**Generation of a human induced pluripotent stem cell (iPSC) line from a patient carrying a P33T mutation in the *PDX1* gene**

by

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**ABSTRACT**

**Homozygous loss-of-function mutations in the gene coding for the homeobox transcription factor *PDX1* leads to pancreatic agenesis, whereas certain heterozygous point mutations are associated with Maturity-Onset Diabetes of the Young 4 (MODY4) and Type 2 Diabetes Mellitus (T2DM). To understand the pathomechanism of MODY4 and T2DM, we have generated iPSCs from a woman with a P33T heterozygous mutation in the transactivation domain of PDX1. The resulting *PDX1* P33T iPSCs generated by episomal reprogramming are integration-free, have a normal karyotype and are pluripotent *in vitro* and *in vivo*. Taken together, this iPSC line will be useful to study diabetes pathomechanisms.**

**1. Resource table**

|  |  |
| --- | --- |
| Name of Stem Cell line | *PDX1* P33T iPSC1 |
| Institution | *Institute of Diabetes and Regeneration Research* |
| Person who created resource | Xianming Wang |
| Contact person and email | Heiko Lickert heiko.lickert@helmholtz-muenchen.de |
| Date archived/stock date | April 2014 |
| Origin | Human dermal fibroblasts |
| Type of resource | Induced pluripotent stem cells from a woman carrying a *PDX1* P33T Mutation |
| Sub-type | Cell line |
| Key transcription factors | OCT4, SOX2, NANOG, LIN28, KLF4, and L-MYC |
| Authentication | Identity and purity of cell line confirmed |
| Link to related literature | Not available |
| Information in public databases | Not available |
| Ethics | Informed written consent obtained |

**2. Resource details**

The Tübingen Family Study for T2DM (TÜF study, N=2500) was screened for known rare mutations in the MODY4 gene *PDX1*. By mass spectrometry-based genotyping, one heterozygous *PDX1* P33T carrier could be identified and recruited for full-thickness skin biopsy. From the biopsy material, the epidermal layer was separated from the dermis by dispase digestion and fibroblasts were isolated from the dermis by trypsin digestion using an established protocol (see material and methods). The *PDX1* P33T fibroblasts were expanded using commercially available growth media and deep-frozen in liquid nitrogen. From this collection of dermal fibroblasts, samples were tested for the presence of viruses pathogenic to humans (HBV, HCV, HIV) as well as for the presence of mycoplasma. All cultures were found to be negative for all of these potential contaminants. *PDX1* P33T primary fibroblasts were reprogrammed into iPSCs using nucleofection with three episomal plasmids encoding human *OCT4*, *SOX2*, *NANOG*, *LIN28*, *KLF4*, and *L-MYC* (Fig. 1B). The reprogramming protocol (transfection, reprogramming and expansion) is shown in Fig. 1C. 3 weeks after transfection, many colonies with human embryonic stem cell (hESC)-like morphology appeared that were hand picked by day 21, expanded and frozen down as individual iPSC lines. The analysis of one of these iPSC lines confirmed that *PDX1* P33T fibroblasts were successfully reprogrammed into iPSCs with a normal karyotype (Fig. 1D) and containing the C>A mutation causing a P33T amino acid exchange in the transactivation domain (Fig. 1A, 1E). Integration of the exogenous transgenes in the genome of iPSCs was excluded by semi-quantitative PCR (Fig. 1F). To confirm that this iPSC line was pluripotent, we performed immunofluorescence staining for the pluripotency transcription factors OCT4 and SOX2, as well as for the hESC surface markers SSEA-3, SSEA-4 and TRA-1-81, which were all expressed in the *PDX1* P33T iPSC line (Fig. 2A). To further demonstrate pluripotency of the selected iPSC line we injected 2x106 cells subcutaneously into NOD/SCID mice to generate teratomas. The histological analysis of the induced teratomas revealed that all tissues from all three germ layers were differentiated confirming pluripotency in this *in vivo* assay (Fig. 2B). Taken together, we have successfully reprogrammed *PDX1* P33T dermal fibroblasts into pluripotent iPSCs that can be used to study a point mutation in the transactivation domain of PDX1 to study the development of diabetes.

**3. Materials and methods**

**Ethics statement**

The study adhered to the Declaration of Helsinki. All participants gave informed written consent, and the study protocols were approved by the local ethics board (Ethics Committee of the Eberhard Karls University Tübingen).

**Study participants**

The ongoing TÜF study currently includes more than 3000 non-related individuals at risk for type-2 diabetes mellitus (T2DM), i.e., healthy subjects with a family history of T2DM, a body mass index ≥27 kg/m2, impaired fasting glycaemia, and/or previous gestational diabetes (Stefan N, Machicao F, Staiger H, Machann J, Schick F, Tschritter O, Spieth C, Weigert C, Fritsche A, Stumvoll M, Häring HU). From all TÜF participants, the medical history, smoking status, and alcohol consumption habits were queried and documented. Furthermore, all participants underwent physical examination, routine blood tests, bioelectric impedance measurement, and 5-point oral glucose tolerance tests (OGTTs) with insulin and glucose measurements. The current study population comprised 2500 individuals who spent DNA for genotyping, were not on any medication known to influence glucose tolerance, insulin sensitivity, or insulin secretion, and who had complete OGTT data sets.

Using the mass spectrometry-based genotyping platform massARRAY from Sequenom (Hamburg, Germany) and the manufacturer’s iPLEX software, the 2500 subjects were screened for known rare mutations in maturity onset of diabetes (MODY) genes that were described in the literature to co-segregate with MODY phenotypes in families. We identified seven individuals with heterozygous mutations in *PDX1* (MODY4) (McKinnon and Docherty, 2001). We identified seven individuals with heterozygous mutations in *PDX1* (MODY4). From these cases, one glucose-tolerant female *PDX1* Pro33Thr (P33T) carrier (aged 40 years; BMI 23.0 kg/m²) could be recruited for full-thickness skin biopsy.

**Skin biopsy, isolation and testing of dermal fibroblasts**

A full-thickness skin specimen was taken by punch biobsy from the upper arm in the deltoid muscle region. After removal of adipose tissue remnants and visible blood vessels, the sample was digested overnight at 4°C with 10 U/mL dispase II (Roche Diagnostics, Mannheim, Germany) in 50 mM Hepes pH 7.4, 150 mM NaCl. Thereafter, the digest was heated for 30 min at 37°C under continuous shaking (1200 rpm). Using forceps, the dermis was separated from the epidermal layer, and fibroblasts were isolated from the dermis by digestion with 0.2% collagenase CLS I (Biochrom, Berlin, Germany) in DMEM, 10% BSA for 45 min at 37°C under continuous shaking (1200 rpm). For purification of the fibroblasts, the digest was filtered through a 70 µm mesh and centrifuged. The pelleted cells were resuspended, grown for three days in DMEM, 10% FCS, and subsequently further expanded in Medium 106 supplemented with low serum growth supplement (Invitrogen, Thermo Fisher Scientific, Waltham, MA, USA). Samples of dermal fibroblasts were tested for the presence of viruses pathogenic to humans, i.e., HBV, HCV, and HIV, with Genesig PCR-based detection kits from Primerdesign Ltd. (Chandler's Ford, UK) and for the presence of mycoplasma with a PCR test kit from PanReac AppliChem (Darmstadt, Germany) and, in parallel, by DNA staining with DAPI. All cultures were found to be negative for the tested contaminants.

**iPSC generation**

Primary fibroblasts from patient were reprogrammed into pluripotent stem cells by using a non-integrating Episomal iPSC Reprogramming Kit (Invitrogen, Cat.no.A14703). This kit contains mixture of three vectors which has the oriP/EBNA-1 (Epstein-Barr unclear antigen-1) backbone that delivers six reprogramming factors: *OCT4*, *SOX2*, *NANOG*, *LIN28*, *KLF4*, and *L-MYC (Yu et al., 2011)*. Human fibroblasts at 75-90% confluent were transfected using the Amaxa 4D-Nucleofector transfection system and a nucleofector kit for human dermal fibroblast (Lonza, Cat.no.VPD-1001), plated onto geltrex-coated culture dishes, incubated in supplemented fibroblast medium. This medium contained knockout DMEM/F-12 (Life technologies), 10% FBS of ESC-qualified (Life technologies), 1% MEM non-essential amino acids (Life technologies), 10 µM HA-100 (Santa Cruz) and 4 ng/ml bFGF (Life technologies). At 24 hours after transfection, the medium was exchanged with N2B27 medium supplemented with 0.5 µM PD0325901 (Stemgent), 3 µM CHIR99021 (Stemgent), 0.5 µM A-83-01 (Stemgent), 10 µM HA-100 (Santa Cruz), 10 ng/ml hLIF (Life technologies) and 100 ng/ml bFGF. The basic N2B27 medium contained DMEM/F12 with HEPES (Life technologies), 1x N2 supplement (Life technologies), 1x B27 supplement (Life technologies), 1% MEM non-essential amino acids, 1x Glutamax (Life technologies) and 1x  β-Mercaptoethanol (Life technologies). On day 15 after transfection, the medium was exchanged with Essential 8 medium and monitored for the emergence of iPSC colonies. Around 3 weeks after transfection, undifferentiated iPS colonies were picked and transferred onto fresh geltrex-coated culture dishes for expansion.

**iPSC characterization**

DNA was extracted from iPSCs by using standard procedure. Markers for the episomal backbone were amplified by semi-quantitative PCR to exclude transgene integration. Primers are as follows: *oriP* forward: TTCCACGAGGCTAGTGAACC. *oriP* reverse: TCGGGGGTGTTAGAGACAAC; *EBNA-1* forward: ATCGTCAAAGCTGCACACAG. *EBNA-1* reverse: CCCAGGAGTCCCAGTAGTCA. For karyotype analysis, we used the cells growing in logarithmic phase. They were fed with fresh medium the night before adding colcemid for 2 hours. Cells were then trypsinized, treated with hypotonic solution (0.075 m KCl) for 20 min and fixed with methanol : acetic acid (3:1). Metaphases were spread on microscope slides, and chromosomes were classified according to the International System for Human Cytogenic Nomenclature using the standard G banding technique. At least, 20 metaphases were counted per cell line, and the final karyotype was stated if it was present in more than 85% of them. For teratomas, 2x106 iPSCs were injected into the right hind leg of immunocompromised NOD/SCID mice. Tumors were excised after 8 weeks, fixed, embedded in paraffin, sectioned and stained with hematoxylin/eosin (Takahashi et al., 2007).

**Mutation analysis**

Genomic DNA was isolated from *PDX1* P33T and control iPSCs using standard procedure. PCR amplification with a set of primers flanking the mutation site was performed in those two samples. PCR products were sequenced using the reverse primer by Sanger sequencing on an ABI 3130 genetic analyzer (Applied Biosystems). Primers are as follows: *PDX1* forward: GGAGTGTGCAGCAAACTCAG, *PDX1* reverse: ACGCGTGAGCTTTGGTAGAC.

**Immunofluorescence imaging**

Cells were fixed with 4% paraformaldehyde for 30 min and then permeabilized in PBS containing 0.2% Triton X-100. Cells were blocked with PBS containing 3% BSA, and incubated with primary antibodies overnight at 4°C. Then secondary antibodies were incubated for 1 hour at room temperature after washing with PBS. Images were acquired on a laser scanning microscope. The following antibodies and dilutions were used: goat anti-OCT3/4 (1:500, Santa Cruz), goat anti-SOX2 (1:500, Santa Cruz), rat anti-SSEA3 (1:50, Invitrogen), mouse anti-SSEA4 (1:500, Cell signaling) and mouse anti-TRA-1-81 (1:50, Millipore).

**Author disclosure statement**

There are no competing financial interests in this study.

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