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Generation of a homozygous LRP2 knockout human embryonic stem cell line (FDCHDPe010-A-56) by CRISPR/Cas9 system

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Abstract

LRP2 is mainly expressed in the cell membrane of epithelia, maintaining normal endocytosis of nutrients from the extracellular microenvironment and mediating growth factor signals. The deficiency of LRP2 can result in abnormal lysosomal and mitochondrial function as well as insufficient resistance to oxidative stress. LRP2-KO animals show enlarged eyes and malfunction of the retinal pigment epithelium (RPE). We were able to generate an LRP2-KO human embryonic stem (ES) cell line using CRISPR/Cas9 gene editing and differentiate the mutant ES cells into RPE cells. Thus, this LRP2-KO human ES line will facilitate studying cellular mechanisms of eye disease due to LRP2 deficiency.

2. Resource utility

Low-density lipoprotein receptor-related protein 2 (LRP2) is a cell surface protein mainly expressed in the apical surface of epithelia. LRP2 has been shown to be a multifunctional receptor, playing roles in maintaining normal endocytosis of nutrients and other substances, as well as mediating growth factor binding. Deficiencies of LRP2 can result in perturbed membrane trafficking and dysfunctional lysosomes and mitochondria (Marzolo MP, 2011). Humans with recessive LRP2 mutations develop Donnai-Barrow syndrome with craniofacial anomalies including ocular hypertelorism, forebrain defects, and mild holoprosencephaly (Christ et al., 2012; Rosenfeld et al., 2010). LRP2 knockout mice show an enlarged ocular

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Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Appendix A. Supplementary data

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.scr.2021.102342>.

appearance, and exhibit abnormal retinal pigment epithelium (RPE) endocytosis (Cases et al., 2017; Patel et al., 2007). To establish human disease models, we generated an LRP2-KO human embryonic stem cell (HESC) line using CRISPR/cas9 system. Differentiating LRP2-KO ES cells into RPE cells will further studies of LRP2 function in ocular development and diseases.

3. Resource details

To generate the LRP2 knock-out HESC line, we used a CRISPR/cas9 system based on *Staphylococcus aureus* Cas9 (SaCas9), which edits the genome with efficiencies similar to those of SpCas9, while being > 1 kb shorter (Ran et al., 2015). To improve the efficiency of screening for mutated clones, a DNA fragment containing the CMV promoter sequence, GFP sequence, and poly-A sequence was inserted into XhoI endonuclease sites of the px601 plasmid (Addgene #61591) by homologous recombination. A guide RNA was designed targeting the second exon of the common sequence of three transcripts (exon17 of transcripts 1 and 2; exon 3 of transcript 3) of LRP2 (Fig. 1A) by utilizing <http://crispor.tefor.net/crispor.py>. The synthesized oligo was inserted into the vector described above. Then, the plasmid was transfected into wild-type HESCs (H9 [Wi Cell Research Institute, Madison, WI, USA]) by lipofection. Forty-eight hours later, GFP positive cells were sorted by FACS and seeded as single cells in the presence of ROCK inhibitor.

Among all the expanded HESC clones, a single clone carrying a 2-bp deletion (Fig. 1B), as confirmed by Sanger sequencing, was chosen for further research. The deletion resulted in a frameshift mutation at amino acid No.96 (No.870 of transcripts 1,2; NO.107 of transcript 3) in the common sequences of the three transcripts, leading to a premature stop codon at amino acid No.117 (No.891 of transcripts 1,2; NO.128 of transcript 3; Fig. S1A), and truncation of the subsequent 3764 amino acid that contains critical domains, conserved sites, including the transmembrane domain (Fig. S1B). In addition, the CRISPR cut site in the LRP2 protein is predicted to be part of LDLR class B repeat (No.415–4304aa of transcript 1,2; No.1–3541aa of transcript3) and thus may disturb the formation of the predicted beta-propeller structure, which is critical for ligand release and recycling of the receptor (Davis et al., 1987; Springer, 1998).

The LRP2 gene-edited cell line showed morphologies typical of pluripotent stem cells (Fig. 1E). Immunostaining studies with the LRP2-KO HESC line showed the expression of several pluripotency markers, including OCT4, SOX2, and Nanog (Fig. 1C). Flow cytometry analysis further confirmed comparable percentages of OCT4 positive cells (>98%) in the LRP2-KO HESC line and the wild-type HESC line (Fig. 1D). Karyotype analysis demonstrated that the LRP2-KO cell line had a normal female karyotype (46, XX), with no gross chromosome structure abnormalities (Fig. 1I). Trilineage differentiation assays were conducted in vitro to confirm the expression of markers for ectoderm (PAX6), mesoderm (BRACHYURY), and endoderm (FOXA2) (Fig. 1F). Short tandem repeat (STR) analysis showed that the LRP2-KO HESC line matched the parental cell line of origin. These cells were free of mycoplasma contamination (Fig. 1J). Off-target analyses were conducted using primers from <http://crispor.tefor.net/crispor.py>, and Sanger sequencing confirmed that no predicted off-target sites were present in the LRP2 mutant HESC line. LRP2-KO HESC

cells were subsequently induced to differentiate into RPE, which displayed a polygonal morphology, produced pigment like human RPE, and expressed typical RPE markers ((ZO-1 in the cell membrane, MITF in the nucleus and RPE65 in the endoplasmic reticulum and plasma membrane) (Fig. 1G) (Buchholz et al., 2013; Foltz and Clegg, 2017). The absence of detectable levels of LRP2 protein in the differentiated LRP2-KO cells was confirmed by Western blot (Fig. 1H). The above pieces of information of the LRP2-KO hESCs were summarized in Resource Table and Table 1.

4. Materials and methods

4.1. Cell culture

Wild-type HESC and LRP2-KO HESC lines were cultured in mTeSR™1 (Stem Cell Technology) on Matrigel®-coated plates (Corning). When colonies reached 70–80% confluency, ReLeSR™ (Stem Cell Technology) was used to detach and dissociate large clones. Cells were passaged at a 1:3 ratio, and single cells were obtained using Accutase (Sigma-Aldrich) before plasmid transfections and FACS sorting. Post-FACS recovery medium was utilized to promote adherence of single cells (Peters et al., 2008).

4.2. Gene targeting

LRP2-sgRNA was designed, synthesized, and cloned into the vector described above. Lipofetamine3000 (ThermoFisher Scientific) was then used to transfect 5 μ g of the engineered plasmid into 5 \times 10⁵ HESCs. GFP positive cells were sorted through FACS and seeded as single cells until large enough for screening. Clones were manually picked and genomic DNA used for Sanger sequencing using primers listed in Table 2. Only clones that showed appropriate indels at the designed sgRNA targeting site were selected for further analyses.

4.3. Immunostaining

Passaged cells were seeded on a 24-well plate and cultured for 3–4 days. After 3 washes with PBS, cells were fixed in 4% paraformaldehyde for 10–15 min, permeabilized with 0.2% Triton X-100 for 15 min, and blocked in 4% bovine serum albumin for 30 min at room temperature. Cells were then incubated with primary antibodies at 4 °C overnight, followed by secondary antibodies for 1 h at room temperature. Both primary and secondary antibodies were diluted in the blocking medium. Cell nuclei were stained with DAPI (Abcam) for 5 min at room temperature. Images were taken by an inverted fluorescence microscope (Leica Microsystems, Germany). The antibodies used are listed in Table 2.

4.4. Flow cytometry analysis

Typically, 1 \times 10⁶ cells were washed twice with PBS and fixed in 4% formaldehyde for 15 min at room temperature. Cell permeabilization was performed by slowly adding 100% cold methanol to pre-chilled cells to a final concentration of 90% methanol, and then incubating for an additional 10 min on ice. Cells were subsequently incubated with primary antibody for 1 h and then with the corresponding secondary antibody for 30 min at room temperature. The primary and secondary antibodies were diluted with 3% BSA. Cells were resuspended in 500 μ l pre-chilled PBS, detected with flow cytometry (Beckman coulter Inc, MoFlo

XDP), and analyzed for percentages of signal-positive cells among total cells by Summit5.2 software.

4.5. Differentiation of HESC and LRP2-KO HESC

Trilineage differentiation assays were carried out according to instructions of the Trilineage differentiation kit (Stem Cell Technology). Briefly, appropriate amounts of ES cells were seeded on Matrigel-coated plates. Then, cells were treated with lineage-specific differentiation medium respectively. About 5 or 7 days later, typical germ layer markers were detected by immunostaining. The antibodies used are listed in Table 2.

For directed differentiation of LRP2-KO HESC cells into RPE, a previously published protocol was used with mild modification (Foltz and Clegg, 2017) and cytokines were added step by step to induce stem cell transformation.

4.6. Western blot

Cells were washed twice with cold PBS, incubated with RIPA lysate containing 1% PMSF on ice for 15 min, and centrifuged at 12000 rpm for 15 min to obtain the supernatant. After SDS-PAGE electrophoresis (Tanon Science Inc, Shanghai), the lysates were transferred to 0.45um PVDF membranes and incubated with LRP2-specific polyclonal antibody (Proteintech Group) at 4°C overnight. Then incubated for 1 h at room temperature with secondary antibody, rinsed, and detected by chemiluminescence with HRP substrate (Millipore). The antibodies used are described in Table 2.

4.7. Karyotype analysis

Cells in their logarithmic growth phase were treated with 10ug colchicine and then incubated for 4 h at 37°C, 5% CO₂. Single cells were obtained using Accutase. Standard cytogenetic procedures were performed by ZhenHe Bioscience Inc, Shanghai using the GTG-band method.

4.8. STR analysis

STR analysis was authenticated by iCell Bioscience Inc, Shanghai.

4.9. Off-target analysis

Potential off-target sites (POTs) were identified using the website service <http://crispor.tefor.net/crispor.py> to predict possible site-specific cleavage by CRISPR/Cas9. The PCR products of POTs were confirmed by Sanger sequencing. POT primers are listed in Table 2.

4.10. Mycoplasma test

Mycoplasma tests were performed using the EZ-PCR Mycoplasma Test Kit (Biological Industries, BI) following the manufacturer's instructions.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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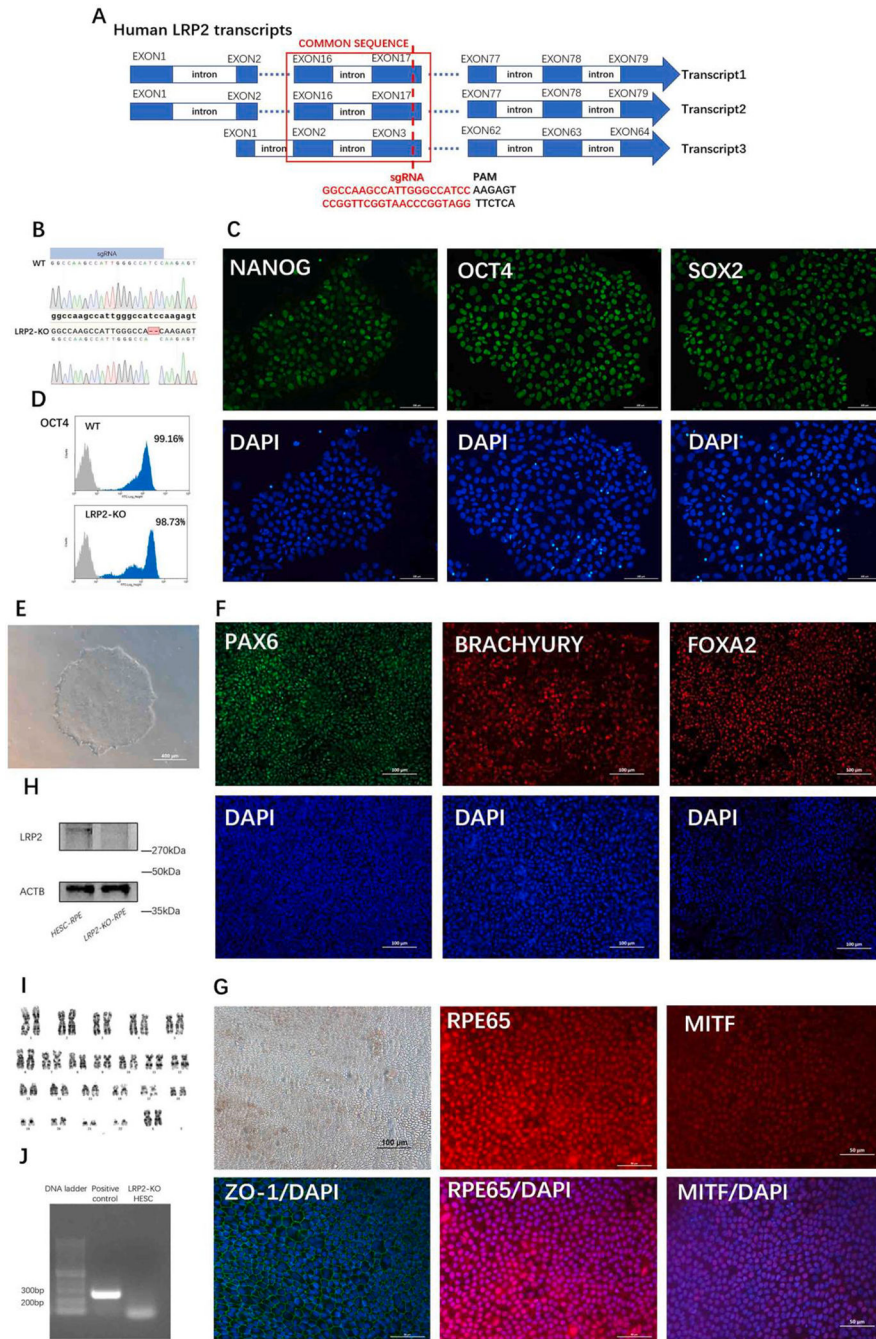


Fig. 1. Characterization of LRP2 knockout human embryonic stem cell line (FDCHDPe010-A-56).

Table 1

Characterization and validation.

| Classification | Test | Data | Result | Data |
|--|--|------|--|----------------------------|
| Morphology | Photography | | Normal | Fig. 1 panel E |
| Pluripotency status evidence for the described cell line | Qualitative analysis (i.e. Immunocytochemistry, western blotting) [mandatory] | | Positive for OCT4, SOX2, NANOG | Fig. 1 panel C |
| Karyotype | Quantitative analysis (i.e. Flow cytometry, RT-qPCR) | | Flow cytometry: Oct4: > 98% | Fig. 1 panel D |
| Genotyping for the desired genomic alteration/allelic status of the gene of interest | Karyotype (G-banding) and higher-resolution, array-based assays (KaryoStat, SNP, etc.) | | 46XX, Resolution 400 | Fig. 1 panel I |
| Verification of the absence of random plasmid integration events | PCR across the edited site or targeted allele-specific PCR | | PCR + sequencing: Homozygous 2-bp deletion | Fig. 1 panel B, H |
| Parental and modified cell line genetic identity evidence | PCR | | WB: Completely knock- out | N/A |
| Mutagenesis / genetic modification outcome analysis | Transgene-specific PCR | | N/A | N/A |
| | PCR/Southern | | PCR detection: No plasmid backbones | Figure S1 panel C |
| | STR analysis, microsatellite PCR (mPCR) or specific (mutant) allele seq | | 9 loci tested | Available with the authors |
| | Sequencing (genomic DNA PCR or RT-PCR product) | | DSS818, D13S317, D7S820, D16S539, vWA, Th01, AMEL, TPOX, CSFIPO, 100% matched | Available with the author |
| | PCR-based analyses | | PCR + sequencing: Homozygous 2-bp deletion | Fig. 1 panel B |
| | Southern Blot or WGS; western blotting (for knock- outs, KOs) | | N/A | N/A |
| Off-target nuclease analysis- | PCR across top 5/10 predicted top likely off-target sites, whole genome/exome sequencing | | WB: Completely knock- out | Fig. 1 panel H |
| Specific pathogen-free status | Mycoplasma | | No off-target effect | Available with the author |
| Multilineage differentiation potential | Trilineage differentiation | | Negative | Fig. 1 panel J |
| Donor screening (OPTIONAL) | HIV 1 + 2 Hepatitis B, Hepatitis C | | Expressing three germ layers formation: Ectoderm (PAX6), Mesoderm (BRACHYURY) and Endoderm (FOXA2) | Fig. 1 panel F |
| Genotype - additional histocompatibility info (OPTIONAL) | Blood group genotyping | | N/A | N/A |
| | HLA tissue typing | | N/A | N/A |

Table 2

Reagents details.

| Antibodies and stains used for immunocytochemistry/flow-cytometry | |
|---|--|
| Antibody | Dilution Company Cat # and RRID |
| Pluripotency Markers | Rabbit anti-OCT4 1:100 for immunostaining 1:60 for flow cytometry Abcam Cat# ab181557, RRID: AB_2687916 |
| | Rabbit anti-SOX2 1:100 Abcam Cat# ab92494, RRID: AB_10585428 |
| | Rabbit anti-NANOG 1:100 Abcam Cat# ab21624, RRID: AB_446437 |
| Differentiation Markers | Rabbit anti-PAX6 1:100 BioLegend Cat# PRB-278P, RRID: AB_291612 |
| | Rabbit anti-BRACHYURY 1:100 Abcam Cat# ab209665, RRID: AB_2750925 |
| | Rabbit anti-FOXA2 1:100 Abcam Cat# ab108422, RRID: AB_11157157 |
| RPE Markers | Rabbit anti-ZO-1 1:100 Thermo Fisher Scientific Cat# 402200, RRID: AB_2533456 |
| | Mouse anti-MITF 1:100 Abcam Cat# ab3201, RRID: AB_303601 |
| | Mouse anti-RPE65 1:100 Novus Biologicals Cat# NB100-35 RRID: AB_10002148 |
| Western Blot analysis | Rabbit anti-LRP2 1:300 Proteintech Cat# 9700-1-AP, RRID: N/A |
| Secondary antibodies | Alexa Fluor 594 AffiniPure Donkey Anti-Rabbit IgG (H + L) 1:1000 Yeasen Cat# 34212ES60, RRID: N/A |
| | AlexaFlour488 goat anti-rabbit IgG 1:1000 Thermo Fisher Scientific Cat# A-11008, RRID: AB_143165 |
| | AlexaFlour555 goat anti-mouse IgG 1:1000 Thermo Fisher Scientific Cat# A-21422, RRID: AB_2535844 |
| | Peroxidase-Conjugated Goat Anti-Rabbit IgG (H + L) 1:5000 Yeasen Cat# 33101ES60, RRID: N/A |
| Nuclear stain | DAPI 1:1000 Abcam Cat# ab104139, RRID: N/A |
| Site-specific nuclease Nuclease information | N/A |
| Delivery method | FACS |
| Selection/enrichment strategy | FACS |
| Primers and Oligonucleotides used in this study | Forward/Reverse primer (5'-3') |
| Targeted mutation analysis/sequencing | Target LRP2, 2nd Exon of common sequence of three transcripts GCAGTATCTGGAGAATCTCTGTTTG/ GAGTTTCCACTAAATCTTGTCAITCAGC |
| gRNA oligonucleotide/crRNA sequence | GGCCAAGCCATTGGGCCATCC |
| Potential random integration-detecting PCR | PB1 ATACGATGTTCCAGATTACGCT/ GGTGTTTCGTCCTTCCACAAG |

Antibodies and stains used for immunocytochemistry/flow-cytometry

| Antibody | Dilution | Company Cat # and RRID |
|---|--|------------------------|
| PB2 | CGTGTTTATCTCGTCAACTTGTGG/CCAGTTTTGGAAACAAGAGTCCACTAT | |
| PB3 | CTCGAGGCCGTTGACATTGAT/GTGGCACCCGGTAGTTAGCC | |
| POT1 Top off-target mutagenesis predicted site sequencing | CTTTGCCCGGCCAAGAAATTC/TCTGTCAAGGCATCATGCTGGG | |
| POT2 | GTGGCATTCCCGAATTCTGGC/GTGTTCACACCCAGAGCCTGAG | |
| POT3 | CAGATGGTCAGAGCAGGCTC/TGATGAACCCCTTGGGCCAAAG | |
| POT4 | CAGACGTGCCCGATGAAGAGA/CCACAGGAAACACTAGGCCAGT | |
| POT5 | AGTTTACTTGGTGTTCATTACCCA/TGGGCATTTGGAGGGACATCG | |

1. Resource Table

| Unique stem cell identifier | FDCHDPe010-A-56 |
|---|---|
| Alternative name(s) of stem cell line | LRP2-KO hESCs |
| Institution | Eye & ENT Hospital, Shanghai Medical School, Fudan University, Shanghai, China |
| Contact information of distributor | Jie You, 513yj45@163.com; Ling Chen, linglingchen98@hotmail.com |
| Type of cell line | ESC |
| Origin | Human |
| Additional origin info | Age: blastocyst stage Sex: female, 46, XX Ethnicity: N/A |
| Cell source | N/A |
| Clonality | Clonal |
| Method of reprogramming | N/A |
| Cell culture system used | mTeSR™1 |
| Genetic modification | Yes |
| Type of modification | Induced mutation |
| Associated disease | Endocytosis deficiency disease |
| Gene/locus | Gene:LRP2 Locus:2q31.1 |
| Method of modification | CRISPR/Cas9 |
| Site-specific nuclease (SSN) delivery method | Plasmid transfection |
| All genetic material introduced into the cells | Cas plasmid Karyotyping |
| Analysis of the nuclease- targeted allele status | |
| Method of the off-target nuclease activity surveillance | Targeted PCR/sequencing |
| Name of transgene or resistance | N/A |
| Inducible/constitutive system | Transient expression of Sacas9 and GFP under CMV promoter |
| Data archived/stock date | December 2020 |
| Cell line repository/bank | N/A |
| Ethical approval | This study was approved by the ethics committee of Fudan University affiliated Eye & ENT Hospital (KJ2011-04) |