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ABSTRACT

Studying the cellular function of microRNAs requires genetic strategies to generate their loss-of-function. Recently, a novel approach of targeted genomic deletion was proposed, which is based on induction of site-specific DNA cuts with Cas9/gRNA ribonucleoprotein complexes, combined with homologous recombination-dependent insertion of cassettes that contain sequences for Cre-lox or FLP-FRT systems. Here, we provide a technical report describing application of this CRISPR/Cas9-directed homologous recombination procedure to the generation of human tumor cells in which conditional knockout of an X-linked cluster of microRNAs (miR-105/miR-767) can be induced. We describe the successive steps of genetic engineering and cell clone selection that allowed us to generate cells with the expected genome editing.

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Application of CRISPR/cas9-Directed Homologous Recombination to the Generation of Human Tumor Cells with Conditional Knockout of an X-Linked MicroRNA Locus

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Abstract

Studying the cellular function of microRNAs requires genetic strategies to generate their loss-of-function. Recently, a novel approach of targeted genomic deletion was proposed, which is based on induction of site-specific DNA cuts with Cas9/gRNA ribonucleoprotein complexes, combined with homologous recombination-dependent insertion of cassettes that contain sequences for Cre-lox or FLP-FRT systems. Here, we provide a technical report describing application of this CRISPR/Cas9-directed homologous recombination procedure to the generation of human tumor cells in which conditional knockout of an X-linked cluster of microRNAs (miR-105/miR-767) can be induced. We describe the successive steps of genetic engineering and cell clone selection that allowed us to generate cells with the expected genome editing.

Keywords: CRISPR/cas9; MicroRNA; FLP recombinases; LoxP; Dulbecco's medium; T4 DNA ligase

Introduction

MicroRNAs (miRNAs) are small noncoding RNAs that exert important cellular functions by repressing post-transcriptional gene expression through binding to target mRNAs [1]. More than 60% of all human genes are predicted to be regulated by a total of over 2,000 mature miRNAs. Some miRNAs are expressed in virtually all cell types, whereas others are highly tissue-specific with a distinct function depending on cell type or organ. miRNAs play key roles in most biological processes, including cell division and death, cellular metabolism, intracellular signaling, immunity and cell movement. Not surprisingly, disruption of miRNA expression has been functionally linked to various pathological and occasionally malignant outcomes [2]. Specific miRNA expression patterns, which have been associated with particular diseases, hold great prognostic value. In cancer, oncogenic miRNAs as well as tumor suppressor miRNAs have been identified, and therapeutic strategies directed against such cancer-related miRNA are being considered [3,4].

The physiological roles of most miRNAs still need to be deciphered. Therefore, tools allowing manipulation of miRNA activity are required. Gain-of-function by over-expression of the miRNA is relatively easy, and can be achieved by transfection of synthetic microRNAs or by enforcing expression of primary miRNA transcripts [5,6]. Loss-of-function analyses are less obvious. miRNA inhibitors based on synthetic antisense molecules or miRNA sponges, which act by binding and sequestering miRNAs away from their natural targets, are available [7]. However, such inhibitors have some disadvantages, including incomplete masking of miRNA function, and uncontrolled off-target effects.

Genome engineering is a powerful tool for dissecting biological mechanisms. The Clustered, Regularly Interspaced, Short Palindromic Repeats (CRISPR) / CRISPR-associated protein 9 (Cas9) system provides a rapid and efficient technology for targeted genome editing. In association with a specifically designed guide RNA (gRNA), Cas9 can achieve site-specific DNA recognition and cleavage [8]. A constraint in this genome editing process is the compulsory presence of a Protospacer Adjacent Motif (PAM) sequence near the Cas9 cleavage site. In most cases, the site-specific DNA double-strand breaks (DSB) induced by Cas9 triggers a non-homologous end-joining (NHEJ) process of DNA repair, leading to small insertions or deletion in the nucleotide sequence. This procedure is therefore exploited to generate loss-of-function of protein coding genes, via alteration of the open reading frame. Short miRNAs are less amenable to this editing process, as many of them do not carry the required PAM motif within their sequence.

An alternative use of the CRISPR/Cas9 technology, which would be better adapted to manipulate miRNAs, has been proposed. In this setting, Cas9 cleavages are used to direct homologous recombination-dependent insertion of cassettes that contain LoxP or FRT sequences up- and downstream of the miRNA locus, thereby allowing subsequent deletion of the embedded sequence upon expression of Cre or FLP recombinases. This procedure requires that template DNA sequences with homologous arms are provided to the cells, in order to stimulate homology-directed repair (HDR) of the Cas9-induced DSB [9]. Examples where this technology was used to delete a miRNA locus remain however scarce [10,11]. Here, we report successful application of this procedure to the generation of human tumor cells in which a miRNA locus can be conditionally deleted. The locus targeted in our study corresponds to an X-linked cluster of two miRNAs (miR-105 and miR-767), which were recently shown to display aberrant activation in wide variety of tumors, and to exert oncogenic potential [12,13].

Materials and Methods

Cell culture and transfection

HT1080, LB2201-MEL, Mi13443, SK-MES1, GLCP1 cell lines were cultured in Iscove's modified Dulbecco's medium (IMDM, Life

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DNA transfection was performed in a T75 flask, with 2 to 6 millions cells, using Lipofectamine 2000® Reagent (Invitrogen). Five hours after transfection, the medium was replaced. The amount of transfected DNA was 5 µg of Cas9/sgRNAs vectors and 5 µg of donor pEZ-Frt-lox-5' or pEZ-Frt-lox-3' vectors. Prior to transfection, pEZ-Frt-lox-5' vector was linearized 5' to the left homology arm by digestion with the EcoRV restriction enzyme, and the pEZ-Frt-lox-3' vector was digested by EcoRV and Xhol restriction enzymes. Transfectants were selected for 15 days in medium containing 0.8 to 2 mg/ml of genetin, depending on the type of cells. Two weeks after transfection, integration of the donor DNA was tested by PCR amplification with primers encompassing the recombiant fragment on genomic DNA. Cell populations showing effective recombination were cloned by limiting dilutions.

For Cre or FLP recombination, cells were transiently transfected using Lipofectamine 2000® Reagent (Invitrogen) in 6-well plates with 2 µg of CMV-Cre or pCAGGS-FLPe vectors, and cloned by limiting dilution 72h after transfection.

Plasmid design and construction

The pX330-U6-Chimeric_BB-CHb-hSpCas9 vector (available at Addgene, and kindly provided by P. Coulie) was digested using Fast-Digest BbsI (Thermo Scientific) and double-stranded oligonucleotides corresponding to different spacer sequences were ligated with T4 DNA ligase (Thermo Scientific) generating different sgRNAs. Double-stranded oligonucleotides for spacer sequences were obtained by annealing pairs of complementary oligos (Eurogentec) composed of the spacer sequence flanked by adapter sequences (Forward: 5'-TTTGTGTAATGGGATCGTTTGG; Reverse: 5'-attaCTCGAGccatagactggtacttaccgaga). PCR products were purified (QIAGEN) and cloned into the plasmid pEZ-Frt-lox-DT vector (Addgene, and kindly provided by P. Coulie) was digested using Fast-Digest HindIII (Thermo Scientific) and linearized 5' to the left homology arm by digestion with the EcoRV restriction enzyme, and the pEZ-Frt-lox-DT vector was digested by EcoRV and Xhol restriction enzymes. Transfectants were selected for 15 days in medium containing 0.8 to 2 mg/ml of genetin, depending on the type of cells. Two weeks after transfection, the donor DNA was tested by PCR amplification with primers encompassing the recombiant fragment on genomic DNA. Cell populations showing effective recombination were cloned by limiting dilutions.

RNA preparation and RT-qPCR evaluation of miRNA expression levels

We isolated total RNA using the TRIzol Reagent (Roche) according to the manufacturer's protocol, and used 100 ng of this RNA for reverse transcription with the miRCURY LNA Universal RT microRNA PCR kit (Exiqon). The resultant cDNA was diluted 20 times, and a 2.5 µl aliquot was used in a SYBRGREEN qPCR with LNA specific primers for miR-105 and miR-767 (Exiqon). RNU44 was used as internal control.

Flow cytometry cell sorting

HT1080 #72.2.25.9 clone was transiently transfected by pTM945-Cre-IRESC-cherry vector or control vector pTM945-mCherry, coding both for mCherry fluorescent protein. Two days later, cells were sorted by fluorescence-activated cell sorting (FACS, FACSaria TM III, BD Biosciences) based on mCherry signal. The sorted populations were harvested for RT-qPCR analysis 6 to 34 days after reseeding.

Detection of gRNA efficiency

HT1080 cells were transfected with pX330-U6-Chimeric_BB-CBh-hSpCas9 vector carrying 8 different sgRNAs, named Cas9/sgRNA1-8. Three days after transfection, DNA extracted from those cells was treated with RNase A and submitted to SURVEYOR* Mutation Detection Kit, according to the manufacturer's recommendations (Transgenomic). In brief, the genomic region flanking the CRISPR/Cas9 target site was first

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amplified by PCR using PrimeSTAR HS DNA polymerase (Takara). After migration through agarose gel, PCR products were purified using QIAquick Gel Extraction Kit (Qiagen). 2 µg of the purified PCR products were mixed with 10x Surveyor Buffer (100 mM Tris, 500 mM KCl, 15mM MgCl₂) and water to a final volume of 20 µl, and subjected to a re-annealing process to enable heteroduplex formation: 95°C for 10min, 95°C to 85°C ramping at −2°C/s, 85°C to 25°C at −0.25°C/s, and 25°C hold for 1 minute. After re-annealing, PCR products were treated with 1 µl of SURVEYOR nuclease and SURVEYOR enhancer S (Transgenomics) during 1 hour at 42°C. DNA samples were run in a 2% agarose gel, in TAE 1x buffer supplemented with ethidium bromide. Quantification was performed by calculating relative band intensities using ImageJ software.

Results and Discussion

General strategy for the generation of cells with conditional knockout of MIR105/767

The general strategy to obtain cells where the X-linked MIR105/767 locus can be conditionally deleted is described in Figure 1 and each step is described in details below. In brief, the procedure involved successive steps of CRISPR/cas9-directed homologous recombination to permit integration of neomycin-loxP/FRT cassettes 3' and 5' to the MIR105/767 genomic locus, as well as exposure of cells to Cre and FLP (Flippase) recombinases to leave only single loxP sites on both sides. At each step of the procedure, a cell clone with the appropriate integration/recombination was selected, and used for the subsequent step.

Selection of efficient single guide RNAs (sgRNAs)

Targeting of the Cas9 nuclease to a specific site on the genome is commonly achieved through its association with a chimeric RNA construct, termed single guide RNA (sgRNA). The sgRNA includes the tracrRNA sequence, which allows association of the RNA molecule with the Cas9 enzyme, and the spacer sequence, which binds the genomic target by nucleotide complementarity. Not all sgRNAs are equally efficient. The first step to achieve our construction was therefore to test different sgRNAs, and to select those that stimulate site-specific cleavage by Cas9 with the highest efficiency (Figure 2). Using a spacer RNA design algorithm (http://crispr.mit.edu), we designed four sgRNAs for each side of the MIR105/767 locus. The corresponding sequences were inserted in the pX330-U6-Chimeric_BB-CBh-hSpCas9 vector, which also carries a human codon-optimized Cas9 coding sequence. These different Cas9/sgRNA vectors were then transfected into HT1080 cells, generating DSBs at precise sgRNA targeted sites. The error-prone NHEJ process results in the formation of mutation or small insertions or deletion. Genomic DNA was collected from transfectants after three days. DNA cleavage efficiency was evaluated by mutation detection assay using the Surveyor® Mutation Detection kit. Thus, DNA
fragments carrying the expected cleavage site were amplified by PCR. Amplicons were denatured by heat, and then allowed the re-anneal slowly. They were then exposed to the Surveyor nuclease, which cuts heteroduplexes but not homoduplexes of DNA. Nuclease-treated DNA fragments were electrophoresed in an agarose gel, and the cleavage efficiency was evaluated by calculating the ratio between the cleaved and uncleaved band (percentage of indel). Using this method, we identified the sgRNAs that directed the most efficient Cas9-mediated cleavage either 5' (sgRNA1, 9.3% indel) or 3' (sgRNA8, 12.9% indel) to the MIR105/767 locus. The left homology arm (LHA5', 306bp) and the right homology arm (RHA5', 692bp) corresponded to genomic sequences located upstream and downstream the Cas9/sgRNA1 cutting site, respectively.

We transfected Cas9/sgRNA1 and pEZ-FRT-lox-5' vectors in six different human cell lines: embryonic kidney cells (HEK293), two melanoma cell lines (Mi13443 and LB2201-MEL), two lung carcinoma cell lines (GLCP1 and SKMES1), and a fibrosarcoma cell line (HT1080). We selected cells of male origin, as these contain only one X chromosome. Following transfection, cells were selected for two weeks in neomycin-containing medium, and part of the resistant populations was harvested for DNA extraction. Integration of the Neo-1loxP/2FRT cassette was assessed by PCR amplification with one primer matching a genomic sequence upstream of the LHA5' and another primer corresponding to a sequence within the cassette. Of the six transfected cell lines, only three (HT1080, GLCP1 and SK-MES1) showed evidence of integration of the Neo-2loxP/2FRT cassette (Figure 3).

We decided to derive clones from the transfected HT1080 cell population, in order to isolate clones harboring the appropriate integration event. Out of 113 clones, 4 showed integration of the Neo-2loxP/2FRT, as evidenced by positive signals following PCR amplification with indicated primers (Figure 4). Following verification of PCR products by sequencing, only clones #72, #76 and #83 showed perfect recombination. The remaining clone (#29) showed deletions in the intersection between homology arms and the cassette sequence. Overall, we observed a 2.5% (3/113) efficiency of homologous recombination directed by CRISPR/Cas9 towards the 5' side of the MIR105/767 locus in HT1080 cells. Clone HT1080#72 was selected for the subsequent steps.

**Cassette removal by Cre recombinase**

In order to obtain cells where the Neo-2loxP/2FRT cassette was removed and only one loxP sequence remained 5' to the MIR105/767 locus, HT1080#72 cells were transiently transfected with a vectors encoding Cre recombinase (CMV-Cre). Sub-clones were isolated, and screened for effective loxP recombination by PCR amplification with primers matching sequences in LHA5' and RHA5' homology arms (Figure 5). Out of five tested clones, two clones (#72.2 and #72.3) showed effective recombination. We chose clone HT1080 #72.2 for the subsequent steps aiming at introducing a second loxP site 3' to the MIR105/767 locus.

**Cassette removal by Cre recombinase**

We next performed directed integration of a Neo-1loxP/2FRT cassette 3' to the MIR105/767 locus. In HT1080#72.2 cells, we constructed a vector (pEZ-FRT-lox-3') in which left and right homology arms were inserted on each side of the Neo-1loxP/2FRT cassette.
Cassette (Figure 6). The left homology arm (LHA5', 774bp) and the right homology arm (RHA3', 692bp) corresponded to genomic sequences located upstream and downstream of the Cas9/sgRNA8 cutting site, respectively. Restriction sites used for insertion of the RHA3' into the vector were chosen in order to delete the neighboring loxP site.

HT1080#72.2 cells were transfected with Cas9/sgRNA8 pEZ-FRT-lox-3' vectors, and following neomycin selection, resistant clones were derived. These clones were screened for integration of the Neo-1loxP/2FRT cassette by PCR amplification on genomic DNA, using primer pairs matching either sequences within the cassette or genomic sequences outside of the homology arms. Recombinant clones are expected to produce a signal with both PCRs. PCR amplification of PCBD2 served as control. According to PCBD2 amplification, only 113 of these were analyzable. Control samples included the total population of HT1080 cells transfected with pX330-sgRNA1/pEZ-FRT-lox-5' (HT1080 sgRNA1), untransfected HT1080 cells, salmon sperm DNA (DSS), and water.

**Figure 4:** PCR screening for Neo-2loxP/2FRT cassette insertion in HT1080 cell clones.
The schematic draw depicts the annealing sites of the PCR C primers used to detect ‘‘floxing’’ of the 5’ cassette. The PCR product is expected at a size of 408bp in case of appropriate loxP recombination (1888bp in non-recombinant cells). PCR in naïve cells is expected to yield a 355bp product. Five clones isolated from the CMV-Cre-transfected HT1080#72 cell population were tested. Control samples included untransfected HT1080 cells, salmon sperm DNA (DSS), and water.

**Figure 5:** PCR screening for Cre-induced loxP recombination at the 5’ cassette.

HT1080#72.2 cells, which had been transfected with pX330-sgRNA8 and pEZ-FRT-lox-3’ vectors, were selected in neomycin and cloned. DNA from 40 clones was tested for insertion of the Neo-1loxP/2FRT cassette insertion 3’ to the MIR105/767 by PCR. The upper panel indicates the position of the primers and expected product size of the two PCR (D and E). PCR results for the PCBD2 control sequence shows that only 33/44 clones were analyzable. Control samples included untransfected HT1080 cells, and water.

**Figure 6:** PCR screening for Neo-1loxP/2FRT cassette insertion 3’ to the MIR105/767 locus in HT1080 cell clones.
We next aimed to delete the cassette integrated 3’ to the MIR105/767 locus, but without removing the single loxP site. To this end, HT1080#72.2.25 cells were transiently transfected with a vector encoding Flippase, which induces recombination between FRT sites. Following transfection, cellular clones were isolated, and screened for effective FRT recombination by PCR amplification with primers matching sequences in LHA3’ and RHA3’ homology arms (Figure 7). Out of 21 tested clones, 8 clones (38%) showed effective FRT recombination. Among these, clone HT1080 #72.2.25.9, in which the MIR105/767 locus is now surrounded by two loxP sites, was chosen for subsequent analyses.

Cre recombinase-mediated knockout of the MIR105/767 locus

Since HT1080#72.2.25.9 cells contain loxP sequences on both sides of the MIR105/767 locus, their exposure to Cre recombinase is expected to induce deletion of the corresponding genomic region. To test this, HT1080#72.2.25.9 cells were transiently transfected with the CMV-Cre vector. Previous experiments established a 40% efficiency of transfection in HT1080 cells, implying that only part of the transfected HT1080#72.2.25.9 will effectively express Cre recombinase. We therefore decided to verify successful deletion of the MIR105/767 locus in clones isolated from the CMV-Cre transfected HT1080#72.2.25.9 cell population. Following derivation of the clones, their DNA was extracted and submitted to PCR screening with three different pairs of primers allowing unambiguous determination of the presence or absence of the MIR105/767 locus (Figure 8). Among 24 tested clones, 7
MIR105/767 locus can be CRISPR/Cas9-directed homologous recombination, which allowed us respectively (Figure 9).

6% residual expression level was observed for miR-105 and miR-767, expression of these two miRNAs in Cre-exposed cells, as only 5.6% and qPCR in FACS-sorted cells. The results confirmed marked loss of deletion, MIR105/767 PCR screening with the above-mentioned primer pairs (Figure 8). The Genomic DNA was extracted from FACS sorted cells, and submitted to lacking Cre recombinase (pTM945-mCherry), was treated in parallel.

(FACS) and reseeded. A control group, transfected with a similar vector vector, which expresses both Cre recombinase and the mCherry fluorescent protein. Thus, HT1080#72.2.25.9 cells were transfected with pTM945-Cre-mCherry, and two days later cells with the highest level of fluorescence were selected by fluorescence-activated cell sorting (FACS) and reseeded. A control group, transfected with a similar vector lacking Cre recombinase (pTM945-mCherry), was treated in parallel. Genomic DNA was extracted from FACS sorted cells, and submitted to PCR screening with the above-mentioned primer pairs (Figure 8). The results showed efficient enrichment of cells with deletion, although a small proportion of non-recombined cells remained (Figure 8). We next tried to facilitate the knockout procedure by avoiding the process of cellular cloning that followed CMV-Cre transfection. To this end, we replaced CMV-Cre with the pTM945-Cre-IREs-mCherry vector, which expresses both Cre recombinase and the mCherry fluorescent protein. Thus, HT1080#72.2.25.9 cells were transfected with pTM945-Cre-IREs-mCherry, and two days later cells with the highest level of fluorescence were selected by fluorescence-activated cell sorting (FACS) and reseeded. A control group, transfected with a similar vector lacking Cre recombinase (pTM945-mCherry), was treated in parallel. Genomic DNA was extracted from FACS sorted cells, and submitted to PCR screening with the above-mentioned primer pairs (Figure 8). The results showed efficient enrichment of cells with MIR105/767 deletion, although a small proportion of non-recombined cells remained (Figure 8). We also analyzed the expression of miR-105 and miR-767 by RT-qPCR in FACS-sorted cells. The results confirmed marked loss of expression of these two miRNAs in Cre-exposed cells, as only 5.6% and 6% residual expression level was observed for miR-105 and miR-767, respectively (Figure 9).

Altogether, we described a genetic engineering strategy based on CRISPR/Cas9-directed homologous recombination, which allowed us to create a human tumor cell line in which the MIR105/767 locus can be conditionally deleted. Our data therefore confirm the feasibility of this strategy, and provide several guidelines concerning the experimental procedures. CRISPR/Cas9-directed homologous recombination was found to occur with an expected efficiency (2.5% and 12.1% efficiency for the 5’ and 3’ position, respectively). One of the pitfalls of the CRISPR/Cas9 technology is the presence of many off-target mutations induced by Cas9, which renders comparisons between genetically modified cells uncertain. This is however not a problem in our cellular model, as comparisons will be made within the final clone (HT1080#72.2.25.9), between two cell groups that differ only for the presence or absence of the MIR105/767 locus.

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