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GASTROINTESTINAL TUMOURS, COLORECTAL

79O Clinical performance of Immunoscore® in early colon cancer in the Asian population

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Background: Immunoscore® is an in vitro diagnostic test predicting the risk of relapse in early-stage Colon Cancer (CC), by measuring the host immune response at the tumor site. This risk-assessment tool provides independent and superior prognostic value than the usual risk parameters and is intended to be used as an adjunct to the TNM classification for clinical decision. In the present study, we investigated Immunoscore® clinical performance in the Asian population from the international SITC-led validation study (Pagès et al. The Lancet 2018).

Methods: Out of the 2681 eligible stage I-III patients of the international Immunoscore® study, 423 were collected from 4 expert centers in Asia including Japan (n=330), China (n=35), and India (n=58). Patients were classified by Immunoscore® based on pre-defined cutoffs, either in 5 (IS 0-4) or 2 categories: IS Low (IS 0-1) and IS High (IS 2-4). Time to recurrence (TTR) was compared between Immunoscore® categories.

Results: Immunoscore® Low and High were observed in 37% (n=158) and 63% (n=265) of the Asian cohort, respectively. Immunoscore® was positively and significantly correlated with TTR. After 5 years, 86.9% (95% CI 82.7-91.4), and 77% (95% CI 70,5-84,1) of Immunoscore -High and -Low patients respectively were event free (HR =0.52; 95% CI 0.32-0.86; p=0.0085). When adjusting the model with Immunoscore®, age, gender, T-stage, N-stage, sidedness and MSI, and when stratified by center, Immunoscore® remained a significant parameter (HR=0.45; 95% CI 0.22-0.91; p=0.027). When stratified into 5 Immunoscore® categories, TTR rates at 5 years were 100%, 96%, 84%, 80%, and 73.5% for IS4, IS3, IS2, IS1, IS0, respectively. These results were similar to those found in European and North American patients.

Conclusions: Immunoscore® is a strong prognostic indicator of the risk of recurrence in stage I-III CC patients who receive standard of care treatment in real-life clinical practice in Asia. This first standardized immune-based assay risk assessment tool can be used reliably to guide clinical decision according to each patient information.

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80MO Gut microbiome analysis for predicting neoadjuvant chemoradiotherapy response in locally advanced rectal cancer patients

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Background: The gut microbiome has been reported to be involved in antitumour immunotherapy and chemotherapy responses; however, evidence-based research on the role of the gut microbiome in neoadjuvant chemoradiotherapy (nCRT) responses of locally advanced rectal cancer (LARC) patients is scarce. This research aims to evaluate the feasibility of the gut microbiome in predicting nCRT responses in LARC patients.

Methods: We collected 167 faecal samples from 84 LARC patients before and after nCRT in our institution and 31 faecal samples from healthy individuals for 16S ribosomal RNA sequencing. We used the AJCC tumour regression grade (TRG) system to evaluate the nCRT responses and accordingly divided patients into two groups. Patients with TRG scores of 0-1 were grouped as responders (R group), and those with TRG scores of 2-3 were grouped as non-responders (NR group). After characterizing the gut microbiome and identifying biomarker bacteria related to nCRT responses, we constructed a random forest classifier for nCRT response prediction of a training set of 37 baseline samples and validated the classifier with the remaining 47 baseline samples.

Results: Taxonomic differences in relation to nCRT responses were noticed in baseline faecal samples, including overrepresentation of butyrate-producing bacteria (Dorea and Anaerostipes) in R, and overrepresentation of Coriobacteriaceae and Fusobacterium in NR. During nCRT, a decline in bacterial richness related to therapeutic responses was observed. Furthermore, microbiome alterations imposed by nCRT were represented by a decrease in LARC-related pathogens and an increase in Lactobacillus and Streptococcus, and the increase of Streptococcus was exclusively shown in R subgroup. Ten variables were selected for the classifier, including Dorea, Anaerostipes and Streptococcus, and the area under the curve reached 93.57% (95% CI: 85.76%～100.00%) in the training set and 73.53% (95% CI: 58.96%～88.11%) in the validation set.

Conclusions: The gut microbiome plays a role in nCRT responses and provides potential biomarkers to predict nCRT responses. Further validation in a larger sample size is needed.

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