearson correlation and linear regression.

**Results:** Ciprofloxacin use decreased (p < 0.001) and aztreonam use increased (p = 0.03) following policy revision. There was no change in meropenem, ceftriaxone or pip–tazo use. In all, 5445 isolates were evaluated; the proportion susceptible to ciprofloxacin (p < 0.001), aztreonam (p < 0.001), and pip–tazo (p = 0.049) increased. A significant inverse linear association between ciprofloxacin use and susceptibility was detected (p < 0.001; correlation p < 0.001). Furthermore, pip–tazo, aztreonam and meropenem susceptibility were inversely correlated with ciprofloxacin use (univariate pip–tazo r = -0.39 p = 0.045; aztreonam r = -0.69 p < 0.001; meropenem r = -0.53 p = 0.008), with a linear relationship apparent (pip–tazo p = 0.089; aztreonam p = 0.001; meropenem p = 0.016). Surprisingly, there was a significant positive linear association between aztreonam use and susceptibility (r = 0.61 p = 0.004).

**Conclusions:** These data suggest that an antibiotic policy revision, successfully reducing ciprofloxacin use, correlated with an increase in ciprofloxacin susceptibility among Gram-negative organisms. Furthermore, this was also associated with an increase in susceptibility to B-lactam antibiotics, in spite of increased use of aztreonam. Therefore, reducing quinolone exposure within a population appears to exert a favourable effect on both quinolone and B-lactam susceptibility of Gram-negative organisms.

**Figure.** Correlation of ciprofloxacin DDD with ciprofloxacin and β-lactam.

**Life without ciprofloxacin: implementation and consequences of a fluoroquinolone ban for a tertiary referral hospital**

K. Burns*, S. Foley, M. Morris-Downes, F. Fitzpatrick, H. Humphreys, E. Smyth (Dublin, IE)

**Objectives:** An outbreak of *Clostridium difficile* infection (CDI) due to PCR ribotype 027 affecting 42 patients occurred in our hospital between July 2008 and March 2009. The reported association between
fluoroquinolone use and *C. difficile* colitis and evidence that *C. difficile* 027 isolates tend to be fluoroquinolone-resistant, prompted the outbreak control team to recommend a complete ban on the prescription of fluoroquinolone antimicrobials as one component of the multifactorial outbreak management programme, effective September 2008. This report describes the practicalities of introducing a fluoroquinolone ban, the efforts to maintain the ban and some of the observed consequences of the ban.

**Methods:** The hospital’s clinical microbiology team, surveillance scientist and antimicrobial pharmacist collected data regarding the impact of this ban on rates of inpatient *C. difficile* infection, fluoroquinolone resistance in *E. coli* bacteraemia isolates and the use of other antimicrobial agents.

**Results:** At the peak of the outbreak of CDI, there were on average 16 new cases diagnosed per month. Following closure of the outbreak, the number of new cases of CDI has declined to an average of 7.8 per month. Compared with 2007, fluoroquinolone use for inpatients during 2008 declined by 59% (19.07 DDD/100BD to 7.82 DDD/100BD). However, for the same period, meropenem use increased by 43% (1.34 DDD/100BD to 1.92 DDD/100BD). The proportion of fluoroquinolone resistance in *E. coli* isolates from bloodstream infections in our hospital has decreased from 25% in 2008 to 5% for quarters 1 & 2 2009.

**Conclusion:** Implementation of a fluoroquinolone ban has proved challenging, but has rewarded with a reduction in cases of CDI and fluoroquinolone resistance in *E. coli*. Such an intervention may be a useful adjunctive measure in the management of outbreaks of infection due to *Clostridium difficile* ribotype 027. Of concern, is the increased use of broad spectrum agents such as meropenem. Further effort is required to limit the use of such agents, particularly in the context of the recent emergence of carbapenemase producing Enterobacteriaceae and the lack of new anti-Gram-negative agents.

**O94** Do published studies provide accurate estimates of the association between antibiotic exposure and acquisition of antibiotic-resistant bacteria?

M.A. Cataldo, G. De Angelis, M. Cipriani, R. Cauda, E. Tacconelli* (Rome, IT)

**Objectives:** Antibiotic stewardship is usually included in a multifaceted approach to combat the spreading of antibiotic resistant bacteria (ARB) into the healthcare setting. Numerous papers have demonstrated that prior antimicrobial drug exposure is a strong risk factor for infection due to ARB. However, the association between antibiotic therapy and the acquisition of ARB is still unclear and it is often confounded by scarce data on antibiotic usage. Our objectives were to define major limits of the available evidence and to explore the sources of heterogeneity.

**Methods:** Two meta-analyses were performed to determine whether antibiotic exposure is a risk factor for the isolation of ARB. Target bacteria were: methicillin-resistant *Staphylococcus aureus* (MRSA) and carbapenem-resistant *Acinetobacter baumannii* (CRAB). The I2 test was calculated to assess whether results varied no more than might have been expected by the play of chance. The subgroup analysis was performed by stratifying sampling frame for inclusion, definition of case subjects and controls, study design, geographic area of the study, presence of adjustment of covariates and length of time in which antibiotic exposure was detected. A significant heterogeneity was considered for I2 > 50%.

**Results:** Seventy-eight studies (60 related to MRSA and 18 studies to CRAB) were considered eligible for inclusion. All studies were cohort, case-control or prevalence survey. Patients who had taken antibiotics had a risk increased by 1.8 (95% CI, 1.7−1.9) and by 1.3 (95% CI, 1.2−1.4) fold of acquiring MRSA and CRAB, respectively. Significantly heterogeneity was detected for study design, definition of controls, sampling frame for inclusion, endemic / epidemic setting, adjustment for covariates. A regression analysis revealed that the heterogeneity was linked to the length of time in which antibiotic exposure was detected before isolation, selection of the control group, and sampling frame for inclusion.

**Conclusions:** Our analysis confirms that the quality of the evidence available on the association between antibiotic therapy and the acquisition of antibiotic-resistant bacteria is poor. Specific guidelines focused on methodological issues to address the epidemiology of antibiotic-resistant infections are urgently needed.

**O95** Divergent intentions to use a local antibiotic guideline: a theory of planned behaviour survey

P. Cortoos*, B. Schreurs, W. Peetermans, K. De Witte, G. Laekeman (Leuven, Brussels, BE)

**Background:** In order to improve antimicrobial practice, correctly identifying antibiotic guideline barriers, and assessing their relative importance are important factors. The Theory of Planned Behaviour (TPB) permits such assessment and has been used already for evaluating antibiotic use (1). According this theory, the intention driving guideline use, is fuelled by three factors: attitude; subjective norm (SN) (perceived social pressure regarding guidelines); and perceived behavioural control (PBC) over the guideline. Using a TPB-based questionnaire, we wanted to study how guideline use is affected in our hospital.
Temporal effects of a restrictive antibiotic policy on hospital-acquired Clostridium difficile, methicillin-resistant Staphylococcus aureus and extended-spectrum β-lactamase producing coliforms in a district general hospital

S. Dancer, P. Kirkpatrick, D. Corcoran*, F. Christison, D. Farmer

Methods: Following a persistent problem with cases of Clostridium difficile, a restrictive antibiotic policy was imposed on a 400-bedded district general hospital. This policy banned the use of cephalosporin and quinolone antibiotics unless released by the microbiologist. Hospital pharmacists upheld the policy on the wards and stocks of restricted agents were removed from all wards except intensive and emergency care.

Results: During the six months before the policy was introduced, the hospital experienced an average monthly rate of 1.099 MRSA cases/1000 pt bds; 2.398 C. difficile cases/1000 pt bds; and 1.480 cases ESBLs/1000 pt bds. The average monthly consumption of ceftriaxone over the whole 22-month period. These were calculated as the number of cases per month per 1000 patient-occupied bed-days (1000 pt bds) for the whole hospital. In addition, we determined each new case of hospital-acquired C. difficile, methicillin-resistant Staphylococcus aureus (MRSA) and extended-spectrum β-lactamase-producing coliform (ESBLs) infection for the whole 22-month period. The changing epidemiology of staphylococci worldwide, whether some specific genetic traits of the human host favor the some virulence traits are highlighted; it remains to be determined that there is no specific background strain associated with IE; however some virulence traits are highlighted; it remains to be determined whether some specific genetic traits of the human host favor the occurrence of S. aureus IE.

Conclusion: There is no specific background strain associated with IE; however some virulence traits are highlighted; it remains to be determined whether some specific genetic traits of the human host favor the occurrence of S. aureus IE. MSSA: The 114 MSSA isolates were seldom resistant to erythromycin (16/114, 1.4%) and almost fully susceptible to all other antibiotics. Phenotypic results were highly correlated with genomic data from microarray. All MSSA isolates were assigned to 19 ST. Their ST diversity evaluated by the lambda modified Simpson was not different when compared to a set of 114 S. aureus invasive isolates collected throughout France during the EARS study in 2006–2007 (88.31% vs 91.09%). Surprisingly we noticed that 8 isolates belonged to ST398. Genomic DNA microarray comparison of the 114 MSSA IE isolates with 152 MSSA nasal carriage isolates highlighted that several specific determinants or gene alleles (e.g., bone sialoprotein, elastin binding protein, modulins) were preferentially harbored by MSSA IE isolates.

Conclusions: The genetic diversity of S. aureus strains from IE suggests that there is no specific background strain associated with IE; however some virulence traits are highlighted; it remains to be determined whether some specific genetic traits of the human host favor the occurrence of S. aureus IE. MSSA, including CA-MRSA are infrequent.

Improved discrimination of highly-clonal ST22-methicillin-resistant Staphylococcus aureus (MRSA)-IV isolates achieved by combining spa, dru and pulsed field gel electrophoresis typing data

A. Shore*, A. Rossney, P. Kinaney, O. Brennan, O. Sherlock, E. Creamer, D. Sallivan, R. Cinney, R. Goering, H. Humphreys, D. Coleman (Dublin, IE; Omaha, Nebraska, US)

Objective: The pandemic ST22-methicillin resistant Staphylococcus aureus (MRSA)-IV strain has been endemic in Irish hospitals since 2002, where it is designated as antibogram-resistogram type-pulsed-field group (AR-PFG) 06–01 and is similar to the UK epidemic strain EMRSA-15. Differentiating isolates of this strain is difficult as they exhibit a limited number of pulsed-field gel electrophoresis (PFGE) patterns.
patterns and spa types. This study investigated whether combining PFGE and spa typing with DNA sequencing of the SCCmec-associated direct repeat unit (dru typing) would significantly improve isolate discrimination.

Methods: One hundred and seventy-three MRSA isolates recovered in one Irish hospital during 2007 and 2008 were investigated using AR, PFGE, spa, dru and SCCmec typing. One isolate representative of each of the spa types identified underwent multilocus sequence typing.

Results: Ninety-seven percent of isolates (168/173) exhibited AR-PFG 06-01 or closely related AR patterns and 163 of these harboured SCCmec IVh. Isolates representative of the 17 PFG-01 spa types were identified as ST22. Combining PFGE, spa and dru typing data significantly improved discrimination of the 168 PFG-01 isolates yielding 65 type combinations with a Simpson’s Index of Diversity (SID) of 96.53 compared to a pairwise combinations which yielded 37, 44 and 43 type combinations with SIDs of 90.84 for spa and dru, 91.00 for spa and PFGE and 93.57 for dru and PFGE; respectively, or b) individual typing methods which yielded 21, 17 and 17 types with SIDs of 66.9, 77.8 and 81.34 for spa, dru and PFGE, respectively. Analysis of epidemiological information for a subset of PFG-01 isolates validated the relationships inferred using combined PFGE, spa and dru typing data.

Conclusions: This study demonstrates that the combination of PFGE, spa and dru typing improves discrimination and epidemiological tracking of highly clonal ST22-MRSA-IV isolates.

O099 External quality assessment of genotyping techniques for methicillin-resistant Staphylococcus aureus

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Background: After detection of meticillin resistant Staphylococcus aureus (MRSA), genotyping may be necessary to proceed with infection-preventive measures. This external quality assessment study determines the performance of genotyping techniques for MRSA in participating laboratories and was organised by Quality Control for Molecular Diagnostics (QCMD) (www.qcmd.org).

Methods: The EQA panel for MRSA genotyping was distributed to 19 participants in 8 countries in August 2009 and consisted of 10 samples (2 identical, 5 genetically related and 5 unique, as determined originally with pulsed-field gel electrophoresis [PFGE]) of viable MRSA strains in Muller Hinton broth. A different letter signified the detection of a different genotype, whereas a different number signified the detection of a different subtype. All data were reported in relation to the reference strain in panel sample MRSATP09-01.

Results: Out of the 19 potential participants, 14 (74%) responded. Four of the non-responders withdrew officially indicating ‘panel used for research’ (n=1) and ‘assay not offered’ (n=3). The majority of datasets were generated by PFGE (n=11), with the remainder generated by AFLP (n=2) and spa typing (n=2). Seventy-three percent of participants typed all samples correctly, all with PFGE. Results obtained from spa-typing and amplified fragment length polymorphism (AFLP) were found to be less discriminatory than those obtained with PFGE.

Discussion: We present the first EQA programme for the genotyping of MRSA. PFGE was implemented by most of the participating laboratories. However, most protocols proved to be suboptimal, resulting in inferior resolution in the higher or lower fragment regions. This suggests that further assay optimisation is required. The lack of resolution was most evident with the closely related MRSA strains in the panel. Results generated using AFLP and spa-typing showed less discriminatory power compared to PFGE. Participants reported a range of criteria for determining genotype and subtype. The guidance according to Tenover et al was the most prominent method. Future EQA distributions will gather information on the cutoff values used by participants. To improve the performance and quality of MRSA genotyping and subtyping, both laboratories and manufacturers should be encouraged to participate in EQAs. The availability of EQA panels for detection and typing should also be developed for other important (nosocomial) infectious agents.

O100 Usefulness of DiversiLab rep-PCR system for typing and follow-up of Pseudomonas aeruginosa strains colonizing cystic fibrosis patients: comparison with PFGE and MLST techniques

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Objective: rep-PCR typing method has been recently proposed as alternative to the classical PFGE for Clinical Microbiology Laboratories. This method demonstrated their utility in outbreaks typing whereas non-experience in the follow-up of chronically colonized patients is available. The aim of this work was to evaluate the ability of the rep-PCR DiversiLab system (bioMérieux) to discriminate a well-typed collection of P aeruginosa strains from cystic fibrosis (CF) patients.

Material and Methods: A collection of 49 P aeruginosa strains recovered from sputum samples of 24 CF-patients (1994–2009) were studied. Strains were classified as first colonizer (n=24), sporadic or intermittent (n=13), and persistent colonizers (n=12). First colonizer was defined as the first P aeruginosa isolate detected from sputum in each CF-patient. In four patients, first colonizers were identical to the follow-up isolates, so were also classified as persistent. Genetic relationships were analyzed by PFGE-Spel and MLST and after compared with those obtained by DiversiLab, which generates patterns by use of microfluidic chips. Follow-up of CF-patients include comparison of the first colonizer, sporadic and chronic isolates as well as possible persistence and cross-colonization.

Results: Among the 24 first colonizer strains, 22 PFGE patterns and 21 unrelated STs were detected. rep-PCR DiversiLab confirmed these data with discrepancies only in one strain. Two strains belonging to ST312 were classified by DiversiLab as unrelated, and another two strains grouped in ST274 had different PFGE and DiversiLab patterns. The 13 sporadic strains were obtained from 7 CF-patients. Genetic relationship was not detectable among them using either PFGE or MLST tools, and DiversiLab confirmed this pattern of heterogeneity except in one strain. Chronic colonizers (12 + 4 first colonizer strains) were obtained from 4 CF-patients (2–5 strains per patient). The three typing methods agreed with the result that particular host-specific stable clones were detected in different patients, with no genetic relation between them.

Conclusions: DiversiLab system based on rep-PCR technique is a reliable method useful for Clinical Microbiological Laboratories in the follow-up and colonization dynamic of CF-P aeruginosa strains. This technique is considerably less laborious than the classical PFGE and MLST and genetic results for our first colonizers, sporadic or persistent strains are comparable.

O101 Sequence types of carbapenem-resistant Acinetobacter baumannii strains in Greece during the last decade

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(Larissa, Athens, Serres, Napoli, GR)

Objective: During the last decade, carbapenem-resistant Acinetobacter baumannii isolates are increasingly isolated; in the ICUs of many regions worldwide such isolates currently represent the vast majority of A. baumannii recovered from hospital infections. The aim of the present study was to analyse the genetic relatedness of multidrug resistant A. baumannii isolates recovered from ICU patients in different regions in Greece.

Methods: One hundred A baumannii isolates that were derived from 2001 to 2009 from 10 hospitals located in four different geographical regions in Greece were included in the study. Antimicrobial susceptibilities to carbapenems were determined by the reference agar dilution method. The isolates were tested by PFGE and sequence-based typing (ST) using ompA, cseL and blatOXA-51-like sequences.

Results: Eighty-one (81%) of the isolates were carbapenem-resistant. Eleven different ST-types were revealed. Thirty-four isolates (34%) belonged to ST-group 2 (corresponding to EU clone I), 55 (55%) to ST-group 1 (EU clone II) and the remaining 11 were sporadic isolates
Differentiation of Austrian \emph{Salmonella} serotypes using high-resolution melting curve analysis

\textbf{J. Zeinzinger}, A. Stöger, C. Kornschober, R. Mach, F. Allerberger, W. Ruppitsch, A. Pietzka (Vienna, AT)

\textbf{Objectives:} Effective epidemiological surveillance requires the accurate subtyping of strains. The standard method for differentiation of \emph{Salmonella} strains is serotyping. Despite the utility of serotyping, testing with a complete set of sera is time consuming and requires a well-trained technician; problems associated with antiserum production and occurrence of strains for which a serotype antigen cannot be detected prompted reference laboratories to pursue molecular approaches for serotyping.

The aim of this study was to assess the usefulness of high-resolution melting (HRM) curve analysis on the LightCycler 480 PCR system as a tool for accurate and fast molecular typing of \emph{Salmonella enterica} subsp. \emph{enterica} strains.

\textbf{Methods:} A collection of \emph{Salmonella} isolates representing diverse serotypes was recently analysed using Amplified Fragment Length Polymorphism (AFLP) (1). A phylogenetic cluster comprising the serotypes Blockley, Vorchow, Braenderup, Manhattan and Muenchen was chosen to evaluate the potential of HRM analysis for molecular typing. A 171 bp fragment of the gyrB gene (gyrB) was amplified for HRM curve analysis on a LightCycler 480 instrument (Roche Diagnostics, Penzberg, Germany).

\textbf{Results:} HRM curve analysis of a 171 bp amplicon of the gyrB gene resulted in five different melting curves (Figure 1), and thus allowed the rapid and accurate discrimination of the investigated serotypes.

\textbf{Conclusion:} HRM analysis is a new single-step closed-tube screening method for fast mutation detection and can therefore be used to discriminate even genetically closely related samples. HRM analysis has the potential to complement the classical serotyping of \emph{Salmonella} isolates due to its discriminatory power and simplicity.

Reference(s)


\textbf{O103} Direct high-resolution genotyping of \emph{Chlamydia trachomatis} positive swabs from women in Southampton using ompA and three variable-number tandem repeats

Y. Wang, R. Skilton, E. Andrews, I. Clarke, P. Marsh* (Southampton, UK)

\textbf{Objectives:} Genital chlamydial infection is the commonest diagnosed sexually transmitted infection in the UK. \emph{Chlamydia trachomatis} infections are caused by strains which fall into two pathovars: ‘serovars’ ophthalmogranuloma venereum (LGV) and \emph{C. trachomatis} inogenitalis, which may reflect backgrounds of particular demographics relating to age group, geography, high-risk sexual behaviour, and sexual networks.

\textbf{Methods:} 162 endocervical swabs were taken at the Southampton GUM clinic and tested by routine diagnostic PCR for the presence of \emph{C. trachomatis}. Positive samples were genotyped by use of a variable number tandem repeat (VNTR)-ompA sequencing technique. Isolates were cultured from the positives where possible.

\textbf{Results:} Of the 162 samples, 86 were fully typed by VNTR-ompA. Only one mixed infection (E & F) in one sample was confirmed. The commonest genotypes were D, E & F, comprising 20%, 45% and 15% of the genotyped positives respectively. Within each of these genovars there were multiple VNTR sub-types. 69 of the swabs yielded culturable isolates able to passage multiple times.

\textbf{Conclusions:} This is the first comprehensive fine molecular epidemiology genetic typing survey of \emph{C. trachomatis} in the UK. Amongst the common genotypes, there are a significant number of defined sub-types, which may reflect backgrounds of particular demographics relating to age group, geography, high-risk sexual behaviour, and sexual networks.

\textbf{O104} Comparison of \emph{Listeria monocytogenes} strains from food and human origin by amplified fragment length polymorphism


\textbf{Objectives:} \emph{Listeria monocytogenes} is a foodborne pathogen, responsible for neurological, systemic and gastro-intestinal disease with a mortality up to 30%. For the investigation of \emph{L. monocytogenes} epidemiology highly discriminatory typing methods are needed. The aim of our study was to develop an Amplified Fragment Length Polymorphism (AFLP) for \emph{L. monocytogenes}, to analyze isolates from clinical human and food origin and determine the possibility of differentiation between human and food isolates by AFLP.

\textbf{Methods:} Based on genome sequence analysis we selected restriction enzyme combination HindIII-G and HpyCHV4-C. With this combination, a collection of 279 \emph{L. monocytogenes} strains was typed, consisting of 168 human clinical isolates from the Netherlands Reference Laboratory for Bacterial Meningitis (RBM), 111 food isolates from the Food and Consumer Product Safety Authority (VWA), 3 complete genome sequenced strains (ATCC BAA-679 (=EGDe), F2365, HCC23) and \emph{L. monocytogenes} type strain ATCC 15313. As such, this \emph{L. monocytogenes} collection is one of the largest collections in the world comparing both clinical and food isolates.

\textbf{Results:} AFLP patterns of the 279 \emph{L. monocytogenes} isolates were grouped in two major clusters and a few individual isolates. Cluster I included 100 human isolates and 37 isolates of food origin. The human
cluster I isolates mainly consisted of the virulent serotype 4b (63/100, 63%) and serotype 1/2b (14/100, 14%). The cluster I isolates originating from food consisted mainly of serotype 1/2b (15/37, 40.5%). These food isolates formed a subcluster within cluster I. Cluster II included 68 human and 74 food isolates, mainly serotype 1/2a (69.1% and 35.1%, respectively).

**Conclusion**: AFLP allows discrimination of *L. monocytogenes* in two major clusters. The two clusters show segregation of the virulent 4b serotype into AFLP cluster I, whereas serotype 1/2a predominates in AFLP cluster II. Within cluster I, it is possible to differentiate most food 1/2b isolates from human isolates.

**O105** Investigation of an outbreak of CTX-M-15-producing *Escherichia coli* of sequence types 131 and 1441 in a neonatal surgical ward: comparison of typing methods
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**Objectives**: The spread of *E. coli* producing the CTX-M-15-type of extended-spectrum β-lactamase (ESBL) was ongoing in a surgical ward caring for newborns since at least, September 2008 and was finally recognised in late December. Various typing methods were applied and compared with pulsed-field gel electrophoresis (PFGE) to verify the outbreak and to determine the number of affected children.

**Methods**: Subsequent to clinical sampling, 125 children hospitalised September-December were screened for ESBL-bacteria in stool. January-June 2009, newly admitted children were screened at admission and twice weekly. 51 ESBL- *E. coli* isolates were detected in 26 children, of which 6 later were found to carry isolates of several PFGE-types. The 51 isolates were typed by PFGE, multiple-locus-variable number tandem repeat analysis (MLVA), a “mini” multiple-locus-sequence typing (mMLST) method (fumC, purA and dnaJ genes) and by Phene Plate (PnP) biochemical fingerprinting.

**Results**: When the outbreak was revealed, five children had developed infections with ESBL- *E. coli* of two PFGE-types, A (ST 131) and B (ST 1441), later determined to be the outbreak strains. One or both types spread to a total of 21 children. Altogether, 38 isolates (20 children) were of type A and 7 isolates (5 children) of type B. In addition six children carried isolates of six distinct PFGE-types (C-H), only found in one child each. MLVA generated the same strain differentiation profile as PFGE. mMLST accurately detected the same STs of PFGE-types as detected by standard MLST (http://mlst.ucc.ie/mlst/dbs/Ecoli), although it did not differentiate ST 131 isolates of different PFGE-types (A and C). PfP-typing differentiated isolates such that little correlation was observed with PFGE. By monitoring resistance patterns of isolates we could not predict the identity of isolates.

**Conclusion**: If transmission is ongoing for an extended time period, several types of ESBL-producing bacteria may be detected in an outbreak and all isolates, including screened as well as repeat isolates, should be typed to identify affected patients. Only genetic methods gave satisfactory typing results in investigating this outbreak. MLVA generated identical results as those of PFGE and is, thus, attractive, being faster, less-costly and producing results that are easier to communicate. The mMLST, although accurately detecting the STs, despite using only three house-keeping genes, was less discriminatory than PFGE or MLVA.

**O106** Deep sequencing for accurate and high-throughput HPV genotyping in clinical samples

**Objectives**: Human papillomavirus (HPV) typing is useful for studies on HPV transmission, natural history, pathogenesis, and prevention and for clinical management of HPV-related lesions. HPV typing methods based on Sanger sequencing or reverse hybridization show poor accuracy in multiple infections. Moreover, discordant results have been reported when using different typing methods even in single infection. Aim of the study was to develop an HPV typing method based on 454 Life-Sciences ultradeep pyrosequencing in order to dissect the contribution of each HPV type in multiple infections and to identify possible HPV sequence variants.

**Methods**: A group of 50 HPV-DNA positive cervical samples, including 40 with multiple infections, were selected for deep pyrosequencing. For each cervical sample, a library of amplicons targeting a conserved region of HPV-L1 was generated and sequenced in multiplex reactions on a 454 Life-Sciences platform. Multiple alignment of sequences was performed with ClustalW2, followed by clustering analysis based on sequence identity (Jalview 2.4). A representative sequence was selected for each cluster and aligned with the non redundant database of nucleotide sequences, in order to identify either multiple infections or contaminant genomic DNA. Results from deep sequencing were compared with Sanger sequencing and with the Inno-LiPA HPV genotyping test.

**Results**: An overall analysis of results showed the sensitivity of HPV deep sequencing was higher than other typing methods, since it could detect HPV types representing less than 1% of sequences in multiple infections, at variance with Sanger sequencing, which failed in most cases of multiple infection, and the Inno-LiPA assay, which could not detect HPV types representing less than 8% of sequences in multiple infections nor those not included in the probe set. Moreover, deep sequencing allowed identification of unclassified HPV types and detection of HPV sequence variants within types.

**Conclusions**: Deep sequencing may be a sensitive and accurate high-throughput method for HPV genotyping in clinical samples.

**Antifungal therapy under the microscope: from fungus to mouse to man** (Symposium supported by Gilead)
J. Adler-Moore* (Pomona, US)

Clinical outcomes from invasive fungal infections involve a complex interplay between the infecting organism, antifungal treatment and the host immune response. Factors such as the host's neutropenic status are well known to influence outcome and may be of particular relevance if the antifungal treatment is fungistatic rather than fungicidal, but the immune response involves far more than neutrophils alone. Cytokine changes may correlate with both clinical response and clinical failure. In this symposium the faculty will show how changes in *in vitro* may correlate with responses *in vivo* in animal models and therefore predict the response in the human host.

**MRSA: from molecular epidemiology to molecular screening** (Symposium supported by Roche Molecular Diagnostics)

**S108** Do animal models help predict host responses to fungal infections and antifungal treatments? Choosing therapy on the basis of efficacy not safety
J. Adler-Moore* (Pomona, US)

Clinical outcomes from invasive fungal infections involve a complex interplay between the infecting organism, antifungal treatment and the host immune response. Factors such as the host's neutropenic status are well known to influence outcome and may be of particular relevance if the antifungal treatment is fungistatic rather than fungicidal, but the immune response involves far more than neutrophils alone. Cytokine changes may correlate with both clinical response and clinical failure. In this symposium the faculty will show how changes in *in vitro* may correlate with responses *in vivo* in animal models and therefore predict the response in the human host.
Selection of efficient primers and probes is complicated by the known sequence diversity among the various types of SCCmec cassettes. As a consequence, primer and probes are designed to cover the most common SCCmec types encountered in clinical MRSA isolates. Considering the enormous diversity of SCCmec sequences, rational primer selection can only be a best compromise between the coverage of as many SCCmec variants as possible and losing analytical sensitivity due to primer multiplexing problems. Therefore incrustivity rates may differ among the various PCR assay concepts.

Methods: Three commercial PCR tests targeting the SCCmec-orfX junction were evaluated for analytical sensitivity, time-to-result and for their performance to cover animal-associated MRSA strains of the clonal complex CC398 next to human epidemic MRSA strains.

Results: With exception of MRSA strains harboring “uncommon” SCCmec elements, all of the investigated human epidemic and animal-associated MRSA strains were detected by the Roche LightCycler MRSA Advanced Test, but the latter strains presented with a different Tm-value in melting curve analysis. DNA sequencing revealed single-nucleotide polymorphisms (SNPs) within the S. aureus orfX region characteristic for MRSA CC398 strains, which are obviously covered by the proprietary sensor hybridization probe of the assay. All MRSA strains covered by the LightCycler MRSA Advanced Test also tested positive in the BD GeneOhm MRSA and the Cepheid Xpert MRSA test, but either these real-time PCR tests had no option to perform Tm-analysis or viewing of melting curves.

Conclusions: As a practical application of the newly identified SNPs, we present the use of this commercial real-time PCR test for the direct detection and simultaneous identification of animal-associated MRSA strains. All of the investigated MRSA CC398 strains harbored at least one of the novel SNPs in the SCCmec-orfX junction – represented by a characteristic Tm of 55.5°C in subsequent melting curve analysis. Since such a Tm-shift was not observed with any non CC398 MRSA strains yet, it may serve as a molecular marker for the presence of MRSA CC398.

Antibacterial susceptibility testing and implications for resistance surveillance and treatment

Problems with low level resistance against quinolones

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Bacterial resistance to quinolones is related to decreased permeability, active efflux, drug modification, target modification or target protection. Recent studies indicate that certain genes (recA, recC, tolC, fis, ruvC, xseA, xseB) also contribute to the intrinsic resistance of E. coli to quinolones. Microbiological and clinical aspects of low level quinolone resistance have been more often studied in enterobacteria. In these organisms, a single gyrA mutation causes resistance to nalidixic acid and MICs of fluoroquinolones as low as 0.125–0.25 mcg/ml (still higher than MICs of <0.008–0.06 mcg/ml for wild-type isolates). This mechanism favours the appearance of additional mutations in gyrA or in other topoisomerase-encoding genes, finally resulting in high level resistance. Target protection by Qnr proteins (often encoded by plasmid genes), decreased permeability by porin modifications or active efflux of chromosomal (particularly RND transporters) of plasmid (QepA proteins, QepAB) origin also determine low level quinolone resistance. The Aac(6′)-Ib-cr enzyme modifies quinolones with a piperazinyl substituent. Both in vitro and in vivo data suggest that these additional low-level mechanisms may also represent an initial step for acquisition of increased resistance. Low level resistance mechanisms may be difficult to detect because they translate into MICs below current EUCAST or CLSI breakpoints. Interestingly, plasmid-mediated mechanisms may not sufficiently compromise the activity of nalidixic acid, which results in decreased susceptibility or low-level fluoroquinolone resistance in the absence of nalidixic acid resistance, which is in contrast with the usual consequences of mutations in topoisomerase genes. As quinolone efficacy is related to Cmax/CMI and AUC/CMI parameters, small variations (of even only 2–4 dilutions) due to low-level resistance mechanisms may contribute to therapeutic failure. Animal models and clinical data suggest a poor outcome of patients with severe infections caused by Salmonella, Klebsiella (and presumably other enterobacteria) with low level fluoroquinolone resistance. Because of these reasons, it would be important to know actual MICs of quinolones for clinical isolates, and to obtain additional information on quinolone resistance mechanisms. This will allow a better knowledge of risk factors for acquiring low level resistant strains, and a better definition of the actual therapeutic relevance of these organisms.

Evolution and epidemiology of β-lactamases in Enterobacteriaceae

Problems with low level resistance against glycopeptides

A. Soriano* (Barcelona, ES)

The emergence of methicillin-resistant Staphylococcus aureus (MRSA) strains has complicated the treatment of S. aureus infections. Vancomycin is currently a cornerstone in the treatment of bacteremia and infectious endocarditis (IE) due to this pathogen, but evidence linking vancomycin minimum inhibitory concentration (MIC) of 4–8μg/ml to a high failure rate of vancomycin has led to the susceptibility breakpoint being considered when the MIC is ≤2μg/ml. However, vancomycin treatment failure is not uncommon even when MRSA strains are fully susceptible (MIC ≤2μg/ml), and studies have described a reduction in vancomycin efficacy against MRSA strains with high MIC but within the susceptible range. The presentation will deal with the different methods for determining the vancomycin MIC and discuss the implications of understanding the relationship between vancomycin MIC and vancomycin efficacy.

Evolution and epidemiology of β-lactamases in Enterobacteriaceae
Emerging resistance mechanisms in ESBL-producing strains in Europe. Delivery of crucial health services in hospitals and in the community is at stake.

**Objective:** ESBL producing strains are increasingly reported to present additional resistance mechanisms. These multidrug resistant strains should be detected early to rationalize drug treatment and avoid increased selection of resistance. The aim of this study was to detect the presence of AmpC, carbapenemases and plasmid-mediated quinolone resistance (PMQR) (qnr, aac(6’)-Ib-cr and qepA) mechanisms in ESBL-producing strains by genotypic assays and compare their efficiency versus phenotypic methods.

**Methods:** ESBL- and AmpC-producing strains were identified by the double-disk test and double disk synergy test, respectively. Carbapenemases were phenotypically detected by the Hodge test. MIC of fluoroquinolones was detected by Etest. AmpC, carbapenemase, qnr, aac(6’)-Ib-cr and qepA genes were identified by multiplex PCR and sequencing. Topoisomerase II mutations were detected by sequencing of the quinolone-resistant determining region.

**Results:** In 2009, 200 ESBL-producing Enterobacteriaceae isolates were collected at the Microbiology Unit of the Padua Hospital. ESBL belonging to different classes (TEM, SHV, CTX-M and OXA) were characterized by genotypic analysis. Qnr and aac(6’)-Ib-cr genes were found in 26% and 8% isolates, respectively. Qnr was mostly present in Klebsiella pneumoniae, while aac(6’)-Ib-cr was found exclusively in Escherichia coli. QepA was not found. Both genes were localized on plasmids and could be both transformed and trans-conjugated in acceptor strains. MIC of fluoroquinolones on these acceptor strains indicated a 20–100 increased resistance due to the plasmid-mediated mechanism. However, high-level resistance to fluoroquinolone in the wild-type strains was due to the additional presence of topoisomerase mutations in strains presenting both ESBL and PMQR. AmpC were detected in 5.5% isolates of Enterobacter spp. and Proteus mirabilis. Carbapenemases were found in 3% isolates of E. aerogenes, E. coli and K. pneumoniae. Carbapenemases were subsequently genotypically characterized as IMP, VIM, OXA, KPC CMY or SME types.

**Conclusions:** Emerging resistance mechanisms were found in ESBL-producing strains, with PMQR being the most frequent. While genotypic assays implement phenotypic testing of AmpC and carbapenemases, they are the only methods available up to date for detection of PMQR. Hence, both phenotypic and genotypic methods should be employed to rationally direct the pharmacological treatment.

**Objective:** The changing epidemiology of carbapenem-resistant Enterobacteriaceae carriage in hospitalized patients

**Background:** Klebsiella pneumoniae (KP) ranks second as cause of Gram-negative sepsis at our medical center and forty five percent of the isolates display an extended spectrum β-lactamase producer (ESBL) phenotype. Starting in January 2006, the prevalence of carbapenem-resistant (CR) KP isolates increased significantly. Similar trends have been recorded worldwide.

In April 2006, an extensive infection control program was started in our medical center. In 2008 this program included surveillance to identify potential carbapenem-resistant Enterobacteriaceae (CRE) carriers among asymptomatic hospitalized patients being contacts of patients with KP-CR clinical infection and all patients admitted to the general ICU and to the hemat-o-ncology wards. The present study describes the results of this program.

**Methods:** Rectal swabs were obtained weekly and plated on KPC selective agar. Suspected colonies were identified by Vitek II system. Susceptibility testing for imipenem, meropenem, and ertapenem was performed using E-test (AB Biodisk) in accordance with the manufacturer’s instructions. The molecular mechanism underlying resistance to carbapenems was assessed by PCR amplification of blaKPC and KP specific genes directly from bacterial isolates.

**Results:** During a 22-month period we assessed 8650 samples from 3239 patients (1810 patients in 2008 and 1429 in 2009). Of the 105 CRE carriers identified in 2008 (5.8% of patients tested), 100 (95.2%) were KP-CR carriers and 5 (4.8%) were CR Enterobacter sp. and/or E. coli sp. carriers. As the carrier rate decreased in 2009 (40 of 1429 tested patients, 2.8%; p < 0.001) the proportion of CRE carriers other than KP-CR increased significantly (11 of 40 positive patients, 27%; p < 0.001).

All of CRE isolates were found to carry blaKPC gene.

**Conclusions:** Our results show that during the present outbreak of CR-KP, a large number of hospitalized patients considered at risk are asymptomatic carriers and certainly constitute a major reservoir for the nosocomial spread of the organism. The presence of multiple CRE isolates suggests transfer of the genetic element encoding this β-lactamase between Enterobacteriaceae species in the gastrointestinal tract.
Impact of EUCAST breakpoints on susceptibility levels of nosocomial Gram-negatives in Belgium


Objectives: The implementation of EUCAST breakpoints was simulated on the susceptibility rates of isolates from 8 teaching hospitals in Belgium, collected from 1998 to 2002 as part of the MYSTIC study, against 5 antibiotics.

Materials and Methods: E-tests were used on 6993 unduplicated Enterobacteriaceae (EB) and 2409 *P. aeruginosa* isolates collected over a ten year surveillance study from patients admitted in ICU, hematology and general wards. Results were analysed using both CLSI and the new EUCAST breakpoints.

Results: Among the EB (n=6993), susceptibility rates according to CLSI and EUCAST breakpoints did not significantly decrease for meropenem (MEM); 99.6% and 99.1% respectively. A significant decrease in susceptibility rates (P<0.0001) was seen for cefazidime (CAZ): 83.8% to 75.5% (P<0.0001), for cefepime (CPE): 96.9% to 88.0% (P<0.0001), for pip/tazo (TAZO): 84.1% to 78.4% (P<0.0001) and for ciprofloxacin (CIP): 83.1% to 80.2% (P<0.0001).

Susceptibility rates for *E. aerogenes* isolates (n=766), among which TEM-24 and SHV-4 ESBL-producing isolates, decreased from 94.0% to 77.4% for CPE (P<0.0001) and from 54.1% to 32.4% for TAZO (P<0.0001) using CLSI and EUCAST criteria respectively; susceptibility rates for MEM did not decrease significantly and remained high at 96.3% and 94.2% respectively.

After implementation of EUCAST breakpoints, susceptibility rates of *P. aeruginosa* (n=2409) for CAZ and CPE were not affected: 72.3% and 61.2% respectively. MEM remained the most active agent against *P. aeruginosa* though a decrease in susceptibility was observed from 81.6% to 75.2% (P<0.0001). The activity of TAZO is affected the most with a decrease in susceptibility from 80.4% to 69.3% (P<0.0001).

Conclusions: When implementing EUCAST breakpoints carbapenem activity against EB does not change whereas an important decrease in susceptibility from 80.4% to 69.3% (P<0.0001) using CLSI and EUCAST criteria respectively; susceptibility rates for MEM did not decrease significantly and remained high at 96.3% and 94.2% respectively.

Characteristics of the multi-resistant bacteria that actually diffuse in the Centre region, France, in and out of healthcare institutions

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Objectives: Epidemiological study involving the teaching hospital, 20 general hospitals, 7 local hospitals, 16 private clinics, 12 rehabilitation-care centers, 5 psychiatric clinics, 30 nursing homes (NHs) and 19 in town clinics (17 inpatients, 2 outpatients), to document the diffusion of multiresistant bacteria (MRB) into the region (2.8 millions inhabitants).

Methods: During 15 days, all MRB isolated from diagnostic clinical samples were documented and strains were centralized. After identification control, antibiotic susceptibility testing was performed (standard procedures). Genetic diversity of strains was studied (PFGE).

Results: The study involved 346,251 patient-days and 244,091 resident-days. During the study, 43,379 diagnostic clinical samples were performed: 7,564 blood cultures, 2,130 deep pus, 1,054 respiratory tract samples, 17,768 urines, 606 intravenous devices, 12,889 superficial pus. From the 43,379 clinical samples, 281 MRB were obtained (0.6%): 56% from urine (1.5% of urine samples), 23% from superficial pus (0.6% of pus), 9% from respiratory tract (5% of respiratory tract samples), 5% from deep pus, 4% from blood and one from intravenous devices.

MRB belonged to 14 species. *S. aureus* (36%) and *E. coli* (31%) predominated, followed by *E. cloacae* (9%), *P. aeruginosa* (8%), *K. pneumoniae* (5%) and *A. baumannii* (2%). Vancomycin-resistant *E. faecalis* or *E. faecium* were not recovered. Diversity was the highest in healthcare institutions (HCIs). By contrast, *S. aureus* predominated in NHs. *E. coli* among outpatients. 70% of MRSA strains were non-multiresistant (usually named CA-MRSA). 79% of ESBL-producing *E. coli* strains were CTX-M. MRSA and ESBL-producing *E. coli* strains were (1) mostly resistant to fluoroquinolones (93 and 60% respectively), (2) genetically diverse and distinct from clones classically spreading into HCIs, (3) widely spread in HCIs, NHs and outpatients, (4) responsible for rare outbreaks, but in NHs. *E. cloacae*. *K. pneumoniae*, *P. mirabilis* and *A. baumannii* were the most involved in outbreaks into HCIs, and were associated with a lower genetic diversity.

Conclusion: MRD are unfrequent, but their diffusion is large, especially for recent MRSA and ESBL-producing *E. coli* clones. Prevalence is the highest into HCIs, but MDR diffuse now out of HCIs, and especially in NHs.

We suggest that an effective alert system to detect emerging and/or epidemic phenomenon should involve MDR survey in HCIs, NHs and in town-clinical laboratories.

Antimicrobial susceptibilities of Gram negative bacteria and antibiotic consumption in a Greek tertiary hospital, 2001–2008

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Objective: To examine differences in antibiotic susceptibility of Gram negative bacteria and in antibiotic consumption in a Tertiary Hospital, within 7 years of operation.

Methods: All clinical samples from inpatients. Identification and susceptibility testing, using the Wider® semi-automated system with CLSI breakpoints. Antibiotic consumption expressed as Defined Daily Doses (DDD) per patient-day.

Results: 1550 and 706 isolates identified during 2008 and 2001, respectively.

*E. coli* non-susceptibility rates were significantly higher in 2008 for Cefotaxime (12.5%; 69/551 isolates vs. 4.5%; 21/266 in 2001), Cefepime (14.9%; vs. 3.8%); Cotrimoxazole (31.2% vs. 18.4%); Gentamicin (9.6% vs. 3.7%); and Ciprofloxacin (21.6% vs. 3.3%) (for all, p<0.01).

*K. pneumoniae* non-susceptibility increased significantly for Cefotaxime (55.1%; 97/176 isolates in 2008 vs. 35.6%; 21/59 in 2001), Cefturoxime (58.5% vs. 31.8%); Cotrimoxazole (51.1% vs. 18.6%); Cefepime (53.4% vs. 5.1%); and Ciprofloxacin (51.7% vs. 13.2%) (for all, p<0.01).

*P. aeruginosa* non-susceptibility increased for Gentamicin (26.5%; 61/230 in 2008 vs. 13.1%), Piptazo (15.2% vs. 10.9) and Cefepime (25.6% vs. 16.3%). In 2008, non-susceptibility rates to anti-pseudomonal antibiotics ranged from 18.2% (Meropenem) to 26.1% (Ciprofloxacin). *A. baumannii* non-susceptibility increased significantly for Piperacillin (82.2%; 180/219 isolates vs. 37.8%; 17/45, p<0.01). In 2008, non-susceptibility rates ranged from 52.1% (Cefepime) to 86.6% (Ciprofloxacin).

Pan-Drug Resistant (PDR) – to B-lactams, Carbapenems, Amikacin, Ciprofloxacin and Colistin) bacteria isolated in 2008: *Klebsiella* (12), *A. baumannii* and *P. aeruginosa* (1 each). No PDR isolates were found in 2001.

Consumption of antibiotics with activity against Gram negatives increased by 30.3% (15.9 DDD/100 hospital-days in 2008 vs. 12.2 in 2001). Increase was more marked for Carbapenems (3.2 vs. 1.1; p<0.03), Fluoroquinolones (6.4 vs. 4.3) and Colistin (0.05 vs. 0.03), whereas decreased was the consumption of 3rd Generation Cephalosporins (2.1 in 2008 vs. 2.3 in 2001) and the anti-pseudomonal penicillins (3.8 vs. 4.0).

Conclusion: Non-susceptibility rates of Gram negative bacteria markedly increased within 7 years and PDR strains emerged. This paralleled the increased consumption of wide-spectrum antibiotics (mainly Carbapenems and Fluoroquinolones) and of antibiotics used as last-resource (Colistin).
Recent epidemic emergence of blaNDM-1 metallo-β-lactamase in enteric organisms from India is mostly linked to A/C plasmids

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Objective: Metallo-β-lactamases are powerful resistance mechanisms that can generate insensitivity to virtually all β-lactam antibiotics. The recent epidemic emergence of this resistance mechanism in Klebsiella spp., E. coli, Enterobacter cloacae, Citrobacter freundii and Providencia rettgeri in geographically distant areas of India and the UK is a major cause for concern. This project was initiated to determine the genetic vehicle(s) responsible for the rapid emergence and dissemination of the blaNDM-1 MBL in enteric organisms.

Methods: Species identification and antibiotic susceptibility profile of 67 blaNDM-1 harbouring enteric isolates collected from Chennai (south India) and Haryana (North India) was performed using the Phoenix machine. Isolates were typed by pulsed field Gel electrophoresis after XbaI digestion. Plasmids were visualized by ethidium bromide staining following PFGE of SI partially digested plags. Plasmids carrying blaNDM-1 were further identified by probing of the same gels using a 32P labelled blaNDM-1 and A/C rep probes. Transconjugants were selected following matting with J53 on MacConkey plates containing azide and 0.5 mg/L meropenem. Plasmid analysis on A subset of transconjugants (20) was performed by replicant typing and SI PFGE and subsequent probing. A/C plasmid analysis was further performed using a set of 12 primers designed to amplify sections of the backbone of A/C plasmids and DNA probing with A/C probes.

Results: All isolates from the North of India were Klebsiella pneumoniae and carried A/C plasmids of size 50kb (9), 80–90kb (2), or 118kb (11). However, in the south of India isolates were of various enteric species and gave numerous different pulsed field gel restriction types. Furthermore plasmids found in the isolates from the south were of many different sizes ranging from 100kb to 375kb in size. Probing indicated that most plasmids carrying blaNDM-1 were of rep A/C type (19/20) only 1/20 tested were found to be carried on the F plasmid. Transconjugants were selected for all strains except the small plasmids from the North of India. Transconjugants gave plasmids of mostly the same size but examples were found of size changes following transconjugation including both increasing and decreasing size. PCR on transconjugants and parents indicated changes in the A/C plasmid backbone.

Conclusions: blaNDM-1 emergence in enteric organisms in India is linked mostly to A/C plasmid types of varying sizes ranging from 50kb to 375kb.

Risk factors for intestinal carriage of Enterobacteriaceae with extended-spectrum β-lactamase-producing phenotype on a medical ward


Background: Intestinal carriage is a reservoir for invasive infection with ESBL producing Enterobacteriaceae (ESBL PE) and their dissemination. The aim of the study is to establish the risk factors for intestinal carriage in patients admitted on a medical ward with infectious and noninfectious diseases.

Method: A prospective study conducted between 1st Aug and 31st Oct 2009 on patients hospitalized for more than one week. Patients were screened on discharge (convenience sample). Rectal swabs were placed in 1 ml sterile 0.9% saline then inoculated on cultured media Chrom ID ESBL Biomerieux. The results were confirmed with double disc diffusion assay according to CLSI. Univariate and multivariate analyses were performed.

Results: 153 patients were screened (46% male, median age 53.8 years) from which 129 patients (84%) were admitted for infectious diseases. 64 ESBL PE were isolated (carrier rate 41.83%). ESBL PE included: E. coli (39), Klebsiella spp. (21), Proteus spp. (2), Serratia spp. (2). Variables associated with ESBL PE carriage by univariate analysis: length of stay (p = 0.03), length of antibiotic use (p = 0.02), use of ceftriaxone (p < 0.01), use of ciprofloxacin (p = 0.003). In multivariate analysis, only length of stay (p = 0.004) and use of ciprofloxacin (p = 0.001) were independently associated with carriage of ESBL PE.
Risk factors of death among hospitalized patients with tuberculosis: a report from Iran

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Method:
The retrospective study was carried out at the National Research Institute of Tuberculosis and Lung Disease (NRITLD) in Tehran, Iran from May 2003 to Dec 2009. Patients with documented pulmonary TB were included. A death case is considered as a case that died during the treatment of TB from any causes. Data was gathered from medical records and compared between two groups of patients who died and the group who didn’t die during their treatment. These variables include age, sex, nationality, history of smoking and opium, HIV status, history of TB treatment, co-morbidity, symptoms and sign of TB, cavitary lesion, and other demographic, clinical and radiological factors. All data were entered into SPSS (Version 15.0). The Cox-proportional hazard model was used for the significant factors with survival.

Results:
In this study, 1897 tuberculosis patients were included. The mean age was 50.18±21.13 years and 54±20 in all patients and in death group respectively, a difference that was statistical significant. 973 were male (51.3%) and 76.8% of the patients were Iranian and the remaining 440 (23.2%) were from the neighboring countries. During the hospitalization, 163 (8.6%) patients died. The mean duration of admission was 34±36.8 days (Median = 22 days, Range 1–365). Totally among whom HIV test was performed, 32 (22.2%) cases of the death group and 82 (14.3%) of the control group were found to be HIV positive that reach statistical significance.

The mean duration of symptoms to admission was 8.27±16.79 months. Notably, cough, dyspnea, and fever were more commonly seen in death group (P <0.05).

During the course of treatment, 231 (12.2%) developed drug-induced hepatitis that 45 (19.5%) of the patients died (p <0.05). In χ² analysis, male sex, Iranian nationality, opium addiction, HIV positive status, concomitant respiratory and immunosuppressive diseases and MDR-TB were statistical significant in death group.

In the stepwise Cox regression model, is showed that TB history, smoking, co-morbidity, involvement of lung, cavitary lesion, Drugs induced hepatitis, WBC <4000 and >10000 and age >65 affected the in-hospital mortality rate (Table 1).

Conclusion: Identifying these risk factors may improve clinical outcome of patients.

Table: Cox-proportional hazard model of factors

<table>
<thead>
<tr>
<th>Multivariate logistic regression</th>
<th>Crude HR</th>
<th>HR</th>
<th>95% CI</th>
</tr>
</thead>
<tbody>
<tr>
<td>TB history</td>
<td>2.270</td>
<td>1.562</td>
<td>1.023–2.383</td>
</tr>
<tr>
<td>Smoking</td>
<td>0.538</td>
<td>0.621</td>
<td>0.443–0.871</td>
</tr>
<tr>
<td>Co-morbidity</td>
<td>0.326</td>
<td>0.424</td>
<td>0.295–0.610</td>
</tr>
<tr>
<td>Involvement of lung</td>
<td>0.899</td>
<td>0.498</td>
<td>0.311–0.798</td>
</tr>
<tr>
<td>Cavitary lesion</td>
<td>1.650</td>
<td>1.379</td>
<td>0.960–1.980</td>
</tr>
<tr>
<td>DII</td>
<td>2.155</td>
<td>1.592</td>
<td>1.112–2.282</td>
</tr>
<tr>
<td>WBC</td>
<td>1.425</td>
<td>2.169</td>
<td>1.555–3.027</td>
</tr>
<tr>
<td>Age &gt;65</td>
<td>1.896</td>
<td>1.688</td>
<td>1.165–2.445</td>
</tr>
</tbody>
</table>

Clinical mycobacteriology

Conclusions: ESBL PE carriage rate after hospitalization and treatment in our medical ward is high. Length of stay and use of ciprofloxacin are important risk factors for intestinal carriage with ESBL PE.

The aim of this study is to describe the prevalence of tuberculosis and non-tuberculous mycobacteria isolates in paediatric patients during a two year period (November 2007 to November 2009) in a health district of Madrid (Spain).

Methods: Four hundred and ninety eight specimens from paediatric patients were processed for mycobacterial study. All of them were prepared for auramine stain and decontaminated by NaOH-N-acetylcyesteine method. When the specimen was a gastric acid, it was neutralized before with bicarbonate of sodium. After decontamination each specimen was cultured in liquid and solid medium (MIGT and Coletos, respectively). If growth was detected a Ziehl-Neelsen stain was done. Accuprobe kit (Gen-Probe) was used to identify Mycobacterium tuberculosis Complex or Mycobacterium avium Complex strains. Other Non Tuberculosis Mycobacteria (NTM) were identified by solid hybridization using GenoType Mycobacterium kit (Hain Lifescience).

Results: Thirty two (6.42%) out of 498 specimens received were positive: 17 Mycobacterium tuberculosis Complex (53.13%), 9 Mycobacterium avium complex (28.12%), 4 Mycobacterium avium Complex (12.5%) and 2 Mycobacterium lentiflau (6.25%). They were obtained from different specimens from 22 patients:

- M. tuberculosis Complex: 14 gastric juice, 2 pleural liquid and 1 sputum.
- M. abscessus: 7 sputum, 2 bronchoalveolar lavage.
- M. avium Complex: 2 fine needle aspiration biopsies (FNAB), 1 gastric juice and 1 bronchoalveolar lavage.
- M. lentiflau: 2 FNAB

Five out of 22 patients were cystic fibrosis patients in 4 of them the microorganism isolated was M. abscessus. In the other one, M. lentiflau was recovered.

Conclusions: The most common specimens received were those of the respiratory tract, where M. tuberculosis was the most prevalent mycobacteria followed by M. abscessus. On the other hand in FNAB specimens the species isolated were M. avium Complex, and M. lentiflau. M. abscessus is the most common mycobacteria isolated in cystic fibrosis patients in this population during this period.

Seroprevalence of human immuno-deficiency virus infection among patients diagnosed with sputum smear positive pulmonary tuberculosis at an infectious diseases hospital, Kano, Nigeria

Y. Mohammed* (Kaduna, NG)

Objective: The main objective of the study is to estimate the HIV seroprevalence among patients diagnosed with sputum smear positive pulmonary tuberculosis (PTB).

Methods: In order to estimate the HIV seroprevalence one thousand six hundred and ninety-two (1,092) males (1,066) and females (626) patients aged 15 years and above, with no previous TB treatment that presented to the chest clinic with symptoms like cough, night sweats, fever, weight loss, chest pain etc, and whose initial sputum smears demonstrated acid fast bacilli (AFB) by direct smear sputum microscopy using Ziehl-Nelsen (ZN) stain at least two specimens in line with WHO recommendation. Each patient was offered confidential HIV testing accompanied by pre and post-test counseling accordingly. Those that agreed to be screened for HIV antibodies had blood sample taken for the test and performed according to the standard hospital practice and followed guidelines developed by the National HIV Rapid Test Algorithm using ELISA Test of Capillus, Genie 11 and Determine HIV kit.

Results: The overall HIV prevalence was 38%, of that value, male, accounted for 37% and females 41%. There was no statistical difference. However, the prevalence is 48% in the age group 25–34 years as
Different clinical isolates of *Mycobacterium tuberculosis* induced distinctive pulmonary inflammation in mice

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**Background:** *Mycobacterium tuberculosis* (Mt) is a virulent intracellular pathogen that infects and persists in host macrophages, resulting in granuloma formation and collagen deposition in the lung. The mechanisms that confer resistance to Mt or results in establishment of disease are poorly understood. Data from the literature suggest that differences in Mt virulence contribute to setting up of the disease. In order clarify this aspect, our purpose is to investigate the immune response and lung pathology in mice infected with Mt obtained from distinct clinical isolates. The isolates were recovered from patients with noncavitary (SV 009) or extrapulmonary (SV 068) active tuberculosis. 

**Methods:** Female Balb/c mice were infected intratracheally with 1×10^5 CFU/100 μL of Mt clinical isolates. Neutrophils and mononuclear cells recruitment to the lung were accessed by bronchoalveolar lavage at 30 days post infection and lung histology were evaluated on 30 and 60 days post infection.

**Results:** Mice infected with SV 068 showed 22% more neutrophils (9×10^3/mL) and 70% more mononuclear cells (6×10^3/mL) recruited to bronchoalveolar space 30 days post infection, when compared with mice infected with SV 009, 5×10^5 mL and 4.5×10^5 mL respectively. The histology analysis of lung tissue, demonstrated that animals infected with SV 068 present greater number of foamy macrophages containing aggregations of Mt, especially at 60 days post infection. Also, in this period, we observed the presence of more intense infiltrate of neutrophils in perivascular and perivascular spaces when compared with animals infected with SV 009.

**Partial Conclusion:** Our preliminary findings suggest that the host defense can vary accordingly to the type of clinical isolation, leading to a correlation between the virulence and the source of infection.

Infection of a knee joint with *Mycobacterium avium* in a patient with sarcoidosis

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**Objective:** Infections of osteoarticular tissue caused by *Mycobacterium avium* are reported in the literature but are still rare. *Mycobacterium avium* is found throughout the environment, the transmission is still unknown. Patients show a variety of symptoms and the septic process is insidious which is leading to a delay of diagnosis. Most patients reported on were immunocompromised. Potential treatments are either surgery, antituberculous drugs or both.

**Method:** We present a case of a 33 year old Caucasian male with a *Mycobacterium avium* infection of the knee joint.

**Results:** In March 2009, a 33 year old Caucasian male with previously documented sarcoidosis presented in a cancer university hospital with pain and swelling in the right knee joint. The patient underwent knee arthroscopy and consequently developed purulent knee arthritis and a lateral joint fistula. Repetitive debridements were performed. The histological examination of the resected tissues showed granulomatous inflammation. *Mycobacterium avium* was confirmed via culture. In addition to surgery the patient was treated with ethambutol, clarithromycin and rifabutin. The fistula persisted and therefore treatment was changed to air dressing. At the request of the patient he was sent to our specialist department for septic surgery. Repetitive debridements were started. Tissue samples revealed *Pseudomonas aerogenosa* and *Staphylococcus haemolyticus*. Tests for *Mycobacterium avium* were positive. Because of superinfection with the listed bacteria ethambutol was replaced by ciprofloxacin. The soft tissue quality improved. In August 2009 a ALT flap was transplanted. Postoperative progress was uncomplicated – the patient was discharged in September 2009. We recommended treatment with clarithromycin, ciprofloxacin and rifabutin for another 7 months. Mobilisation at full weight bearing as pain allowed was started at discharge. Definitive treatment options have to be reevaluated 6 months after last surgery. A total knee replacement in the case of negative microbiological tests is optional.

**Conclusion:** In immunocompromised patients with osteoarthritis the infection with ATM (atypical *Mycobacterium*) should always be considered. Treatment should include both: surgery and antituberculous drugs. Knowing the *in vitro* resistance of most ATM against antituberculous drugs, it’s debatable whether the superinfection of other bacteria is clinically relevant for the symptoms and should be treated with priority.

*Mycobacterium conceptionense* (M. fortuitum group) catheter-related bloodstream infection in an immunocompromised patient – necessity for antibiotic treatment after removing the central venous catheter?

A. Uschinsky*, D. Schobel, S. Zimmermann (Heidelberg, Baden-Baden, DE)

**Objective:** Atypical Mycobacteria can cause disease in both healthy and immunocompromised individuals. They can rarely cause disseminated infections. Nevertheless infections in immunocompromised patients by atypical mycobacteria are described.

**Results:** We report a case of a 54-year-old man with diffuse large b-cell lymphoma (DLBCL) stadium III E B of the stomach, proximal duodenum, axillary, inguinal and cervical lymph nodes after six cycles R-CHOP 14 and one cycle R-DHAP chemotherapy received via central venous catheter (CVC) who develops leucopenia and anemia. Blood culture reveals *Mycobacterium fortuitum*. On admission to our hospital several days later a blood sample reveals leucocytosis (10.97×10^3 cells/litre), low hemoglobin level (9.8 g/dl) and thrombocytosis (517×10^7 platelets/litre). The C-reactive protein level was 43.9 mg/l. The patient has no fever. Blood cultures taken simultaneously peripherally and via CVC reveal both *Mycobacterium conceptionense* (*Mycobacterium fortuitum* group). The CVC is removed, but routine culture is negative for Mycobacteria. Because of a sustained bacteremia for more than ten days and an underlying
immunocompromise antibiotic treatment with clarithromycin (500 mg twice daily) and amikacin (15 mg/kg once daily) is done for two weeks in accordance with the guidelines of the American Thoracic Society (ATS). A repeat blood culture after therapy is sterile.

**Conclusion:** In literature there are only few descriptions of invasive infections with rapidly growing *Mycobacterium fortuitum*. In a setting of underlying immunocompromised disease we treat bloodstream infection, advocate a duration of two weeks after having removed the catheter and review literature for the necessity for antibiotic treatment.

**O143** Human *Mycobacterium bovis* infection in Buenos Aires: epidemiology, microbiology and clinical presentation

**E. Cordova**, X. Gonzalo, A. Boschi, M. Lossa, M. Robles, S. Poggi (Buenos Aires, AR)

**Objectives:** Describe the clinical, epidemiological, and microbiological characteristics of a series of cases of *M. bovis* infection in humans diagnosed in the Infectious Diseases ‘Francisco J. Muñiz’ Hospital, Buenos Aires, Argentina.

**Methods:** Analytic and retrospective study of clinical, epidemiological and laboratory findings of 39 patients with confirmed diagnosis of *M. bovis* infection (1996–2008).

**Results:** N = 39. Male: 28/39 (72%). Age (median): 45 years. Previous conditions: Diabetes 8/39 (21%), HIV+ 8/39 (21%) (CD4 count (median): 34 cells/mm³), malaria 1/39 (3%). Domicile: Buenos Aires city and Comurabo: 22/22 (100%).

Risk factor for *M. bovis*: 26/28 (93%); a) Occupational exposure: 17/26 (65%) (meat processing plant n = 9; butcher’s shop n = 4; tannery n = 2); b) Consumption of unpasteurized milk 1/24 (4%); c) History of living in rural area: 8/26 (31%).


**Conclusions:** The most important risk factor was occupational exposure. Pulmonary disease, indistinguishable from tuberculosis, was the most frequent clinical presentation. A high proportion of the patients had a compromised immune system with a high mortality among HIV+ patients. In contrast to what is commonly described the most likely route of infection in our series was airborne transmission.

**O144** Features of non-tuberculous mycobacterial pulmonary infections in an eight-year cohort of non-HIV-infected patients


**Background:** Non-tuberculous mycobacterial (NTM) pulmonary infections predominantly affect patients with advanced HIV and those with chronic lung disease. Data on the nature of infection, treatment course and outcomes in the UK are sparse.

**Objectives:** To identify and characterise NTM pulmonary infections with slow growing mycobacteria in non-HIV patients, diagnosed within a south London teaching hospital between 2000 and 2007

- To assess underlying risk factors for infection
- To assess treatment given, incidence of side effects, treatment cure and relapse rates

**Methods:** In this retrospective study 2000–2007, we examined pulmonary NTM infections south London hospital. Cases were identified through the microbiological database and case notes records. Inclusion criteria were: culture positivity for *Mycobacterium kansasi* (MK), *Mycobacterium avium* intracellulare (MAI), *Mycobacterium xenopi* (MX) and *Mycobacterium malmoense* (MM); ≥18 years old; HIV negative; meeting the ATS (American Thoracic Society) clinical criteria. Radiological reports were made by a radiologist. Statistical analyses were made on SPSS v15, using t tests and Mann Whitney U as appropriate.

**Results:** Of 211 patients identified with NTM isolates, 57 met inclusion criteria. Males (76%) with a median age of 60.5 years predominated. Predisposing factors were smoking (76%), alcohol (30.4%) and COPD (39.1%). Radiologically, cavitation (63.6%) and pulmonary infiltrates (31.8%) were common findings. 47 patients were treated, 10 not treated and 5 died. The predominant organism was MK, 35 of 47 cases (74.5%). Of the MK infections, there was a 100% cure rate with a 10% relapse rate over a 3 year follow up period. Treatment courses differed from British Thoracic Society (BTS) guidelines, most patients receiving triple therapy of rifampicin, ethambutol and usually clarithromycin or ciprofloxacin for 9 months. Side effects were uncommon, occurring in 30% of treated infections. The statistically significant predictors of a poor outcome were a low pre-treatment weight and absence of fever.

**Conclusions:** *M. kansasi* is the predominant NTM organism in London. Optimal treatment regimens are unclear. In this study many patients were treated with 3 agents, in counterpart to BTS guidelines. However, adding a third agent to the treatment regimen for MK did not appear to reduce the relapse rate, but did increase the risk of side effects.

![Table. Outcome of patients with *M. kansasi*.](image)

<table>
<thead>
<tr>
<th>Symptom</th>
<th>Treatment success</th>
<th>Relapse/Died</th>
</tr>
</thead>
<tbody>
<tr>
<td>Median age (range)</td>
<td>58 (25–87)</td>
<td>7.5 (59–80)</td>
</tr>
<tr>
<td>Male sex</td>
<td>18 (72)</td>
<td>5 (62.5)</td>
</tr>
<tr>
<td>Median Pre-treatment weight (range)</td>
<td>60</td>
<td>47</td>
</tr>
<tr>
<td>Median weight difference, kg +1.4</td>
<td>−0.1</td>
<td></td>
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</table>
| **p value** | 0.081 | 0.652 | 0.046 | 0.517 | 0.394 | 0.304 | 0.022 | 0.876 | 0.48 | 0.795

**O145** Absence of non-tuberculous mycobacteria recovery in sputum of cystic fibrosis patients despite adequate decontamination: a possible role of specific antimicrobial therapy used in our centre


**Objectives:** Non-tuberculous mycobacteria (NTM) were pathogens of growing importance in non-paediatric cystic fibrosis (CF) patients. In our centre, the prevalence of NTM in these patients observed (0.5%) during the last decade was markedly inferior to those reported in the literature ranging from 6.5% to 24%. The aim of this study was to screen for NTM in adult patients in our centre with 3 different decontamination methods for mycobacterial cultures in order to determine whether the choice of the decontamination technique of samples may have an impact on their recovery in our centre.

**Methods:** Between January and June 2009, consecutive sputum samples from adult patients with clinical suspicion of NTM infection (respiratory function degradation without other microbiologic explanation) were included in this study. 3 different decontamination protocols were
used: N-acetyl-L-cysteine (NALC)-NaOH (DCT1), NALC-NaOH-oxalic acid 5% (DCT2) and DTT-Chlorhexidine 1% (DCT3). Decontaminated specimens were than cultured onto both solid Loewenstein-Jensen slants (LL; BioRad) and liquid MGIT (BD) culture. A sample was considered NTM negative if no NTM isolate was recovered after a standard 42-day incubation protocol.

Results: 36 sputum samples were collected from 26 adult patients during the study period. The median age of patients was 26 years. 88% of the patients received antimicrobial active against mycobacteria for more than 24 months before sputum collection (61% of the patients had fluoroquinolones and 88% had macrolides). No NTM was detected in the 36 specimens with none of the three decontamination techniques.

Conclusions: Long-term use of macrolides and fluoroquinolones may be an explanation for the absence of recovery of NTM in these CF patients. Further studies in other CF centres prescribing similar antimicrobial treatment regimens are warranted to support this observation.

**O146** M. haemophilum outbreak among 9 Swiss women after permanent make-up of the eyebrows

S.G. Giulieri*, M. Cacassemi, T. Eidney, M. Ödman Jaques, C. Voide, D. Guggisberg, C. Hammann, E. Musumeci, E. Masserey, K. Jaton-Ogay (Lausanne, Neuchâtel, CH)

Objective: Between May and September 2009 9 patients were referred to our infectious diseases outpatient clinic because of skin lesions and suppurative lymphadenitis after permanent make-up of the eyebrows. We present the clinical and microbiological characteristics of the patients and the results of the outbreak investigation.

Methods: All but one patient had at least a lymph node fine needle aspiration, whereas skin biopsy of the eyebrow was performed only in 4 cases. Microscopic examination for mycobacteria, culture and broad-range mycobacterial PCR (16 S rRNA) were performed. Diagnosis of the first case was established using broad-range mycobacterium PCR. As PCR was positive for *M. haemophilum*, special culture was performed. After notification to the public health authorities, an investigation was started and all possibly contaminated material was examined for mycobacteria.

Results: All patients presented with an inflammatory lesion of the eyebrow associated with ipsilateral lymphadenitis located within the parotid gland. The lesions appeared 2–6 weeks after permanent make-up of the eyebrows. Fine needle aspiration and skin biopsy of the eyebrow were positive for mycobacteria in 8 and 1 case, respectively. Microscopic examination showed acid-fast bacilli in 6 cases whereas broad-range PCR was positive for *M. haemophilum* in 5 cases. Culture was positive for 7 patients after 14–70 days (median 44 days) and the microorganism was identified as *M. haemophilum*. All patients were treated with various combinations of ciprofloxacin, clarithromycin and either rifampin or rifabutin. Parotidectomy, local eyebrow excision and partial neck dissection were performed in 3 cases. Three patients were in complete remission following surgical intervention, one patient was in partial remission after two months of conservative treatment. The remaining 5 patients were stable after 2–6 weeks of antibiotic therapy (still ongoing). Outbreak investigation showed that all make-up procedures were performed by the same tattoo artist. PCR of the make-up ink was positive in 6 out of 19 samples for *M. haemophilum*, cultures are still negative after 5 weeks.

Conclusions: We report the first *M. haemophilum* outbreak after permanent make-up due to contamination of the make-up ink. PCR analysis of mycobacterial 16S rRNA is an effective tool for early diagnosis and for appropriate selection of culture method. Optimal management of the infection requires further studies.

**Vaccines: from Petri dish to populations**

**O147** Vaccination with Acinetobacter baumannii outer membrane proteins elicits protective immunity against multidrug-resistant and pan-resistant strains

M.J. McConnell*, J. Dominguez-Herrera, Y. Smali, R. López-Rojas, F. Docobo-Pérez, J. Pachón (Seville, ES)

Objective: Over the last two decades the incidence of hospital-associated infections caused by multi-drug resistant *Acinetobacter baumannii* has increased significantly, requiring the development of novel approaches for controlling this infection. The objective of the present study is to develop a prophylactic vaccine for the prevention of *A. baumannii* infection.

Methods: Outer membrane proteins (OMPs) were purified from *A. baumannii* strain ATCC 19606, combined with an aluminium adjuvant, and used to vaccinate C57Bl/6 mice by intramuscular injection. Levels of anti-OMP antibodies in serum were quantified by ELISA, and the ability of serum to prevent bacterial adherence to the A549 epithelial cell line was determined. Mice were challenged with the ATCC 19606 strain and 2 clinical isolates using a disseminated sepsis model, and the following parameters were measured: i) bacterial loads in tissues, ii) serum levels of pro-inflammatory cytokines, and iii) mortality. The ability of serum from vaccinated mice to protect naive mice from infection by passive transfer was determined.

Results: Two doses of the vaccine three weeks apart elicited high levels of OMP-specific antibodies which were able to block bacterial adherence to A549 cells. At 12 hours post-challenge, vaccinated mice had fewer bacteria than control mice in spleens (3.78 vs. 9.07 log10 cfu/g; p < 0.001), kidneys (3.50 vs. 8.33 log10 cfu/g; p < 0.001), and lungs (3.73 vs. 8.95 log10 cfu/g; p < 0.001). Vaccinated mice had lower serum levels of the pro-inflammatory cytokines IL-1β (2.0 vs. 397.59 pg/ml, p < 0.001), TNF-α (59.3 vs. 351.9 pg/ml, p = 0.002), and IL-6 (188.6 vs. 51141.3 pg/ml; p = 0.007) than control mice 12 hours post-challenge. Vaccinated mice had increased survival over control mice after challenge with the ATCC 19606 strain (100% vs. 0% survival; p < 0.001), a multi-drug resistant clinical isolate (70% vs. 10% survival; p = 0.007), and a panresistant clinical isolate (100% vs. 10% survival; p < 0.001). Mice passively immunized with serum from vaccinated mice 3 hours prior to challenge were protected from infection, whereas control mice receiving non-immune serum were unprotected (100% vs. 0% survival; p = 0.003).

Conclusion: Immunization with an OMP-based vaccine protects against infection with multi-drug resistant and panresistant *A. baumannii* in a mouse model of disseminated sepsis. Passive immunization with anti-OMP antibodies provides rapid protective immunity against *A. baumannii* infection.

**O148** Development of C5a peptidase and CspA based recombinant polypeptides as vaccine components against group B streptococci

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Objective: Group B streptococci (GBS) is a major cause of pneumonia, sepsis, and meningitis in newborns and morbidity of immunocompromised adults. It is known that C5a peptidase and CspA allow GBS to evade phagocytosis by disrupting the C5a and several CXC chemokines of the host. The aim of the current study was to construct and investigate C5a-ase and CspA based recombinant polypeptides with predominantly α helix structure and evaluate their immunogenicity.

Methods: Collection of GBS strains consisting of 75 GBS clinical isolates from Russia, Sweden, China, USA and 10 reference strains was analyzed. PCR generated DNA fragments from cspA and sept genes were cloned employing pQE expression vectors (Qiagen, USA). Immunological assays: 1. Subcutaneous immunization of mice and rabbits. 2. Opsonophagocytosis of GBS preliminary incubated with
normal or immune sera with mouse peritoneal macrophages. 3. Protection studies on immune mice intraperitoneally infected with GBS.

**Results:** All DNA samples from 85 GBS strains tested by PCR and hybridization were found to carry cspA gene. Two portions of cspB and two portions of cspA (pB1, pB3 and csp2, csp3) encoding for α helical regions of C5a-ase and CspA were amplified and cloned. Resultant proteins PB1, PB3 and CSP2, CSP3 (M.M. 12kDa, 10kDa and 42kDa, 12kDa, respectively) were successfully expressed in E. coli followed by purification with Ni sepharose. All polypeptides under study generated humoral immune response in mice and rabbits. The antisera were examined for their opsonizing ability against GBS strains of six different serotypes employing mouse peritoneal macrophages. The data demonstrated significant opsonizing effect of anti-PB1, anti-PB3, anti-CSP3 immune sera over the control. Mice preliminary immunized with the polypeptides were studied for development of GBS infection. As result obvious and classless sensitive antibody titers of mice immunized with PB1, PB3 and CSP3 in comparison with control group was determined. In contrast anti-CSP2 antibodies were found to possess neither opsonizing ability nor protective activity in above mentioned experiments.

**Conclusion:** 1. DNA from 85 GBS strains comprised cspA gene. 2. PB1, PB3 and CSP3 with high α helix structure displayed the immunogenic and protective properties that allowed proposing them as vaccine components against GBS.

**O149** Novel combined multiple subunit vaccine protects against extraintestinal pathogenic E. coli

A. Wieser*, S. Schubert (Munich, DE)

**Objectives:** Extraintestinal pathogenic E. coli (ExPEC) are frequent causative agents of sepsis, neonatal meningitis and urinary tract infections. They lead to significant mortality and morbidity in humans as well as live-stock and are a big burden for healthcare providers. With fast rising antibiotic resistance rates among clinical ExPEC isolates preventive vaccination against these pathogenic E. coli is greatly desired.

**Methods:** Based on genome analysis data and in vivo transcription studies we selectively target virulence factors expressed during the course of infection such as iron acquisition systems. Immunogenic regions as well as the unknown three dimensional structure of these proteins were analyzed in silico. MHCI and MHCI epitopes as well as proteasome cleavage sites were also taken into account. Based on this data two synthetic modular vaccine proteins were designed each bearing eight epitope rich subfragments. For each a fully synthetic protein was designed.

**Results:** Enhanced.

**Conclusion:** Combined T-cell and antibody stimulating vaccines containing multiple epitopes are effective against ExPEC in the mouse. Further evaluation is needed to elucidate the potential for use in humans.

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**O150** Dendritic cell vaccination generates protective responses against influenza virus infection: a model explored for effective vaccination of immunosuppressed cancer and stem cell transplant patients

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**Introduction:** We have recently demonstrated the ability to generate robust, antigen-specific T-cell responses following priming of naive, unblinded cord blood lymphocytes with recombinant influenza hemagglutinin (rHA) loaded dendritic cells (DC) (Safdar et al. Vaccine 2009). Toward the goal of validating this model in vivo, we have developed a murine model of DC immunotherapy utilizing a Balb/c-adapted A/New Caledonia H1N1 influenza virus. Here we demonstrate that a single injection of rHA-loaded DCs can generate high antibody titers and associated with protection against lethal influenza virus infection.

**Methods:** Balb/c-adapted A/New Caledonia was generated by 4 serial passages of infected lung pools. Bone marrow stem cells derived from Balb/c donors were incubated in GM-CSF and IL-4 for 6 days to generate immature DCs. DCs were loaded with A/New Caledonia rHA protein and then matured in a cocktail of GM-CSF, IL-4, IL-10, TNF-α, IL-6, and PGE2. Mature DCs were harvested after 24 hours and delivered at a dose of 106 DC by subcutaneous (SC) or intraperitoneal (IP) routes. Mice were bled 4 weeks after vaccination for serum HA-specific antibody (Ab) titers by ELISA. Six weeks after vaccination, mice were challenged with a 10xLD50 of Balb/c-adapted A/New Caledonia influenza virus administered intranasally. Efficacy of the vaccine was determined by survival.

**Results:** Four weeks after vaccination, 3 of 3 mice injected with DCs IP had seroconverted with high titers apparent at 1:250 serum dilutions. In contrast, only 1 of 3 mice injected SC demonstrated seroconversion and only at a serum dilution of 1:25. None of the mice injected with control DCs (not loaded with rHA) demonstrated rHA-specific seroconversion. At six weeks post-vaccination, mice were challenged with a 10 x LD50 of Balb/c-adapted A/New Caledonia. On day 15 post-inoculation, the four mice with HA-specific Ab titers were all alive with no significant changes in weight, appetite, or behavior, whereas the 4 mice with no demonstrable HA-specific Ab titers had all died (p < 0.005).

**Conclusions:** The model demonstrates that robust HA-specific antibody titers may be generated by a single injection of HA-loaded DCs, and that such titers are protective against fulminant influenza infection. This validation of in vitro data suggests that DC immunotherapy for the prevention of influenza in immunosuppressed cancer patients might be feasible and warrants further exploration of the technique.

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**O151** A novel DNA vaccine against toxoplasmosis induces sporozoite specific protective immune response through nonapoptotic cells

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**Objectives:** Toxoplasma gondii is an obligate intracellular parasite infecting all warm-blooded animals, including humans and causes serious clinical presentations. There is no 100% effective drug to treat toxoplasmosis. Development of a vaccine, which can prevent the consequences of acute infection, is an attractive alternative.

Since 1990s, vaccination strategies against toxoplasmosis mainly used DNA vaccine, purified recombinant proteins showed variable protection because vaccine candidate antigens were almost always selected randomly and targeted tachyzoite form which invades the host cell abruptly and immediately embeds itself in a protective parasitophorous vacuole which keeps away the host immune response. Currently, there is substantial evidence about T. gondii oocysts (contains sporozoites) as being the cause of water related outbreaks. After classification of T. gondii oocysts in category B bioterrorism agents...
as a water safety threat, the demand for a protective vaccine against toxoplasmosis has increased. The present study aims to generate first time a DNA vaccine containing a sporozoite specific surface antigen “SporoSAG” to block the sporozoites as they are released from the oocysts in the intestine. To increase the efficacy of the vaccine, antigen specific-CD8 response inducing anti-apoptotic Bcl-xL gene was inserted to the dual expression DNA vaccine. 

**Methods:** During the construction of the dual expression DNA vaccine, SporoSAG was inserted after CMV promoter and anti-apoptotic protein Bcl-xL were inserted in frame with EGFP after IRES (pIRES2EGFP-SporoSAG-Bcl-xL). In *vitro* transfection of BHK-21 cells was performed to show the expression of SporoSAG and Bcl-xL. The functionality of Bcl-xL was demonstrated by Casp3 flow cytometry. Humoral and cellular immune response (CD4/CD8, IFN-γ) were analyzed from sera and spleen cells of vaccinated BALB/c mice by western blot and flow cytometry using purified recombinant SporoSAG protein (Figure 1).

**Results and Conclusion:** Western blot and fluorescence microscopy analyses of pIRES2EGFP-SporoSAG-Bcl-xL transfected BHK-21 cells showed SporoSAG and Bcl-xL expression. Casp3 analyses rationalized Bcl-xL expression that impedes apoptotic cell death. Analysis of sera obtained from vaccinated mice showed anti-SporoSAG antibody response compared to controls. Cellular immune response analyses showed increased CD8 and IFN-γ response compared to controls indicative of protection against toxoplasmosis.

**Materials and Methods:** Chromosomal DNA extracted from *E. coli* 35218 as a positive type I pil strain and fimH gene amplified by using this template in PCR. The PCR product inserted to pBluescript cloning vector and sequenced. Then, the fimH gene sub cloned to pVax eukaryotic expression vector. The recombinant vector sequenced again. COS7 cell line transfected with a complex of pVax/fimH and ExGen 500 poly cationic polymer. Three groups of BALB/c mice immunized with recombinant DNA construct. The first group injected intramuscularly (i.m) with two doses (100 μg for every injection during two weeks) of purified pVax/fimH. The second group injected with the same amount of pVax vector and the third group injected with PBS as negative control. All mice challenged, one week following the second injection, with uropathogenic *Escherichia coli* strain 35218. Moreover, lymphocytes isolated from spleen of immunized mice and cultured for cytokines assay.

**Results:** The sequence of *E. coli* 35218 fimH gene in our research showed more than 97% identity to other fimH sequence reports in GenBank. Expression of fimH gene in transfected COS7 was confirmed by RT-PCR. The result of challenge showed 100 times reduction of *E. coli* colonization in bladder tissue of first group mice. Additionally, IFN-γ titer got rise in first group on compression with others groups.

**Discussion:** fimH gene has a little variation among type I pil positive strains but it has less variation on amino acid sequences. Hence, it was detected more than 97% identity of *E. coli* 35218 fimH sequence reports in GenBank. Expression of fimH in pVax/fimH cassette was confirmed by RT-PCR. Consequently, induction of cellular immune response was showed by increasing of INF-γ titration in immunized mice. So, DNA vaccination has a potential candidate for limiting recurrent urinary tract infection.

**O153** Rabies neutralizing antibody in AIDS patients after rabies post-exposure treatment with doubling the intramuscular doses of conventional regimen and aluminium-adjuvanted tetanus toxoid

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HIV-infected patients with low CD4+ T lymphocyte had a poor Nab response to conventional pre- and post-exposure rabies vaccination. Our previous reports revealed that HIV-infected patients with CD4+ counts <200 /μL did not respond well to conventional intramuscular (IM) post-exposure vaccination or multiple-site intradermal (ID) vaccination. We conducted a prospective study of the Nab response after doubling the IM doses of WHO IM regimen (ESSEN) and aluminium-adjuvanted toxoid (TT) in AIDS persons. Fifteen AIDS patients (age range, 30–46 years) without active opportunistic infections who presented with possible or proven rabies exposure were enrolled. Four patients had severe exposure (WHO category III). All patients had a history of AIDS-related conditions such as opportunistic infections or CD4+ counts <200 /μL. Only 5 patients did not received antiretroviral therapy. All patients were given the post-exposure rabies prophylaxis. They received doubling the doses of IM regimen (2–2–2–2–0) with purified Vero cell rabies vaccine (doubling the IM doses of vaccine in 1–1–1–1–0 ESSEN-IM regimen) but one of the two rabies vaccines on day 0 was dissolved in...
Safety of vaccination with 7-valent conjugated pneumococcal vaccine among HIV-infected adult patients

C.L. Lu*, W.C. Liu, C.H. Wu, S.Y. Chang, C.C. Hung (Taipei City, TW)

Objectives: Patients with HIV infection have a higher incidence and recurrence rates of invasive pneumococcal diseases compared with the persons without HIV infection. An increasing number of clinical studies are reported to evaluate the immunogenicity of 7-valent conjugated pneumococcal vaccine (PCV) among elderly and transplant recipients, but the data on safety of vaccination with PCV among HIV-infected patients are scarce.

Methods: HIV-infected patients aged 18 years or greater were enrolled for vaccination with PCV to prevent invasive pneumococcal diseases from October 2008 to October 2009. Two groups of patients were assessed: group A, recipients of 2 doses of PCV given at a 1-month interval and group B, recipients of 1 dose of PCV. Patients were further stratified to 4 groups according to CD4+ count when primary PCV was administered: group 1, CD4+ <200 cells/mL; group 2, CD4+, 200 to 349 cells/mL; group 3, CD4+, 350 to 499 cells/mL; and group 4, CD4+ ≥500 cells/mL. All patients were given 1-week diary to record any discomfort after vaccination. All statistical analyses are performed by STATISTAT software.

Results: 407 HIV-infected patients were vaccinated with PCV during the study period: 206 patients received two doses and 201 patients one dose. After first dose vaccination, 372 (91.1%) patients who returned their one-week diary for recording side effects were assessed. Among these 372 HIV-infected patients, 124 (33.3%) patients reported discomfort after the vaccination that included injection site soreness (22.8%), pain (8.6%), redness (1.08%), swelling (1.62%), fever (1.62%), headache (1.88%), fatigue (4.30%), cough (1.34%), rash (0.53%), tinnirhorea (0.27%), sneezing (0.27%), and insomnia (0.27%). None of these patients reported severe adverse events that prompted medical attention. The only factor that was found to be associated with occurrence of side effects was high nadir CD4 counts (P=0.04) before vaccination. The associated factors for injection site soreness, the most common side effect after vaccination, included high nadir CD4 counts (P=0.01) before vaccination and high HIV viral load at vaccination (P=0.01). None of the patients who received two doses PCV reported aggravated discomfort after second dose vaccination.

Conclusions: We conclude that vaccination with 7-valent PCV among HIV-infected patients was generally safe and high nadir CD4 counts before vaccination were associated with increased risk for injection side reactions.
and 19F. The introduction of the 7-valent conjugate vaccine (PCV7) resulted in changes in serotype frequency that can also affect pili prevalence. To evaluate this effect we determined the presence of Pi-1 and Pi-2 among a collection of 475 invasive isolates recovered from children after PCV7 introduction (2003–2008). The results were analyzed in terms of pilus islet association with antibiotic resistance, serotype, pulsed-field gel electrophoretic profile (PFGE) and multicollinearity sequence type.

**Results:** Overall, 46.7% of the strains presented one of the pilus islet. As observed in previous studies serotype distribution analysis showed a high correspondence between serotype and the presence and type of pili (Wallace coefficient, W = 0.85). This association was even higher when considering pili and PFGE cluster (W = 0.98). The rIIA islet was identified in 13% of the strains most of them expressing serotype 6B, 9V, 14, 19A and 19F. Pi-2 islet was found to be present in 37% of the pneumococcal strains and was identified mainly among serotypes 1 and 7F. **Conclusion:** A decrease in the presence of the rIIA islet among invasive pneumococcal strains was observed after PCV7 availability. This change is associated with the decrease of vaccine serotypes since the majority of the strains carrying Pi-1 expressed vaccine serotypes. In contrast, Pi-2 islet was more prevalent due to the predominance of serotypes 1 and 7F. Since most of the strains carrying pil islet presented serotypes that are included either in current or future conjugate vaccine formulations, their potential use in a vaccine would offer limited additional benefits.

### Epidemiology and control of *Clostridium difficile* infection

**0157** Final results of the first pan-European *Clostridium difficile* infection survey


**Objectives:** To survey the incidence and demographic, clinical and microbiological characteristics of *Clostridium difficile* infection (CDI) in hospitals in Europe.

**Methods:** We organised a network of 106 laboratories capable of isolating *C. difficile* strains in 34 European countries. In November 2008, 1–7 hospitals per country, depending on population size, tested stool samples of patients aged ≥2 years who were suspected of CDI, or who had developed diarrhea after ≥3 days of hospital admission. CDI was defined by a positive enzyme immunoassay for *C. difficile* toxin A and/or B, a positive cytotoxicity test, or positive culture of a toxigenic strain. Each hospital collected detailed clinical data of the first 10 CDI cases, and sent stool isolates of *C. difficile* for PCR-rbobtyping and characterization of toxin A, toxin B and binary toxin genes. After 3 months, follow-up clinical data were collected.

**Results:** CDI incidence varied across hospitals (mean: 5.5 per 10,000 patient-days per hospital; range: 0 to 36.3). Detailed information was obtained on 509 patients and 395 isolates of these patients were available for characterization. Sixty-two different PCR ribotypes were found, among which 014 (15%), 001 (10%) and 078 (8%) were most prevalent. The prevalence of PCR ribotype 027 was 5%. Most patients had the previously identified risk profile of an elderly patient with co-morbidity and recent antibiotic use. At follow-up, 22% of patients had died and previously identified risk profile of an elderly patient with co-morbidity. The prevalence of PCR ribotype 027 was 5%. Most patients had the most prevalent.

**Conclusion:** In this pan-European, hospital-based study, the incidence of healthcare-associated CDI varied widely between hospitals. The overall and attributable mortality were high. Dominant PCR ribotypes were 014, 001 and 078, whereas 015, 018 and 056 were significantly associated with death to which CDI contributed. Cefazidime use and having recurrent CDI at inclusion were significantly associated with recurrences during follow-up.

**Background:** Following the emergence in 2006 of the PCR-ribotype 027 epidemic clone, surveillance of *Clostridium difficile* infections (CDI) in France was reinforced through the mandatory notification of severe cases or clusters in healthcare facilities (HCF). To complete this strategy, the national public health surveillance institute (InVS) and the *C. difficile* national reference centre (NRC) launched a multicenter, national, prospective survey in 2009.

**Objectives:** To assess CDI incidence in HCF and the geographical distribution and characteristics of strains responsible for CDI.

**Methods:** From March to August 2009, voluntary HCF reported through a web-based questionnaire the total number of new CDI patients by origin and severity, admissions and patient-days (pd). ECDC case definitions were used and data were stratified by type of wards: acute-care (AC) vs. rehabilitation/long-term care (RLTC). HCF were asked to send to the NRC strains isolated in March from patients diagnosed with a CDI for characterisation and typing.

**Results:** 137 HCF participated in the epidemiological component of the survey. On 1st November 2009, a complete dataset was sent by 85 (73%) of 117 HCF with AC wards and 72 (69%) of 105 HCF with RLTC wards. In AC, 1,043 CDI-patients were reported; CDI incidence was 2.18 cases per 10,000 pd (1.05 case per 1,000 admissions). By origin, 686 (66%) cases were healthcare-associated (HA), 598 (87%) of which were acquired in the reporting HCF; 294 (28%) community-associated (CA); 65 (6%) of unknown origin (UO). Among 734 CDI-patients diagnosed in HCF actively following them up for a month, 100 (14%) were severe cases and 25 (3%) died from their CDI. In RLTC, 251 CDI-patients were reported; CDI incidence was 1.31 cases per 10,000 pd. By origin, 231 (92%) cases were HA, 204 (88%) of which were acquired in the reporting HCF; 8 (3%) CA; 12 (5%) of UO. Among 186 CDI-patients diagnosed in HCF actively following them up for a month, 4 (2%) were severe cases and died from their CDI. Last, 237 *C. difficile* strains were sent by 54 HCF to the NRC; their characterisation and typing are underway.

**Conclusions:** Preliminary results from this survey confirm that CDI incidence in France is much lower than reported in other European countries, and suggest that CDI are adequately controlled in French HCF. However, the high proportion of CA cases reported in AC wards suggests the need for further studies. Final results from this survey will be presented in April.

**0159 Prevalence of *Clostridium difficile* in retail meat products in north-eastern Italy**

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Recent studies conducted in Canada, United States and Sweden pointed out that *Clostridium difficile* spores are present in retail ground meat thus suggesting that meat could act as food source of *Clostridium difficile* for human infections.

**Objectives:** The aim of this pilot study was to estimate the occurrence of *Clostridium difficile* in minced beef and pork at retail in North-Eastern Italy.

**Methods:** The cross-sectional study was performed in February-March, 2008, in 150 retail outlets randomly sampled in 3 provinces of North-Eastern Italy. Among those 3 provinces retailer’s sample size was proportional to resident population. In each sampled retailer one laboratory sample of minced meat and one of pork was randomly collected. Each sample was microbiologically processed using the *Clostridium difficile* selective medium Cefoxitine Cycloserine Fructose broth (added with Taurocolate). After 10 days of incubation broth cultures were plated on blood agar base, horse blood red cells added
A review of the epidemiology, risk factors and strain characteristics of *Clostridium difficile* among hospitalized patients: a pilot nested case–control study


**Introduction:** The study aimed to determine the outcomes, mortality and morbidity from *Clostridium difficile* infections (CDI) in the North West of England, and to identify possible differences in risk factors between ribotypes.

**Methods:** Multicentre case control study at three large hospitals in NW England. Cases defined as hospitalized patients with positive *Clostridium difficile* toxin in diarrheal stool samples. Controls randomly selected from matched patients with negative stool samples, at a ratio of 1:1, frequency matched by 10 year age band. Data was abstracted at case note review. Stool samples from cases cultured and typed at regional reference laboratory.

**Results:** Between Sept 9, 2007 and Sept 30, 2008, data on 296 cases and 296 controls collected and analysed. Average age for controls was 77 years. 40.2%(119/296) of controls and 48.3%(143/296) of cases were male. 48 (16%) controls and 97 (33%) cases died during the study period. Of the samples typed, 27.7% were 001, 26.6% were 001 and 20.9% were 027.

In the overall logistic regression model, length of stay, transfer from another NHS hospital, number of different antibiotics, number of days of quinolone antibiotics, degree of comorbidity and number of days of nitromidazole antibiotics were identified as risk factors (see figure). Reduction in odds of CDI with H2-blocker therapy was an interesting finding.

**Discussion:** This study did not find any difference in mortality or morbidity between different strains of *Clostridium difficile*, but did find some differences in risk factors between ribotypes. An unexpected association of H2-blocker therapy with a reduction in odds of CDAD was observed.

**Conclusion:** This study has some limitations. Diagnosis of *Clostridium difficile* associated disease was based on toxin detection, which may not be sensitive or specific. Details to be presented.

**Figure.** Multiple logistic regression model for all ribotypes.

**O160**

**Stronger correlation between antibiotic consumption and incidence of *Clostridium difficile* determined by cultures instead of faecal toxin only**


**Objectives:** The diagnosis of *Clostridium difficile* (*C. difficile*) associated diarrhoea is usually based on the detection of faecal toxin A/B, rather than on stool cultures. Therefore, studies on the correlation between the incidence of *C. difficile* and antibiotic consumption were limited to toxic strains in the past. The aim of this ecological study was to analyse the association between unit-specific antibiotic consumption and the incidence of toxigenic and non-toxigenic *C. difficile* in hospitalised patients.

**Methods:** Unit specific antibiotic consumption data and the incidence of *C. difficile* in 19 units over 5 years were analysed at the University Hospital of Basel, Switzerland. Stool samples were tested for toxin A/B and simultaneously cultured. In a second step, positive cultures were tested for toxin production. In order to analyse specific antibiotics, unit specific length of stay and antibiotics showing a significant association in univariate analysis were entered in a multiple linear regression model.

**Results:** Over 5 years, a total of 165 first isolates of toxin producing *C. difficile* and 413 first isolates of *C. difficile* were detected. The incidence of *C. difficile* overall and of toxin producing *C. difficile* was 0.39 and 0.15 per 1000 patient days, respectively. The correlation (figure) is highly significant in both analyses (p < 0.001), but a higher correlation results when all *C. difficile* strains are included in the model (R = 0.80 vs. R = 0.63). In a multivariate analysis explaining more than 80% of the variance of the incidence of *C. difficile* (R^2 = 0.82), only piperacillin/tazobactam, trimethoprim/sulfamethoxazole, and the aminoglycosides were found to be statistically significant risk factors.

**Conclusion:** We show for the first time, that the correlation between antibiotic consumption and the *C. difficile* incidence rates significantly improves, if detection is not limited to toxin producing strains. Overall antibiotic pressure as a risk factor was previously underestimated due to restriction to the toxin producing strains. Our results underline the importance of the overall pressure of antibiotics that explains the majority of the variance rather than the importance of a single group of antimicrobial agents such as quinolones. Therefore, interventions to
reduce the overall antibiotic consumption might be more successful in controlling C. difficile incidence than interventions focusing on certain groups of antibiotics.
Impact of different antibiotic treatment regimes for respiratory tract infections on emergence of Clostridium difficile

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Background: It has been suggested that treatment of lower respiratory tract infections (LRTI) with broad spectrum antibiotics and newer fluoroquinolones in particular, contributes to selection for Clostridium difficile (C. diff). We studied the prevalence of C. diff carriage, selection for C. diff and development of C. diff infection (CDI) in patients (pts) hospitalized and treated for LRTI and compared the different treatment regimes.

Methods: Pts receiving antibiotic treatment for LRTI in one university medical center and an affiliated teaching hospital were prospectively followed for 30 days with careful monitoring of the development of diarrhoea. Of all patients, stool samples collected on admission, day 5, day 3 after discontinuation of antibiotics and day 30 were cultured for C. diff using selective plates. Cultured isolates were further characterized for toxin production and typed by PCR ribotyping. CDI was defined as the presence of diarrhoea and a positive faeces toxin test.

Results: Of 107 pts included, 45 (41.1%) pts were treated with moxifloxacin, 47 (43.9%) with β-lactam monotherapy and 15 (14.0%) with β-lactam/macrolide combination therapy. The endemic rate of CDI in the participating hospitals is 0.6/1000 pts a year. In total, during the study period, C. diff was cultured in 18.7% (n=20) of pts. 6 (30%) isolates were toxin positive. On admission, baseline prevalence of C. diff carriage was 10.4% (n=10). Of those, one patient had mild CDI and persistent positive cultures for C. diff during the study period.

The overall acquisition rate of C. diff carriage after antibiotic treatment for LRTI in our population was 10.3% (n=11). Acquisition rates of C. diff carriage were 11.1% (n=5) in moxifloxacin, 10.6% (n=5) in β-lactam and 6.7% (n=1) in β-lactam/macrolide treated pts (p=NS). Tests for faeces toxin production were negative in all pts who acquired C. diff. No acquired CDI or relapse of previous CDI occurred during the study period. Risk factors for C. diff carriage and at any time were intravenous antibiotic treatment >7 days (OR 3.89, 95%CI 1.3–11.8) and hospitalization the past 3 months (OR 4.08, 95%CI 1.4–11.9).

Conclusions: In a setting with a low endemic rate, acquisition rates for C. diff during antibiotic treatment for LRTI were 10% and did not lead to CDI. Moxifloxacin was not associated with increased acquisition rates for C. diff as compared to other antibiotics classes prescribed for LRTI.
Azithromycin in the treatment of chronic bacterial prostatitis

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Prostatitis is an inflammatory condition of the prostate that presents with urinary symptoms, prostatic symptoms and sexual dysfunction. It is diagnosed by clinical symptoms and signs, the microscopy of expressed prostatic secretion (EPS) and culture of EPS and segmented urine samples. Prostatitis is chronic when symptoms have been present for at least 3 months. As a part of several scientific research projects we have been prospectively investigating prostatitis syndrome at the Outpatient Department of Urogenital Infections and Sexually Transmitted Diseases, Dr Fran Mihaljevic University Hospital for Infectious Diseases, Zagreb, Croatia, since March 1, 1999 and is still ongoing. We examined more than 3450 patients over 18 years of age with symptoms of chronic prostatitis and no evidence of lower genitourinary tract abnormalities.

Results: a total of 307 patients with chronic prostatitis caused by Chlamydia trachomatis were treated with azithromycin in a total dose of 4.0, 4.5 or 6.0 g for 3–4 weeks. Eradication of Chlamydia trachomatis was achieved in about 80%, with 70% of patients clinically cured. There were no statistically significant differences between these three dosage regimens. A total of 82 patients with chronic prostatitis caused by Ureaplasma urealyticum were treated with azithromycin in a total dose of 4.5 g for 3 weeks. The eradication of Ureaplasma urealyticum was 85% and clinical cure 76%.

Conclusions: azithromycin is an effective and safe antimicrobial drug for the treatment of chronic prostatitis caused by Chlamydia trachomatis or Ureaplasma urealyticum. It is recommended in a total dose of 4.5 g per day, during 3 weeks, administered for 3 days weekly in a dose 1x500 mg po. per day. The results of recently published clinical studies on the treatment of chronic bacterial prostatitis with combination therapy with ciprofloxacin and azithromycin are impressive. We also have a limited, but positive experience.

Azithromycin – new horizons (Symposium supported by Teva)

S171 Azithromycin in the treatment of chronic bacterial prostatitis

S172 The role of azithromycin in the treatment of acute infectious gastroenterocolitis

D. Vukelic (Zagreb, HR)

Acute infectious gastroenterocolitis is a common disease worldwide. In most cases, gastroenterocolitis does not require antimicrobial treatment as it is considered a self-limiting and mild disease of short duration. However, antibiotic therapy is indicated in most severe cases. HIV-positive or immunocompromised patients should also receive antimicrobial treatment. In such cases, antibiotics could decrease the duration of the disease, enable a faster recovery and shorten the carrier state. Azithromycin proved effective in the treatment of acute infectious gastroenterocolitis. Two studies involving US military personnel in Thailand indicated that a single azithromycin dose (1 g) or a 3-day regimen (500 mg/day) were comparable or superior to ciprofloxacin or levofloxacin in empirical treatment of acute diarrhea. Efficacy of azithromycin in the treatment of traveler’s diarrhea in infants and children has also been suggested.

Campylobacter enterocolitis is the most frequent form of acute bacterial diarrhea affecting humans, particularly children and young adults. We evaluated the efficacy and tolerability of a single oral azithromycin for the treatment of Campylobacter enterocolitis in children <12 years of age, administered early in the course of the disease compared to a standard 5-day erythromycin regimen or no antibiotic. Our study suggests that a single azithromycin 30 mg/kg administered early in the course of Campylobacter enterocolitis in children <12 years of age effectively eradicates the pathogen and accelerates clinical cure attainment and that it is clinically superior to an early commenced 5-day erythromycin regimen.

S173 Current and future issues in resistance of respiratory pathogens: is the horizon still bright?

R. Kozlou (Smolenš, RU)

Respiratory tract infections (RTIs) continue to be the major causes of morbidity and mortality worldwide. Lower respiratory tract infections (LRTIs), including CAP, were ranked third in a list of the 30 leading causes of death worldwide in 1990. Out of all pathogens, S. pneumoniae, H. influenzae, M. catarrhalis and “atypical” pathogens still remain to be the most prevalent ones, independently on the country. Traditionally, β-lactamase, modern macrolides and respiratory fluoroquinolones (for adults only) are drugs of choice for the therapy of RTIs. But antimicrobial resistance among these pathogens continues to be the major challenge for the physicians in all countries. A total of 2,449 S. pneumoniae from 23 cities of Central, North-Western, Southern, Privolgsk, Ural, Siberian and Far-Eastern regions of Russia were studied from 1999 to 2009. β-lactams

quino...
Non-typeable Haemophilus influenzae, the "unrevealed pathogen" (Symposium supported by GlaxoSmithKline Biologicals)

S174 Clinical effectiveness of azithromycin in an era of multidrug resistance: results of a prospective international, multicentre observational study (SUPoRTI)

B. Baricic (Zagreb, HR)

Azithromycin after twenty years of extensive use is still one of the most prescribed antibiotics in the treatment of bacterial, respiratory tract infections. Multidrug resistance (MDR) is reported worldwide, but clinical consequences of MDR still remain controversial. SUPoRTI study was designed to evaluate efficacy of a 3-day azithromycin therapy in the treatment of respiratory tract infections in adults and children and to compare results with early clinical trials. SUPoRTI study is a multicenter, prospective non-comparative phase IV study, which included 550 patients with bacterial upper and lower respiratory tract infections. Three countries and 26 centers participated in the study. Only outpatients were included in the study. The trial included patients with acute pharyngitis, sinusitis and otitis media as well as patients with acute exacerbation of chronic bronchitis and mild to moderate community acquired pneumonia. Azithromycin was administered orally. Clinical effectiveness was assessed after the third or fourth visit and dynamic of clinical scores was assessed throughout the study. We present the results of effectiveness and safety of azithromycin obtained in this study.

S178 The role and pathogenicity of non-typeable Haemophilus influenzae in invasive and mucosal respiratory diseases

A.W. Crripps *, D.C. Otczyk, M. Ravuru, WP Hausdorff (Gold Coast, AU; Wavre, BE)

Non-typeable Haemophilus influenzae (NTHI) is a common commensal of the human respiratory tract mucosa. It is a fastidious Gram-negative cocobacillus that resides exclusively in the human host. To date, NTHI infection has been accepted largely as opportunistic and to occur particularly in cases in which the host's immune status or physiological barriers have been compromised, for example in acute exacerbations of chronic obstructive pulmonary disease in adults and otitis media (OM) in young children. However, there is increasing evidence that, despite the absence of a polysaccharide capsule, NTHI causes significant invasive disease as well as mucosal respiratory infections in subjects without predisposing risk factors. In both developed and developing countries, NTHI may cause septicaemia and meningitis in children at a prevalence at least equal to that caused by a single, major Streptococcus pneumoniae serotype. In developed countries, especially in the post H. influenzae vaccine era, it is difficult to estimate the current disease burden, although some countries have suggested an increasing number of cases of invasive disease reported in the literature. Maternal gentamicin-tract infection has been identified as a source of highly fatal, early onset neonatal NTHI septicaemia. The most significant mucosal infections known to be caused by NTHI are OM, sinusitis and conjunctivitis. Approximately one-third of the bacterial isolates from OM and sinusitis are NTHI. In the post-PCV-7 era, a proportionate increase in the frequency of recovery of NTHI from mucosal isolates has been demonstrated in children and adults in the United States. Furthermore, several lines of evidence suggests NTHI may also play an important role in paediatric community acquired lower respiratory infections, especially in children with recurrent and persistent bronchitis & pneumonia. Further studies are warranted to understand the public health importance of NTHI, as a pathogen. This review suggests that NTHI, as a cause of invasive disease, has been underestimated and that there is an important invasive disease burden. NTHI appears to be more commonly responsible for mucosal respiratory infections than previously recognized.

S179 Clinical implications related to NTHI: from treatment to potential prevention

J. Van Eldere * (Leuven, BE)

Guidelines on the treatment of respiratory tract infections (RTI) may need to be re-evaluated considering the increasing importance of non-typeable Haemophilus influenza (NTHI).

- Reports comparing the prevalence of bacterial pathogens in acute otitis media and acute bacterial sinusitis in children prior to and after the introduction of the 7-valent conjugated pneumococcal vaccine (PCV7) show replacement of Streptococcus pneumoniae vaccine types with non-vaccine types. They also show an increased prevalence of NTHI.
- Recent reports confirm that NTHI are associated with recurrent and protracted morbidity.
- There are signs that the β-lactamase-dependent β-lactam resistance in NTHI is being replaced by a non-β-lactamase-dependent resistance mechanism that may render the use of current first-line treatment antibiotics, such as amoxicillin-clavulanic acid and second-generation cephalosporins, ineffective.

Worldwide, β-lactamase production accounts for the majority of H. influenzae ampicillin resistance. Mutations in penicillin-binding proteins are another β-lactam resistance mechanism. These H. influenzae strains are called β-lactamase-negative, ampicillin-resistant or BLNAR. BLNAR strains are less susceptible to ampicillin but also to amoxy-clavulanate and to second- or third-generation cephalosporins. BLNAR strains were, until now, rare and increases in minimum inhibitory concentrations (MIC) were limited, making use of amnopenicillins in high doses still warranted. This situation is changing. Most notably, for example, BLNAR strains have increased significantly in Japan. Similarly, in some European countries (Spain and France), an increasing prevalence of BLNAR is also seen. Some of these strains have increased MIC values that make treatment with amnopenicillins or second- or third-generation cephalosporins ineffectual. A further increase of BLNAR strains might challenge our current guidelines for treatment of RTI that advocate use of amoxy-clavulanate or second-generation cephalosporins as first-line treatment options. Based on the observed effects of PCV7, the possible clinical implications of new vaccines should be explored.

S180 The need for surveillance: a call for action

M.P. Slach * (Abingdon, UK)

In order to monitor the impact of Hib vaccination on the epidemiology of invasive Haemophilus influenzae disease, an international collaboration
was established in 1996. By 2006, 28 countries had responded and provided national surveillance data on invasive *H. influenzae*. By 2000, 14 of these countries had incorporated the Hib conjugate vaccine into their infant immunization schedules and routinely serotyped all clinical *H. influenzae* isolates. A total of 10,081 *H. influenzae* infections were reported between 2000 and 2006; of these, 2,836 (28%) were due to Hib and 4,466 (44%) to non-typeable *H. influenzae* (NTHi). It was found that the incidence of NTHi was almost twice that of Hib (0.28 versus 0.15 per 100,000 cases) and that both Hib and NTHi infections were more common in infants and the elderly. Moreover, the incidence of NTHi was much higher than Hib in the first month of life (11.4 versus 1.2 per 100,000 cases) and infections were more likely to occur in the first week of life, suggesting vertically acquired infection. Overall, however, the median age at disease was higher for NTHi infections than for Hib (58 versus 5 years, p < 0.0001). NTHi infections were also associated with: a higher case fatality ratio (CFR; 366/3172 [11.5%] versus 88/2005 [4.4%]; p < 0.0001), particularly among infants (17.4% versus 2.9%; p < 0.0001); and a higher proportion of NTHi infections among women of child-bearing age. In addition, one-third of reported meningitis cases were due to NTHi. The CFRs for Hib and NTHi meningitis were similar in EU-IBIS data (4.1% versus 4.2%) but in England and Wales, the CFR was much higher for NTHi meningitis (17% versus 5%). The reasons for this unclear. In conclusion, there is a need for continued, large-scale, clinico-epidemiological surveillance to collect data on clinical presentations of NTHi, risk factors, management and NTHi-attributable death.

References


**Emerging trends in fungal infections**

**K182 Emerging trends in fungal infections**

*C. Lass-Flörl*° (Innsbruck, AT)

The frequency and diversity of serious fungal infections does increase and severely immunocompromised patients are particularly vulnerable to infection from moulds and yeasts. *Candida* and *Aspergillus* species are the predominant pathogens. *Candida* bloodstream infections are associated with high morbidity and mortality in both neutropenic and non-neutropenic critically ill patients. Risk factors associated are diverse and include exposure to broad spectrum antimicrobial agents, mucosal colonisation, indwelling vascular catheters, surgery and cancer chemotherapy. Differences in geographical epidemiology are emerging, in particular regarding a shift towards non-albicans species. This shift has been correlated with routine fluconazole administration. *Aspergillus* spp. can cause a wide spectrum of diseases in humans, including allergy, superficial infection, and invasive disease. Invasive aspergillosis has emerged as a leading cause of morbidity and mortality in immunocompromised patients. The most important species are *Aspergillus fumigatus* followed by *Aspergillus flavus*. Contemporaneously, infections with rare moulds are on rise. *Zygomycetes*, *Trichosporon*, *Fusarium*, *Alternaria*, *Pseudallescheria* and dematiaceous fungi are recognized more frequently. The emergence of these organisms is multifactorial and can be related to more intense immunosuppression, the prolonged survival of patients, and the selective pressure of broad spectrum antifungal agents used for prophylaxis or therapy. Among these rare mould infections, the *zygomycetes* are the most commonly encountered, and appear to be associated with the use of voriconazole. *Aspergillus terreus*, a species that is resistant to amphotericin B, and less frequently, *A. astus* and *A. lentulus*, have been noted increasingly as causes of invasive aspergillosis in some tertiary care centres. *Scedosporium* with innate resistance to many antifungal agents have emerged as major causes of disseminated infections, followed by infections due to *Fusarium* species. Dematiaceous, or brown-black, fungi, most often associated with chronic localised infections, are now increasingly reported as a cause of disseminated infection in immunosuppressed hosts. Watchful surveillance, rapid detection of disease, adequate treatment and effective control measures are highly warranted in the optimal management of these difficult to treat fungal infections.

**Impact of the commensal flora on health and diseases**

**K183 Impact of the commensal flora on health and diseases**

*L. Engstrand*° (Stockholm, SE)

Our adult bodies harbour approximately ten times more microbial cells than human cells and their genomes (the microbiome) endow us with physiological capacities that strongly influence our well-being. However, our microbiome is largely unexplored and there is a great need to increase our understanding of the interactions between our human and microbial genomes. The sequencing of the human genome constituted a starting point in the understanding of human biology at a global scale, yet today there is a growing agreement that human health and disease cannot be understood without considering the microbial communities. Now when the human microbiome project has been launched a number of international consortiums are starting up with efforts to explore the role of the human microbiota in health and disease. Many lines of evidence suggest a role for both commensal and transient microbes in the status of human health as well as for the risk of contracting certain diseases. During the last years molecular microbiology has revolutionized the landscape of microbiology and will continue to do so by providing new solutions for microbe identification and characterization. Next-generation sequencing has opened up new areas of research for people in the field of intestinal, skin, oral cavity and other microbiomes. The high-throughput sequencing platforms we now have access to will hopefully also help to increase our understanding of host-bacteria interactions, immune maturation and mechanisms behind chronic disease development. An interdisciplinary approach must be taken on comprising medical, epidemiological, computational, and biotechnology expertise focusing on understanding the human microbial communities and their effect on human health. Application of different “omics”-methods and computational systems biology methods to unique biobanks will be required in order to map out the human microbiome as well as the human cellular machinery interacting it.

**ESBL-producing *E. coli* in the community**

**S185 How big is the threat in the outpatient setting?**

*N. Woodford*° (London, UK)

*E. coli* with CTX-M enzymes are globally the most prevalent ESBL producers. They are often isolated from urines of patients attending general practice, but there are few data to assess accurately the extent of the community burden. The prevalence of ESBL producers in faeces from healthy people is typically <5% in Europe. In a recent multicentre study of non-hospitalized patients with infections, one third of the ESBL producers (mainly *E. coli*) were from those with no recent health care contact (Ben-Ami et al. Clin Infect Dis. 2009;49:682). In the UK, ESBL-producing *E. coli* cause c. 2,500 cases of bacteraemia p.a., and may be estimated to cause c. 50,000 urinary tract infections p.a. Many belong to the globally-disseminated O25:H4-ST131 uropathogenic clone and have CTX-M-15 ESBL, though CTX-M-3 is equally common in this clone in Belfast, a city where the ST131 clone is present in the faeces of 40% of nursing home residents. CTX-M-15 ESBL is associated with InhA multi-resistance plasmids, while CTX-M-3 in Belfast is encoded on Inh1 plasmids. These plasmids cannot readily be lost even in the absence of antibiotic selective pressure, since they encode multiple “addiction” systems. Hence ESBL producers may serve as long-term community reservoirs of resistance genes. Foreign travel may also be associated
with gut colonization by ESBL-producing isolates, and the ESBL present often reflects the type most prevalent in the countries visited. Food remains an under-explored potential source for ESBL-producing *E. coli*. Raw chicken has been sampled in the UK, with CTX-M group 2 and 8 ESBLs found in meat imported from South America; these types account for <1% of ESBLs from clinical infections. There are currently no data to suggest wide presence of CTX-M-15 ESBL in foodstuffs; it may be found in *E. coli* from animals, but the strains are usually distinct from the dominant human clinical types. ESBL producers are often multi-resistant. Carbapenems are the drugs of choice for serious infections, but resistance may emerge in strains with reduced permeability, as observed in a UK nursing home resident who had no recent hospitalization or carbanenem exposure. Carbapenemase-producing *E. coli* are rare, although isolates with NDM-1 metallo-carbapenemase in addition to CTX-M-15 and acquired AmpC enzymes give cause for concern lest they become as prevalent as those with ‘traditional’ CTX-M-15 enzyme, or follow them into the community setting.

**S186** How does changing epidemiology alter our management and prevention strategies?

J. Pitout (Calgary, CA)

Since 2000 *Escherichia coli* producing CTX-M enzymes (especially CTX-M-15) have emerged worldwide as important causes of community-onset urinary tract (UTIs) and blood stream infections due to extended-spectrum β-lactamase (ESBL) producing bacteria. Molecular epidemiology studies suggested that the sudden worldwide increase of CTX-M-15-producing *E. coli* is mostly due to a single clone named ST131 and that foreign travel to high-risk areas such as the Indian subcontinent might play in part a role in spread of this clone across different continents. The carbapenemes are widely regarded as the drugs of choice for the treatment of severe infections due to ESBL-producing Enterobacteriaceae. Empiric antibiotic coverage for these resistant organisms should be considered in community patients presenting with sepsis involving the urinary tract especially in patients with certain risk factors such recent antibiotic use, residence in a long-term care facility, recent hospitalization, males older than 65 years and recent travel to a high-risk area. Failure to initiate appropriate antibiotic therapy from the start appears to be responsible for higher patient mortality. Studies from different parts of the world shows that that up to 5 percent of the population in the community can become as prevalent as those with ‘traditional’ CTX-M-15 enzyme, or follow them into the community setting.

**The integrated diagnostic platform versus the stand-alone microbiology laboratory**

**S188** The integrated diagnostic platform

J. Van Eldere (Leuven, BE)

Clinical microbiology is subject to rapid evolution due to the need for rapid and more complex diagnostics, the increasing difficulty in recruiting trained personnel as well at the medical as at the technical level, the need for proven cost-efficiency and the increasing overhead costs associated with quality control. On the other side, there are new opportunities following the introduction of new techniques such as PCR, MALDI-TOF and in particular the availability of automated inoculation and plate reading systems to replace manual labour.

Reactions to these challenges differ, ranging from outsourcing to non-hospital based specialized microbiology labs to various forms of cooperation between smaller labs. This cooperation can exist in centralizing a part of or almost all activity in a central hospital-based lab or can be a network with a division of labor between collaborating labs. All these solutions share one factor. By increasing size, they seek to increase cost-efficiency and facilitate the introduction of new, specialized and expensive techniques. Outsourcing is often rejected because it risks reducing microbiology to a purely analytical activity with little microbiologist-dependent added-value. Concentrating smaller microbiology labs in one central lab or networking may not always be possible for practical reasons and will again increase the distance between clinical microbiologists and some of the microbiological tests. A solution that can assure a sufficient lab size even in medium-sized hospitals without the need for collaboration with other labs or outsourcing is integration of the microbiology lab with other pathology labs such as clinical chemistry or clinical hematology. This kind of integration can combine economy of scale with conserving the microbiological activity within the hospital and thus the close link between microbiology and infectious disease and infection control specialists. Integration of laboratories in its simplest form can exist in sharing of machines and lab space. It can also lead to an integration of all diagnostic activity according to common workflows. An example is an integrated unit for molecular testing performing all nucleic acid based testing; microbiological, hematological but also human genetics or forensic medicine. This integrated lab demands new ways of organizing lab activity. Essential to the integrated lab is a separation of medical and technical expertise and medical and organizational responsibility.

EBV, CMV and virus hepatitis in solid-organ transplant recipients

**S189** EBV and CMV-specific immunity

M.K. Brenner (Houston, US)

Following allogeneic stem cell transplantation, patients have profound and prolonged immunosuppression. This is most severe after HLA-mismatched transplants that require extensive T cell depletion to prevent graft-versus-host disease, and in recipients of cord blood transplants, which contain few memory T-lymphocytes. The consequence is a high morbidity and mortality from infection and disease relapse. We have been developing two approaches to repopulate the immune system following transplantation to reduce both types of risk. Our first approach is to isolate viral and fungal antigen reactive T lymphocytes from donor blood and expand them *ex vivo* before infusing them into the stem cell recipients. We have generated T lymphocytes that are specific for common viruses such as Epstein–Barr virus, cytomegalovirus, and adenovirus, and engineer them to expand efficiently *in vivo*. They have proved effective at preventing and treating serious virus illness in the target patient populations and we are now extending this approach to the treatment of fungal disease. Our second approach is to remove alloreactive T cells from donor PBMT and infuse these deleted T cells to produce broad immune reconstitution. As a further safety measure to prevent GvHD from the infused cells, we incorporate a new suicide gene composed of a modified caspase 9 that can be activated by a small molecule drug. Early clinical results show high safety and efficacy of the approach.

We have also developed tumor-specific cytotoxic T lymphocytes, using both native and chimeric receptors directed to tumor associated antigens. We express the chimeric receptors in virus specific T lymphocytes, thus gaining the benefit of both an antiviral and an antitumor response from the same infused T-cells. These approaches appear to be extremely cost effective and to have a high margin of safety.

**Hepatitis E: monitoring and treatment**

J. Isopet (Toulouse, FR)

Hepatitis E virus (HEV) infection is now considered as an emerging infectious disease in industrialized countries. HEV genotypes 3 and 4...
Screening procedures have a significant impact on incidence of methicillin-resistant Staphylococcus aureus. How many patients do you need to screen for methicillin-resistant MRSA to find a positive? Results from a screening programme in a UK teaching hospital G. Jones*, J.K. Sutton, S. Aplin, D. Browning (Southampton, UK)

Objectives: Screening for methicillin-resistant Staphylococcus aureus (MRSA) became mandatory in the UK for all elective and day case admissions from April 2009 and will be mandatory for all emergency admissions from April 2011. Data to assess the effectiveness of this strategy at an individual hospital level are lacking. We analyzed our screening programme data to determine the number needed to test (NNT) to detect a colonised patient across a range of clinical specialties, and develop a risk assessment strategy for MRSA screening.

Methods: MRSA screens of nose and groin were performed using chromogenic agar, with additional sites such as wounds and catheters included when present. In our hospital, MRSA screening data were resolved prospectively to individual patient level as opposed to a commonly utilized approximation using matched census (admission) data. Screening data were mapped to a patient administration system database containing relevant specialty codes. Mismatches where no screening results existed for individual patients were investigated weekly and included identification of patients in specific categories excluded from screening. Screening efficiency by specialty was fed back weekly to clinical teams to drive improved performance. Rates of MRSA positivity and NNT to detect a positive patient were determined for each specialty.

Results: For the 12 months from October 2008, the laboratory performed >160,000 MRSA swabs on 51,855 individuals costing 600,000 Euros. Screening efficiency for elective admissions improved from 60% to 99% (2228/2249) and for emergency admissions from 76% to 97% (2996/3077). Overall, 1.2% of hospital admissions were MRSA positive, with 1.6%, 0.7% and 0.6% being MRSA positive in emergency, elective and day case cases respectively. The highest MRSA positivity rates were seen in emergency cases in hepatology (4.3%), interventional radiology (3.7%) and vascular surgery (3.3%). 1.5% of elective vascular surgery patients were MRSA positive. The lowest MRSA positivity rate was in day case orthopaedics where 1,006 patients were screened without detecting a single positive patient. NNT to detect a positive ranged from 24 to >1,000 depending on clinical speciality and admission type.

Conclusions: Accurate data on results of MRSA screening can be used to assess both risk for individual patient admissions and the cost effectiveness of screening in specific patient groups, and to enhance the efficiency of the screening process.
Impact and cost-effectiveness of MRSA screening

**O197** Long-term control of endemic methicillin-resistant *Staphylococcus aureus* in a tertiary centre: a segmented regression analysis of a stepwise approach

J. Rodríguez-巴ñot*, L. García, E. Ramírez, C. Luptón, M.A. Muntañ, C. Velasco, J. Gálvez, M.D. del Toro, A. Millán, L. López-Cerero, A. Pascual (Seville, ES)

**Objectives:** We evaluated the long term efficacy of several bundles of control measures against endemic methicillin-resistant *Staphylococcus aureus* (MRSA) in a 1000-bed tertiary hospital.

**Methods:** A quasi-experimental study of interrupted time series was performed. The outcome variables were hospital-wide bimonthly rates (cases per 1,000 patient-days) of nosocomial infection and bacteraemia due to MRSA from January 2005 to December 2008. The interventions were as follows: Intervention 1 (In1), implemented in January 1997: active surveillance of MRSA colonisation of patients and healthcare workers (HCW) in wards with ongoing MRSA transmission as suspected by the analysis of clinical epidemiologic data; and intervention 3 (In3), implemented in January 2001: active surveillance of readmitted patients and patients admitted from other centers. For the analysis, segmented regression was used. The following model was adjusted: \[ Y = b_0 + b_1 \cdot \text{time} + b_2 \cdot \text{In1} + b_3 \cdot \text{time after In1} + b_4 \cdot \text{In2} + b_5 \cdot \text{time after In3} + \epsilon, \]

where \( b_1 \) = baseline time trend, \( b_2 \cdot \text{level change after In1} \), \( b_3 \cdot \text{trend change after In1} \), \( b_4 \cdot \text{level change after In2} \), \( b_5 \cdot \text{trend change after In3} \), and \( b_7 \cdot \text{trend change after In3} \).

**Results:** The rate of colonisation/infection and bacteraemia in the preintervention period (1995–1996) was 0.56 and 0.10, respectively. Neither the level nor the trend changed after In1. Rates were significantly reduced to 0.28 and 0.04 after In2, and to 0.07 and 0.02 after In3, respectively, and were kept in those levels since 2008. There was no significant changes in the rate of bacteraemia due to methicillin-susceptible *S. aureus*. The results cannot be explained by changes in the case-mix or antibiotic consumption. The segmented regression model is shown in the table.

**Conclusion:** Sustained control of endemic MRSA in tertiary centres is possible by active screening of patients and HCW, contact precautions, and control of high risk patients at hospital admission.

<table>
<thead>
<tr>
<th>MRSA colonisation/infecion</th>
<th>Coefficient (95% CI)</th>
<th>( P )</th>
<th>MRSA bacteraemia</th>
<th>Coefficient (95% CI)</th>
<th>( P )</th>
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<td>( b_1 ) -0.004 (-0.16; 0.008)</td>
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<td>0.001 (-0.003; 0.004)</td>
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<td>( b_2 ) 0.03 (-0.08; 0.14)</td>
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<td>-0.018 (-0.050; 0.014)</td>
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<tr>
<td>( b_3 ) 0.001 (-0.016; 0.018)</td>
<td>0.8</td>
<td>0.002 (-0.003; 0.006)</td>
<td>0.4</td>
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<tr>
<td>( b_4 ) 0.06 (-0.05; 0.18)</td>
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<td>-0.05 (-0.08; -0.02)</td>
<td>0.002</td>
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<td>-0.006 (-0.010; -0.001)</td>
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<td>( b_6 ) 0.07 (-0.01; 0.16)</td>
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<td>0.002 (-0.022; 0.026)</td>
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<tr>
<td>( b_7 ) 0.04 (0.03; 0.05)</td>
<td>&lt;0.001</td>
<td>0.003 (0.000; 0.006)</td>
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**O198** Diagnostic yield and financial consequences of anatomic sites tested using rapid diagnostic tests for methicillin-resistant *Staphylococcus aureus*

M.W. Wassenberg*, J. Klaymans, A. Troelstra, M. Bonten on behalf of the Dutch Rapid MRSA Diagnostics Study Group

**Objectives:** The Dutch MRSA screening strategy requires sampling of multiple sites and with rapid diagnostic testing (RDT) conventional cultures are mandatory as back up. We determined cost-effectiveness of a less extensive screening regime using RDT without back up cultures in a prospective multi-center study.

**Methods:** All patients at risk of MRSA colonisation and fulfilling the criteria for pre-emptive isolation in 14 hospitals between 12/05 and 06/08 were eligible. In addition to conventional cultures, BD GeneOhmTM MRSA PCR (‘IDI’, BD Diagnostics) or the Xpert MRSA assay (‘GeneXpert’, Cepheid) was performed directly on patient material. In a nested cohort study the chromogenic agar MRSA-ID (bioMérieux) was tested. Cost-efficacy is determined assuming isolation measures would have been based on single site testing of the nares without back up cultures. Isolation of MRSA at any site tested using broth enrichment culture was the gold standard.

**Results:** 1764 patients (mean 48 years, 56% male) were enrolled. 3.3% carried MRSA; after hospitalization abroad 1.6% (20/1225), contact with pigen 15.0% (29/193) and contact screening related to MRSA positive patients 2.8% (8/289). The sensitivity of screening of the nares using IDI PCR, GeneXpert and MRSA-ID was 69.2%, 56.3% and 61.5%, respectively with negative predictive values >98.4% for all tests. Costs per patient tested were £56.62, £70.92 and £8.06 for IDI PCR, GeneXpert PCR and MRSA-ID, respectively. Isolation days avoided were 2.3%-5.2% higher with single site testing compared to multiple site testing because of higher specificity (and lower sensitivity). Test costs per isolation day avoided were £25.00, £34.48 and £49.41 for IDI PCR, GeneXpert PCR and MRSA-ID respectively. As compared to “nares-only” multiple site testing prevented respectively, 4 and 6 false negative cases using IDI PCR (4/853, 0.5%) and GeneXpert PCR (6/911, 0.7%) at the additional costs of respectively £148.55 and £161.78 per patient. Chromogenic agar testing of multiple sites prevented 4 FN results (4/428, 0.9%) at no additional costs.

**Conclusion:** Although the recommended multiple site sampling strategy has a higher sensitivity than “nares-only” screening without back up cultures, our results demonstrate that in a low endemic setting the benefits of such a strategy are limited, and the costs are high. Financial consequences of the missed MRSA patients have to be determined to draw definite conclusions.

**O199** Modelling the cost-effectiveness of screening and decolonization in the control of methicillin-resistant *Staphylococcus aureus*

J.V. Robotham*, N. Graves, B.D. Cookson, J. Wilson, A.G. Barnett, J. Edgeworth, R. Batra, B.S. Cooper (London, UK; Brisbane, AU; Bangkok, TH)

**Objectives:** To use transmission dynamic models to assess the cost-effectiveness of defined screening and decolonisation strategies in the control of methicillin-resistant *Staphylococcus aureus* (MRSA).

**Methods:** We developed a dynamic transmission model of MRSA in intensive care units (ICUs) to evaluate the effectiveness and cost-effectiveness of screening and topical decolonisation (both nasal ointment and body wash-based antisepctic protocol). The model was parameterized using evidence from multiple sources (data, literature and expert opinion) including full parameter uncertainty. Thirteen strategies were compared, including decolonisation of all admissions, decolonisation of patients identified as MRSA positive through screening (comparing conventional cultures, chromogenic agars and polymerase chain reaction (PCR)-based techniques) and targeting interventions to high risk patients. Incremental costs and health benefits of the alternatives were evaluated under different settings of prevalence, proportion of high risk patients and ICU size.

**Results:** Compared to a baseline strategy of decolonisation of clinical infections only, all other strategies were cost-saving and gave increased health benefits. Decolonisation of all patients was the most cost effective option, saving £60,000/quality adjusted life year (QALY) gained. For screening, and decolonisation of identified MRSA positives, PCR had the greatest ability to reduce MRSA transmission (giving a 94% reduction in infections per 100 admissions, compared to 64% with conventional culture). Including parameter uncertainty, the best decision depended on the decision maker's willingness to pay for health benefits: at a value of £20,000–30,000 per QALY, admission screening with PCR combined with decolonisation of identified positives was the best strategy. However, there was uncertainty in this decision, reflecting parameter uncertainty,
and the expected value of perfect information on the parameters was high (~£10,000).

**Conclusion:** With no microbial resistance to decolonisation agents, all decolonisation strategies were cost-effective, particularly decolonisation of MRSA positive admissions identified through PCR screens. These models allow uncertainty in decision making to be quantified and highlight parameters on which more information is needed to ensure cost-effective decisions, in this case the probability of progressing from colonisation to infection for decolonised and ‘un-decolonised’ patients.

### Future high-throughput microbiology laboratory

**S204 I believe in mass-spectrometry**

X. Nassif* (Paris, FR)

MALDI-TOF mass spectrometry: a revolution in the identification of pathogens in clinical laboratories. In the management of bacterial infections, identification of the pathogen following growth remains essential to propose as soon as possible the most appropriate treatment before the availability of antibiotic susceptibility. The strategy for most common pathogens requires Gram staining, the results of simple tests such as determination of oxidase and catalase activity and appropriate phenotypic tests using commercial identification kits and/or automated systems. A new proteomic strategy is progressively changing this strategy by identifying bacterial or fungal species grown on plates within minutes. Matrix assisted laser desorption ionisation time-of-flight mass spectrometry (MALDI-TOF-MS) of intact bacteria yield reproducible spectrum depending upon strain or species. Using whole viable bacteria we describe here the application of MALDI-TOF-MS to the identification of bacterial pathogens isolated in routine clinical microbiology laboratories. Our aim was, once a primary isolate of a bacterium has grown onto a plate, to identify spectral prints, in the MALDI-TOF spectrum, that can be used to recognize the genus or the species. MALDI-TOF-MS was performed using bacteria obtained from one isolated colony. Over 400 clinically relevant bacterial species were selected. For each of these species one or several references strain was (were) selected to establish spectral prints. For each strain, only peaks that were conserved in the spectra of all 10 isolated colonies and with a relative intensity above 0.1 were retained, thus leading to a set of 3 to 30 selected peaks per strain. For each group of pathogens the database was validated using a set of isolates identified using mostly 16S RNA sequencing. The use of this strategy to identify bacterial species in clinical microbiology laboratories will be presented.

### Climate change and parasitic infections in Europe

**S206 Expansion of leishmaniasis and other parasitic diseases in Europe**

B. Eccengård* (Umeå, SE)

**Objectives and Methods:** To give an overview over climate change in Europe with some regional examples and the knowledge we have on its influence on the prevalence of parasitic infections with the use of review of literature.

**Results:** The northern part of Europe, the Arctic will have three times higher temperatures than the rest of the world due to climate change. We have a lot to learn from what is happening in the circumpolar area for adaptation strategies. Parasitic infections as Leishmania, Opisthorchis, Echinococcosis multilocularis and alveolaris are expanding along with Giardia intestinalis as some examples. The impact will differ regionally.

**Conclusion:** Given the dynamis and the complexity of climate/sensitive infectious disease, particularly those transmitted by mosquitoes or rodents Europe needs to develop and sustain surveillance and early warning systems with a regional focus.

### Food for thought: tackling the problem of food-borne infection in the elderly

**S209 The elderly patient as a sitting duck for food-borne infections: causes and consequences**

L. Medeiros* (Columbus, US)

According to the United Nations, the world population of elderly will surpass that of children under age 15 by the year 2045. Health resources will shift with population growth; thus, measures to reduce health cost through preventive care are prudent. Illnesses from food-borne pathogens are avoidable if technologies are used to maximize safety of food and water, populations are educated in self-care, and medical therapies are advanced for early diagnosis and treatment. Since self-care strategies require alteration of usual cultural and habitual behavior, education efforts have limited success with the elderly. Why is it difficult to teach the elderly how to handle food safely and what are the consequences for failure to heed professional advice? Medically, when is a person elderly? When does the body begin senescence and susceptibility to opportunistic infections increase? The aging immune system is the primary reason for susceptibility to food-borne pathogens in the elderly. Natural, senescent immunity is exacerbated by the immune insufficiency of chronic disease and pharmacological therapies common in the population. Immune insufficiency associated with malnutrition becomes a causative factor as the physical and mental capacity of the aging individual deteriorates. Poor hygiene, failure to handle and store foods safely, and inability to distinguish between safe and tainted food may all be consequences of diminished mental or general health. For those in group housing, failure of care staff to heed food handling guidance could affect the health of multiple residents due to wide-spread exposure and immune insufficiency. Yet, acceptance of well-meaning advice to change poor health habits is limited due to lack of trust in the efficacy of the information, information that is contrary to cultural and traditional practices, or the failure to recognize and accept the decline of physiological and mental health. The challenge to the health professional that is providing food safety guidance is to recognize the social, health and mental barriers that control the ability of the individual to act on the advice. The goal is no food-borne illness in the world, but reality is that when preventative care is no longer possible, palliative care must take its place.

### Paediatric infectious diseases

**S215 Aetiology of community-acquired pneumonia in children during the influenza A (H1N1) outbreak**

L. Michelin*, J. Fracasso, P. Garrido, V. Buffon, L. Generosi, P. Oliveira Filho (Caxias do Sul, BR)

**Objective:** In July 2009, a respiratory illness outbreak caused by influenza A virus (H1N1–2009) was identified in Caxias do Sul, Brazil. The aims of the study is to determine the impact of influenza A H1N1 2009 on the viral etiology of pneumonia among children admitted at General Hospital of Caxias do Sul from July 01 to August 31, 2009.

**Methods:** Retrospective medical chart reviews on the pediatric hospitalized patients diagnosed with acute respiratory infection between July and August 2009. We evaluated demographic data, clinical and laboratory findings. Nasopharyngeal aspirates for detection of respiratory viruses were analyzed by indirect immunofluorescence (IFI) and real-time polymerase chain reaction (RT-PCR).

**Results:** A total of 53 children were hospitalized for severe acute respiratory disease, according to the criteria established by the Health Ministry of Brazil. Most patients were male (60.3%) and had less than one year of age (35.8% with less than 6 months and 26.4% between 6 and 12 months). Comorbidities were identified in 9.4%. Fifteen patients were referred for the intensive care unit, and one third of them required mechanical ventilation. No deaths occurred. Six patients (11.3%) had
confirmed influenza A (H1N1) and in 27 children (50.9%) were identified respiratory syncytial virus (RSV) as the etiologic agent of pneumonia.

**Conclusion:** As in previous years, respiratory syncytial virus has remained as predominant agent in the etiology of viral pneumonia in spite of the outbreak of influenza A (H1N1) experienced in 2009.

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**Norovirus infection in hospitalized Australian children**

**A. Kesson**, N. Benwell, E. Elliott (Westmead, Sydney, AU)

**Objective:** Norovirus, previously the Norwalk agent, is a common cause of acute gastroenteritis. We determined the incidence and relative impact of norovirus in children with acute diarrhoea admitted to a tertiary paediatric hospital in New South Wales, Australia.

**Methods:** Faecal samples were collected from children presenting to our Hospital with episodes of acute diarrheal illness over a 12 month period (2007). The viral pathogens, rotavirus and adenovirus were detected using immunochromatography and norovirus was detected using enzyme linked immunosorbent assay.

**Results:** During this 12 month period, faecal samples were collected from 3962 children who presented with diarrhoea to our Hospital and viral pathogens were detected in 294 of these children who required hospital admission. 231 of 294 (78.5%) children with gastroenteritis required a hospital stay of one week or less, median 1 day and 212 had a single viral stool pathogen detected of which 63 (30%) were norovirus, 56 (26%) were adenovirus and 93 (44%) were rotavirus. Dual viral infections were detected in 19 (8%). Norovirus infections most commonly presented in spring (September-November, with an October peak) in infants (age less than 12 months). Of the 63 patients with a hospital stay greater than one week, 28 (44%) had norovirus infection, 16 were non-oncology patients who developed nosocomial infection after admission for another condition. The 25 oncology patients were older and had a longer hospital stay (median 11 days) than non-oncology patients and 7 (28%) had nosocomial infection due to norovirus.

**Conclusion:** We have demonstrated the impact of community-acquired norovirus gastroenteritis and the high frequency of nosocomial norovirus infection in a tertiary paediatric hospital. With the advent of rotavirus vaccination, norovirus may become the major viral pathogen causing gastroenteritis in Australian children.

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**Impact of rapid PCR detection of enteroviruses in spinal fluid in children with meningitis**

**K.M. Huizing**, C.M. Swantick, A.M. Landstra, A.A. van Zvet, P.A. van Setten (Arnhem, NL)

**Objectives:** We hypothesized in this study that the use of a rapid PCR on enteroviruses in spinal fluid significantly reduces the duration of hospitalization, and use of antibiotics. We expected that these reductions would lead to lowering of hospital costs.

**Methods:** The study group comprises children admitted to the hospital from April 2009 until November 2009 with confirmed enterovirus meningitis. Since 2009 we performed the PCR on enteroviruses in spinal fluid in our hospital. The results are available within 3 hours. This study group was compared to a historical control group that consisted of children who were admitted in 2007 and 2008 with confirmed enterovirus meningitis. In the historical control group, results for enterovirus PCR tests were available after 3 to 7 days. We analyzed both groups for clinical and laboratory parameters, length of hospital stay, use of antibiotics and estimated overall costs.

**Results:** The study group and historical control group were comparable with respect to clinical and laboratory data. A significant difference was found between the groups in length of hospital stay (p < 0.0001). The mean duration was 6.7 days in the 2007–2008 group (range 2.3–41.0 days) versus 1.8 days in the 2009 group (range 0.8–4.55 days). The mean duration of use of antibiotics was also significantly reduced (p < 0.0001) from 4.8 days (range 1.3–12.8 days) to 0.75 days (range 0.1–1.5 days). Overall costs were 2900 euro lower per patient in the 2009 group.

**Conclusion:** Our data show that in children with enterovirus meningitis the use of a rapid PCR results in a significant reduction of hospital stay and duration of antibiotic treatment. Subsequently, it also leads to an important reduction of hospital costs. The rapid enterovirus PCR is an important diagnostic tool in daily management of children with meningitis.

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**Predictive model for diagnosis of neonatal sepsis**

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Early diagnosis of neonatal sepsis is essential to prevent severe complications and avoid unnecessary use of antibiotics.

**Objective:** To develop a predictive model for the diagnosis of neonatal sepsis.

**Methods:** This case–control study was conducted in QSNICH, Bangkok. Data were derived from the medical records of 45 sepsis and 135 non-sepsis neonates for early sepsis, and 52 sepsis and 156 non-sepsis cases for late sepsis, during the period 1 October 2004–30 September 2007. Potential predictors consisted of risk factors, clinical conditions, laboratory data, and treatment modalities. The models were developed based on multiple logistic regression analysis.

**Results:** The incidence of early and late proven neonatal sepsis was 1.27 and 1.46%, respectively. For early neonatal sepsis, the equation and score consisted of 5 variables: length of stay pre-sepsis, poor feeding, abnormal oxygen saturation (<92%), thrombocytopenia (<150,000/mm³), and leucopenia (<5000/mm³). For late neonatal sepsis, the model had 6 variables: poor feeding, abnormal heart rate (outside the range 100–180 x/min), abnormal temperature (outside the range 36–37.9°C), abnormal oxygen saturation, abnormal leucocytes (according to Manroe’s criteria by age), and abnormal pH (outside the range 7.27–7.45). The area below the ROC curve were 87.8 and 95.5% for early and late neonatal sepsis, respectively. Validation used subsets of the original data-set, twice for each model, and produced areas below the curve of 82.2 and 86.2% (for the early group) and 96.3 and 93.6% (for the late group). For early sepsis, score 1 had a sensitivity of 73.3% and specificity of 84.4%. For late sepsis, score 2 had a sensitivity of 88.5% and specificity of 90.4%.

**Conclusion:** 2 predictive models were developed, one for proven early-onset and another for proven late-onset neonatal sepsis. Derivation and preliminary validation produced good results.

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**Failure of oral colistin to prevent colonization with extended-spectrum β-lactamase-producing enterobacteria in newborns hospitalized at a neonatal intensive care unit**

**V. Strenger***, T. Gischliesser, G. Zarfel, G. Feierl, A.J. Grisold, L. Massoud, B. Reich, W. Müller, B. Urlesberger (Graz, AT)

**Objectives:** Colonisation and infection with extended-spectrum β-lactamase producing Enterobacteriaceae (ESBL-E.) is an emerging problem at Neonatal Intensive Care Units (NICU). ESBL-E. often show additional antimicrobial resistance. Colistin is reported to be effective in treatment of infections with multiresistant enterobacteria as well as for selective digestive decontamination (SDD). Over the last years several outbreaks of ESBL-E. colonisation occurred at our NICU.

**Methods:** For prophylaxis of necrotizing enterocolitis (NEC) all term and preterm born neonates hospitalised at the NICU of the Medical University of Graz routinely receive gentamicin orally (15 mg/kg/d). Patients are routinely screened at least twice a week for ESBL-E. in stool specimens. ESBL-E. colonised patients subsequently are cohorted. From May 2005 through September 2007, gentamicin was replaced by colistin (8 mg/kg/d) administered orally during ESBL-E. outbreak situations. We retrospectively analysed all neonates colonised with ESBL-E. from May 2005 through September 2007 regarding influence of colistin on colonisation with ESBL-E.. Genetic relatedness of strains was assessed by using repPCR-technique.
Results: During the study period 3 ESBL-E. outbreaks were observed and 30 (2.02%) out of 1488 neonates have been colonised with ESBL-producing Klebsiella pneumoniae (ESBL-Kp, n = 22) or Klebsiella oxytoca (ESBL-Ko, n = 8). 12 out of 22 pts. colonised with ESBL-Kp and 1 out of 8 pts. colonised with ESBL-Ko had received oral colistin at time of colonisation with ESBL-E. Four different clones of ESBL-Kp and 2 different clones of ESBL-Ko were isolated indicating occurrence of patient-to-patient transmission.

Conclusion: Despite administration of Colistin during outbreaks of ESBL-E, colonisation, additional colonizations (including patient-to-patient transmission) were observed. Thus, oral colistin (8 mg/kg/d) does not prevent colonisation with ESBL-E. Further analyses are needed to assess its usefulness for SDD.

Success stories about control of nosocomial antimicrobial resistance – yes, we can!

KPC control (Israel)
M.J. Schwaber* (Tel Aviv, IL)

Containment of a nationwide outbreak of KPC-producing Klebsiella pneumoniae via a centrally-coordinated public health intervention.

Background: Since 2006, Israeli hospitals have faced a clonal outbreak of carbapenem-resistant Klebsiella pneumoniae, producing the serine carbapenemase KPC-3. Locally- implemented infection control measures in affected hospitals failed to contain spread. A nationwide intervention was launched to contain the outbreak and introduce a strategy to control future dissemination of antibiotic-resistant bacteria in healthcare facilities.

Methods: In March 2007, the Ministry of Health issued guidelines mandating physical separation of hospitalized carriers of carbapenem-resistant Enterobacteriaceae (CRE) and dedicated staffing, and appointed a professional task force charged with containing the spread of the epidemic strain. The task force paid site visits at acute care hospitals, evaluated infection control policies and laboratory methods, supervised adherence to the guidelines via daily census reports on carriers and their conditions of isolation, provided regular feedback on performance to hospital directors, and intervened additionally when necessary. During 2008, the intervention was extended to long-term care facilities, and in June 2008 national guidelines for active surveillance were issued. The primary outcome measure was the incidence of nosocomial CRE cases diagnosed by clinical culture in acute care hospitals.

Results: By March 2007, over 1200 patients were affected in the nation’s acute care hospitals. Prior to the nationwide intervention, the monthly incidence of nosocomial CRE climbed steadily, peaking at over 180 cases. Crude 30-day mortality was >30%. With the intervention, the continuous rise in incidence of CRE acquisition was halted, and by the end of the 14-month initial intervention period the number of new monthly cases was reduced to 46. Following the introduction of active surveillance guidelines, monthly incidence fell further, reaching a low of 24 as of October 2009. A direct correlation was observed between compliance with isolation guidelines and success in containment of in-hospital CRE transmission.

Conclusions: A centrally-coordinated public health intervention has succeeded in containing a nationwide outbreak of CRE in Israeli hospitals after local infection control measures failed. The intervention demonstrates the importance of strategic planning and national oversight in combating antimicrobial resistance.

MALDI-TOF in clinical microbiology

Microbiological identification by routine use of MALDI-TOF
M. Droucourt* (Marseille, FR)

The analysis of bacterial protein profile obtained after matrix-assisted laser desorption ionization time-of-flight (MALDI-TOF) mass spectrometry (MS) emerged over the past years as a new method for the accurate identification of bacterial isolates. MALDI-TOD-MS protein profiling can be achieved within minutes thus speeding the identification; it is a cheap technology including the decreasing cost for mass spectrometers; protein profiles and issued identifications are reproducible and robust; and new generation mass spectrometers are smaller machines easily implanted within the laboratory. All these parameters make MALDI-TOF MS the technology to be introduced in any modern microbiology laboratory, including the point-of-care laboratory.

Databases, the crucial part of the process, now comprise of most of the bacterial species routinely encountered in the microbiology laboratory. Despite the fact that some Gram-positive organisms remain “MALDI-TOD-MS resistant” in part because of underlying taxonomic weaknesses and in part because of database weaknesses, MALDI-TOF is definitely the first line method for the routine identification of bacterial isolates in the 21 century, pushing biochemical profiling and even the gram staining off the laboratory towards the museum of bacteriology.

Bacterial typing
T. Han* (Giessen, DE)

Rapid identification and typing of Listeria species by matrix-assisted laser desorption ionization-time of flight mass spectrometry. Listeria monocytogenes is a food-borne pathogen that is the causative agent of human listeriosis, an opportunistic infection that primarily infects pregnant women and immunologically compromised individuals. Rapid, accurate discrimination between Listeria strains is essential for appropriate therapeutic management and timely intervention for infection control. A rapid method involving matrix-assisted laser desorption ionization-time of flight mass spectrometry (MALDI-TOD MS) that shows promise for identification of Listeria species and typing and even allows for differentiation at the level of clonal lineages among pathogenic strains of L. monocytogenes is presented. A total of 146 strains of different Listeria species and serotypes as well as clinical isolates were analyzed. The method was compared with the pulsed-field gel electrophoresis analysis of 48 Listeria strains comprising L. monocytogenes strains isolated from food-borne epidemics and sporadic cases, isolates representing different serotypes, and a number of Listeria strains whose genomes have been completely sequenced. Following a short inactivation/extraction procedure, cell material from a bacterial colony was deposited on a sample target, dried, overlaid with a matrix necessary for the MALDI process, and analyzed by MALDI-TOD MS. This technique examines the chemistry of major proteins, yielding profile spectra consisting of a series of peaks, a characteristic “fingerprint” mainly derived from ribosomal proteins. Specimens can be prepared in a few minutes from plate or liquid cultures, and a spectrum can be obtained within 1 minute. Mass spectra derived from Listeria isolates showed characteristic peaks, conserved at both the species and lineage levels. MALDI-TOD MS fingerprinting may have potential for Listeria identification and subtyping and may improve infection control measures.

MALDI-TOF-MS of surface-associated and stable intracellular proteins for identification and resistance profiling of human pathogens
H.N. Shah* (London, UK)

Microbial classification and identification is today based largely upon comparative 16S rRNA sequencing analysis. There is, however, a desire to retain a polyphasic approach as microorganisms are far too diverse to be unequivocally delineated by a single method. Proteomics, in the form SDS-PAGE, MLEE or IEF profiles, have had a long history of applications and have shown excellent congruence with genomic methods such as DNA-DNA reassociation. The arrival of MALDI-MS and ESI-MS has made the study of the proteome so accessible that within less than a decade platforms are now available for clinical applications. Thus, the development of intact cell MALDI-TOF mass spectrometry is
approaching maturity and its uptake by diagnostic laboratories has been increasing steadily. Extensive databases e.g. AmamosTec (>100,000 MS spectra), negligible sample preparation and rapid analysis have been the main reasons for its success. No specific guidelines present in the MS spectra are either surface-associated on intracellular ribosomal proteins, consequently, at present, little information can be obtained using solely this approach to gain information on antibiotic resistance patterns. More in-depth analysis involving 1D, 2D and LC-MS-MS methods are required. Using such approaches, new information on antibiotic resistance mechanisms are becoming apparent and providing an excellent tool to elucidate complex mechanisms where genome analysis alone cannot provide a solution.

**Yeast identification**

G. Haase* (Aachen, DE)

Identification of clinical yeasts is an important task in the mycological laboratory especially in view of a rising number of patients with respective opportunistic mycoses. Reliable species identification can be used as a first guidance for initiation of an appropriate antifungal therapy. Classical phenotypical identification of yeasts is often tedious and needs up to 3 days for obtaining a reliable result. A further obstacle is the limited databases of commercially available systems and test results with variable outcome for a given species. Genetic identification by in situ hybridization or by sequence analysis is relative expensive in terms of consumables per test. After initial introduction of mass fingerprinting for species identification of bacteria by Claydon et al. 1996 availability easy-to-handle instruments and equipped with sophisticated analysis software facilitated use of this technique also for identification of yeasts in the last years. Qian et al. (2008) described the use a fixation step by using alcohol as an essential prerequisite for obtaining improved mass signatures in case of yeasts. In a comparative study Marklein et al. (2009) could show that usage of a commercial MALD-TOF MS-based microbial identification system (MALDI BioTyper System, Bruker Daltonics) was superior to an essential prerequisite for obtaining improved mass signatures in case of yeasts. In a comparative study Marklein et al. (2009) could show that usage of a commercial MALD-TOF MS-based microbial identification system (MALDI BioTyper System, Bruker Daltonics) was superior to otherwisedifficult-to-achieve identification of potentially pathogenic Prototheca spp., a group of algae with a yeast-like cultural appearance. Of note, Marinach et al. (2009) demonstrate that MALDI MS is capable to estimate Fluconazole resistance in case of *C. albicans*. In conclusion, MALDI-TOF MS fingerprinting turned out as a very promising tool for reliable and rapid (hands-on time <5 min) identification of clinical yeasts with low costs for consumables per identification (<1 €). This approach was not so much hampered by influence of the morphology of the fungus and cultural conditions e.g. culture media and minor changes in incubation temperature when compared to MS-based identification of hyphomyces. So this technique facilitates high through put and objective identification of yeasts when using a quality-checked database.

**Infections in the elderly, new concepts**

**HIV and aging**

R. Casula* (Rome, IT)

Epidemiological data show that HIV-infected population is aging, mainly as a result of prolonged survival due to potent antiretroviral regimens that can successfully control viral replication, thus preventing AIDS-related events, but also of a late diagnosis of HIV infection in older patients. No specific guidelines have been developed for the clinical management of older HIV-infected patients but clinicians must take into account several factors that are peculiar of this population, like the presence of co-morbidities, the pharmacokinetics characteristics of the elderly, a possible higher incidence of drug-related toxicity and a different response to antiretroviral therapy.

In older HIV-infected population, morbidity and mortality still remain high as a consequence of an increased risk of non-AIDS related conditions compared to age-matched HIV-seronegative subjects. These conditions include cancers, neurocognitive disorders, cardiovascular, liver, kidney and bone diseases. Many factors contribute to non AIDS-related co-morbidities and they can be related to the population characteristics (e.g. higher prevalence of traditional health-related risk factors like diabetes, hypertension, hyperlipidemia and smoking), to antiretroviral drugs (e.g. association between long term exposure to protease inhibitors and higher risk of cardiovascular disease, tenofovir exposure and renal or bone dysfunction) or to the HIV-infection itself (e.g. association between age-related events and low CD4 cells count or higher levels of inflammation markers found in HIV-positive patients). The pharmacokinetic characteristics of the elderly are peculiar, with a possible modification of drug absorption, distribution and hepatic or renal clearance that results in a high inter-individual pharmacokinetic variability. Moreover, interactions between antiretrovirals and drugs frequently prescribed for non HIV-related co-morbidities can further contribute to this variability. As a consequence, plasma drug levels can drop below effective concentrations promoting treatment failure or can become high resulting in toxicity.

Many data shows that, despite a high rate of virological suppression (usually attributed to high adherence to the therapy), older patients had a significantly slower CD4 cells count reconstitution than younger subjects. The causes for such finding could be due to several factors like the late diagnosis and treatment of HIV infection on the one hand, or the thymic involution and immunosenescence during aging on the other hand. Many studies indicated that suboptimal CD4 cells increase is associated to a higher risk of non AIDS-associated morbidity and mortality (for cancer, heart and liver disease) in this patient population.

In conclusion, as the prevalence of older HIV-infected patients is increasingly growing, additional research is needed to fully understand factors contributing to the peculiar evolution of HIV infection and associated co-morbidities in this age group, in order to optimize the clinical care of this population.

**Infectious disease outbreaks in nursing homes**

M. Pajol* (Hospitalet Llobregat, ES)

Advances in health care have condued in developed countries to an aging population. Long-term care facilities (LTCF) are institutions which provide health care to people unable to manage themselves in the community. Most residents are elder and have multiple comorbidities. Residents will stay at LTCF for months or years. Hence, comfort, dignity and socialization are important issues. In order to control costs, many post-acute patients who used to stay in acute care hospitals for a long time, are now currently transferred to LTCF. This situation has led to the necessity of invasive devices such as urinary and vascular catheters and feeding tubes. This fact increases the incidence of nosocomial infections, as does the one observed in hospitals. Several significant differences can be pointed out between hospitals and LTCF, most notably the nurse-patient ratio, the availability of microbiological cultures, laboratory and diagnostic equipment on site and the access to costly antibiotics. In addition there are few LTCF with infection control staff. Most of them lack of nosocomial infections surveillance programs and also of antibiotic policy strategies. In general, rates of colonization by multiresistant bacteria in residents of LTCF are higher than those observed in hospitalized patients. For example, some studies have shown that rates of methicillin resistant *Staphylococcus aureus* (MRSA) carriage among LTCF residents can reach 50%, while in hospitals are generally below 1–2%. Although it is possible to detect outbreaks, MRSA infections in LTCF are sporadic, related to pressure ulcers acific guilier less serious than those seen in hospitals. The prevalence of multidrug resistant Gram-negative (MDR-GNB) bacteria is also high among LTCF residents, particularly among those with facal incontinence and antibiotic exposure. MDR-GNB is frequently
Herpes zoster: is there a role for vaccination? M. Rothberg*(Springfield, US)

Herpes Zoster (shingles) is caused by reactivation of the varicella zoster virus. It is characterized acutely by a painful rash, and 10–20% of patients experience prolonged pain (postherpetic neuralgia), which in rare cases can last for years and be debilitating. Both the incidence and severity of zoster increase with age. Treatment options for zoster and post herpetic neuralgia are limited and costly. A shingles vaccine was licensed in Europe and the United States in 2006 following the completion of the Shingles Prevention Study, a randomized controlled trial of 38,546 healthy adults; vaccination decreased both the incidence and severity of zoster over a median of 3 years. Primary efficacy was measured by a burden of illness score which combined incidence, duration and severity of pain. The vaccine decreased burden of illness by 61%, but the effects varied by age. Efficacy in preventing acute zoster declined with age at vaccination, and there was minimal efficacy past age 80 years. Vaccination reduced the incidence of post-herpetic neuralgia at all ages by 66%. This was achieved by preventing acute zoster among patients aged 60–69 years, and attenuating disease in patients aged >70 years. Side effects were mild, but serious adverse events were more common in the vaccination group (1.9 percent vs. 1.3 percent, P=0.03). Debate about the use of the vaccine revolves not around the effectiveness, but the cost-effectiveness, as the vaccine is expensive (£136 per dose). Published analyses have found incremental cost-effectiveness ratios ranging from £18,500 to £76,500 per quality-adjusted life year. The vaccine appears to be most cost-effective among 65- to 70-year-olds, as the incidence of disease in this age group is high, but vaccine recipients are still able to mount a satisfactory immune response. Despite recommendation by the Centers for Disease Control that all adults aged >60 years receive the shingles vaccine, uptake in the US has been slow. Barriers to vaccination include difficulties with vaccine storage, variable insurance coverage, and competing priorities for primary care doctors. Since licensure, the cost of the vaccine has increased by 30%. Moreover, studies of willingness-to-pay suggest that current vaccine pricing is not acceptable to patients. In conclusion, the shingles vaccine appears to be effective in reducing morbidity, but the cost is high and universal vaccination over age 60 years may not currently represent good value.

Rapid diagnosis and resistance testing in mycobacteria

Improved sensitivity of rapid detection of Mycobacterium tuberculosis in clinical specimens by real-time PCR
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Objective: Our aim was to compare the use of DNA amplification by two polymerase chain reaction (PCR) tests for the detection of Mycobacterium tuberculosis directly in human respiratory and extrapulmonary specimens. For this purpose, the sensitivity and specificity of culture and smear diagnostics as well as the Cobas Amplicor PCR test and the Cobas TaqMan MTB real-time PCR test were compared in a trial study.

Methods: The PCR assays employed was the Cobas Amplicor M. tuberculosis test and the real-time PCR Cobas TaqMan MTB test (Roche Diagnostics, Switzerland), which use the 16S rDNA as the target template. Eight hundred and seventy-eight samples from 763 patients submitted to our clinical microbiology laboratory were processed by enriched culture analysis, direct microscopy and PCR. Rifampicin susceptibility testing was performed with culture-based MGIT assays and rpoB sequence analysis.

Results: Out of the 878 clinical specimens, 120 were from TB-positive patients. In comparison with culture, the sensitivity of the real-time PCR test Cobas TaqMan MTB test and the Amplicor M. tuberculosis test were 99.0% and 95.5% for smear-positive samples and 83.0 and 72.1% for smear-negative samples, respectively. Interestingly, 15 specimens from TB-positive patients were real-time PCR positive and Amplicor PCR negative. These specimens included 8 airway samples and 7 extra-pulmonary samples. A single TaqMan MTB test positive and culture negative specimen was found. The specificity of the M. tuberculosis PCR tests were challenged with DNAs and cultures from strains of Mycobacterium ulcerans and M. marinum, which are the mycobacterial species most closely related to the M. tuberculosis complex, resulting in negative PCR test results. Less than 2% of the isolates were rifampicin resistant, reflecting the low level of M. tuberculosis drug resistance in Norway.

Conclusions: A comparison of two M. tuberculosis-specific PCR tests performed, and the sensitivity of the real-time PCR test Cobas TaqMan MTB test was clearly superior to that of the Amplicor M. tuberculosis PCR test. The improved sensitivity, rapidity and less labour-intensive format of the Cobas TaqMan MTB test make this a valuable tool in routine tuberculosis diagnostics.

A high-throughput method for the simultaneous detection of drug resistance and genotypic mutations in M. tuberculosis isolates
I. Bergoul*, A. Schuitema, P. Klätsker, R. Anthony (Amsterdam, NL)

Objective: To make the genetic screening of tuberculosis (TB) isolates suitable for low-income countries as well as endemic countries with high prevalence/incidence of drug-resistant TB. The emerging epidemic of drug-resistant TB calls for rapid diagnosis and early detection of drug resistance. This allows immediate and appropriate treatment of the patient and could thereby reduce the spread of multidrug-resistant (MDR) or extensively drug resistant TB (XDR-TB).

We have recently developed an MTB-specific multiplex assay, based on Multiplex Ligation-dependent Probe Amplification (MLPA). This method allows simultaneous detection of multiple dispersed DR mutations and genotype-specific mutations in the Mycobacterium tuberculosis (MTB) genome and has proved to be highly specific.

Method: The current read-out of MLPA is done by capillary electrophoresis, a method that is expensive and time-consuming and therefore difficult to implement and sustain in low-income countries. Recent developments in biotechnology have raised the opportunity to transfer the assay to a liquid array. Current MLPA-probes were modified to be compatible with such a system. To cover the increasing prevalence of MDR- and XDR-TB isolates, targets revealing resistance to several important second-line drugs (e.g. fluoroquinolones) were included in the MLPA assay, as well as additional genotypic markers.

Results and Conclusion: The newly included MLPA-probes were very specific for the targeted SNPs, allowing the detection of prevalent second-line drug resistance mutations and a further delineation of Mtb complex members. The genotyping abilities of the MLPA assay were additionally increased by the discovery of a new genotypic marker. There will be an explosion of SNP discovery in the next years as data from high throughput sequencing projects become available. Methods allowing informative SNPs to be rapidly detected will then become increasingly valuable.

Furthermore, we feel that the new analysis method for MLPA will specifically be of added value in low-income countries with high endemicity of DR-TB. The liquid array allows multi-parameter testing and could provide a standard platform for several diagnostic and
screening tests, which are traditionally performed by several different methods. Therefore, MLPA combined with this detection system can bring molecular typing of MTB clinical isolates closer to the patient than is currently feasible.

**O235** Application of the rapid detection system for *M. tuberculosis* complex and rifampicin resistance Xpert MTB/RIF in decontaminated respiratory specimens, non-respiratory specimens and culptus

L. Deforges, J.M. Le Glannec, N. Lanay, R. Vergyne, A. Minaret, M. Marzouk, M. Marmiesse*, N. Finaström, P. Legrand (Creteil, Maurens-Scopont, FR)

**Objectives:** GeneXpert (Cepheid) is an automated real-time PCR system which is very easy to use and suitable for emergency use. The principle of the Xpert MTB/RIF test, running on GeneXpert, is to detect *M. tuberculosis* complex and mutations in the gene rpoB that cause resistance to rifampicin. This is done directly from at least 500 μl of a respiratory sample. After 15 min treatment of the sample all stages of the sample preparation and PCR takes place within the instrument in 1 h 30.

Some restrictions of use led us to validate this system on various types of samples.

**Methods:** Respiratory samples were decontaminated with NACl/NaOH and 500 μl of decontaminated product added to 1.5 ml of lysis buffer (provided with the Xpert product). For non-respiratory non-decontaminated samples (CSF, pleural liquid and biopsies) the sample volume was sometimes too low. In these cases distilled water was sometimes added to 500 μl. For solid culture one colony was resuspended in 500 μl of distilled water, for liquid culture 500 μl of medium were centrifuged prior to addition of lysis buffer. Fifteen decontaminated respiratory samples (PDP) and 24 non-pulmonary samples (PNP) were tested in the Xpert MTB/RIF assay, solid culture, Cobas TaqMan MTB test and cultures were tested with probes from GenProbefor identification.

**Results:** Twelve PPD of 15 were negative in Xpert MTB/RIF and the COBAS TaqMan MTB Test. Culture was also negative for 10 of these. In two samples atypical mycobacterium was isolated. 3 PDP were positive in Xpert and COBAS and showed no mutations in rpoB. The culture confirmed *M. tuberculosis* sensitive to rifampicin in these 3 cases. 20 PNP of 24 were negative by both PCR techniques and culture. Four of 24 (1 CSF, 1 pleural, 2 lymph node biopsies) were positive by both techniques and showed no mutations in the rpoB gene. The culture confirmed *M. tuberculosis* sensitive to rifampicin in these 4 cases. Nine culture isolates tested were identified as *M. tuberculosis* by Xpert and GenProbe. One isolate was determined resistant to rifampicin in Xpert. This was confirmed by susceptibility testing.

**Conclusion:** These preliminary results obtained on a limited number of samples show a perfect match for Xpert MTB/RIF with conventional laboratory tests irrespective of the nature of the sample tested.

**O236** Evaluation of the GeneXpert® MTB/RIF assay for the rapid detection of rifampicin resistance in *Mycobacterium tuberculosis* isolates

C.Cavusoglu, A. Nazli* (Trakya, TR)

**Introduction:** *Mycobacterium tuberculosis* is one of the most significant causes of death from an infectious agent. The incidence of pulmonary tuberculosis in Turkey is nearly 27.9 per 100,000 populations. The proportion of multidrug resistant tuberculosis among new cases is 2.9% and among previously treated cases is 15.5%. DNA sequencing studies demonstrate that 95% of rifampicin (RIF)-resistant *M. tuberculosis* strains has a mutation within the 81-bp hotspot region of the rpoB gene. The GeneXpert® MTB/RIF Assay (Cepheid, Sunnyvale, California) is a novel real-time PCR-based method for the diagnosis of tuberculosis and rapid detection of RIF-resistance in clinical specimens. However, there is a limited data about the performance of the GeneXpert® MTB/RIF Assay to detect different rpoB gene mutations.

**Objectives:** We aimed to determine the performance of the GeneXpert® MTB/RIF Assay for detection of the mutation within the 81-bp hotspot region of the rpoB gene in RIF-resistant *M. tuberculosis* isolates.

**Methods:** A total of 37 *M. tuberculosis* isolates (27 RIF-resistant, 10 RIF-susceptible), were included in the study. Drug susceptibility testing for RIF had been previously performed with the proportional method on 7H10 medium due to the criteria of the CLSI. Mutations in the rpoB gene for each isolate had also been determined by DNA sequencing.

**Results:** Thirteen different mutations (531-TTG, 526-CGC, 531-TGG, 526-TAC, 522-TGG, 516-TAC, 515-ATC, 533-CGG, 533-CGC, 526-TGC, 513-CCA, 490-CAT, and insertion of CGG between 514 and 515) were studied in 27 RIF-resistant *M. tuberculosis* isolates (Table 1).

<table>
<thead>
<tr>
<th>No. of isolates</th>
<th>Nucleotide changer(s)</th>
<th>GeneXpert MTB/RIF result/ unbounded probe(s)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>490 CAG to CAT</td>
<td>S*</td>
</tr>
<tr>
<td>2</td>
<td>513 CAA to CCA</td>
<td>R* (B)</td>
</tr>
<tr>
<td>2</td>
<td>514 515 ins. CGG</td>
<td>R (B)</td>
</tr>
<tr>
<td>2</td>
<td>516 GAC to TAC</td>
<td>R (B)</td>
</tr>
<tr>
<td>2</td>
<td>516 GAC to GTC</td>
<td>R (B)</td>
</tr>
<tr>
<td>2</td>
<td>522 TCG to TGG</td>
<td>R (C)</td>
</tr>
<tr>
<td>2</td>
<td>526 CAC to CGC</td>
<td>R (D)</td>
</tr>
<tr>
<td>2</td>
<td>526 CAC to TAC</td>
<td>R (D)</td>
</tr>
<tr>
<td>2</td>
<td>526 CAC to TGC</td>
<td>R (D)</td>
</tr>
<tr>
<td>3</td>
<td>531 TCG to TTG</td>
<td>R (E)</td>
</tr>
<tr>
<td>3</td>
<td>533 CTG to CCG</td>
<td>R (E)</td>
</tr>
<tr>
<td>1</td>
<td>515 ATG to ATC</td>
<td>R (B, E)</td>
</tr>
<tr>
<td>1</td>
<td>533 CTG to CCG</td>
<td></td>
</tr>
</tbody>
</table>

*Susceptible; °Resistant.

**O237** Detection by genotype MTBDRsl test of complex resistance mechanisms to second-line drugs and ethambutol in multidrug-resistant strains of *Mycobacterium tuberculosis*


**Objectives:** The Genotype MTBDRsl test aims at rapid detection of ethambutol, fluoroquinolones and second line aminoglycosides (amikacin, kanamycin) and cyclic peptide (capreomycin) in *Mycobacterium tuberculosis* (MtB).

**Methods:** A set of 41 MDR (multidrug-resistant) and 8 XDR (extensively drug-resistant) MtB strains has been tested by MTBDRsl and DNA sequencing of the resistance-determining regions in gyrA and gyrB (fluoroquinolones), rpsl (streptomycin), rrs and tlyA (aminoglycosides-cyclic peptide) and embB (ethambutol).

**Results:** The values of sensitivity/specificity of the MTBDRsl test were as follows: fluoroquinolones 87/96%, amikacin 100/100%, kanamycin 77/100%, capreomycin 80/98% and ethambutol 57/92%. Analysis of the discrepant results indicated that 3 FQ-resistant strains (including one XDR) with mutations in gyrB were missed by MTBDRsl, and that one FQ-susceptible strain, identified as resistant by MTBDRsl, had a double
mutation T80A-A90G in GyrA not conferring resistance to FQ. Five strains (including 2 XDR) without mutation in rrs were mono-resistant to aminoglycosides or cyclic peptide and were missed by MTBDRsl. Finally, 16/28 ethambutol-resistant strains had a mutation at codon 306 in embB while 2/24 ethambutol susceptible strains had such a mutation.

**Conclusions:** MTBDRsl efficiently detects the most common mutations involved in resistance to fluoroquinolones, aminoglycosides-cyclic peptide and ethambutol and accurately assesses susceptibility to amikacin. However, due to mutations not included in the test (particularly in gyrB) or yet-uncategorized resistance mechanisms (particularly those related to ethambutol and to aminoglycosides-cyclic peptide mono-resistance), the wild-type results yielded by the MTBDRsl test need to be confirmed by drug susceptibility testing when the prevalence of resistance is high.

**[O238] Molecular diagnosis of tuberculous meningitis – a 4-year experience**

A. Mendes*, S. Almeida, S. Fernandez, K. Rodrigues, A. Santos, H. Ramos (Oporto, PT)

**Objectives:** Tuberculous meningitis (TBM) is the most severe form of extrapulmonary tuberculosis, with high mortality rates and serious long-term consequences. Accurate and early diagnostic confirmation is essential in patient management. The purposes of this study was to, retrospectively, evaluate the performance of a molecular test for the detection of *Mycobacterium tuberculosis* complex in cerebrospinal fluid specimens (CSF), compared with culture and microscopy, and correlate the results with clinical findings.

**Methods:** Between November 2005 and September 2009, 118 CSF specimens were sent to the Molecular Biology Unit of Centro Hospitalar do Porto, with requests for *M. tuberculosis* molecular detection (MTD, GenoType, Hain), with mycobacterial culture (MGITTM and Lowenstein-Jensen) and microscopy examination performed in the Microbiology laboratory. MTD test was performed as described by manufacturer, but after mechanical cell lysis, nucleic acid purification was carried out in EZ1 BioRobot (Qiagen). Presence of amplification inhibition was verified in every sample. MTB diagnosis was based in laboratory results and clinical criteria, such as patient response to anti-bacillary therapy.

**Results:** 118 samples from 107 patients were studied. Molecular detection of *M. tuberculosis* complex was positive in 5 cases, which were confirmed by cultural methods. Microscopy revealed acid-fast bacilli in one sample. MTB diagnosis (laboratory and clinical criteria) was established in 17 cases, 12 being presumptive. All 17 patients showed altered cytology with pleocytosis. Protein level was elevated in 16 samples (0.55–10.5 g/L). Compared with MTB diagnosis, MTD showed a sensitivity of 30%, specificity of 100%, positive predictive value (PPV) of 100% and a negative predictive value (NPV) of 89%.

**Conclusion:** Our results suggest the potential role of molecular methods in confirming diagnosis of MTB, with short turnaround time results (2.5 h), high PPV, and similar sensitivity as culture (30%). Results must be interpreted in parallel with clinical findings and conventional microbiology methods. The use of molecular tests should not exclude a diagnosis of MTB (NPV-89%). More studies would help improve the adequacy of these methods.

**[O239] Real-time PCR for broad detection of the *Mycobacterium tuberculosis* complex and medically important atypical mycobacteria**

G. Abeldaim*, R. Carl-Johan, E. Scensson, L. Kirsbeom, J. Blomberg, B. Herrmann (Uppsala, Gotenburg, SE)

**Objectives:** To determine the sequence of the rnpB gene, coding for the ubiquitously present ribonuclease P RNA, and develop a real-time PCR for detection of the *Mycobacterium tuberculosis* complex and atypical mycobacteria.

**Methods:** The rnpB sequences of 17 *Mycobacterium* spp. were determined. Based on obtained rnpB sequences, two quantitative real-time PCRs for detection of the *M. tuberculosis* complex (Mytu PCR) and atypical mycobacteria (Myat PCR) were developed and combined into a single tube format. The analytical sensitivity of the PCR assay was determined with serial dilutions of target DNA. The specificity of the duplex PCR assay was tested with 21 mycobacteria species (55 strains), and 35 bacteria species other than mycobacteria. The PCR assay was evaluated on 10 samples from a quality control panel (QCMD) and on 442 clinical samples. The results were compared with the results of culture, direct microscopic examination and the Roche Amplicor PCR.

**Results:** Obtained rnpB sequences showed hypervariable regions enabling species specific identification and PCR design. The analytical sensitivity for detection of the *M. tuberculosis* complex was <50 copies/reaction, while for atypical mycobacteria it was 500 copies/reaction. The assay was specific and did not detect any of 35 non-mycobacterial bacteria spp. The Mytu PCR specifically detected all four species of the *M. tuberculosis* complex and the Myat PCR detected all tested 17 atypical mycobacteria species, except 2 of 7 strains from the *M. avium* complex. The PCR assay correctly detected all 10 samples from QCMD quality assurance panel. In analysis of 442 clinical specimens *M. tuberculosis* was detected in 40 cases (9%) by Mytu PCR, in 38 cases (8%) by the Roche PCR, in 46 cases (10%) by culture and in 23 (5%) cases by direct microscopic examination. The atypical mycobacteria were detected by Myat PCR in 18 (4%) cases, in 12 (3%) culture cases, and in 8 cases (2%) by direct microscopic examination.

**Conclusion:** Sequence determination of the rnpB gene is useful for *Mycobacterium* species identification.

Our duplex real-time PCR was shown to detect strains from both the *M. tuberculosis* complex and tested atypical mycobacteria strains. The PCR assay has a broader detection range of mycobacteria than commercial standard PCR method and has a sensitivity similar to culture.

**[O240] Molecular differentiation of *Mycobacterium tuberculosis* complex members from non-tuberculous mycobacteria**

M. Slany*, J. Scobodova, I. Pavlik (Brno, CZ)

**Objective:** Most mycobacterial infections are still caused by *Mycobacterium tuberculosis* complex (MTC) members; however, infections caused by non-tuberculous mycobacteria (NTM) are increasing, particularly among immunocompromised patients. NTM are ubiquitous in the environment and are responsible for several diseases in humans known as mycobacterioses. More than 128 mycobacterial species are currently described. Conventional species-specific identification and proper patient management are delayed due to the slow-growing nature of mycobacteria, their biochemical properties and antituberculous drugs sensitivity testing. We propose simple molecular based method using multiplex PCR (mPCR) for rapid detection and differentiation of NTM from MTC followed by sequence analysis used for NTM identification.

**Methods:** In the frame of study were have analysed: 50 MTC and 57 NTM isolates collected in 2009 in the Czech Republic; 14 non mycobacterial (non myco) reference strains. Bacterial supernatant applied as DNA template for the mPCR reaction targeting rpoB gene was used for detection and differentiation of isolates as MTC or NTM. One amplicon of 235 bp from MTC members or a single amplicon of 136 bp from NTM are expected. More studies would help improve the adequacy of these methods.

**Conclusion:** The mPCR reaction with template DNA from mycobacteria yielded the expected amplicons. We assume that proposed mPCR is specific for mycobacteria because analysis of non myco strains resulted in any amplicons. Detection limit for proposed mPCR was 50 copies per reaction, which facilitated its use for analysis of DNA extracted directly from clinical samples (spuza or biopsies). DNA sequencing of the 16S rRNA gene confirmed the status of analysed bacterial isolates and enabled precise isolate identification to the species level. Different NTM (Table 1) causing mycobacterial infections in humans were detected using this approach.

**Conclusion:** The mPCR used in this study allowed rapid detection and differentiation of primary cultures as MTC, NTM or non myco. Specific NTM identification is possible in second step by sequence
Surveillance of antibiotic resistance in leprosy by a new real-time PCR assay for specific detection and quantification: GenoType® LepraeDR was applied blindly. Results were compared with those obtained by the genotypic method (PCR sequencing) and the phenotypic reference method (mouse footpad) in vitro.

Methods: A real-time PCR assay based on amplification of the specific Mptb52.16 target was designed including an internal amplification control to identify false negative results. The detection limit was established in artificially contaminated raw milk samples and the optimized assay applied to 96 naturally contaminated raw milk samples. The potential of the real-time PCR assay to detect viable MAP was explored by expression accessing the Mptb52.16 target in raw milk samples and inoculated Dubos broth.

Results and Conclusions: The method showed 100% inclusivity and exclusivity when testing 11 MAP strains, 22 non-MAP mycobacteria, and 16 raw milk microflora strains. The detection limit in artificially contaminated raw milk was 2.42 × 10^4 MAP cells/ml milk. In a survey of naturally contaminated samples obtained from dairy herds with a known history of paratuberculosis, 47.8% pre-milk and 51.9% main milk of naturally contaminated samples obtained from dairy herds with a known history of paratuberculosis (John’s disease) in ruminants. Crohn’s disease is an inflammatory gastrointestinal tract disease in humans, presenting with similar symptoms and pathological changes in the gut as John’s disease in cattle. Therefore, it was suggested that MAP could be one of the etiologic factors of the disease. The aim of the present study was to develop a MAP-specific real-time PCR assay providing the additional possibility of detecting viable MAP.

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during pre-emptive therapy controls further replication episodes without
valganciclovir administration in solid organ transplant (SOT) patients at
high risk for CMV infection.

Methods: SOT recipients at high risk for CMV infection, those that are seronegative and receive a seropositive graft, were followed for 18 months after transplantation. CMV viral loads (VL) were determined by real-time PCR, and the CMV-specific immune response was characterized by flow cytometry by the detection of CD4+, CD8+ and CD3+ T cells expressing CD69 and secreting IFN-g and IL-2. Preemptive treatment was administered when VL reached 1,000 copies/ml. Once a CMV-specific immune response was detected no treatment was administered and patients were closely monitored.

Results: Eleven patients with a median age of 53 years were included. Between 2 and 7 weeks after transplantation, all patients experienced CMV replication episodes that ranged from 787 to 1,432,217 copies/ml. All of them were resolved after administration of valganciclovir. Between we performed HHV-6B transplantation a CMV-specific immune response was detected in all patients. After this, 33 replication episodes were detected, 32 of which (97%) were controlled by the host immune system without the administration of treatment (VL ranging from 10 to 31,317 copies/ml). Furthermore, although the number of positive PCR results was similar before and after the acquisition of immunity, VL levels were significantly lower (p = 0.017) after immunity than before with median values of 1,696 copies/ml and 20,110 copies/ml, respectively. From week 39 to week 51 all replication episodes were 1,000 copies/ml and no new replication episodes were detected after week 51.

Analysis of the immune response demonstrated that IL-2 was secreted from CD4+ T cells significantly earlier than IFN-g (6 vs 8.5 weeks post-transplant; p = 0.001). Additionally, IFN-g was secreted from CD4+ T cells significantly earlier than from CD8+ T cells (9 vs 12 weeks post-transplant; p = 0.005).

Conclusion: Pre-emptive therapy promotes the acquisition of an early immune response after transplantation in SOT patients at high risk for CMV infection. We demonstrate that the immune response elicited during pre-emptive therapy confers immunity to later CMV replication events.

**O244 Break-through HHV-6B infections during antiviral prophylaxis after liver transplantation**

I. Lautenschlager*, R. Logins, T. Karlsson, K. Höckerstedt (Helsinki, FI)

Objectives: Human herpesvirus-6 (HHV-6) activation, mostly of the variant B, is common after liver transplantation. Most HHV-6 reactivations are asymptomatic, but symptoms such as encephalitis, hepatitis or graft dysfunction have been described. The clinical experience on antiviral therapy is very limited, but based on in vitro studies, the current antiviral drugs effective against cytomegalovirus (CMV), have also activity against HHV-6. However, ganciclovir is less effective against HHV-6B than HHV-6A. The aim of our study was to investigate the efficiency of antiviral prophylaxis, given to the CMV-seronegative risk patients receiving the graft from the seropositive donor, in preventing HHV-6B reactivation.

Methods: Of 232 consecutive adult liver transplant patients 36 belonging to the CMV high risk group received valganciclovir (or ganciclovir) prophylaxis up to 3 months after transplantation. The patients were frequently monitored for CMV by real-time quantitative PCR and HHV-6 reactivations were demonstrated by the antigenemia test in PBMC by using indirect immunoperoxidase staining and monoclonal antibodies against HHV-6B and HHV-6A. Intragraft HHV-6 infection was demonstrated in liver biopsies by using the same antibodies and immunostaining.

Results: During antiviral prophylaxis, no break-through CMV infections were recorded. On the contrary, HHV-6 antigenemia was detected in 13/36 (36%) patients appearing mean 12 days (range 7-22 days) after transplantation. All reactivations were caused by HHV-6B. In three cases HHV-6 antigens were also detected in the transplant associated with graft dysfunction.

Conclusions: HHV-6B reactivations were common during antiviral prophylaxis after liver transplantation. At least in three cases also the transplant was infected. Valganciclovir/ganciclovir prophylaxis did not prevent HHV-6B infections in adult liver transplant patients.

**O245 Diagnosis of polyomavirus-associated nephropathy in renal-allograft recipients by real-time polymerase chain reaction and urine cytology**


Objective: Polyomavirus-associated allograft nephropathy (PVAN) frequently results in allograft dysfunction in renal transplant patients in the era of powerful immunosuppressive agents. BK virus (BKV) is the dominant causal agent whilst JC virus (JCV) accounts for the rest. Although renal biopsy is considered as the diagnostic standard for PVAN, patients with BKV and JCV for their plasma and urine samples within one week of renal biopsy. The biopsy results were obtained on 7 PVAN patients, exclusive BKV viruria was detected in all patients with BKV-associated PVAN and exclusive JCV viruria was detected in 2 patients with JCV-associated PVAN. BKV viremia exceeded the cut-off threshold value (10^4 copies/ml) was found in all 5 BKV-associated PVAN patients. JCV viremia was found in one JCV-associated PVAN patient. The use of decoy cells as a marker of PVAN was not beneficial for the diagnosis. A less invasive surrogate method is helpful. This study evaluated the clinical utility of urinary decoy cells and urine and plasma BKV/JCV real-time polymerase chain reaction (PCR) in the diagnosis of PVAN in renal transplant recipients with allograft dysfunction.

Methods: In a retrospective analysis, 22 renal transplant patients with allograft dysfunction and with renal biopsy results were evaluated. All patients were given real-time PCR assays for BKV and JCV for the diagnosis of PVAN (5 BKV- and 2 JCV-associated) and 15 patients with pathological diagnosis other than PVAN. Urine cytology was evaluated for decoy cells within 1 week of renal biopsy in all patients.

Results: In the 7 PVAN patients, exclusive BKV viruria was detected in all patients with BKV-associated PVAN and exclusive JCV viruria was detected in 2 patients with JCV-associated PVAN. BKV viremia exceeded the cut-off threshold value (10^4 copies/ml) was found in all 5 BKV-associated PVAN patients. JCV viremia was found in one JCV-associated PVAN patient. The use of decoy cells as a marker of PVAN was not beneficial for the diagnosis. A less invasive surrogate method is helpful. This study evaluated the clinical utility of urinary decoy cells and urine and plasma BKV/JCV real-time PCR methods may help in the diagnosis of PVAN among renal transplant patients. BKV viremia (>10^4 copies/ml) is highly associated with BKV nephropathy whilst the cut-off value for JCV requires further investigation.

**O246 Norovirus-related severe and chronic diarrhoea in renal transplant adult recipients**


Objective: Noroviruses (NoV) and Sapoviruses (SpV) are two separate genera in the Caliciviridae family. NoV are an increasingly recognized cause of transient gastroenteritis in immunocompetent individuals and have been recently implicated in chronic diarrhea in immunocompromised patients. However, clinical and epidemiological spectrum of Caliciviridae infections in renal transplant recipients is still poorly defined.

Methods: We undertook a single-center retrospective analysis of the clinical and virologic features of Caliciviridae infection, diagnosed by reverse transcription polymerase chain reaction (RT-PCR) from July 2008 to September 2009. Genotypes and variants were identified by genome sequencing. Other infectious agents were ruled out.

Results: Eleven renal transplant adult recipients were identified as having Caliciviridae infection, including 10 NoV and 1 SpV. All of them were given an induction immunosuppressive therapy relayed by a triple maintenance therapy. The median time from transplantation to symptoms and from then to diagnosis were 21 months (range: 1-83) and 30 days (range: 9-154), respectively. All patients had protracted
Evolution of anelloviridae strains in serial blood and biopsy samples from a renal transplant patient

P.Biagini,* B.Dussol, Y. Berland, P.de Micco (Marseille, FR)

Objectives: The Anelloviridae family is composed of multiple viral species belonging to the prototype TT virus. Biology and implications for host health of this intriguing viral family is still a matter to debate. In order to better understand the evolution of anelloviridae strains in the immunocompromised host, we performed a molecular analysis of serial blood and biopsy samples from a kidney transplant recipient.

Methods: Viral DNA was extracted from plasma samples using the High pure viral nucleic acid kit (Roche). Biopsy tissue samples were pre-digested using proteinase K, and nucleic acids were further extracted using the same approach. Rolling circle amplification (RCA) using Phz29 DNA polymerase was performed on extracted materials in order to optimise the detection of viral DNA. Anelloviridae detection was performed using a highly conserved PCR system; amplified products were further cloned and sequenced, and submitted to phylogenetic analyses.

Results: The evolution of viral strains detected in blood samples was bimodal: 1) prior to kidney transplant (T-90 days to T0), the genetic diversity exhibited by anelloviridae sequences was moderate; 2) on the other hand, multiple variants were detected from T+15 to T+420 (end of follow-up). Regarding the biopsy samples, although the first sample (T+11) was PCR negative, an anelloviridae sequence was identified in the second sample (T+170). Interestingly, this sequence was identical or nearly identical to a cluster of sequences identified in the blood of the patient before transplant.

Conclusion: This study suggests that a transplant is able to be colonized by an anelloviridae strain identified previously in the blood of the corresponding patient. It confirms also that major changes in anelloviridae dynamics occur in the blood of patients undergoing immunosuppressive treatments. Precise analysis of biological and molecular data collected in this study is exposed.

O249 Reduced IgG antibody avidity in organ transplant recipients after varicella-zoster-virus vaccination

M.Prelog, J. Schönlaub,* M.Zlany, L. Zimmerhackl, R. Würzner (Innsbruck, AT)

Objectives: Varicella-zoster virus (VZV) infection may cause significant morbidity and mortality in the immuno-compromised patient. VZV vaccine induces both humoral and cellular immunity. However, there is no clear correlation between IgG antibody titers and protection against infection. Antibody protection is a function of both concentration and affinity (=chemical binding strength). Avidity is a measure of functional affinity. It has been suggested that studies of vaccine efficacy should incorporate analysis of avidity, since high avidity is a marker of memory priming. The present study was designed in order to answer the question as to whether solid organ transplant (SOT) recipients have a lower VZV IgG antibody avidity, despite having protective IgG antibody levels after vaccination, or not.

Methods: The serum samples of SOT recipients were evaluated for IgG antibody levels against VZV and IgG antibody avidity. Twenty-eight patients were included in the study (20 had had liver transplantation, 3 heart transplantation, 5 kidney transplantation) and had received a single dose of Varivax (Aventis Pasteur, Lyon, France) prior to transplantation. The control group consisted of 50 healthy children, 36 of whom had had clinical and serological confirmed varicella infection after wild-virus contact or 14 of whom had varicella vaccination with a single dose of varicella vaccine, Varilrix.

Results: Median IgG antibody levels were 800 U/ml in wild-virus infected controls, 810 U/ml in vaccinated controls and 630 U/ml in SOT recipients. Median relative avidity index (RAI) was 89% for wild-virus infected controls, 94% for vaccinated controls and 82% for transplant recipients (p=0.01 compared to wild-virus infected controls, p=0.002 compared to vaccinated controls).

Conclusions: In conclusion, IgG antibody avidity in SOT recipients may serve as a substitute marker to evaluate humoral immunity against VZV. This is of particular importance in the clinical setting of exposure to VZV when considering VZV-specific immunoglobin and/or acyclovir treatment in order to prevent clinical relevant re-infection and varicella-caused complications as a result of exposure to VZV after transplantation. However, the role of humoral protection against VZV has to be evaluated in long-term follow-up, since also cellular immunity may play a crucial role in defence against viral infections.

O248 Relationship of viral load Epstein-Barr virus as a marker of lymphoproliferative disease after liver transplant

J.Hernandez, M. Naca, J. Casasola, J. Arellano, R. Farfan*(Distrito Federal, MX)

Background: Lymphoproliferative disease (ELPT) are a heterogeneous group of lymphoid disorders that can develop in patients undergoing solid organ transplantation. The incidence ranges between 2% adults and 10% in children and reach a mortality rate between 40 and 70%. The wide range of clinical presentations ranging from a mononucleosis syndrome and lymphadenopathy, masses to multiple organ dysfunction.

The risks identified in pediatric patients post transplant are the early ages, the use of Tacrolimus, a high viral load and a concomitant low cellular immune response.

Objectives: To describe the relationship between EBV viral load as a predictive marker for the presence of ELPT and clinical characteristics of patients after transplantation of liver in the Hospital Infantil de Mexico “Federico Gomez” in the period January 2005 to January 2008.

Methods: A descriptive, retrospective and observational study of a series of cases.

Results: From January 2005 to January 2008, nine liver transplants were performed, three were high risk by serology (EBV D+/R+), of which one ELPT development at 100 weeks post-transplant viral load of 1450 genomes/ml plasma. The time of reactivation of EBV infection on average for the nine patients was 3.3 weeks after transplantation. Seven patients belonged to age group <5 years (high risk by age). And 4 ELPT developed ELPT viral loads >800 genomes/mL of plasma. Five of nine patients developed ELPT with viral loads >800 genomes/mL. The patient number 9 ELPT present two events with added diagnosis of acute cellular rejection by biopsy in his second event of ELPT and high viral loads.

Conclusions: Viral load >800 genomes/mL accompanied by elevation in liver enzyme values of up to four or more times their normal levels were related to the development of ELPT.

O247 Evolution of anelloviridae strains in serial blood and biopsy samples from a renal transplant patient

P.Biagini,* B.Dussol, Y. Berland, P.de Micco (Marseille, FR)

Objectives: The Anelloviridae family is composed of multiple viral species belonging to the prototype TT virus. Biology and implications for host health of this intriguing viral family is still a matter to debate. In order to better understand the evolution of anelloviridae strains in the immunocompromised host, we performed a molecular analysis of serial blood and biopsy samples from a kidney transplant recipient.

Methods: Viral DNA was extracted from plasma samples using the High pure viral nucleic acid kit (Roche). Biopsy tissue samples were pre-digested using proteinase K, and nucleic acids were further extracted using the same approach. Rolling circle amplification (RCA) using Phz29 DNA polymerase was performed on extracted materials in order to optimise the detection of viral DNA. Anelloviridae detection was performed using a highly conserved PCR system; amplified products were further cloned and sequenced, and submitted to phylogenetic analyses.

Results: The evolution of viral strains detected in blood samples was bimodal: 1) prior to kidney transplant (T-90 days to T0), the genetic diversity exhibited by anelloviridae sequences was moderate; 2) on the other hand, multiple variants were detected from T+15 to T+420 (end of follow-up). Regarding the biopsy samples, although the first sample (T+11) was PCR negative, an anelloviridae sequence was identified in the second sample (T+170). Interestingly, this sequence was identical or nearly identical to a cluster of sequences identified in the blood of the patient before transplant.

Conclusion: This study suggests that a transplant is able to be colonized by an anelloviridae strain identified previously in the blood of the corresponding patient. It confirms also that major changes in anelloviridae dynamics occur in the blood of patients undergoing immunosuppressive treatments. Precise analysis of biological and molecular data collected in this study is exposed.
**O250** Characteristics and timing of bloodstream infections following orthotopic liver transplantation: a single-centre experience

B. McGecorn*, A. Gilleece, A. McCormick, S.F. Fitzgerald, L. Fenelon, K. Schafer (Dublin, IE)

**Aims:** To analyse the characteristics of bloodstream infections (BSI) occurring in orthotopic liver transplant (OLT) recipients in an Irish tertiary care hospital during the 2 year period from July 1st 2007 to June 30th 2009. To compare the findings with data from a previous time period.

**Methods:** The incidence, timing, aetiology and microbiology of BSIs in OLT recipients were obtained retrospectively. 124 OLTs were performed from July 1st 2007 to June 30th 2009. Chart reviews were performed on all patients who had positive blood cultures up to 12 weeks post-OLT. Bacteremia or fungaemia was considered to be significant according to the CDC criteria. Previous related literature was reviewed.

**Results:** Overall the incidence of BSI at our transplant centre has decreased (2007-2008) compared to (2008-2009). In an attempt to further reduce the incidence of BSI post-OLT we plan to target IV catheter-related sepsis at our centre.

**Conclusion:** The overall number of BSI involving multiresistant pathogens in the ONIKO-KISS patient group is rather low. Rates of MRSA and VR *E. faecium* were varying in the observation period and sometimes higher than the corresponding rates for Germany derived from EARSS [European Antimicrobial Resistance Surveillance System; www.scmc.org/earss]. However, the low overall numbers must be taken into account. ESBL producing *E. coli* were not seen before 2007 but thereafter with a high percentage in comparison to EARSS data for 3rd generation cephalosporin resistant *E. coli*.

<table>
<thead>
<tr>
<th>Year</th>
<th>MRSAT- aureus total no. (%)</th>
<th>ESBL producing <em>E. coli</em> total no. (%)</th>
<th>Vancomycin resistant <em>E. faecium</em> total no. (%)</th>
<th>Total no. of blood culture isolates</th>
</tr>
</thead>
<tbody>
<tr>
<td>2004</td>
<td>2/7 (29%)</td>
<td>0/2 (0%)</td>
<td>0/2 (0%)</td>
<td>2/9 (100%)</td>
</tr>
<tr>
<td>2005</td>
<td>0/3 (0%)</td>
<td>0/3 (0%)</td>
<td>0/1 (10%)</td>
<td>4/13 (31%)</td>
</tr>
<tr>
<td>2006</td>
<td>3/5 (60%)</td>
<td>0/2 (0%)</td>
<td>0/2 (0%)</td>
<td>6/9 (22%)</td>
</tr>
<tr>
<td>2007</td>
<td>1/4 (25%)</td>
<td>1/4 (25%)</td>
<td>0/1 (10%)</td>
<td>3/9 (22%)</td>
</tr>
<tr>
<td>2008</td>
<td>2/5 (40%)</td>
<td>0/2 (0%)</td>
<td>0/1 (10%)</td>
<td>3/8 (31%)</td>
</tr>
<tr>
<td>2009</td>
<td>2/5 (40%)</td>
<td>0/3 (0%)</td>
<td>0/1 (10%)</td>
<td>3/9 (22%)</td>
</tr>
</tbody>
</table>

**O252** Quantification of CMV DNA in plasma by real-time PCR for management of allogeneic stem cell transplant recipients

L. Cardeñoso, S. Agudo*, M.J. Moreno, S. Rodrigo, O. Muñoz, V. Rivero, M. López-Brea (Madrid, ES)

The objective was to evaluate a quantitative real time PCR in plasma samples for monitoring active CMV infection in allogeneic stem cell transplant (allo-SCT) patients and try a new strategy for the initiation of CMV preemptive therapy.

We studied 395 plasma samples obtained of 51 CMV infection episodes from 32 allo SCT patients between January 2007 and February 2009. 29 out of 32 received one or more course of preemptive therapy upon positive AG and/or TNAI-PCR results and 6 (19%) developed CMV end-organ disease (4 colitis and 2 neutonits). All patients were monitored post-STC with antigenemia pp65 CINAPo®. Argene (AG) and conventional quantitative PCR, COBAS® Amplicor® CMV after automatic extraction COBAS® Ampliprep® TNAI kit, Roche (TNAI-PCR). A positive sample was defined by AG ≥2×10⁴ PMNs and/or TNAI-PCR ≥600 copies/μL. All samples were retrospectively tested using a real time PCR Affigene® CMV trender after automatic DNA extraction with NucliSENS® easyMag®; bioMérieux (rt-PCR); data lower than 57 copies/μL were considered as negative. An episode was defined as the period between the first positive sample by antigenemia and/or TNAI-PCR, until the first negative sample by both techniques. Plasma samples were positive in 28.3%, 30.6% and 46% by AG, TNAI-PCR and rt-PCR, respectively. Rt-PCR detected 72% of AG positive samples vs 60% by TNAI-PCR. AG was not evaluable in 30 samples (7.5%). Sixteen samples (53%) were positive by rt-PCR vs 7 (23%) by TNAI-PCR. 12% of samples were only positive by rt-PCR. The range for rt-PCR was 63–2.77×10⁴ copies/μL vs 605–2.7×10⁴ copies/μL by TNAI-PCR. Episodes were detected in 46 (90%), 38 (82%) and 41 (89%) by AG, TNAI-PCR and rt-PCR, respectively. Six episodes (11.8%) were only detected by AG (all PCRs negative). Five episodes (11.8%) were detected only by PCR assays. Thirty-four episodes out of 51 episodes (66.7%) were detected by both PCR techniques, in 14 out of 34 (41.2%) were detected earlier by RT-PCR than TNAI-PCR (median = 7 days), and in 5 (14.7%) TNAI-PCR was earlier than RT-PCR (median = 3 days). Concordance between PCRs assays was 79% (k = 0.6). Strategy based on the quantification of CMV DNA in plasma could be established in >153 copies/μL (curve ROC, graphic 1) for triggering the initiation of CMV preemptive therapy in this clinical setting. Rt-PCR can be introduced to allow the more sensitive, rapid, and accurate diagnosis of CMV reactivation infection in SCT recipients, which allowed for preemptive therapy to be administered as early as possible.
Invasive *Candida* infections occur in many different patient populations. Critical care is widely acknowledged as an important predisposing factor, with a third of candidaemia episodes occurring in the ICU. This is chiefly because ICU patients are exposed to many of the risk factors, which include compromises to natural barriers of infection; *Candida* colonisation and alterations in normal flora; and the presence of debilitating diseases or immunsuppression, particularly neutropenia. Invasive *Candida* infections also occur outside the ICU, as the cardinal risk factors are present in a variety of patient types, including patients undergoing major abdominal surgery; bone marrow and solid-organ transplant patients; and patients undergoing cancer chemotherapy. Although risk factors for invasive *Candida* infections are well characterised, definitive diagnosis remains problematic due to the long lead times associated with blood culture and histopathology. Targeted treatment, i.e. selection of an antifungal agent tailored to a particular *Candida* species with known antifungal susceptibility, is rarely possible initially. Consequently, pre-emptive and empirical strategies, which make use of the limited information available to guide treatment decisions, are commonly employed.

Patients with invasive *Candida* infections are often severely ill prior to developing a fungal infection. Therefore, rapid initiation of therapy is vital, as the risk of mortality increases significantly with any delay in treatment. However, it is also important to consider carefully the choice of agent, as differences exist in microbiological and clinical efficacy. Many cases of invasive *Candida* infections are caused by species that are potentially resistant to older antifungals, particularly fluconazole. Therefore, if the causative agent is unknown, or is suspected to be a fluconazole-resistant species (i.e. *C. glabrata* or *C. krusei*), a broad-spectrum antifungal agent should be selected first-line, with recent guidelines recommending echinocandins as the best overall choice.

Differences also exist between the echinocandins, particularly with regard to their suitability for use in certain patient populations. Therefore, careful assessment of individual cases is the optimal basis for selection of therapy. Mecafungin, which was evaluated in an extensive clinical trial programme and has to date been administered in 600,000 patients worldwide, is a recognised treatment option.
Antimicrobial resistance: rising to the challenge exploring new territories to fight microbial resistance (Symposium supported by bioMérieux)

Emerging resistance mechanisms: current status and future risks

D Livermore* (London, UK)

Recent years have witnessed dramatic shifts in the prevalence and nature of antibiotic resistance. Key changes include: (i) the rise and, in some countries, subsequent decline of MRSA, also (ii) the rise of quinolone and cephalosporin resistance in Enterobacteriaceae, particularly E. coli and Klebsiella spp., with CTX-M ESBLs increasingly the dominant source of the cephalosporin resistance, (iii) the proliferation of A. baumannii with OXA carbapenemases and (iv) the ‘loss’ of fluoroquinolones against gonorrhoea, with resistance rates as high as 90% in China. Treatment shifts predicated on these problems are now exerting their own selection pressure, favouring the spread of yet further resistances. The greatest concern for hospital medicine is the emergence of Enterobacteriaceae with acquired carbapenemases, including the IMP, VIM, and NDM metallo-types, the class A enzyme KPC and the class D enzyme, OXA-48. At present, Enterobacteriaceae with these enzymes are proliferating in different parts of the world: NDM in India, OXA-48 in Turkey, VIM in Greece and KPC in the US – but the stability of this distribution is unpredictable, in view of migration and medical tourism. In general, the IMP, VIM and NDM enzymes are spread by plasms, whilst accumulation of K. pneumoniae isolates with KPC enzyme largely involves dissemination of the ST258 clone. ‘Loss’ of the carbapenems against Enterobacteriaceae would be a public health catastrophe, in view of the lack of alternative therapies for infections due to multiresistant Gram-negative bacteria. A shift that should be of greater concern than it is presently receiving is the erosion of the anti-gonococcal activity of cephaporsins. Owing to changes to PBPs, porins and efflux it is increasingly common to see N. gonorrhoea isolates with cefixime and ceftriaxone MICs of 0.12–0.5 μg/mL, representing the edge of treatability, again with a lack of convenient alternative therapies. Future risks are harder to predict but potentially include transferable resistance to new anti-Gram-positive agents, and it is notable here that many soil streptomyces can degrade daptomycin. Some organisms were the sources of several other resistance genes that have spread to mobile DNA and into clinical pathogens. But, as the saying goes, ‘Prediction is very hard, especially when it concerns the future’ and only two things are certain: that neither evolution nor resistance surprises have stopped yet.

Individual determinants of antibiotic prescription

J.C. Lucet* (Paris, FR)

The use of antibiotics in the hospital setting is shaped by cultural and behavioural aspects as well as by clinical situation and microbiological considerations. An understanding of the determinants of antibiotic prescription is critical to explain current patterns and to devise programs to reduce inappropriate use. Physician behaviour is explained by such factors as lack of information, marketing campaigns to increase use of newer products and fear of adverse outcome with ineffective prescription. Studies of antibiotic use patterns consistently demonstrate frequent inappropriate prescribing and low adherence to antibiotic prescription (ABP) guidelines, a factor likely to increase the emergence of resistant organisms. Behavioural aspects of the antibiotic prescription remain largely unknown. We explored beliefs and perceptions associated with measured knowledge about ABP in two French university hospitals. Physicians in charge of ABP in inpatient hospital wards were asked to participate. Volunteers completed in a same meeting (less than 1
ESBLs and AmpCs – understand the mechanisms

S61

Contribution of procalcitonin for guidance of antibiotic therapy in respiratory tract infections

P. Schuetz* (Basel, CH)

Lower respiratory tract infections (LRTI) account for almost 10% of the burden of morbidity and mortality in western countries. LRTIs comprise a continuum of different severities of infections ranging from typically self-limiting acute bronchitis, to more severe acute exacerbation of chronic pulmonary disease (AECOPD) and to life-threatening bacterial community-acquired pneumonia (CAP). Clinical signs and symptoms, and traditional laboratory parameters are unreliable to distinguish viral from bacterial LRTI. As a consequence, up to 75% of LRTI are treated with antibiotics, despite the main viral origin leading ultimately to emergence of bacterial resistance. To limit antibiotic overuse, rapid and more accurate differentiation of clinically relevant bacterial LRTI from other causes is key.

A novel approach to estimate the probability of a bacterial origin of LRTIs is measure-ment of serum procalcitonin (PCT) levels. PCT increases rapidly upon infection (3–6 hours) and decreases upon recovery. PCT correlates with severity and has prognostic implications. Its kinetics makes it a good marker for assessing the effectiveness of treatment, which is a prerequisite for safe guidance of antibiotic therapy. PCT levels can be used to guide antibiotic therapy in individual patients as a surrogate biomarker. Antibiotic stewardship based on PCT cut off ranges has successfully been implemented in patients with LRTI in different clinical settings. Thereby, initiation or continuation of antibiotics was more or less discouraged (<0.1 ug/L or <0.25 ug/L) or encouraged (>0.5 ug/L or >0.25 ug/L) (Figure 1). If PCT values are increased and antibiotics therapy is initiated, repeated PCT measurements are recommended and antibiotics can be discontinued using the same cut-off ranges. This clinical algorithm was prospectively tested in different intervention trials in the emergency room, in the intensive care unit, in primary care and recently, this concept has been externally validated in a large Swiss nation-wide multi centre trial including over 1350 patients. Overall, PCT-guided antibiotic stewardship reduced antibiotic prescription rate by 40–50% in patients with acute bronchitis or AECOPD; in CAP, it reduced the initial prescription rate by about 10%, but importantly shortened the duration of antibiotic therapy by 65% with a similar outcome in patients with all severities. Similarly, PCT guidance safely reduced antibiotic exposure by more than 75% in primary care patients with upper and lower RTI. Thereby, PCT guidance significantly reduced antibiotic-related side effects, especially diarrhoea and nausea.

The septic syndrome is far too heterogeneous and complex to be reduced to a single cut-off of any surrogate marker. Biomarker must always be evaluated in the context of a careful clinical and microbiological assessment. As the kinetics of biomarkers are of particular diagnostic and prognostic interest, repeated measurements should always be performed, especially if antibiotics are withheld.

Emerging bacterial resistance to antimicrobial agents calls for more efficient efforts to reduce the unnecessary use of antimicrobial agents in self-limited and non-bacterial diseases. Embedded in a clinical algorithm, PCT-guided antibiotic stewardship offers great potential to safely and markedly reduce antibiotic exposure and antibiotic-associated side effects.

Figure 1. Clinical algorithm for antibiotic guidance in LRTI.

ESBLs and AmpCs – understand the mechanisms

S271

Current trends in epidemiology of ESBLs and acquired AmpCs

J. Pitout* (Calgary, CA)

Since 2000, Escherichia coli producing CTX-M enzymes (especially CTX-M-15), have emerged worldwide as important causes of community-associated urinary tract infections (UTIs) and bloodstream infections due to extended-spectrum β-lactamase (ESBL) producing bacteria. Molecular epidemiology studies suggested that the sudden worldwide increase of multi-resistant CTX-M-producing E. coli (especially CTX-M-15) is mostly due to a single clone named ST131 and that foreign travel to high-risk areas such as the Indian subcontinent might play in part a role in spread of this clone across different continents. Clone ST131 that produce CTX-M ESBLs (i.e. most often CTX-M-15 but also CTX-M-3 and CTX-M-14) is associated with IncFII and IncI1 multi-resistance plasmids and certain virulence factors such as mxi,ompT and usp. Community-associated acquisition and infections due to enterobacteria with plasmid-mediated AmpC β-lactamases are a relatively recent phenomenon and have been described in the UK, Canada and USA. The spread of clones in the community setting have not been described for enterobacteria that produce plasmid-mediated AmpC β-lactamases. Empircic antibiotic coverage for these resistant organisms should be considered in community patients presenting with sepsis involving the urinary tract especially in patients with certain risk factors such recent antibiotic use, residence in a long-term care facility, recent hospitalization, males older than 65 years and recent travel to a high-risk area. If this emerging public health threat is ignored, it is possible that the medical community may be forced in the near future to use the carbapenems as the first choice for the empirical treatment of serious infections associated with urinary tract infections originating from the community.
The role of plasmids and bacterial clones in the spread of ESBLs and acquired AmpCs

A. Carattoli* (Rome, IT)

A multidisciplinary approach is currently applied to study the acquisition and spread of antimicrobial resistance in clinically-relevant bacterial pathogens: the established surveillance is implemented by molecular characterization of the strains by genotyping, identification of the resistance gene types, virulotyping analysis and replicon typing of the circulating plasmids. Multilocus sequence typing is also used to document the international occurrence of successful, healthcare-associated and community-acquired clones.

Many of these clones are often resistant to multiple antibiotics and multidrug resistance is often encoded by extrachromosomal elements, called plasmids. Plasmids evolve as an integral part of the bacterial genome, providing resistance genes that can be easily exchanged among bacteria of different origin and source, through the natural process of conjugation.

Particular plasmid families are playing a major role in the diffusion of ESBLs such as CTX-M, SHV, TEM and acquired AmpCs. For instance, IncFII, IncA/C, IncM, IncN and IncI1 plasmids carrying ESBLs are considered as “epidemic resistance plasmids”, being detected in resistant bacteria of different origin and sources. The emergence of the CTX-M-15 enzyme has been associated to the spread of the highly virulent E. coli O25:H4-ST131 clone carrying plasmids belonging to the IncF group. Other CTX-M variants have been amplified locally, such as CTX-M-9 and CTX-M-14 in Portugal and Spain, CTX-M-3 in eastern countries associated to specific plasmid families. TEM-52 and CTX-M-1 disseminated prevalently on IncI1 plasmids among E. coli of human and animal origin. The identification of KPC-2-positive IncN and ColE-like plasmids in K. pneumoniae from USA and Colombia suggests that these plasmids could contribute to the rapid spread of the gene. Acquired AmpCs widely disseminated on IncA/C and IncI1 plasmids.

The occurrence of the particular epidemic plasmids seems tightly linked to positive selection exerted by the antimicrobial use, incrementing their prevalence compared to that observed in bacterial populations that are not pre-selected for antimicrobial resistance.

Many questions remain unanswered about mechanisms driving the successful dissemination of a specific plasmid type or a bacterial clone. However, the recognition of successful clones and plasmids is an essential first step that may lead eventually to the design of intervention strategies at preventing their spread.

Mutational modifications of ESBL and AmpC activities

T. Palzkill* (Houston, US)

The class A TEM-1 and SHV-1 β-lactamases are common plasmid-encoded β-lactamases in Gram-negative bacteria. These enzymes efficiently hydrolyze penicillins and many cephalosporins but are not effective catalysts for extended-spectrum cephalosporins and thus do not provide resistance against these drugs. However, variants of TEM-1 and SHV-1 that can hydrolyze extended spectrum cephalosporins have evolved in clinical isolates over the last two decades, which has limited treatment options. These evolved enzymes, termed extended-spectrum β-lactamases (ESBLs), contain from one to five amino acid substitutions that result in increased catalytic efficiency of the enzymes for hydrolysis of extended spectrum cephalosporins. Site-directed and random mutagenesis studies have revealed that these amino acid substitutions commonly found in the evolved variants increase the catalytic efficiency for hydrolysis of extended spectrum cephalosporins and, in some cases, stabilize the evolved enzymes. The evolution of high level resistance involves a process of mutational changes in the active site that increase catalysis but often decrease protein stability. This, in turn, leads to the acquisition of secondary mutations that increase the in vivo half life of the enzyme. The interactions between amino acid substitutions and the resultant impact on the evolution of ESBL activities will be discussed.

AmpC β-lactamases are highly efficient for hydrolysis of many cephalosporins, however, they exhibit lower activity towards extended-spectrum cephalosporins. Nevertheless, AmpC mediated resistance to extended-spectrum cephalosporins can occur due to high levels of enzyme production or through mutations in the enzyme that result in increased hydrolysis of the drugs. Several amino acid substitutions as well as small insertions and deletions in AmpC enzymes have been reported to increase resistance to extended spectrum cephalosporins and have been associated with increased hydrolysis of these antibiotics. The mutational changes occur in regions in the vicinity of the active site and may act by increasing access for the bulky oximecephalosporins. In addition, random mutagenesis experiments have revealed positions where amino acid substitutions alter the substrate specificity of the enzyme. The impact of amino acid substitutions on the evolution of extended spectrum cephalosporin hydrolysis by AmpC enzymes will be discussed.

Non-tuberculous mycobacterial infections

Non-tuberculous mycobacterial pulmonary infections

E. Tortoli* (Florence, IT)

The lung can be easily affected by inhalation of aerosolized mycobacteria and is by far the most frequent site of human mycobacteriosis. In HIV-negative patients, the disease is undistinguishable from tuberculosis and is characterized by very slow progression. The manifestations range from absence of symptoms to cavitary disease, and X-ray may reveal fibrosis, upper lobe cavitation, nodular or parenchymal opacity, and pleural thickening. The most affected are elderly patients with predisposing pulmonary conditions (e.g. silicosis, obstructive pulmonary disease, pneumoconiosis, previous tuberculosis, bronchiectasis or cancer). The symptoms include cough, fever, weight loss, weakness and respiratory insufficiency. The NTM most frequently responsible for disease belong to the Mycobacterium avium complex; in Europe, infections caused by Mycobacterium xenopi and, particularly in northern countries, those caused by Mycobacterium malmoense are also quite frequent whereas, in the USA, infections caused by Mycobacterium kansasii are more prevalent.

In AIDS patients the radiographic picture is often normal or may reveal mediastinal or hilar adenopathy, and the progression of disease is very rapid. The most frequent symptoms are cough, fever and weight loss. The patients have usually a CD4 lymphocyte count lower than 100/mL. In recent years, the widespread use of highly active anti-retroviral treatments has dramatically reduced the frequency of mycobacterial diseases, including the pulmonary ones, in HIV-positive patients. Recently pulmonary infections due to NTM have increasingly been reported in patients with cystic fibrosis.

Because of the high risk of contamination of the sputum by environmental mycobacteria, it is estimated that less than 30% of the isolations of NTM from the respiratory tract have clinical relevance. The strict observance of the criteria of the American Thoracic Society is essential for a correct diagnosis.

Buruli ulcer disease: epidemiology, clinical manifestations, diagnosis, treatment

F. Portaels*, D. Walsh, W. Meyers (Antwerp, BE; Bangkok, TH; Washington, US)

Buruli ulcer (BU), caused by Mycobacterium ulcerans is the third most common human mycobacteriosis worldwide after tuberculosis and leprosy.

BU is endemic in rural wetlands of tropical countries of Africa, America, Asia and Australia but remains uncommon in non-African countries. A few cases have been reported in non-tropical areas. Incidence rates vary greatly by continent, country, and in areas within a country. Known incidence rates currently are highest in West Africa.

Children 15 years old or younger account for approximately 75% of cases. Risk factors include tropical climate, exposure to stagnant water,
unprotected water sources, hygiene, trauma to skin and HIV infection. *M. ulcerans* disease presents a spectrum of forms related partly to patient delay in admission to hospital. Estimated incubation periods range from 2 weeks to several years. The nonulcerative forms represent the first stages of the disease. Early stages are often ignored by the patients and may sometimes heal spontaneously.

The clinical diagnosis can be difficult even for experienced health professionals, hence the importance of microbiologic confirmation. Four laboratory tests are currently in use:

1. Direct smear of exudates from ulcerated lesions in situ, or fine needle aspirates (FNA) from nonulcerated lesions, or biopsy specimens
2. In vitro cultivation of *M. ulcerans* from exudates, FNA or biopsies.
3. Gel-based or quantitative real-time PCR targeting IS2404.
4. Histopathologic examination (important in both BU diagnosis and differential diagnosis).

Numerous other infectious and noninfectious diseases and neoplasms are diagnosed among clinically suspected cases of BU. Tropical phagedenic ulcer is the most common diagnostic problem.

Options for therapy for BU are surgery, antibiotics, or combinations of both. Antibiotic therapy for all forms is gaining acceptance. The World Health Organization (WHO) recommends, if not contraindicated, the directly observed use at least an 8-week course of oral rifampin and streptomycin by intramuscular injection. This antibiotic treatment may also be combined with surgery. Other antibiotic regimens, especially those administered completely orally, are under evaluation.

Severe ZN positive lesions (large ulcers and disseminated forms) should receive specific antibiotherapy and should be surgically treated without delay to avoid deterioration of lesions and possible bone dissemination.

**Conclusion:** This investigation highlights that failure in disinfection of injecting material could generate severe infections with highly resistant bacteria related to non regular medical cares. Efforts should focus on control of hygiene practices in non hospital settings based on appropriate guideline recommendations.

### S278 Management of non-tuberculous mycobacterial lymphadenitis in children

*J. Amir*° (Petah Tiqwa, IL)

The spectrum of clinical manifestations caused by nontuberculous mycobacteria (NTM) in immunocompetent individuals comprises three major categories: lymphadenitis, pulmonary infections and skin/soft tissue infections. Lymphadenitis due to NTM strikes mainly young children whereas pulmonary and skin/soft tissue infections are common in adults.

The frequency of NTM lymphadenitis has increased over the past few decades. Diagnosis is based on clinical presentation, PPD skin test and bacterial isolation from nodal aspiration or incision. *Mycobacterium scrofulaceum* was the most common cause in the 1970s, replaced by *M. avium-intracellulare* complex (MAC) and *M. haemophilum* in last two decades. Management options are surgery, antibiotics or “observation only”. Complete excision of the infected lymph node has been considered the optimal therapy by most researchers, however, it is associated with various side effects such as unacceptable scarring with or without keloid formation, wound breakdown, secondary staphylococcal infection and facial nerve paresis. Most facial nerve damage is transient, although in approximately 2% permanent palsy developed. Incision and drainage is performed when the lesions are too large to be excised. Few retrospective case series have demonstrated superiority of complete excision over incision and drainage. Pharmacologic therapy with clarithromycin alone, or combined with other antimycobacterial agents such as rifampicin, rifabutin, or ethambutol have been reported. On the other hand, there are no controlled clinical trials showing the efficacy of chemotherapy versus placebo. Very few cases of “observation only” in children with NTM lymphadenitis were reported in the past. A recently published study described the natural history of 92 immunocompetent children with cervical NTM lymphadenitis. In most cases, the skin over affected lymph nodes underwent violaceous changes, with discharge of purulent material for 3–8 weeks. Total resolution was achieved within 6 months in 71% of the patients, and within 9–12 months in the remainder. No complications were observed, and at 2 years follow-up, a skin-colored flat scar in the region of the drainage was noted.

In conclusion, The optimal therapy for this condition is still controversial. Nevertheless, it seems that antibiotics are not very effective in treating immunocompetent children. A randomized, controlled trial examining surgical excision versus spontaneous healing is warranted.

### S279 Why malaria prophylaxis sometimes fails?

*V. Kremery*,° J. Sokolova, L. Seng Duong (Bratislava, Trnava, SK)

Reasons for antimalarial prophylaxis failure include:

i. poor adherence to antimalarial agents
ii. malabsorption of antimalarial drugs
iii. interactions with other medications
iv. adverse reaction leading to treatment interruptions
v. underdosing the patient
vi. in vitro resistance

In case of clinical failure standby treatment is recommended, if no health infrastructure is available. Commonly used antimalarials for prophylaxis in travelers include mefloquine or atovaquon-proguanil. In prophylaxis failure therapy with artemisin based combination drugs (ACT) is indicated. Special conditions exist for IPT (Intermittent Preventive Treatment) in pregnant women in endemic areas and children. For long term travelers/residents prophylaxis in hyperendemic areas is usually ineffective.

**Conclusion:** It is important to be aware of the reasons for failure of prophylaxis and how to treat them.
Artemisinin resistance
H. Noedl° (Vienna, AT)

Within the past 10 years virtually all malaria-endemic countries have officially adopted artemisinin-based combination therapies (ACTs) as first or second line therapy for the treatment of *P.* falciparum malaria. Artemisinins have become the most essential class of antimalarials, their impact comparable only to that of chloroquine in the mid 20th century. Spreading artemisinin resistance could therefore have a devastating impact on malaria control efforts throughout the malaria-endemic world. In the current situation losing a single class of antimalarial drugs to resistance may severely impact the ability of many countries to treat falciparum malaria.

The concept of artemisinin resistance has been a contentious one for many years, with some authorities suggesting that it was unlikely to arise in the first place. However, recent data indicate that the first cases of genuine artemisinin resistance have already emerged in western Cambodia. We may already be losing artemisinis in selected parts of the world.

Our data showing individual parasite isolates resistant to high doses of artemisinins, prolonged parasite clearance times, and reduced in vitro drug response indicate that the phenomenon is not limited to a relatively small proportion of the parasite isolates and probably also to a relatively small area in Southeast Asia. Once it starts spreading, resistance to artemisinin derivatives, currently the most essential antimalarial drugs, could very well be the most devastating event in the history of malaria control in the 21st century. Artemisin-resistant malaria is a new emerging disease that will require new treatment and control strategies to limit the impact and spread of resistance to the rest of the malaria-endemic world.

Microbial colonization of respiratory tract: does it always predict a nasty outcome?

Clinical significance of *Pneumocystis* colonization
A. Morris* (Pittsburgh, US)

*Pneumocystis* pneumonia has long been recognized as a cause of morbidity and mortality in immunocompromised populations, particularly those with human immunodeficiency virus (HIV) infection. *Pneumocystis* colonization is defined as detection of the organism or its DNA without signs or symptoms of pneumonia. Sensitive molecular techniques such as polymerase chain reaction are frequently utilized to identify colonization. Accumulating evidence suggests that colonization with *Pneumocystis* may be an important clinical phenomenon. The clinical significance of colonization is not yet fully understood, but it may be important for several reasons. Colonized persons may be at risk of developing *Pneumocystis* pneumonia. Even if colonized individuals do not themselves develop *Pneumocystis* pneumonia, they might transmit the organism to others. Exposure to *Pneumocystis*-colonized animals leads to colonization of normal animals and to the development of clinical disease in immunosuppressed animals. Colonization in persons receiving long-term anti-*Pneumocystis* prophylaxis may also lead to the development of mutations that have been associated with drug resistance. Furthermore, *Pneumocystis* may play a role in progression of lung diseases such as chronic obstructive pulmonary disease (COPD). The presence of *Pneumocystis* in the lungs, even at low levels as seen in colonization, produces inflammatory changes similar to those seen in COPD, with increases in the numbers of neutrophils and cytotoxic CD8+ lymphocytes. Colonization with *Pneumocystis* has been demonstrated in HIV-infected subjects, and HIV-infected smokers are particularly susceptible to *Pneumocystis* colonization regardless of CD4 cell count or use of *Pneumocystis* prophylaxis. *Pneumocystis* colonization is also increased in non-HIV-infected patients with COPD and is directly related to the severity of the disease. Models of *Pneumocystis* colonization in mice with smoke exposure and in non-human primates infected with an HIV/simian immunodeficiency virus chimera demonstrate the development of COPD-like changes. These studies suggest that treatment or prevention of *Pneumocystis* colonization in at-risk populations may be a novel therapy for COPD.

Virus oncogenesis: mechanisms and clinical aspects

E.BV-associated tumours
D.A. Thorley-Lawson* (Boston, US)

Epstein–Barr virus is a human herpesvirus that is known to infect and efficiently drive the activation and proliferation of resting B cells in vitro. It achieves this through the expression of nine latent proteins. However, *in vivo* EBV persists in a benign, dormant state in resting memory B cells. The link between these two observations is that *in vivo* EBV uses its latent proteins to activate newly infected cells in lymphoid tissue so that the cells can then differentiate through the germinal center to become resting memory cells. In doing so the virus infected cells mimic the normal process whereby antigen activated B cells become long term memory cells. At each stage of the process EBV uses different combinations of latent proteins. If at any stage the infected cell is unable to progress into the resting memory state it is at risk of becoming a tumor expressing the pattern of latent proteins characteristic of its particular stage of infection. Thus EBV is associated with several human malignancies including Burkitt’s lymphoma, Hodgkin’s disease, immunoblastic lymphoma, nasopharyngeal carcinoma and gastric carcinoma. Each of these tumors expresses a different pattern of latent proteins reflecting their origins from specific stages of the viral life cycle. Recently it has been shown that EBV also expresses ~40 miRNAs in latently infected cells. miRNAs are thought to play critical regulatory functions in normal and malignant cells but the roles of the EBV miRNAs remain unclear. It is also unknown if they are expressed in a tumor specific pattern like the latent proteins. In this presentation I will:

1. Discuss the mechanism of how EBV establishes persistent infection in memory B cells including recent evidence on how EBV usurps the germinal center process to gain access to the memory B cell compartment.
2. Detail how the model of EBV persistence explains the origin of the EBV associated tumors especially the lymphomas.
3. Demonstrate tumor specific expression profiles of miRNAs and a possible functional significance of these expression patterns.

Polyoma virus-associated tumours
J.M. Pipas* (Pittsburgh, US)

Some polyomaviruses induce tumors in their natural hosts or in test animals. Tumorigenesis by these viruses is effected by a number of different mechanisms depending on the specific virus. Studies with simian virus 40 have shown that this virus targets key cellular regulatory proteins, in particular the tumor suppressors pRb and p53 to stimulate cell proliferation and to block cell death. Our laboratory uses a combination of genetics, proteomics, gene expression arrays and transgenic and knockout mice to understand how the action of SV40 proteins on these cellular targets leads to tumorigenesis. This talk will review this research and present a model for SV40-induced transformation and tumorigenesis.
Innate immunity to pathogens: from genes to cells

**Objective:** Panton-Valentine Leukocidin (PVL) positive *Staphylococcus aureus* is an emerging pathogen associated with highly lethal necrotizing pneumonia. PVL is a bi-component β-barrel pore-forming toxin that has been shown to cause cell death in neutrophils. However, the precise mechanisms leading to necrotizing pneumonia are not fully understood and the role of PVL herein is controversial. We therefore aimed to investigate the mechanism by which PVL might contribute to the development of severe lung inflammation.

**Methods:** Recombinant PVL was generated and its cytotoxic properties were verified by patch clamp and FACS. The inflammatory potential of PVL was tested on alveolar macrophages using microarray profiling, PCR and ELISA. Signaling pathways were investigated using western blotting and microarray. In *vivo* role of PVL was then studied in a murine pneumonia model, in which lung tissue and lavage fluid was assessed for cell-influx and cytokine/chemokine release.

**Results:** PVL rapidly induces pore formation and death of neutrophils. In contrast, alveolar macrophages were found less sensitive to the toxic effects and only succumbed after prolonged incubation. Microarray assays performed 1 h after addition of PVL to alveolar macrophages revealed the selective induction of 29 genes upon stimulation. Bioinformatic analysis disclosed the upregulation of NFκB target genes. These data were verified by PCR and on protein levels and suggest that PVL selectively induces NFκB associated inflammation in *vivo*. Inhibitor studies and gene reporter assays further confirmed this finding. Furthermore, PVL-induced lung inflammation in mice confirmed the inflammatory potential of PVL, as illustrated by a rapid influx of neutrophils and enhanced levels of pro-inflammatory cytokines and chemokines within the pulmonary compartment.

**Conclusions:** Our data demonstrate that PVL, beside its pore-forming properties on neutrophils, is able to strongly induce inflammation via NFκB activation in alveolar macrophages, leading to pneumonia in *vivo*.

**Conclusion:** Our results not only suggest a novel mechanism for delta lgt-LTA mediated immune activation in human blood cells that involves an opsonization-dependent uptake and recognition process of LTA but also provide a conclusive explanation for the controversial findings obtained in previous experiments comparing the immunostimulatory capacity of delta lgt-LTA and wt-LTA.
Amphotericin B mediates killing in *C. neoformans* through induction of oxidative burst rather than through pore formation at the membrane


**Objectives:** Amphotericin B (AmB) is an antifungal drug widely used for the treatment of fungal infections, such as cryptococcal meningoencephalitis, which is caused by the encapsulated fungal pathogen *Cryptococcus neoformans*. AmB binds to ergosterol and forms pores at the membrane, resulting in cell death. However, other reports indicate that AmB also acts as an oxidant. In this work we have studied the effect of AmB on *C. neoformans*.

**Methods:** We have compared three viability methods: XTT assay, prodium iodide staining, and colony forming units enumeration. XTT is reduced in the mitochondria by living cells, producing a compound that is quantified spectrophotometrically. Prodium iodide is a DNA-binding fluorescent compound that only penetrates in the cells once they lose the membrane integrity. Finally, CFUs enumeration estimates the ability of the cells to replicate and form visible colonies.

**Results:** While AmB inhibited the formation of colonies at concentrations above 0.5-1 mg/L, the cells did not become permeable to prodium iodide in the same conditions, suggesting that AmB has other effects on *C. neoformans* different than pore formation. When viability was measured using the XTT assay, a correlation with the CFUs results was observed, confirming that AmB exerts its killing effect intracellularly. However, we also observed a “paradoxical effect” in which cells treated with high AmB concentrations (4-16 mg/L) produced higher levels of reduced XTT than cells treated with intermediate AmB concentrations (0.25-1 mg/L). Since this “paradoxical effect did not correlate with CFUs appearance, we argued that it might reflect an induction of the electron transfer in the mitochondria, as a consequence of an increased oxidative burst induced by AmB. So we measured the amount of reactive oxygen species (ROS) in the cells using dihydrofluorescein, a compound that when is attacked by free radicals releases fluorescence. Our results demonstrated that AmB induced a strong release of ROS in the cells, which correlates with the metabolic inactivation measured by the XTT assay.

**Conclusions:** Although AmB can bind to ergosterol and produce pores at the membrane, our results indicate that this antifungal drug induces killing in *C. neoformans* mainly through an induction of a strong oxidative burst. These findings confirm that Am B has multiple effects on the cells, which suggests an explanation for the low antifungal resistance to this compound observed among clinical isolates.

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Characterization of class I-restricted epitopes of *Trypanosoma cruzi* HSP70 protein recognized by Chagas’ disease patients

C. Marañón*, A. Egui Machado, B. Carrilero, M. Segovia, C. Thomas, M.C. López (Armilla, Murcia, ES)

**Objectives:** The protozoan parasite *Trypanosoma cruzi* is the aetiologic agent of Chagas disease or American trypanosomiasis, which affect near 20 million people with severe consequences in terms of morbidity and mortality. The host’s ability to generate a parasite-specific immune response plays an essential role in the control of the infection and the severity of the disease. In particular, efficient CD8+T cell responses are required for the immune control of the infection. Heat shock proteins have been characterized as immunodominant CD8+antigens in several bacterial infections and tumours, but not still in parasitic diseases. The aim of this work is to know whether *T. cruzi* HSP70 is processed and presented to CD8+T lymphocytes during natural infection.

**Methods:** Peptides containing HLA-A*0201-binding motifs were selected using bioinformatics, and their binding affinity were evaluated using T2-binding assays. HSP70-immunized or *T. cruzi* infected C57BL/ A2/Kb transgenic mice were used to predict immunodominant epitopes within the protein by cytotoxicity assays. The recognition of candidate peptides by circulating lymphocytes from chagasic patients were assessed through IFN-γ secretion tests.

**Results:** Thirty peptides were selected as putative HLA-A*0201 binders and synthesized. Of these, 16 candidates were selected and their recognition was tested by splenocytes of C57BL/A2/Kb mice immunized with HSP70 protein or, alternatively chronically infected with *T. cruzi*. No significative peptide recognition was observed in non-infected or non-immunized animals, and two peptides were significatively recognized by both immunized and infected mice. When the recognition of these two peptides by circulating lymphocytes of chagasic patients was tested by IFN-γ secretion assays, both peptides were well recognized by chagasic patients in different stages of the disease.

**Conclusion:** The data above demonstrate that *T. cruzi* HSP70 is an immunodominant CD8+ epitope, which is naturally processed and presented during Chagas disease progression. CD8+ T cell response against microbial HSP70 has been shown to be protective in other infections like tuberculosis. Since currently no vaccine against Chagas disease is available, the characterization of new parasite antigens providing protective responses will be of great value in order to fight against *T. cruzi* infection.

Differential induction of *in vitro* CD4+/CD8+ T-cell responses by live vs. killed *Leishmania major*

M. Nateghi Rostami*, A. Khamestipour, A. Miramin Mohammadi, E. Eskandari, A. Sarraf-Nejad, H. Keshavarz (Tehran, IR)

**Objectives:** Different clinical trials of killed *Leishmania* vaccines showed a limited efficacy compared to inoculation of live *Leishmania major* (leishmanization=LZ) against cutaneous leishmaniasis (CL). The reason for the discrepancy in efficacy of live and killed vaccines is not yet

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(87%). Caspase-1−/− mice had a 100-fold increase in fungal loads in the kidneys of the deficient animals and showed preferential growth of *Candida* in the pyelum of the caspase-1−/− mice accompanied by remarkably little inflammation (Figure). In contrast, ASC−/−mice did not have higher fungal loads, but they showed a significantly stronger inflammatory reaction in the kidneys. ASC−/−–spleenocytes showed a higher TNF production after *Candida* stimulation. NLRP3−/− and P2X7−/− did not display an increased susceptibility to disseminated candidiasis. Local bioactive IL-1β and INFγ in *in vivo* was only affected in the caspase-1−/− mice, but not in the ASC−/−, NLRP3−/− or P2X7−/− animals. In addition, caspase-1 was constitutively active in ROS deficient monocytes and *C. albicans* induced IL-1β production was not reduced in the absence of ROS.

**Conclusions:** Caspase-1-dependent processes are important in anti-fungal host defense during *Candida* sepsis. In contrast to current thinking, these process are not dependent on the inflammasome components, ASC, NLRP3 and the ATP receptor P2X7. These data thinking, these process are not dependent on the inflammasome activation. ASC plays an important role in disseminated fungal host defense during candidiasis. Local bioactive IL-1β and INFγ in *in vivo* was only affected in the caspase-1−/− mice, but not in the ASC−/−, NLRP3−/− or P2X7−/− animals. In addition, caspase-1 was constitutively active in ROS deficient monocytes and *C. albicans* induced IL-1β production was not reduced in the absence of ROS.

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**O296** Characterization of class I-restricted epitopes of *Trypanosoma cruzi* HSP70 protein recognized by Chagas’ disease patients

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**Methods:** Peptides containing HLA-A*0201-binding motifs were selected using bioinformatics, and their binding affinity were evaluated using T2-binding assays. HSP70-immunized or *T. cruzi* infected C57BL/A2/Kb transgenic mice were used to predict immunodominant epitopes within the protein by cytotoxicity assays. The recognition of candidate peptides by circulating lymphocytes from chagasic patients were assessed through IFN-γ secretion tests.

**Results:** Thirty peptides were selected as putative HLA-A*0201 binders and synthesized. Of these, 16 candidates were selected and their recognition was tested by splenocytes of C57BL/A2/Kb mice immunized with HSP70 protein or, alternatively chronically infected with *T. cruzi*. No significative peptide recognition was observed in non-infected or non-immunized animals, and two peptides were significatively recognized by both immunized and infected mice. When the recognition of these two peptides by circulating lymphocytes of chagasic patients was tested by IFN-γ secretion assays, both peptides were well recognized by chagasic patients in different stages of the disease.

**Conclusion:** The data above demonstrate that *T. cruzi* HSP70 is an immunodominant CD8+ epitope, which is naturally processed and presented during Chagas disease progression. CD8+ T cell response against microbial HSP70 has been shown to be protective in other infections like tuberculosis. Since currently no vaccine against Chagas disease is available, the characterization of new parasite antigens providing protective responses will be of great value in order to fight against *T. cruzi* infection.

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**O297** Differential induction of *in vitro* CD4+/CD8+ T-cell responses by live vs. killed *Leishmania major*

M. Nateghi Rostami*, A. Khamestipour, A. Miramin Mohammadi, E. Eskandari, A. Sarraf-Nejad, H. Keshavarz (Tehran, IR)

**Objectives:** Different clinical trials of killed *Leishmania* vaccines showed a limited efficacy compared to inoculation of live *Leishmania major* (leishmanization=LZ) against cutaneous leishmaniasis (CL). The reason for the discrepancy in efficacy of live and killed vaccines is not yet
known, in *vivo* and in *vitro* studies on T-cell function against live/killed stimulatory effect might provide valuable information.

**Methods:** Nine leishmanin skin test (LST) positive donors with history of self healing CL (HCL) and seven healthy LST negative donors were included in this study. CD4+CD8+CD14+ cells were isolated from peripheral blood. 5,6-carboxyfluorescein diacetate succinimidyl ester (CFSE) labeled CD4+ or CD8+ lymphocytes were cultured in the presence of 1:10 of mitomycin treated autologous monocytes and 100 micro g/ml killed *Leishmania* lysate (KLL) or 2.5×10^7/ml live *Leishmania* major (LLM). Cells were harvested after 7 days of incubation at 37°C and analysed for proliferation using flow cytometry. Culture supernatants were collected on day 3 for IL-5, IL-10, IL-13 and IFN-g titration using sandwich ELISA method.

**Results:** In HCL volunteers, upon stimulation with KLL, the number of proliferated CD4+ or CD8+ T-cells (at division 4) was significantly more than unstimulated cells or control LLL stimulated cells (P<0.05 for CD4+ and P<0.001 for CD8+ cells). Cells from HCL donors showed a significantly higher IL-10 production to LLM stimulation compared with KLL stimulation (P<0.001 for CD4+ and P<0.0005 for CD8+ cells) or comparing controls (P<0.05 for CD4+ and P<0.01 for CD8+ cells). Stimulation of CD4+ T cells with LLM (P<0.001) or KLL (P<0.05) induced a significantly higher IFN-g production compared to cells from controls, but LLM induced significantly more IFN-g than KLL (P<0.05). On the CD8+ compartment, a significantly higher IFN-g production was observed when the cells were stimulated with LLM (P<0.05).

**Conclusion:** While killed *Leishmania* induced more proliferation response in purified T cells of HCL volunteers, live *Leishmania* induced cytokine production in T cells without a significant induction of proliferation. The results from healed CL volunteers in this study might be implicated in further investigations on T-cell function against live/killed *Leishmania* vaccination in *vivo*.

**Conclusions:** The decreased cytokine production by immune cells bearing this SNP. Functional assays demonstrated a loss-of-function phenotype of the SNP, as shown by the decreased cytokine production by immune cells bearing this SNP.

In contrast, the dectin-1 Y238X SNP did not influence susceptibility to candidaemia or that of oropharyngeal candidiasis in HIV-infected patients. Patients with meningitis had a somewhat higher prevalence of the A allele in rs2305619 and the C allele in rs3816527, but this was not significant. In addition, no differences were found for number of days spent in ICU or disease severity. During active meningococcal infection, in patients with meningococcal septic shock, peak plasma concentration of pentraxin 3 appeared to be dependent on PTX3 genotype. Patients homozygous for the A allele in rs3816527 had higher peak plasma concentrations of PTX3 than other individuals (P<0.05). Instead, patients homozygous for the A allele in rs3816527, had lower peak plasma concentrations than AC and CC individuals, this approached significance (P=0.09) (Figure 1).

**Conclusions:** These findings indicate that in patients with septic shock PTX3 plasmaconcentrations are in part dependent on PTX3 genotype for the rs2305619 and rs3816527, but these SNPs do not affect susceptibility to meningococcal disease.

**Figure 1.** Pentraxin 3 peak plasma concentrations during meningococcal septic shock according to PTX3 genotype. Medians and interquartile ranges are presented. P value by Mann–Whitney test.
Serious Gram-positive infections: the need for new treatment options (Symposium supported by Astellas)

J. Garau, A. MacGowan, D. Nathwani, M. Niederman (Barcelona, ES; Bristol, Dundee, UK; Mineola, US)

Serious Gram-positive infections are becoming increasingly difficult to treat because of the escalating incidence of multidrug-resistant pathogens, such as methicillin-resistant Staphylococcus aureus (MRSA). In order to improve clinical outcomes and to select the most appropriate therapy, it is essential to consider pharmacokinetic (PK) and pharmacodynamic (PD) parameters, such as PD targets and their relation to dosing and the use of PK parameters as measures of exposure. In addition, AU/UC/MIC ratios should be used to predict clinical efficacy, and the relationship between MICs and dosing requirements should be considered.

In patients with suspected multidrug-resistant infections, prompt initiation of appropriate therapy is an important determinant of mortality. In some European hospitals MRSA strains account for >40% of all S. aureus isolates so it is crucial that the chosen therapy provides appropriate coverage for MRSA. Current treatment guidelines for serious Gram-positive infections, such as hospital-acquired pneumonia (HAP) and complicated skin and soft tissue infections (cSSTIs), recommend the use of vancomycin or linezolid for infections caused by MRSA. However, the role of these agents in the treatment of serious Gram-positive infections is still uncertain and there is currently an unmet need for additional agents that are effective against serious Gram-positive infections caused by both methicillin-susceptible S. aureus (MSSA) and MRSA.

Telavancin is a rapidly bactericidal lipoglycopeptide with a novel dual mode of action and a broad spectrum of activity against clinically important Gram-positive pathogens, including MRSA. In phase 3 trials, telavancin has demonstrated non-inferiority compared with vancomycin for the treatment of cSSTIs and HAP (including ventilator-associated pneumonia) caused by Gram-positive pathogens, including MSSA and MRSA. These results suggest that telavancin would be a promising addition to current therapeutic options in the management of serious Gram-positive infections caused by MSSA and MRSA.

The medical and public health impact of rapid molecular testing (Symposium supported by Cepheid)

M. Jeevan, D. Goff, N. El Helali, J. Kluytmans (Antwerp, BE; Columbus, US; Paris, FR; Breola, NL)

Despite notable advances in recent years, molecular diagnostics applications for infectious disease detection have yet to reach their full potential. Often performed in specialized laboratories far removed from where patient care decisions are made, specimens usually spend more time in transit than in actually being analyzed, and once samples do arrive in the lab, further delays are incurred by obligatory dependence on batch processing.

The chief limitations of current molecular diagnostic approaches are not due to the underlying technology, but rather in how this technology is implemented. Real-time PCR is perfectly capable of generating results within a few minutes. However, the processes leading up to the analytical steps are often unwieldy and performed in batches within a high-complexity laboratory environment. Moreover, the requirement for complex procedures ties the availability of molecular diagnostic test results with the limited availability of highly trained personnel.

In many cases, medical value of a diagnostic result is tied directly to how quickly results can be linked to patient management and/or treatment decisions. Fortunately, technologies for nucleic acid detection are now evolving in the direction of modern clinical chemistry analyzers, the most successful of which allow for random access, high throughput, and STAT testing capability. In addition, by virtue of the simplicity afforded by integrated, automated sample processing, the technology is fully capable of being decentralized in order to minimize the impact of sample transport on turnaround time. This symposium will focus on the “need for speed” in driving maximum medical impact for four different areas relevant to molecular diagnostics—respiratory infections, group B strep prophylaxis, blood cultures positive for staphylococci, and pre-surgical prophylaxis.

Current and future management of fungal infections (Symposium supported by Pfizer)

C. Kibbler* (London, UK)

Objectives: Despite increasing understanding, the treatment and prevention of invasive fungal infections (IFIs) remains a major challenge. IFI is an important cause of complications and mortality among hospitalised patients, especially among immunocompromised patients in the haematology setting. The potential of voriconazole (VORI) as primary and secondary prophylaxis for IFI has recently been evaluated in clinical trials in patients with haematological disease having undergone allogeneic transplantation.

Methods: In the primary prophylaxis study IMPROVIT (A), patients ≥12 years were randomised to receive oral VORI or oral itraconazole (ITRA) from the day of transplantation, for 100–180 days; the primary composite endpoint was success of prophylaxis at Day 180 (i.e. survival without developing proven/probable IFI or discontinuing prophylaxis for
>14 days during the first 100 days). In the secondary prophylaxis study
VOSIFI (B), patients ≥18 years with proven/probable IFI in the previous
12 months received VORI 4 mg/kg/12 hours IV or 200 mg/12 hours PO
within 48 hours post-conditioning chemotherapy, for 100–150 days; the
primary endpoint was the incidence of proven/probable IFI during the
subsequent 12 months.

Results: In A, the success of prophylaxis was significantly higher in
the VORI group (n = 234) compared with the ITRA group (n = 255) at
Days 100 (55% vs. 41%; 95% CI: 6%, 24%; p = 0.007) and 180 (49% vs
35%; 95% CI: 7%, 24%; p = 0.0004). Significantly more patients treated
with VORI than ITRA (54% vs 40%; p = 0.0014) had sufficient days
of prophylaxis (median: 97 vs 68 days). While the incidence of IFI
was low in both arms (VORI: 1.3%, ITRA: 2.4%), 3 patients receiving
ITRA developed IFI compared with none on treatment with VORI.

In B (n = 42), 3 cases of IFI occurred: 1 recurrent
Candida albicans fungaemia (fatal) and 1 new case of zygomycosis, at Day 3, 16, and 66 after transplant,
respectively (incidence: 7%). The most common VORI-related adverse
events were hepatotoxicity, nausea, headache and hallucinations/visual
impairment (<15%). In A, there was no difference in 180-day survival
(85% in each treatment group); in B, 11 patients (24%) died (median:
136 days post-transplant) but only 1 from IFI.

Conclusions: Based on the results of these prophylaxis studies, VORI
is an effective and safe option for both primary and secondary prevention
of IFI after allogeneic transplantation.

Microorganisms as human carcinogens: a list
without an end

L. Gissmann* (Heidelberg, DE)

The current estimation of the cancer cases that are related to infectious
events varies between 18 and 20% and there is evidence that this
cancer number is still growing. Besides Helicobacter pylori and some parasites
there are mostly viruses for which a causative relation to malignant
diseases has been demonstrated. Establishing such a link depends on the
epidemiologic profile of the disease and the putative causal infectious
agent as well as its biologic properties in experimental cell culture and
in vivo models. Often one of the classical Koch's postulates (isolation
of the putative agent from the affected tissue) cannot be fulfilled and, in
some instances, not even traces of the microbe (i.e. its nucleic acid) can
consistently be found in the tumor. Therefore it is not certain that cancer
is the late and rare consequence of a chronic infection where replication of
the infectious agent does no longer take place and gene functions are not
required for maintenance of the tumor growth. Therefore a combination
of observational and experimental strategies has to be applied to collect
enough evidence and to initiate attempts for preventive measures that
target the infectious agent such as development of vaccines. Examples
of classical and innovative approaches will be presented.

Reporting β-lactam susceptibility tests on
Enterobacteriaceae

J. Turnidge* (North Adelaide, AU)

The emergence of extended-spectrum β-lactamases (ESBLs) in
Enterobacteriaceae (ENTB) in the 1980s began to alter the laboratory
approach to β-lactamase detection in Enterobacteriaceae. Prior to that
time, tests for β-lactams were reported according to the test result,
and specific detection of acquired narrow spectrum β-lactamases such
as TEM-1 was not sought. With the arrival of ESBLs, detection and
confirmation was considered very important, and the default position
arose that the presence of an ESBL in a test clinical strain, whatever the
MIC of the organism, required the reporting of the organism as resistant
to cephalosporins of all types. Many susceptibility testing methods
recommended the use of ESBL screening and confirmation tests on a
routine basis. However, a number of issues have emerged routine use
over the years:
1. The problem of defining an adequate number of substrates to ensure
   sufficiently sensitive screening.
2. The lack of simple and reliable phenotypic methods to detect ESBLs
   in species with inducible AmpC β-lactamases.
3. The failure of current ESBL detection methods to provide advice
   on the interpretation of a positive screening test but a negative
   confirmation test, especially if the isolates are “susceptible”
   to extended-spectrum cephalosporins using method-recommended
   breakpoints.
4. Animal model data showing that the response to treatment of ENTB
   (measured as in vivo killing) is correlated with the MIC of the strain,
   and not the presence or absence of an ESBL

A range of recent studies has suggested that failures of treatment
with extended-spectrum cephalosporins are likely when strains of
ENTB have MICs elevated above the wild-type. Further, application
of pharmacokinetic/pharmacodynamic principles to the most widely
recommended dosing schedules of cephalosporins have shown that the
susceptibility breakpoints recommended by many methods have been too
high. Lower breakpoints for injectable cephalosporins are now published
by CLSI and EUCAST, with recommendations to optionally conduct
specific ESBL tests, for instance if there is an epidemiological need.
These newer cephalosporin breakpoints put us in a position where almost
all ESBL-producing and plasmid-borne AmpC-producing ENTB will be
detected and reported as I or R with the new breakpoints, and specific
β-lactamase testing will not be required. This is appropriate for clinical
reports whose major purpose is to guide therapy in individual patients.

Reporting β-lactam susceptibility tests on
Enterobacteriaceae

D. Livermore* (London, UK)

It is argued that treatment outcomes, e.g. for ESBL producers, can
be predicted from MICs, irrespective of the resistance mechanism.
Proponents of this view contend that it is unnecessary for clinical
laboratories to edit susceptibility data on the basis of resistance
mechanisms and that these should only be sought, if at all, for purposes
of epidemiological surveillance.

Several outcome studies support this view (though others do not) and
it would have great merit in a perfect world where routine MICs
were rapidly and precisely determined for clinical isolates. The reality
is very different. MICs, if measured at all in clinical laboratories,
are determined, late, on a geometrical scale with four-fold run-to-run
variation. In this imperfect reality an ESBL producer with a cephalosporin
MIC of 1 mg/L (probably responsive to cefotaxime
in vivo) cannot
be reliably distinguished from one with an MIC of 4 mg/L (probably
not responsive) and it is simpler and safer to follow the precautionary
approach of seeking the ESBL and, if this is found, reporting the isolate
as resistant.

A further advantage of seeking mechanisms is that – using selective
primary culture media or chromogenic tests – they can be found by 24-h
post specimen, as against 48-h for a precise MIC. This differential, which
is only likely to increase with the coming of molecular methods to detect
resistance mechanisms, may be critical, allowing the association between
early effective therapy and reduced mortality in severely-ill patients.
Antiretroviral therapy

O324 | Longitudinal evaluation of lipoprotein-associated phospholipase A2 as a cardiovascular disease-associated biomarker in relation to abacavir therapy


Objectives: As there exists still some concern about the potential relationship of Abacavir (ABC) and myocardial infarction (MI), and some authors have postulated that the increase in the risk of MI might be caused because of pro-inflammatory state, as increase and decrease of the risk follows quickly the start and resume of ABC, we decided to longitudinally evaluate Lipoprotein-associated phospholipase A2 (Lp-PLA2), a widely accepted marker of vascular inflammation and cardiovascular disease during ABC therapy in HIV patients due the lack of accuracy of other markers as IL6, IL8, hs-CRP or TNFα.

Methods: Eleven consecutive HIV-positive patients starting ABC-containing HAART were sampled at 0, 6 and 12 months after the start of ABC. Eleven HIV-positive patients on ABC sparing HAART were individually matched for other potential cardiovascular disease markers as hypertension, sex, age, smoking status, cholesterol and diabetes, and were sampled as controls.

Results: There were 4 women and 7 men in the cases matched against the same proportion of males/females. Median age was 42 years old (32–54) and 42 (30–54) for men in cases and control, respectively and 40 (35–46) and 40 (33–46) for women in cases and controls respectively. Results are depicted in Table 1. Values of LpPLA2 are expressed in ng/mL. Mean values for every patient at any given time point were higher than clinical cut points established in 2006 (low risk Lp-PLA2 <200 ng/mL). Interestingly, there was an increase in mean LpPLA2 in all four groups 6 months after the change in HAART, followed by a decrease. At 6 months there were no differences in men regarding ABC, but at 12 months there was an increase in men taking ABC whereas there was a decrease in men without ABC (p=0.02). Women did not show any differences.

Conclusion: There is an increase in Lp-PLA2 during therapy with ABC in men, but because there were no MI during the one year follow-up among the two groups, the mean Lp-PLA2 values are more than 3 times higher than clinical cut points and Lp-PLA2 seems to exhibit a “risk threshold” we cannot rely on LpPLA2 as a cardiovascular marker in our population.

<table>
<thead>
<tr>
<th>Mean (range)</th>
<th>Start</th>
<th>6 months</th>
<th>12 months</th>
</tr>
</thead>
<tbody>
<tr>
<td>Men</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>ABC</td>
<td>614.4 (483.1–812.3)</td>
<td>702.9 (582.3–860.9)</td>
<td>669.92 (497.3–835.94)</td>
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<tr>
<td>No ABC</td>
<td>653.74 (517.3–778.1)</td>
<td>693.6 (615.2–769.5)</td>
<td>620.8 (483.1–764.5)</td>
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<tr>
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<tr>
<td>ABC</td>
<td>535.7 (450.9–661.6)</td>
<td>548.8 (480.9–670.2)</td>
<td>566.83 (483.8–685.94)</td>
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<tr>
<td>No ABC</td>
<td>644.6 (503.1–763.8)</td>
<td>646.4 (542.3–723.4)</td>
<td>652.72 (472.3–806.6)</td>
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</table>

O325 | Effectiveness of tenofovir-abacavir containing HAART in pretreated HIV-1 infected patients


Objectives: Although there has been an increase in available antiretroviral for pretreated patients, their high cost and short time since approved make nucleoside reverse transcriptase inhibitors (NRTI) to be the most widely used backbone. However, since pre treated patients usually harbored mutations in reverse transcriptase, frequently tenofovir (TDF) and abacavir (ABC) are the only NRTI available. Since there are no reports about the combination of ABC and TDF, ans some concern about drug-drug interaction, we made a retrospective review to establish the effectiveness of ABC plus TDF as a NRTI backbone of HAART in pretreated patients.

Methods: A single clinic retrospective study including all HIV-1 infected pretreated patients ≥18 years of age starting ABC-TDF irrespective of their prior HAART. The effectiveness was evaluated in an ITT analysis.

Results: Forty-six patients, 31 men (67%) with a mean age of 43 years (28–65) and median CD4 cell count of 447 (75–1935). Mean HIV-1 viral load was 29400 copies/mL (19–85600). Among the sample 12 patients (26%) had undetectable viral load when starting the combination. Failure, as defined, occurred in 26 patients (57%), with 21 patients (46%) having virological failure. The other 5 patients resumed therapy because side effects to any of the drugs (4 patients) or lost to follow up (1 patient). Among these 5 patients, 3 had undetectable HIV-1 viral load when stopped therapy. Median duration of therapy for non-failure patient was 27 months (11–54) and 12 months (3–33) for patients who resumed therapy. When stratified by viral load at the start of therapy we found that patients who had undetectable viral load had better chance to keep on therapy than patients who started with detectable viral load 8/12 (66%) vs 12/34 (35%), almost reaching statistical significance (p=0.061).

Conclusion: TDF-ABC backbone should not be routinely used in HIV pre-treated patients. However, if the patient has undetectable viral load, the combination might be used with a high chance of success at 96 weeks follow-up in an ITT analysis.

O326 | Optimization of antiretroviral treatment of HIV-patients with viral loads below 1,000 copies/mL based on genotyping data

J. Mier-Mota*, L. Lopez-Cortes, P. Viciana, P. Perez-Romero (Seville, ES)

Objectives: Despite the success of antiretroviral therapy (ART) in the majority of patients, a percentage of patients receiving ART have sustained low-level viremia with viral loads (VL) between 20 and 1,000 copies/mL. The objective of this study was to determine whether the early optimization of the treatment based on the resistance pattern determined in patients with VL below 1,000 copies/mL results in the decrease of the VL to undetectable levels.

Methods: Our laboratory has developed a method for amplifying and sequencing the protease and retrotranscriptase genes from the plasma of patients with VL between 20 and 1,000 copies/mL. In this method HIV-RNA is concentrated using RNA affinity columns and is used as a template for high fidelity RT-PCR. The products are sequenced and mutations determined and analyzed. Using this method we studied HIV patient samples collected from September 2008 to September 2009. Genotyping data were obtained for each patient and ART was modified according to the resistance pattern and previous clinical history.

Results: Genotyping was determined for 37 patients that fulfilled the requirements of sustained low-level viremia. Resistance mutations were detected in 89% of the sequences. The most common mutations in the protease were at positions 10 (40.5%), 71 (16.2%) and 90 (18.9%). The most common mutations in the retrotranscriptase associated with resistance to nucleoside analogs were at positions 67 (27.1%), 184 (27.1%) and 215 (37.5%), while the most prevalent mutations associated with resistance to non-nucleoside analogs were at positions 98 (10.4%), 100 (14.6%) and 103 (16.7%).

After genotyping, 17 patients received an optimized treatment regimen. In 15 of these patients (88.2%) the VL became undetectable, in one patient (5.9%) the VL decreased significantly but not to undetectable levels and in one patient (5.9%) the VL was undetermined. Of the 20 patients that did not undergo treatment change, in 4 patients (20%) the VL decreased to undetectable levels, in 9 patients (45%) the VL remained between 20 and 1000 copies/mL, in 3 patients (15%) the VL increased to over 1,000 copies/mL and in 4 patients (20%) the VL was undetermined.

Conclusion: The developed method allows for genotyping of patients with VL between 20 and 1,000 copies/mL. Treatment changes based on these genotyping data have clinical significance since the VL decreased to undetectable levels in the majority of the patients who underwent treatment change.
Lack of correlation between plasma residual viraemia and total HIV-DNA in PBMCs of successfully treated patients


Objectives: The origin of residual viremia (RV) in HAART-treated HIV-seropositive patients (pts) is unknown. Many investigators interpret RV as the result of ongoing cycles of replication, others as the reactivation of virus from latently infected cells. The aim of the study was to correlate the level of HIV-RNA in plasma and level of HIV-DNA in PBMCs in a cross-sectional analysis.

Methods: 195 HAART-treated pts who achieved virological suppression, as defined by two consecutive plasma HIV-RNA measurements <50 copies/ml, from at least 18 months were enrolled. On the basis of RV levels, the pts were subdivided in 4 groups: pts with undetectable plasma RNA level (UL, <1 copy/ml), pts with low level (LL, 1–10 copies/ml), pts with high level (HL, >10–50 copies/ml) and pts with viral blip (VB, >50–400 copies/ml). RV was quantified by an ultra-ultrasensitive method based on a modified Amplicor HIV-1 Monitor 1.5 (Roche Molecular Systems, USA), with a detection limit of 1 copy/ml. To quantify the total proviral HIV-DNA copy number in PBMC, the Real Time TaqMan protocol published by J-P Viard was adapted, with a sensitivity of 5 copies/10⁶ PBMCs.

Results: 66 (33.8%) pts were UL, 63 (32.3%) were LL, 41 (21%) were HL and 25 (12.8%) were VB. UL pts had highest number of nadir CD4-cells compared to other groups (UL: 360 cells/ml, LL: 315 cells/ml, HL: 279 cells/ml and VB: 305 cells/ul; mean values). Not significant difference was detected in CD4 cell count in the four groups of pts (698, 764, 680 and 691 cell/ul, respectively; mean values). Twenty two patients had undetectable level of proviral DNA in PBMCs (10 UL, 2 LL, 9 HL and 1 VB). The 12 patients with undetectable proviral DNA but detectable residual viremia had a median of 22 copies of HIV-RNA copies/ml (range 12–81 copies/ml). Finally, 11 out of 31 (35.5%) pts with more than 1,000 copies of HIV-DNA/10⁶ PBMCs had undetectable level of RV.

Conclusion: A lack of correlation between HIV proviral DNA and residual viremia levels in a cohort of virologically long term suppressed pts was demonstrated. This study confirms the complex origin of RV and the need to evaluate the relevance of the impact of the new potent drugs, such as Integrase Inhibitors and CCR5 Inhibitors, on episomal viral DNA, on RV and on the long term treatment success.

Prevalence of secondary drug-resistant mutations to antiretroviral drugs in Iranian HIV-infected patients

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Objective: Several studies have reported increasing number of therapeutic failures with antiretroviral drugs in HIV infected patients. The emergence of viral resistant strains is a major problem for the medical management of infected individuals. In this study we aimed to determine the prevalence of secondary antiretroviral resistance-associated mutations in Iranian HIV infected patients.

Methods: A total of 40 HIV infected patients under antiretroviral drug treatment were enrolled in this study. All of the patients were received antiretroviral treatment for at least 1 year. One protease inhibitor (PI) or one nonnucleoside transcriptase inhibitor (NNRTI) in combination with 2 nucleoside transcriptase inhibitors (NRTI) are considered for antiretroviral therapy. The HIV pol region including viral protease and reverse transcriptase genes were amplified and sequenced for determining genotyp, subtype and antiretroviral resistance-associated mutations.

Results: Sequencing of the samples revealed that 40% of strains belonged to subtype B, 20% subtype A, 35% were A/D and 5% were CRF01-AE recombinants. Drug resistance-associated mutations identified more common in subtype A/D recombinant. Virus samples from 30% of participants showing no drug resistance mutation and 70% of them carried ≥2 drug resistance mutations. Dual-class drug-resistant virus (NRTI and NNRTI) was present in 22% of participants, and 43% had virus with triple-class drug resistance.

The prevalence of NRTI mutations was 77% with M184V and V118I present in 55% and 48% of samples respectively. The prevalence of NNRTI mutations was 66% which P225H mutations were present in 30% of study specimens. The prevalence of PIs mutations was 44%. Major PIs mutation L90M was seen in 45% and minor protease inhibitor mutation A71V was detected in 50% of samples. The other major PIs mutations were V32I, L33F, M46I, I54V, V86T, and I84V. The highest frequency of resistance to PIs was related to nevirapine (60%, high level resistance) and saquinavir (60%, intermediate resistance). For NNRTI, the frequencies of resistant isolates were 56% to nevirapine, 44% to delavirdine and 44% to efavirenz, and for NRTI was 56%, high level resistance.

Conclusions: Our study showed a high prevalence of secondary resistance mutations in Iranian HIV infected patients. Continued surveillance of resistance patterns is warranted to guide therapeutic approaches as selection of second-line regimens in Iran.
Sensitivity, specificity and inter-test agreement of interferon-gamma release assays for the diagnosis of latent tuberculosis infection in HIV-infected individuals with advanced immunodeficiency

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Objective: Treatment of latent tuberculosis (LTBI) in HIV+ patients reduces the incidence of TB. Interferon-gamma release assays (IGRAs) may be more specific in diagnosing LTBI than the tuberculin skin test, but their sensitivity at lower CD4 counts has not been established. We studied the effect of CD4 count on IGRA results.

Methods: T-SPOT.TB® ELISPOT assays, incorporating ESAT-6 and CFP-10, and Quantiferon® 3G® ELISA assays, incorporating ESAT-6, CFP-10 and TB17.7, were performed in HIV+ patients with CD4 counts <250×10^6/L (n=72, median CD4 count = 124×10^6/L) and HIV+ controls with CD4 >250×10^6/L (n=160, median CD4 count = 460×10^6/L). Active TB was excluded in all patients. ELISA and ELISPOT responses were related to patient characteristics.

Results: ELISA responses were positive in 21% (n=15) of patients with CD4 <250×10^6/L and 37% (n=49) of those with CD4 >250×10^6/L (difference of 10%, 95% CI –2–22%, p=0.15). ELISPOT responses were positive among 8% (n=5) of patients with CD4 <250×10^6/L and 15% (n=22) of those with CD4 >250×10^6/L, (difference of 7%, 95% CI –2–16%, p=0.13). However; when multivariate regression analysis was used to adjust for LTBI risk factors such as origin from countries of high TB prevalence, ELISA and ELISPOT results were independent of CD4 count.

Migration from countries with a high prevalence of TB (COHP) was associated with positive results on multivariate analysis: in those from COHP the OR for positive ELISA was 2.7 (95% CI 1.5–5), p=0.03; and OR for positive ELISPOT was 4.0 (95% CI 1.6–10), p=0.003. Injection drug use, incarceration and homelessness were not associated with positive results. Significantly, 17% (7/41) of individuals with no risk factor for LTBI had a positive ELISA, and 5% (2/41) had a positive ELISPOT.

30% (70/232) of patients had one or more positive IGRa result, of whom only 32% (21/70) were positive on both tests. Agreement between the two IGRAs was moderate, Cohen’s kappa = 0.37. There was no association between inter-test agreement and CD4 count. Origin from a COHP was associated with a higher level of agreement between positive tests. Conclusions: ELISA and ELISPOT responses were independent of CD4 count. Disagreement between the tests is frequent, and not related to CD4 count. Discordant results are more common in patients with lower pre-test probability of LTBI and, given the high rate of positive results in those with no risk factor for LTBI, may represent false positive results.

Clinical experience with Tspot.TB™ for diagnosis of tuberculosis in HIV-negative and HIV-positive patients

L. Turtle*, T. Kemp, J. Darroch, N. Beeching, M.B. Beadsworth (Liverpool, UK)

Aims: IFN-γ release assays (IGRA) had principally been developed for the diagnosis of latent tuberculosis infection (LTBI) and appear more sensitive and specific than than tuberculin skin testing. IGRA may also offer an attractive option for assisting in diagnosis of active TB. Several studies have been published comparing IGRA with conventional diagnosis. As part of on-going assessment of TB diagnostic approaches we assessed the reliability of IGRA within our cohort at the regional Tropical and Infectious Diseases Unit (TIDU).

Methods: All patients who underwent Tspot TB testing within the TIDU, since testing was introduced in Jan 2008, were included. Comparison was made with M. tuberculosis culture and with a final diagnosis of TB (the administration of a full course of TB therapy). The comparison was also performed separately for both HIV+ and HIV− patients.

Results: 73 Tspot.TB tests were performed on 72 patients; 32% of patients (n=23) were HIV+, 8 were not HIV tested. 76% of patients (n=55) had mycobacterial culture results available (36%, n=20 HIV+), 94% of patients (n=68) had data on the administration of TB therapy; 35% (n=24) received TB therapy (7 HIV+). The kappa coefficient for agreement between Tspot TB and culture of M. tuberculosis for all patients was 0.42 (standard error (SE) 0.13); the kappa value for receipt of TB therapy was 0.47 (SE 0.12). For HIV+ patients (n=23) the kappa value compared with culture was 0.38 (SE 0.22) and for TB therapy was 0.27 (SE 0.2). For HIV- and untested patients (n=46) the kappa value for culture was 0.43 (SE 0.16) and the kappa value for TB therapy was 0.56 (SE 0.15). The sensitivity of Tspot TB in all patients compared with culture was 69.2% (95% CI 57–81.4), specificity 76.8% (95% CI 67.8–89.4), positive predictive value 50% (95% CI 36.8–63.2) and negative predictive value 89.2% (95% CI 81–97.4). Compared with receipt of TB therapy in all patients the sensitivity of Tspot TB was 58.3% (95% CI 45.3–73.1) and specificity 86.7% (95% CI 77.7–95.7). Further analysis will be presented.

Conclusion: The performance of IGRA (Tspot TB) in our everyday clinical use, compared with other published studies is poorer for both HIV positive and negative patients. This indicates the need for further prospective studies to be undertaken before recommending IGRA as a diagnostic tool in active TB.

Usefulness of interferon-gamma release assays for latent tuberculosis screening in patients candidate for TNF-α therapy


Objectives: Reactivation of Mycobacterium tuberculosis infection is a major complication of anti-tumor necrosis factor (TNF-α) treatment. Thus, screening for latent tuberculosis infection (LTBI) is mandatory before starting anti-TNF therapy. The TST has 2 main disadvantages: the low specificity with false positive results in BCG vaccinated subjects and lower sensitivity in presence of immunosuppressive therapy resulting in false negative results. Diagnosis of LTBI may benefit from new interferon-gamma release assays (IGRA). The aim of this study was to investigate the performance of QuantiFERON-TB Gold In Tube (QFT-GIT) assay and its agreement with TST in the screening of LTBI in patients with an immune-mediated inflammatory diseases candidate for anti-TNF therapy.

Methods: We consecutively enrolled 215 patients affected by rheumatoid arthritis (n = 77), psoriatic arthritis (n = 38), psoriasis (n = 64), ankylosing spondylitis (n = 8), Crohn’s disease (n = 22), and Behcet’s disease (n = 6) were enrolled. Screening included: clinical evaluation, chest X-ray, TST and QFT-GIT. 106 patients were on corticosteroid and/or immunosuppressive drugs and 20 were BCG-vaccinated.

Results: Of the 215 patients, 34 (15.8%) had a positive, 152 (70.6%) a negative, and 29 (13.4%) had an indeterminate QFT-GIT result. In 122 (65.5%) patients the TST and QFT-GIT were both negative, in 30 (16%) patients both the tests were positive, while 34 (18%) had discrepant results between TST and QFT-GIT. Agreement between two tests was 81.7% (k=0.53). A diagnosis of LTBI was considered in 38 cases (17.6%). By univariate analysis, we observed an association between BCG vaccination and discordant QFT-GIT/TST+ (OR = 6; 95% CI: 2.3–37.1; p < 0.001) and between the immunosuppressive therapy and an indeterminate QFT-GIT tests (OR = 2.79; 95% CI: 1.06–7.6; p = 0.02), No association between the immunosuppressive therapy and discordant QFT-GIT/TST− (OR = 0.16; 95% CI: 0.01–1.8; p < 0.09) was found.

Conclusion: Our results show that QFT-GIT may be helpful for screening LTBI in patients candidates for anti-TNF-α therapy not only to confirm positive TST results but also to discriminate false-negative TST results as a consequence of previous long-term immunosuppressive treatments. The performance of QFT-GIT seems to not be affected by immunosuppression in our patients. IGRA appears to offer a better chance than TST for monitoring TB infection during anti-TNF-α therapy.
**O333** Diagnosis of tuberculosis infection in patients awaiting transplantation


**Objectives:** To compare the tuberculin skin test (TST) with the QuantiFERON® TB Gold-in-Tube (QFT-GIT) for the diagnosis of tuberculosis infection (TBI) in patients prior to transplantation.

**Methods:** A prospective, cross-sectional study of the patients evaluated for liver and haematopoietic progenitor transplantation in a teaching hospital in Spain, from July 2008 to September 2009. Simultaneous QFT-GIT and two steps TST were performed.

**Results:** 92 patients were screened for TBI, 69 (75%) candidates to liver transplantation (LT) and 23 (25%) to haematopoietic progenitor transplantation (HPT). Sixty-five (65.2%) were men, mean age of 55 years. Fifty two (56.2%) presented some risk factor for TBI and 23 (25%) had BCG-vaccination. In the LT group, 67 (97.1%) patients were diagnosed with cirrhosis with a mean MELD score of 13.8. In the HPT group, 21 (91.3%) patients had received chemotherapy, at least, in the previous 6 months. Thirty eight (41.3%) patients had a positive TST (35 with the 1st TST and only 3 with the 2nd one), and also 38 (41.3%) had a positive QFT-GIT. Among LT patients, there were 31 (44.9%) positive TST and 31 (44.9%) positive QFT-GIT results, and among HPT patients 7 (30.4%) positive TST and 7 (30.4%) positive QFT-GIT results. In the LT group, a MELD score >18 (OR 0.09, CI95% 0.02–0.55; p=0.01) and albumin <30 (OR 0.23, CI95% 0.07–0.82; p=0.02) were associated with a lower likelihood of positive TST but not with QFT-GIT results. Discordant results were observed in 11 QFT-GIT+/TST− patients and in 11 QFT-GIT−/TST+ patients and in 11 QFT-GIT+/TST−, QFT1-GIT+/TST− results were associated with MELD score >18 (9.8, CI95% 1.6–62; p=0.02). There were only 3 (3.3%) indeterminate QFT-GIT results.

**Conclusions:** QFT-GIT and TST are both feasible tests for diagnosing TBI in patients considered for LT and HPT. Higher MELD score and hypoalbuminemia were associated with a lower likelihood of positive TST, but not with QFT-GIT.

**Molecular virology**

**O334** Epstein–Barr virus gene expression patterns in paediatric liver transplant recipients

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**Objectives:** Determination of EBV gene expression patterns in association with EBV DNA load monitoring might be more informative and effective tool in monitoring EBV infection in immunosuppressed patients, allowing earlier detection of EBV related lymphoproliferations and therapeutic intervention in time. The aim of this study was to analyse latent and lytic EBV transcript levels, in relation to EBV DNA load in peripheral blood lymphocytes in immunosuppressed paediatric patients after liver transplantation (LTx).

**Methods:** Thirty patients after LTx were included in this study. Mean±SD age at LTx was 24.1±13.0 months. Mean follow-up was 36.2 months (range 4.7–122.8 months). Multiple blood samples prospectively collected at different time points during post-transplant checkups were used for EBV load measurement and viral gene expression analysis. Quantitative analysis of latent (EBNA1, EBNA2, LMP1, LMP2) and lytic (BZLF1) gene expression was performed in 75 samples by two-step RT real-time PCR. The B95−8 cell line was used as a calibrator, and the expression level of EBV genes was normalized to the expression levels of the endogenous control (HMBS gene). Simultaneously EBV DNA load was monitored using quantitative real-time PCR method.

**Results:** In children after LTx several distinct patterns of EBV gene expression were identified. Majority of samples (53/75, 71%) showed latency 2 profile (LMP1±LMP2 expression), in 10 samples (13%) latency 3 was found (EBNA2 + other latent transcripts), whereas latency 0 (LMP2 only expression) was detected in 8 samples (11%). Additionally, in 4 samples from 4 children lytic infection (BZLF1 expression) was identified. In three cases it was accompanied by a simultaneous presence of latent transcripts. In most children (12/16) in whom multiple blood samples were analysed EBV gene expression patterns varied over time. Similarly, expression level of particular EBV genes varied over time up to 5-log fold in individual patients. EBV latency pattern was not associated with the EBV DNA level. Similarly, the appearance of lytic infection (detectable BZLF1 expression) did not lead to a significant increase of EBV copy number. However, viral load correlated significantly (p<0.05) with the LMP1 and LMP2 expression levels (both r=0.29), but not with EBNA1 or EBNA2 transcript levels.

**Conclusion:** The activity of LMP1 and LMP2 genes may influence EBV DNA load in immunosuppressed paediatric patients.

**O335** Prevalence of papillomavirus in HIV-positive patients

M. Lorenzo, M.P. Romero-Gomez* (Madrid, ES)

**Objective:** The aim of the present study was to determine the prevalence and genotype distribution of concurrent anogenital human papillomavirus (HPV) infection in male patients infected with the human immunodeficiency virus (HIV), using polymerase chain reaction and reverse hybridization.

**Methods:** HPV testing was performed on anal cytology specimens collected from 65 HIV-seropositive men from January to October 2009. Results of de anal cytology also were collected.

**Conclusions:** Anal samples were collected by a trained nurse and cytological specimens were prepared using a liquid based collection method (ThinPrep). The samples were loaded onto the EasyMAG system (bioMérieux, Durham, NC) and DNA extractions were made according to the manufacturer's protocol. The genotyping was performed with a new technological platform using a low density Microarray CLART® Papillomavirus 2 (Genomica, Spain). All samples were analyzed for the presence of the following HPV types: 6, 11, 16, 18, 26, 31, 33, 35, 39, 40, 42, 43, 44, 45, 51, 52, 53, 54, 56, 58, 59, 61, 62, 66, 68, 70, 71, 72, 73, 81, 82, 83, 84, 85 and 89.

**Results:** HPV DNA was detected in 58 (89.2% of samples). The most frequently detected HPV types were HPV 53 (29.2% of the positive samples), HPV 16 (24.6%), HPV 33 (24.6%), HPV 51 (23%), HPV 58 (21.5%), HPV 59 (18.5%) and HPV 68 (16.9%). We found only seven patients with one genotype infection of HPVs. Twenty nine patients (44.6%) with normal anal cytology had high and low risk HPV. In six patients we found high risk HPV and abnormal cytology [3 patients had low-grade squamous intraepithelial lesion (LSIL), 2 patients with grade 1 anal intraepithelial neoplasia (AIN-I) and 1 patient with atypical squamous cells of undetermined significance (ASCUS)].

**Conclusions:** A wide variety of HPV genotypes was detected, and coinfection with multiple genotypes was common in our patients. HPV screening in HIV-positive patients even in cases of normal anal cytology can be useful for detecting those patient with risk to develop cancer.

**O336** Natural polymorphism of UL23 thymidine kinase and UL30 DNA polymerase among herpes simplex virus type 1 and 2 strains


**Objectives:** Genotypic detection of herpes simplex virus (HSV) resistance to antivirals is based on thymidine kinase (UL23) and DNA polymerase (UL30) gene sequencing. The interpretation of results requires distinguishing resistance mutations from natural interstrain sequence variations. The objective of this work was to assess extensively the natural polymorphism of pUL23 and pUL30 among HSV strains.

**Methods:** Three laboratory strains (KOS, G-HSV-2, MH2) and 54 clinical isolates (27 HSV-1 and 27 HSV-2) were studied. Forty strains
were collected from patients who had not received any previous anti-HSV treatment, and 14 strains exhibited acyclovir and foscarnet phenotypic susceptibility using a plaque reduction assay. The entire open reading frame of UL23 and UL30 genes was sequenced. Nucleotide and amino acid sequences were compared with that of reference strains from Genbank: accession numbers X14112 (HSV-1 strain 17) and Z86099 (HSV2 strain HG52).

**Results:** The interstrain identity of UL23 gene ranged from 99.3% to 100% at the nucleotide level in the 57 HSV strains investigated. There were 19 and 11 variant nucleotides for HSV-1 and HSV-2 strains, respectively. Overall, 19 amino acid changes were identified for HSV-1 strains and 7 amino acid changes for HSV-2 strains (that is, 5.1% and 1.9% of the total codons of the protein, respectively). The analysis of UL30 gene showed >99.5% interstrain identity among all HSV strains. Surprisingly, in HSV-1 strains, 113 variant nucleotides were evidenced, of which 72% produced silent mutations, whereas in HSV-2 strains, only 28 were evidenced, of which 32% produced silent mutations. Thirty and 18 amino acid changes distributed across UL30 DNA polymerase were described for HSV-1 and HSV-2 strains, respectively, corresponding to 2.4% and 1.3% of the total codons of the protein. Of note, one HSV-2 isolate harboured a deletion at codons 1106–1111 in the C-terminal region of pUL30. For both viral proteins, 71 out of 74 amino acid changes identified lied within nonconserved regions.

**Conclusion:** Our results show that UL23 thymidine kinase and UL30 DNA polymerase are highly conserved among HSV strains, with a weaker variability for HSV-2 strains. Beside previously described mutations, a number of previously undescribed natural variations were identified. This work provides the natural polymorphism map of pUL23 and pUL30 among both HSV-1 and HSV-2 strains that will be helpful for HSV genotypic antiviral resistance testing.
Community-acquired MRSA and MSSA

Clonal composition and antimicrobial resistance of Panton-Valentine leukocidin-positive Staphylococcus aureus in Wales

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(Swansea, Cardiff, UK)

Objectives: Panton-Valentine Leukocidin (PVL)-positive S. aureus typically cause skin/fat-tissue abscesses, haemorrhagic pneumonia and necrotising fasciitis. Wide dissemination of PVL-positive CA-MRSA clones, i.e. USA300 and USA400, requires continuous surveillance. We investigated the molecular epidemiology and antibiotic resistance of PVL-positive S. aureus obtained at two institutions in Wales.

Methods: Two cohorts of PVL-positive S. aureus were studied: i. 19/560 (3.4%) consecutive wound isolates from NHHS Microbiology Swansea PVL-positive by PCR (ABMU); ii. PVL-positive S. aureus strains submitted to Specialist Antimicrobial Chemotherapy Unit, NHHS Microbiology Cardiff (SACU; n=61), using meca, PVL, and arginine catabolic mobile element (ACME) PCR, pulsed-field gel electrophoresis (PFGE), spa-, and SCCmec-typing. Susceptibility testing was performed using BD Phoenix.

Results: meca prevalence was significantly different between ABMU 2/19 (10.5%) and SACU 35/61 (57.4%) strains (p<0.001). ABMU MRSA strains exhibited t011-MRSA-IVd and t437-MRSA-V genotypes. The majority of ABMU strains were diverse MSSA containing 3 strains each of spa-types 021 and t314 (15.8%) and the new spa-type t4791. The SACU cohort comprised a predominant clone (n=16; 26.2%) t008-MRSA-IVA, confirmed as USA300-0114 by PFGE and presence of ACME. Other clones included: t044-MRSA-IVc (n=5; 8.2%); t002-MRSA-IVA (n=3; 4.9%) and t127-MRSA-IVA (n=2; 3.3%).

Two new spa-types were encountered (1 MRSA, 1 MSSA, assignment pending). Resistant strains (n=80): oxacillin 45%, gentamicin 5%, tobramycin 36%, erythromycin 28%, clindamycin 1%, tetracycline 18%, trimethoprim 16%, and ciprofloxacin 1%. D-test revealed 36% inducible clindamycin resistant (CR), 5% constitutive CR, and 59% clindamycin sensitive strains in 22 48h (n=1), 48h (n=2), nodata (n=2)

Conclusions: There was a striking difference of antibiotic resistance and clonal composition of the two cohorts. USA300-0114 was the most prevalent clone in the SACU cohort and other globally distributed clones were also represented. None of these clones were found in the unselected ABMU cohort. While molecular epidemiologic analysis of strains submitted to referral units provides valuable information, this needs confirmation by investigation of unselected isolates from the same area.

Frequency of PVL-positive community-associated MRSA and livestock-associated MRSA among patients in Belgian acute-care hospitals


Objectives: Healthcare-associated strains of methicillin-resistant Staphylococcus aureus (HA-MRSA) are endemic in Belgian hospitals for two decades. Recently, PVL-positive community-associated MRSA (CA-MRSA) and livestock-associated MRSA ST398 strains (LA-MRSA) have been identified in Belgium. We determined the relative frequency of MRSA strains by genotype in patients in acute-care hospitals as part of an ongoing surveillance program since 1995.

Methods: All hospitals were invited to collect three consecutive, non-duplicate MRSA isolates from hospitalised patients in 2005 and 2008 (five isolates in 2003). MRSA were confirmed by PCR for nuc and meca genes and genotyped by spa- and SCCmec-type. MLST was performed on a subset of strains (n=20).

Results: Of MRSA isolates from 315 patients in 109 hospitals, 53% were detected on admission or ≤48 hours after admission, compared to 36% in 2005 and 2003. Five PVL-positive strains (1.6%) of ST30-SCCmec IV (n=4) and ST5-SCCmec IV (n=1) were detected. PVL-positive MRSA represented 1.2% and 0.2% of MRSA from hospitalised patients in surveys of 2005 and 2003, respectively. Two patients with LA-MRSA ST398 (0.6%), showing spa-type t011, were identified. LA-MRSA isolates were found in 0.9% and 0.4% of MRSA in 2005 and 2003, respectively.

Conclusion: The proportion of patients with MRSA that are imported in hospitals was over fifty percent in Belgium in 2008. However, LA-MRSA and PVL-positive MRSA strains only represent a small proportion (<3%) of the burden of MRSA strains in this patient population in 2008. The frequency of PVL-positive MRSA and LA-MRSA has remained stable since 2003.

Distribution of MRSA during surveys in 2003, 2005 and 2008

Table 1: Distribution of MRSA during surveys in 2003, 2005 and 2008

<table>
<thead>
<tr>
<th>MRSA genotype</th>
<th>2003 (n=518)</th>
<th>2005 (n=327)</th>
<th>2008 (n=315)</th>
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</thead>
<tbody>
<tr>
<td>ST1-SCCmec IV</td>
<td>30.6%</td>
<td>33.1%</td>
<td>35.0%</td>
</tr>
<tr>
<td>ST5-SCCmec IV</td>
<td>26.6%</td>
<td>27.3%</td>
<td>25.9%</td>
</tr>
<tr>
<td>ST80-SCCmec IV</td>
<td>10.6%</td>
<td>10.9%</td>
<td>11.8%</td>
</tr>
<tr>
<td>ST398-SCCmec IV</td>
<td>12.9%</td>
<td>12.3%</td>
<td>12.4%</td>
</tr>
<tr>
<td>ST22-SCCmec IV</td>
<td>3.4%</td>
<td>3.6%</td>
<td>3.4%</td>
</tr>
<tr>
<td>ST30-SCCmec IV</td>
<td>0.4%</td>
<td>0.4%</td>
<td>0.4%</td>
</tr>
<tr>
<td>ST5-SCCmec IV</td>
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<td>0.2%</td>
</tr>
<tr>
<td>ST5-SCCmec IV</td>
<td>0.2%</td>
<td>0.2%</td>
<td>0.2%</td>
</tr>
</tbody>
</table>

Association of PVL with staphylococcal pyogenic skin infections

A.M. Kearns*, M. Ganner, I. McCormick Smith, C. Perry, B.D. Cookson, M.J. Ellington (London, UK)

Objectives: Whilst the role of PVL in staphylococcal disease remains contentious, the association of PVL-positive S. aureus (PVL-SA) with recurrent skin and soft tissue infections is compelling. Following the introduction of initiatives for enhanced ascertainment of PVL-related disease in England, we sought to investigate the clinical and epidemiological features of pyogenic skin infections cause by PVL-positive versus PVL-negative S. aureus.

Methods: Isolates of S. aureus submitted to the national Staphylococcus Reference Unit (SRU) recovered from pyogenic skin infections (boils, abscesses, carbuncles etc) from patients throughout England, Wales and Northern Ireland during 2008 were included for study. Isolates were characterised by toxin gene profiling (including PVL), meca testing and DNA fingerprinting by pulsed-field gel electrophoresis. Patient demographic data and clinical features including the site of the lesion(s) and recurrence of infection were analysed.

Results: During 2008, a total of 1230 isolates of S. aureus from pyogenic skin infections were submitted to the SRU for characterisation. Of these, 835 were MSSA and 395 were MRSA (68 and 32% respectively). Patients were aged 0 to 95y (median 30y); the male:female ratio was 1:1.

A total of 800 (65%) isolates were PVL-positive; the majority of which (523; 65%) were LA-MRSA. Comparison of cases according to PVL status showed PVL-SA were recovered from younger cohorts (median 26y) and were commonly associated with buttock, thigh and/or axilla lesions (50% cases). In contrast, PVL-negative SA were associated with older
individuals (median 38y) with lesions from a wide range of body sites, the commonest sites being breast or back (11% each). Recurrent infections were more apparent among the PVL group (30 vs 20% cases). A multiplicity of strains/lineages was identified. Of 10 different clones of PVL-MRSA identified, 3 lineages (USA300, European and South West Pacific clones) predominated.

**Conclusion:** PVL-SA from pyogenic skin infections predominantly occurred in younger individuals, most commonly affecting the buttocks and/or axillae; a third of infections were recurrent. These data have important implications for recognising, diagnosing and managing such infections in the community.

**O342** Staphylococcus aureus skin and mucosa infections in primary healthcare in Denmark: a 12-year population-based study

M. Dalager-Pedersen*, M. Søgaard, M. Mølgaard, H.C. Schonheyder (Aalborg, DK)

**Objectives:** A rise in community onset S. aureus infections has been observed in several European countries. The objective of this study was to ascertain trends of S. aureus infections in primary healthcare in Denmark.

**Methods:** We conducted the study within the North Denmark Region (pop. 495,000 inhabitants) 1996 though 2008. We retrieved information on bacteriological specimens collected from skin and mucosal surfaces by general practitioners and practicing specialists. We further obtained data on redeemed dicloxacillin prescriptions which is the preferred antibiotic for S. aureus infections in Denmark. Our unit of observation was a specimen, S. aureus isolate or prescription with no similar record within the previous year. According to this definition we limited the study to the years 1997–2008. By use of direct standardization, we computed annual age- and gender standardized rates of bacteriological specimens, S. aureus isolates and prescriptions of dicloxacillin per 100,000 person-years (pyr).

**Results:** A total of 108.758 specimens were obtained of which 42.778 (39%) yielded S. aureus. The rate of specimens doubled during the study period reaching 2399 per 100,000 pyr in 2008. The rate of S. aureus isolates increased until 2003 and remained fairly stable thereafter (842 per 100,000 pyr in 2008). Among children 0–14 years old, the rate of S. aureus isolates increased steeply from 1997 to 2002 followed by a gradual decrease thereafter (peak 145 per 100,000 pyr in 2002). The rising incidence of bacteriological cultures and antibiotic prescriptions, especially in children, contributed to the rising trend but in recent years there has been a further increase of S. aureus isolates from other sources and age groups.

**Conclusion:** The rising incidence of bacteriological cultures and anti-staphylococcal antibiotic prescriptions indicate an increasing attention to S. aureus infections in primary health care in Denmark. National campaigns for prudent use of antibiotics may have been an incentive to perform more bacteriological cultures. Impetigo, especially among children, contributed to the rising trend but in recent years there has been a further increase of S. aureus isolates from other sources and age groups.

**Table MRSA details from long-term care facilities in Northern Israel**

<table>
<thead>
<tr>
<th>Status</th>
<th>No. Screened</th>
<th>Positive MRSA (%)</th>
<th>Antibiotic susceptibility profile</th>
<th>MRSA molecular characterization</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Facility A</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Residents</td>
<td>19</td>
<td>15</td>
<td>5 (20)</td>
<td>5 GEN; CIP; CLI; ERY</td>
</tr>
<tr>
<td>Staff</td>
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<tr>
<td><strong>Facility B</strong></td>
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<tr>
<td>Residents</td>
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<td>11</td>
<td>2 (18)</td>
<td>2 GEN; CIP; CLI; ERY</td>
</tr>
<tr>
<td>Staff</td>
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<td>0 (0)</td>
<td></td>
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<tr>
<td><strong>Facility C</strong></td>
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<td>Residents</td>
<td>18</td>
<td>17</td>
<td>2 (12)</td>
<td>2 CIP; CLI; ERY</td>
</tr>
<tr>
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<td><strong>Facility D</strong></td>
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<tr>
<td>Residents</td>
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<td>0 (0)</td>
<td></td>
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<tr>
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<td><strong>Facility E</strong></td>
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<td>Residents</td>
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<td>Staff</td>
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<td>0 (0)</td>
<td></td>
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<td><strong>Facility F</strong></td>
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<tr>
<td>Residents</td>
<td>125</td>
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<td>13 (10)</td>
<td>15 CIP; CLI; ERY</td>
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<tr>
<td>Staff</td>
<td>100</td>
<td>100</td>
<td>10 (10)</td>
<td>15 CIP; CLI; ERY</td>
</tr>
</tbody>
</table>

**Antifungal resistance and molecular mycology**

**O344** Azole-resistant environmental aspergilli and Aspergillus terreus in Denmark, Austria and Spain

K. Mortensen*, E. Mellado, C. Lass-Fårø, J.L. Tudela, M. Arendrup (Copenhagen, DK; Madrid, ES; Innsbruck, AT)

**Objectives:** To investigate if azole resistant aspergilli and A. terreus are present in the environment and in commercial compost in Denmark (DK), Austria (A) and Spain (ES).

**Methods:** Soil samples were collected from the surroundings of the main hospitals in Copenhagen (CPH), Innsbruck (25) and Madrid (31), flowerbeds in a amusement park in the centre of Copenhagen (23) and finally from compost bags purchased in DK (26), A (25) and ES (28).
Two grams of soil/compost were suspended in 5 ml 0.2 M NaCl-1% Tween and 100 µl plated on Sabouraud agar and 50 µl on each of 4 RPMI-1640–2% glucose agars containing itraconazole (4 mg/l), voriconazole (1 mg/l), posaconazole (0.5 mg/l) and no antifungal, respectively, and incubated at 37°C. Identification of aspergilli was based on standard micro- and macro-morphological criteria. Aspergillus isolates which grew on the azole containing agars underwent susceptibility testing using EUCAST E.DEF 9.1 microdilution method for itraconazole, posaconazole and voriconazole and β-tubulin sequencing unless they were able to grow at 48°C. The promoter and entire coding sequence of the cyp51A gene were sequenced for azole resistant isolates.

Results: From a total of 185 samples A. fumigatus was recovered in 139 (DK: 50/76, 66%; A: 49/50, 98%; ES: 40/59, 68%), A. niger in 36 (DK: 4/76, 5%; A: 5/50, 10%; ES: 27/59, 46%), A. terreus in seven (DK: 0/76; A: 7/50, 14%; ES: 0/59), A. nidulans in four (DK: 1/76, 1%; A: 0/50; ES: 3/59, 5%), A. f.latus in three (DK: 2/76, 3%; A: 0/50; ES: 1/59, 2%), A. lentulus (ES: 1) and A. sp (ES: 2, molecular identification pending). A total of four A. fumigatus isolates (three from the amusement park in CPH and one from surroundings of CPH University Hospital (CPHUH)) displayed elevated MICs to itraconazole (>4 mg/l), posaconazole (0.5–4 mg/l) and voriconazole (4–>4 mg/l). All harboured the TR-L98H resistance mechanism. Additionally, one A. niger infected CD one A. niger with elevated itraconazole MIC’s of 4 mg/l and 2 mg/l, respectively, were recovered from CPHUH.

Conclusion: Multi-azole resistant A. fumigatus is present in the environment in DK. The resistance mechanism is identical to that of environmental isolates in the Netherlands. In ES and A only Aspergillus species with intrinsic resistance to either azoles or amphotericin B were found. No link to commercial compost could be detected. Resistant aspergilli should be considered in aspergillosis, even in antifungal drug-naive patients.

Impact of CYP51A mutations associated with azole-resistance on in vitro growth rates and in vivo virulence of clinical A. fumigatus isolates

E. Maxvidas*, J. Meletiadis, M. Arendrup, W.J. Melchers, J.W. Mouton, P. Verweij (Nijmegen, NL; Athens, GR; Copenhagen, DK)

Objectives: The emergence of multi-azole resistant Aspergillus fumigatus (AF) causing invasive aspergillosis has raised the question of whether the evolution of azole-resistance has an impact on virulence and therefore on clinical outcome. The aim of this study was to determine whether acquired azole resistance in fungi through mutations in CYP51A or other unknown genes comes with a cost in fitness.

Methods: The virulence study included a) 8 multi-azole resistant AF clinical isolates with different mutations in the CYP51A gene (3 strains with TR-L98H, 1 each with M220I, M220V, M220K, G54W, G138C) b) 3 wild-type azole susceptible (WT) strains as reference and c) 2 isogenic isolates with no CYP51A mutations (1 susceptible and 1 resistant strain) which were serially recovered from a single patient pre- and post-antifungal treatment. Microsatellite-typing method and CSP-method were performed to verify the genetic relationship of the 2 isolates. Susceptibility testing was performed based on the CLSI-M38A method. RT-PCR was performed to determine the CYP51A expression. In vitro growth rates were determined using a previously described kinetic system (Meletiadis et al JCM 2001) and defined as the incubation time needed to reach a hyphal growth of 70 microm. In vivo virulence was determined based on the 15-day mortality in each of 52 groups of 572 outbred i.v infected C57BL/10 mice (11 mice/group × 13 AF strains × 4 different CFU inocula).

Results: There was a marked reduction of virulence of the post-treatment azole-resistant isogenic isolate 2 (0% 15-day mortality) compared to a) the reference WT groups (57.6% average mortality, p < 0.05) b) the CYP51A groups (47.72% average mortality, p < 0.05) and c) the pre-treatment azole susceptible isolate 1 (90.91% mortality, p < 0.05). There was no difference (p < 0.05) in virulence for all CYP51A mutants compared to the WTs. The in vitro growth rates of the AF CYP51A mutants were not different compared to those of the AF WT control but it was significantly reduced when compared to the resistant isolate 2. Linear correlation was found between in vitro growth rates and in vivo virulence (R² 0.99, slope 2.28, p < 0.001). Moreover, CYP51A elevated RNA levels implicate 14α-methylase in an important role in azole resistance but not in virulence.

Discussion: Acquired antifungal resistance can lead to dramatic decrease of virulence of AF. However, CYP51A mutations associated with acquired azole resistance did not affect AF virulence.

Infections due to Candida spp. with reduced susceptibility to caspofungin in France


Objectives: Resistance to caspofungin in Candida spp. is rare with less than 25 cases reported so far in the literature. We thus analyzed the characteristics of infections due to isolates with reduced susceptibility to caspofungin collected at the French Natl Reference Center (NRCMA) between 2004 and 2009.

Methods: All Candida spp. received at the NRCMA are routinely tested for their susceptibility to caspofungin in AM3 medium using the EUCAST method. Those with caspofungin MIC > 0.5 µg/ml (Desnos-Ollivier AAC 2008, 52:3092), were analyzed by sequencing the hot-spot regions of the FKS genes. Initial isolates were also analyzed when available and serial isolates were genotyped using polymorphic microsatellite markers. All medical charts of patients harbouring such isolates were reviewed.

Results: For the 14 episodes involving isolates with reduced susceptibility to caspofungin, patients (sex ratio M:F = 10:4, mean age: 44y) were diagnosed with candidemia (n = 8), other invasive infections (n = 4) and oropharyngeal candidiasis (n = 2). Underlying diseases were hematological malignancies (n = 6), solid organ transplant (n = 2), HIV infection (n = 1), and other conditions (n = 5). Candida species were 7 C. albicans, 6 C. glabrata, and 1 C. krusei. All 14 isolates have been recovered after the patient was treated with caspofungin for a duration ranging from 10 days to several months. All had mutation in FKS genes. Among 10 patients for whom a previous isolate was available, paired isolates shared identical genotypes. Furthermore, for each pair, the isolate recovered before caspofungin treatment had higher susceptibility (MIC < 0.25 µg/ml) to caspofungin than the second ones, and had wild-type FKS genes.

Conclusions: Caspofungin resistance in Candida spp. was always associated with prior exposure to the drug in severely ill patients. Further analysis should uncover if other factors such as treatment's duration influence its occurrence. Invasive infections due to various species of Candida spp. with acquired reduced susceptibility to caspofungin deserve attention.

Innovative multiplex diagnostics for Candida spp. using MLPA

G. Dingemans*, R. Boezen, C. Klaassen, M. Reijans, J. Meis, T. Boekhout, G. Simons (Maastricht, Utrecht, Nijmegen, NL)

Objective: Candida yeasts are the fourth most common source of nosocomial bloodstream infections. Especially during the last decade, the prevalence of opportunistic Candida infections has increased and has become a serious threat to high risk patients.

To date, most molecular diagnostic tools are based on ribosomal regions. Although broadly applied, these target genes have difficulties discriminating closely related species, causing misidentification and underestimation of polymicrobial infections. This results in an urgent need of high discriminatory and accurate detection methods for clinical purposes using novel probes.

The aim of this project is to improve molecular diagnostics of yeast-related infections.

Methods: A novel DNA based diagnostic system using Multiplex Ligation-dependent Probe Amplification (MLPA) technology serves as
our platform for molecular diagnostics using newly developed diagnostic probes. A Candida-MLPA assay containing probes for C. albicans, C. dublinensis, C. krusei, C. tropicalis, C. parapsilosis, C. glabrata, C. guilliermondii, and C. lastariae has been developed.

Results: The specificity of the assay was validated on 50 Candida/non-Candida spp. from CBS Fungal Biodiversity Centre. In addition, 95 clinical isolates were screened with the MLPA assay and the results were compared with AFLP profiles. In case of any discordance the identity of the strain was established by sequencing the ITS region. Furthermore, the total screening encompassed phylogenetically related species, including 31 Candida spp., 4 Pichia spp. and S cerevisiae. The Candida-MLPA assay showed a 100% concordance with the ITS sequences. The analytical sensitivity of the Candida-MLPA assay was established on 100 fg gDNA, which represents less than two yeast cells. Conclusions: We have demonstrated that an assay based upon the MLPA technology was able to identify 8 Candida spp. in one reaction. Multiple infections, up to 7 species in one sample, could be identified. Due to the nature of the MLPA technology highly complex assays are possible providing room for additional probes like a generic Candida probe or probes for other emerging species. The specificity and sensitivity of this multiparameter assay shows great potential for a fast and comprehensive screening approach for clinically relevant Candida spp. in a diagnostic setting.

Evaluation of publicly available sequence information in the NCBI nr/nt database to identify fungi isolated from clinical samples

Objectives: Defining the specific etiology of a fungal infection is critical to the selection of appropriate antifungal therapy. Morphologic identification of fungi can take days to weeks and requires an experienced mycologist. Sequence-based identification of fungi could expedite identification but it has been estimated that up to 20% of fungal sequences deposited in NCBI are incorrect. A reliable database of clinically relevant fungal sequences is critical for advancing molecular diagnosis of fungal infections. The purpose of this study was to compare morphologic identification to sequence identification of fungi isolated from clinical samples.

Methods: Fungi isolated from clinical samples at Barnes-Jewish Hospital and St. Louis Children’s Hospital were identified based on morphological and/or biochemical characteristics. DNA was extracted from the fungi using the BDI GeneOhm kit with a 5 min lysis followed by heating at 95°C for 15 min. The ITS1 – 5.8s rRNA-ITS2 region from 133 isolates was amplified and PCR products were bi-directionally sequenced on an ABI 3130. Trimmed sequences were then aligned with sequences in the NCBI nr/nt database using BLAST. Filamentous fungi and yeast from 33 genera and 55 species were included in the study.

Results: For 64 of the 133 isolates sequenced, the morphological identification matched the sequence-based identification. Morphologic and sequence based identification were disparate in 38 cases. For 31 of the isolates, the sequence-based identification was equivocal; that is, the morphologic identification was found in the top ten “hits” in the sequence database, but the morphologic identification was not the first choice or there were other choices that were equal probability matches. Sequence identification performed well for most yeast species, and for some filamentous fungi, such as Aspergillus, Sciciodiortum and Fusarium spp. Sequence identification was not as accurate for identification of dermatophytes, Zygomycetes, and dematiaceous moulds.

Conclusions: Use of the NCBI sequence database for identification of clinical isolates of fungi may result in incorrect identification and administration of appropriate antifungal therapy. Once our data have been compiled into a database of fungal sequences, we will conduct challenge experiments for the identification of clinical isolates.

Population genetics, phylogeny and genomics
C. Bachrieser* (Paris, FR)

Legionella pneumophila is a human pathogen that was recognized only about 30 years ago. It is the causative agent of Legionnaires’ disease, a severe pneumonia that is transmitted through inhalation of aerosols of contaminated water. Shortly after its discovery, the ability of Legionella to multiply intracellularly in fresh water protozoa was discovered. This long lasting co-evolution between the eukaryotic host and Legionella has led to the selection of a panoply of virulence factors, which allow to exploit important cellular processes during infection. Compelling evidence for the importance of protozoa in the evolution of this bacterium comes from analysis of complete genome sequences. A key feature of the L. pneumophila genomes is the presence of a high number and wide variety of eukaryotic like proteins and protein domains probably acquired through horizontal gene transfer and/or convergent evolution. In the last years several different typing methods aiming in investigating the molecular epidemiology of L. pneumophila have been developed. Furthermore, the access to whole genome sequences of several L. pneumophila strains allowed to apply large scale comparative genomics studies using DNA arrays. A higher genetic diversity among environmental isolates with respect to clinical isolates and the presence of specific clones of L. pneumophila overrepresented in human disease or causing legionellosis world wide, were identified. Recently we applied new generation sequencing to further investigate the evolutionary history and population structure of the worldwide distributed epidemic and endemic clone L. pneumophila Paris as well as the newly emerging clone Lorraine.

Cell microbiology
C.R. Roy* (New Haven, US)

We are interested in the dialogue between intracellular pathogens and eukaryotic host cells. To better understand how pathogens communicate with the host we have been studying bacterial proteins that function in the manipulation of host cellular processes. This lecture will describe proteins produced by the intracellular pathogen Legionella pneumophila that are delivered into eukaryotic cells by a specialized “type IV” secretion system. These bacterial proteins function to prevent fusion of lysosomes with vacuoles containing L. pneumophila and promote fusion of the pathogen-occupied vacuole with endoplasmic reticulum-derived vesicles. Several of these bacterial proteins modulate the activity of small GTP-binding proteins belonging to the ARF and Rab families. The biochemical activities of these bacterial effector proteins and their specificity for host targets will be discussed.

Travel medicine: an emerging field of infectious diseases
P Parola*, P Gautret, P Schlagenhauf (Marseille, FR; Zurich, CH)

Some 80 million individuals from industrialized nations travel to the developing world each year and it is estimated that more than 200 million people now reside outside their country of birth. In recent years, growth in international travel has been estimated at approximately 6% per year, and European travellers represent the vast majority of international travellers. Travel medicine focuses on protecting the health of the individual and protecting the wider community in which that individual lives, works or travels. Initially derived from infectious diseases and tropical medicine, the specialty now encompasses primary care, migrant medicine, occupational medicine, wilderness medicine, as well as international health.
Travelers can spread new and re-emerging infectious diseases that initially appear in developing countries, and act as ideal sentinels for the early detection of these diseases. Over the past decade, the global public health community has been facing the challenges brought on by the emergence and rapid worldwide spread of novel influenza strains, SARS, chikungunya virus, and drug-resistant tuberculosis amongst other pathogens. Modern transportation and the growth of tourism, immigration, and business travel were factors that contributed to dissemination of these high impact pathogens.

Specialized travel/tropical medicine clinics in Europe are ideally situated to effectively detect emerging infections and to track ongoing trends in travel-related illness and emerging agents in collaboration with laboratories of microbiology. Over the past decade, both global and regional provider-based surveillance networks have emerged that have provided, for the first time, systematic and robust data that define the spectrum of illness and the places of exposure to the most significant health risks that face travelers.

**Infection control: zero tolerance?**

*W. Gruninger* (Vienna, AT)

With a declining arsenal of antibiotics to treat infections, it was increasingly clear that the traditional orientation toward control of HAIs (hospital acquired infections) needed to shift to one where preventing the occurrence was the priority throughout the institution. There has to be a global capacity for the political, financial, managerial, and technical support needed for worldwide initiatives. These considerations were all addressed when diseases like smallpox, polio, measles, dracunculiasis, lymyatic filariasis, onchocerciasis, Chagas disease, and Hansen disease were targeted for eradication. This model doesn’t exactly work for HAIs, because we deal with many different organisms and types of infections, humans are not the only reservoir, many of the organisms are normal flora, and relatively limited scientific and operational resources have actually been dedicated to preventing HAIs.

New technologies and procedures, more virulent pathogens and increasing resistance will continue to challenge the healthcare community in its efforts reduce HAIs.

If one looks theoretically at all of the infections that occur, one could divide them up into two main groups; some that are preventable and some that are not. The ones that are preventable are preventable through the implementation of practices, behaviors and procedures, and following a very strict clinical pathway. Others are not probably preventable, and that is the irreducible amount.

The ‘getting to zero’ movement is the product of three forces: the expansion of external pressures on infection control programs, the intrusion of suboptimal evidence, and the convergence of quality improvement and infection control. The ‘zero’ obsession has a number of worrisome, unintended consequences. It sets up unrealistic expectations on the part of the public and healthcare administrators, leading to unreasonable demands on infection control programs. It fosters a punitive culture, since someone must be at fault for causing infections. It separates infection control from safety and quality, when infection control concerns trump other important safety issues. It has shifted the development of interventions away from an approach based on local risk assessment to the promotion of a one-size-fits-all approach. Healthcare workers and hospital epidemiologists have become demoralized when the expectations for getting to zero persist but the elusive zero has not been attained.

The concept of “targeting zero HAIs” is controversial, because many people believe it sets unrealistic or impossible expectations that all HAIs are preventable and that any HAI that may occur was due to an error or a broken process. Targeting ‘zero’ is problematic, because it does not address the variation in the risk of HAIs in different patient populations or settings, it does not address the denominator or time frame that is necessary to understand rates of infection, and it inherently seems scientifically unrealistic.

“Getting to zero” is a sound bite that misleads the public and is not helpful to hospital epidemiologists. The “zero” approach to HAIs is rigid, dishonest, and anti-intellectual, and it dives a culture of blame.

**MRSA screening: what else to know**

*M.J. Struelens* (Stockholm, SE)

Healthcare associated staphylococcal infection represents a major health and economic burden world wide. The in vitro diagnostic industry has in recent years invested significantly to develop and market advanced SA/MRSA screening tests for clinical and public health decision support in healthcare facilities. Successful technology innovation meets longstanding medical needs of timely detection of SA/MRSA carriers to accelerate control of transmission. The purpose of SA/MRSA screening is two-fold: (1) to adapt individual therapeutic and prophylactic treatment regimens and (2) to isolate and decolonize carriers early on to reduce secondary nosocomial transmission. Novel screening tests include enhanced culture-based methods and molecular-based DNA detection methods. Significant enhancement of culture based MRSA screening has been achieved with marketing of new generation of selective, cefoxitin-containing chromogenic agar media. The best performing media provide MRSA detection within 16 to 48 h post sampling with variable sensitivity (ranging 50–99%) and good to excellent specificity (>95%). A more sophisticated, semi-automated system of luminescent growth detection in selective liquid media proved insufficiently sensitive in clinical trials. Several PCR systems are commercially available for MRSA screening. PCR assay time varies from 75 min to 6 h. Analytical complexity ranges from multi-step manual procedure of sample preparation, DNA extraction, amplification and hybridisation to fully automated systems with minimal sample preparation. Diagnostic accuracy of PCR tests varies according to test, test version, sample site and reference method used as gold standard with sensitivity range of 70–100% and specificity range of 90–99%. Impact of rapid MRSA screening on transmission control effectiveness depends on many contextual factors, including workflow integration and clinical turn-around time, case-mix and type of care, MRSA incidence and prevalence, infection control policy, compliance with infection control measures and intervention study design. Cost-effectiveness evaluation should carefully examine these parameters for each test before routine implementation.

**The threat of a new influenza A pandemic**

*I. Capua* (Legnaro, IT)

The emergence and spread of the 2009 pandemic H1N1 virus (H1N1 2009) from the animal reservoir raises questions on the future approach to influenzavirus infections. We have evidence demonstrating that influenzavirus genes migrate across continents and animal species, and assemble themselves in combinations which are a threat to animal and human health, resulting in panzootics like H5N1 or pandemics like H1N1 2009. The latter contains a unique combination of genes from three species and two hemispheres. In a globalized environment, mapping gene movement across species and national borders and identifying mutations and gene constellations with pandemic potential or virulence determinants is essential to enact prevention and control strategies at a global level. This is in line with, and possibly the best example of, the ‘One Health’ vision: a multidisciplinary collaborative approach to improve the health of humans, animals and the environment endorsed by the UN Food & Agriculture Organisation, the World Organisation for Animal Health (OIE) and the World Health Organisation.

Vast improvements in capacity building have been achieved as a result of the H5N1 global crisis. Thousands of viral isolates with zoonotic
potential have been obtained through surveillance efforts, although the genetic information has not been exploited fully. In addition, the circulation of efflux pumps in certain species including dogs, pigs and horses has been neglected.

Time has come to invest in a novel approach to efflux pump infections, abandoning prefixed compartments linked to geographical origin or species of isolation, and analyse the efflux gene pool as one entity.

We propose capitalising on existing achievements and investments to develop an international network and a permanent observatory which will improve our understanding of the dynamics of the efflux virus gene pool in animals and humans. This will generate essential information to support both public and animal health.

The “One Health” initiative would result in international synergies, bridging gaps between medical and veterinary scientists, permanent monitoring of virus evolution and epidemiology and the best exploitation of investments in capacity building. Above all it could be a challenge and opportunity to implement the “One Health” vision, and possibly act as a model for other emerging zoonotic diseases.

**Antimicrobial activity against carbanem resistant Gram-negative bacteria**

**O359 In vitro activity of antimicrobials in combination against clinical strains of extreme drug-resistant Acinetobacter baumanii to all antibiotics including polymyxin B in Singapore**


(Singapore, SG)

**Objectives:** We have used polymyxins since 1990s in Singapore. Emergence of extreme-drug-resistant(XDR) *Acinetobacter baumanii*(AB) infection resistant to all available antibiotics including polymyxins have finally occurred. Combination therapy may be the only viable option until new antibiotics become available. We assess the *in vitro* activity of various antimicrobials and elucidate the most effective combination therapy against these XDR AB.

**Methods:** Five XDR AB strains from 4 different patients (1 with haematological malignancy and 3 with severe burns injuries) were identified, after weeks of polymyxins therapy. MICs were determined according to a modified CLSI broth-dilution method. Time-kill studies (TKS) were performed with approximately $10^5$ CFU/ml at baseline with the maximum, clinically achievable, unbound concentration (mg/L) of PB (2), (R)rifampin (2), (M)eropenem (64), (C)cefepime (200) and (T)tigecycline (2) alone and in combination against these 5 isolates.

**Results:** All isolates were resistant to all antibiotics including PB (MICs 16–128 mg/L). In TKS, CP provided a killing effect of $>99\%$ ($>2$ log kill) from baseline inoculum at 24 h for all 5 strains. CM & MR exhibited killing effect of $>99\%$ from baseline inoculum at 24 h for 4 strains. MP exhibited killing effect of $>99\%$ from baseline inoculum at 24 h for 3 strains. CR, TM & PR exhibited killing effect of $>99\%$ from baseline inoculum at 24h for 2, 1, & 1 strains, respectively. Four strains had 3 or more antibiotic combinations that provided killing effect of $>99\%$ from baseline inoculum at 24 h, while 1 strain had only 1 antibiotic combination that was effective.

**Conclusions:** Clinical isolates of AB resistant to PB is also resistant to all major antibiotic classes with no compromise in biofitness; in contrary to previous reports that illustrate PB resistant AB with a substantial deficit in biofitness *in vitro*. We had shown that CP, CM, MR, MP may be potential antibiotic combinations as pre-emptive therapy for XDR AB infections and the effective combinations were strain specific. Our study warrants further investigations.

**O360 In vitro antibacterial activity of ceftazidime in combination with the β-lactamase inhibitor NXL104**


**Objective:** NXL104 is a novel β-lactamase inhibitor that has been shown in *in vitro* and in *vivo* to inhibit both class A and class C β-lactamases; it is currently in phase 2 of clinical development in combination with ceftazidime (CAZ). The objective of the study was to evaluate the antibacterial activity of CAZ/NXL104 combination against characterized Enterobacteriaceae species.

**Methods:** Activity of CAZ/NXL104 combination was tested on 222 strains of Enterobacteriaceae representing most clinical species. The panel included 49.5% CAZ-resistant isolates, 11% CAZ-susceptible, 1.3% CAZ-indeterminate, 22.5% β-lactamases. Minimal Inhibitory Concentrations (MIC) were determined with NXL104 at fixed ratios of 1:1 to 16, or at fixed concentrations of 2, 4, and 8 μg/mL.

**Results:** CAZ/NXL104 combinations were active against all isolates and had significantly lower MICs than CAZ alone, cefotaxime, ceftaxalone, cefepime, or piperacillin/tazobactam (MIC90s $>128\,\mu g/mL$). MICs50 and MIC90s for CAZ with fixed concentrations of NXL104 were $<0.125–0.5$ and 1–4 μg/mL, respectively, and 1–2 and 4–16 μg/mL, respectively, with fixed ratios. Potentiation of CAZ by NXL104 was generally 16 to 512-fold for TEM, SHV, CTX-M or KPC producers. Against KPC producers, NXL104 reduced CAZ MICs from $>128$ to $<0.25–8\,\mu g/mL$. Potentiation of 8 to 512-fold was observed against AmpC enzyme producers.

**Conclusion:** The CAZ/NXL104 combination exhibits a broad spectrum activity against resistant Enterobacteriaceae isolates, and represents an important next-generation of β-lactam/β-lactamase inhibitor combination.

**O361 Activities of tigecycline in combination with colistin or meropenem against KPC carbapenemase-producing Enterobacteriaceae by time-kill analysis**

S. Pourmaras, E. Neou, A. Poulou*, G. Vrioni, A. Tsakris (Larissa, Serres, Athens, GR)

**Objectives:** Enterobacteriaceae producing KPC carbapenemases cause hospital infections often associated with therapeutic failures and increased mortality. The treatment of these infections usually requires the use of tigecycline or colistin as a last-resort drug. The objective of this study was to test the *in vitro* activity of tigecycline against KPC-producing Enterobacteriaceae.

**Methods:** The KPC-producing isolates comprised four *Klebsiella pneumoniae*, two *Escherichia coli*, one *Enterobacter cloacae* and one *Serratia marcescens*. The *K. pneumoniae* and *E. coli* isolates were randomly selected among those representing different clonal types. MICs were obtained using the macrodilution method in fresh Mueller–Hinton broth (MHB), before performing time-kill assays by inoculating 5x105 CFU/mL of the test organisms in 3 ml MHB. *E. coli* ATCC 25922 was used as control. Antibiotics (tigecycline, colistin and meropenem as single agents and in combinations) were added at concentrations 1x and 2x the MIC for each isolate. Aliquots were removed at times 0, 2 h, 4 h, 6 h, 8 h, 16 h and 24 h post-inoculation, serially diluted and plated on MH agar plates for enumeration of viable colonies. Each time-kill experiment was performed twice. As bacterial activity was defined a $\geq 3$ log10 CFU/mL reduction in viable cells with respect to the original inoculum.

**Results:** Macrodilution MIC values were 0.25 to 2 mg/L for tigecycline, 0.5 to 1 mg/L for colistin and 2 to 16 mg/L for meropenem. In time-kill assays, tigecycline and meropenem as single agents were mostly bacteriostatic for the first 6–8 hours of incubation with bacterial regrowth to follow, while colistin alone was ineffective. The tigecycline plus colistin combination was in most cases bactericidal after 4 to 8 h of incubation and in some cases also synergistic compared with
tigecycline alone, although bacterial regrowth was observed after 8 to 16 h. The tigecycline plus meropenem combination was in most cases also bactericidal after 4 to 6 h of incubation and thereafter regrowth was observed.

**Conclusion:** The results of the present study indicate that tigecycline alone could be a therapeutic option for infections due to multidrug resistant KPC producers when bacteriostatic activity is adequate or in combination with colistin or meropenem when bactericidal activity is necessary. Additional *in vivo* tests may be warranted to fully assess the killing kinetics of tigecycline against KPC producers when the immune system is competent.

**O362 Activity of temocillin against carbapenem-resistant clinical Enterobacteriaceae**


**Objectives:** Until recently, carbapenems retained near-universal activity against Enterobacteriaceae but resistance is now emerging, mediated either by combinations of ESBL or AmpC enzymes and porin loss or by carbapenemases. The prevalent emerging carbapenemases vary by country: KPC enzymes in the USA and Israel, OXA-48 in Turkey, VIM in southern Europe and NDM in Italy. The UK sees small numbers of isolates with each of these types, some imported, some representing domestic spread. Most are multiresistant. We examined their susceptibility to temocillin, a 6-β-methoxy derivative of tigecyclin, notable for stability to ESBLs and AmpC.

**Methods:** The 81 isolates tested variously had KPC (n = 10), SME-1 (1), IMP (13), VIM (5), NDM (17) or OXA-48 (19 carbapenemases) or had combinations of impermeability with an AmpC enzyme or ESBL (16); they included 52 Klebsiella spp., 18 Enterobacter spp., 6 E. coli and 5 others. Transformants and transconjugants were prepared in E. coli DH5α and 362−1, respectively. Carbapenemase genes were identified by PCR and sequencing; MICs were measured by CLSI agar dilution.

**Results:** MICs for isolates with KPC carbapenemases were from 16–64 mg/L (geometric mean 40 mg/L) and introduction of a KPC plasmid into E. coli only raised the MIC from 8 to 16 mg/L; by contrast MICs for isolates with metallo-β-lactamases were >128 mg/L in 22/36 cases, and introduction of plasmids coding NDM carbapenemase (the commonest MBL in the UK) into E. coli DH5α raised the temocillin MIC from 4 to >64 mg/L. Temocillin MICs for isolates with OXA-48 were >128 mg/L in 18/19 cases, and the MIC shift on transformation of E. coli DH5α was from 4 to >128 mg/L. Temocillin MICs for isolates with combinations of porin loss and AmpC or an ESBL were from 8 to 128 mg/L (geometric mean 25 mg/L).

**Conclusion:** If the dosage can be raised from the present 2 g bds, temocillin may be a therapeutic option in some infections due to Enterobacteriaceae with KPC carbapenemases or combination of AmpC or ESBL and porin loss, not against those with OXA-48 or metallo-carbapenemases.

**O363 Interactions mediating the positioning of mercapto-phosphonate inhibitors in the active site of metallo-β-lactamases**


**Objective:** Metallo-β-lactamases (MBL) represent an emerging problem due to their capacity to hydrolyze almost all β-lactam antibiotics, including last generation cephalosporins and carbapenems. Due to the presence of two chelating functions (sulfanyl and phosphonato), the mercapto phosphonic acids (phosphonates analogues of mercapto carboxylic acids) are potential candidates for MBL inhibitors.

**Methods:** The inhibitory effect of 14 mercapto-phosphonate derivatives against representatives of the three subclasses of MBLs (VIM-4 (B1), CphA (B2) and L1 (B3)) was previously reported [1]. Here, in order to determine the interactions mediating the positioning of the inhibitors in the active site of each enzyme, crystallographic and docking studies were performed with 10a and 18, both inhibitors being active against the three subclasses.

**Results:** The crystallographic structure of the CphA-10a and CphA-18 indicated that the sulphydr atom of 10a and the phosphonato group of 18 interact with the zinc ion respectively. Molecular modelling on the VIM-4 (B1) and FEZ-1 (B3) enzymes with 10a and 18 also brought to light different binding modes depending on the enzyme and the inhibitor, consistent with the crystallographic structures.

**Conclusions:** The investigation of mercapto-phosphonate derivatives as MBL inhibitor has allowed us to find potent inhibitors active on representative members of all the three MBL subclasses. Moreover, on the basis of structural and modelling data, the inhibitory strength of these compounds will be improved further.

**Reference(s)**


**Infection in the immunocompromised host**

**O364 Hormographiella aspergillata: an emerging mould in acute leukaemia patients?**


**Objectives:** Invasive fungal infections (IFI) are a major cause of morbidity and mortality in hematological patients. The emergence of non-Aspergillus molds has been observed in recent years. *Hormographiella aspergillata* is a Basidiomycete and has previously been implicated in human infections rarely. We describe 3 cases of IFI with *H. aspergillata* occurring within one year on the hematological ward at the University Hospital Basel.

**Methods:** Patients were hospitalized in single rooms with special high-efficiency particle air filters. Surveillance fungal cultures of air filters were carried out regularly. No primary mold prophylaxis was performed. Screening for mold infections was performed by twice weekly measuring serum galactomannan and weekly pulmonary CT scans. Sabouraud agar was inoculated for fungal cultures. The identification of *H. aspergillata* by culture was molecularly confirmed. Susceptibility testing was performed by Etest.

**Table 1. Minimal inhibitory concentrations of antifungals against Hormographiella aspergillata patients isolates**

<table>
<thead>
<tr>
<th>Compound</th>
<th>Case 1</th>
<th>Case 2</th>
<th>Case 3</th>
</tr>
</thead>
<tbody>
<tr>
<td>Amphotericin B</td>
<td>not done</td>
<td>0.5 mg/l</td>
<td>0.5 mg/l</td>
</tr>
<tr>
<td>Caspofungin</td>
<td>not done</td>
<td>2 mg/l</td>
<td>&gt;32 mg/l</td>
</tr>
<tr>
<td>Voriconazole</td>
<td>not done</td>
<td>0.125 mg/l</td>
<td>0.25 mg/l</td>
</tr>
<tr>
<td>Fluconazole</td>
<td>not done</td>
<td>not done</td>
<td>&gt;256 mg/l</td>
</tr>
<tr>
<td>Posaconazole</td>
<td>not done</td>
<td>not done</td>
<td>not interpretable</td>
</tr>
</tbody>
</table>

**Results:** In one year, 3 cases of pulmonary IFI with *H. aspergillata* in leukemic patients, undergoing prolonged periods of severe neutropenia, were found. One patient (case 1) also had cerebral and ocular involvement in autopsy. This patient had positive blood cultures with *H. aspergillata*. In all patients pulmonary CT showed infiltrates, bronchoalveolar lavage performed failed however to identify the causative microorganism and serial serum galactomannan measurements remained negative. In contrast, specimens collected by VATS grew *H. aspergillata* in both patients where it was performed (cases 2+3). *In vitro* susceptibility testing was done in 2 cases (Table 1). Treatment consisted of caspofungin in one patient (case 1), after severe hepatotoxicity due to azoles, and of second generation azoles in the others. An evaluation of the *in vivo* efficacy of antifungal treatment in this series is difficult. All patients died, one due to the disseminated
IFI (treated with caspofungin), 2 due to progression of the underlying hematological disease and allogeneic transplant related complications. **Conclusions:** Despite the accumulation of 3 cases of an unusual IFI with *H. aspergillata*, no hospital source was detected. Due to the rarity of cases reported there is no established treatment for *H. aspergillata*. Standardized antifungal susceptibility testing of filamentous fungi has been established only recently and breakpoints with proven clinical relevance have yet to be identified. Voriconazole might be a valuable treatment option.

How to improve microbial documentation in febrile neutropenia? Impact of implementing an automat in the ward and addition of DNaeima detection


**Objectives:** Febrile neutropenia (FN) is the most frequent complication of high-dose chemotherapy-induced neutropenia. Only 30% of FN episodes are microbiologically documented by routine procedures, mainly by blood cultures (BC). We wondered whether shortening the time before incubation could improve this figure. In addition, we searched microbial DNA by the Septisfast® test.

**Methods:** Adult patients were eligible at their 1st FN episode if they were neutropenic (PMN <0.5×10^9/L), febrile (≥38.3° or twice ≥38° within 8h), and had a central venous catheter (CVC). At onset of fever, we collected 4 BC bottles (2 aerobic and 2 anaerobic) sampled through the CVC. They were immediately incubated in the ward (BacT/Alert3D®). Septisfast was performed on 1.5 ml of blood sampled at the same time. In parallel, 2 standard BCs (1 aerobic and 1 anaerobic bottles) were routinely sampled (1 CVC and 1 peripheral) and sent to the laboratory for incubation. Each patient was assessed for microbial documentation in the blood, either BC positivity or DNA detection; and the time elapsed between blood sampling and documentation, when this latter was positive. Pairwise analyses were performed using the McNemar test for documentation rate and the Wilcoxon signed-rank test for times for positivity.

**Results:** 120 consecutive FN episodes were included from Feb 2008 to Mar 2009: 97 (80%) acute leukemia/myelodysplasia, 26 (17%) lymphoproliferative malignancies and 4 (3%) others with 18 (15%) episodes in allogeneic and 16 (13%) in autologous stem cell transplantation. The rate of BC positivity was 30% (36 episodes) in the study process and 28.3% (34 episodes) in the routine process (McNemar’s χ² = 0.67, p = 0.41). In the microbiologically documented episodes, the time elapsed between incubation and positivity was significantly shorter for the BC bottles incubated in the ward (median rank: 12.525 min [7.55–25.57]) than for the routine BC bottles (median rank: 13.503 min [9.531–43.533]) (p<0.002). The Septisfast test was positive in 9 episodes (7.5%) that were positive also by the BC testing. In 8 additional episodes, the Septisfast® test showed low DNA content out of the threshold, which was nevertheless concordant with positives BCs.

**Conclusion:** Immediate incubation of blood cultures in the ward and detection of DNaeima with the Septisfast test did not improve the rate of microbial documentation for FN episodes when compared to BC routine process. However, it reduced the time to positivity.

Aetiology of eye infections in hospitalized ophthalmological patients

M.M. Wroblewska*, G. Broniek

**Objectives:** Ophthalmological patients are prone to nosocomial infections due to advanced age and common underlying medical conditions. Eye infections caused by multi-drug resistant (MDR) pathogens may further contribute to loss of vision in already visually disabled persons. Antimicrobial therapy is often difficult due to unsatisfactory penetration of many agents into the eye. Empiric therapy should be based on data comprising most prevalent pathogens, including MDR pathogens.

Methods: Specimens for bacteriological and fungal culture were obtained from patients hospitalized in ophthalmological hospital (2005–2009). Samples were cultured and isolates identified according to standard microbiological techniques.

**Results:** In total 1662 specimens were cultured, including swabs from conjunctiva, cornea, throat, nose, wounds and cornea conservation medium. The samples yielded 328 isolates, comprising 293 strains of bacteria and 7 strains of yeast-like fungi. Among bacteria predominated staphylococci – 197/293 (67.23%), followed by enteric rods – 36/293 (12.29%), non-fermenting rods – 20/293 (6.87%) and streptococci – 19 (6.48%). Among alarm pathogens there were methicillin-resistant *S. aureus* (MRSA) strains (4/50, 8.00%), high-level aminoglycoside resistant (HLLAR) strains of enterococci (1/8, 12.50%), extended-spectrum β-lactamase producing – ESBL(+) enteric rods (2/36, 5.56%) and ESBL(+) Gram-negative nonfermenting rods (4/20, 20.00%). Methicillin-resistant coagulase-negative staphylococci (MCNS) comprised 28/147 (19.05%) strains. Among all cultured microbial isolates there were 7/300 (2.33%) strains of fungi. Predominated *Candida parapsilosis* (4/7 strains), followed by *C. albicans* (2/7) and *C. glabrata* (1/7).

**Conclusion:** In ophthalmological specimens predominated Gram-positive cocci, mainly staphylococci. The presence of MCNS (19%) may be important in therapy of biofilm-associated implant infections. In this study there was a high percentage (20%) of ESBL(+) Gram-negative nonfermenting rods. Among yeast-like fungi *Candida parapsilosis* was more often isolated than *C. albicans*. This is clinically relevant as *C. parapsilosis* tends to form a biofilm on artificial materials, increasingly used in ophthalmic surgery.

These are the natural representations of the texts.
**Campylobacter sp. bacteremia in Taiwan, 1999–2008**

**C.Y. Chuang**, Y.T. Huang, C.H. Liao, P.I. Lee, P.R. Hsuve (Taipei City, TW)

**Objectives:** Bacteremia caused by *Campylobacter* species is rarely described in Asia. We investigated the bacteriology and clinical presentation of *Campylobacter* bacteremia in Taiwan.

**Methods:** There were 28 episodes of *Campylobacter* spp. bacteremia in 28 patients occurred from January 1999 to December 2008 in National Taiwan University Hospital. All the 28 isolates were identified by conventional phenotypic methods and later confirmed by using previously described multiplex PCR (cadF, hipO and aspg gene detection) and 16S RNA gene sequencing up to 900 base pairs. Medical records previously described multiplex PCR (cadF, hipO and aspg gene detection) and were reviewed in 24 patients.

**Results:** The most common species is *C. coli* (N = 17 [60.7%]) followed by *C. fetus* and *C. jejuni* (N = 6 [35.2%] and N = 5 [29.4%]; respectively). One isolate was identified as *C. coli* by multiplex PCR which is not consistent with the result of 16S RNA gene sequencing (*C. jejuni* strain SWU0713; accession number: gb GQ479831.1). Of the 24 cases with available medical records, 17 patients were male with a median age of 45.7 (range of age was from 7.75 to 80.67 years old). The main underlying conditions were hemato- oncological disease (41.67%), followed by hepatic decompensation (37.5%), renal insufficiency (33.3%) and liver cirrhosis (25%). There were 7 patients (29.17%) were in usage of steroid. The most common clinical manifestations were intra- abdominal infection (54.16%), primary bacteremia (10 patients, 41.67%), and cellulitis (4.1%). The mean Pitts bacteremic score was 1.58 (range from score 0 to score 9). There were 6 patients’ systolic blood pressure were below 90mmHg (25%). And consciousness change were noted in 8 patients (33.3%). Leucocytosis were noted in 12 patients (50%), and the mean value of white blood cell counts were 11,065.3/ul (Range was from 4,050/ul to 21,340/ul). And the mean value of e-reactive protein was 6.56mg/dl. Third generation antibiotics was the most commonly used empirical treatment regimen (50%) and Amoxicillin/clavulanic acid was 20.83%. The mean hospitalization stay was 12.96 days. All cause mortality at 14 days was 4.16% (N = 1) and 16.67% (N = 4) at 30 days.

**Conclusions:** *Campylobacter coli* is the leading species causing invasive Campylobacteriosis in immunocompromised patients in Taiwan.

**Experimental treatments in animal models**

**C. jejuni** (N=17[60.7%]) followed by *C. fetus* and *C. jejuni* (N=6[35.2%] and N=5[29.4%]; respectively). One isolate was identified as *C. coli* by multiplex PCR which is not consistent with the result of 16S RNA gene sequencing (*C. jejuni* strain SWU0713; accession number: gb GQ479831.1). Of the 24 cases with available medical records, 17 patients were male with a median age of 45.7 (range of age was from 7.75 to 80.67 years old). The main underlying conditions were hemato-oncological disease (41.67%), followed by hepatic decompensation (37.5%), renal insufficiency (33.3%) and liver cirrhosis (25%). There were 7 patients (29.17%) were in usage of steroid. The most common clinical manifestations were intra-abdominal infection (54.16%), primary bacteremia (10 patients, 41.67%), and cellulitis (4.1%). The mean Pitts bacteremic score was 1.58 (range from score 0 to score 9). There were 6 patients’ systolic blood pressure were below 90mmHg (25%). And consciousness change were noted in 8 patients (33.3%). Leucocytosis were noted in 12 patients (50%), and the mean value of white blood cell counts were 11,065.3/ul (Range was from 4,050/ul to 21,340/ul). And the mean value of e-reactive protein was 6.56mg/dl. Third generation antibiotics was the most commonly used empirical treatment regimen (50%) and Amoxicillin/clavulanic acid was 20.83%. The mean hospitalization stay was 12.96 days. All cause mortality at 14 days was 4.16% (N = 1) and 16.67% (N = 4) at 30 days.

**Conclusions:** *Campylobacter coli* is the leading species causing invasive Campylobacteriosis in immunocompromised patients in Taiwan.

**Antifungal drugs improve survival by immunomodulation rather than by reduction of fungal burden in experimental cerebral aspergillosis**

I. Ullmann, R. Strahm, S.L. Leib, S. Zimmerli° (Berne, CH)

**Objectives:** To evaluate the antifungal and immunomodulatory effects of antifungal drugs we used a lethal model of cerebral aspergillosis in non-immunosuppressed infant rats.

**Methods:** Eleven-day-old male Wistar rats were infected by intracerebral injection of 7.17 log10 colony-forming units of *Aspergillus fumigatus* conidia. Treatment started 22 h after infection and was given for 10d. Regimens were (i) caspofungin (CAS) 1 mg/kg/d i.p. qd, (ii) liposomal amphotericin B (L-AmB) 5 mg/kg/d i.p. qd, (iii) both drugs combined at the same dose, and (iv) voriconazole (VCZ) starting at 15 mg/kg bid and increasing the dose to compensate for auto induction of metabolism. In survival experiments censored at 11d brains were examined at the time of death. To monitor cerebral disease progression, animals were sacrificed 2, 3, 5, and 11d after infection. Brain homogenates were analyzed by quantitative fungal culture, a flow-cytometry based assay for cytokine quantification, and ELISA for galactomannan (GM) detection. Animals with symptoms of severe disease were sacrificed for ethical reasons.

**Results:**

1. Survival experiments [Fig. A]: Compared to controls (4.4±2.7d), survival times were significantly increased by treatment with CAS alone (10.3±1.7d; p < 0.0001) and combined with L-AmB (9.3±2.8d; p < 0.0001) as well as VCZ (10.1±2.2d; p < 0.0001). In contrast, survival time of animals treated with L-AmB alone (4.3±3.1d) was not different from untreated controls.

2. Fungal culture: The cerebral fungal burden declined over time in all animals including untreated ones. Interestingly, there was no significant difference between controls and treated animals.

3. GM: GM peaked later than the CFU counts in all treatment groups except L-AmB. There were no significant differences in GM indices regarding treatment and time.

4. Cytokines: At 2d after infection both IFN-γ and TNF-α [Fig. B] levels were significantly higher in animals treated with L-AmB alone (135.8±93.9pg/mg and 25.8±22.2pg/mg) compared to CAS (24.1±20.8pg/mg and 6.3±8.4pg/mg; p < 0.001), and VCZ (13.8±8.0pg/mg and 2.0±1.9pg/mg; p < 0.001). No differences were found for IL-1β and IL-10. IL-6 was undetectable in most animals but elevated in severe disease.

**Conclusion:** In this lethal model of cerebral aspergillosis mortality is not determined by the antifungal drug’s effect on cerebral fungal burden but by its modulation of the host’s immune response.

**Receptor for advanced glycation end-products is protective during murine tuberculosis**

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**Objective:** The development of active tuberculosis after infection with *Mycobacterium* (M.) tuberculosis is almost invariably caused by a persistent or transient state of relative immunodeficiency. Multidrug-resistant strains are on the rise and the frequent occurrence of co-infection with the human immunodeficiency virus makes the treatment and outcome of tuberculosis even more worrisome. The receptor for advanced glycation end products (RAGE) is a promiscuous receptor that is involved in pulmonary inflammation and infection. We here aimed to investigate the role of RAGE in tuberculosis.

**Methods:** RAGE deficient (RAGE−/−) and normal wild-type (WT) mice were intranasally inoculated with live virulent *M. tuberculosis*.

**Results:** While lungs of infected WT mice expressed RAGE, in particular on endothelium, *M. tuberculosis* pneumonia was associated with an enhanced expression of pulmonary RAGE. Lung inflammation was increased in RAGE−/− mice, as indicated by histopathology, percentage of inflamed area, lung weight and cytokine and chemokine levels. In addition, lung lymphocyte and neutrophil numbers were increased in the RAGE−/− mice. RAGE−/− mice displayed higher mycobacterial loads in the lungs after 3 weeks of infection, while they showed similar loads...
in the liver at 3 and 6 weeks. Finally, RAGE−/− mice displayed body weight loss and a worsened M. tuberculosis induced mortality (Figure).

Conclusion: These data suggest that RAGE plays a beneficial role in the host response to pulmonary tuberculosis.

**O371** Imipenem or meropenem plus clavulanate combination improves survival of mice infected with M. tuberculosis


**Background:** Due to the emergence of extensively drug resistant strains (XDR) of M. tuberculosis, new antibacterial agents are desperately needed. Although β-lactam antibiotics are not considered as antituberculous drugs, it has been recently shown *in vitro* that the combination of meropenem and clavulanate has synergic activity against M. tuberculosis.

**Objectives:** We wished to evaluate in the murine model of tuberculosis the activity of penems alone and combined with clavulanate against M. tuberculosis.

**Methods:** Swiss mice were infected intravenously with 3.105 M. tuberculosis H37Rv and treated the day after inoculation for 4 weeks. Treatment groups consisted of 10 mice. The test groups were treated with clavulanate (100mg/kg) alone, imipenem (100mg/kg) and meropenem (100mg/kg) alone or combined with clavulanate whereas a positive control group was treated with isoniazid (25mg/kg) and a negative control group was held without treatment. At the end of treatment, surviving mice were sacrificed and lungs harvested. Treatment efficacy was assessed on survival rate, spleen weights and lung CFU counts.

**Results:** at the end of the 4 weeks, the mortality rates were the following: untreated 60%, isoniazid 0%, clavulanate 30%, imipenem 10%, meropenem 30%, imipenem-clavulanate 0%, meropenem-clavulanate 0%. The combination of imipenem or meropenem plus clavulanate significantly improved survival (p<0.01 vs untreated mice). On the other hand, imipenem and meropenem combined with clavulanate did not prevent splenomegaly (591 and 573mg) whereas isoniazid did (304mg) (p>0.05). Among groups of mice with 100% survival, only isoniazid reduced lung CFU counts (−1.2log10 CFU vs D0), the penem-clavulanate combinations did not prevent bacterial growth (+0.9 to 1.4log10 CFU vs D0).

**Conclusion:** although less active than isoniazid, the combinations of imipenem or meropenem and clavulanate improve survival of mice infected with M. tuberculosis and should be further evaluated.

**O372** Evaluation of the efficacy of anti-staphylococcal human therapies in a severe PVL pneumonia model


**Objectives:** Many strains of *S. aureus* harbour the Panton Valentine Leukotoxin (PVL) phage and can cause severe necrotising pneumonia in young immunocompetent patients. *In vitro* studies showed that some anti-staphylococcal drugs can induce or inhibit the PVL production. Animal models are needed to evaluate new treatment strategies in such infections. We compared the efficacy of 4 antibiotic human therapies in a severe model of PVL necrotizing pneumonia in rabbits.

**Methods:** 2 isogenic and fully-susceptible *S. aureus* strains were used to induce pneumonia: RN6390 PVL− and LU0853 PVL+. Animals were randomized to no treatment (controls) or to a 48h IV human equivalent dosage of either vancomycin (VA) (continuous perfusion Css=30mg/l), cloxacillin (CLOX 2g/6h), clindamycin (CLI 600mg/8h) or linezolid (LZO, 600mg/12h). Serum levels were measured by microbiological assay or HPLC, pharmacokinetic data were obtained, and evaluation of efficacy was based on bacterial counts in lungs (mean±SD) and the residual quantity of PVL (ng/residual CFU).

**Results:** Several inocula were tested to perfect this model. Here are the results for an inoculum of 8.5 log CFU/mL (table).

<table>
<thead>
<tr>
<th>Treatment</th>
<th>PVL− strain</th>
<th>% early mortality</th>
<th>PVL+ strain</th>
<th>% early mortality</th>
</tr>
</thead>
<tbody>
<tr>
<td>Control</td>
<td></td>
<td>100%</td>
<td>CLI</td>
<td>0%</td>
</tr>
<tr>
<td>VA</td>
<td>0.00±0.58</td>
<td>75%</td>
<td>LZO</td>
<td>0%</td>
</tr>
<tr>
<td>CLOX</td>
<td>0.00±0.00</td>
<td>100%</td>
<td>LZO</td>
<td>0%</td>
</tr>
<tr>
<td>CLI</td>
<td>3.00±1.32</td>
<td>80%</td>
<td>LZO</td>
<td>0%</td>
</tr>
<tr>
<td>LZO</td>
<td>7.10±0.00</td>
<td>0%</td>
<td>LZO</td>
<td>0%</td>
</tr>
</tbody>
</table>

**Conclusion:** No significant efficacy was obtained with VA. LZO, CLOX and CLI were highly efficacious against both strains with a complete sterilization of lungs and spleen for CLOX and CLI (CLOX = CLI > LZO > VA).

**Early mortality:** VA did not reduce the mortality rate. 0% of early mortality was obtained with CLOX and CLI. LZO slightly reduced the mortality rate (CLOX = CLI > LZO > CLOX). LZO reduced by half the PVL quantity. CLI was strongly effective on pulmonary PVL reduction (CLI > LZO > CLOX > VA).

**PVL assessment:** VA and CLOX did not reduce the residual PVL quantity significantly. LZO reduced by half the PVL quantity. CLI was strongly efficacious on pulmonary PVL reduction (CLI > LZO > CLOX > VA).

**Conclusion:** Different therapies in a severe *S. aureus* pneumonia model were tested. CLOX was strongly bactericidal contrasting with the persisting production of PVL. LZO and CLI reduced the PVL production and the residual bacterial content in this model. Other studies are under way to evaluate the impact of such strategies in a MRSA-PVL model.

**O373** The colonizing ability of *E. coli* strains isolated from patients with inflammatory bowel disease

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**Objectives:** *E. coli* strains of the phylogenetic group B2 were isolated more frequently from patients with IBD compared to healthy controls. Furthermore, B2 strains with ExPEC genes were found more frequently among IBD patients with active disease compared to patients with inactive disease. It is of great interest to further characterise those strains. The objective was to investigate the colonising traits of *B2 E. coli* strains isolated from patients with IBD in a gastrointestinal animal model.

**Methods:** Two B2 *E. coli* strains from IBD patients and one *E. coli* isolate from a healthy person were investigated. Strains were also compared to the probiotic *E. coli* Nissle 1917 and to the laboratory *E. coli* MG1655. Growth rate was determined *in vitro*. The adhesion capacity was assessed in the human epithelial intestine cell line (Int-407). The colonising ability was tested by colonisation of the large intestine of streptomycin treated mice. Different colonisation, competition and inoculation procedures were tested in this model.

**Results:** Both IBD strains had increased growth rate compared to the *E. coli* from the healthy person and the *E. coli* Nissle strain. Likewise, the IBD strains had an increased adhesion capacity in the cell adhesion assay. In the animal model all strains were able to colonise the gastrointestinal tract in high levels when inoculated alone. In competition with the probiotic Nissle strain both IBD strains co-colonised, though to a log higher (in CFU/g faeces) than Nissle, when inoculated in equal high levels. When *E. coli* Nissle was inoculated in high levels compared to IBD strain in low levels the strains also co-colonised at the end of the experiment. The *E. coli* strain from the healthy person also co-colonised with *E. coli* Nissle in intestine of the mice, but stabilised at a log lower than Nissle strain, when inoculated in equal high levels and two logs lower when inoculated at a lower level than *E. coli* Nissle.

**Conclusion:** B2 strains had increased growth rates and adhesion abilities compared to *E. coli* isolated from a healthy person and *E. coli* Nissle. Furthermore, *E. coli* from IBD patients had an increased ability to co-colonise with the probiotic *E. coli* Nissle strain.
New antibacterial agents

MUT056399, a new drug candidate against S. aureus: PK parameters and safety

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Background: MUT056399 is a novel antistaphylococcal agent targeting the essential enzyme FabI. We present here its key properties: in vivo efficacy, preclinical pharmacokinetics and safety, finally the pharmacology data of phase I.

Methods: Standard procedures were used for evaluation of PK parameters. Preclinical safety studies were conducted on mice, rat and dogs in GLP conditions. In vivo assays were performed using the mice models of septicaemia and thigh infection using methicillin-susceptible and non susceptible S. aureus (MSSA and MRSA). Linezolid and vancomycin were used as comparators.

In Phase I, ascending doses of MUT056399 formulated in HPBCD were administered to healthy volunteers by iv infusions.

Results: PK studies in 3 species indicated that MUT056399 given iv was rapidly cleared from the blood (T1/2 -3.5h). The MUT056399 molecule was well distributed among tissues without accumulation.

In the thigh infection model with MRSA strains, after a single sc administration the mean static dose was 143 mg/kg/d in nephropic mice and 45 mg/kg/d in immunocompetent mice.

In the mouse septicaemia model using a single sc administration of MUT056399, the mean ED50 against MSSA ATCC 29213, was 21.6 mg/kg/day, against MRSA strains the mean ED50 was 31 mg/kg/day and 49.6 mg/kg/day for a GISA strain. In GLP safety studies in rats and dogs MUT56 399 did not affect CV, CNS or respiratory functions.

In Phase I, the administration of a single intra venous doses from 10 mg/d to 1.2 mg/d was safe.

Conclusion: MUT056399 is a novel highly potent antistaphylococcal agent with a clean safety profile. These properties support MUT056399 as a very promising candidate for a novel drug to treat severe staphylococcal infections.

Efficacy of two novel antimicrobials, BC-3781 and BC-3205, in a murine MRSA-pneumonia model

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Background: BC-3781 and BC-3205 are two new antimicrobial agents of the pleuromutilin class, which are both in an early stage of clinical development for intravenous and/or oral treatment of skin and skin structure infections (SSSI) and community-acquired pneumonia (CAP). BC-3781 and BC-3205 exhibit excellent antimicrobial activity against a range of relevant bacteria frequently identified in SSSI and CAP including methicillin-resistant Staphylococcus aureus (MRSA).

Invasive severe infections caused by MRSA, particularly those involving persistent bacteraemia and necrotizing pneumonia are associated with high mortality. Since treatment with currently available antibiotics is often unsatisfactory novel antibacterials with improved efficacy against severe MRSA infections are urgently needed.

Methods: Murine pulmonary infections caused by MRSA were established in neutrophenic female BALB/c mice. Mice were grouped (n=6) and subcutaneous therapy using BC-3781, BC-3205, linezolid or vancomycin started 2 h post infection (1.5×10⁶) with a single dose and continued for two days with a bid dosing regimen. Lungs of mice were dissected on day 3 after start of infection. The bacterial burden in pulmonary tissues was determined using standard plating techniques.

Untreated animals died on day 2. An Emax dose response model was used to obtain the bacteriostatic dose levels and the maximum killing potency of all tested compounds.

Results: BC-3781 and BC-3205 showed excellent efficacy with a reduction of 3−4 log10 CFU/lung being achieved with doses of 160 mg/kg BC-3205 and BC-3781, respectively. For the same reduction of viable MRSA in lungs a dose of 240 mg/kg/day linezolid was required. The maximum killing potency of vancomycin was only ~1.3 log10 CFU/lung at a dose of 480 mg. BC-3781 and BC-3205 ensured 100% survival already at daily doses greater than 20 and 40 mg/kg, respectively. Doses of >60 mg/kg/day linezolid and >240 mg/kg/day vancomycin, were needed for 100% survival.

Conclusions: Both compounds, BC-3205 and BC-3781, demonstrated excellent efficacy in a murine pulmonary infection caused by MRSA. Both compounds, BC-3781 and BC-3205, showed superior efficacy compared to the standard of care antibiotics linezolid and vancomycin.

BAL30072, a new sulfaient with excellent in vitro and in vivo activity against Escherichia coli producing extended-spectrum β-lactamases

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Objectives: BAL30072 is a novel sideromone monocylic β-lactam belonging to the sulfaents. We evaluated its in vitro antimicrobial activity of this compound against a panel of Escherichia coli clinical isolates and studied its efficacy against peritonitis and sepsis in mice caused by an ESBL-producing strain of E. coli.

Methods: The antimicrobial activity of BAL30072 was tested against 39 strains (20 wild type and 19 ESBL-producers). MICs were determined using agar dilution on Mueller-Hinton agar supplemented with 2, 2′-bipyridyl to induce iron transport. In vivo efficacy was evaluated against a CTX-M-15-like-producing E. coli strain using a lethal peritonitis sepsis model in neutropic ICR mice. Survival was monitored for seven days after infection. E. coli inocula ranged from 2.5×10⁷ to 5.0×10⁸ cfu/mouse (2–5 X LD50) and BAL30072 was administered intraperitoneally 3 times daily for 3 days (doses of 100 mg/kg down to 12.5 mg/kg) following infection. Saline was administered to the untreated control group and meropenem was administered to the treated control group.

Results: MIC50/MIC90 of BAL30072 for wild type, and ESBL-producing E. coli were 0.125/0.5, and <0.0625/1 mg/L, respectively (ranges <0.0625–1 and <0.0625–256 mg/L, respectively). The MIC of BAL30072 against the ESBL-E. coli used in the mouse model was <0.0625 mg/L. In vivo experiments in mice infected intraperitoneally with various E. coli inocula showed that, at doses from 100 mg/kg down to 12.5 mg/kg, BAL30072 conferred protection similar to meropenem (90–100% survival). Survival in the placebo group was 0–33%.

Conclusion: BAL30072 is an effective antibacterial agent against clinical isolates of E. coli, including ESBL-producing strains. It is highly effective treatment against infection caused by ESBL-producing E. coli as demonstrated in mice peritonitis-sepsis model.

AchN-490 and other aminoglycosides vs. carbapenem-resistant Entrobacteriaceae isolated in the United Kingdom


Objectives: AchN-490 is a novel sisomicin derivative stable to nearly all aminoglycoside-modifying enzymes. We compared its activity with that of other aminoglycosides vs. clinical Enterobacteriaceae representing the diversity of carbapenem resistance types now emerging in the UK. Most were multiresistant.

Methods: The 81 isolates comprised those with the Class A carbapenemases KPC (n =10) or SME-1 (1); Class B enzymes, IMP (13), VIM (5) and NDM (17) and the Class D enzyme, OXA-48 (19) or with combinations of impermeability plus an AmpC or ESBL (16). They included 52 Klebsiella spp., 18 Enterobacter spp., 6 E. coli and 5 others. Carbapenemase genes were identified by PCR and sequencing as were those encoding the 16S rRNA methylases ArmA and RmtA-C. MICs were measured by CLSI agar dilution.
Results: ACHN-490 was active against all 64 non-NDM+ isolates at <2 mg/L, with 95% of MICs between 0.06 and 0.5 mg/L. Isepiamcin was active at 8 mg/L against 62 of these 64 whereas 35%, 61% and 19% were resistant to gentamicin at 4 mg/L, tobramycin at 4 mg/L and amikacin at 16 mg/L, respectively. Among the 17 isolates with the NDM-1 enzyme – many from patients with prior medical contact on the Indian subcontinent – 16 harboured armA or rmtC and were resistant to ACHN-490 and to all other human-use aminoglycosides at >32 mg/L; armA and rmtC were absent from the sole ACHN-490-susceptible NDM-1-positive strain. Apramycin, a veterinary analogue, was active at 4–8 mg/L against (i) control strains, (ii) the NDM-1-positive isolates with armA or rmtC and (iii) all other strains except a Serratia with SME-1 enzyme (MIC > 128 mg/L).

Conclusion: ACHN-490 had potent activity vs. all the carbapenem-resistant isolates screened except those with combinations of NDM-1 enzyme and ArmA or RmtC rRNA methylases; the international prevalence of these enzymes needs urgent surveillance. Evasion of ArmA and RmtC by apramycin is striking and may facilitate future human drug development.

Novel antimicrobial agent NI02 displays potent activity against a range of pathogenic bacteria
S.K. Sandford*, M. Upton (Manchester, UK)

Objectives: The ever increasing resistance of pathogenic bacteria towards the current arsenal of antimicrobial therapeutics emphasizes the urgent requirement for development of novel agents. It is currently estimated over 50% of clinical infections are also biofilm associated, therefore, agents that are effective against multiple resistant, biofilm forming would be extremely advantageous. The aim of the current study was to assess the effect of novel antimicrobial agent (NI02) against a range of pathogenic bacteria and against a clinical isolate Staphylococcus epidermidis that displays methicillin resistance and a biofilm phenotype.

Methods: The deferred antagonism method was used to assess the range of activity of NI02 against a selection of pathogenic Gram-positive and Gram-negative bacteria. The traditional biofilm forming assay was also employed using preparations of NI02 with an inhibitory activity of >2560 AU/ml to coat microtiter wells and also to treat mature (48 hour) biofilms.

Results: The deferred antagonism assay showed NI02 to have good activity against a range of Gram-positive pathogens including vancomycin resistant enterococci, methicillin resistant Staphylococcus aureus, Streptococcus pneumoniae, Streptococcus pyogenes, Listeria sp., Bacillus subtilis and Bacillus cereus and Gram-negative isolate Moraxella catarrhalis. NI02 also showed good activity against Staphylococcus epidermidis biofilms as coating microtiter plate wells resulted in complete inhibition of biofilm development and treatment of mature biofilms resulted in a significant reduction in biofilm density (P ≤ 0.001).

Conclusion: The results obtained in the current study demonstrate the broad-spectrum activity of antimicrobial agent NI02 against a range of pathogenic bacteria and the ability of the inhibitor to prevent and disrupt biofilms.

Carbapenemases other than KPCs: MBL and OXAs
S. Edelstein* (Smolensk, RU)

Gram-negative bacteria producing acquired metallo-β-lactamas (MBLs) represent one of the greatest challenges for modern antimicrobial therapy. MBL producers commonly exhibit resistance not only to a broad-spectrum of β-lactams but also to a variety of non-β-lactam agents owing to association of MBL genes with those affecting different groups of antibiotics. The IMP and VIM enzymes are the most common acquired MBLs. These enzymes were first reported in Japan and Europe but are now broadly disseminated in many countries of all populated continents. Production of acquired MBLs is most often observed in P. aeruginosa, with VIM-2 being the most ubiquitous enzyme, and less frequently in Acinetobacter spp. and in Enterobacteriaceae, mainly in Klebsiella pneumoniae and Enterobacter cloacae, with VIM-1 or VIM-4 being the most typical variants in the latter species. MBLs of other genetic groups were either identified in isolates causing sporadic infections and local outbreaks (e.g. GIM-1, SIM-1, KHM-1, AIM-1) or as endemic types in some geographic areas (e.g. SPM-1 in Latin America). However, the recent reports of the international importation of SPM-1 from Brazil to Switzerland and of NDM-1 from India to the UK provide continuing evidence of the increasing complexity of MBL epidemiology. The prevalence of MBL-producers varies significantly among different countries and their epidemiology now ranges from sporadic monoclonal outbreaks to polyclonal endemicity. Furthermore, MBL-producing strains are no longer confined to nosocomial environment but are being identified also in residents of long-term-care facilities and even in patients with community-acquired infections. The association of MBL genes with a variety of non-β-lactam mechanisms (e.g. Tn402-like transposons in the case of blaVIM genes), broad host range plasmids and highly epidemic clones (e.g. P. aeruginosa clones CC235 and CC111) were implicated in the rapid spread of these important resistance determinants.

S. Sandford, M. Upton (Manchester, UK)

Objective: The increasing resistance of pathogenic bacteria towards the current arsenal of antimicrobial therapeutics emphasizes the urgent requirement for development of novel agents. It is currently estimated over 80% of clinical infections are also biofilm associated, therefore, agents that are effective against multiple resistant, biofilm forming would be extremely advantageous. The aim of the current study was to assess the effect of novel antimicrobial agent (NI02) against a range of pathogenic Gram-positive and Gram-negative bacteria.

Methods: The deferred antagonism method was used to assess the range of activity of NI02 against a selection of pathogenic Gram-positive and Gram-negative bacteria. The traditional biofilm forming assay was also employed using preparations of NI02 with an inhibitory activity of >2560 AU/ml to coat microtiter wells and also to treat mature (48 hour) biofilms.

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Conclusion: The results obtained in the current study demonstrate the broad-spectrum activity of antimicrobial agent NI02 against a range of pathogenic bacteria and the ability of the inhibitor to prevent and disrupt biofilms.

L. Poiret* (Le Kremlin Bicêtre, FR)

Class D β-lactamase-mediated resistance to β-lactams has been increasingly reported during the last decade. Those enzymes also known as oxacillinases or OXAs are widely distributed among Gram negatives. They usually possess a narrow spectrum β-lactam hydrolysis profile, but some of them do possess the ability to hydrolyse carbapenems, even at a low level. They have been named Carbapenem-Hydrolysing class D β-Lactamases, or CHDLs. CHDLs are known to be intrinsic in some Gram negative rods, including Acinetobacter baumannii (OXA-51-like enzymes) and Pseudomonas aeruginosa (OXA-50-like enzymes), but usually play a minor role in the natural resistance phenotypes. Besides those naturally-occurring CHDLs, others have been identified as acquired. They have been mostly identified in Acinetobacter spp. (mostly in A. baumannii), and belong to four distinct groups according to their amino acid sequences, namely the OXA-23, OXA-40, OXA-58, and OXA-143 groups. The genes encoding those CHDLs in A. baumannii are either plasmid- or chromosome-encoded. Interestingly, the blaOXA-23 progenitor was shown to be Acinetobacter radioresistens, a non-pathogenic and environmental species. Despite their weak ability to hydrolyse carbapenems, those CHDLs are responsible for high level resistance to those compounds when their expression is associated with other mechanisms such as efflux overexpression, penicillin-binding protein modifications, or porin loss. Another CHDL, OXA-48, distantly related from those CHDLs identified in A. baumannii, has been identified in several Enterobacteriaceae species, and mostly in Klebsiella pneumoniae. The blaOXA-48 gene which has been found to originate from the Shewanella spp. is plasmid-mediated, increasingly reported in different countries, and responsible for resistance to carbapenems when associated with permeability defects. Acquired CHDL encoding genes have been mostly identified in association with insertion sequences that are either responsible for their expression and their acquisition. In particular, both the blaOXA-48 and blaOXA-23 genes have been identified inside composite integron structures (IS199- and ISA1b-made, respectively).
Molecular epidemiology of carbapenem-resistant \textit{Acinetobacter baumannii}: genes, plasmids and clones
N. Woodford* (London, UK)

Carbapenems (excluding ertapenem) are treatments of choice for infections caused by multi-resistant \textit{A. baumannii} so the emergence of carbapenem resistance is a serious problem. As with other Gram-negative species, carbapenem resistance has been attributed to multiple mechanisms, including reduced permeability through loss of outer membrane proteins, altered penicillin-binding proteins and over-expression of weakly carbapenem-hydrolyzing \beta-lactamases, but the major mechanism is carbapenemase production. Diverse carbapenemases have been reported in \textit{A. baumannii}, differing in their regional prevalence: isolates with IMP or VIM metallo-enzymes are globally scattered; those with SIM-1 are associated particularly with the Far East, while NDM-1 has been observed only rarely. OXA class D enzymes are the dominant carbapenemases in \textit{A. baumannii}, with 5 phylogenetically distinct groups identified. OXA-51-like enzymes are intrinsic to the species, and are only associated with carbapenem resistance when up-regulated by an adjacent insertion sequence, usually ISAba1. By contrast, OXA-23-like, OXA-40-like, OXA-58-like and OXA-143 carbapenemases have all been acquired via horizontal gene spread. These enzymes usually confer clinically significant carbapenem resistance, although the MICs for individual isolates are influenced by the particular gene present, its copy number, and presence of accessory mechanisms (e.g. loss of the CarO porin). The blaOXA genes may be located on the chromosome, as part of large resistance islands, or on plasmids. Local outbreaks of carbapenem-resistant \textit{A. baumannii} typically include a predominant strain, and strains from epidemiologically unlinked sites may show sufficient similarity to be regarded as the same clone. There are two dominant carbapenem-resistant clones in the UK, ‘OXA-23 clone 1’ has OXA-23 enzyme, and the ‘South-east clone’ has ISAba1-up-regulated OXA-83 enzyme; both have affected >50 hospitals and belong to sequence group 1 (based on ompA, csuE and blaOXA-51-like alleles), which is European clone II. In other countries there may be greater evidence for horizontal gene spread in addition to strain spread, as observed for OXA-72 (an OXA-40-like enzyme) in a Taiwanese hospital. There are few therapeutic options for infections caused by carbapenem-resistant strains other than a polymyxin or glycylcycline and effective infection control remains essential to control their spread and impact.

Tuberculosis at the cutting edge
S389 New insights into host–pathogen responses in TB
A. Lalvani* (London, UK)

Host–pathogen interactions determine the outcomes of tuberculosis infection by influencing key control points in the natural history of infection, including progression from latent infection to active disease and the clinical spectrum of active disease itself. Our understanding of the natural history and epidemiology of tuberculosis infection are based on two key century-old tools, the tuberculin skin test and chest radiography. The advent of new, more accurate markers of infection presents an opportunity to re-evaluate our conventional understanding of the host–pathogen relationship in tuberculosis, including the natural history and epidemiology of tuberculosis infection. The application of interferon-gamma release assays in epidemiologically well-defined tuberculosis outbreaks and longitudinal cohorts points towards a new class of host–pathogen interaction in a subset of tuberculosis contacts that likely involves a transient, self-resolving infection. This entity was not previously appreciated and has significant implications for our understanding of the host–pathogen interaction in tuberculosis infection which will be discussed. T cell-based testing for tuberculosis infection has also uncovered a role for BCG vaccine in preventing infection despite \textit{M. tuberculosis} exposure. The implications of this phenomenon for the design and evaluation of new tuberculosis vaccines, as well from tuberculosis control, will be discussed. Newer biomarkers, measuring multiple facets of the host response to tuberculosis infection and disease, have recently been developed and may enable discrimination between the several stages in the natural history of tuberculosis infection, eg differentiating between active and latent tuberculosis infection. These new types of biomarkers will be reviewed as well as the new insights they could provide for our understanding of the host–pathogen equilibrium in tuberculosis infection.

Genomics and therapeutics
S385 N.W. Woodford° (London, UK)

New medicines for tuberculosis (NM4TB): Tuberculosis (TB) is one of the oldest infectious diseases known to man and has infected one third of the world’s population. As a result, new drugs are required to address the current treatment failures. A few of the new medicines in the pipeline are currently in the late preclinical stage, is a candidate for inclusion in combination therapies for both drug-sensitive and extensively drug-resistant TB.

Use of epidemiological methods in making rational treatment decisions in infectious diseases
S389 From case reports to causality: how can we quantify rare adverse events, how should they be considered in the treatment decisions?
R. Platt* (Boston, US)

Rare adverse events after drugs, vaccines, and other therapeutic agents are usually identified after the product is licensed and in widespread use. Historically, surveillance for these has relied on case reports. While case reports have identified many important problems, they have drawbacks, including unknown sensitivity for detecting events of interest and inability to provide the quantitative estimates of risk that are needed to make informed decisions about the balance of benefits and risk. Quantitative information about risks and also about benefits is becoming increasingly available through the secondary use of electronic health data - both electronic medical records and administrative data - collected during the routine delivery of health care. Among the earliest examples is the U.S. Centers for Disease Control's Vaccine Safety Datalink, which performs both active, near real-time, surveillance for vaccine-associated adverse events, and retrospective epidemiological studies. These methods are being modified to work in groups of health plans with tens of millions of members, and to address the sequelae of exposures to drugs as well as vaccines. An important feature of these methods is that they require minimal sharing of confidential personal
Pharmacodynamics of anti-staphylococcal antibiotics

Molecular analysis of extended-spectrum

Massive emergence of multidrug-resistant Enterobacteriaceae

Optimizing therapy exploits the specific antibiotic pharmacodynamic parameter that best predicts resistance development is key for successful patient outcome. Understanding the relationships between antibiotic pharmacokinetics and pharmacodynamics, target organism, site of infection and the potential for resistance development is key for successful patient outcome. Optimizing therapy exploits the specific antibiotic pharmacodynamic parameter that best predicts in vivo efficacy. For example, in the case of β-lactams, improving the time above the MIC for the targeted pathogen may be accomplished by prolonging the infusion time or utilizing continuous infusion administration. For aminoglycosides, use of high-dose once-daily therapy should increase the Cmax/MIC. Recently, based on the need to improve the performance of vancomycin, higher troughs have been recommended. Higher troughs are needed in order to achieve a higher AUC/MIC ratio which is thought to be important to achieve a higher AUC/MIC ratio which is thought to be important for serious infections like complicated bacteremia, infective endocarditis and pneumonia. Additional factors that affect antibiotic performance include the ability to reach the site of infection (barriers to penetration) and conditions at the site of infection such as pH, protein binding and inoculum. This lecture will discuss specific antibiotic PK/PD characteristics, conditions at the site of infection that diminish antibiotic activity and opportunity to improve performance.

MRSA bacteraemia and endocarditis – treatment considerations

MRSA bacteremia and endocarditis represent some of the most challenging and difficult infections to overcome with antibiotics. Understanding the relationships between antibiotic pharmacokinetics and pharmacodynamics, target organism, site of infection and the potential for resistance development is key for successful patient outcome. Optimizing therapy exploits the specific antibiotic pharmacodynamic parameter that best predicts in vivo efficacy. For example, in the case of β-lactams, improving the time above the MIC for the targeted pathogen may be accomplished by prolonging the infusion time or utilizing continuous infusion administration. For aminoglycosides, use of high-dose once-daily therapy should increase the Cmax/MIC. Recently, based on the need to improve the performance of vancomycin, higher troughs have been recommended. Higher troughs are needed in order to achieve a higher AUC/MIC ratio which is thought to be important for serious infections like complicated bacteremia, infective endocarditis and pneumonia. Additional factors that affect antibiotic performance include the ability to reach the site of infection (barriers to penetration) and conditions at the site of infection such as pH, protein binding and inoculum. This lecture will discuss specific antibiotic PK/PD characteristics, conditions at the site of infection that diminish antibiotic activity and opportunity to improve performance.

Surveillance of ESBL

Massive emergence of multidrug-resistant Enterobacteriaceae in blood culture isolates of children in Ghana


Objective: To evaluate the prevalence of antimicrobial resistance in Enterobacteriaceae isolated from blood cultures of children in rural Ghana.

Methods: Between October 2007 and June 2009 blood cultures were collected from children admitted to the Agogo Presbyterian Hospital located in the rural area of the Ashanti – Akim North District with a population of about 135,000. Peds Plus™ bottles and the BacTec™ 9050 system were used and detected strains were identified by Gram staining, selective subcultures, biochemical testing and specific agglutination tests. Minimum inhibitory concentration (MIC) of isolated Enterobacteriaceae and production of extended-spectrum-β-lactamases (ESBL) was determined by the Etest™ method.

Results: In this study isolated Enterobacteriaceae (n=178) were non-typhoid Salmonella enterica (NTS) (113), Salmonella Typhi (39), Escherichia coli (15) Klebsiella sp. (9), Shigella boydii (1) and Enterobacter sp. (1). NTS were highly resistant to ampicillin (80.5%), cotrimoxazole (82.3%), chloramphenicol (83.2%) and tetracycline (10.6%). No strain was resistant to ciprofloxacin, but one strain had reduced susceptibility to ceftriaxone. The majority of S. Typhi strains were also resistant to ampicillin (69.2%), cotrimoxazole (60.0%), chloramphenicol (66.7%), and tetracycline (60.0%), but all were completely susceptible to ciprofloxacin and ceftriaxone. All E. coli isolates were resistant to ampicillin and 20% produced ESBL. Resistance to cotrimoxazole (93.3%), tetracycline (86.7%), chloramphenicol (53.3%) and ciprofloxacin (26.7%) was frequently detected. All Klebsiella strains were resistant to ampicillin and tetracycline and 77.8% produced ESBL. Only one strain was susceptible to cotrimoxazole, 77.8% were resistant to chloramphenicol and one third to ciprofloxacin. The Enterobacter strain produced ESBL and was only susceptible to ceftriaxone and ciprofloxacin.

Conclusion: The study indicates that the majority of Enterobacteriaceae causing bacteraemia in children in the study area are resistant to the majority of local available antibiotics. Moreover this massive emergence of multidrug-resistant Enterobacteriaceae and ESBL producing E. coli and Klebsiella strains in clinical isolates indicates a serious medical and economic burden for African healthcare systems. Surveillance programs and prevention strategies have to be established to face this challenge.

Molecular analysis of extended-spectrum β-lactamase dissemination in Escherichia coli within families


Objectives: The means of transmission of ESBL-producing E. coli (ESBLEC) isolates in the community are poorly understood. We previously reported that the prevalence of faecal carriage with ESBLEC was higher in relatives of patients with urinary tract infections (UTI) caused by these organisms.in 54 households The aim of this study was to analyse the molecular relationship of the ESBLEC within families settings and the plasmids identified.

Methods: We studied 72 ESBL-producing E. coli isolates (34 CTX- M-14, 31 SHV-12, 3 CTTX-M-9, 3 CTTX-M-15 and 1 CTTX-M-32) from 19 families of patients with UTI caused by ESBLEC where at least one family member was infected (19 patients with UTI and 23 relatives). All isolates were evaluated by XbaI PFGE, the molecular the relatedness was determined by the UPG method using the Dice similarity index on Fingerprinting 0 Phylogenetic groups were assigned by multiplex PCR. Transfers of bla genes were carried out by conjugations experiments and transformation by electroporation into J53 and DH10 E. coli, respectively. Plasmids were compared by size using S1 nuclease digestion and by the patterns resulted of southern hybridization of HindIII-digested plasmidic patterns in 5 families (3 with CTX-M14 and 2 with SHV-12). The CTX-M14 bla gene hybridized with a single 20 kb hybridization band in 9 plasmids, whereas SHV-12 bla gene was located in fragments with different sizes in 13 plasmids.

Conclusions: Common source or horizontal transmission of the same ESBL-producing strain or plasmid was found in 63% of the families with ESBLEC carriers. The acquisition of different clones producing different ESBL enzymes by members of the same household was less frequent in our study, but denote other routes of spread in the community.
High frequency of faecal colonization with ESBL-producing Enterobacteriaceae among Swedish persons after travelling outside the Scandinavian countries


Objective: High frequency of faecal colonization with ESBL-producing Enterobacteriaceae among Swedish persons after travelling outside the Scandinavian countries.

Methods: From September 1st, 2008 to March 31, 2009, persons attending vaccination clinics in southeast Sweden planning to travel outside Scandinavia for <3 months, were asked to participate. Faecal samples and questionnaires were collected before and after travel. Faecal samples were cultured on chromogenic media: chromID ESBL (bioMérieux) and chromogenic UTI-medium (Oxoid) with discs containing cefotaxime, ceftazidime, cefepime, piperacillin/tazobactam, meropenem and linezolid. Isolates with suspected ESBL-pheno type were subcultured and confirmed according to the methods of the extended ESBL definition suggested by the Swedish Reference group for Antibiotics (SRGA) (www.srga.org).

Results: Of 262 enrolled persons, 231 submitted faecal samples and questionnaires before and after travel and were included for analysis. Before and after travel, 9 (4%) and 73 (32%) persons were colonised by ESBL-PE, respectively. No KPC were found. E. coli was the most commonly found species. Gender, age, use of oral cholera vaccination or antibiotics and duration of travel were similar among persons acquiring ESBL-PE during travel (travel associated (TA)-carriers, n = 69) and persons never colonised by ESBL-PE (non-carriers, n = 154). TA-carriers more often reported diarrhoea (54%) or other abdominal symptoms (25%) during travel, compared to non-carriers (38% and 13%). Business was a more common cause for travelling among TA-carriers (12%) than non-carriers (6%), whereas TA-carriers more often reported travelling as “backpackers”, 16% vs. 8%. The frequencies of TA-carriers after travel to the most visited countries (>10 travellers/country) were: India 82%, Egypt 57%, Peru 36%, Thailand 37%, South Africa 27% and Tanzania 24%, respectively.

Conclusions: Travel increases the risk of faecal colonisation by ESBL-PE. Acquisition of ESBL-PE during travel is associated with abdominal symptoms such as diarrhoea.

Comparative epidemiology of faecal carriage of extended-spectrum β-lactamase-producing enterobacteria in 2 hospitals specialized in liver diseases in Egypt and in France


Objective: To compare the carriage of ESBL-PE producing enterobacteria in Egypt and in France.

Methods: Two recent studies identified admission to a room previously occupied by a methicillin-resistant Staphylococcus aureus (MRSA) or a vancomycin-resistant enterococci patient as an independent risk factor for acquisition of these bacteria. The aim of our study was to determine whether admission to an ICU room previously occupied by a multidrug-resistant Gram negative bacilli (MDRGNB) carrier increase the risk of acquiring these bacteria by subsequent patients.

Results: Of 262 enrolled persons, 231 submitted faecal samples and questionnaires before and after travel and were included for analysis. Before and after travel, 9 (4%) and 73 (32%) persons were colonised by ESBL-PE, respectively. No KPC were found. E. coli was the most commonly found species. Gender, age, use of oral cholera vaccination or antibiotics and duration of travel were similar among persons acquiring ESBL-PE during travel (travel associated (TA)-carriers, n = 69) and persons never colonised by ESBL-PE (non-carriers, n = 154). TA-carriers more often reported diarrhoea (54%) or other abdominal symptoms (25%) during travel, compared to non-carriers (38% and 13%). Business was a more common cause for travelling among TA-carriers (12%) than non-carriers (6%), whereas TA-carriers more often reported travelling as “backpackers”, 16% vs. 8%. The frequencies of TA-carriers after travel to the most visited countries (>10 travellers/country) were: India 82%, Egypt 57%, Peru 36%, Thailand 37%, South Africa 27% and Tanzania 24%, respectively.

Conclusions: Travel increases the risk of faecal colonisation by ESBL-PE. Acquisition of ESBL-PE during travel is associated with abdominal symptoms such as diarrhoea.
Intestinal colonization with Gram-negative bacteria and subsequent ICU-acquired bacteraemia during selective digestive decontamination

E.A.N. Oostdijk*, M. Bonten (Utrecht, NL)

Objectives: In a recent study (NEJM 2009;360:20) selective digestive decontamination (SDD) was, compared to Selective Oropharyngeal Decontamination (SOD), associated with a significant reduction in ICU-acquired bacteraemia caused by Gram-negative bacteria (GNB). The difference between SDD and SOD is intestinal tract decontamination and standard 4 days of cefotaxime during SDD (and not during SOD). We hypothesized that intestinal colonisation with GNB was associated with subsequent ICU-acquired GNB bacteremia in patients receiving SDD.

Methods: Retrospective cohort study in a tertiary care ICU in the Netherlands, including all patients that had received SDD between Sept 2008 and Sept 2009. Rectal carriage with GNB was determined twice weekly during ICU-stay. For each patient-day the status of intestinal GNB colonization was determined, creating patient-days with and without intestinal GNB colonization. Incidence densities of ICU-acquired GNB bacteraemia were calculated for 1,000 patient-days with and without intestinal GNB colonization.

Results: 730 patients (7762 patient-days at risk) were included and 650 (89%) had >1 episode of rectal GNB colonization during ICU-stay. 23 patients (3.2%) had >1 episode of ICU-acquired GNB bacteremia. Incidences of ICU-acquired GNB bacteraemia were 6.1 and 1.9 per 1,000 patient days for the periods with and without intestinal GNB colonization (relative risk 3.78 (95%CI 1.66–8.61)). The median onset of ICU-acquired bacteremia with and without intestinal GNB was 12 (IQR 37.5) and 8.5 (IQR 14.3) respectively (p=0.4); 3 and 2 ICU-acquired bacteremias occurred within the first 4 days after ICU-admission. 10 (43%) Episodes of bacteremia were preceded by rectal colonization with the same species, being most frequently Serratia spp. (n = 3) and Pseudomonas aeruginosa (n = 3). 3 patients had already lost rectal carriage at the time of bacteremia with the same species.

Conclusion: Intestinal colonization with GNB during SDD is associated with an almost 4-fold risk of developing GNB bacteraemia. 78% of ICU-acquired bacteremia occurred after day 4, indicating that this association seems not to be influenced by cefotaxime use.

Characterization of CTX-M15-producing Klebsiella pneumoniae associated with an outbreak in a neonatal intensive care unit. A follow-up study shows long-term faecal colonization and transmission to family members

I.H. Lühr*, S. Rettedal, K. Oymar, A. Sandeijord, O. Natås (Stavanger, Tromsø, NO)

Objective: Molecular characterization of a multiresistant extended-spectrum β-lactamase (ESBL)-producing Klebsiella pneumoniae-strain associated with an outbreak in a neonatal intensive care unit (NICU) at Stavanger University Hospital, Norway. Evaluate long term colonization in affected newborns and transmission to family members.

Methods: Rectal/fecal samples were cultured on modified MacConkey agar and on chrom ID ESBL-plates (bioMérieux). Susceptibility testing was performed by disk diffusion and Etest. ESBL-production was confirmed by double disk approximation test. β-lactamase-genes were detected by PCR and typed by DNA sequencing. Clonal relatedness was examined by PFGE. A follow-up study has been initiated. Monthly rectal/fecal samples are collected from the newborns and their families.

Results: The outbreak was disclosed Jan 30th 2009 after identification of multiresistant K. pneumoniae in clinical samples from three patients. Subsequently, 58 children were found to be colonized with ESBL-producing K. pneumoniae after screening all patients in the NICU (26/27 colonized) and children discharged from the NICU or maternity ward during Nov 2008 to Jan 2009 (28/500 colonized). After cohorting and strengthened infection control measures another four children (4/89) at the NICU were colonized during Feb to April. Only one patient had a severe clinical infection (septicaemia) and recovered successfully after treatment with meropenem. All isolates (n = 58) expressed resistance to aztreonam, 3rd and 4th generation cephalosporins, clavulanic acid synergy as well as co-resistance to aminoglycosides, trimethoprim-sulfamethoxazole and nitrofurantoin. CTX-M-type (group1) was confirmed by PCR and DNA sequencing. All isolates examined (n = 17) displayed an indistinguishable Xba1-PFGE-pattern. 49 colonized children and 80 family members were included in the follow-up study. After nine months of follow-up, 45 children (92%) are still colonized. Transmission to 16 family members (20%) has been detected.

Conclusions: This is the first major hospital outbreak caused by ESBL-producing Enterobacteriaceae in Norway. The outbreak onset was about two months before the ESBL-producing K. pneumoniae-strain was identified. A subclinical outbreak like this is difficult to detect unless patients are regularly screened. Long time carriage in newborns is a possible reservoir for the spread of ESBL-producing bacteria in hospitals and in the community.
ESBL positive follow-up culture. The median colonisation time was 192 days (95% CI 172–216), the first quartile 56 days (95% CI 41–69) and the third quartile 365 days (95% CI 334–391) (Figure). For 575 pts the first positive isolate was cultured during admission. Of the 470 with a follow up culture the proportion of pts with a positive isolate after week 1 was 63% and after week 2 58%.

Conclusions: At least 75% of pts remain ESBL positive for at least 2 months and 25% of the pts is still carrier after one year. This implicates that flagging should be continued until screening cultures at (re-) admission are shown to be negative. At least 60% of the patients remain ESBL positive during hospitalisation. Since the real percentage is likely higher due to interference of antimicrobial therapy with culture results, the advice to perform 2-weekly surveillance cultures should be reconsidered.

**Individual risk factors for colonization with carbapenem-resistant Klebsiella pneumoniae among residents in post-acute-care facilities in Israel: a matched case–control study**

D. Ben-David*, S. Masarwa, S. Nason-Venezia, G. Smolian, H. Mishali, I. Friental, B. Rubinowitch, Y. Carmeli, M.J. Schwaber for the PACC CRKP working group

Background: Since 2006, a nationwide outbreak of carbapenem-resistant Klebsiella pneumoniae (CRKP) has been reported in acute-care hospitals in Israel. In a point-prevalence study in post-acute-care facilities (PACFs), we previously identified type of ward, prolonged length of stay (LOS) and infection control policies as ecological factors associated with CRKP colonization. It is important to distinguish between ecological and individual-level risk factors in order to direct interventions appropriately. Here we extended our analysis to assess individual risk factors for colonization among residents without history of CRKP carriage.

Methods: A point-prevalence study was conducted in 12 PACFs. Rectal swabs were obtained from residents without a history of CRKP carriage in 33 wards. Suspicuous colonies growing on CHROMagar™ KPC plates were speciated and tested for carbapenem susceptibilities by VITEK 2, supplemented by Etest®. We used a nested, matched case–control study design to assess individual risk factors for colonization. Cases were defined as patients with positive rectal screening. Controls were selected from patients with negative rectal screening, matched to cases by ward. Patient data collected from medical records included demographic characteristics, comorbid conditions, presence of skin lesions, presence of invasive devices, antibiotic exposure, number of colonized roommates, and PACF LOS.

Results: Of 1004 residents without history of CRKP colonization was detected in 119 (12%). Covariates entered into the multivariable model included: Norton score, antibiotic exposure during the past 3 months, skin lesions, receipt of amoxicillin–clavulanate during the past month, and presence of other resistant pathogens (OR1.6, 95% CI 1.06−2.6, p=0.03).

Conclusion: This nested, matched case–control study identified an important modifiable risk factor for CRKP colonization not identified in the ecological analysis: antibiotic exposure. Antibiotic control programs may have an important role in decreasing the burden of CRKP in PACFs.

**Invasive candidiasis in ICU**

**O405 Candidaemia in 536 intensive care units, 2001–2008**

E. Meyer *, F. Schwab, P. Gastmeier, C. Geffers (Berlin, DE)

Background: We analyzed the epidemiology and secular trends in candidemia within a network of 536 German ICUs reporting data to the German Surveillance System for Nosocomial Infections.

Methods: CDC standard definitions were used for diagnosis of nosocomial laboratory confirmed primary bloodstream infection (BSI). Incidences were calculated by BSI per 100 patients, incidence densities by nosocomial BSI per 1000 patient days and per 1000 central venous catheter (CVC)-days. Results: 536 ICUs submitted data of 1,942,745 patients, 6,881,170 patient-days and 4,740,019 CVC. Fungi were isolated in 492 of the 6,608 positive BSIs. Of them, 335 BSIs were associated with C. albicans and 325 were CVC-associated (97%). C. albicans ranked fifth in the most frequent isolated pathogens in BSIs. The mean CVC-associated BSI rate with C. albicans stayed stable over time with 0.06 per 1000 CVC-days and it was 0.02 for non-albicans Candida (2006–2008). For monomicrobial C. albicans BSIs, the mean time from ICU-admission to onset of infection was 14 days. Crude ICU-mortality of all pathogens was highest for C. albicans with 19%. Primary BSI differed by type of ICU or hospital and was highest in university hospitals as well as in paediatric, surgical and cardiopulmonary ICUs.

Conclusion: In critically ill patients C. albicans versus non-albicans Candida remained the predominant species in our network of 536 ICUs and ranked fifth of the top pathogens causing primary BSI with a crude mortality of 19%. The mean incidence of candidemia with 0.06 C. albicans BSI/1000 CVC-days remained unchanged over an eight year period.

**O404 Seasonal and ascending trends in the incidence of extended-spectrum β-lactamase-producing E. coli and Klebsiella sp. in two German university hospitals**

K. Kaiser *, U. Frank, A. Conrad, E. Meyer (Freiburg, Berlin, DE)

Objectives: In the present study, the incidence of extended spectrum [β]-lactamase (ESBL) producing strains were analysed for general trends and seasonality.

Methods: Monthly data on ESBL producing strains were collected retrospectively at two large university hospitals in the Southwest and Northeast Germany. For the analysis we focussed on E. coli, Klebsiella pneumoniae and Klebsiella oxytoca for consistency both between the two settings and during the study periods. Multivariate time-series analyses were carried out to explain variations in the monthly incidence densities of ESBL cases (E. coli-and/or Klebsiella-related ESBL cases per 100 patient days) in the two settings (Berlin and Freiburg). For the final models, we were able to incorporate variables for the ascending linear trends and other variables representing the average monthly temperature.

Results: Our models show that in general all the incidences of ESBL cases show an increasing trend. In addition, all incidences of ESBL cases responds positively to the average temperature, meaning that in summer when the temperature is high more ESBL cases were detected than during winter months (See Figure for details). The study methodology was also applied to the incidences of MRSA in the two settings, but an association with the average temperature could not be detected.

Conclusion: In the present study, we affirmed that ESBL-producing E. coli and K. pneumoniae are an emerging problem in German hospitals. Furthermore, we demonstrated that the monthly incidence of ESBL strains is highly correlated with the mean monthly temperature, a fact which should be considered in experimental studies as an additional parameter influencing the incidence of ESBL.
Incidence of candidaemia and antifungal sensitivity in critically ill patients

M. Mascellina*, A. Oliva, C. Gallinelli, R. Niconia, F. Chiarini (Rome, IT)

Introduction: The incidence of invasive candidaemia is increasing all over the world, mainly in critically ill and immunocompromised patients. A shift to non-albicans species and a growing resistance to the common antifungal have been noticed over the last years.

Objectives: Aim of our study was to analyze the different Candida species isolated from bloodstream infections and the related antifungal susceptibility pattern over a three year period at Policlinico Umberto I of Rome.

Methods: 7574 blood cultures were analyzed from 2007 to 2009 by both automated and manual methods. Candida species isolates were identified using chromogenic culture media and by API system (Bio-Merieux). VITEK-2 cards were used to perform the antifungal agents sensitivity to the following drugs: fluconosine, amphotericin B, fluconazole, itraconazole, voriconazole, voriconazole-susceptible C. glabrata. To determine the susceptibility or resistance patterns, CLSI breakpoints were used.

Results: The overall incidence of invasive candidaemia during the three years under study was 4.75% with a marked increase from 2007 to 2009 (3.85% to 7.5%). The species isolated were the following: C. albicans 37.6%, non-albicans species 62.4% (C. krusei 30.2%, C. glabrata 21.7%, C. parapsilosis 5.6%, C. tropicalis 3.8%, C. lusitaniae 1.1%). We observed that the detection of C. albicans raised from 7.1% in 2007 to 55.5% in 2009, whereas C. krusei, C. parapsilosis and C. tropicalis incidence decreased over the three year period. C. glabrata was almost the same during the whole period (28.6% in 2007, 22.2% in 2009). As far as C. albicans is concerned, we noticed an increase of resistance to amphotericin B (from 0% in 2007 to 6.6% in 2009) and voriconazole (from 0% in 2007 to 13.4% in 2009). C. krusei showed a raising resistance to amphotericin B, fluconazole, itraconazole and voriconazole (from 0% to 40%, from 25% to 80%, from 25% to 50%, from 0% to 20%, respectively). In C. glabrata a marked increase of resistance to all the antifungal agents was observed. All the isolates of C. parapsilosis were resistant to voriconazole; in contrast, C. tropicalis was susceptible to all antifungal agents.

Conclusions: Our study confirms the high incidence of candidaemia in the setting of critically ill patients. C. albicans resulted to be the most prevalent species. The overall rate of resistance increased over the study period in all the Candida strains under consideration.

Low prevalence of azole-resistant isolates causing fungaemia in patients admitted to intensive care units

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Objectives: The widespread use of azoles may be responsible for an increasing number of episodes of fungaemia caused by fluconazole-resistant isolates. We previously showed that, during 2000–2006, only 3.5% of fungaemia episodes occurring in patients admitted to intensive care units (ICUs) were caused by a fluconazole-resistant isolate. In the present study, we assess the proportion of episodes of fungaemia caused by azole-resistant strains in patients recently admitted to ICUs (2007 to 2009).

Methods: From February 2007 to June 2009, we recorded 80 episodes of fungaemia in 78 patients admitted to the ICUs of a tertiary hospital in Madrid, Spain. The distribution of episodes by ICU was as follows: general, 41.2%; neonatology, 32.5%; major heart surgery, 11.2%; C. tropicalis (n = 6; 7.5%); C. albicans + C. parapsilosis (n = 3; 3.8%). Arxula adeninivorans (n = 1; 1.2%), Rhodotorula mucilaginosa (n = 1; 1.2%), and Trichosporon inkin (n = 1; 1.2%). The antifungal susceptibility (MIC50/MIC90/MIC range [μg/ml]) of the isolates was 0.25/≤0.125–≥128 for fluconazole and <0.015/0.125≤0.015–4 for voriconazole. According to the CLSI M27-A3 breakpoints, the isolates were classified as susceptible, (96.2%) and resistant (3.8%) to fluconazole and as susceptible (97.4%), susceptible–dose-dependent (1.3%), and resistant (1.3%) to voriconazole. Three patients had fungemia caused by fluconazole-resistant isolates. The isolates were voriconazole-resistant (C. glabrata), voriconazole-susceptible–dose-dependent (A. adeninivorans), or voriconazole-susceptible (R. mucilaginosa). The 3 patients were admitted to the general ICU (C. glabrata and A. adeninivorans) and the major heart surgery ICU (R. mucilaginosa) and only one had recently received fluconazole. Outcome was favourable in 2/3 patients.

Conclusions: Fungemia caused by fluconazole-resistant isolates occurred only in adult ICUs. Only 3.7% of cases of fungemia were caused by azole-resistant isolates, and this proportion has not increased recently in our hospital. J. Guinea (CP09/00055) is contracted by FIS.

Evaluation of the risk for invasive candidiasis in intensive care patients after cardiothoracic surgery

C. Kratzer*, S. Tobudic, A. Schiferer, H. Fischer, A. Lassnig, W. Graninger, E. Presterl (Vienna, AT)

Objectives: To improve the diagnostic procedures for invasive Candida infections critically ill patients after cardiothoracic surgery, a prospective surveillance study was performed at our cardiothoracic intensive care unit (ICU) of the Medical University of Vienna.

Methods: Patients admitted to the cardiothoracic ICU for at least 4 days between December 2006 and December 2008 were enrolled into the study. Two times weekly surveillance cultures (n = 4718) for superficial sites were analyzed for the presence of Candida. To determine the risk for invasive candidiasis, the following data were assessed: age, sex, Simplified Acute Physiology Score SAPS II, the European System for Cardiac Operative Risk Evaluation (EuroSCORE), length of ICU stay and hospital stay, type and duration of cardiothoracic procedure, number of redo surgeries, additional gastrointestinal (GIT) surgery, parental nutrition, severe Candida colonization, bacteremia, severe sepsis, leukocytosis or leucopenia and the highest Sequential Organ Failure Assessment (SOFA) score.

Results: A total of 198 patients were included into the study, 10 ICU patients (5%) developed invasive Candida infections. Age, gender, SAPS II and euroSCORE of patients, the type and duration of cardiothoracic procedures and parental nutrition were no significant risk factors in our study population. In all invasive Candida infection patients severe Candida colonization (p < 0.001), leukocytosis >14 G/l or leukopenia <4 G/l (p = 0.03) and a SOFA score >8 (p = 0.002) were found. The risk for invasive Candida infections in cardiothoracic ICU patients was calculated using the following determinants: severe Candida colonization, leukocytosis or leucopenia, highest SOFA score >8, redo surgical procedures >2 and additional GIT surgery.

Conclusion: Cardiothoracic ICU patients are at risk for invasive Candida infections at the presence of severe Candida colonization, leukocytosis or leucopenia, a SOFA score >8, additional GIT surgery and when undergoing multiple cardiothoracic interventions >3.

Functional IL-10 and IL-12B polymorphisms are associated with persistent Candida spp. bloodstream infection


Objectives: Candida bloodstream infections cause significant morbidity and mortality in hospitalized patients. While clinical and microbiologic factors affecting prognosis have been identified, the impact of immune responses, mediated by cytokines, on outcomes of infection remains
be studied. The present study assessed the role of genetic variation in cytokine genes on susceptibility and/or clinical outcomes of candidemia.

**Methods:** Single nucleotide polymorphisms (SNPs) in six cytokine genes (IFN-γ, IL-10, IL-12B, IL-1B, IL-8) and one cytokine receptor gene (IL-12RB) were genotyped and analyzed with logistic regression in 365 patients with candidemia and 351 non-infected controls. In addition, the presence of these SNPs and measured concentrations of pro-inflammatory cytokines were further analyzed for association with persistent fungemia (≥5 days of positive blood cultures) in 325 Americans with candidemia. Other variables were assessed including type of *Candida* spp. identified, total parenteral nutrition (TPN), dialysis dependence, malignancy, immunocompromised state, renal/liver failure. Variables with p<0.10 on univariate analysis were further analyzed using multivariable logistic regression.

**Results:** None of the SNPs examined were associated with susceptibility to candidemia. Mean age of candidemia patients was 55 years (±21.3), with 44% female, 32% African American, 58% immunocompromised, 31% active malignancy, 10% neutropenic, 43% recent surgery, 21% receiving total parenteral nutrition (TPN), 12% dialysis, 25% liver disease, and 49% ICU residence. The following species were identified: *C. albicans* (43%), *C. glabrata* (27%), *C. parapsilosis* (17%), *C. tropicalis* (12%), *C. krusei* (3%), >1 *Candida* species (6%). Overall, persistent fungemia occurred in 15% of cases. In the multivariable model, persistent candidemia was significantly associated with (OR, [95% CI]): TPN (2.69 [1.28–5.62]), dialysis dependence (3.45 [1.36–8.74]), IL10 rs1800896 (3.07 [1.31–7.12]) and IL12B rs41292470 (4.34 [1.38–13.8]). In addition, significantly lower pro-inflammatory cytokine concentrations were measured in serum from patients with persistent fungemia (rs1800896 (3.07 [1.31–7.12]) and IL12B rs41292470 (4.34 [1.38–13.8]).

**Conclusions:** SNPs in IL-10 and IL12B were associated with persistent fungemia in candidemia patients, which also associated with low serum concentrations of pro-inflammatory cytokines. This may provide insights for future targeted management strategies for patients with this high mortality condition.

**O410** An echinocandin vs. a comparator antifungal in *Candida* bloodstream infections: a meta-analysis

Y. Golan*, D. Harrison, K. Fahrbach (Boston, US)

**Objective:** Mortality from *Candida* bloodstream infections (CBSI) is high if not treated adequately. In recent clinical trials of CBSI, treatment with an echinocandin resulted in higher success rates. However, superiority has not been demonstrated. Given similarities in trial design and definitions, data from these trials can be combined in a metaanalysis. We compared the efficacy, measured as global clinical success at the end of intravenous therapy, of an echinocandin vs. a comparator AF agent in the treatment of CBSI.

**Methods:** We used standard metaanalysis methodology and a random effect model. We conducted a literature search to identify all randomized, controlled, trials (RCTs), assessing the efficacy of an echinocandin (caspofungin, micafungin, anidulafungin) in CBSI. To evaluate whether the comparator (fluconazole or amphotericin preparations) success rates were consistent with previously published data, we conducted an additional literature search of all RCTs in which these agents were evaluated. Articles were reviewed independently by 2 reviewers. The corresponding authors and sponsors were approached for additional data.

**Results:** 8 RCTs were included: 3 comparing an echinocandin to comparator antifungal (CAF), 1 comparing two echinocandins, and 4 comparing amphotericin preparations to fluconazole. The summary odds ratio for global success was 1.58 (95% CI 1.07–3.54) in favor of echinocandin therapy. The removal of a high-recruting center that had a high anidulafungin response-rate had an insignificant impact on the results (OR 0.90, 95% CI 1.10–1.94). Global success rates observed in all included RCTs of fluconazole (5 treatment arms), amphotericin (4 arms) and the echinocandins (5 arms) were 62%, 73%, and 83%, respectively. In the echinocandin trials, success rates observed in the CAF arms were consistent with prior published trials. In an additional analysis that included only CBSI caused by *C. albicans*, echinocandin therapy resulted in higher success rate vs the CAF (74%; 95% CI 69–78% vs 59%; 95% CI 51–66%).

**Conclusions:** In patients with CBSI, as compared to amphotericin preparations or fluconazole, echinocandin therapy is associated with higher global success rates. This better effect is maintained when restricting the analysis to *C. albicans*, suggesting that effectiveness differences may be unrelated to the level of fluconazole susceptibility.

**O411** Candidemia in neonatal intensive care unit, Malaysia: a success story

A.R. Zaidah*, M. Zeehaida, H. Habshah, WM. Zahirudin, S. Saraiya, R. Noraida, H. Van Rostenberghe (Kelantan, MY)

**Objectives:** Neonates in intensive care units were susceptible of having blood stream infections because of invasive procedures and underdeveloped immune system. Prolonged hospitalization and broad spectrum antibiotics further risk the development of candidemia. This report was written to share the success story in controlling the candidemia after a major outbreak in 2004 by adopting strict infection control practice, in which indirectly resulted in the reduction of candidemia in our neonatal intensive care unit (NICU).

**Methods:** This is a retrospective laboratory based analysis study from January 2001 to August 2009. Spectrum and distribution of *Candida* isolated from blood cultures taken from the NICU at Hospital Universiti Sains Malaysia before and after a major outbreak in 2004 was analyzed. The prevalence of candidemia before and after outbreak was compared and the trends of *Candida* spp. were determined. *Candida* spp. was identified using standard microbiological tests and a commercialized identification system, API-32C system.

**Results:** Altogether, 413 *Candida* were isolated during the study period. Generally, there was a significant reduction in the prevalence of candidemia after 2004 for both *Candida albicans* and non-albicans. The reduction was sustained for the past five years. *Candida parapsilosis* (40%) was the predominant species isolated followed by *Candida albicans* (24.8%), *Candida glabrata* (15.2%) and *Candida tropicalis* (12.4%).

**Conclusion:** Adherence to strict infection control practice is important to control candidemia. *Candida parapsilosis* was the major species implicated in candidemia among our neonates.

**O412** Is there any factor prompting early central venous catheters removal from cancer patients with candidemia?

E. Velasco*, R. Portugal (Rio de Janeiro, BR)

**Background:** Few studies have addressed the timing of CVC removal as a prognostic factor of mortality in cancer patients with candidemia.

**Objective:** To evaluated the clinical factors associated with early central venous catheter removal in cancer patients with candidemia who survived >3 days after the index blood culture.

**Methods:** This is a retrospective analysis from a candidemia study conducted between January 2001 and June 2005 at an oncology cancer center in Brazil. Eligible patients were those whose catheters were eventually removed. We excluded patients who died within 72 h after the candidemia onset or had catheters in place for ≤48 h. Early catheter removal was defined as those catheters withdrawn ≤72 h after the onset of candidemia.

**Results:** We enrolled 164 patients with a 10.4% overall mortality rate. Multivariate analysis revealed the temporary nontunnelled central venous catheter type (OR, 5.06; 95% CI 2.16–11.83) as the only variable independently associated with early removal. Among the 82 episodes not catheter related, 52 catheters (63%) were removed at doctor’s discretion due to the urgency for cancer treatment continuation. Most of these removal (n=46) occurred within 3 days of the index blood culture. No differences in the overall mortality rates were seen among patients with early or delayed catheters removal (P>0.05). Nevertheless, stratified analysis showed a survival benefit (P=0.04) of early removal in the subgroup of patients with performance Karnofsky score >60.
Conclusion: This study showed short-term nontunneled central venous catheter type as the only factor associated with early catheter removal. There were a high proportion of removed catheters with the purpose of not interrupting the underlying cancer treatment. Overall, early catheter removal did not have a beneficial impact on mortality. Nevertheless, the observed favorable survival benefit of early over late catheter removal in the subgroup of patients without significant medical illnesses merits further investigation. Clinical trials enrolling sufficient number of homogeneous patients are necessary to analyze the impact of central venous catheter management on the outcome of cancer patients with candidemia.

Strategies to stay one step ahead of bacteria (Symposium supported by Janssen-Cilag)

**S413** The bacterial challenge: time to react  
J. Garau* (Barcelona, ES)  
The changing pattern of antimicrobial resistance presents a challenge which needs to be met on many fronts. This, combined with the lack of development of new antimicrobials, necessitates a review of current treat-ment strategies. Strategies which will be discussed in this symposium will include the benefits of appropriate empirical antimicrobial treatment for serious infections, and more rational ways of administration (higher doses and varying infusion times) of some antimicrobials. Resistance development is well monitored in Europe, with resources such as the European Antimicrobial Resistance Surveillance System (EARSS), and additional country and local surveillance (e.g. PEG-surveillance in Germany, Austria and Switzerland). Data will be presented on resistance profiles and evolution rates within the intensive care unit, where the challenge is to contain and prevent the spread of resistance. These data are critical for the rational choice of adequate empirical antibiotic treatment which will not lead to failure. This can be achieved using broad-spectrum, potent agents, which are least likely to select for resistance, before changing to a more targeted therapy (de-escalation) once susceptibilities have been determined. These methods allow us to use our limited armamentarium effectively. If this approach is not followed, the risk of failure and increased mortality associated with initial inadequate antibiotic treatment, the emergence of resistant strains while on therapy, and their subsequent spread to others, are the main consequences. The number of new antibiotics to treat multidrug-resistant pathogens in the pipeline are too few, particularly those against Gram-negative bacteria and those with new mechanisms of action. New strategies are needed to close the gap between the burden of infections due to multidrug-resistant bacteria and the development of new antibiotics.

**S414** Optimizing β-lactams by reducing resistance development  
D. Livermore* (London, UK)  
The development of resistance to antibiotics has long been a thorn in the side of the infectious disease physician. Dr Livermore will discuss current resistance issues from a microbiological perspective. The concept of potency and how it relates to minimal inhibitory concentrations (MICs) and breakpoints will be covered, with particular reference to carbapenems and *Pseudomonas aeruginosa*, where simple mutations leading to loss of the ‘carbapenem-specific’ porin OprD can confer frank resistance to imipenem whereas resistance to meropenem or doripenem additionally requires some upregulation of efflux. For reasons that remain obscure, these latter combinations of mechanism usually have a lesser effect on doripenem MICs than those of meropenem. In these circumstances there is potential for the dosing of carbapenems to affect the likelihood of resistance development, though any practical significance remains to be confirmed in clinical studies, particularly for the meropenem / doripenem comparison.  

In contrast to *P. aeruginosa*, carbapenem-resistance in *Acinetobacter* spp. is due to OXA-carbapenemases. Some low-level producers may remain marginally susceptible to imipenem (not meropenem or doripenem) but there seems little general scope to overcome resistance by dosage adjustment for any of the compounds. Among Enterobacteriaceae, carbapenem resistance can arise either via combinations of porin loss together with production of extended-spectrum or AmpC-lactamasises or via the production of true carbapenemases. The former mechanism, mostly seen in *Klebsiella* or *Enterobacter* spp, affects ertapenem more than any other analogue and this compound therefore seems most likely to act as a selector; the true carbapenemases – including IMP, VIM and NDM (New Delhi Metallo) zinc-enzymes as well as the KPC and OXA-48 serine types affect all carbapenems, and it seems unlikely that any could be overcome by dosage adjustment, though some might, in the future, be overcome by carbapenem/inhibitor combinations.

**S415** Optimizing β-lactam antibiotics by maximizing PK/PD  
F. Pea* (Udine, IT)  
Consideration of pharmacokinetic (PK) and pharmacodynamic (PD) principles can be useful to optimise dosing of β-lactam antibiotics. β-lactams have time-dependent action, with time above the minimal inhibitory concentration (MIC) critical for maximum efficacy. PK/PD data can be used in Monte Carlo simulations to predict probabilities of obtaining an exposure target for a given dose. Evidence from Monte Carlo simulations, animal models and clinical studies have led to real-world recommendations, such as using extended infusions and other strategies to maximise efficiency of β-lactams. Prolonged and continuous infusions can give better efficacy, can lower the likelihood of resistance developing through higher trough levels and eliminate or at least reduce the need to increase the dose, β-lactam antibiotics that can be dosed via continuous/prolonged infusions include penicillins, cephalosporins and carbapenems. However, data should be assessed for each antimicrobial. For example, doripenem exhibits linear pharmacokinetics and does not accumulate with repeated dosing over 7 days, which supports its use as a prolonged infusion. Dr Pea will compare differences between carbapenems and classic β-lactams. Dosing strategies for different carbapenems will be discussed, including their stability and safety profiles. Practical considerations for prolonged infusions include having knowledge of the relationship of serum levels to target organ levels for different antimicrobials and an awareness of differences in PK and PD parameters among diverse patient groups. Dr Pea will conclude with a discussion on which particular patient populations, such as those with *Pseudomonas* infection, may benefit most from continuous infusions. He will also discuss the effect of different comorbidities, such as use in patients with severe sepsis or septic shock and with renal failure or glomerular hyperfiltration, and how their pathophysiology can affect drug levels.

**S416** Novel β-lactams: what makes them different?  
T. Welte* (Hanover, DE)  
Dr Welte will discuss β-lactams which are newly approved and in late-stage development from a clinical perspective. Discussion will include summaries of in vivo data including pivotal clinical studies, recent meta-analysis, such as activity studies against *Pseudomonas* and *Acinetobacter*, and new clinical data on carbapenems, such as doripenem data dosed at 1 g. The use of intravenous antibiotics for patients with renal failure will be discussed, including considerations when using hemofiltration and continuous renal replacement therapy (CRRT). Comparative safety data will be presented for the carbapenems and recent health economic and hospital utilization datasets will also be discussed. Dr Welte will illustrate his talk with examples, particularly of patients who have failed therapy, with reasons for failure, which can be complex. Techniques and approaches to minimise the possibility of treatment failure will be discussed, such as appropriate initial empiric treatment and prolonged infusion. The presentation will conclude with a brief review of β-lactams currently in the pipeline including ceftobiprole, ceftaroline, and faropenem.
Cytomegalovirus infection: strategies, recommendations and future solutions (Symposium supported by DiaSorin)

S422 Epidemiology of human cytomegalovirus with focus on mother/child transmission

G. Jahn* (Tübingen, DE)

Human cytomegalovirus (HCMV) affects 30–100% of adults worldwide depending on geography and lifestyle by the age of 40 years. Two possible sources of sexual transmission of HCMV are virus in the female cervix and in semen of men. The frequency of HCMV infection in adults correlates with the number of sexual partners and sexual experience. This β-herpesvirus is the virus most commonly transmitted to the fetus before birth, occurring in 0.3–2% of all live births. Another even much more frequent transmission route of mother-child is breastfeeding. The local viral reactivation of the HCMV antibody positive mothers during lactation is highly frequent and self limited and follows unimodal kinetics. The vertical transmission rate from mother to child is about 40%. Also horizontal HCMV transmission from newborns and young children to their mothers or other individuals taken care of those infants happens. Children may shed the virus in saliva and urine for months or years, but the relative portion of this kind of horizontal transmission from children to children or from children to adults is unknown. Also the horizontal transmission among adults, besides sexual intercourse, is not well described, but unlikely. In medical care, HCMV can be transmitted by blood products or organ transplantation. As with all other herpesviruses, HCMV has the ability to establish latent/silent infection in the host after primary infection. Activation from silent infection can occur under immunosuppression, during pregnancy and during lactation. Individuals can be infected with multiple strains, meaning secondary infection as exogenous reinfection or endogenous reactivation may occur. HCMV disease with various symptoms can result from either primary or secondary infection, also in primary infection disease is more severe and more frequent. The outcome of congenital HCMV infection is variable. About 10–15% of infected newborns exhibit clinical symptoms at birth such as CNS sequelae with hearing loss, cognitive impairment and cerebral palsy. Remarkably from 85–90% of HCMV infected newborns who are asymptomatic at birth will later develop hearing loss in about 15%. In both symptomatic and clinical asymptomatic newborns, sequelae often are not apparent in the first months or years of life. That all is an urgent need for specific HCMV diagnostic procedures and interpretations for pregnant women and newborns to guide the solid management of fetal/infant infection.

Contemporary challenges in β-lactamase inhibition

S435 Inhibition of KPC β-lactamase

J. Spencer* (Bristol, UK)

The growth of antimicrobial resistance, and in particular the proliferation of ESBL-producing Enterobacteriaceae, means that carbapenems are increasingly front line therapy for nosocomial infections. In consequence numerous carbapenem-hydrolysing β-lactamases have emerged and begun to disseminate across geographic and species boundaries. Several class A carbapenemases have now been described. Of these the KPC enzymes are of the most immediate clinical relevance. Growing numbers of reports indicate the presence of KPC variants in Enterobacteriaceae, notably from the Eastern United States and Israel but also in China and a number of South American and European countries. KPC-expressing isolates frequently contain additional β-lactamases as well as other resistance determinants, severely limiting treatment options and affecting patient outcomes. Although class A carbapenemases have been extensively studied, the molecular basis for this activity has remained obscure in light of their close structural resemblance to other class A enzymes. It is now established that the acylenzyme formed when carbapenems react with class A β-lactamases such as TEM or SHV can adopt two conformations, and that associated tautomeration ultimately results in inhibition. However, equivalent studies are yet to be reported for the species formed when carbapenems associate with class A carbapenemases. Using X-ray crystallography we have now studied the interactions of the carbapenem meropenem with a model class A carbapenemase (SFC-1 from Serratia fonticola) in which we have used directed mutagenesis to trap the substrate and acylenzyme complexes. These structures show that SFC-1 binds carbapenems in a single well defined orientation where, in contrast to carbapenem-inhibited enzymes like SHV, the β-lactam amide nitrogen remains close to the active site Ser-130. We propose that this model represents productive binding of substrate and is likely to apply to other class A carbapenemases, including KPC enzymes.

One approach to combating carbapenemase-producing organisms is to combine β-lactams with an appropriate β-lactamase inhibitor. However, available β-lactamase-inhibitor combinations are variably effective against carbapenemase producers. Accordingly, a number of β-lactamase inhibitors under development have been tested against KPC and other class A carbapenemases. Recent results in this area will be reviewed.

S437 Designing class C inhibitors

M. Page* (Basel, CH)

Many Gram-negative bacteria, especially Pseudomonas aeruginosa, Acinetobacter baumannii and Enterobacteriaceae, including Enterobacter, Citrobacter and Serratia species, possess chromosomally encoded Class C β-lactamases (AmpC) that are important determinants of resistance towards a broad range of β-lactam antibiotics. Even carbapenems lose activity when confronted with class C lactamases if the organism also has restricted outer membrane permeability. For example, loss of the OprD outer membrane porin of P. aeruginosa, which is essential for the rapid entry of imipenem into the periplasm, will lead to high-level resistance if a class C β-lactamase is expressed. In the last decades, a number of AmpC enzymes have been mobilized on plasmids or other genetic elements and have spread to organisms such as Escherichia coli and Klebsiella pneumoniae that did not usually express AmpC. Carbapenem-resistant strains of K. pneumoniae that have altered porin expression and a plasmid-encoded AmpC β-lactamase have been reported from several countries. In general, class C lactamases are not well inhibited by the clinically available β-lactamase inhibitors clavulanic acid, sulbactam and tazobactam. Insights into the mechanism of class C β-lactamases and how this knowledge can be applied to the design of novel inhibitors.

S438 OXA carbapenemases and their inhibition

M. Galleni* (Liège, BE)

The catalytic efficiency of the class D β-lactamase depends critically on an unusual carboxylated lysine as the general base residue for both the enzyme acylation and deacylation steps of catalysis. Different class D β-lactamase’s X-ray structures indicate that the active site Lys-70 is surrounded by a hydrophobic core comprising residues such as Val-117, Phe-120 and Trp-154. Evidence is presented that the interaction between the indole group of Trp-154 by the carboxylated lysine is essential for the stability of the post-translationally modified Lys70. Substitution of Trp-154 by Gly, Ala or Phe yielded non carboxylated AmpC β-lactamase have been reported from several countries. In general, class C lactamases. This presentation will review the fundamental steps in the mechanism of class C β-lactamases and how this knowledge can be applied to the design of novel inhibitors.
Finally, the deacylation impaired W154A mutant was used to determine the structure of the acyl-enzyme complex with benzylpenicillin. Stopped-flow and quenched-flow experiments indicate that the deacylation step is clearly rate limiting for the OXA-10 \( \beta \)-lactamase. The observation of acyl-enzyme complex with the K70C mutant by X-ray crystallography also suggests that the deacylation step is rate limiting but the acylation step is also affected for the lysine mutants. Indeed, the values of the acylation constants (k2) are clearly lower than with the wild-type enzyme. The catalytic efficiencies of the V117T mutant decrease for all substrates tested. The structure of the V117T OXA-10 mutant indicates that the Lys-70 is partially carboxylated at pH 8.0 in monomer A whereas monomer B contains a non-carboxylated Lys-70. This confirms that the valine residue in the hydrophobic core is important to promote the carboxylation of the Lys-70.

It has been reported that class D \( \beta \)-lactamas are inhibited by chloride ions. Interestingly, in we could show that the inhibitor is due to the replacement of the side chain carboxylate group of the modified lysine by chloride ion. Finally, the structural modifications induced also the appearance of a detectable carbenapenemase activity in OXA variants.

Finally, the deep analysis of structure-function relationship for class D \( \beta \)-lactamas yielded a new approach for the selection and synthesis of new inhibitors.

Community-acquired MRSA: emerging cause of pneumonia

**Pathogenicity: what does question the role of PVL?**

A. Norrby-Teglund* (Stockholm, SE)

Community-acquired methicillin-resistant *Staphylococcus aureus* (CA-MRSA) has emerged as a major health problem world-wide. CA-MRSA is a frequent cause of skin and soft-tissue infections, and has also been reported to cause rapidly progressing life-threatening infections with unusually severe pathology, including necrotizing pneumonia, severe sepsis and necrotizing fasciitis. A large number of epidemiological and clinical studies have established a strong association between these severe CA-MRSA infections and strains harbouring the pore-forming toxin Panton-Valentine Leukocidin (PVL). Although compelling, epidemiological data alone is insufficient to establish a role of PVL in disease pathogenesis. However, this issue has been addressed in a large number of studies utilizing different experimental systems including PVL-deficient mutants and various in vitro models. The results of these studies have been highly conflicting, and consequently, this topic is a matter of great debate in the staphylococcal field. The current progress toward understanding the enhanced virulence potential of CA-MRSA with special emphasis on PVL, but also including other relevant staphylococcal virulence factors, will be summarized and discussed during this talk.

Epidemiology and epidemic of CA-MRSA pneumonia

G. French* (London, UK)

Healthcare-associated MRSA (HA-MRSA) infection is now widespread throughout the world. Recently, new strains of community-associated MRSA (CA-MRSA) have emerged that affect people with no history of healthcare contact. These are community strains of MSSA that have acquired mecA. They are generally more virulent than HA-MRSA and can cause primary infection in healthy people, including children. CA-MRSA often possess genes encoding the putative virulence factor Panton-Valentine Leukocidin (PVL). CA-MRSA clones can be defined by multilocus sequence (ST) and SCCmec type. CA-MRSA have appeared in most countries of the world. They are common in the USA and much less common, but increasing, elsewhere. There are many different clones whose distribution differs geographically. Some are particularly successful. USA300 (ST8-IV PVL+) has replaced USA400 (ST1-IV PVL+) as the commonest type in the USA. The ‘European clone’ (ST80-IV PVL+) is common in Europe and the ‘South West Pacific’ clone (ST30-IV PVL+) in the Far East and South America. In Europe there is great clonal diversity and new types are continually being reported, including the pig-associated ST398 strain (usually PVL−) that is common in Denmark and the Netherlands but now spreading elsewhere. Although new CA-MRSA clones continue to appear, successful older ones are being introduced into new geographical areas by travellers and immigrants. CA-MRSA pneumonia is uncommon worldwide but increasing. It may follow influenza in previously healthy people and may cause fatal necrotizing disease, usually associated with PVL-producing CA-MRSA. PVL-positive staphylococci produce necrotizing pneumonia in animal experiments but the role of PVL in human disease is still under debate. Although PVL+ USA300 is the most frequent strain causing pneumonia, this may be because it is common; it remains to be seen whether other types of CA-MRSA, including PVL− strains, also have this ability. With the continuing spread of CA-MRSA and the on-going influenza pandemic, we can expect the incidence of severe CA-MRSA pneumonia to increase. HA-MRSA pneumonia in ventilated patients is well recognised and has a poor prognosis. CA-MRSA is now spreading in hospitals and becoming increasingly multi-drug resistant (MDR). Physicians should be aware of the threat of hospital-acquired pneumonia with virulent, PVL-producing MDR CA-MRSA and national and international organisations should provide appropriate surveillance systems for CA-MRSA.

Preventing catheter-related infection: light and shadow

W. Zingg* (Geneva, CH)

Many patients require a central venous catheter or an arterial line. Although indispensable and of benefit, vascular access devices pose a potential risk of complications due to central line-associated bloodstream infections (CLABSI). The risk for CLABSI varies between 1 to 7 episodes or more per 1000 catheter-days depending on ward-type, institution and socio-economic status of the country. Most successful CLABSI prevention strategies are multimodal and include a combination of effective single intervention measures. Some measures are “procedural”, such as using maximal sterile barrier precautions at catheter insertion, avoiding the femoral site, strict hand hygiene and applying a non-touch technique for catheter handling, opening hubs on antiseptic-impregnated pads, change of tubing only when indicated, and avoiding unnecessary access to the system. Furthermore, any indication for a central line insertion must be justified and catheters should be removed as soon as possible. Other intervention measures are more “technical”, such as chlorhexidine-containing products for skin antisepsis, chlorhexidine dressings at the catheter insertion site, impregnated catheters with antibiotics or chlorhexidine and silver-sulfadiazine, access devices coated with silver particles, and closed infusion systems. A promising approach in CLABSI prevention is the use of lock-solutions consisting of taurolidine-citrate, ethanol, EDTA or citrate/methylene-blue/paraben.

Although there is evidence that some intervention combinations or bundles are effective, no specific combination should be considered superior to another. However, effort, complexity and costs may limit the possibility to apply all measures together. Even more important, infection prevention measures, and especially procedures, are of no use if they are not respected in daily practice. Most episodes of CLABSI are identified in the intensive care unit where care is complex. In such an environment, attention may be drawn away from infection control measures. Thus, infection control measures must be simple and easy to integrate into daily practice. Furthermore, it is indispensable to promote an infection control culture among nurses and physicians to ensure that prevention measures are observed under stress conditions. Although technical devices may be of help in stress situations, the failure to adopt a safety culture cannot be replaced by the use of impregnated catheters, chlorhexidine dressings or lock solutions.
### Antimicrobials against biofilm-based catheter-related infections: new perspectives

G. Donelli* (Rome, IT)

Antimicrobials against biofilm-based catheter-related infections: new perspectives. In the last decades, different strategies have been developed to prevent microbial colonization of intravascular catheters through surface adsorption or incorporation in the device polymer matrix of antibiotic/antifungal agents. However, the currently available medicated catheters have shown to inhibit microbial biofilm formation for relatively short periods, mainly due to the massive release of the loaded antimicrobial agents in the first 24h followed by a slow release at sub-inhibitory concentrations until drug exhaustion. This phenomenon involving the risk of emergence of antibiotic-resistant strains. To overcome these limitations, we focused our research efforts in developing different experimental approaches to prevent microbial colonization of central venous catheters based on the adsorption of antimicrobial agents to synthesized and properly functionalized polyurethanes with the aim to control drug adsorption and release. Firstly, we have impregnated appropriately functionalized polyurethanes with two antibiotics with different mechanisms of action, rifampicin and cefamandole nafate, along with pore forming agents such as albumin and polyethylene glycol. This in vitro model exhibited a good polymer/antibiotic affinity and the ability to obtain a controlled release of large amounts of antimicrobials for up to 23 days. These results suggest that the entrapping of antibiotic molecules and pore-formers in properly functionalized polyurethanes may represent a promising approach to prevent catheter colonization and onset of bacterial resistance. Other antibiotic strategies we are dealing with concern: i) the development of antimicrobial polymers by the use of polyurethanes able to coordinate metal ions (Ag+, Zn2+, etc); ii) the exploiting of the biofilm matrix-degrading enzyme, Dispersin B, to allow a better penetration of antibiotics through the microbial biofilm, thus improving their activity; iii) the development of a magnetic nanoparticles-based targeting system to fight catheter-related infections by an in situ, on demand, antimicrobial treatment.

### Fever in the returning traveller

#### Fever in the returning traveller

N. Beeching* (Liverpool, UK)

This presentation will focus on the changing epidemiology of fevers imported from this region reflected in travel infection databases, and use brief vignettes to highlight important clinical diagnostic and management issues. As in all travellers, a detailed travel, exposure and immunisation history is essential, combined with knowledge of patient comorbidities that may predispose to acquiring certain infections. In general, malaria is less likely to be the cause of fewer than other infections, contrasting strongly with the differential diagnosis in travellers arriving from Africa. However, recent increases in malaria transmission in tourist areas such as Goa remind us of the need to maintain a high index of suspicion and continually to review pretravel advice on prevention. The emergence of artemisinin resistance in the Thai-Myanmar border area is a concern for the future.

In most recently returned travellers, arbovirus infections such as dengue and chikungunya are common causes of fever and can be confirmed using molecular techniques in the first week of illness and serological tests thereafter. Confrontation of scrub typhus is less common than is tick typhus in travellers from Africa. Leptospirosis is associated with fresh water activities popular with tourists in South East Asia, such as white water rafting and “tubing”, but imported schistosomiasis from this area is rare. Eosinophilia is more likely to be due to other enteric or systemic helmintic or flute infections.

Enteric fevers are common in travellers from the Indian subcontinent, with recent predominance of paratyphoid A, which is often resistant to fluoroquinolones and multidrug resistant to other first line agents. Empirical treatment while awaiting culture results and resistance data should avoid such agents and include a third generation cephalosporin and/or azithromycin. Antimicrobial resistance is common in infections imported from this area, including extended spectrum β-lactamase producing Gram negative bacteria, and multidrug resistant tuberculosis. Respiratory infections are common in any traveller, and influenza has been demonstrated to be the most frequent vaccine preventable infection acquired by tourists in South East Asia. Recent experience with SARS and ongoing concerns in the region about avian influenza remind us of the continued risk in this region of the emergence of novel virus infections spread by the respiratory route.

#### Fever in travellers from South America

E. Gotuzzo* (Lima, PE)

In a study performed by Geo Sentinel and published recently, it was found that, among North Americans, fever after a travel to South America is not very common and that it includes malaria, salmonellosis, dengue, etc. It is important to make geographic distinctions:

1. In Mexico: amebiasis, hepatic abscess and typhoid fever should always be included.
2. In Central America: typhoid fever and dengue are the main causes of fever. Histoplasmosis and toxoplasmosis have been detected in immunosuppressed patients.
3. In South America: Malaria by *P. falciparum* and *P. vivax* are frequent causes of fever. Since 1991, the frequency of typhoid has decreased with more than 90%. The strains of *S. typhi* continue to be sensitive to chloramphenicol, ampicillin and fluoroquinolones. By contrast with Asia, multidrug resistant strains have not been detected. Dengue and enteric hepatitis are frequent causes of fever. In Peru, brucellosis (as well as in Mexico and Venezuela) and bartonellosis should be considered as important diseases. Occasionally, regional mycoses such as histoplasmosis (exposure to caves) and paracoccidioidomycosis are seen.

#### Computer-assisted diagnosis of fever in travellers

J. Van den Ende* (Antwerp, BE)

Kabisa, a computer based tutorial for tropical medicine, has been developed since 1992, the first version in foxpro, the second in C++, the third in MS Access XP and the last in Delphi. (Van den Ende et al. 1997a) For developing countries it is a didactic tool that challenges the student with cases electronically assembled from a randomly generated disease and randomly chosen related presenting symptoms. The student should find the diagnosis with a set of disease characteristics, available in the context of a hospital in developing countries. The logical engine is based upon both pattern recognition and Bayesian logic. For a Western context the programme offers also an expert system for imported fever, based on a prospectively generated database of over 2000 patients. The expert module is innovative with the suggestion of new tests based on the data already provided by the user. In this suggestion, a threshold driven logic is followed (Pauker & Kassirer 1980) for the highest ranked diagnosis strong excluders are asked for, once this diagnosis is worked out less probable hypotheses are examined also. Ranking of suggested tests takes into account power, feasibility, risk and cost. During the session, real examples will be played and the application of the logic shown. If wanted, detailed explanation of the programming can be given. Participants are invited to bring their laptop; the program will be installed and distributed for free.

Reference(s)

Reducing hospital-acquired infections. What is new?

Hospital resources and capabilities in dealing with highly infectious diseases: EuroNHID data from a survey of 44 isolation facilities in 14 European countries


Objective: Highly Infectious Diseases (HIDs, e.g. Viral Haemorrhagic Fevers and SARS) are life-threatening, human-to-human transmissible diseases that may cause Public Health emergencies, requiring special procedures for their containment. To review isolation hospital resources, the European Network for Highly Infectious Diseases project conducted, through a specifically developed checklist, a survey in the facilities designed to deal with HIDs. These data from 44 facilities in 14 European Countries are described.

Methods: The checklist, including 10 items and 44 questions, was developed through a “networking strategy”: a project partner with specific expertise sent drafts for comments and amendments. Final agreement had been reached during a meeting involving all partners. Facilities to be surveyed were selected by national authorities, and are those planned for giving care to patients affected by HIDs. In site surveys were conducted from March to November 2009.

Results: Totally, 481 hospital beds in 350 rooms are available, and in 185 of them it is possible to give intensive care. These facilities are mainly recently built/renovated (70% after 2000). Most of surveyed facilities use these beds routinely, while in 10 isolation facilities they are reserved to HIDs only. Among technical issues, about 90% of facilities are equipped with anterooms, negative pressure inside the isolation area, and high-efficiency filtration of exhausting air. Availability of other technical features (autoclave, scaling of the room, use of adequate material, communication systems, negative pressure indicators, self-closing doors) varies among countries. Four facilities have a BSL-4 laboratory in the same centre/city, while BSL-3 laboratories are available in the same centre/city for 36 facilities. In 60% of facilities, staff is specifically trained, including physicians and nurses with Infectious Diseases and Intensive Care background.

Conclusion: According to preliminary data analysis, generally the hospital resources in isolation are adequate, despite the fact that different levels of preparedness among different countries are still present, in particular in the field of intensive care capabilities and availability of trained staff. These data will represent a valuable tool both for surveyed facilities, in order to identify their strengths and weaknesses, and for European authorities, providing an “on-the-field” evaluation of European hospitals’ capabilities in dealing with HIDs.

Effects of selective digestive and selective oropharyngeal decontamination on bacteremia and respiratory tract colonization with highly resistant micro-organisms

A.M. De Smet", J. Kleytmans, H. Blok, M. Bonten, M. Bootsm (Amsterdam, Breda, Utrecht, NL)

Background: Selective Digestive tract Decontamination (SDD) and Selective Oropharyngeal Decontamination (SOD) were associated with improved day-28 survival in intensive care patients, but the effects on infections and respiratory tract colonization with Highly-Resistant Microorganisms (HRMO) are unknown.

Methods: SDD, SOD and standard care (SC), during periods of six months each, were evaluated in an open clustered group-randomized cross-over study in 13 ICUs, with the order of interventions randomized per center. SOD consisted of four times daily topical application of tobramycin, colistin and amphotericin B in the oropharynx. SDD consisted of SOD and topical application of the same antibiotics in the stomach and four days of intravenouscefotaxime. Cultures of respiratory tract were obtained twice weekly during SDD and SOD, and on clinical indication only during SC. HRMO were defined according to Dutch guidelines. All blood and respiratory tract culture results were evaluated.

Results: 5,927 patients were available for analysis: 1,989 (SC), 1,904 (SOD) and 2,034 (SDD). Compared to SC, odds ratios (OR) for ICU-acquired bacteremia were 0.48 (95% CI 0.38–0.60) during SDD 0.66 (95% CI 0.53–0.82) during SOD. OR for ICU-acquired bacteremia caused by HRMO during SDD were 0.41 (95% CI 0.18–0.94) as compared to SC, which corresponds to a rate reduction of 59%, an absolute risk reduction (ARR) of 0.6% and a number needed to treat (NNT) of 170. As compared to SC, the OR for SDD was 0.37 (95% CI 0.16–0.85), which corresponds to a rate reduction of 63%, an ARR of 0.7% and a NNT of 145. ICU-acquired colonization of Gram negative bacteria was highest among patients receiving SC. ORs for acquiring HRMO colonization, as compared to SC, were 0.58 (0.43–0.78) and 0.65 (0.49–0.87) for SDD and SOD respectively, corresponding to 38% and 32% rate reductions, 5.5% and 4.6% ARR and with NNT of 18 and 22, respectively. Acquired colonization with cefotaxime-resistant or colistin-resistant pathogens was lowest during SDD.

Conclusions: As compared to SC, ICU-acquired bacteremia and respiratory tract colonization with HRMO were 48% and 59% lower during SDD and acquired respiratory tract colonization with HRMO was 38% lower during SOD.

Prevention of catheter-related bacteremia with a daily ethanol-lock in haematology patients with tunnelled catheters. Randomized placebo-controlled trial

B.J. Rijnders", L. Slobbe (Rotterdam, NL)

Objective: Catheter-related bacteremia (CRB) results in significant attributable morbidity and mortality. In this randomized double-blinded placebo-controlled trial, we study the efficacy and safety of a daily ethanol-lock on prevention of CRB in patients with a tunnelled central venous catheter (CVC).

Methods: From 2005 until 2008, each CVC lumen of adult haematology patients was locked for 15 minutes per day with either 70%-ethanol or placebo, following which the lock-solution was flushed through. As a primary endpoint, rates of endoluminal CRB in each group were compared.

Results: The catheter-based ITT-analysis was based on 376 patients, accounting for 448 catheter episodes and 27,745 catheter days. For ethanol-locks, the incidence of CRB per 1000 days of CVC-use was 0.70 compared to 1.19 in patients allocated to placebo (incidence rate ratio 0.59; p=0.19). In patients who classified for endoluminal CRB according to the strictest definition (positive hub culture and concurrent bacterial strain detected in blood) a 3.6-fold, but not statistically significant reduction of CRB was observed for patients receiving ethanol (2/226 versus 7/222; p=0.103). No life-threatening adverse events were observed. More patients receiving ethanol discontinued lock therapy (11/226 versus 1/222; p=0.006) or continued with decreased lock frequency (10/226 versus 0/222; p=0.002), due to subjective discomfort, especially facial flushing and drowsiness.

Conclusion: In this study, the use of ethanol-locks non-significantly reduced the incidence of endoluminal CRB. However, further studies are needed as the overall low incidence of endoluminal precludes definite conclusions. Alternative sources of bacteremia, like microbial translocation during mucositis or exoluminal CRB may have been more important in this patient population.

Different strokes: a co-relational modelling study of common (community and acute hospital) HCAI reduction targets, variable dynamics and antibiotic prescribing

I. Matiland", R. Kato, M. Ibeto, M. Quilaghashi, A. Galeri (Blackpool, UK)

Objectives: Reducing healthcare associated infections (HCAI) in hospitals & community has been priority for department of health (DH). Blackpool Victoria Hospital, large district acute hospital covers
Decontamination of sink wastes and traps is associated with hand hygiene compliance in 13 European intensive care units (ICUs).

Objectives: To compare the incidence of nosocomial Gram-negative sepsis in a neonatal intensive care unit (NICU) before and after the introduction of quarterly dismantling, cleaning and disinfection of sink wastes and traps.

Methods: Prospective surveillance of all late-onset (neonate >72 hours of age) nosocomial Gram-negative sepsis in the NICU over a 40-month period from July 2006 to October 2009. Gram-negative bacteria isolated from blood or cerebrospinal fluid were included. Sepsis rates during 24 months before the introduction of quarterly cleaning and disinfection of sink wastes and traps in July 2008 were compared with the 16 months following. Patient demographic information collected includes sex, gestation, birth weight, multiple birth, day of onset of sepsis and outcome. Data from environment screening of sink faucets and drains are documented.

Results: Twenty-one episodes of sepsis occurred in 21 neonates during the period from July 2006 to June 2008. There was 1 meningitis (E. coli), 1 meningitis and bacteraemia (Enterobacter species) and 19 bacteraemia’s (6 E. coli, 4 Klebsiella pneumoniae, 7 Enterobacter species, 1 Proteus mirabilis and 1 Pseudomonas aeruginosa). After introduction of quarterly cleaning and disinfection of sink wastes and traps 3 episodes of sepsis have occurred in 3 neonates during the 16 months from July 2008 to October 2009. These were 3 bacteraemia’s (2 Klebsiella species and 1 Acinetobacter species). Before introduction of this practice, there were an average of 10.5 episodes of Gram-negative sepsis per annum compared to 2.25 per annum currently (p < 0.001).

Conclusions: No significant infrastructural work took place during this 40 month period. There was no significant change in medical, nursing, hygiene or infection control staffing numbers. The antibiotic policy remained unchanged. The number of admissions to the NICU was stable (1239 in 2006; 1215 in 2007 and 1232 in 2008), although the percentage of neonates <1500g birth weight increased from 99 (8%) in 2006 to 137 (11.3%) in 2007 and 154 (12.5%) in 2008. The reduction in the rate of Gram-negative sepsis as very low birth weight admissions increased was unexpected. Methods to reduce Gram-negative sepsis are complex and multifactorial infection control measures are required. Nonetheless, we found quarterly dismantling, cleaning and disinfection of sink wastes and traps was associated with a reduction in Gram-negative sepsis.
A survey examining promotion of hand hygiene in healthcare through campaigns and programmes coordinated at a national/sub-national level

E. Mathai*, B. Allegranzi, C. Kilpatrick, S. Bagheri Nejad, W. Graafmans, D. Pittet (Geneva, CH)

Objective: The WHO First Global Patient Safety Challenge “Clean Care is Safer Care” (CCiSC) recognises the importance of nationally coordinated activities in achieving its goal of reducing healthcare-associated infection (HAI) through improved hand hygiene in healthcare. A baseline survey of existing hand hygiene national/sub-national initiatives was conducted in 2007 and repeated in early 2009 to assess current status and to generate information on factors contributing to their success.

Methods: Campaigns and programmes promoting hand hygiene in healthcare were identified through WHO regional offices and experts in the field. An online survey using a structured questionnaire was conducted during March-April 2009.

Results: In 2009, 38/38 campaigns/programmes identified (18/20 in 2007) completed the survey. Of the 38, 29 were active national/sub-national level initiatives from all WHO regions, except for Africa; 21 (72.4%) were initiated after the launch of CCiSC in October 2005. The main targets of hand hygiene promotion were general, district and university hospitals, with increasing coverage of long-term care facilities and primary care. The scope varied from awareness raising to well scaled-up activities with ongoing evaluation. Most activities (20/29) obtained funding from multiple sources with governments among the main funders; governments were responsible for initiating 25/29 (86.2%) campaigns/programmes. Through the 2009 survey, the facilitator role played by CCiSC in initiating activities and the support with tools and recommendations emerged very clearly. Barriers were identified, but the perceived significance of specific barriers varied considerably. Those related to commitment (priority and support) and resource availability were important across all regions. A range of indicators to measure the impact of the initiative was reported with process indicators being more common.

Conclusion: Hand hygiene is being promoted in healthcare in several countries at national/sub-national level with clear objectives, strategies and governmental support. Such embedding through policies and resource allocation is important for sustainability. Actions to improve commitment from different stakeholders are needed. Indicators for measuring impact need to be more uniform and more widely implemented. Further actions to initiate coordinated activities across the world, including countries with limited resources, are required.

Effect of a multifaceted intervention on adherence to hand hygiene among healthcare workers: a cluster randomized trial

D. Mertz*, N. Dafoe, S. Walter, K. Brazil, M. Loeb (Hamilton, CA)

Objectives: Compliance with hand hygiene among health care workers (HCWs) is widely felt to be a key factor in reducing the spread of nosocomial infections. The objective of this study was to evaluate the impact of a multi-faceted intervention to increase adherence of hand hygiene among healthcare workers (HCWs) and assess the effect on the incidence of nosocomial meticillin-resistant Staphylococcus aureus (MRSA).

Methods: A cluster randomised controlled trial was conducted from June 2007 to May 2008 in 30 units of three tertiary care hospitals in Hamilton, Ontario, Canada. Study units included eight medical, four general surgery and eight intensive care units. Following a three month baseline period of data collection, 15 units were randomly assigned to the intervention arm (performance feedback, small group teaching seminars, posters) and 15 to usual practice. Hand hygiene was observed during randomly selected fifteen-minute periods on each unit and the incidence of MRSA measured using surveillance specimens.

Results: 3812 (48.2%) of 7901 opportunities for hand hygiene in the intervention group resulted in adherence compared to 3205 (42.6%) of 7526 opportunities in the control group (P < 0.001). However, there was a significant increase of adherence compared to baseline adherence (15.4% in the control and 16.2% in the intervention group) for both groups (Figure). There was no reduction in the incidence of nosocomial MRSA in the intervention group.

Conclusion: Among HCWs in Ontario tertiary care hospitals, adherence to hand hygiene significantly increased with a multi-faceted intervention. Moreover, there was a marked increase in adherence to hand hygiene in both study groups. No resulting difference in MRSA rates between patients in the two study groups could be observed.

Glove use in infection control – is this a significant barrier to hand hygiene compliance?

C. Fuller, J. Savage, S. Besser, S.P. Stone* (London, UK)

Objectives: WHO guidelines stipulate that gloves are required for specific clinical procedures, but warn that they are not a substitute for disinfecting or cleaning hands. It has been suggested previously that wearing gloves could be a barrier to good hand hygiene compliance but the literature is divided as to whether healthcare workers (HCWs) are less likely to clean their hands when wearing gloves. We carried out a large multicentre study to determine whether wearing gloves was associated with poorer hand hygiene compliance.

Methods: 232 hours of observations (7020 observations) were carried out on 15 Intensive Therapy Units (ITUs) and 41 Acute Care of the Elderly/General Medical (ACE/GM) wards in 20 hospitals in England & Wales, whilst conducting a randomised controlled trial of an intervention to improve hand hygiene compliance (FIT trial N0256159318, NRR website). Glove use was not part of the intervention. Hand hygiene moments & behaviours were recorded using a rigorously standardised hand hygiene observation tool (the HHOT), and noting whether the HCW was using gloves or not. Compliance with & without gloves was compared overall & for different hand hygiene moments.

Results: Of the 7020 observations, 1729 (25%) were associated with glove use in both ITUs and ACE/GM wards. Gloves were used in 78% of high risk hand hygiene moments (aseptic technique, body fluid exposure) and in 16% of low risk moments (before & after patient
Achieving sustained improvement in hospital hygienic cleaning using peer-group benchmarking

P. Carling*, B. Dick, E. Eck (Boston, Toledo, Pasadena, US)

Objectives: Ongoing contamination of surfaces in the “patient zone” (Pittet 2007) has become increasingly recognized as playing a role in the transmission of major healthcare-associated pathogens. Over the past five years an indirect monitoring system has been used to improve environmental hygiene related to discharge cleaning in almost 100 hospitals. In view of these results, we undertook a prospective evaluation of a multi-hospital benchmarking program to further analyze this approach for improving the thoroughness of disinfection cleaning (TDC) at discharge.

Methods: The TDC of fourteen high touch objects was evaluated using a fluorescent dye based targeting method in two hospital systems consisting of 12 hospitals (Group A) and 7 hospitals (Group B) administratively related within each group but geographically and functionally independent institutions. A three phase intervention was utilized as previously described (ICHE 2008; 29: 1035−41). TDC scores were provided to the environmental services administration at each hospital and on a regular basis as part of system-wide quality assurance reviews for each system. At each meeting TDC scores were reviewed and the most effective programmatic and educational interventions shared.

Results: As noted in the Figure, pre-intervention (Phase I) TDC scores averaged 39% (95% CI 27.4 to 50.1) in group A hospitals and 53% (95% CI 33.1 to 72.8) in group B hospitals. Following education alone (Phase II), scores in both hospital groups improved group A hospitals improving to 70.1% and group B hospitals to 68%. Subsequently (Phase III) and as a result of serial feedback and peer group benchmarking (F/Us), overall TDC continued to improve in group A hospitals to 88% and group B hospitals to 77%. As noted in the Figure, high levels of improvement were documented for sustained periods of time (to date, 6 to 16 months).

Conclusions: (1) Phase I of the study disclosed previously unsuspected differences in TDC despite the existence of similar cleaning policies in all hospitals. (2) Group benchmarking of TDC scores favorably impacted additional improvement in cleaning. (3) The ongoing transparency engendered by the system-wide programs has made it possible to sustain gains for up to 18 months. (4) The development of a patient-safety oriented, non-punitive environment as well as individual hospital and system-wide leadership support were recognized as critical components of the success of the program.

Antimicrobial consumption – experience from ESAC and other surveillance studies

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Reprints: B. Jans*, K. Latour, E. Broex, A. Muller, V. Vankerckhoven, R. Stroobants, H. Goossens on behalf of the European Surveillance of Antimicrobial Consumption (ESAC) Point Prevalence Survey carried out during a maximum of 2 weeks from May to June in 270 European countries in 2008. The survey included all inpatients wards and collected information on the treated patients with indications and diagnoses. The analyses were restricted to patients above 65 years which were divided into 2 age year groups (G1: 65−75; G2: 76+).

Results: Data for treated patients were obtained for 1,579 patients in G1 and 1,032 patients in G2. Among all the treated patients, G2 received less AM combination (G1: 6%; G2: 24%) and parenteral AM (G1: 65%; G2: 57%). The top three AM classes prescribed were similar in both groups and corresponded to combinations of penicillins with β-lactamase inhibitors (G1: 18%; G2: 24%), fluoroquinolones (G1: 3%; G2: 19%) and third-generation cephalosporins (6% for both groups). Infections represented 74% and 45% of all indications in G1 and G2, respectively.

Conclusion: The results of this study showed differences between the 2 elderly age groups, particularly in the proportion of AM combination, parenteral use, and infection site. It became clear that in line with the improved quality of life of the elderly population in industrialized countries, the treatment of G1 is more comparable to that of younger adults. Importantly, future analyses on AM use should take several age groups of the elderly population into consideration.

O469 The ESAC point prevalence survey: antimicrobial prescribing in 2 age groups of elderly patients from 49 hospitals in 28 European countries in 2008

B. Amadeo*, P. Zarb, G. Giavazzi, A. Muller, V. Vankerckhoven, P. Dacey, H. Goossens on behalf of the ESAC Hospital Care sub-project Group

Objectives: As ageing population rises fast, elderly aged above 65 years are usually considered as one group in literature. However, if infections are more frequent and more severe in the elderly, they also have specific features related to different subgroups of the elderly patients. This study aimed to identify and to assess the variability of antimicrobial (AM) use between 2 age groups of elderly patients.

Methods: Data were extracted from 49 hospitals of the European Surveillance of Antimicrobial Consumption (ESAC) Point Prevalence Survey carried out during a maximum of 2 weeks from May to June in 28 European countries in 2008. The survey included all inpatients wards and collected information on the treated patients with indications and diagnoses. The analyses were restricted to patients above 65 years which were divided into 2 age year groups (G1: 65−75; G2: 76+).

Results: Data for treated patients were obtained for 1,579 patients in G1 and 1,032 patients in G2. Among all the treated patients, G2 received less AM combination (G1: 33%; G2: 24%) and parenteral AM (G1: 65%; G2: 57%). The top three AM classes prescribed were similar in both groups and corresponded to combinations of penicillins with β-lactamase inhibitors (G1: 18%; G2: 24%), fluoroquinolones (G1: 3%; G2: 19%) and third-generation cephalosporins (6% for both groups). Infections represented 74% and 45% of all indications in G1 and G2, respectively.

Conclusion: The results of this study showed differences between the 2 elderly age groups, particularly in the proportion of AM combination, parenteral use, and infection site. It became clear that in line with the improved quality of life of the elderly population in industrialized countries, the treatment of G1 is more comparable to that of younger adults. Importantly, future analyses on AM use should take several age groups of the elderly population into consideration.

O470 The European Surveillance of Antimicrobial Consumption: point prevalence survey of antimicrobial prescriptions in 270 European nursing homes

B. Jans*, K. Latour, E. Broex, A. Muller, V. Vankerckhoven, R. Stroobants, H. Goossens on behalf of the European Surveillance of Antimicrobial Consumption (ESAC) Nursing Homes subproject group

Objectives: Facing the treat of antimicrobial resistance in healthcare settings, optimising the use of antibiotics (AB) in the nursing home (NH)
population is an important priority of quality of care. However, data on AB-use in European (EU) NHs are scarce. The European Surveillance of Antimicrobial Consumption (ESAC) NH sub-project team, funded by the European Centre for Disease Prevention and Control, carried out a methodology in order to measure and describe AB prescriptions among residents living in EU NH.

**Methods:** In April 2009, a PPS was carried out in 301 NH in 19 EU countries. Inclusion criteria for residents were to be present in the NH for at least 24 hours and to receive systemic AB on the day of the PPS. Data were obtained from nursing notes, medication administration records and staff in relation to AB prescribing, characteristics, risk factors and determinants at NH- and at resident level.

**Results:** Data were available for 17 countries and 270 NH (29,360 NH-beds). The mean number of beds by NH was 108 (20–621 beds). Among 27,614 eligible residents, 1740 (median 5.9%, 0–30%) received an AB on the PPS-day. In 20 NH no residents received AB. In the total NH-population 4% (0–57%) had an urinary catheter, and of these, 17% received an AB. Wounds were present in 10% of the population (0–75%) and AB were prescribed in 15% of them. Vascular catheters were uncommon (0.78%) but 36% of this sub-population used an AB. Among residents with AB, 24% had a recent hospital stay. In total 1757 AB molecules were used. AB were administered orally in 90%, parenteral in 9% and nasal (decolonisation MRSA) in 1%. 53% of all treatments concerned urinary tract (prophylactic: 25%) and 29% the respiratory tract (empirical: 92%). 51% of all prescribed regimens were empirical treatments (RTI: 53%, UTI: 23%), 32% was prophylactic (UTI: 89%, RTI: 5%) and 16% was for a documented infection (UTI: 72%). The prevalence of AB use was significantly lower in NH with regular training of prescribers (p=0.02), with written guidelines for appropriate AB-use (p=0.01) or with a NH therapeutic formulary (p=0.0002) compared to NH without these tools.

**Conclusion:** Strong differences in AB-prevalence and device-use were observed in EU NH. Both micro (case-mix)- and macro determinants (cultural differences) partially contribute to these differences. The high proportion of AB-use for urinary tract, especially the important part of uroprophylaxis, was surprising and needs to be explored.

**O471 Impact of medical care and coordination on antibiotic policy and consumption: data of the European Surveillance of Antimicrobial Consumption (ESAC) nursing home subproject**

K. Latour*, E. Broex, A. Muller, N. Drapier, V. Vankerkhoven, R. Stroobants, H. Goossens, B. Jans on behalf of the European Surveillance of Antimicrobial Consumption (ESAC) Nursing Home subproject group

**Objectives:** The aim was to explore medical care and coordination in European nursing homes (NH) and their effect on antibiotic (AB) policy and use.

**Methods:** The European Surveillance of Antimicrobial Consumption (ESAC) NH subproject explored the medical care and coordination and AB policies by using a standardised questionnaire which had to be completed by participating European NHs. Residents: The questionnaire was completed by 270 NHs in 16 European countries. Medical care was provided by personal general practitioners (GP), by an employed medical staff or by both in 67.3%, 20.3% and 12.4% of the NH, respectively (n=266). A NH working with GPs was visited by a median of 26.3 personal GPs per 100 NH beds (min.0.3-max.96.6 per 100 beds) while in other NHs the medical staff consisted of a median of 2 physicians (min.1-max.14). A coordinating physician (CP) of medical care was assigned in 68.4% of the NHs (n=256). The most reported tasks of the CPs were to develop an infection prevention policy (77.7%), to train nursing staff (76.0%), and to develop medical care strategies (70.9%). The presence of a CP in a NH did not result in a significantly lower number of AB prescriptions compared to NHs without a CP (median AB prevalence 5.78% vs. 5.71%; p=0.46). However, NHs where the CP developed an infection prevention policy showed a significant lower rate of AB use in comparison to NHs where the CP did not have this specific task (median 5.2% vs. 8.7%; p=0.0097).

Furthermore, the presence of a CP led to a significant higher availability of a restrictive AB list compared to NHs without an assigned CP (median 17.4% vs. 6.3%; p=0.018).

Private institutions were more likely to work with GPs than public NHs (59.2% vs. 40.8%), which in their turn had a greater tendency (84.9% vs.15.1%) to work with an employed medical staff (p < 0.001). Working with visiting GPs in the NH made it more difficult to develop a restrictive AB list compared to NHs with a medical staff (5.6% vs. 43.1%; p < 0.001). However, the number of visiting GPs per 100 beds did not significantly influence (categorical variable: <20, 20–40, >40 GPs/100 beds; median 5.06%, 6.19% and 6.67%, respectively) the prevalence of AB use (p=0.15).

**Conclusion:** Although an impact of an appointed CP in the NH on the prevalence of AB use could not be demonstrated, his role in developing a restrictive AB list and infection prevention policy was clearly shown in our survey.

**O472 The European Surveillance of Antimicrobial Consumption (ESAC) survey of wound prevalence and antibiotic use in 270 European nursing homes in 2009**

E. Broex*, K. Latour, A. Muller, N. Drapier, V. Vankerkhoven, R. Stroobants, H. Goossens, B. Jans on behalf of the ESAC Nursing Homes Subproject group

**Objectives:** To define wound prevalence, its determinants and its relation with antibiotic (AB) use in European nursing homes (NHs).

**Methods:** A point prevalence study, on AB use, characteristics of residents and characteristics of the NH was conducted in European NHs in 2009.

**Results:** Results from 270 NHs in 16 European countries are available. A median of 9.7% (11.7% mean) of all NH residents (n=26,063) was diagnosed with an undefined wound. Among residents treated with ABs (n=1734), 24% had a wound. However, when considering wound- and AB prevalence (dichotomized above and below the median) at institutional level there was no significant relation (p=0.19). Of the AB using residents 2.5% was treated (i.e. prophylactic, empirical or documented) for a wound infection (WI). Among AB using residents with wounds 7% was treated for a WI. Remarkable is that 1.5% of the residents reported not to have wounds treated for a WI. Of the AB treated NH residents that were admitted to a hospital within the last three months, 35% had a wound. Of those without hospital admission, 20% had a wound (p < 0.0001). Escherichia coli accounted for 47% of the microorganisms (MOs) detected among residents without a wound, in contrast to only 24% (p = 0.0002) for residents with a wound. Methicillin-resistant Staphylococcus aureus was found among 15% of residents with a wound, and 4% of those without (p=0.00015).

Residents with a wound received more often empirical (55%) or documented AB treatments (22%) than residents without a wound (49%, p=0.045 and 15%, p=0.0012, respectively). Prophylactic ABs were used less for patients with (22%) than for those without wounds (36%, p <0.0001). Residents with in contrast to those without wounds received more often combinations of penicillins and β-lactamase inhibitors (JO1CR, 21% vs. 13%, respectively, p <0.0001) and cephalosporins (J01D, 13% vs. 7%, p = 0.012). On the contrary, residents with wounds received other antimicrobials (JO1X) significantly less (18% vs.31%, p <0.0001). Finally, residents with compared to those without wounds received less often oral ABs (83% vs. 93%, respectively, p <0.0001) but significantly more often parenteral ABs (15% vs. 7%, p <0.0001).
Antimicrobial consumption – experience from EAC and other surveillance studies

O473 Antibacterials for systemic use in Belgian hospitals
S. Vaerenberg, E. Hendrickx, B. Catry* for the Belgian Antibiotic Policy Coordinating Committee

Objectives: The aim of the present study is to explore differences in antimicrobial consumption in Belgian hospitals including differences between ward types. This report was restricted to antibacterials for systemic use (WHO-ATC classification J01C).

Methods: Belgian hospitals were invited to report their antimicrobial use to the federal Scientific Institute of Public Health (IPH), which was responsible for the data collection, conversion into defined daily doses (DDD), analysis and feedback. The data collected were split up for non-pediatric and pediatric wards. There is also an optional reporting of intensive care wards and hematology-oncology wards.

Results: The overall results are shown in Table 1. The optional reporting was highly variable over different unit types (range of unit types: 8–44).

The median antibacterial use per bed-day was more than twice as high in ICU compared to NPD (1150 vs. 456 DDD/100 bed-days for 2006 and 1209 vs. 536 DDD/1000 bed-days for 2007). The median antibacterial use in HAO (787 DDD/1000 bed-days in 2006, 943 DDD/10000 bed-days in 2007) was situated in the between the use on NPD and HAO. For 2007, a higher increase in variation in ICU was observed.

Conclusion: Overall incidence of antimicrobial use slightly increased during the observation period, possibly biased by the different number of participating hospitals in the second year of observation. The methodology allows a close trend follow up, with the possibility to compare the consumption between different unit types over time. From 2008 onwards, participation is obliged for the majority of Belgian hospitals.

Table 1. Hospital use expressed as DDD/1000 bed-days (subgroup J01)

<table>
<thead>
<tr>
<th>Class</th>
<th>ATC</th>
<th>2006 (n= 28) Mean</th>
<th>Range</th>
<th>2007 (n= 55) Mean</th>
<th>Range</th>
</tr>
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<tbody>
<tr>
<td>Beta-lactam antibiotics, penicillins</td>
<td>J01C</td>
<td>234</td>
<td>186-275</td>
<td>255</td>
<td>186-250</td>
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<tr>
<td>Other beta-lactam antibiotics</td>
<td>J01D</td>
<td>109</td>
<td>10-175</td>
<td>184</td>
<td>17-244</td>
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<td>Quinolones and fluoroquinolones</td>
<td>J01M</td>
<td>65</td>
<td>6-102</td>
<td>67</td>
<td>7-115</td>
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<td>Other antibacterials</td>
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<td>35</td>
<td>2-61</td>
<td>37</td>
<td>7-104</td>
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<tr>
<td>Macrolides, lincosamides and syreepenemopneumomycins</td>
<td>J01Y</td>
<td>23</td>
<td>6-36</td>
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<td>0-22</td>
<td>9</td>
<td>0-29</td>
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<td>Tetracyclines</td>
<td>J01A</td>
<td>3</td>
<td>0-13</td>
<td>3</td>
<td>0-46</td>
</tr>
<tr>
<td>Amphenicols</td>
<td>J01B</td>
<td>6</td>
<td>0-11</td>
<td>3</td>
<td>0-25</td>
</tr>
<tr>
<td>Total</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>492</td>
<td>344-694</td>
<td>524</td>
<td>242-792</td>
</tr>
</tbody>
</table>

O474 Increased antibiotic use in Swedish intensive care units, 1999–2008
M. Edström*, H. Gill, G. Fransson, J. Ström, S. Walther, H. Hanberger on behalf of the ICU-Strama and the Swedish ICU registry

The ICU-Strama programme was developed ten years ago and is used for regular audit of antibiotic use, antibiotic resistance and infection control procedures in Swedish ICUs. It is a joint project between the ICU-Strama and the Swedish Intensive Care Registry. A central component has been a web-based application which includes a system for automatic feedback.

The purpose of this report is to increase awareness of the usefulness of the programme and provide a ten-year trend analysis of antibiotic consumption.

Material and Methods: The data on antibiotic consumption based on the anatomical therapeutic chemical (ATC) classification system were collected from 64 Swedish ICUs and entered into the database using the web application. Antibiotic consumption was expressed as defined daily doses (DDD) per 1,000 occupied bed day (DDD1000). We used the annually updated DDD calculated by the WHO Collaborating Centre for Drug Statistics Methodology as the average maintenance dose per day in adults for the main indication of the drug (http://www.whocc.no/atcddd).

Data were analysed using the non-parametric test for trend across ordered groups and Spearman’s rank correlation using STATA/SE 9.2 (StataCorp LP, College Station, TX, USA) and SPSS version 11.5 (SPSS Inc., Chicago, IL, USA). Statistical significance was assumed if P < 0.05.

Results: The survey found a variation in the method of data collecting for antimicrobial consumption among hospitals. The lack of an appropriate pharmacy information technology and inadequate education and training on antimicrobial consumption data collection and reporting are some
of the main issues of concern. Results from the evaluation of the consumption trends demonstrate the need to monitor hospital-wide and individual specialty wards/units separately. Limitations of the ATC/DDD system have been identified and taken into consideration when interpreting the results.

**Conclusion:** Variation exists in the methods of collecting and reporting for antimicrobial consumption. The study has shown that setting up of antimicrobial consumption databases expressed in DDD/100 bed-days can be done at a local level. An antimicrobial consumption database should be available in all hospitals to facilitate the close monitoring of antimicrobial consumption, frequent feedback reporting to the prescribers and also to supplement the surveillance of microbial resistance.

<table>
<thead>
<tr>
<th>[O476] Antibiotic prescribing in outpatients: hospital and seasonal variations in Ujjain, Madhya Pradesh, India</th>
</tr>
</thead>
<tbody>
<tr>
<td>A. Pathak*, K. Mahadik, S. Dhaneria, G. Marrone, C. Lundborg on behalf of APRIAM Group</td>
</tr>
</tbody>
</table>

**Objective:** To explore seasonal patterns of antibiotic prescribing for selected infectious disease complaints for children up to 5 years and adults (> 18 years) reporting to out patient clinics of two hospitals in Ujjain. **Methods:** This was cross sectional study; during 15 months period from 15th November 2007 to 15th February 2009. It covered 4 seasons, 2 winters, one summer and one rainy season. First consultations of all patients for suspected infectious aetiology at outpatients of two hospitals (one for profit and other academic) were included. A diagnosis prescribing form was filled by the treating consultant for each patient irrespective of whether an antibiotic was prescribed or not. An average of 70% of available consultants participated. Each prescribed antibiotic was coded according to the WHO Collaborating Centre for Drug Statistics Methodology, ATC classification index with DDD 2009. All DDDs were calculated/1000 patients/diagnosis (DDD/TPD). Sta 10.0 was used for appropriate statistical tests.

Table. Number of patients per diagnosis, prescription rate with commonest prescribed antibiotic groups with Defined Daily Doses/1000 patients/diagnosis (DDD/TPD) per group

<table>
<thead>
<tr>
<th>Diagnosis</th>
<th>Number of patients</th>
<th>Overall prescription rate %</th>
<th>Name and DDDs/TPD of commonest antibiotic group/antibiotic</th>
</tr>
</thead>
<tbody>
<tr>
<td>URTI†</td>
<td>728</td>
<td>38.6</td>
<td>Quinolones 435.8</td>
</tr>
<tr>
<td>Ear discharge</td>
<td>105</td>
<td>96.2</td>
<td>Co-amoxiclav 152.7</td>
</tr>
<tr>
<td>Pneumonia</td>
<td>422</td>
<td>89.4</td>
<td>Quinolones 1889</td>
</tr>
<tr>
<td>Vaginal discharge</td>
<td>1361</td>
<td>72.2</td>
<td>Levofloxacin 1597.8</td>
</tr>
<tr>
<td>Doxycycline</td>
<td>9183</td>
<td>72.2</td>
<td>Metronidazole 11632.5</td>
</tr>
<tr>
<td>URTI†</td>
<td>647</td>
<td>96.1</td>
<td>Quinolones 3647.2</td>
</tr>
<tr>
<td>Diarrhoea</td>
<td>525</td>
<td>73</td>
<td>Metronidazole 2893</td>
</tr>
<tr>
<td>Dysentery</td>
<td>69</td>
<td>53</td>
<td>Imidazole group 713</td>
</tr>
<tr>
<td>SSTIT*</td>
<td>575</td>
<td>92.4</td>
<td>Co-trimoxazole 4032.5</td>
</tr>
</tbody>
</table>

*URTI: Upper respiratory tract infection; †UTI: Urinary tract infection; *SSTI: Skin and soft tissue infections.

**Results:** Out of a total of 5,733 patients antibiotics were prescribed in 3,732 (66.3%). These prescriptions contained 1–3 antibiotics, with a mean of 1.28 antibiotics per prescription. Indications were respiratory tract infections (32.2%), vaginal discharge (26.3%), urinary tract infections (16.3%), skin and soft tissue infections (15%), diarrhoea (9.2%) and prophylaxis (1%). Quinolones were the commonest group prescribed. Antibiotic prescribing was 37% less in academic hospital (P < 0.001). Prescribing peaked in rainy season with 70% of patients prescribed antibiotics. The independent predictors of antibiotic prescribing were seasons (2nd winter > 1st winter), facility (for profit > academic), age groups (adults > children), education level (illiterate > more educated), productive cough at presentation, ear discharge, pneumonia and dysentery. The number of patients per diagnosis, prescription rate with commonest prescribed antibiotic group with DDDs/TPD per group is shown in table.

**Conclusions:** Statistically significant association between antibiotic prescribing and seasons, for profit hospital, age groups, education level, symptom of productive cough at presentation, ear discharge, pneumonia and dysentery was found. High use of quinolones is a cause of concern.

<table>
<thead>
<tr>
<th>[O477] Systemic antifungal therapy in European hospitals. Data from the ESAC point prevalence surveys 2008 and 2009</th>
</tr>
</thead>
<tbody>
<tr>
<td>P. Zarb*, B. Amadeo, A. Muller, V. Vankerkhoeven, P. Dacey, H. Goossens on behalf of the ESAC Hospital Care sub-project group</td>
</tr>
</tbody>
</table>

**Objectives:** To determine the variability of antifungal treatment in European hospitals and to identify targets for quality improvement in antifungal prescribing. **Methods:** The European Surveillance of Antimicrobial Consumption (ESAC) Point Prevalence Survey (ESAC-PPS) was carried out during a period of two weeks in 50 European hospitals in 2008 and in 134 hospitals in 2009. A web-based application was developed for online data entry by the hospitals. Antimycotic prescriptions were recorded using the WHO ATC classification including ‘antimycotics for systemic use’ (J02) and terbinafine (D01BA02). Demographic data on treated patients, indications, and diagnoses were collected. **Results:** From a total of over 85,000 admitted patients, 25,201 (29%) received antifungals. Patients receiving antifungals amounted to 1,309 (3.8% of all antimicrobials) receiving a total of 3,125 therapies (mean 2.4, range 1–7). Dual therapy was used in 487 (37%) patients, and triple therapy in 24% of patients. The most commonly prescribed antifungal was fluconazole, accounting for 60% of all antifungal therapy followed by caspofungin (10%). The most frequently used antifungal-antibacterial combinations included fluconazole plus either a quinolone or a β-lactam, mainly for medical prophylaxis. The proportion of parenteral use within the total antifungal prescriptions was 47%. The oral route accounted for 60% of fluconazole prescriptions. In 38% of cases the site of infection was undefined whilst the most common sites were respiratory (20%), gastro-intestinal (16%) and ENT (4%). The medical specialty accounted for the majority (69%) of antifungal use. Hospital acquired infections represented 46% of all the indications followed by medical prophylaxis at 30%.

**Conclusion:** These ESAC-PPS results showed minimal variation in treatment for fungal infections. This was mainly observed in the predominance of fluconazole. However, high use of fluconazole can increase the prevalence of other fungi, e.g., Candida glabrata, and therefore increase the need for newer antifungals which are active against inherently resistant pathogens. Ongoing surveillance will enhance efforts to limit the extent of antifungal use and resistance. Antifungal prophylaxis in the immunocompromised host needs further exploration.

**ESAC-PPS methodology is the right tool for such analysis.**

<table>
<thead>
<tr>
<th>[O478] European Surveillance of Antimicrobial Consumption: outpatient systemic antiviral use in Europe</th>
</tr>
</thead>
<tbody>
<tr>
<td>N. Adriaenssens*, S. Coenen, A. Muller, V. Vankerkhoeven, H. Goossens on behalf of the ESAC Study Group</td>
</tr>
</tbody>
</table>

**Objectives:** To assess the total outpatient systemic antiviral use in Europe and to identify the antiviral substances most commonly used before the outbreak of the A/H1N1 pandemic as a historical reference. **Methods:** The European Surveillance of Antimicrobial Consumption (ESAC; www.esac.ua.ac.be) project, now funded by the European Centre for Disease Prevention and Control (ECDC; agreement number 2007/001), continues to collect data on antimicrobial consumption for all Member States, candidate countries and European Free Trade Association-European Economic Area countries using the anatomical
Emergence and spread of GES-type-expressing resistance in agents of hospital-acquired respiratory infection.

**Results**: Total outpatient systemic antiviral use in 2007 in 11 European countries varied by a factor of 6.9 between the country with the highest (1.5 DID in the Netherlands) and the country with the lowest (0.2 DID in Finland) use. In most countries substances to treat HIV infection (ATC J05AE, J05AF01–07, J05AF09, J05AG, J05AR, J05AX02, J05AX05 and J05AX07–09) represented more than 50% of the total outpatient systemic antiviral use. In Finland, Denmark, Italy and Luxembourg nucleosides and nucleotides excluding reverse transcriptase inhibitors (ATC J05AB) represented more than 80% of the total outpatient antiviral use. The use of neuraminidase inhibitors (ATC J05AH) was the highest in Austria (0.02 DID) and varied from 3.42% in Denmark to no use reported in Belgium.

**Conclusion**: Our study demonstrates a variation of outpatient systemic antiviral use in Europe as striking as that of outpatient systemic antibiotic, antimycotic and antifungal use. More in-depth data on outpatient systemic viral use from more countries are needed to explain this variation. The ESAC data facilitate auditing of antiviral prescribing and evaluation of the implementation of guidelines and public health policies e.g. those related to A/H1N1.

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**Objective**: Worldwide emergence and spread of multidrug resistant *A. baumannii* (AB) is a matter of concern. We studied the microbiologic, epidemiological and molecular characteristics of GES-like producing AB isolates (GPAB) recovered from 5 different Belgian hospitals. 

**Methods**: Antibiotic susceptibilities were determined by agar disk diffusion, VITEK2, and Etest MIC determination. ESBL, carbapenemase coding genes and their genetic environment were analyzed by PCR-sequencing. OXA-51 and ADC-like coding genes were also characterized and the isolates were typed by PFGE. β-lactamase activities were confirmed by gel diffusion, VITEK2, and Etest MIC determination. ESBL, carbapenemase and carbapenem-resistant reverse transcriptase inhibitors were further analyzed by IEF, abain, and clavulanic acid and corresponding to GES was visualized at pl of about 6.

**Conclusion**: AB harboring blaGES-11 and -12 alleles were detected recently in France and in UK but were not yet reported elsewhere. The blaGES-14 variant is reported here for the first time in a pan-resistant AB isolate. This event further highlights the potential of acquisition of resistance genes by AB and the risk of travel import of multi-resistant bacteria with the possible subsequent inter/intra-hospital spread in acute care hospitals.

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**Results**: MRSA were more prevalent in H48 respiratory *S. aureus* (77/171, 45%) than in H48 blood *S. aureus* (72/231, 31%), but had a similar non-susceptibility profile. Of 796 H48 respiratory Enterobacteriaceae, 37/231, 31%), but had a similar non-susceptibility profile. Of 796 H48 respiratory Enterobacteriaceae, 37/231, 31%), but had a similar non-susceptibility profile. Of 796 H48 respiratory Enterobacteriaceae, 37% were *E. coli*, 28% *Klebsiella*, 20% *Enterobacter* and 14% other genera, compared with estimates of 59%, 18%, 9% and 14% respectively among H48 blood isolates (combined data, BSAC Surveillance Programme). Preliminary results for isolates tested up to October 2009 were compared with those for H48 blood isolates from the similar 2008 BSAC Bacteraemia Resistance Surveillance Programme.

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Antimicrobial resistance among invasive Streptococcus pyogenes isolates in Portugal
A. Fries*, M. Ramirez, J. Melo-Cristino (Lisbon, PT)

Objectives: Although S. pyogenes is universally susceptible to penicillin, in the treatment of complicated Group A Streptococci (GAS) infections such as necrotizing fasciitis or STSS, the association of penicillin with clindamycin has been advocated. Resistance to the latter has been described in GAS, associated with resistance to macrolides. The aim of this work was to evaluate the resistance of GAS invasive isolates to several antimicrobial agents and to further characterize the macrolide resistance isolates.

Methods: A total of 306 invasive GAS isolates recovered in Portugal during 2000–2008 were tested for susceptibility to penicillin, vancomycin, erythromycin, tetracycline, levofloxacin, chloramphenicol, clindamycin, quinupristin-dalfopristin, and linezolid by disk diffusion. Intermediate susceptibilities were confirmed by MIC determination using E-test strips. Resistance genotypes were determined by PCR.

Results: All the 306 GAS isolates were susceptible to penicillin, vancomycin, chloramphenicol, quinupristin-dalfopristin, and linezolid, and only two (0.7%) presented reduced susceptibility to levofloxacin (MIC > 3 and ≤ 4 μg/ml). A total of 32 isolates (10.5%) were resistant to erythromycin. Of these, 20 were also constitutively resistant to clindamycin (cMLSb phenotype, 62.5%), whereas 12 presented the M phenotype (37.5%). The cMLSb phenotype was associated with the presence of the erm(B) gene, whereas the M phenotype was associated with mef(A). Non-susceptibility to tetracycline was found in 42 isolates (13.7%), of which 8 also expressed the cMLSb phenotype and 1 the M phenotype.

Conclusion: Erythromycin resistance among invasive GAS isolates in Portugal did not vary significantly during 2000–2008, contrary to what has been reported for isolates causing pharyngitis, whose macrolide resistance decreased from 1999 to 2006. The macrolide resistance observed in this study for invasive GAS isolates (10.5%) is in line with reports from other countries, as well as with the overall rate reported for pharyngitis isolates in Portugal during 2004–2006 (13.2%).

Effect of ertapenem on susceptibility of imipenem to Pseudomonas aeruginosa six years later
D. Goff*, J. Mangino (Columbus, US)

Objectives: There is continued concern that ertapenem (E) will negatively effect imipenem (I) susceptibility to Pseudomonas aeruginosa (PA). One purpose is to monitor E effect on (I) susceptibility to PA from 2003–2008. Other antipseudomonal on the formulary, piperacillin/tazobactam (P/T), ceftazidime (C), and tobramycin (T), were also examined.

Methods: Antibiotic susceptibilities to I, P/T, C, and T were determined by microdilution MIC using Microscan panels. E was not on Microscan panels until 2007, so Etest was used prior to 2007. Change in I susceptibility was analyzed using Mantel-Haenszel $\chi^2$ test for linear trend. A Poisson model was used to estimate change in carbapenem defined daily doses/1000 patient days (DDD) over time. A rate ratio (RR) was calculated to compare carbapenem usage between 2003 and 2008 with a 95% confidence interval.

Results: P. aeruginosa susceptibility to I, P, T, and C remained the same over 5 years and improved in year 6. An overall $\chi^2$ test (p = 0.010) indicated a difference in percentages over time. The Mantel-Haenszel test for linear trend (p = 0.004) indicated an increasing trend in percentages over time. 91% ESBL K. pneumoniae and 100% ESBL E. coli and K. oxytoca isolates tested to E were susceptible MIC < 2. Total carbapenem use had significantly increased from 2002 (28DDD/1000PD) to 2008 (42DDD/1000PD) RR = 1.08 (95%CI, 1.01–1.15, p = 0.017). E was 13–44% of all carbapenem use; the increase was significant RR = 1.24 (95%CI, 1.06–1.47, p = 0.006).

Conclusion: The use of ertapenem did not negatively effect the susceptibilities of imipenem, P/T, C, or T to PA. P. aeruginosa susceptibility to imipenem, P/T, C and T remained the same or improved over these 6 years.

Growing role of community-acquired MRSA infections in the United States: a 10-year trend of replacement and expansion

Objectives: To describe the role of Community-Acquired (CA) MRSA in inpatient and outpatient staphylococcus aureus infections over a 10 year period in the US.

Methods: The study used the TSN Network surveillance database (Euroftns Mednet) for the period 1998 to 2007. The database contains information on isolate source, setting (ambulatory or hospital), geographic region, and demographic characteristics such as gender and age. Identiﬁed CLSI breakpoints were used for all the time points. CA-MRSA phenotype was deﬁned by a resistance proﬁle that includes the absence of gentamicin/cotrimoxazole resistance, and the absence of ciprofloxacin/ clindamycin/ erythromycin co-resistance. Using multivariate logistic regression, we computed adjusted phenotype prevalences and odds ratios (OR) with 95% conﬁdence intervals (CI).

Results: The study consisted of 824,307 S. aureus isolates. MRSA prevalence continuously increased over the 10 year period from 32.7% in 1998 to 53.8% in 2007 (OR 2.4, 95%CI 2.3–2.5). CA-MRSA represented an increasing proportion of MRSA from 22.3% in 1998 to 53.8% in 2007 (OR 2.4, 95%CI 2.3–2.5). CA-MRSA prevalence were observed for all age-groups, isolate sources, inpatient or outpatient settings, and across all geographic regions of the US. However, a comparatively larger statistically signiﬁcant temporal increase of CA-MRSA occurred in children and young adults as compared to the elderly, and in abscess and wound isolates when compared to blood and sputum. By 2007, 81.5% of all MRSA isolates were categorized as CA-MRSA among children, while CA-MRSA represented 48.9% of MRSA isolates from the elderly. In 2007, out of all MRSA, CA-MRSA represented 85.7% of all abscess, 75.4% of wound, 43.6% of blood and 30.4% of...
Resistance of staphylococci isolated from infected hip arthroplasties in Norway


Objectives: Antibiotic prophylaxis is commonly used during prosthetic surgery both systemically and locally in cement. We have examined bacterial findings from specimens taken during revision due to deep infection reported to the Norwegian Arthroplasty Register (NAR). Susceptibility to aminoglycosides (gentamicin, tobramycin and netilmicin) and β-lactamase-stable penicillins (meticillin, oxacillin and cloxacillin (the meticillin-group) is presented. These antibiotics are the most commonly used in prophylaxis and in treatment of prosthetic joint infections (PJI).

Methods: We collected bacterial findings from operations reported as revisions for infection to NAR. The information was collected from notes from the ten hospitals in Norway that reported most revisions for infection from 1987 to 2007. In this period 730 revisions were reported to NAR from these ten hospitals. The total number of reported revisions was 1443 from all Norwegian hospitals. In this study we included operations with one or more positive sample. The bacteria were tested against different antibiotics at different hospitals and in different time periods. We used the χ² test for linear trend to evaluate changes in distribution of sensitive, intermediate and resistant (S, I, R) bacteria over time. We excluded the first five-year period due to low number of cases compared to the latter three five-year periods (5 vs. 31, 38 and 70, respectively).

Results: The most frequent bacteria isolated were coagulase-negative staphylococci (CoNS) (37%), and S. aureus (SA) (17%). Overall 153 operations with CoNS and 74 with SA were found. Among CoNS 53% of the bacteria were resistant to aminoglycosides. The proportion of resistance increased from 35% in 1993–1997 to 43% in 1998–2002, and to 55% in 2003–2007 (p < 0.1). The overall resistance of CoNS to the meticillin-group (MRSE) was 62%. We found that 45% were MRSE in 1993–1997. The proportion increased to 50% in 1998–2002 and to 76% in 2003–2007 (p = 0.002). All S. aureus were sensitive both to aminoglycosides and to the meticillin-group.

Conclusion: The proportion of MRSE was increasing with time in the present study. There was also a tendency to increased resistance to aminoglycosides among CoNS. No MRSA was found. This study shows that the development of antibiotic resistance is an increasingly important challenge in the management of PJI.

Emergence and spread of resistance

S. Baka*, A. Lykas, A. Panopoulos, I. Pattakis, A. Spatiho, I. Tsouma, S. Demeridou, E. Kouskoumi (Athens, GR)

Objectives: Pseudomonas aeruginosa is considered a “high-risk” pathogen responsible for severe intensive care unit (ICU) – acquired infections. In an era of increasing resistance, nosocomial infections caused by P. aeruginosa are very common despite the application of preventive measures in ICU leading to prolonged hospital stay, increased morbidity, mortality and treatment cost. Very often, in the last years, clinicians are left with very few antimicrobials as therapeutic options. Therefore, we aimed to study the susceptibility profile of P. aeruginosa clinical isolates against an extended panel of antibiotics in the last 2 years.

Methods: Beginning January 2008 to October 2009 all strains of P. aeruginosa isolated from surgical patients in the ICU were studied. In order to identify aerobic microorganisms we inoculated the specimens on blood agar, MacConkey, Manitol Salt and Sabouraud Dextrose agar, and then incubated the plates at 37°C for 24 hours, whereas anaerobic cultures were carried out on Wilkins-Chalgren agar at 37°C for 48 hours. The identification of isolated strains and their susceptibility test to antibiotics using an extended panel of antibiotics were carried out with the automated system VITEK 2 (bioMérieux, Marcy l’Etoile, France).

Results: A total of 52 isolates from 21 patients in 2008 and 49 isolates from 19 patients in 2009 were studied. An increased resistance in all antimicrobials studied (except for colistin), was observed. The most active antimicrobials against P. aeruginosa isolates during 2008 and 2009 were piperacillin with 15% and 32% resistance, respectively, piperacillin/tazobactam 8% and 17%, gentamicin 21% and 50%, amikacin 18% and 43%, tobramycin 18% and 47%, ceftazidime 29% and 46%, and cefepime 26% and 49%, respectively. Thirty-six percent of the isolates were resistant to imipenem in 2008 and 37% in 2009 while for meropenem the resistance was 31% and 40%, respectively, and for tigecycline 36% and 58%, respectively. Finally, colistin was the least resistant among all antimicrobials tested (9% in 2008 and 2% in 2009).

Conclusion: The development of resistance must be carefully monitored in hospitals. Due to an increased use of tigecycline in our ICU, an emerging resistance to this new and promising antimicrobial was observed. Colistin maintained significant in vitro activity against P. aeruginosa isolates and should be considered in critically ill patients with difficult-to-treat infections.

Surveillance of drug resistance of Mycobacterium tuberculosis patterns in clinical sputum samples

C.D. Kalanga*, M. Tembo (Lusaka, ZM)

Introduction: Testing for first line anti tuberculosis drugs formed the back bone of the study based on routine drug susceptibility testing since these drugs are widely used in the world and tested for in rounds of proficiency testing among reference laboratories. Therefore the need to determine the susceptibility and resistance patterns of Mycobacterium tuberculosis in 641 clinical samples for diagnosis and from retreatment samples in the period between 2000 and 2009.

Objective: To determine the drug resistance patterns for Mycobacterium tuberculosis in clinical samples.

Methodology: This was a retrospective descriptive study conducted at chest diseases laboratory. 641 Tuberculosis positive cultures by proportion methods. Data of the drug resistance survey conducted during this period was excluded.

Results: The total number of strains examined was 641, showing drug resistance to one, more drugs in sputum. Total resistant strains 228 (31.7%), Mono resistance to Streptomycin 54 (8.4%), Isoniazid 23 (3.5%), Rifampicin 7 (1.09%), Ethambutol 4 (0.64%). Resistance to two drugs Rifampicin and Isoniazid 41 (6.3%), Streptomycin and Isoniazid 11 (1.7%), Streptomycin and Rifampin 12 (1.8%), Isoniazid and Ethambutol 3 (0.46%), Resistance to three drugs Streptomycin + Isoniazid + Rifampicin 11 (1.7%), Isoniazid + Rifampicin + Ethambutol 3 (0.46%), Streptomycin + Isoniazid + Ethambutol 1 (0.15%) and resistance to all four drugs included 15 (2.3%).

Discussion: The trend seen in the study period shows that proportions of resistance to Rifampicin and Isoniazid was increasing suggestive of secondary drug resistance.

Conclusion: out of 641 positive cultures tested for drug susceptibility, 228 were resistant to one, two, three and four drugs. Multi drug
Four major drug-resistant mycobacterial strains isolated between 2001–2008 in Konya, Turkey

Objectives: In our study, we aimed to detect the presence of M. tuberculosis with the BACTEC MGIT 960 (Mycobacteria Growth Indicator Tubes, Becton-Dickenson) system (2007–2008) in clinical samples containing suspected pulmonary and extrapulmonary tuberculosis and also to determine the resistance of the isolated M. tuberculosis strains against four major antimicrobial drugs. The study period was between 2001 and 2008.

Methods: From 2001 to 2006, antimicrobial susceptibility tests to isoniazid (INH), streptomycin (SM), ethambutol (EMB) and rifampin (RIF) on 635 Mycobacterial strains were performed using the radiometric BACTEC 460TB system. From 2007 to 2008, antimicrobial susceptibility tests on 270 Mycobacterial strains were performed with the BACTEC MGIT 960 SIRE kit.

Results: Of the 1039 M.tbc spp., antibiotic susceptibility tests were performed on 905. We observed that 84.8% (767/905) were susceptible to all 4 antibiotics, 15.2% (138/767) were resistant to at least one of the 4 antibiotics. Mono resistance rates to INH, SM, RIF, and EMB were 4.4, 4.3, 0.6 and 0.4, respectively. Total monodrug resistance was observed in 6.7% of 905 the Mycobacterial isolates. Resistance to two drugs was observed in 48 (5.3%) isolates, to three drugs in 24 (2.7%) isolates and to four drugs in 5 (0.5%) isolates. The prevalence of MDR (Multidrug Resistance) in 905 Mycobacterial isolates was 4% (36/905).

Conclusions: According to these results it could be concluded that, drug resistance which requires immediate solution, continues to be a major problem in our region.

Figure. The annual numbers of culture-positive specimens, the number of susceptibility tested cultures, the number of cultures susceptible to four drugs tested, the number of cultures resistant to at least one drug from 2001 to 2008.

Antimicrobial resistance in Chinese Clostridium difficile strains
H. Huang, A. Weintraub, H. Fang, S. Wu, Y. Zhang, C.E. Nord* (Stockholm, SE, Shanghai, CN)

Objectives: Clostridium difficile infection is the leading cause of nosocomial diarrhea. The emergence and spread of resistance in C. difficile are complicating the treatment and prevention. The purpose of the present study was to investigate the antimicrobial susceptibility patterns and resistance mechanisms of Chinese C. difficile strains.

Methods: 110 toxigenic C. difficile isolates collected between December 2008 and May 2009 at Fudan University Hospital Huashan were analyzed for their antibiotic susceptibility patterns using the agar dilution method. The heteroresistance to metronidazole in fresh isolates were detected by disc diffusion and Etest methods. Resistance molecular basis was investigated using polymerase chain reaction (PCR) and DNA sequencing.

Results: 16 different PCR ribotypes were identified with a dominant clone 017 accounting for 37.3% of the isolates, followed by 001 and H. Ribotype 027 was not found but one isolate belonged to ribotype 078. All the isolates were susceptible to vancomycin and piperacillin/tazobactam. However, 18 of 78 (23.1%) isolates were found to be transient heteroresistant to metronidazole. Resistance to moxifloxacin, ciprofloxacin, levofloxacin, erythromycin, clindamycin, tetracycline, rifampin, rifaximin and fusidic acid was found in 61.8%, 100%, 66.4%, 85.3%, 88.1%, 62.7%, 29.1%, 29.1% and 8.2% of the isolates, respectively. The isolates of common PCR ribotypes were more resistant than the uncommon ribotypes. The prevalence of resistance genes and mutations among the resistant isolates was as follows: ermB, 69.1%; tetM, 97.1%; gyrA mutation, 63.2%; gyrB mutation, 4.4%; gyrA and gyrB mutation, 32.4%; rpoB mutation, 100%, respectively. The fusA mutation was only found in one isolate with minimum inhibitory concentration (MIC) of 4 mg/L.

Conclusions: Many C. difficile isolates now show an alarming pattern of resistance to the antimicrobial agents used in China. Isolates of common PCR ribotypes are more resistant than uncommon ribotypes, especially the dominant strain 017. Most of the resistance mechanisms which have been identified in C. difficile are similar to those in other Gram-positive bacteria.

Molecular architecture and antigenic structure of flaviviruses
F. Heinz*, K. Staissny, H. Holzmann, S. Kiermayr (Vienna, AT)

The genus Flavivirus in the family Flaviviridae comprises about 70 different virus species, many of which are arthropod-borne and transmitted to their vertebrate hosts by mosquitoes or ticks. Among those, the most important human pathogens are yellow fever virus, dengue viruses types 1 to 4, Japanese encephalitis virus, West Nile virus and tick-borne encephalitis virus. Depending on specific and different natural host systems, these viruses differ with respect to their areas of geographical distribution but – at least in some instances – have the potential to emerge as new pathogens in previously non-endemic regions. Flaviviruses are positive-stranded RNA viruses that have a lipid envelope and only three structural proteins, designated C (capsid), M (membrane) and E (envelope). Non-infectious, immature particles – containing a precursor of the M protein (prM) – are formed intracellulary and the proteolytic cleavage of prM by the cellular protease furin generates mature and infectious virions shortly before their release from infected cells.

With respect to their structure, flaviviruses are among the best-studied enveloped viruses. The atomic structures of E proteins of several flaviviruses have been determined using X-ray crystallography, and the architectures of both immature and mature virions are known from cryo-electron microscopic studies. Through the combination of structural and immunological investigations, we have gained a detailed understanding of the effects of antibody-binding to the virus and its different antigens. This includes the definition of virus neutralization and antibody-mediated enhanced (ADE) of infectivity at a molecular level. The latter phenomenon has been proposed to play an important role in the immunopathology of severe forms of dengue virus infections (hemorrhagic dengue fever and dengue shock syndrome) in the course of sequential infections with different dengue serotypes. All of these structural insights have also shed new light on the different degrees of cross-reactivity between flaviviruses, including the existence of cryptic epitopes that are recognized by broadly flavivirus cross-reactive
antibodies without leading to neutralization. The current picture of antibody interactions with flaviviruses will be presented in the context of their biological significance.

**Treatment of invasive aspergillosis: pharmacokinetics vs. resistance**

P. Verweij* (Nijmegen, NL)

The class of the azoles have become the most prominent class of compounds for the management of invasive aspergillosis. The clinically licensed triazoles with activity against *Aspergillus* include itraconazole, voriconazole and posaconazole. The azoles are also the only drugs that can be administered orally. The azoles interact with the biosynthesis of ergosterol, which is an important component of the fungal cell membrane. Intrinsic resistance to azoles has been documented for *A. calidoustus*, but the vast majority of species are susceptible in *vitro*. Recently, *Aspergillus* species with acquired resistance to azoles have been reported, especially in *A. fumigatus*. It appears that resistance may develop during azole therapy, especially in patients with chronic therapy including patients with chronic infection and aspergillosis. Another route of resistance development may be exposure of *Aspergillus* toazole fungicides that are used in our environment. Patients would then inhale azole-resistant conidia and develop azole-resistant aspergillosis. The consequence of this route of transmission is that azole-resistant disease may occur in patients without previous exposure to azole compounds. Azole resistance is commonly due to mutations in the Cyp51A-gene and is associated with different phenotypes. Isolates may be resistant to a single azole compound, but more commonly a cross-resistant phenotype is observed. Several cases of azole-resistant aspergillosis have been reported and commonly these patients failed to respond to azole therapy. Azole-resistant *A. fumigatus* isolates remain virulent and are capable of causing invasive disease in patients at risk. The efficacy of azole compounds against azole-resistant isolates, with different resistance mechanisms, has been investigated in experimental models of invasive aspergillosis. These indicate that the minimal inhibitory concentration has major impact on the efficacy of the azole. Elevated MICs are associated with loss of efficacy of the azole compounds in *vitro*. The use of azoles should be avoided in patients with azole-resistant aspergillosis, if possible. Alternative agents such as lipid-formulations of amphotericin B or caspofungin appear to retain their efficacy against azole-resistant isolates. A significant problem is the early diagnosis of azole-resistance as in the majority of cases an isolate is not obtained and, if an isolate is cultured, in *vitro* susceptibility testing causes delay in treatment with effective agents.

**Living in the ideal CM/ID world**

J. van der Meer* (Nijmegen, NL)

Infectious diseases in our time pose a tremendous challenge to the medical community. We are confronted with emerging infectious diseases, increasing antimicrobial resistance, stagnant development of new antibiotics, poor quality of antimicrobial prescribing, poor compliance with hospital hygiene, a revolution in microbiology, increasing numbers of immuno-compromised and frail patients, and upcoming immunotherapeutic possibilities. To cope with these problems in a successful way, synergy between clinical microbiologists and clinicians with infectious disease expertise is needed more than ever. In my view, the profile of the ideal microbiologist is that of a well-trained physician who received a specialty training which encompasses laboratory skills (microbiology, molecular biology), practical training in clinical infectious diseases, epidemiology and public health, hygiene, research and communication.

**Nocardia infections**

P.R. Hsueh* (Taipei City, TW)

Nocardiosis is an uncommon bacterial infection with a wide variety of clinical manifestations in immunocompetent and immunocompromised patients. The number of cases reported in the literature is increasing. This might be due to an absolute increase in the number of immuno-compromised patients but also to improvement in laboratory techniques to detect nocardiosis. Host resistance to nocardial infection depends on neutrophils in early lesions and then the cell-mediated immunity. The most common predisposing factors to opportunistic nocardia infections are long-term steroid usage, chronic obstructive pulmonary disease, neoplastic disease, and human immunodeficiency virus infection. Clinical manifestations of nocardiosis range from cutaneous infections caused by traumatic inoculation in normal hosts to severe pulmonary and central nervous system diseases in immunocompromised hosts. The genus of *Nocardia* is rapidly expanding
and the species distribution varies with different geographical locations. Previous studies also emphasized the importance of determining the species of *Nocardia*, because different species and isolates vary in their antimicrobial susceptibility patterns. Sulphonamides have been used in the treatment of nocardiosis since the 1940s and are still the drugs of choice and the most common antimicrobials used to treat these infections. Sulphonamide monotherapy, however, was associated with mortality rates of almost 50% for patients with central venous system (CNS) nocardial infections. In addition, patients with non-CNS infections who had overwhelming or disseminated disease had a high mortality rate when treated with sulphonamides alone. However, currently available therapeutic alternatives are scarce and only comprise amoxicillin/clavulanate, carbapenems (imipenem, meropenem, doripenem, and ertapenem) and amikacin. Resistance to previously administered drugs, the toxicity and intolerance of the antimicrobials and even therapeutic failure necessitate the search for alternative agents. Results from in vitro studies suggest that nemonoxacin (TG-873870), a non-fluorinated quinolone, linezolid and tigecycline show promise as alternatives for the treatment of nocardiosis. Further clinical trials are needed to clarify their role in the treatment of these infections.

**Novel influenza A (H1N1)**

- **O501** Efficacy and safety of oseltamivir-zanamivir combination compared to each monotherapy for seasonal influenza: a randomized, double-blinded, placebo-controlled trial


  **Objective:** Evaluation of oseltamivir-zanamivir combination efficacy and tolerance is of interest given the (H1N1) 2009 virus pandemic.

  **Methods:** A randomized, placebo controlled, double blind study was conducted during the 2009 seasonal Influenza epidemic to evaluate oseltamivir-zanamivir combination. Adults with influenza like illness for less than 36 hours and a positive Influenza A rapid test diagnosis were randomized to oseltamivir 75 mg orally twice daily plus zanamivir 10 mg by inhalation twice daily (OZ), oseltamivir plus inhaled placebo (O) or zanamivir plus oral placebo (Z). Virological success was defined by a nasal viral load (RT-PCR) J2 <200 copies genome equivalents (cgeq) / ml. Clinical response was assessed by time to alleviation as symptoms.

  **Results:** Overall 541 patients were included (OZ, n = 173; O, n = 192; Z, n = 176). In the intention-to-treat analysis conducted in the 447 patients with confirmed Influenza A, the virological response was 46%, 59%, and 34% in OZ, O and Z arms (p = 0.025, p = 0.028 for OZ/O and OZ/Z comparisons). Mean viral load decrease D0-D2 was 2.14, 2.49, and 1.68 log10 cgeq /mL (p = 0.060, p = 0.016 for OZ/O and OZ/Z comparisons). The time of disappearance of symptoms were 4, 3, 4 days (p = 0.030, p = 0.77 for OZ/O and OZ / Z) The combination was well tolerated.

  **Conclusions:** Monotherapy of oseltamivir remains the first line antiviral strategy for the ongoing Influenza pandemic. The lesser effect of the oseltamivir-zanamivir combination should be further investigated.

- **O502** Effectiveness and safety of neuraminidase inhibitors in reducing influenza complications: a meta-analysis of randomized controlled trials

  M. Falagas, P. Koltesi, E. Vouloumanou, P Rafaillid*\*, A. Kapaniklis, J. Rello (Athens, GR; Tarragona, ES)

  **Objective:** Several studies provide evidence that neuraminidase inhibitors can reduce the duration of influenza symptoms. Yet, data regarding their effectiveness in reducing influenza complications are scarce.

  **Methods:** We evaluated the effectiveness of neuraminidase inhibitors in reducing influenza complications and mortality of patients with seasonal influenza, by performing a meta-analysis of randomized controlled trials (RCTs) retrieved from PubMed, Cochrane and Scopus databases, comparing neuraminidase inhibitors with placebo.

  **Results:** Eleven RCTs (10 double-blinded, 1 with an open-label design) were included; 8 involved adults and adolescents. In total, 5315 patients were included; 3491 (65.7%) with confirmed infection. Total influenza-related complications occurred significantly less likely in otherwise healthy patients with confirmed infection treated with antivirals versus placebo [7 RCTs, 2621 patients, OR (odds ratio)=0.71, 95% confidence interval (CI)=0.58–0.87]. This finding was more pronounced in high-risk patients (4 RCTs, 475 patients, OR = 0.26, 95% CI=0.15–0.47), compared with otherwise healthy patients (p < 0.01). In the comparisons regarding other respiratory complications, a trend in favour of antivirals was observed. Regarding acute otitis media specifically, a significant difference was observed. Significantly fewer antibiotics were also administered in patients with confirmed infection treated with antivirals versus placebo (6 RCTs, 1921 patients, OR = 0.77, 95% CI=0.62–0.96). No differences were found in the comparisons regarding the safety outcomes of our meta-analysis. Mortality data were scarcely reported. No deaths were reported in the respective trials.

  **Conclusions:** Neuraminidase inhibitors appear to be effective in reducing total influenza-related complications both in otherwise healthy with confirmed infection and high-risk patients. They also reduce additional antibiotic consumption.

- **O503** Clinical characteristics of influenza A H1N1–2009 outbreak at a public university hospital in the north-eastern region of Rio Grande do Sul, Brazil


  **Objectives:** In July 2009, a respiratory illness outbreak caused by influenza A virus (H1N1–2009) was identified in Caxias do Sul, Brazil. The aim of this work is to describe the clinical and epidemiologic characteristics of hospitalized patients at a public university hospital for viral pneumonia who had laboratory confirmed H1N1–2009 infection.

  **Methods:** Retrospective medical chart reviews on the hospitalized patients between July and August 2009. H1N1–2009 infection was confirmed in specimens with the use of a real-time reverse-transcriptase–polymerase-chain-reaction assay.

  **Results:** From July 1 through August 30, 2009, a total of 40 cases of confirmed H1N1–2009 pneumonia were identified among 124 patients hospitalized for acute respiratory illness at the Caxias do Sul General Hospital. More than half of the 40 patients were between 20 and 49 years of age, and only 10 had preexisting medical conditions. All patients had fever, cough, dyspnea or respiratory distress, increased serum lactate dehydrogenase levels and lymphopenia. Thirty-seven patients required mechanical ventilation, and five died.

  **Conclusions:** In 2009, our region had the coldest winter season in many years. Influenza infections are common cause of respiratory diseases in our city, but on this year there was an increase of visits to doctors for influenza-like illness and also flu-related hospitalizations. Comparisons with seasonal influenza suggest that pandemic influenza A (H1N1– 2009) disproportionately affects younger ages and causes generally mild disease, but during the outbreak we noticed that H1N1–2009 infection had caused severe pneumonia and death in many previously young to middle-aged healthy persons.

- **O504** Hospitalized cancer patients with severe infections due to the novel influenza A (H1N1) in Brazil

  E. Velasco*, J. Salhuh, V.M. Gonçalves, V. Oliveira, T. Moreno, S. Rocco (Rio de Janeiro, BR)

  **Background:** The novel influenza A (H1N1) pandemia exposes immunocompromised cancer patients under chemotherapy to an increased risk of mortality.

  **Objective:** To describe clinical characteristics, treatment, and outcome of cancer patients with 2009 Influenza A (H1N1) infection.
**Methods:** A descriptive study of hospitalized cancer patients at an Oncology Cancer Center in Brazil between July 8 and September 1, 2009 who were tested positive for the 2009 H1N1 virus with the use of a RT-PCR assay and/or a direct fluorescence antibody staining.

**Results:** As of 1 September, 24 cases were tested positive for influenza virus infection. Median age was 14.5 years (2–69 years). Underlying cancer diagnoses were: acute leukemia, 7 (29%); solid tumors, 6 (25%); lymphoma, 6 (25%); multiple myeloma, 3 (12%) and chronic leukemia, 2 (8%). All patients had fever and acute respiratory symptoms. Previous chemotherapy (79%), neutropenia (50%) and history of steroids therapy (37%) were commonly present. No patients had laboratory-documented bacterial infections at the illness onset, however all received antibacterial agents at presentation. Seventeen patients developed bilateral pulmonary infiltrates and severe hypoxemia was present in 15 cases (88.2%). Of these, 11 underwent mechanical ventilation. Twenty-two patients were treated with oseltamivir and, in 37.5% of them a double dose was prescribed. Median time from fever to antiviral therapy start was 5 days (range: 0–20 days). Antiviral therapy was started within 48 h of symptoms in only 10 patients (22%). Main reasons for therapy delay were the lack of specificity symptoms in neutropenic patients and the initial difficulty to obtain antiviral drugs. Five patients died (21%), and two of them never received oseltamivir. In the other 3 cases, the therapy was only started 8, 9 and 15 days after hospital admission.

**Conclusions:** This study presents a series of cancer patients with H1N1 virus infection with an elevated mortality. We observed a high number of cases in young patients. Considering the clinical data, a nosocomial transmission cannot be ruled out. Our data shows a possible association of mortality with a lack or a delay of antiviral therapy initiation. A faster availability of antiviral medication for therapy and prophylaxis and vaccination programs should be reinforced among cancer patients, close contacts and healthcare workers.

**Epidemiology of severe paediatric patients with novel influenza A (H1N1) in Korea**


**Objectives:** Since the first outbreak of novel influenza A (H1N1) in May 2009, the virus has been spread throughout local communities. More than 4,000 diagnosed cases are being reported daily as of November 2009. One of the major infection routes is the educational institutions, so children and teenagers have very high risk of viral exposure. Recently, mass outbreaks were reported from 870 schools within one week. Korea Centers for Disease Control and Prevention (KCDC) is operating nationwide monitoring system for severe hospitalization cases. The objective of this study is to highlight demographics, infection risk factors and clinical courses.

**Methods:** Novel influenza A (H1N1) patients who were hospitalized in intensive care unit or had pneumonia in needs of intubation were categorized as severe pediatric patients. Between June and October, total of 22 cases under the age of 18 were identified as severe patients. After the medical chart review, we had an interview with the doctor in charge. All the patients were laboratory-confirmed novel influenza A (H1N1) virus infection by means of real-time polymerase chain reaction. Based on the Advisory Committee on Immunization Practices, the patients with high-risk medical conditions were defined as having higher risk for influenza complications.

**Result:** Among the reported 22 severe cases, 15 were male and 7 were female. Ages ranged from 2 months to 18 years old (median 7, standard deviation 5.4). Fourteen patients (63%) had high-risk medical conditions such as 1) age less than 59 months (6 cases), 2) chronic respiratory disease (3 asthma cases), 3) neuro-developmental disorder (3 cases), 4) congenital heart disease (1 case) and 5) leukemia (1 case). Total of 7 patients have expired. Patients took anti-viral agent (Tamiflu®) average 2 days after onset. Thirteen patients received ventilator care, 7 did not and 2 were unsure. Viral pneumonia was the most common complication (17 cases, 77%) and 3 patients exacerbated into acute respiratory distress syndrome. Initial symptoms were fever and cough (18 cases, 81%) each.

There were 11 leukocytosis, 3 leucopenia and 3 thrombocytopenia cases on complete blood count.

**Conclusions:** Half of patients with high-risk medical conditions have expired. Considering current situations, we need to maintain high-risk medical conditions category and to have continuous tracking for severe pediatric patients with novel influenza A (H1N1).

**Table 1. Characteristics or status of Korean pediatric patients with influenza A(H1N1), June–October 2009**

<table>
<thead>
<tr>
<th>Characteristics/Status</th>
<th>No. of patients (N = 22)</th>
<th>Percentage (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Age group</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>0–23 months</td>
<td>1</td>
<td>4.5</td>
</tr>
<tr>
<td>24–59 months</td>
<td>5</td>
<td>22.7</td>
</tr>
<tr>
<td>5–18 years</td>
<td>16</td>
<td>72.7</td>
</tr>
<tr>
<td><strong>Sex</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Male</td>
<td>15</td>
<td>68.1</td>
</tr>
<tr>
<td>Female</td>
<td>7</td>
<td>31.9</td>
</tr>
<tr>
<td><strong>High-risk medical conditions</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ages under 59 months</td>
<td>6</td>
<td>27.2</td>
</tr>
<tr>
<td>Neurodevelopmental condition</td>
<td>3</td>
<td>13.6</td>
</tr>
<tr>
<td>Chronic pulmonary condition</td>
<td>3</td>
<td>13.6</td>
</tr>
<tr>
<td>Congenital heart disease</td>
<td>1</td>
<td>4.5</td>
</tr>
<tr>
<td>Immunosuppression</td>
<td>1</td>
<td>4.5</td>
</tr>
<tr>
<td><strong>Antiviral treatment (Tamiflu®)</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Unsure</td>
<td>2</td>
<td>9.0</td>
</tr>
<tr>
<td>≤2 days after illness onset</td>
<td>15</td>
<td>68.1</td>
</tr>
<tr>
<td>&gt;2 days after illness onset</td>
<td>5</td>
<td>22.7</td>
</tr>
</tbody>
</table>

**Nosocomial pneumonia**

**OS056 Ventilator-associated pneumonia rates in 12 intensive care units between 1995 and 2006, Lyon, France**

P.B. Sow*, D. Latringer-Maguin, T. Benet, D. Barutin, P. Vanhems (Lyon, FR)

**Objective:** The aim of this study was to describe trends of ventilator acquired pneumonia (VAP) incidence in 12 intensive care units (ICU) by taking into account of individual major risk factors of VAP.

**Methods:** A prospective surveillance in 12 ICUs participating in the national nosocomial infection surveillance network in South-East France between 1995 and 2006 was done. The VAP was defined base on clinical, radiological and bacteriological findings, according to the national protocol. Yearly incidences of VAP were described. The risk of VAP by time was modelled using a Cox proportional hazard model with the year of admission in ICU as the main exposure. The tested covariates were age, gender, and SAPSII.

**Table 1. Characteristics, incidences and risks of ventilator associated pneumonia in 12 intensive care units included in a surveillance program network, 1995–2006, Lyon, France**

<table>
<thead>
<tr>
<th>Year of admission</th>
<th>No. of patients</th>
<th>No. of VAPs*</th>
<th>VAP incidence per 1000 patient-days</th>
</tr>
</thead>
<tbody>
<tr>
<td>1995</td>
<td>366</td>
<td>48</td>
<td>13.0</td>
</tr>
<tr>
<td>1996</td>
<td>557</td>
<td>52</td>
<td>9.6</td>
</tr>
<tr>
<td>1997</td>
<td>524</td>
<td>34</td>
<td>7.2</td>
</tr>
<tr>
<td>1998</td>
<td>706</td>
<td>75</td>
<td>10.6</td>
</tr>
<tr>
<td>1999</td>
<td>1,678</td>
<td>198</td>
<td>11.8</td>
</tr>
<tr>
<td>2000</td>
<td>1,135</td>
<td>166</td>
<td>14.6</td>
</tr>
<tr>
<td>2001</td>
<td>1,191</td>
<td>182</td>
<td>15.2</td>
</tr>
<tr>
<td>2002</td>
<td>1,669</td>
<td>277</td>
<td>16.4</td>
</tr>
<tr>
<td>2003</td>
<td>1,552</td>
<td>239</td>
<td>15.4</td>
</tr>
<tr>
<td>2004</td>
<td>1,451</td>
<td>249</td>
<td>17.0</td>
</tr>
<tr>
<td>2005</td>
<td>1,539</td>
<td>259</td>
<td>16.7</td>
</tr>
<tr>
<td>2006</td>
<td>1,622</td>
<td>1936</td>
<td>11.9</td>
</tr>
</tbody>
</table>

**Mean age** (years), SD: 57 (16) |

**Mean SAPSII** (20) |

**P values** (18) |

**Adjusted HR** (19) |

**Notes** |

**VAP incidence** (41) |

**SAPSII** (42) |

**NOSOSAP** (43) |

**SOP** (44) |

**SD** (45) |

**CI** (46) |

**P** (47)
SAPSII (P < 0.001), significant by the Pearson khi square test. After multivariate analysis, VAP risk per year decreased between years 1996 to 1998, increased continuously until 2001 and stabilized between 2002 and 2006, compared to 1995 (global Hazard Ratio=0.96; 95% CI [0.81–1.14]).

Conclusion: Despite of an increase of risk factors as age and SAPSII scores of ICU patients by time, we observed that the adjusted VAP risk between 2002 and 2006 were stable. These results should be a consequence of the implementation of specific prevention measures related to ICUs practitioners.

**O507** Attributable mortality of ventilator-associated pneumonia: a meta-analysis

M. Agrafiotis, I. Siempos, T. Ntaidou, M. Falagas* (Athens, GR)

Objective: To investigate whether ventilator-associated pneumonia (VAP) is a true cause of mortality in the intensive care unit (ICU) setting.

Methods: We performed a meta-analysis of available data obtained through search of PubMed and relevant bibliographies without time restrictions. A conservative DerSimonian-Laird random effects model was employed to calculate pooled odds ratios (OR) and 95% confidence intervals (CIs).

Results: Out of 968 retrieved reports, 44 papers fulfilled our inclusion criteria. Presence, as opposed to absence, of VAP was associated with higher mortality in the ICU setting (OR: 1.96, 95% CI: [1.26, 3.04]). This result persisted when matched case control studies (OR 1.73, 95% CI: [1.23, 2.45]) or studies in which VAP was microbiologically confirmed in all patients (OR: 2.20, 95% CI: [1.01, 4.81]) were evaluated separately. VAP was still associated with higher mortality when the impact of immunosuppression was controlled (OR: 1.74, 95% CI: [0.95, 3.16]); a finding that did not reach statistical significance. Though, presence of VAP was not associated with higher mortality in the subgroup analysis of studies including patients who received appropriate initial antimicrobial treatment (OR 1.64 [0.68, 3.96]).

Conclusion: Presence, compared to absence, of VAP seems to be associated with higher mortality in critically ill patients. Appropriateness of initial antimicrobial treatment in such patients may moderate this association.

**O508** Impact of antiseptic based oral care on rates of ventilator-associated pneumonia in intensive care unit patients: a meta-analysis

K. Van de Vyver, S. Labeau, N. Brusselaers, D. Vogelaers, S. Blox* (Ghent, BE)

Objective: Ventilator-associated pneumonia (VAP) is the most frequent nosocomial infection in the intensive care unit. Reducing inoccult of oral pathogenic microorganisms by adequate oral care could prevent VAP.

Methods: A systematic review of the literature concerning oral decontamination with chlorhexidine or povidone-iodine vs. oral care without use of an antisepticum resulted in a significant reduction of the incidence of oral care with use of chlorhexidine (n patients = 1862) and 2 that assessed the effect of oral care with use of povidone-iodine (n patients = 109). The use of an antisepticum resulted in a significant reduction of the incidence of VAP with a RR of 0.63 (95%CI 0.50–0.81; p=0.0002). These results are valid for chlorhexidine (RR 0.68; 95% CI 0.53–0.88; p=0.004) and povidone-iodine (RR 0.38; 95% CI 0.19−0.75; p=0.005). Among studies important differences exists concerning concentrations of the antiseptic used, frequency of oral care, and study methodology and diagnostic criteria for VAP. Clinical heterogeneity was confirmed statistically and was moderate ($\chi^2=43$; p = 0.08) for the trials using chlorhexidine and high ($\chi^2=66$; p=0.09) for those assessing povidone-iodine. Subgroup analyses revealed most beneficial effects with concentrations of 0.12% and 2% chlorhexidine and 10% povidone-iodine, and in a population of cardiac surgery patients.

Conclusions: This analysis shows that oral decontamination with an antiseptic reduces the incidence of VAP significantly. Both chlorhexidine and povidone-iodine show this effect. However, further research is needed to make recommendations about the concentration and frequency of application.

**O509** Efficacy of panobacumab, an IgM monoclonal antibody, in hospital-acquired pneumonia caused by Pseudomonas aeruginosa


Objectives: Despite adequate antibiotic therapy Hospital Acquired Pneumonia (HAP) and Ventilator Associated Pneumonia (VAP) caused by P aeruginosa are of the most common and deadliest nosocomial infections. Panobacumab, a fully human IgM/kappa monoclonal antibody targeting P aeruginosa serotype O11, was evaluated as a new therapeutic modality for treatment of VAP/HAP.

Methods: Patients with HAP caused by P aeruginosa O11 were enrolled in a Phase IIa open trial to be treated with Panobacumab 1.2 mg/kg (days 1, 4, 7) in addition to standard antibiotic therapy.

Results: 17 patients, (23–83 years) with VAP (n = 14) or HAP (n = 3) were treated with Panobacumab. Thirteen patients (completers) received 3 infusions and 4 patients (non-completers) received 1 infusion. The study drug was safe and well tolerated. Panobacumab revealed a pharmacokinetic profile similar to a native IgM. Panobacumab could be detected in BAL samples collected after treatment indicating the antibody to reach the inflamed lung tissue. Clinically the initial mean CPIS and APACHE II score were 8.53 (7–11) and 18.2 (6–33) with an expected mortality of 29.6%. The overall observed mortality within 30 days after starting treatment was 17.6%. Despite an APACHE II score of 18.5 and expected mortality of 30.6% all complers survived within the first 30 days while non-completers showed a survival rate of 25%. Resolution of pneumonia was achieved by 9 out of 13 completers in 9.9±4.3 days (mean±SD) including two patients who were initially inadequately treated. An early administration of the antibody seems to correlate positively with the resolution of pneumonia. The mean Cmax after the third dose of Panobacumab was higher in patients with resolution than in those with continuation of pneumonia (34.8 versus 28.5 mg/L) as well as in those with eradication of P aeruginosa versus those with continuation (37.3 versus 27.7 mg/L).

Conclusions: A survival of 100% was observed in patients that completed the full treatment cycle with 3 doses of Panobacumab indicating efficacy of the antibody treatment. Early administration of Panobacumab and high Cmax levels seem to correlate positively with the resolution of pneumonia and eradication of P aeruginosa. The current data is promising and warrant further trials with Panobacumab.

**O510** Tigecycline in the treatment of multidrug-resistant Acinetobacter baumannii pneumonia

M.S. Tasbakan, H. Paliuluku, O. Sipahi*, M. Tasbakan, S. Aydemir, F. Bacakoglu (Izmir, TR)

Objectives: Nosocomial infections by multidrug-resistant (MDR) A. baumannii are important causes of mortality in intensive care units
**Daptomycin – clinical experience**

**[S113]**

**Daptomycin for the treatment of infective endocarditis:** High-dose daptomycin for infective endocarditis

**Microbiologic eradication rate did not result in good clinical results in toxicity.**

- Daptomycin

**EvaluatetheefficacyoftigecyclineinMDR A.baumannii (ICU).Thetreatmentchoicesarelimited.Theaimofthisstudywasto**

- vs 58.9 respectively.

**Results:** There were a total of 34 cases (18 male, mean age 66.79±14.34 years) fulfilling our inclusion criteria. On the admission 17 cases were diagnosed as community-acquired pneumonia and 12 were diagnosed as chronic obstructive lung disease. 27 cases (79.4%) had comorbidities and the most common comorbidity was atherosclerotic heart disease (8 cases) followed by diabetes mellitus (5 cases), cerebrovascular disease (5 cases), respectively. When A. baumannii was isolated from respiratory samples 19 patients were considered as ventilator-associated pneumonia and 15 were considered as hospital-acquired pneumonia.

All isolates were sensitive to tigecycline, whereas all were resistant to piperacillin/tazobactam and ceftazidime. 74%, 56%, 41% and 24% were resistant to imipenem, cefepime/azatulbactam, amikacin and netilmicin, respectively. Then, the use of a mean duration of 9.6±5.2 days. Microbiologic eradication (on day 3 and 7) was observed in 21 cases (61.8%). Tigecycline was combined with cefepime/azatulbactam in 12 cases, with netilmicin in 6 cases and with amikacin in 3 cases. Nine of 21 cases with microbiologic eradication were lost whereas mortality was 100% in the other 13 cases (p=0.0006). Mortality and microbiologic eradication rates were not different in combination vs monotherapy (p > 0.05). Mortal cases were older than the survivors (71.1±12.6 vs 58.9±15.9, p = 0.02). Toxicity developed only in one case as liver toxicity.

**Conclusion:** Our findings show that microbiologic eradication rate of tigecycline in MDR A. baumannii is not very low. However this microbiologic eradication rate did not result in good clinical results in terms of mortality probably due to comorbidities.

**Daptomycin – clinical experience**

**[O511]** Daptomycin for the treatment of infective endocarditis: results from European Cubicin® Outcomes Registry and Experience (EU-CORE)

P. Dohmen *, A. Guleri, N. Petrosiello, R. Utthi, V. Gonzalez Sanz, R.A. Seaton, V.J. Gonzalez-Ramallo, R. Hetzer, M. Heep, H.J. Thurston, R.L. Chaces (Berlin, DE; Lancaster, UK; Rome, Naples, IT; Zaragoza, ES; Glasgow, UK; Madrid, ES; Basel, CH)

**Objective:** Randomized controlled trials are scarce in endocarditis and excluded dialysis, were retrospectively reviewed at 4 academic medical centres. This subset analysis included all patients with IE defined by modified Duke criteria. Charts were reviewed for demographics, comorbidities, antimicrobial therapy, microbiological cultures, clinical outcomes, and adverse events.

**Methods:** Consecutive patients treated with HD DAP for ≥72h, including dialysis were retrospectively reviewed at 4 academic medical centres. This subset analysis included all patients with IE defined by modified Duke criteria. Charts were reviewed for demographics, comorbidities, antimicrobial therapy, microbiological cultures, clinical outcomes, and adverse events.

**Table 1.**

<table>
<thead>
<tr>
<th>Primary Organism</th>
<th>Right-sided endocarditis (RIE)</th>
<th>Left-sided endocarditis (LIE)</th>
</tr>
</thead>
<tbody>
<tr>
<td>MRSA (n=31)</td>
<td>6 (19.4%)</td>
<td>9 (29.0%)</td>
</tr>
<tr>
<td>VRE (n=5)</td>
<td>1 (20.0%)</td>
<td>1 (20.0%)</td>
</tr>
<tr>
<td>No organism isolated</td>
<td>20 (64.5%)</td>
<td>16 (51.6%)</td>
</tr>
</tbody>
</table>

**Clinical and Microbiological Outcomes**

Duration of bacteraemia (days)

| MRSA (n=31) | 6 (1–30) | 12 (6–18) |
| VRE (n=5)   | 3 (1–3)  | 12 (1–12) |

Duration of fever (days)

| MRSA (n=31) | 4.5 (1–21) | 8 (6–16) |
| VRE (n=5)   | 10 (1–44)  | 12 (6–79) |

Duration of leukocytosis (days)

| MRSA (n=31) | 8.5 (3–13) |
| VRE (n=5)   | 12 (1–79)  |

Duration of HD DAP (days)

| MRSA (n=31) | 8 (3–27) |
| VRE (n=5)   | 12.5 (4–48) |

Length of stay (days)

| MRSA (n=31) | 15 (6–47) |
| VRE (n=5)   | 25 (10–91) |

Median dose of HD DAP (mg/kg/day)

| MRSA (n=31) | 9.7 (0.0–14) |
| VRE (n=5)   | 9.8 (0.0–12) |

**Clinical outcome**

| MRSA (n=31) | 1 (0.0%) |
| VRE (n=5)   | 3 (75.0%) |

**Medical failure**

| MRSA (n=31) | 1 (3.2%) |
| VRE (n=5)   | 1 (20.0%) |

**Organism persisted**

| MRSA (n=31) | 1 (0.0%) |
| VRE (n=5)   | 1 (20.0%) |

**Safety**

| EOT APK <150IU/L | 20 (87.0%) |

**Results:** 45 patients were identified. Baseline characteristics: Median age 53 years (range 24–93), APACHE II 7 (0–28). 57.8% hospitalization ≤1 year. 22.2% MRSA infection ≤1 year. 32.8% injection drug use, 28.9% diabetes, 22.6% renal disease. 23 (51.1%) patients had right-sided IE (R1E), 20 (44.4%) patients had left-sided IE (LIE), and 2 (4.4%) patients had both RIE and LIE. Characteristics and outcomes of patients with RIE or LIE are presented in Table 1. The median days of bacteraemia, as determined from clinical cultures, for MRSA RIE and LIE were 6 days (1–30) and 12 days (6–18), respectively. Overall clinical cure and microbiological eradication was 76.1% and 86.4%, respectively. The median dose of HD DAP for RIE vs. LIE were 9.7 mg/kg/day (8.0–11.4) vs. 9.9 mg/kg/day (8.0–12.1), respectively. Safety: 87% patients had concomitant antibiotic therapy, most commonly aminoglycosides (71, 26%) or carbapenems (46, 17%). The majority of pts received DAP doses of 6 mg/kg (62%) or higher (21%). The clinical outcome per IE type were:

- **Right sided endocarditis,** success 92%, failure 5%, non-evaluable (NE) 3%.
- **Left sided endocarditis,** success 76%, failure 9%, NE 14%.
- **Right plus left sided endocarditis,** success 89%, NE 11%.

The proportion of pts with low Creatinine clearance (<30 mL/min) improved from 17% (46/276) initially to 13% (35/276) at the end of DAP treatment. Serious AEs were reported in 34 (12%) pts and 20 (7%) pts discontinued the study drug due to AEs.

**Conclusions:** Daptomycin appears effective and well tolerated against a variety of clinical presentations of infective endocarditis. Success rates and adverse event profile, including renal safety were comparable to those observed in the pivotal trials. Further clinical studies on infective endocarditis e.g. on the impact of DAP at higher doses might be warranted.

**[O512]** High-dose daptomycin for infective endocarditis

R. Kullar *, S. Dacus, C. Crank, J. Segreti, S. Cosgrove, J. Zhao, D. Levine, M. Rybak (Detroit, Chicago, Baltimore, US)

**Objective:** Infective endocarditis (IE) is a serious infection associated with high morbidity and mortality. IE due to methicillin-resistant Staphylococcus aureus (MRSA) and enterococci including vancomycin-resistant strains (VRE) has been associated with high failure rates. Daptomycin (DAP) has activity against both MRSA and VRE strains. We evaluated the safety and efficacy of high-dose (HD) DAP (≥8 mg/kg/day) for MRSA and VRE IE.

**Methods:** Consecutive patients treated with HD DAP for ≥72h, including dialysis were retrospectively reviewed at 4 academic medical centres. This subset analysis included all patients with IE defined by modified Duke criteria. Charts were reviewed for demographics, comorbidities, antimicrobial therapy, microbiological cultures, clinical outcomes, and adverse events.
end-of-therapy (EOT) creatinine phosphokinase (CPK) levels <150 IU/L (15–452). No patients were discontinued from therapy due to myopathy or any other adverse events.

Conclusion: Efficacy and safety of HD DAP were favourable in a cohort of pts with IE. Further studies with a larger cohort are warranted.

**OS13** Evaluation of safety and tolerability of daptomycin in the treatment of osteomyelitis: results from a European Registry

R.A. Seaton¹, P. Gargalianos-Kakolyris, K. Malizos, F. Romero-Candau, A. Carretta, J. Hernández-Quero, M. Militz, S. Reus Bañuls, G. Riccio, M. Heep, H. Thorton, K. L. Chaves (Glasgow, UK; Athens, Larissa, GR; Seville, ES; Bari, IT; Granada, ES; Marnau, DE; Alicante, ES; Pietra Ligure, IT; Basel, CH)

Objectives: Osteomyelitis (OM) is a complicated and diverse disease and long term efficacy and safety of an antibiotic is an important determinant in selecting the optimal therapy. This is the first report of a large series of OM cases treated with daptomycin (DAP) across many countries in Europe.

Methods: Data were collected as part of the European CUBICIN² Outcomes Registry and Experience (EU-CORE) program, a retrospective, non-interventional, observational, multicenter study designed to describe the clinical use of DAP. All patients (pts) who had a diagnosis of OM were selected from the database. Pts who were treated with at least one dose of DAP and for whom any safety parameter was assessed were included in safety population. Efficacy population was a subset of the safety population where clinical outcome (cure, improved, failure, or non-evaluable) was assessed by the investigators. Pts enrolled from Jan 2006 to Aug 2009 were included.

Results: Of 2581 pts enrolled 161 (55.4%) male, 42% ≥65 years were diagnosed with OM. 90 (56%) cases of OM were non-prosthetic device related, 50 (31%) were permanent prosthetic device related, 21 (13%) were temporary prosthetic device related. For 103 pts (64%) primary pathogens have been reported. S. aureus (45/103) was the most frequent species, with MRSA (n = 19) as significant subset. Coagulase-negative Staphylococci (41/103) ranked second. Most pts received DAP doses ≥6 mg/kg (76%). Median duration of DAP outpt therapy was 29 days (range: 4–82), and inpt therapy was 14 (range: 1–246). Overall clinical success (cured or improved) was seen in 73% (118/161) of pts and failure in 9% (14/161). 18% of pts were non-evaluable (29/161). In subgroup analyses, clinical success was observed in 72% (65/90) of pts without devices, 72% (36/50) of pts with permanent devices and 81% (17/21) of pts with temporary prosthetic devices. Serum creatine phosphokinase (CPK) values were reported in 68% (109/161) of pts during DAP therapy. In 86% of pts (94/109) CPK levels remained within normal range. Discontinuation of DAP due to treatment failure was reported for 2 pts (1%) only. Serious AEs were reported in 3% (5/161) of pts. AEs leading to study drug discontinuation were reported in 5% (8/161).

Conclusion: DAP at doses ≥6 mg/kg once daily was the most frequent dose regimen used for osteomyelitis in Europe. DAP was well-tolerated also for longer treatment duration. These promising results warrant confirmation in additional studies.

**OS14** Daptomycin versus vancomycin for methicillin-resistant Staphylococcus aureus bacteraemia with reduced in vitro susceptibility to vancomycin

P. Osaki Kiyun, C. Moore, N. Perri, N. Haque, S. Donabedian, M. Zerres * (Detroit, US)

Background: Poor outcomes in MRSA bacteraemia have been associated with reduced in vitro susceptibility to vancomycin, yet still within the susceptible range. Data for alternative management in these cases is lacking, particularly with daptomycin (DAP).

Methods: We conducted a case-control study evaluating treatment with VAN or DAP for MRSA-B with a VAN MIC of 1.5 or 2 μg/mL. Patients were matched 2:1 by level of risk source, APACHE-II score at onset of infection and age. Respiratory infections were excluded. Failure was a composite of: 30-day mortality, microbiologic failure (positive cultures >10⁴ from index culture) and/or recurrence of MRSA-B within 30 days of end of tx.

Results: DAP treated patients (n = 37) were compared to VAN treated patients (n = 74). VAN MIC was 1.5 (46 v 85%) and 2.0 (54 v 15%), p <0.01. Source of infection was similar between groups including endocarditis (27 v 24%), skin (38 v 32%), catheter (19 v 19%), device (8 v 11%) and other (8 v 14%). Age, comorbidities, APACHE II score (14 v 14) and requirement of ICU admission (24 v 21%) was similar between groups, p >0.05. Immunosuppression (24 v 7%) was more common in the DAP group, p <0.05. Factors significantly associated with failure: ICU at onset of infection, nursing home residence, CV disease, ARF, and Vancomycin MIC of >2 were greater in the DAP group. In subgroup analyses, between groups, baseline comorbidities, risk level of source and APACHE-II scores were similar, although immunosuppression and isolates with VAN MIC=2 were greater in the DAP group. This study shows that DAP may be associated with better outcome of infection as compared to VAN, and trended toward lower 30-day mortality, particularly in subjects with MRSA endocarditis.

**OS15** Daptomycin against highly resistant Enterococcus faecium invasive infections


Objective: Treatment recommendations for invasive enterococcal infections advocate synergistic combinations such as ampicillin plus gentamicin. In case of resistance to one or even both of the drugs, vancomycin therapy is proposed, albeit it is poorly bactericidal. The Swiss surveillance program reports resistance of Enterococcus faecium to aminopenicillin and high-level gentamicin to be as high as 82% and
49%, respectively (www.anrexis.ch). This leaves the clinician with a therapeutic conundrum since no established therapeutic regimen exists. Daptomycin is approved for complicated skin and soft tissue infections with Gram-positive bacteria and showed efficacy against E. faecium in the experimental endocarditis model.

**Methods:** We report a case series of 11 patients with severe E. faecium infections treated with daptomycin at the University Hospital Basel between 2007 and 2009. All strains were resistant to ampicillin (MIC > 8 mg/l), but susceptible to vancomycin. 7/11 strains were also highly resistant to gentamicin (MIC > 500 mg/l).

**Results:** All patients were treated with multiple broad-spectrum antibiotics prior to isolation of E. faecium and had severe underlying diseases: Five had haematological malignancies, two had repeated episodes of cholangiosepsis, two suffered from severe atherosclerosis after multiple vascular surgical procedures, one had undergone liver transplantation and one had colon cancer. Foci were mainly blood stream infections or cholangitis. The reasons for daptomycin treatment were renal failure (n = 3), vancomycin failure (n = 4) despite vancomycin susceptibility (MIC ≤ 4 mg/l), outpatient parenteral therapy (n = 2) and uncontrolled infection (n = 2).

With one isolate from a patient with persistent bacteremia, in vitro kill-curves were performed, showing a bactericidal effect of daptomycin (loss of Pseudomonas aeruginosa population of 2 log with 2 mg/l and 10 mg/l of the drug). In contrast, 10 mg/l of vancomycin was bacteriostatic. Daptomycin was used in a dose of 6 mg/kg/d. 7 patients recovered, 4 patients died. Death was related to uncontrollable infection in only one case, the other deaths were attributable to the underlyng diseases.

**Conclusion:** Our case series suggests that salvage therapy with daptomycin was likely to be efficient in 7/11 patients with refractory invasive infections due to multi-resistant E. faecium. Thus, daptomycin might be a safe option in such cases.

**PK/PD approaches in Gram-negative infections**

**O516 Pharmacokinetic evaluation of intravenous colistin following two different dose regimens in multidrug-resistant infections**

M. Cusato*, R. Imberti, P. Villani, L. Carnesale, G. Iotti, G. Accetta, M. Langer, M. Regazzi (Pavia, Milan, IT)

**Objectives:** Infections caused by multidrug-resistant Gram-negative bacteria are a growing clinical problem and are associated with significant morbidity and mortality. We evaluated colistin concentrations at steady-state in plasma samples and bronchoalveolar lavage (BAL) of critically ill patients admitted to our ICU.

**Methods:** Nineteen patients (16M, 3F) aged 20–70 years and affected with ventilator-associated pneumonia were enrolled. Six patients received 1 million IU of colistin methanesulphonate (CMS) intravenously every 6 hours; thirteen patients received 2 million IU every 8 hours for at least 2 days. Blood samples were collected from each patient at baseline (predose) and at time intervals after the end of CMS infusion. BAL was performed in all patients at 2 hours post-infusion. Colistin plasma and bronchoalveolar concentrations were measured using a selective and sensitive high performance liquid chromatography assay with fluorescence detector. Pharmacokinetic parameters were determined by non-compartmental analysis using Infuse KineticTM 4.0 software.

**Results:** Patients receiving 1M IU/6h had mean ± SD Cmax and Cmin plasma concentrations at the steady-state of 1.57 ± 0.57 and 1.10 ± 0.43 µg/ml, respectively. Mean ± SD AUC(0–6h), t1/2 and Vd were 6.40 ± 2.32 µg·h/ml, 8.36 ± 4.94 h, and 220.46 ± 76.61 L/h, respectively. Patients receiving 2M IU/8h had mean ± SD plasma Cmax and Cmin levels at steady-state of 2.21 ± 1.08 and 0.98 ± 0.70 µg/ml, respectively. Mean ± SD AUC(0–8h), t1/2 and Vd were 11.54 ± 6.20 µg·h/ml, 5.87 ± 2.56 h, and 143.24 ± 116.47 L/h, respectively. Cmax/MIC and AUC(0–24h) /MIC ratios (MIC = 2 µg/ml) were 0.79 ± 0.07 and 12.79 ± 4.65, 1.1 ± 0.54 and 17.30 ± 9.30, after administration of 1M IU and 2M IU, respectively. Colistin was undetectable in BAL under both regimens. A complete eradication of bacteria was observed in 12/13 of our patients with the 2M IU/8h dosing schedule.

**Conclusions:** In critically ill patients, the 2M IU/8h dose regimen provided higher Cmax and AUC than the 1M IU/6h schedule; this may be a therapeutic advantage because the AUC/MIC and Cmax/MIC ratios are strongly associated with efficacy. Further studies are needed to provide important clinical answers, from individualising treatment to optimising dosage and reducing adverse effects.

**O517 Pharmacokinetic/pharmacodynamic modelling of polymyxin B, rifampicin and tigecycline against pandrug-resistant Acinetobacter baumannii in an in vitro model**

T.P. Lim, W. Lee, S. Sasikala, T.Y. Tan, L.Y. Hsu, T.T. Tan, A.L. Kwa* (Singapore, SG)

**Objective:** Outbreaks of pandrug-resistant (PDR) Acinetobacter baumannii (AB) have emerged in Singapore. Combination therapy is often the remaining viable option until new antibiotics are available. While polymyxin B (P) may remain a viable treatment option, heteroresistance has become a major problem. We evaluate the efficacy of P, rifampicin (R) and tigecycline (T) combined against PDR AB isolated from our local hospitals.

**Methods:** PDR AB isolates from all public hospitals in Singapore were collected from 2006–07. MICs were determined according to a modified CLSI broth-dilution method. Time-kill studies (TKS) were then performed with the maximum, clinically achievable, unbound concentration (mg/L) of P (2), R (2) and T (2) alone and in combination against the PDR AB isolates. A hollow-fiber infection model (HFIM) was used to validate our quantitative assessment of combined killing against 2 isolates (selected based on the unique genotype that represents the PDR AB population). Resistance selection of the 2 isolates against P alone in the HFIM were quantified using drug-free and selective (P at 3x MIC) media.

**Results:** Among 361 non-repeat AB isolates screened, 29 PDR AB isolates found were susceptible to P (MICs 1–2 mg/L) and resistant to all antibiotic classes whereas R MICs ranged from 2–16 mg/L. In TKS, P, R and T alone was bacteriostatic with regrowth by 24 h in all isolates. P+R, P+T and R+T achieved >99% kill from baseline in 15/29, 14/29 and 8/29 isolates with no regrowth at 24 h. These assessments were consistent with observation in HFIM studies where we observe bacterial killing up to 120 h with P+R. Pharmacokinetic validation of the HFIM studies were satisfactory. Minimal killing of the 2 isolates was seen when exposed to P alone. Regrowth was seen at 24 h due to selective amplification of resistant sub-population(s) on P supplemented plates. Repeat MIC testing of the resistant isolates confirms P resistance (MICs 32–128 mg/L).

**Conclusions:** We have shown that our PDR AB has the propensity to exhibit heteroresistance and combination therapy with P is needed. P+R may be a potential antibiotic combination as therapy for PDR AB infections. The in vivo relevance of our results warrants further investigations.

**O518 Pharmacodynamic evaluation of the intracellular activity of tobramycin, doripenem, levofloxacin, and colistin towards Pseudomonas aeruginosa after phagocytosis by human THP-1 macrophages**

J. Buyck*, P.M. Tulkens, F. Van Bambeke (Brussels, BE)

**Objectives:** P. aeruginosa (Pa) is capable of invading epithelial and phagocytic cells (Mol. Biol. Cell 2005; 16: 2577–85), which may play an important role in the initiation and persistence of the infection process. As no data is available about antibiotic activity against intracellular Pa., we have developed a 24-h infection model using THP-1 cells, a human cell line known to be permissive for infection by several important human pathogens. This model has now been used to test for the activity of 4 different antibiotics representing all 4 classes of drugs used in clinics to treat pseudomonal infections.

**Methods:** Phagocytosis of bacteria (opsonized with human serum) was allowed for 2 h (bacteria/macrophage ratio: 10), extracellular bacteria
were eliminated by washing and incubation for 60 min with gentamicin at 50 × MIC, and infected cells (5–7 × 10^6 CFU/ml per cell prot.) incubated with antibiotics (0.01 to 100 × MIC). Activity against bacteria in broth (1 × 10^8 CFU/ml) was determined in parallel (same con. span). Activity was expressed as change from the initial inoculum after 24h, and the data used for fitting a concentration-response curve (Hill equation) and for calculation of the Emax and Cstatic pharmacodynamic parameters (AAC 2006; 50: 841–51).

Results: The table shows that while TOB and DOR were cidal in broth (Emax ~ −3 log CFU), their intracellular maximal efficacy was markedly reduced (less negative Emax) towards intracell. Pa. LVX was also affected but to a lesser extent. CST, bacteriostatic against extracell. bacteria, also showed decreased intracellular efficacy. In addition, CST and TOB showed a 6 to 9 fold decrease of relative potency (higher Cstatic) when comparing intracell. and extracell. CST.

Conclusions: The model shows that, as for other intracell. bacteria, antibiotics are considerably less active and, for 2 classes, less potent, against intracellular forms compared to bacteria in broth, irrespective of their mode of action. This may contribute to the difficulty of eradicating P. aeruginosa in vivo.

### Table 1: Pharmacodynamic Parameters for CIP

<table>
<thead>
<tr>
<th>Antimicrobial</th>
<th>MIC (μg/ml)</th>
<th>IC50a (μg/ml)</th>
<th>Cstaticb (μg/ml)</th>
<th>Cmax/MIC</th>
<th>Emaxc (μg/ml)</th>
<th>R2d</th>
</tr>
</thead>
<tbody>
<tr>
<td>Teicoplanin (TOB)</td>
<td>0.5</td>
<td>−2.85±0.10</td>
<td>0.86</td>
<td>0.92</td>
<td>−1.22±0.22</td>
<td>7.95</td>
</tr>
<tr>
<td>Dicloxacillin (DOR)</td>
<td>0.06</td>
<td>−5.19±0.22</td>
<td>0.90</td>
<td>0.96</td>
<td>−1.22±0.22</td>
<td>0.95</td>
</tr>
<tr>
<td>Levofloxacin (LVX)</td>
<td>1−2</td>
<td>−3.17±0.30</td>
<td>0.15</td>
<td>0.89</td>
<td>−2.40±0.21</td>
<td>0.50</td>
</tr>
<tr>
<td>Colistin (CST)</td>
<td>2</td>
<td>−1.21±0.11</td>
<td>0.34</td>
<td>0.99</td>
<td>−0.20±0.17</td>
<td>18.94</td>
</tr>
</tbody>
</table>

a determined by precipitation in MII broth. b maximum decrease in log CFU compared to initial inoculum for a 24h period. c static concentration (in μg/ml), resulting in no apparent bacterial growth (number of CFU identical to the original inoculum). d determined by graphical interpolation.

O519 Population pharmacokinetics and pharmacokinetic–pharmacodynamic metrics for delafloxacin


Objectives: To develop a population pharmacokinetic (PK) model for delafloxacin (DFX) and use that model to estimate pharmacokinetic–pharmacodynamic (PK-PD) indices in Phase 2 patients treated for complicated skin and skin structure infections (cSSSI). Methods: Data from 3 Phase 1 studies (1 single dose, two multiple dose) and 1 Phase 2, cSSSI study were pooled to develop a population pharmacokinetic model. All doses were administered by IV infusion; doses ranged from 50 to 600 mg. The Phase 2 study employed doses of 300 or 450 mg BID. Intensive PK sampling was employed in all Phase 1 studies while Phase 2 patients contributed 4−5 samples at steady-state over one dosing interval. Population PK modeling was performed using Monte Carlo Parametric Expectation Maximization as implemented in S-ADAPT 1.5.6. Two and 3 compartment models were explored using linear and/or nonlinear elimination. Steady-state AUC and Cmax estimates were calculated using individual PK parameter estimates for Phase 2 patients and indexed to observed bacteria MICs to calculate PK-PD indices. Previous animal studies have indicated that free-drug AUC/MIC ratios (AUC/MIC) of 9.3 and 14.3 are associated with net bacterial stasis and 1-log10 CFU reduction, respectively, for Staphylococcus aureus.

Results: The final analysis dataset included 103 subjects (86 from Phase 1, 17 from Phase 2) and 2273 plasma concentrations. A 2 compartment model with a mix of linear and nonlinear elimination provided the most robust fit to the data (R^2=0.965, observed=1.02*fitted − 0.032). All parameters were estimated with excellent precision; inter-individual variability in the parameters that define clearance (linear clearance, intrinsic clearance, and Michaelis-Menten constant) ranged from 24−70%. Twelve patients had requisite MIC data to calculate a PK-PD index, all AUCss:MIC estimates were above 100 (range: 108−3754); all 12 patients were classified as clinical and microbiological cures. The median (min – max) fCmax:MIC ratio was 191 (18.8−565). Seven patients had MRSA as their primary pathogen; MIC values were universally low (0.004−0.06).

Conclusions: Development of a population PK model allowed for the estimation of drug exposure in a Phase 2 cSSSI study using relatively sparse PK sampling. Based on PK-PD indices from the Phase 2 study, 300 and 450 mg (BID) clinical doses were appropriate for the treatment of cSSSI. Results also support coverage of MIC values up to 1.0 mg/mL.

O520 Pharmacokinetics and penetration of ciprofloxacin into bronchial secretions of critically ill patients with chronic obstructive pulmonary disease

P. Kontou*, K. Chatziika, G. Pitosoa, A. Boutou, P. Argyropouloa, I. Kioamis (Thessaloniki, GR)

Objective: Ciprofloxacin (CIP) is one of the antibiotics of choice for the treatment of severe exacerbations of Chronic Obstructive Pulmonary Disease (COPD). Antibiotic penetration into the site of infection is critical for obtaining an optimal clinical outcome. Since in COPD patients the infection develops within the airway lumen, it is important to know the drug concentrations that are achieved in bronchial secretions (BS). The purpose of this study was to evaluate CIP’s pharmacokinetic (PK) profile in plasma and penetration into BS of mechanically ventilated COPD patients, when administered at the currently recommended dose of 1200 mg per day.

Methods: Nineteen critically ill COPD patients received a 1-hour infusion of 400 mg CIP q8h. They all had a respiratory infection as well as risk factors for Ps. aeruginosa and they were intubated. Serial blood and BS samples were obtained at steady state. Concentrations were determined by a validated HPLC assay. Penetration ratio was calculated by dividing the 24h area under the curve (AUC0−24) of BS by the AUC0−24 of plasma. The pharmacodynamic (PD) parameters for CIP were also calculated.

Results: Mean±SD values for volume of distribution, clearance, half-life and AUC0−24 were 174.3±85.42 L, 27.32±9.53 L/h, 5.5±2.34 h and 47.58±18.07, respectively. The mean peak (C max) and trough levels in plasma were 5.32±1.76 and 1.05±0.59 mg/L, respectively. In BS, a mean C max of 3.11±1.27 mg/L was achieved in 3±1.03 hours and the penetration ratio was 1.17±0.61. Thirteen patients demonstrated penetration equal to or even more than 100%. The PD target of AUC0−24/MIC ≥125 in plasma, that has been shown to be predictive of efficacy for Gram-negative infections, was attained in all patients and in the majority of them (74%) at MICs of 0.125 and 0.25 μg/ml respectively but in only 3 patients and in none at higher MICs (0.5 and 1 μg/ml). Slightly better results were obtained for the PD threshold of C max/MIC ≥ 10.

Conclusions: CIP exhibits excellent penetration into BS. There is wide interindividual variability in its PK parameters in critically ill COPD patients and inadequate PD exposure against bacteria with MICs ≥0.5 μg/ml. Our data confirm the need for combination therapy against pathogens with high MICs such as Ps. aeruginosa, as well as the institution of therapeutic drug monitoring for individualizing antimicrobial dosing in order to optimize the efficacy of antibiotic therapy in the ICU.

Biofilm infections – diagnostic, prophylactic and therapeutic methods

S521 Diagnosis of biofilm infections

T. Bjarnsholt* (Copenhagen, DK)

The initial problem or challenge with all infections is to identify the infecting organisms and the focus of the infection. This is usually not a problem for acute infections since the bacteria are readily obtained by swapping or sampling the infected area. For chronic infections it is usually more problematic. An exception is cystic fibrosis (CF) in which the easy accessible purulent sputum coughed up by the patients on a regular basis harbor the bacteria. For the other chronic infections routine sampling has been either using a swab, a scrape or a biopsy, however all
might fail to sample the bacteria. In a chronic wound the swab will only collect bacteria on the surface not the bacteria embedded in the wound bed. On the other hand, since the bacteria are very heterogeneously distributed chances are that a biopsy fails to contain any bacteria. Also for implant and catheter related infection diagnosing the bacteria prove difficult. Five to 10 years ago the bacteria on these surfaces and biofilm in general were considered unculturable. Here the problem is surface adherence, the bacteria simply attach extremely well to the surface of the foreign bodies. It is not that they are unculturable, they have to be released from the surface, and vigorously vortexing or even mechanical scraping is not enough. The implant or catheter has to be treated with ultra sound (sonication) to release the bacteria.

The problems of diagnosing the bacteria in these chronic infections are far from solved. Today bacteria can be detected by: culturing, PCR, microscopy or diagnostic imaging. Each method has its advantages and limitations. For culturing, the problem is to collect the bacteria, either next to the surface, which is sampled, or from the catheter or implant. PCR will detect even tiny amounts of available DNA or RNA available in the sample. Additionally, just because a bacterium is present does not necessarily indicate that it contributes to the pathogenesis of the infection. Microscopy such as Gram-staining or fluorescence in situ hybridization (FISH) enables direct visualization of the infecting bacteria and the surrounding tissue and inflammatory cells. Again the bacteria need to be present in the collected sample, which means many biopsies need to be analyzed for a correct diagnostics of e.g. a wound. On the other hand if only a few bacteria are present they might be very hard and statistically impossible to observe using traditional staining such as Gram.

**Antibiotic therapy of biofilm-forming group A streptococcal infections**

L. Baldassarri* (Rome, IT)

*Streptococcus pyogenes* (group A streptococcus, GAS) is responsible for a diverse range of clinical manifestations, from mild skin/soft tissue infections and pharyngitis to more serious manifestations, such as bacteremia, cellulitis, purpura fulminans, meningitis, pneumonia, and necrotizing fasciitis.

The drug of choice for streptococcal infections treatment still remains penicillin. In fact, the ability of penicillin and its related antibiotics (e.g., amoxicillin) to kill group A streptococci has not changed in more than 50 years and, to date, there has never been a report on a group A streptococcus resistant to this class of antibiotics. On the other hand, macrolide resistance has been showing an increasing trend, with resistance rates which vary considerably in different countries, reaching up to almost 30% in some part of Europe.

Effective treatment is of utmost importance, even for streptococcal pharyngitis, as it is primarily aimed at preventing non-suppurative and supplicative complications and decreasing infectivity. Even if not frequently, *S. pyogenes* infections may fail to respond to antibiotic therapy leading to persistent throat carriage and recurrent infections. Such failures cannot always be explained with the occurrence of antibiotic resistance determinants. It was first suggested that erythromycin-resistant *S. pyogenes* may escape antmicrobial treatment and the host immune response through invasion of epithelial cells. Later, as GAS have recently been shown to be able to form biofilm, and being such character known to provide organisms with an improved antibiotic resistance besides supporting colonization and persistence, biofilm has been suggested as possibly responsible for unexplained treatment failures and recurrences due to susceptible microorganisms.

Preliminary data have shown that biofilm may be produced, and/or up-regulated, in *S. pyogenes* in response to either antibiotic treatment, other therapeutic molecules or environmental stimuli. In particular, subMIC antibiotic concentrations appear to stimulate biofilm formation; such phenomenon is being observed with increasing frequency for a number of microorganisms, both for biofilm and other virulence factors. The latest findings on what is it known on biofilm produced by *S. pyogenes*, its possible role in the pathogenesis of streptococcal infections, and on the interactions between antibiotics and other therapeutic molecules and streptococcal biofilm, will be examined.

**Diagnosis and treatment of Aspergillus biofilms**

C. Williams* (Glasgow, UK)

*Aspergillus fumigatus* causes infections in both immunocompromised hosts and patients with chronic lung infections. The initial establishment of *A. fumigatus* infections involves the germination of conidia and subsequent hyphal invasion of the lung tissues. Histology and microscopic examination of bronchopulmonary lavage samples reveals the presence of numerous *A. fumigatus* hyphae in the form of a complex mesh like structure, similar to other fungal biofilms.

We have developed an in vitro model of an Aspergillus fumigatus biofilm. This model possesses the classical elements of biofilm growth, namely multicellularity, matrix production and sessile resistance and shows has distinct developmental phases both genotypically and phenotypically.

I will discuss the in vitro antifungal activity of voriconazole, amphotericin B and caspofungin and how this model may relate to the use of antifungals in the clinic. Also how a better understanding of the biology of *Aspergillus fumigatus* in vitro may lead to a different approach to diagnosis of invasive fungal infection.

**Challenges and solutions for determining pharmacokinetics of antimicrobials in the human body**

O. Langer* (Vienna, AT)

Most drugs exert their effects not within the plasma compartment, but in defined target tissues into which drugs have to distribute from the central compartment. Unfortunately, a complete and lasting equilibration between blood and tissue cannot always be taken for granted. Drug distribution processes may be characterized by a high intertissue- and intersubject variability and target site drug levels may substantially differ from corresponding plasma levels. Suboptimal target site concentrations may have important clinical implications, as it is a potential explanation for therapeutic failures. In particular for antimicrobial agents knowledge of drug tissue distribution is of primal importance as tissue drug exposure has been shown to be directly related to outcome of therapy.

Therefore, determination of drug tissue penetration plays an important role in antimicrobial drug development. Positron emission tomography (PET) is nuclear imaging method, which can be used to study the tissue distribution of drugs labeled with positron-emitting radionuclides, such as carbon-11 or fluorine-18, non-invasively. These types of studies have been termed PET-microdosing studies, as the amount of drug administered in a PET study is usually less than 100 microgram. Due to low administered drug doses, the potential toxicological risk to human subjects is very limited. Consequently regulatory authorities require reduced preclinical safety testing as compared to conventional phase I studies. In the present talk, recent applications of PET-microdosing in antimicrobial drug development will be reviewed.

**PK modelling: obtaining PK profiles despite sparse sampling**

J.B. Bulitta*, A. Bingölbali, C. Landersdorfer (Albany, US)

**Objectives:** Tissue penetration studies pose a significant challenge for pharmacokinetic/pharmacodynamic (PK/PD) modelling, especially if only one tissue sample can be obtained per patient. We sought to systematically evaluate the ability of various optimized and non-optimized clinical trial designs to determine the rate and extent of tissue penetration and their between subject variability (BSV).
Methods: Monte Carlo simulations with a 2-compartment model were performed in Berkeley Madonna to simulate plasma and tissue concentrations of 1000 patients for intravenous moxifloxacin as an example drug. Simulation scenario A assumed that the tissue concentration is proportional to the concentration in the peripheral compartment. For scenario B, rate and extent of tissue penetration were estimated and tissue volume fixed to a small value. Population optimal sampling times were determined in WinPOPT (V1.2). For 12 sampling schedules, 100 datasets of 48 patients were drawn randomly and analyzed by the MC-PEM algorithm in S-ADAPTV1.56 using the truemodel (2400 population PK analyses in total). Bias and precision of mean population PK parameters and variances representing BSV were calculated.

Results: Except for designs that sampled both plasma and tissue at the same time in all patients, in scenario A bias was <8% and precision <19% for population means and bias was generally <25% and precision <30% for BSV for all PK parameters. For scenario B and designs with 5 optimized plasma sampling times and one tissue sample per patient: (1) Designs with all tissue samples at the same time showed bias up to 48% for extent of tissue penetration and up to 78% for rate of tissue penetration. (2) A design with random tissue sampling times had bias <7% and precision <2% for all population means. (3) A design with four groups (each: n=12) of patients each sampled at one optimized tissue sampling time achieved bias <3% and precision <13% for all population means and bias <18% and precision <33% for all BSV estimates.

Conclusions: Tissue samples should be obtained at multiple optimized time points to determine the rate and extent of penetration, even if only one tissue sample per patient can be obtained. Designs with serial plasma samples at population optimal times were beneficial. Designs with one plasma and one tissue sample per patient at all the same time performed poorly and benefited from a full Bayesian approach for PK analysis.

Role of pharmacokinetics in early stages of antimicrobial development

U. Theuretzbacher * (Vienna, AT)

The importance of diligent pharmacokinetic (PK) profiling in the early drug research and development stages to reduce late attrition rate has been increasingly recognized over the last decade and major advances have been made. Based on the results of ADMET screening (absorption, distribution, metabolism, and excretion) during the lead optimization phase, relevant predictive information on the pharmacokinetic behavior of a preclinical candidate is typically obtained in two or three animal species before admission to humans. The preclinical PK assessment provides the input for in vitro and in vivo PK/PD (pharmacodynamic) models that evaluate exposure-effect relationships. Such PK/PD models are powerful tools for dose selection for the clinical phases of drug development. If phase 1 PK data are available, population based PK/PD models support effectively dose selection for late stage clinical trials. Moreover, a PK/PD guided approach can provide decision support for susceptibility breakpoints as well as strategies to mitigate resistance development. Recent late stage clinical failures illustrate the importance of understanding the impact of PKs such as protein binding and concentrations at infection sites and incorporating them early into adequate PK/PD evaluations.

Management of infections caused by viruses in haematopoietic stem cell recipients

Epstein–Barr virus infections

J.M. Middeldorp * (Amsterdam, NL)

Epstein–Barr virus (EBV) infection in immune suppressed transplant recipients is a frequent and potential life-threatening complication. EBV causes B-cell lymphoproliferative disorders, collectively named PTLD, which may lead to malignant lymphoma if left untreated. The incidence, clinical appearance and severity of PTLD may be quite variable, requiring appropriate risk-stratification at onset and accurate and standardized diagnostic monitoring approaches in the post-transplant period aiming at early identification of EBV involvement and distinction from rejection and other (infectious) complications. The biology and pathogenesis underlying PTLD in solid organ (SOT) and stem cell transplant (SCT) recipients has different features, with implications for diagnosis and treatment. Primary infection in the SOT and nearly all (re)active EBV infections in SCT pose the highest risk for fatal complications. A distinction should be made between early and late-onset PTLD, the former being directly EBV driven and frequently reversible by simple therapeutic intervention. The latter should be seen as a consequence of misdiagnosed early EBV-driven B-cell amplification, allowing additional genetic defects to accumulate, thereby increasing the malignant phenotype, which frequently require more severe intervention strategies, including chemotherapy.

Early PTLD can be recognized by dynamic increases of EBV-DNA load in blood over relatively short time intervals. In SOT this EBV load is usually cell associated, whereas in SCT both cell and plasma DNA loads are observed. Whole blood may be a preferred well standardized sample for diagnostic monitoring. Dependent on the type of transplant, therapeutic intervention may vary from a (mild-moderate) reduction of immunosuppressive treatment (IST), via use of Rituximab (rX) to infusion of ex vivo activated EBV-reactive T-cells. A persistent decrease of EBV-DNA load may be taken as a sign of therapeutic efficacy, and monitoring EBV-reactive T-cells by tetramer FACS or ELISPOT tests may provide information on patient’s immune capacity to conquer EBV-driven B-cell proliferation and restore EBV latency on the long term. Treatment failure is indicated by persistent increases of EBV-DNA over time, and should be taken as sign for more drastic intervention.

During early PTLD EBV-infected cells frequently disseminate via the circulation, and thus becomes easily detectable, whereas late PTLD may be confined to tissue with little circulating cells. EBV transcription profiling has revealed differences EBV gene expression in biopsy material and circulating EBV-carrying cells in patients with early PTLD, suggesting transcription regulation in affected lymphoid tissues. Furthermore analysis of EBV gene expression in PTLD lesions at the single cell level, reveals heterogeneous EBV gene expression, reflecting more complex underlying pathogenic events rather than simple proliferation of latency-III (growth program) expressing B-cells. Infrequent measuring of EBV DNA loads is not considered a proper diagnostic approach, because mere EBV DNA levels may vary between patients. These generally have no clinical implication when being stable over time. It is suggested that frequent (weekly) measurement of changes in EBV-DNA load at early times post-transplant using sensitive and standardized techniques, coupled to appropriate and timely EBV load-guided therapeutic intervention may reduce and even prevent PTLD in the transplant setting.

Adenovirus infections

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Human Adenoviruses (HAdV) are a highly genetically divergent group of DNA viruses consisting of seven species with 54 types. A few of these HAdV types (1, 2, 5 and 31) are clearly associated with infections in immunosuppressed patients as well as for example haematopoietic stem cell recipients. These HAdV types are not typical opportunistic agents but are associated with less severe diseases in immunocompetent patients.

HAdV can persist for several months to years after an acute infection even in immunocompetent hosts and are more prevalent in children than in adults. Complications due to HAdV in haematopoietic stem cell recipients may originate from HAdV persistence and de novo infections. Due to HAdV persistence, diagnosis of HAdV disease cannot be made by mere detection of HAdV DNA. In case of organ related HAdV diseases, diagnosis is feasible by HAdV detection at the putative infection site, e.g. in case of cystitis by HAdV detection in urine. HAdV infection can also lead to potentially fatal disseminated infections.
HAdV disease. Main risk factors are young age, lymphopenia, T cell depletion and high dosage of immunosuppressive drugs. Diagnosis of the disseminated HAdV disease has been simplified by HAdV load testing in peripheral blood samples using quantitative HAdV PCR. High virus loads (>1e6 genome equivalents/ml) were clearly associated with disseminated disease whereas low virus loads (<1e4 genome equivalents/ml) can be observed in case of HAdV latency. However, a precise threshold HAdV load value has not yet been determined. Disseminated disease may be predicted in case of rapidly rising HAdV loads in blood.

Pathophysiology of HAdV disseminated disease includes massive virus replication in affected organs as for example the liver which may be infected by interaction of HAdV capsids with clotting factor X. Furthermore binding of HAdV capsids to platelets, formation of immune complexes with preformed HAdV specific antibodies as well as induction of cytokines may contribute to the pathophysiology of disseminated HAdV disease.

An antiviral treatment for HAdV disease has not yet been established. Cidofovir may have beneficial effects if applied early but may fail if applied in case of very high virus loads. HAdV specific T-lymphocytes seem to be a promising therapeutic approach because risk of disseminated HAdV disease is clearly associated with lymphopenia. However, HAdV specific T lymphocytes must be prepared before onset of disease in order to be available in time.

What do we expect from MALDI-TOF?

**Objectives:** To compare identification of routine bacterial isolates using the SARAMIS identification system and conventional methods.

**Methods:** Consecutive bacterial isolates from urine- and bloodcultures were identified using conventional biochemical methods or VITEK II. All isolates were subsequently identified using MALDI-TOF (AXIMA®SARAMIS®). Discrepant isolates will be further identified by means of 16S RNA sequencing.

**Results:** A total of 3,695 isolates (1,095 from blood, 2,600 from urine) were included. 71.8% of the isolates showed fully agreement on species-level, for another 9.7% fully agreement on genus-level was achieved. 15.7% of the isolates could not be identified by MALDI-TOF using the identification-score.

In 2.8% of the isolates, the two methods gave different identification. These isolates are currently subject to further characterization by 16S RNA sequencing.

**Conclusion:** MALDI-TOF (AXIMA®SARAMIS®) gives a fast and reliable identification of commonly encountered bacterial isolates in a clinical microbiology laboratory but has certain limitations.

**Objectives:** Automated blood cultivation of patients with suspicion for sepsis is a routine clinical approach. Fast and accurate species identification of microorganisms after signalling of growth is of fundamental interest. Currently, the identification takes up to two days because of the necessity for sub-cultivation and biochemical identification. The presented simple protocol has the potential to shorten the identification time to minutes.

**Methods:** Blood cultures spiked with bacteria or yeast were used for method establishment, inoculated blood cultures and routine samples to optimize and validate the protocol. 1ml of a blood culture was mixed with 200μl of lysis solution followed by vortexing and centrifugation. Thereby, blood cells were disrupted but bacteria and yeast survived. Supernatant was removed and the pellet carefully suspended in wash solution. After centrifugation supernatant was removed and bacteria from the pellet were transferred to a MALDI target directly or after a short extraction procedure. Species ID was achieved by measurement in a MALDI-TOF MS mass spectrometer followed by analysis with the MALDI Biotyper software. The method was optimized by varying volumes and ratios of blood culture liquid and lysis solution.

**Results:** Positive blood cultures showed an average cell density of about 10⁷ cfu/ml and a high number of blood cells. The presented protocol was able to remove blood cells extensively without significant loss of microorganisms. Therefore, resulting MALDI-TOF spectra were of high quality. Different bacterial species (enterobacteria, Gram negative non-fermenting bacteria, staphylococci, enterococci, streptococci, Haemophilus sp.) could be identified with the procedure, reliably. Also yeasts which could not be detected with previously published protocols were identified. In some cases an identification was possible even 1−2h before blood cultures were flagged positive by the automate, showing the high sensitivity of the method. Mixed cultures in most cases lead to non-identification or observation of only one species. Work on bioinformatic algorithms will improve this.

**Conclusion:** The new protocol for species identification from positive blood cultures could be demonstrated as a very fast and accurate alternative to classical methods. Identification time is shortened from...
MALDI-TOF MS for direct bacterial identification from positive blood culture pellets

G. Prod’hom*, A. Bizzini, C. Durussel, J. Bille, G. Greub (Lausanne, CH)

Objectives: Blood cultures are the best approach to establish the etiology of bloodstream infections. Rapid identification of etiological agent of such severe infections is pivotal to guide antimicrobial therapy. The matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) allows the identification at the species level when the score value was >1.7 and <2 and as not valid when the score was <1.7. The identifications obtained with MALDI-TOF MS analysis were compared with biochemical identification.

Results: 122 monobacterial positive blood vials from 76 patients were analyzed. 96 (78.7%) bacterial identifications were obtained with MALDI-TOF MS analysis, of which 69 (56.6% of 122) exhibited a score value >2 and 27 (22.1%) a score value >1.7 and <2. Regardless of the score value, 95 (98.9%) of the 96 bacterial identification obtained with MALDI-TOF MS were correct at the species level and 1 correct at the genus level only. In 26 (21.3%) of cases, no reliable identification was obtained (score value <1.7). 21/26 bacteria (80.8%) were Gram positive, mainly streptococci (n=13) and coagulase-negative staphylococci (n=5). Most unidentified streptococci were Streptococcus pneumoniae. Among the 5 Gram negative bacteria with a score <1.7, 4 were of encapsulated species (2 Klebsiella pneumoniae and 2 Haemophilus influenzae).

Conclusion: The use of an ammonium chloride-driven hemolysis before analyzing directly positive blood cultures by MALDI-TOF MS is a very promising new method allowing fast, accurate and inexpensive identification of the etiological agents of life-threatening bloodstream infections.

Identification and rapid antimicrobial susceptibility testing of bacteria from positive blood culture bottles by using MALDI-TOF MS and Phoenix rapid AST cards

T. Adam*, C. Grüger, U. Göbel (Berlin, DE)

Objectives: Early and appropriate antimicrobial therapy critically determines the outcome of bloodstream infections. Rapid identification (ID) and antimicrobial susceptibility testing (AST) is, hence, mandatory to adjust empirical antimicrobial therapy instituted during the first two hours after onset of symptoms. To reduce the turnaround time (TAT) aliquots from positive blood culture bottles (BC) were subjected to differential centrifugation and gel separation using BD Vacutainer SST II tubes. The preparations were used for direct identification by MALDI-TOF mass spectrometry (MS). In addition, we are optimizing a protocol for rapid AST using the Phoenix BD system.

Methods: Blood cultures were drawn from septic patients and incubated using the Bactec BD blood culture device. In the rapid arm aliquots from consecutive positive BC bottles were processed for direct identification by Mass Spectrometry using the MALDI Biotyper (Bruker) system. Controls were processed according to standard procedures, inoculation of solid media and subsequent ID and AST using the MALDI Biotyper or the Vitrek 2 system (bioMérieux), respectively. In case of discrepant ID results isolates were subjected to 16S rRNA gene sequencing.

Results: So far, we have tested 115 positive BCs. Direct MALDI TOF analysis resulted in 76 (66%) species identifications showing no discrepant results when compared with identification of colonies grown from these BCs. In 9 BCs more than 1 isolate could be grown on plates. Thus, in 73% of monoinfectious BCs MALDI TOF can reveal the etiologic agent in less than 1 h.

Conclusion: As compared to conventional procedures the combined use of MALDI-TOF MS and rapid AST may significantly reduce the TAT in diagnosis of blood stream infections.
We present a novel approach for sample preparation of fungi prior to MALDI-TOF MS improving reproducibility and quality of spectra, significantly.

**Methods:** Fungal species (e.g. *Aspergillus spp.*, *Fusarium spp.*) harvested from solid media were grown over night in liquid medium. Subsequently, cell material was harvested by centrifugation, and washed with water. The pellet was dried well and extracted using 35% formic acid/50% acetonitrile. 1μl of the extract was spotted onto a MALDI target, dried on air, and overlaid with HCCA matrix. Mass spectra were acquired in the linear mode, mass range 2000 to 20000 Da, using a microflex MALDI-TOF mass spectrometer (Bruker Daltonik GmbH, Bremen). Spectra were analysed using the flexAnalysis software, reference libraries were created and bioinformatic analyses were performed with the MALDI Biotyper 2.0 software (Bruker Daltonik).

**Results:** Culture in liquid medium has lead to mycelia without spores and therefore a homogenous cell material. These samples facilitated a successful protein extraction by a simple, short standardised method. Mass spectra generated based on the novel sample preparation method were reproducible and contained many characteristic peaks, thereby leading to a significantly improved identification security. Further, the higher quality of spectra increased the differentiation power of the method and could highlight subspecies differences. A core database of 50 filamentous species has been established and used for first comparative studies. Technical and biological replicates could be identified successfully as well as isolates not included in the database. Reproducibility of results obtained with different mass spectrometers could be demonstrated.

**Conclusions:** The presented approach may lead to significant improvement of fungal identification in clinical or other routine applications.

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**[O540] Diagnosing fungal infections by mass spectrometry**

*J. Nedeva, M. Kazma, M. Strohalm, K. Lemr, M. Stulc, M. Volny, P. Nocak, J. Pol, V. Haulicek*, E. Barreto-Bergter, M. Hajsluch, J.M. Holopainen (Prague, CZ; Rio de Janeiro, BR; Olomouc, CZ; Helsinki, FI)

**Objectives and Method:** Mass spectrometry is presented as a modern analytical tool for fungal strain typing and diagnosing fungal infections. **Results:** Qualitative and quantitative proteomics approaches are documented on various *Aspergillus* strains; virulence protein factors present on fungal spores are identified by peptide mapping, peptide- and de novo-sequencing. Quantitative proteomics is addressed by NOVA-Q in house-developed software improving the precision of results in samples labeled by SILAC. Metabonomics approach is illustrated by the detection of minor macrolide antibiotics produced by Streptomyces strains. Peptidomics is represented by tracking non-ribosomal cyclic peptides and depsipeptides produced by Beauveria, Paecilomyces and Pseudallescheria genera. Peptide profiles are used as chemotaxonomic tools. Patented unique non-ribosomal lasso-peptide structures produced by *Aspergillus* strains: virulence protein factors present on fungal spores are identified by peptide mapping, peptide- and de novo-sequencing. Quantitative proteomics is addressed by NOVA-Q in house-developed software improving the precision of results in samples labeled by SILAC. Metabonomics approach is illustrated by the detection of minor macrolide antibiotics produced by Streptomyces strains. Peptidomics is represented by tracking non-ribosomal cyclic peptides and depsipeptides produced by Beauveria, Paecilomyces and Pseudallescheria genera. Peptide profiles are used as chemotaxonomic tools. Patented unique non-ribosomal lasso-peptide structures are reported as extremely specific fungal markers. Glycomics and lipidomics armory is illustrated by hexosylceramide analysis in *Scedosporium* by Fourier-transform ion cyclotron resonance mass spectrometry. Clinical samples (tissues, whole blood) handling by advanced ambient ionization techniques is reported with special focus to lipids in brain, eye bulb and lungs (murine, porcine). The fungal infections in plants is addressed by DAPPI mass imaging.

**Conclusion:** The current advances in mass spectrometry will lay the experimental foundation for modern sensitive diagnostic tools. We predict that particularly mass imaging of tissues infected by molds will lead to discovery of specific fungal biomarkers.

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**[O541] Comparative evaluation of MALDI Biotyper system, manual biochemical tests and BD Phoenix™ automated microbiology system for species identification of staphylococci**

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**Objectives:** *S. aureus* and several species of coagulase-negative staphylococci are common human pathogens. Therefore, comprehensive and accurate identification of *Staphylococcus* species is of great importance. Several ID methods based on conventional physiological or biochemical characterization are commercially available in manual and automated formats. The presented study aimed to examine the accuracies of manual identification tests, BD Phoenix™ system and MALDI Biotyper system for the discrimination of *Staphylococcus* species.

**Methods:** A total of 301 clinical isolates of staphylococci were studied. For conventional species identification, manual or semi automated biochemical identification systems (bioMérieux, France) were used. All isolates were also identified by Phoenix™ automated microbiology system (BD Diagnostic Systems, USA) as well as by MALDI Biotyper technique (Bruker Daltonik GmbH, Germany) which is based on fingerprinting of mass spectra acquired from fresh bacterial cultures. 16S rRNA gene sequencing was performed as confirmatory approach for discordant cases.

**Results:** Clinical isolates from 31 regions of the Russian Federation were investigated including 101 isolates presumably identified by conventional microbiological methods as coagulase-negative staphylococci and 200 isolates reported as *S. aureus*. A discordance between conventional methods of identification and the other tested technologies was found in 9 (2.9%) cases for MALDI Biotyper technique, and in 29 (9.6%) ones for BD Phoenix™ automated system. Discordant results of ID using the Biotyper and Phoenix were obtained for 24 (8.0%) isolates. Unambiguous species ID was achieved by MALDI Biotyper technique and Phoenix™ automated system in 292 (97.0%) and 277 (92.0%) cases, respectively. Likewise, 8 (3.8%) and 21 (7.0%) isolates, respectively, were identified at the genus level only. Two isolates (0.7%) did not belong to the *Staphylococcus* genus according to both approaches. The discrepant cases were analyzed by 16S rRNA gene sequencing which confirmed the benefits of MALDI Biotyper ID results in most of the cases.

**Conclusion:** The MALDI Biotyper technique was superior to the manual and automated (BD Phoenix) biochemical tests for the species identification of staphylococci.

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**[O542] Comparison of MALDI-TOF MS, the Vitek 2 Anaerobic card and BD BBL Crystal Anaerobe ID kit for identification of anaerobic bacteria**

*A. Ingebreten*, M.Z. Pino, J.V. Bjørnholt (Oslo, NO)

**Objective:** Compare MALDI-TOF mass spectrometry (MS) with established automated identification systems for anaerobic bacteria. All methods were compared to 16s rDNA sequencing.

**Methods:** 66 isolates from our routine diagnostic laboratory cultured on non-selective media to secure pure culture, aged no more than 24−48 hours, underwent Gram staining, catalase testing and spot indole if requested by the identification method. Otherwise standard procedures as specified by manufacturer were followed for VITEK 2 Anaerobic and Corynebacteria identification with VITEK 2 and the BD BBL Crystal Anaerobe ID kit with the BBL autoreader. For sequencing of the 16s rDNA gene, DNA was extracted using the Prepman Ultra protocol (Applied Biosciences) and thereafter performed according to standard procedure using an ABI 3730 sequencer and the BLASTn search tool. Identification of the microorganisms by MS was performed using the Microflex MALDI-TOF mass spectrometer (Bruker Daltonik GmbH) with the Biotyper 2.0 software. Preparation of the bacteria was performed using the ethanol/formic acid extraction procedure according to the manufacturer (Bruker Daltonik GmbH). All bacteria were analyzed in
duplicates. The Biotype and 2.0 software generates a list of species matches ranked by a log score value. In this study we accepted the score value of 1.7 and higher if the duplicates matched each other.

Results: 36 different anaerobic species were identified. Proportion of isolates identified correctly according to species group compared to 16s rDNA sequencing are presented in table 1. Generally MALDI-TOF MS performed better than the 2 automated systems, although short comings were present for some species. Of the two automated systems the VITEK2 Anaerobic and Corynebacteria identification card performed marginally better than the BD BBL Crystal™ Anaerobe ID kit.

Conclusion: The automated systems for anaerobic identification show limited performances. Although the MALDI-TOF MS performed better, significant shortcomings are also present. The latter could be explained by database limitations of the MALDI Biotype 2.0 software, i.e. several subspecies of Fusobacterium nucleatum have been described but are not included. At present 16s rDNA sequencing remains the gold standard but may be somewhat replaced by MALDI TOF MS in the near future depending on further development of the database. The 2 automated identification systems can be used in conjunction to more conventional identification.

Table 1. Proportion of anaerobic isolates correctly identified by MALDI-TOF mass spectrometry, BD BBL Crystal™ Anaerobe ID kit and the VITEK® 2 Anaerobic and Corynebacteria identification card according to species groups

<table>
<thead>
<tr>
<th>16s rDNA sequencing</th>
<th>MALDI-TOF MS</th>
<th>Crystal</th>
<th>VITEK 2 ANA</th>
</tr>
</thead>
<tbody>
<tr>
<td>Actinomyces spp.</td>
<td>5/5</td>
<td>3/5</td>
<td>0/5</td>
</tr>
<tr>
<td>Bacteroides spp.</td>
<td>8/8</td>
<td>7/8</td>
<td>2/8</td>
</tr>
<tr>
<td>Clostridium spp.</td>
<td>16/16</td>
<td>13/16</td>
<td>9/16</td>
</tr>
<tr>
<td>Corynebacterium spp.</td>
<td>7/7</td>
<td>3/6</td>
<td>2/6</td>
</tr>
<tr>
<td>Fusobacterium spp.</td>
<td>10/10</td>
<td>6/10</td>
<td>3/10</td>
</tr>
<tr>
<td>Prevotella spp.</td>
<td>5/5</td>
<td>4/5</td>
<td>2/5</td>
</tr>
<tr>
<td>Propionibacterium spp.</td>
<td>10/10</td>
<td>10/10</td>
<td>6/10</td>
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<tr>
<td>Other</td>
<td>5/5</td>
<td>2/5</td>
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Current emerging bacterial and viral infections

Eco-epidemiology and complete genome comparison of bat SARS coronavirus in China reveal bats as reservoir for frequent recombination


Objective: Despite the identification of SARS-CoV-like viruses in horseshoe bats in China, the evolutionary and possible recombination origin of SARS-CoV remains undetermined. To better define the epidemiology and evolution of bat-SARS-CoV in China and their role as recombination origin of SARS-CoV in civet, a four-year study on coronaviruses in Chinese horseshoe bats in Hong Kong and Guangdong province of southern China was conducted.

Methods: Respiratory and alimentary samples were collected from 1401 Chinese horseshoe bats captured in Hong Kong and Guangdong province of southern China over a four-year period and were detected for coronaviruses by reverse-transcriptase polymerase chain reaction. Five hundred and eleven bats from Hong Kong were also tagged to study the migration pattern of bats and viral persistence. The complete genomes of 10 strains of bat-SARS-CoV obtained at different time were sequenced and compared to the previously characterized genomes.

Results: Bat-SARS-CoV was detected in alimentary specimens from 130 (9.3%) bats, with peak activity during spring. Bats carrying the viruses appeared healthy, with viral clearance occurring between two weeks to four months. Tagging exercise showed that migrations distances of Chinese horseshoe bats in Hong Kong range from 1.86 to 17 km. Complete genome sequencing of 10 strains of bat-SARS-CoV revealed frequent recombination between different strains, especially among the bat viruses in China. Recombination was detected between bat-SARS-CoV Rp3 from Guangxi and Rp1 from Hubei in the possible generation of civet SARS-CoV SZ3, with breakpoint at nsp16/spike region.

Conclusion: Bat-SARS-CoV causes acute, self-limiting infection in horseshoe bats which serve as reservoir for recombination between virus strains from different geographical locations within reachable foraging range. Civet SARS-CoV is likely a recombinant virus arising from bat-SARS-CoV strains closely related to Rp3 and Rp1. Such frequent recombination in these animals may have accounted for the cross-species transmission and emergence of SARS.

Epidemiology and control of Q fever in the Netherlands, 2007-2009


Objectives: Q fever is caused by Coxiella burnetii. Sheep and goats are frequently described as the source. Humans are usually infected through inhalation and half of the infected show symptoms. Before 2007, Q fever was a rare disease in the Netherlands. Since 2005, Q fever emerged in small ruminants and subsequently in 2007 in the human population leading to the largest Q fever outbreak recorded up to date.

Methods: Analysis of data from public health facilities, regional laboratories, the Animal Health Service and the National Institute for Public Health and the Environment to describe the Q fever outbreak occurring in the Netherlands.

Results: In the spring of 2007, Q fever occurred in a village in the province of Noord Brabant with 168 cases. In 2008 and 2009 increasingly larger outbreaks occurred in an increasingly wider area. By November 2009, more than 3000 cases have been notified. Six patients have died. The number of chronic cases is not known. So far, contact with hay/manure and a house location close to an infected dairy goat farm have been identified as important risk factors for human Q fever. In the affected area dairy goat farming is common and goat density per square kilometre is the highest in the Netherlands. Since 2005 and preceding the human outbreaks, abortion waves caused by C. burnetii have been noticed on 27 dairy goat farms and 2 dairy sheep farms in the regions where most of the human cases occurred. Sampling of incriminated farms, animals and surroundings resulted in detection of C. burnetii. Preliminary MLVA analysis points at spreading of a single clone in goats, however the presence of this clone is not yet widely confirmed in humans. Control measures including mandatory veterinary notification as well as hygiene measures during spread of manure, lambing season and mass vaccination of goats and sheep are being implemented. Preliminary results of the monitoring of vaccination indicate a decrease of the abortion rate in the vaccinated groups to zero and a drop in bulk milk levels of C. burnetti DNA.

Conclusion: The Q fever outbreak starting in 2007 in the Netherlands is still on going. It is mainly restricted to the south of the country in an area with intense dairy goat farming. However the epidemic has been expanding to other areas in 2009. The effect of control measures is still to be awaited. Epidemiological data point towards the intensive dairy goat farming as the main source of the outbreak.

Evaluation of a diagnostic algorithm for acute Q-fever in an outbreak setting

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Objectives: An outbreak of Q-fever with over 3300 notified cases is ongoing in the Netherlands. Since 2007, immunofluorescence assay (IFA) has been the cornerstone of Q-fever serology in our hospital. IFA, however, is time-consuming and subject to inter-observer variability. Furthermore, the lag phase in antibody response to Coxiella burnetti
renders serology less suitable for diagnosing early disease. Alternative diagnostic approaches include an ELISA for IgM phase II antibodies as screening assay (M II screen). In addition, IS1111 PCR on serum samples is capable of diagnosing acute Q-Fever before antibodies appear. In 2009, we introduced a diagnostic algorithm (figure) for acute Q-fever with the M II screen as initial step. Subsequently, IFA and/or PCR were performed depending on outcome of M II screen, date of onset of disease and inpatient or outpatient setting. When diagnostics were inconclusive a 14-day follow-up serum sample was requested. Here, we evaluated the value of the algorithm in an outbreak setting.

Methods: We retrospectively evaluated outcome of Q-fever diagnostics according to the new algorithm in all patients referred between May 15th and 31st, 2009, with date of onset of disease unknown or <3 months. Results: In the 17-day period, 825 patients were tested. The diagnosis acute Q-fever was made in 256 patients (31%) – in 197 patients on the first serum sample, in 59 patients on the 14-day follow-up serum sample. A negative M II screen was obtained in 69/825 first serum samples resulting in reduction of IFAs performed by more than 80%. Ninety-two M II screen negative patients were diagnosed with acute Q-Fever by positive PCR. Cross-reactivity was documented in 4% of patients with a positive M II screen. Almost 50% of physicians did not list date of onset of disease. Requested follow-up serum samples were not received from 306 patients leading to inconclusive outcomes.

Conclusion: Introduction of the M II screen significantly reduced the number of IFAs performed, while introduction of PCR allowed for diagnosis of acute Q-fever in a substantial number of seronegative patients. Pitfalls to the presented algorithm are the poor communication by many physicians of the first day of disease, which is a critical component in the algorithm, and the suboptimal response to requests for follow-up serum samples implying that cases of acute Q-fever might have been missed.

![Algorithm diagram](image)

**Methods:**
- **ELISA M II screen:**
  - Negative: no acute Q-fever
  - Positive / doubtful: request for follow-up
- **PCR:**
  - Negative: request for follow-up
  - Positive: acute Q-fever
- **IFA and G:**
  - At least M II and O2 positive:
    - Acute Q-fever
  - Only G positive:
    - Only G positive: chronic infection
  - Request for follow-up
- **Other:**
  - Negative: request for follow-up

**Figure 1:** YLL for gastrointestinal infections in Germany.

**Reference(s)**

**Objectives:**
- Evaluation of a new test that detects *C. difficile* – enzyme glutamate dehydrogenase antigen (GDH) and toxin A/B in one step using the culture, like reference method, and to propose an algorithm for the routine diagnosis of CDAD.
- **Methods:** CDAD study was performed to 970 stool samples of patients more than 1 year old, between February and October 2009. It was studied:
  - Detection of GDH and Toxin A/B by ICT Techlab® C.diff Quick chek Complete (Inverness Medical)
  - Culture on CLO plates (Biomerieux).
- **Results:**
  - 90.2% of samples were (−) to GDH, toxin and culture (875); and the 3.4% (33) (+) to those parameters. The 4.8% (47)
were GDH(+), toxin(−) and culture(+), being the 48.9% (23/47) of those samples toxin(+) when direct toxin detection from culture was performed. The 1.3% (13) were GDH(+), toxin(−) and culture(+), recovering by alcohol treatment the 46.1% (6/13) of those samples, being the 15.4% (2/13) toxin(+). The 0.1% (1) was GDH(+), toxin(+) and culture(−); and the 0.1% (1) GDH(+), toxin(+) and culture(+).

The prevalence of toxicigenic CD was 6.1%. The S, E, VPp and VPn of GDH compared to culture were: 98.7%, 97.9%, 81.6% and 99.8%. The algorithm purpose is:

GDH(−)/toxin(−): not CD
GDH(+)/toxin(−): toxicigenic CD
GDH(+)/toxin(−): culture. If culture(+): direct toxin from culture. If toxin(−): toxicigenic CD; if (−): non toxicigenic CD. If culture(−): non toxicigenic CD.

Conclusions: This test is reliable, sensitive and specific for detect CD from stool. The detection of direct toxin from culture allowed to recover the 48.9% of GDH(+)/toxin(−) samples, increasing the prevalence of toxicigenic-CD from 3.4% to 5.8% and with alcohol treatment to 6.1%. This algorithm allows to exclude CD without additional tests when GDH is (−) (90.2% of samples). In 93.6% of samples the results can be obtain in less than 2 hours.

Risk factors and outcome of Chlamydia pneumoniae infection due to the four predominant PCR-ribotypes in the Netherlands

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Background: Chlamydia pneumoniae infection (CDI) due to hypervirulent PCR-ribotypes (types) have been well described. Little is known about other frequently encountered types.

Methods: We studied risk factors and clinical characteristics of the four predominant types in The Netherlands, as observed by The National Reference laboratory at the Leiden University Medical Center, from May 2005 until October 2008.

Results: Among 2047 isolates, the four predominant types were 001 (n = 162; 8% of all isolates), 014 (n = 217; 11%), 027 (n = 305; 15%) and 078 (n = 205; 10%). Patients with types 014 and 078 were younger (age <65 years 39% and 35%, respectively) than patients with types 001 and 027 (26% and 22%, respectively). Type 027 patients less frequently had community associated (CA) CDI than patients with any of the 3 other types (8% vs. 19–25%). Use of clindamycin was a specific risk factor for type 001, when compared the other types (31% vs. 6–7%). Type 078 patients with complicated CDI were younger (<60 years) than patients with types 001, 014 and 027 (19%, vs. 0%, 9% and 11%, respectively). Attributable mortality for types 001, 014, 027 and 078 was 0%, 0%, 3% and 2%, respectively. Patients with type 027 most often had a recurrence >8 weeks after the first infection (10% vs. 3–4% for the 3 other types).

Conclusions: Risk factors for and the clinical course of CDI vary and depend on the involved type. The antibiotics associated with the highest risk of acquisition of CDI relate to the specific type.

Hantavirus infections show a high variability in the intensity of symptoms depending on the hantavirus strain, but also individual differences were observed. Gender- and patient-specific risk factors in susceptibility and severity and chronic infections, have often been discussed. Therefore, we analyzed epidemiologic and clinical data to identify risk factors for severity.

Methods: Hantavirus-infected patients (18 men and 4 women) hospitalized in the Department of Nephrology from 2002 through 2008 were included. The diagnosis was confirmed by detection of circulating anti-hantavirus IgG- and IgM-antibodies. Demographic data, underlying diseases, biopsy, cardiac, ultrasound and laboratory findings were recorded.

Results: The men-to-women ratio for diagnosed hantavirus infections in Germany is 2.6:1. The higher incidence of infection in men seems to be caused by the way of transmission and corresponds with other rodent-borne zoonoses. Gender or pre-existing conditions did not influence the clinical presentation. Thrombocytopenia precedes organ failure and severe courses were associated with lower platelet levels. Platelet levels are therefore predictive for severe organ failure and, already early after the onset of first symptoms, a useful marker for identifying patients at risk for severe disease.

Conclusion: Gender or pre-existing conditions did not influence the clinical presentation in hantavirus infected patients, however severe courses might be predicted for patients with low platelet levels.

Objectives: In Italy, an equine outbreak of West Nile virus (WNV) infection was reported in 1998 in Tuscany region. The virus re-emerged in 2008 with the occurrence of equine and human cases of WNV neuroinvasive infection in Veneto and Emilia Romagna regions. Aim of the study was to report WNV surveillance activity performed in Veneto region in 2008–2009 and to investigate WNV strains circulating in Italy.

Methods: Since September 2008, our Centre performed surveillance of WNV disease by the following diagnostic tests: WNV-RNA detection in plasma and CSF; WNV isolation in Vero cell cultures, detection of WNV IgM and IgG by ELISA followed by PRNT confirmation. A seroepidemiology survey in at risk population resident in Rovigo province was also performed.

Results: Five cases (4 identified retrospectively) of WNV meningoen-
of the effect of this mutation predicted a higher stability of the NS3 protein at high temperatures, such as in avian hosts.

Conclusion: Since 2008, an outbreak of WNV infection, characterised by the occurrence of cases of severe meningococcalbacteraemia, is ongoing in north-eastern Italy. Genome sequencing of WNV isolates and molecular modelling has provided insight into the mechanism of WNV re-emergence in Italy, since the virus has acquired the Thr249Pro change in WNV-NS3 helicase, a trait associated with avian virulence, rapid geographic diffusion, and human outbreaks.

O552 Human babesiosis: an emerging zoonosis also in Italy?

Preliminary serological data


Objective: Aim of this study was to investigate on the seroprevalence of babesioses in people resident/working in areas where some Babesia species have been detected in the animals [1–4].

Methods: Blood samples (n = 687) from clinically healthy people (foresters, veterinarian, breeders, residents) living in at risk areas of Northern and Central Italy were collected. Sera obtained were tested for the presence of specific IgG by using the indirect immunofluorescence assay on sale for B. bocas, B. canis, B. equi and B. microti (opportually adapted), and the western blot by us recently designed for B. divergens.

Results: A total of 21 out of the 240 (8.75%) sera so far analysed proved reactive: 2/32 (6.2%) to B. bovis, 2/64 (3.1%) to B. equi, and 4/64 (10.4%) to B. microti. Sera tested for B. canis (n = 32) and B. divergens (n = 153) proved negative. No cross-reactions were evidenced.

Conclusions: Our preliminary immunological findings on Italian human population suggest a possible high seroprevalence of babesial infections, greater than to date suspected, that have to be confirmed by the more extensive serological trials programmed. The unexpected high circulation of antibodies to B. microti out of the United States confirms the recent report of an autochthonous case of human babesiosis due to B. microti from Europe [5]. However, it requires to be studied in depth, by the molecular analysis of the corresponding coagulins in some cases available, which may allow not only the conclusive identification of the species involved, but also its genetic relationship with the clustering strains.

Reference(s)


Worldwide dissemination of resistances

O553 First description of carbapenem non-susceptible K. pneumoniae isolates from Germany harbouring the OXA-48 carbapenemase

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Objective: Multidrug resistance in Enterobacteriaceae is of utmost clinical importance since new antibiotics with activity against gram-negative bacteria will be introduced in the next five years. OXA-48 carbapenemases have been described as an emerging resistance mechanism recently.

Methods: Susceptibility testing was performed by Vitek 2 and Etest. Carbapenemase production was detected by a microbiological assay employing cell-free extracts and parallel testing of the effects of selective β-lactamase inhibitors. In addition a modified Hodge test was performed. PCRs for known carbapenemase genes followed by sequencing were performed. The number of β-lactamases was determined by isoelectric focusing. A pulsed-field gel electrophoresis (PFGE) was performed and Plasmid transfer by transformation was tried.

Results: Four non-copy K. pneumoniae isolates from an universal hospital in Freiburg (Southern Germany) were tested because of elevated MICs in Vitek 2. The modified hodge test was positive in all isolates and the microbiological assay demonstrated a carbapenemase activity which was not inhibited by EDTA, clavulanic acid, clocxacillin or 3-aminoophenylboronic acid. Imipenem MICs varied between 1 mg/L and >32 mg/L, meropenem MICs were in the range of 0.38 mg/L to >32 mg/L. PCRs for KPC, VIM, IMP and GES were negative, whereas PCRs and subsequent sequencing showed the presence of OXA-48. Transformation of an OXA-48 harbouring succeeded; no resistance to non-β-lactam antibiotics was co-transferred. PFGE band patterns were related in all four isolates. By isoelectric focusing two β-lactamases with a pI of 5.4 and 7.2, respectively, were found.

Conclusion: This is the first description of OXA-48 in K. pneumoniae isolates from Germany. Some strains showed carbapenem MICs in the susceptible range, highlighting the difficulties in detection of this resistance mechanism.

O554 Multidrug-resistant Klebsiella oxytoca carrying blaIMP-8 associated to OXY-hyperproduction isolated in an intensive care unit from a community Spanish hospital

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Objective: To study the antimicrobial resistance mechanisms of broad-spectrum cephalosporin-resistant Klebsiella oxytoca strains with reduced susceptibility to carbapenems isolated in an intensive care unit from a 200-bed community hospital.

Methods: Nine K. oxytoca isolates recovered from clinical (4) and surveillance (5) cultures during a 3-month period were studied. Susceptibility testing was performed by broth microdilution and disc diffusion (CLSI). Phenotypic β-lactamase characterisation included screening and confirmatory test for ESBL, modified Hodge test for suspected carbapenemase production (CLSI), and isoelectrofocusing (IEF). β-lactamases were analyzed by PCR and sequencing. The clonal relationship among isolates was determined by PFGE with XbaI and cluster analysis was conducted by using UPGM with tolerance 1%.

Results: All isolates were intermediate or resistant to β-lactams (amoxicillin-clavulanate, piperacillin–tazobactam, cefotaxim, cefotaxime, ceftazidime, cefepime, and aztreonam), quinolones, trimethoprim-sulphamethoxazole, tobramycin and ticarcycline. Susceptibility was retained only to gentamicin, amikacin, colistin, and carbapenems (MIC of imipenem: 2 mg/L; MIC range of meropenem: 0.5–1 mg/L; MIC range of ertapenem: 1–2 mg/L). The nine isolates showed a negative double disc test for ESBL detection and a positive modified Hodge test for carbapenemase detection. IEF showed two bands per strain, one with pl slightly higher than 6.5 and another with pl of 8.2. All isolates showed an indistinguishable profile by PFGE (100% similarity). The gene encoding the metallo-β-lactamase IMP-8 was found in all isolates. In addition, all strains presented a G-to-A transition at position 5 of the −10 hexamer of the blaOXY promoter, which has been associated to an increased amount of β-lactamase produced (OXY-hyperproduction), explaining the resistance to aztreonam displayed by all strains.

Conclusion: An outbreak caused by multi-drug resistant K. oxytoca in ICU patients from a community hospital was microbiologically characterised. This is the first report on IMP-8-producing K. oxytoca in Spain.
Multifocal detection of KPC-producing Klebsiella pneumoniae in Italian hospitals


Background: Worldwide emergence and spreading of Klebsiella pneumoniae carbapenemases (KPCs) is a matter of clinical concern. In Italy, a single KPC-producing K. pneumoniae isolate was reported until now (Florence University Hospital, October 2008). Here we report the multifocal detection of KPC-positive nosocomial isolates of Klebsiella pneumoniae obtained from inpatients admitted to different Italian hospitals during 2009.

Methods: Antimicrobial susceptibility was evaluated using the VITEK2 system (bioMérieux, Marcy l’Etoile, France) and confirmed by the Etest method (bioMérieux). Synergy tests based on EDTA and boronic acid were performed to screen for different carbapenem resistance mechanisms. Carbapenemase production was first studied by the modified Hodge test and then confirmed by PCR using primers specific for the detection of blaKPC-type alleles. Molecular typing was also performed to assess clonal relationship.

Results: From May to October 2009, KPC-producing Klebsiella pneumoniae isolates were detected in 5 Hospitals located in Northern Italy. Isolates showed a multidrug-resistant phenotype, including (in addition to β-lactams), fluoroquinolones, amikacin, tobramycin, and trimethoprim-sulfamethoxazole. MICS of ertapenem, imipenem, and meropenem were ≥8 mg/L. Susceptibility was retained only for gentamicin, colistin, and tigecycline. Molecular typing showed the occurrence of few clones, although most of strains were clonally related. Epidemiological analysis revealed that two patients had been transferred among hospitals causing inter-hospitals transmission. Intra-hospital diffusion was also observed.

Conclusions: Following the first case reported in 2008, KPC-producing K. pneumoniae strains appear to be emerging in Italian hospitals. Due to the ability to rapidly spread, the multifocal detection of these strains is a finding of major concern. Monitoring and epidemiologic surveillance are therefore needed. From a therapeutic point of view, KPC-producing K. pneumoniae represent a new challenge for physicians and microbiologists. Based on in vitro results, colistin and tigecycline could represent therapeutic options for treating infections caused by these MDR pathogens.

First outbreak of Klebsiella pneumoniae producing KPC-2 in France

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Objectives: KPC-producing K. pneumoniae (KPC-Kp) are increasingly reported worldwide, mostly in the USA, Israel and Greece, and are associated with higher patient mortality. We report here the first nosocomial dissemination of KPC-Kp isolates mediated by a contaminated duodenoscope.

Methods: KPC-Kp isolates were characterized by standard biochemical methods, by susceptibility testing, by PFGE, plasmid analysis, MLST and transposon Tn4401-typing. Antibiotic resistance genes were sought by PCR and sequencing.

Results: A 85-year old patient with bladder cancer, (hospital K-Bicêtre, France) admitted for severe gastro-intestinal bleeding, underwent endoscopy to stop bleeding. Five days later, he was screened positive for KPC-Kp, resistant to all available antibiotics except gentamicin and colistin. Despite increased awareness and reinforced hygiene precautions, MDR screening of hospitalized patients in the same surgical unit identified two KPC-Kp(-) patients. Concomitantly, a patient from a neighbouring hospital that underwent endoscopy at the same gastro-enterology ward was diagnosed KPC-Kp positive. These patients had endoscopy on separate days (two weeks apart) but with the same endoscope. Bacterial cultures from this endoscope revealed KPC-Kp.

Retrospective analysis of all the patients that had gastroscopy with the same endoscope, identified a Greek patient with KPC-Kp faecal carriage that was directly transferred from the hospital of Chania (Crete, Greece) two months earlier. Since this patient, 17 patients, being mostly from regional hospitals and out-patients, underwent gastroscopy with the same endoscope. Out of 10 patients that could be screened, 6 were KPC-positive and 2 got infected (one bacteremia and one biliary) with KPC-Kp.

Conclusion: Although the risk of endoscopy-related infection is low, changes of endoscope reprocessing by replacing glutaraldehyde decontamination bath by automated per-acetic acid washers (to prevent Creutzfeldt-Jacob), may have been deleterious to this endoscope. This report identified he spread of a panresistant enterobacterial isolate in our hospital, and at a regional level in Paris.

First detection in Europe of plasmid-mediated fluoroquinolone resistance qnrD determinant

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Objectives: To investigate the presence of the newly-described plasmid-mediated determinants of quinolone resistance qnrC and qnrD among Enterobacteriaceae isolated in the North-East of Italy.

Materials and Methods: We collected 756 non-replicate Enterobacteriaceae, isolated during 2007 and 2008 in five different microbiology laboratories in the North-East of Italy and selected for being non-susceptible to fluoroquinolones and/or resistant to third-generation cephalosporins, qnrC and qnrD were determined by PCR and sequencing.

Results: No qnrC gene was detected, but five strains (0.66% of the total) presented a qnrD gene. They included four Proteus mirabilis and one M. morganii.

No ESBL could be found in either Proteus mirabilis or Morganella morganii. No combination of qnrD with other plasmid-mediated determinant of quinolone resistance was found. All qnrD genes were cloned by heat-shock in E. coli DH5α. They were all located in a conjugative plasmid, which was transferred into the E. coli J53 host strain and selected with 100 µg/ml of Na-azide and 0.5 µg/ml of ciprofloxacin. The ciprofloxacin resistance of the qnrD-producing clinical isolates carrying the plasmid-mediated determinants widely ranged between ≤0.06 and 256 mg/L.

Conclusions: qnrD genes have so far been reported only from China, detected for the first time in Salmonella enterica and, subsequently, in E. coli, and Klebsiella pneumoniae. This is the first report of the qnrD gene in Europe, as well as the first detection of this gene in isolates of the tribe Proteaceae (namely P. mirabilis and M. morganii). This is also the first time that any qnr determinant is found in M. morganii.

Occurrence of PMQR determinants and ESBL in clinical Enterobacteriaceae isolates from an Algerian hospital

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Objectives: β-lactams and fluoroquinolones are the most commonly prescribed antibiotic classes. The aim of this study was to characterize the mechanisms of resistance to those antibiotics in Enterobacteriaceae clinical isolates from an Algerian hospital.

Methods: Sixty-one Enterobacteriaceae strains collected between January to June 2005 in CHU Mustapha Bacha, Algeria, were included in this study: 33 K. pneumoniae, 7 S. marcescens, 6 Enterobacter spp., 6 Proteus spp., 3 C. koseri, 2 S. typhimurium, 2 M. morganii and 1 P. rettgeri. MICS were determined by microdilution broth method. PCR and sequencing were used to screen and identify bla genes (blaTEM, blaSHV, blaOXA, blaCTX-M and plasmid-mediated ampC) and as well as plasmid-mediated quinolone resistance (PMQR) genes (qnrA, qnrB, qnrC, qnrD, qnrS, qepA and aac(6’)-Ib-cr). Linkage of blaCTX-M with ISECp1, IS26 and IS903 insertion sequences was investigated by PCR. Biochemical characterization was performed by isoelectricfocusing.
Worldwide dissemination of resistances

Genetic relatedness among strains was analyzed by pulsed-field gel electrophoresis.

Results: The prevalence of extended-spectrum β-lactamases (ESBL) CTX-M was 45.61% (74/164) with 28 CTX-M-15, 16 CTX-M-3, and 1 CTX-M-14 β-lactamases. Other β-lactamase families were also identified, such as CMY-2 (n=1), TEM-type (n=60) and SHV-type (n=35). IEF confirmed strains as ESBL producers. The association of blaCTX-M genes with other bla genes in the same isolate, namely blaTEM-1 or blaSHV-1, was observed. Multidrug resistance was presented especially with aminoglycosides family (72%). PMQR genes were detected only in 4 quinoline non-susceptible isolates: 3 K. pneumoniae strains had the aac(6′)-Ib-cr gene and 1 M. morgani strain had the recently described QnrD determinant. PFGE analysis revealed a high clonal heterogeneity (>80% similarity) among K. pneumoniae strains (23 unique profile types forming 6 clusters), S. marcescens (5 unique profiles types distributed by 2 clusters), and 2 S. typhimurium strains belonging to the same cluster.

Conclusions: This study revealed the first report of a qnrD gene from an Algerian Hospital. Our work confirms also the geographic spread in Algeria of CTX-M-type β-lactamases, mainly CTX-M-15, and suggests the horizontal transfer of blaCTX-M genes, mediated by mobile elements. Given the emergence of quinolone resistance strains and the dissemination of ESBLs, their continuous spread would have a disturbing development.

16S rRNA methylase containing Enterobacteriaceae in the SENTRY Asia-Pacific region frequently harbour plasmid-mediated quinolone resistance and CTX-M types

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Objectives: 16S rRNA methylases and plasmid-mediated quinolone resistance (PMQR) genes have recently emerged as important resistance mechanisms to aminoglycosides and fluoroquinolones respectively. We examined all 16S rRNA methylase containing Enterobacteriaceae from the Asia-Pacific region (2007–2008) for the presence of PMQR and CTX-M-types, which are already known as a world-wide problem.

Methods: Enterobacteriaceae collected from 10 countries as part of the SENTRY Antimicrobial Surveillance Program during 2007–2008 showing elevated aminoglycoside resistance (amikacin MIC >64 mg/L, and gentamicin and tobramycin ≥16 mg/L) were tested for the 16S rRNA methylase genes (armA, rmtB, and rmtC) by real-time PCR. Isolates positive for 16S rRNA methylase genes were also screened for presence of PMQR genes (qnrA, qnrB, qnrS, aac(6′)-Ib-cr, qepA), and CTX-M encoding genes, using real-time PCR.

Results: 16S rRNA encoding genes were detected in 209 of 4,161 isolates from 5 countries: China (107, 6.9%); India (71, 10.5%); Hong Kong (3, 1.5%); Korea (17, 6.1%); Taiwan (11, 5.0%), among 9 species. armA was found in 136 strains and rmtB in 60 strains; each was observed in all 5 countries. rmtC encoding isolates (n=13) were only from India, observed in 5 species, where previously only described in Proteus mirabilis. 91.4% of all 16S rRNA methylase containing isolates also had either PMQR genes: qnr (n=79, 38%); aac(6′)-Ib-cr (n=66, 32%); qepA (n=20, 10%), or CTX-M genes (n=158, 76%). qepA was found in India and China, exclusively with rmtB and predominantly in Escherichia coli. Multiple PMQR resistance mechanisms was surprisingly frequent, with 32 (15.3%) isolates containing two PMQR genes, predominantly qnr in combination with aac(6′)-Ib-cr. Close to 50% of all 16S rRNA methylase containing isolates also harboured a PMQR gene in combination with CTX-M types.

Conclusion: These results highlight the increasing problem of multiple drug resistance among clinical isolates in the Asia-Pacific region, and the importance of vigilance surveillance programs to monitor emerging resistance trends.

Molecular characterization of multidrug-resistant strains of Salmonella infantis isolated in Italy from human, animals and environment

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Objective: Salmonella infantis represents the third serovar isolated in human infections in Europe, with the majority of strains susceptible to antibiotics. In Italy, since 2004, it is the fourth serovar isolated, and during 2005–2006 multidrug resistant strains emerged in a region of central Italy. In particular strains with R-type ACSSuTkMstx were isolated in human, environment and food of animal origin.

The aim of this work was to evaluate the clonal origin of multiresistant S. Infantis strains isolated from different sources; in addition with the purpose to analyze the molecular basis of antibiotic resistance, resistance gene cassettes were identified and their localization investigated.

Methods: Seventy-two S. infantis strains, isolated between 2002–2008, both susceptible or resistant to antimicrobial drugs, were tested by Pulsed Field Gel Electrophoresis (PFGE) according to Pulse-net protocol. Cluster analysis of PFGE profiles was performed using Bionumerics software. Strains with R-type ACSSuTkMstx have been tested by PCR for the presence of the following gene cassettes: blaTEM, tetA-B-C-G, sul2, strA-B and class 1 integron. Conjugation experiments have been performed in order to establish the location of resistance genes. Plasmids from parental and transconjugant strains were assigned to incompatibility group by PCR-based replicon typing (PBRT).

Results: Cluster analysis performed on PFGE profiles showed a main cluster (genetic similarity>90%) including 49 strains, of which 27 with R-type ACSSuTkMstx. All the 27 strains showed the following resistance genes: blaTEM, tetB, strA-B, sul2, conferring resistance to ampicillin, tetracycline, streptomycin and sulphonamides. In addition they harbour a class 1 integron of 2.2 Kb, including fopA, catB3, aadA4, sul1 gene cassettes, which confer resistance to trimethoprim, chloramphenicol, streptomycin/spectinomycin and sulphonamides. Conjugation experiments showed a unique plasmid harbouring all the resistance genes and belonging to HI1 incompatibility group.

Conclusion: Molecular typing by PFGE and the identification of a plasmid harbouring the resistance gene cassettes demonstrated the circulation of a cluster of S. Infantis, R-type ACSSuTkMstx, during 2005–2006 in a region of central Italy. The presence of a plasmid conferring multidrug resistance could have facilitated the spread of this clone through the environment, food and human.

Multidrug resistance in Salmonella isolates recovered from different food sources in Colombia

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Objectives: Salmonella enterica is the most common etiological agent of food borne salmonellosis worldwide. Ciprofloxacin is the antibiotic of choice for the treatment of these infections. Until date, fluoroquinolone resistance remains uncommon in this bacterium. However, the incidence of nalidixic acid resistance is increasing with isolates showing decreased susceptibility to fluoroquinolones. We have screened a large collection of Salmonella strains to determine the incidence of multi-drug resistance (MDR) and to further characterize the genotypic and phenotypic mechanisms that contribute to this MDR.

Methods: From 2002–2009, 93 Salmonella strains from Colombian foods and exotic animals were obtained from the University of Cordoba (Colombia). The serovar and the susceptibility profile of each strain were determined. Antibiotics representative of 8 different classes were tested and strains that demonstrated resistance to nalidixic acid (NA) were further characterized. PCR was performed to determine the presence of qnr genes. Additionally, efflux activity was evaluated by the EtBr-agar cartwheel method. Ex vivo studies were conducted to assess potential differences on the infection and adherence ability of the isolates.
Results: The most predominant serovars in these isolates were: Uganda (n = 19), Anatum (n = 14), Newport (n = 11) and Braenderup (n = 10); although in total 19 different serovars were obtained. Thirteen isolates were resistant to NA (and/or other antibiotics). Four strains showed increased efflux activity when compared with the controls. This was further confirmed by determining the minimum inhibitory concentration of NA in the presence of the efflux pump inhibitor: phenylalanine-arginine-β-naphthamide (PAβN). Resistance to quinolones was confirmed by PCR through the identification of the qnrB19 gene that confers low-level resistance to this class of antibiotics. Ex vivo assays were useful to clarify the infection and adherence potential of the isolates.

Conclusion: In this study, a large collection of Salmonella isolates obtained from food and exotic animals were resistant to NA and/or other class of antibiotics. These isolates showed different serovars and increased efflux activity along with the presence of the qnrB19 gene. The ex vivo assays contributed to clarify the infection and adherence potential of the isolates. These data highlight the importance of intrinsic and acquired mechanisms of MDR in Salmonella.

Increasing prevalence and population dynamics of MBL-producing Pseudomonas aeruginosa in Russian hospitals

E. Skleenova*, J. D'Souza, O. Sheochenko, M. Edelstein, R. Kozlov on behalf of the ROSNET Study Group

Objectives: To determine the trends in the prevalence and population genetic structure of MBL-producing P. aeruginosa in Russian hospitals over the period of 2002–2007.

Materials and Methods: A total of 1,840 consecutive non-duplicate nosocomial P. aeruginosa isolates collected in 48 hospitals of 31 cities of Russia as part of two national surveillance studies in 2002–2004 (n = 1,053) and in 2006–2007 (n = 787) were tested for MBL production using EDTA-double-disk synergy test and PCR assays for blaVIM and blaIMP genes. All MBL-producing isolates were typed by automated RFLP and MLVA methods. The obtained PCR-RFLP profiles were compared to those of the known integrons.

Results: A total of 48 (4.6%) and 158 (20.1%) isolates collected, respectively, in 2002–2004 and in 2006–2007 were found to produce MBLs. During the first and second study periods MBL producers were identified correspondingly in 3 of 21 and 12 of 26 cities surveyed. By MLVA analysis, all MBL-positive isolates were distributed into two genetic clusters: the predominant one encompassing 23 related MLVA types and corresponding to sequence type (ST) 235 and a minor one comprised of 6 related MLVA types and corresponding to ST234. Isolates of the predominant genetic cluster carried 4 different MBL-integrons whose RFLP profiles matched those of the known integrons harboring blaVIM-2 (GenBank acc. nos. DQ522233 (n = 190), DQ522234 (n = 1), DQ522235 (n = 3)) and blaIMP-1 (DQ522237 (n = 3)). Isolates of the minor genetic cluster carried the blaVIM-2-containing integron (GenBank acc. no. DQ522236; n = 9). VIM-2-producing isolates of the two genetic groups have concomitantly increased in prevalence (ST235: from 4.5% to 18.1%; ST234: from 0.1% to 1.0%) and geographic distribution between the two study periods.

Conclusion: A dramatic increase in the prevalence of MBL-producing P. aeruginosa in Russian hospitals between the periods of 2002–2007 to 2006–2007 was noted owing mainly to a clonal spread.

Community-acquired pneumonia

Usefulness of sputum Gram stain and culture for S. pneumoniae and Haemophilus spp. in the aetiologic diagnosis of community-acquired lower respiratory tract infections and predictive value of serum PCT levels for these bacterial LRTI

M. Ieven*, C. Lammens, A. Vanderstraeten, K. Loens, T. Verheij, P. Little, H. Goossens and the GRACE study team

Objectives: To evaluate (1) the usefulness of sputum Gram stain and culture when applied routinely in the etiologic diagnosis of Community-acquired Lower Respiratory Tract Infections (CA-LRTI) in the GRACE study and (2) to correlate sputum culture results with PCT values in serum.

Methods: From 10/2007 through 05/2008, 711 adult patients with LRTI in the community were included during the first winter in a 3 year prospective study in 11 primary care centers in 8 European countries. Sputum and serum specimens were collected before possible antibiotic therapy was started. Sputa were sent to the local laboratory and processed immediately; sera were stored at −70°C until shipment to the central lab. Quality of sputa was scored according to the number of leukocytes (WBC) and squamous epithelial cells: specimens with ratios of WBC/epithelial cells >1 were defined as good quality sputa. Gram stain and culture were performed according to a standardized protocol. Culture was considered diagnostic when S. pneumoniae or Haemophilus spp were isolated as a predominant microorganism.

Kryptor based procalcitonin (PCT) assay (BRAHMS) was performed according to the manufacturer’s instructions: interpretation of PCT values in relation with bacterial infection was done according to Christ-Crain (Lancet 2004).

Results: Of 711 patients included, 538 (75%) produced sputum: 254 (47.2%) were of good quality. A total of 117/538 (21.7%) of sputa were culture positive: 80 (14.9%) and 37 (6.9%) were positive for S. pneumoniae and other class of antibiotics. These isolates showed different serovars and acquired mechanisms of MDR in Salmonella.

Of 190 (35.1%) sputa were culture positive: 80 (14.9%) and 37 (6.9%) were positive for S. pneumoniae and other class of antibiotics.

Conclusion: In GRACE, a good quality sputum was obtained from a considerable number of patients presenting with LRTI and culture of these specimens had a good diagnostic yield. Gram stain is more sensitive for the detection of pneumococcal CA-LRTI compared to the detection of Haemophilus spp. PCT was found insensitive to predict bacterial infections and guide antibiotic use.

Correlation of the bacterial aetiology with initial procalcitonin levels and duration of antibiotic therapy in lower respiratory tract infections

E. Künzli, K. Woitzek*, F. Dusemund, P. Schuetz, B. Müller, W. Albrich for the ProHOSP Study Group

Objectives: Procalcitonin (PCT) has been established as a reliable and efficient marker for the differentiation between viral and bacterial lower respiratory tract infections (LRTI) and to guide antibiotic therapy. There is conflicting data about a correlation of higher PCT levels with Gram-negative bacteraemia. In the current analysis we correlate the bacterial aetiology with initial PCT-levels and the duration of antibiotic therapy in LRTI.

Methods: Initial PCT levels of patients hospitalized with LRTIs as part of the Swiss multicenter randomized controlled ProHOSP Study were correlated with the identified bacterial aetiology and total antibiotic duration in survivors. PCT was measured using the highly sensitive
Clinical features and outcomes of community-acquired pneumonia due to Haemophilus influenzae

D. Viusus, C. García-Vidal*, J. Adamuz, R. Verdaguer, F. Gudiol, J. Carratalà (Barcelona, ES)

Objective: We sought to determine the clinical features, outcome, and risk factors of community-acquired pneumonia (CAP) caused by Haemophilus influenzae.


Results: Of 3421 consecutive CAP episodes, 192 (5.6%) were caused by H. influenzae. The diagnosis was established with the use of one or more of the following methods: sputum Gram stain and culture (178), blood culture (23), transthoracic needle aspiration specimen culture (5). Other Gram-positive organisms were identified in 12, other Gram-negative organisms in 6 and in 306 patients no causative organisms could be detected.

Conclusion: Initial PCT values differed according to the aetiology of LRTIs with more virulent organisms including pneumococci being associated with higher levels. Considerable overlap between PCT values precluded prediction of the aetiology based on PCT values alone. However, combining knowledge of initial PCT values and causative organisms might predict the required antibiotic duration. At the meeting, we will present the data of the entire 1359 patients of all 6 ProHOSP hospitals.

Clinical prediction score for community-acquired Legionella pneumonia

O. Simonsen*, J. Ringstad (Fredrikstad, NO)

Objectives: Legionnaires’ disease (LD) is an underdiagnosed community-acquired pneumonia (CAP) with high mortality. Although urinary antigen testing has facilitated the microbiological diagnosis during the acute-phase, only 52 of 99 microbiologically verified LD cases from a large outbreak in our region in 2005 tested positive. Previous attempts to design a clinical score have yielded conflicting results. The aim of our study was to assess clinical and biochemical predictors of Legionella pneumonia using outbreak patients.

Methods: All patients with CAP referred to the regional hospital during a period of five weeks in May/June 2005 were included in the study. A clinical protocol was initiated during an early phase of the outbreak. Clinical and laboratory data on entry from patients with Legionella pneumonia and non-Legionella pneumonia were compared.

Results: Complete data sets were present for 91 and 90 patients in the LD-group and non-LD group, respectively. In multivariate logistic regression Legionella pneumonia was associated independently with high levels of C-reactive protein (OR 1.009, 95%CI 1.005–1.013), presence of muscle pain (OR 2.8, 95%CI 1.4–5.9), low serum sodium concentration (OR 0.91, 95%CI 0.84–0.98), and high body temperature (OR 1.45, 95%CI 1.00–2.11). The continuous variables were dichotomized according to the optimal cut-off value. A simple predictive score was derived by assigning one point for each variable (CRP > 175 mg/L, absence of muscle pain, serum sodium < 134 mmol/L, temperature > 38.5 centigrades) resulting in a maximum of 4 points. The area under the receiver operator characteristic of the combined score was 0.85 (95% CI 0.79–0.90), which was better than each parameter alone. The median predictive score was higher in the Legionella group (2 (IQR 2–3) vs 1 (IQR 1–2), p < 0.001). The sensitivity and specificity of a score of ≥3 points was 65% and 92%, respectively, with corresponding values of 86% and 66% for a score of ≥2 points. In the subgroup of LD patients with negative Legionella urinary antigen test (n = 45), a score of ≥3 points and ≥2 points yielded nearly unaltered sensitivity of 67% and 82%, respectively.

Conclusion: A simple score including four routine clinical and biochemical parameters can be used to predict Legionella as aetiological agent of pneumonia, including patients with a negative urinary antigen test. This score will be validated in an upcoming prospective CAP study.

Influence of antibiotic first-dose timing on clinical outcomes in patients with community-acquired pneumonia

S. Luque*, S. Grau, M. Marin-Casino, N. Berenguer, O. Ferrández, M. Espona, M.L. Sorli, J.P. Horcajada, E. Sulas (Barcelona, ES)

Objectives: Databased studies have demonstrated the benefits of an early antibiotic treatment in community-acquired pneumonia (CAP) but results from recent experiences have been less consistent. The objective was to study differences in clinical outcomes between those patients who received antibiotics within 4 h (early antibiotic treatment (ET)) of hospital admission and those who received them after 4 h (delayed antibiotic treatment (DT)).

Methods: Prospective study including consecutively all patients diagnosed with CAP and treated with ceftriaxone from July 2006 until February 2007. Main outcome measures: demographics, pneumonia severity index (PSI), length of hospital stay (LOS), length of antibiotic treatment (LOT), time to clinical stability (TCS) (measured as signs and symptoms resolution) 30-day-mortality and 6-month-mortality. In statistical analysis, “U” Mann–Whitney test for dichotomic variables and Fischer exact test for continuous variables were employed. A value of p < 0.05 was considered statistically significant.

Results: Total patients: 118. Data comparing early ET versus DT are showed in table1.

Conclusions: Only differences in LOS were observed after comparing ET versus DT. Mean LOS was 2.5 days shorter with antibiotic
administration within 4 hours with less than later administration. Timing was not associated with LOT, TCS or short- and long-term mortality.

<table>
<thead>
<tr>
<th>Mean values</th>
<th>Early treatment (47 patients)</th>
<th>Delayed treatment (71 patients)</th>
<th>p</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age (years)</td>
<td>70.6 (95% CI 66.1–75.1)</td>
<td>71.9 (95% CI 68.1–75.8)</td>
<td>0.523</td>
</tr>
<tr>
<td>Male (%)</td>
<td>35 (74.5%)</td>
<td>45 (63.4%)</td>
<td>0.207</td>
</tr>
<tr>
<td>PSI class I</td>
<td>3 (64%)</td>
<td>4 (5%)</td>
<td>0.900</td>
</tr>
<tr>
<td>PSI class II</td>
<td>1 (2.1%)</td>
<td>2 (2.8%)</td>
<td></td>
</tr>
<tr>
<td>PSI class III</td>
<td>17 (4.9%)</td>
<td>19 (2.7%)</td>
<td></td>
</tr>
<tr>
<td>PSI class IV</td>
<td>20 (42.6%)</td>
<td>24 (33.8%)</td>
<td></td>
</tr>
<tr>
<td>PSI class V</td>
<td>16 (34.0%)</td>
<td>27 (38.0%)</td>
<td></td>
</tr>
<tr>
<td>LOS (days)</td>
<td>12.0 (95% CI 9.9–14.1)</td>
<td>14.5 (95% CI 12.0–17.0)</td>
<td>0.041</td>
</tr>
<tr>
<td>LOT (days)</td>
<td>11.3 (95% CI 10.0–12.6)</td>
<td>11.6 (95% CI 10.2–13.0)</td>
<td>0.978</td>
</tr>
<tr>
<td>TCS (days)</td>
<td>11.5 (95% CI 8.6–14.5)</td>
<td>11.5 (95% CI 9.8–13.1)</td>
<td>0.286</td>
</tr>
<tr>
<td>30-day mortality</td>
<td>5 (10.6%)</td>
<td>7 (9.9%)</td>
<td>0.891</td>
</tr>
<tr>
<td>6-month mortality</td>
<td>7 (14.9%)</td>
<td>11 (15.5%)</td>
<td>0.929</td>
</tr>
</tbody>
</table>

**Results:**

Table 1: Immunization status and pneumococcal serotypes

- **Immunized Number Serotypes covered by immunizations**
  - Not covered: PPV and PCV7
  - PPV only: PPV total (%)

<table>
<thead>
<tr>
<th>Immunized</th>
<th>Number</th>
<th>Serotypes covered by immunizations</th>
</tr>
</thead>
<tbody>
<tr>
<td>Yes</td>
<td>6</td>
<td>2</td>
</tr>
<tr>
<td>No</td>
<td>10</td>
<td>1</td>
</tr>
<tr>
<td>Unknown</td>
<td>7</td>
<td>2</td>
</tr>
<tr>
<td>Total (%)</td>
<td>23</td>
<td>5 (22)</td>
</tr>
</tbody>
</table>

**Conclusions:**

CPT demonstrated non-inferiority to ceftriaxone in treating patients hospitalized with moderate to severe CABP in the CE and MITTE study populations of FOCUS 2. Clinical cure rates in the 2 co-primary populations and in patients with a confirmed bacterial infection were numerically higher for CPT compared with CRO. CPT had high clinical cure rates and was well tolerated, with a safety profile similar to ceftriaxone. CPT has the potential to be an effective, well-tolerated treatment option for CABP.

**Objective:** Invasive pneumococcal disease (IPD) is a major cause of morbidity and mortality in the United Kingdom. The 23-valent pneumococcal polysaccharide vaccine (PPV) has been recommended for all adults 65 years and over and younger adults with chronic medical conditions or immunosuppression since 2005. The 7-valent pneumococcal conjugate vaccine (PCV7) was introduced into the routine childhood immunization program in September 2006. We aimed to look at pneumococcal bacteremia serotypes and PCV7 immunization history in our district general hospital population.

**Methods:** Patients who had pneumococcal bacteremia between October 2008 and April 2009 were identified retrospectively. Isolates were sent to the United Kingdom Health Protection Agency reference laboratory for serotyping. Clinical details were acquired via case note review. Immunization status was obtained from general practitioners.

**Results:** We identified 29 adults with pneumococcal bacteremia and obtained clinical details for 28. There were 18 patients for whom PPV is currently recommended. Of these seven (47%) had been immunized, of whom two (29%) died; eight had no history of immunization, of whom two (25%) died. For three cases immunization history was not obtained. The total mortality for this group of 18 was 28%. Pneumococcal serotype results were available for 23 patients. Of these, six patients had received PPV, of whom four (66%) acquired infections with serotypes covered by PPV. Of the ten patients who had not received PPV, nine had serotypes covered by PPV. In total, 5 isolates (22%) were not covered by PPV or PCV7, and 14 isolates (61%) were covered by PPV but not PCV7. The total number of isolates covered by PPV was 18 (78%) (Table 1).

**Conclusion:** In this small study, we observed a high rate of mortality in patients for whom PPV is recommended which was similar in those who had (29%) and had not (25%) received PPV. Uptake of vaccine where recommended was sub-optimal (39%). We observed four cases of apparent failure of the PPV vaccine to protect against IPD with pneumococcal serotypes covered by PPV. This is in keeping with observations that PPV is incompletely protective against IPD. Of the 23 isolates serotyped, 14 (61%) were covered by PPV but not PCV7. As serotypes may spread from the paediatric to the adult population, these may represent serotype-replacement following the introduction of PCV7. Promotion of vaccine uptake and ongoing serotype monitoring is warranted.
Methods: In a prospective, observational study in 22 Dutch hospitals, patients (≥18 years) admitted to the ER with a clinically suspected CAP were included between January 2008 and March 2009. Recent hospitalization (<2 wks), stay in long-term care facilities, known bronchial obstruction or a history of post-obstructive pneumonia, primary or metastatic lung cancer, AIDS/ PCP/ TBC and unconsciousness were exclusion criteria. History taking, physical examination, biochemical and hematological blood testing, blood- and sputum cultures and BINK nephococcal urinary antigen testing were performed in all patients. All pneumococcal bacteraemia isolates were serotyped (at the Netherlands Reference Laboratory Amsterdam). Pneumococcal CAP was defined on the presence of clinical criteria for CAP, radiographic confirmation by a radiologist and isolation of S. pneumoniae from blood or sputum (if dominant flora) or positive antigen testing in urine.

Results: Of 1631 included patients, 1115 had radiographically confirmed CAP and 210 (18.8%) had pneumococcal CAP, diagnosed on isolation of S. pneumoniae from blood culture (n=282, 73.7% of all bloodcultures), sputum culture (n=24), or positive urinary antigen test (n=151). 75 bacteraemia isolates were serotyped. Serotypes 14 (n = 9), 1, 7F, 19A and 22F (n = 8) were most common. Potential vaccine coverage was 28% for the 7-valent, 67% for the 13-valent pneumococcal conjugate vaccine (PCV) and 93% for 23-valent polysaccharide vaccine (PS). In unadjusted analyses, mortality risk in unadjusted but not adjusted analyses [relative risks (RR) = 2.01 (95% CI 1.06–3.81)]. Serotypes 3, 6B, 11A, 14, 18C, 19F and 23F were associated with increased mortality risk in crude analyses but only serotype 6B and 11A were associated with increased mortality risk in adjusted analyses.

Conclusion: In this large population-based study host risk factors appeared to be the strongest determinants of both risk of infection with serotypes according to invasive disease potential as well as mortality outcome.

Figure 1. Serotype distribution and potential vaccine coverage.

Serotype-specific mortality risk among patients with invasive pneumococcal disease: Swedish population-based study

P. Naucler*, J. Darenberg, Å. Örtqvist, B. Henriques Normark (Stockholm, SE)

Objectives: To investigate pneumococcal serotype-specific mortality risk correlated to the serotype invasive disease potential among patients with invasive pneumococcal disease (IPD).

Methods: In Sweden it is mandatory to report IPD and isolates are collected for serotyping and molecular typing. Of 4195 episodes of IPD among adults reported between Jan 2007 to Oct 2009 a total of 3692 isolates were serotyped (88%). A questionnaire study was performed to obtain clinical and socio-demographic information about patients with serotyped IPD [obtained for 1657/3692 patients (45%)]. In a preliminary analysis of the 1657 patients we assessed the absolute serotype-specific 30-day mortality risks and relative risks using regression modeling on group level according to previously defined invasive disease potential [high (serotypes 1 and 7), medium (serotypes 4, 9, 14 and 18) and low (serotypes 3, 6A, 6B, 8, 15, 19, 33 and 38) and for individual serotypes. Risk estimates were adjusted for potential confounders.

Results: Pneumococcal serotype prevalence ranged from 0.05% for serotype 5 to 13.4% for serotype 14 and was stable over the observed period. Absolute mortality risk was highest for serotypes with low invasive disease potential (12.8%) followed by serotypes with medium- (8.6%) and high (4.9%) invasive disease potential. Serotypes with low invasive disease potential (12.8%) followed by serotypes with medium- (8.6%) and high (4.9%) invasive disease potential. Serotypes with low invasive disease potential (12.8%) followed by serotypes with medium- (8.6%) and high (4.9%) invasive disease potential.

with low invasive disease potential were associated with increased mortality risk in unadjusted but not adjusted analyses [relative risks 2.62 (95% CI 1.38–5.00) and 1.61 (95% CI 0.84–3.09) respectively] and a test for trend according to invasive disease potential was significant in unadjusted (p-value: 0.001) but not adjusted (p-value: 0.10) analyses. Patients infected with serotypes of lower invasive disease potential were older, more likely to be diagnosed with meningitis, suffer from chronic disease and immunosuppression (all p-values <0.003). Serotype 3, 6B, 11A, 14, 18C, 19F and 23F were associated with increased mortality risk in crude analyses but only serotype 6B and 11A were associated with increased mortality risk in adjusted analyses.

Conclusion: In this large population-based study host risk factors appeared to be the strongest determinants of both risk of infection with serotypes according to invasive disease potential as well as mortality outcome.