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## Insulin-producing cells derived from human pancreatic non-endocrine cell cultures reverse streptozotocin-induced hyperglycaemia in mice

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**Abstract** *Aims/hypothesis:* The aim of the study was to investigate the potential of human pancreatic non-endocrine cells to transdifferentiate into endocrine cells that would be capable of secreting insulin in response to glucose and ameliorating insulin-deficient diabetes after transplantation. *Materials and methods:* Cell fractions enriched with exocrine cells after human islet isolation were treated with streptozotocin to remove residual beta cells, grown in monolayer culture to allow de-differentiation, transferred to cluster culture for redifferentiation in the presence of activin A, betacellulin, nicotinamide and glucose, supplemented with 10% FCS, and administered to streptozotocin-induced diabetic SCID mice. A subset of cells was transfected with the *IPF1* gene (also known as *PDX1*) before transdifferentiation. *Results:* No insulin was detectable in cell preparations after 5 days of treatment with streptozotocin. In monolayer culture, 90% of the streptozotocin-treated pancreatic cells co-expressed cytokeratin-19 and vimentin at 2 weeks and 60% expressed nestin at 4 weeks. Cell cultures with a high proportion of nestin-expressing cells had greater plasticity for transdifferentiation into cells with phenotypic and functional markers of beta cells, this property being significantly enhanced by transfection with *IPF1* gene and leading to 15±6.7% insulin-positive cells after transplantation vs. 0.01% of cells transplanted after streptozotocin treatment alone. These cells improved glucose control in all of 42 diabetic mice after transplantation, restoring normoglycaemia in

40%. *Conclusions/interpretation:* Human pancreatic cells are a potential source of new glucose-responsive insulin-producing cells that may be developed further for clinical use.

**Keywords** Beta cells · Glucose-responsive · Insulin-producing cells · Pancreatic non-endocrine cells · Transdifferentiation · Transplantation

**Abbreviations** ABNG: activin A, betacellulin, nicotinamide and glucose · BrdU: 5-bromo-2'-deoxyuridine · GLP-1: glucagon-like peptide-1 · Q-PCR: quantitative polymerase chain reaction · STZ: streptozotocin

### Introduction

Pancreatic non-endocrine cells may be a potential source of new beta cells [1–3], as endocrine and exocrine cells in the pancreas share the same developmental origin [4–6]. In culture, endocrine and exocrine cells de-differentiate rapidly and express the same ductal cell marker, CK-19 (human) or CK-20 (rodent) [7–9], indicating that they are de-differentiating in a similar pattern. Furthermore, exocrine and ductal cells of rodents and man have been made to express Pdx1 protein in vitro [10, 11]. Pdx1 is an important transcription factor in pancreatic development and maintenance of the beta cell phenotype [12], and its presence suggests that the exocrine and ductal cells can transdifferentiate into cells with the potential to become endocrine cells and that cells with the ductal phenotype may be an intermediate product between undifferentiated and differentiated cells. Human pancreatic duct cells have been implicated as the origin of new beta cells in systems, without [13, 14] and with [15] the help of ectopic gene expression. Rodent exocrine cells can express insulin [16], supporting the concept that the exocrine cell may be a candidate for new beta cells. However, the goal of generating glucose-responsive beta-cell surrogates in numbers sufficient to reverse diabetes remains elusive and ultimately a human cell source will be required

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for clinical purposes. In an attempt to enhance the efficacy of beta cell generation from human sources, we first extended the culture of the non-endocrine cells to induce partial de-differentiation. We then introduced redifferentiation in these cells by culturing them in an environment that favoured differentiation of endocrine cells *in vitro*, with or without prior ectopic expression of *IPF1* (also known as *PDX1*). Finally, we allowed the partially differentiated cells to mature in a diabetic environment *in vivo* before assessing their ability to correct hyperglycaemia in diabetic mice.

## Materials and methods

### Reagents

Monoclonal antibody to human insulin (I2018), rabbit anti-human  $\alpha$ -amylase antiserum (A8273), glucagon-like peptide-1 (GLP-1) (G3265) and nicotinamide were purchased from Sigma (Sigma-Aldrich, Poole, Dorset, UK). Anti-cytokeratin-19 (Sc-6278) monoclonal antibody and anti-neuroD (Sc-1084) were purchased from Santa Cruz (Santa Cruz Biotechnology, Heidelberg, Germany). Monoclonal antibody against human fibroblast (clone 5B5) and rabbit anti-human Ki-67 antigen antiserum were obtained from Dako (Glostrup, Denmark). Anti-nestin monoclonal antibody (MAB 5326) was purchased from Chemicon International (Temecula, CA, USA). Human-specific vimentin monoclonal antibody (clone V9, Non3005) was purchased from Monosan (Amsterdam, The Netherlands). Recombinant human betacellulin and activin A proteins were from R&D Systems (Oxford, UK).

### Culture of human pancreatic non-endocrine cells

Human pancreases were obtained with permission from the local hospital ethical committee and informed consent from families of organ donors ( $n=16$ , seven male, nine female; age 18–58 years). Cold ischaemia time was  $5.2\pm 1.5$  h (mean $\pm$ SD). The pancreases were subjected to liberase digestion and density gradient fractionation as previously described [17]. Gradient fractions enriched with exocrine cells were collected, washed twice with Hanks' balanced salt solution and cultured in suspension as clusters [18] in CMRL1066 medium (Invitrogen, Inchinnan, UK), supplemented with 10% FCS and 0.95 mmol/l freshly prepared streptozotocin (STZ; Sigma) at 37°C in a humid 5% carbon dioxide incubator for 5 days, with medium and STZ changed daily to remove contaminating beta cells and dead cells. Cell samples were collected daily for genomic DNA preparation (Promega, Southampton, UK) to determine cell number indirectly, and for analysis of insulin content by immunocytochemical staining, RIA and RT-PCR as previously described [17, 18]. After STZ treatment, the cells were cultured as monolayers. They were seeded at  $3\times 10^6$  cells/10 cm Petri dish and grown initially at approximately 70% confluence in CMRL1066 medium with 55  $\mu$ mol/l G418 to inhibit the growth of fibroblasts [9] for up to 7

weeks. Cell samples were analysed at intervals of 5–7 days by immunocytochemistry and RT-PCR [18] to assess phenotypic changes. Quantitative PCR (Q-PCR) was used to confirm key RT-PCR experiments and analysed using published methods [19, 20].

### Analysis of cell proliferation

Cells from the monolayer cultures were dissociated using trypsin/EDTA and counted at intervals. Cell division was assessed using a 5-bromo-2'-deoxyuridine (BrdU) incorporation assay. For this, cells were seeded 2 h earlier, 65 nmol/l BrdU was added, and culture continued for 16 h. The cells were washed and dissociated and centrifuged to form a pellet. The pellet was cryosectioned and stained for both BrdU and Ki67, an endogenous proliferation marker [21, 22], using published methods [18].

### Human IPF1 expression plasmid and transfection

The coding region of the human *IPF1* gene was amplified by PCR using a primer set (Table 1). The cDNA was cloned into the expression plasmid pIRES-N1 [23] and partially sequenced. DNA transfections were performed using lipofectamine 2000 (Invitrogen) according to the manufacturer's instructions. Plasmid carrying the  $\beta$ -galactosidase reporter gene (pCMV $\beta$ ; BD Biosciences, San Jose, CA, USA) was used to establish optimal transfection conditions, and approximately 30% efficiency was achieved. Briefly,  $4\times 10^6$  cells/10 cm Petri dish were seeded 3 h before transfection. Plasmid DNA (16  $\mu$ g) was diluted in 1.5 ml of OptiMEM medium (Invitrogen) in tube A and 60  $\mu$ l of lipofectamine 2000 was diluted with 1.5 ml of OptiMEM medium in tube B. Following incubation at room temperature for 5 min, DNA in tube A was mixed with the lipofectamine 2000 in tube B and incubation was continued at room temperature for another 20 min. Before transfection, the cells were rinsed once with OptiMEM medium and 3 ml DNA/lipofectamine 2000 mixture was added drop-wise onto the cells. The cells were incubated at 37°C in a humid 5% carbon dioxide incubator for 3 h. The transfection mixture was then removed and rinsed once with culture medium, and cultured for another 48 h. The cells were dissociated using trypsin/EDTA and converted into cluster culture [18]. Empty plasmid pIRES-N1 was used as a negative transfection control.

### Transdifferentiation induction

To induce the partially de-differentiated non-endocrine cells into low-degree differentiation *in vitro*, the 4-week monolayer-cultured cells were converted to cluster culture in CMRL1066 overnight [18]. Next morning, the medium was replaced with serum-free CMRL1066 containing 50 nmol/l IGLP-1 (Sigma-Aldrich) and incubated for 3 h. Then, a cocktail of differentiation inducers was added at

final concentrations of 25 pmol/l activin A, 200 pmol/l betacellulin, 10 mmol/l nicotinamide and 16.5 mmol/l glucose (ABNG; added only in cluster culture), supplemented with 10% FCS. The cells were cultured for additional 4–10 days, with medium and ABNG replaced every 2 days. Cell samples were taken and assessed for expression of beta cell markers.

### Semi-quantitative RT-PCR

Total RNA was isolated using an RNA Miniprep Kit (Promega) and quantified using a spectrometer (Gene Quant II; Pharmacia Biotech, Cambridge, UK) at 260 nm wavelength [18]. Briefly, 100 ng of total RNA was converted into first-strand cDNA using reverse transcriptase (Invitrogen) in a volume of 20 µl. The hot-start (Qiagen, Crawley, UK) RT-PCR was used with the following parameters: 95°C for 15 min for one cycle; then 25 cycles of PCR with *Ipf1*, 28 cycles with *NeuroD1* and preproinsulin unless specified otherwise, and 30 cycles with *SLC2A2* (also known as *GLUT-2*) and glucokinase, while β-actin was amplified in parallel for 21 cycles as an internal control using the primers listed in Table 1. The relative quantity of DNA was analysed using a gel program (version 3.0 computer analyser of Media Cybernetics, Silver Spring, MD, USA) and expressed relative to the density of β-actin gene PCR product.

### Quantitative PCR

Q-PCR was performed with the LightCycler-2 (Roche Diagnostics, Lewes, UK) using the SYBR Green I fluorescence kit (Roche Diagnostics) and was mainly used to confirm the key semiquantitative RT-PCR. Target genes, such as human preproinsulin (435 bp), *NeuroD1* (410 bp), *IPF1* (508 bp), *SLC2A2* (523 bp) and glucokinase (597 bp), and the reference gene human β-actin (664 bp) were amplified in duplicate and cDNA from at least three donors was tested for each set of experiments. PCR was amplified in

20 µl with 0.25 µmol/l primers and appropriate amounts of DNA template. PCR-grade water was used as a negative control. Amplification efficiency was assessed by using a series of 10× dilutions of plasmid containing the gene or dilutions of cDNA templates. After an initial 15-min pre-incubation step at 95°C, the following parameters were used: 95°C for 10 s, 53–58°C for 20 s and 72°C for 45 s for 40 cycles. The relative copy number was corrected to 10,000 copies of human β-actin mRNA and expressed as copy number per 10,000 copies of β-actin gene±SD, using the comparative threshold ( $C_t$ ) method [19, 20]:  $2^{-\Delta C_t}$  where  $\Delta C_t = (C_t \text{ of the target gene} - C_t \text{ of the reference gene})$ . The  $C_t$  of the genes was determined using thermocycler software (version 3.5; Roche Diagnostics).

### Immunochemical staining

The methods used have been described previously [18]. Briefly, cultured cells or tissues were mounted with OCT compound (Merck, Lutterworth, Leics, UK) and cryosectioned at 5 µm intervals. The sections were assessed for the presence of specific antigens by peroxidase-based immunocytochemical staining (Vector Laboratories, Peterborough, UK). The primary antibody was replaced with species-related normal serum to validate specific staining. To visualise the antigens, VIP (violet) substrate (Vector Laboratories) was used. At least 5000 cells per sample were counted.

### Animals and surgical procedures

Male SCID mice (20–25 g, C.B-17/Icr), purchased from Charles River Laboratories, Margate, UK, were selected as recipients for transplantation and were maintained in filter cages in the Comparative Biology Centre at King's College London, according to guidelines of the Home Office (UK) for Animal Scientific Procedures. Diabetes was induced by a single injection of STZ (180 mg/kg i.p.) and confirmed by

**Table 1** PCR primer sets

<i>IPF1</i> cloning forward primer	5' CGGGCCGCAGCCATGAACG 3'
<i>IPF1</i> cloning reverse primer	5' CTCCTGCCTCTCATCGTGGTTTCCTG 3'
<i>IPF1</i> PCR forward primer	5' CCGCCGCCGCACCCGTTCC 3'
<i>IPF1</i> PCR reverse primer	5' CGACCCCGCCACCCCGACAG 3'
Preproinsulin forward primer	5'CATCAAGCACATTGTCC 3'
Preproinsulin reverse primer	5'CTGGTTCAAGGGCTTTATTC 3'
<i>NeuroD1</i> forward primer	5' ATGAACGCAGAGGAGGACTCACTG 3'
<i>NeuroD1</i> reverse primer	5' TTGGTGGTGGGTTGGGATAAGC 3'
<i>SLC2A2</i> forward primer	5' GTTTTGGGTGGTCCACTGGATG 3'
<i>SLC2A2</i> reverse primer	5' GCCACAGATCATAATTGCCCAAG 3'
Glucokinase forward primer	5' GCCCCACAGCTCAACACAACCAG 3'
Glucokinase reverse primer	5' CTCCCACCTTCACCAGCATCACC 3'
Nestin forward primer	5' GCGGCTGCGGGCTACTGAA 3'
Nestin reverse primer	5' GGGGGTGCTGGCCAAGGTAG 3'
Human β-actin forward primer	5' CCCAGATCATGTTTGAGACC 3'
Human β-actin reverse primer	5' CCAACAGGAGTACTTGCCTCAG 3'

the presence of hyperglycaemia. The diabetic condition was allowed to stabilise for 7–10 days before transplantation. The diabetic mice were randomly allocated to a transplant recipient group and a sham-operated control group. The surgical procedures have been described [18]. Briefly, under anaesthesia, a median lateral laparotomy was performed and the left kidney was exposed. Approximately 1500 cell clusters (approximately  $2.5 \times 10^6$  cells) in a volume of 50  $\mu$ l were transplanted into the kidney parenchyma tissue by direct insertion of a Hamilton syringe into the kidney at the lower pole, crossing the kidney and reaching the capsule membrane. The cells were discharged into the parenchyma as the syringe was slowly withdrawn. In the sham control group, a cell-free saline injection was made in exactly the same way. Plasma glucose was measured using a G2 blood glucose sensor from MediSense (Abbott Laboratories, Dublin, Ireland).

#### Intraperitoneal glucose tolerance test

The mice were fasted overnight and the plasma glucose level was determined. A glucose solution at 1.5 g/kg body weight was injected intraperitoneally and plasma glucose levels were determined 30, 60, 90, 120 and 180 min after injection.

At the end of the experiments, blood, kidneys and pancreases were removed. Immunohistochemistry was performed on the tissues for markers of endocrine, exocrine cells, ductal cells, fibroblasts, and vimentin- and Ki67-expressing cells. Cell nuclei were counterstained with propidium iodide (Sigma-Aldrich) and analysed by fluorescence or confocal microscopy. Cells that stained positive and the total number of transplanted cells (total grafted cells) were counted under light fluorescence microscopy and the percentage of positive cells was derived by counting a total of 1500 graft cells per staining. The concentration of human-specific C-peptide was determined by RIA (DSL, Webster, TX, USA). Organs from sham-operated mice were studied in parallel as a negative control.

#### Data analysis

All data are expressed as mean $\pm$ SD unless specified otherwise and statistical differences between groups were determined by ANOVA (Microsoft Excel, Office 2000). Differences between groups were considered significant when  $p < 0.05$ .

## Results

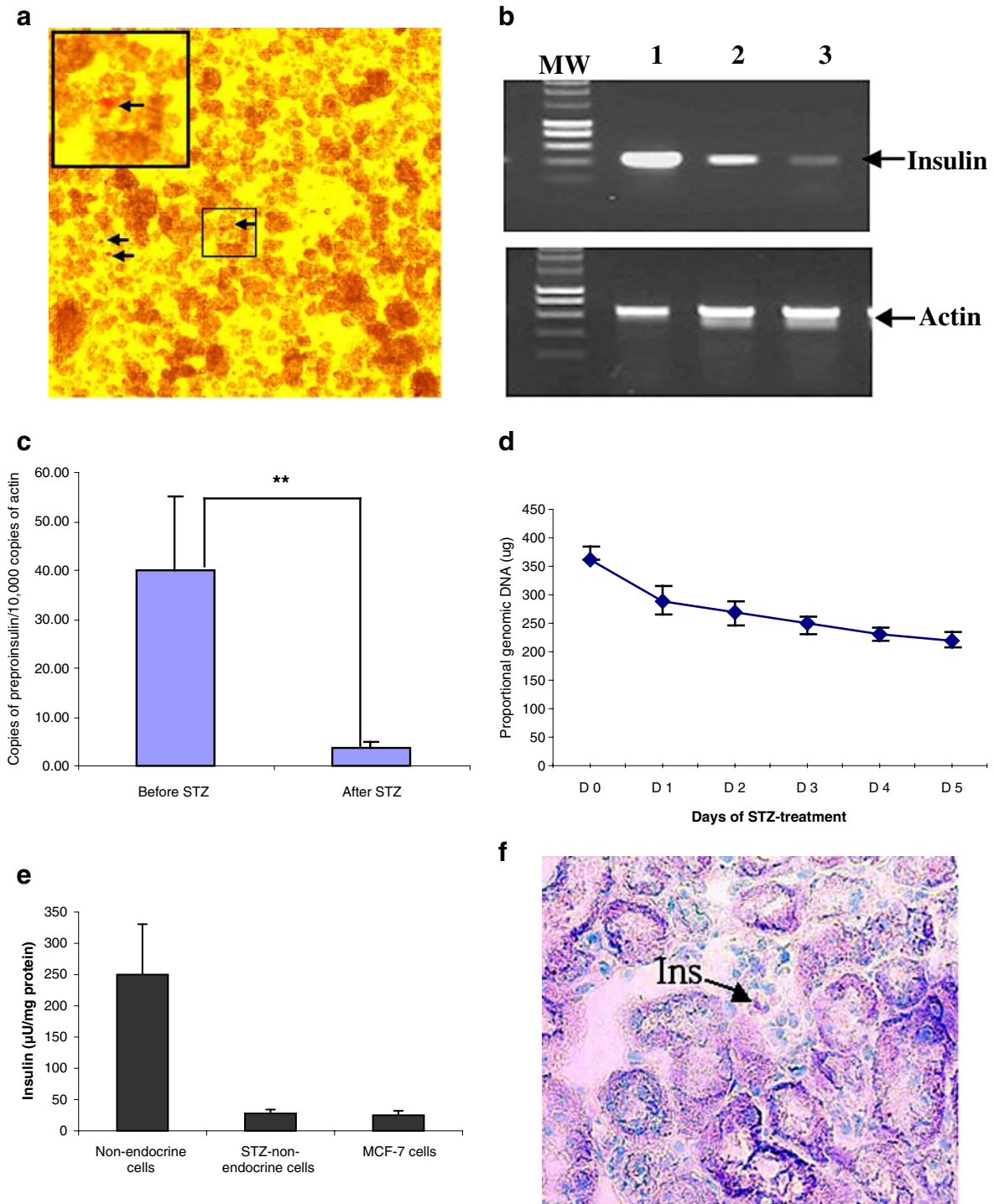
### Removal of beta cells from human pancreatic non-endocrine cell preparations

Under light microscopy, the exocrine-cell-enriched cell fractions contained  $< 0.3\%$  insulin-positive cells (Fig. 1a)

by dithizone staining. Following STZ treatment, beta cells were not detectable by dithizone staining ( $n=16$ ) or by anti-insulin immunocytochemical staining ( $n=5$ , data not shown). The cells were predominantly exocrine cells ( $79 \pm 12\%$  amylase-positive) and ductal cells ( $15 \pm 11\%$  cytokeratin-19-positive,  $n=16$ ). The expression of preproinsulin mRNA ( $n=5$ ) was significantly reduced, as determined by semiquantitative RT-PCR (Fig. 1b) following STZ treatment, consistent with the data from the Q-PCR. The number of copies of preproinsulin mRNA/10,000 copies of human  $\beta$ -actin mRNA was reduced from 40 to 3.5 following STZ treatment, a ten-fold decrease (Fig. 1c;  $n=4$ ,  $p < 0.01$ ). Insulin protein was not detectable by RIA [18] (Fig. 1d;  $n=5$ ). Cell death occurred during STZ treatment and the cell mass was reduced by 20%, as assessed by the reduction of genomic DNA (Fig. 1e;  $n=4$ ). In a further confirmation of the removal of beta cells, STZ-treated cells were implanted in the kidneys of the STZ-induced diabetic SCID mice. Fewer than 0.01% of graft cells were subsequently found to be positive for insulin (Fig. 1f,  $n=4$ ), a 30-fold decrease in beta-cell number, confirming the removal of most beta cells by the isolation procedure and STZ treatment.

### Expression of transient markers

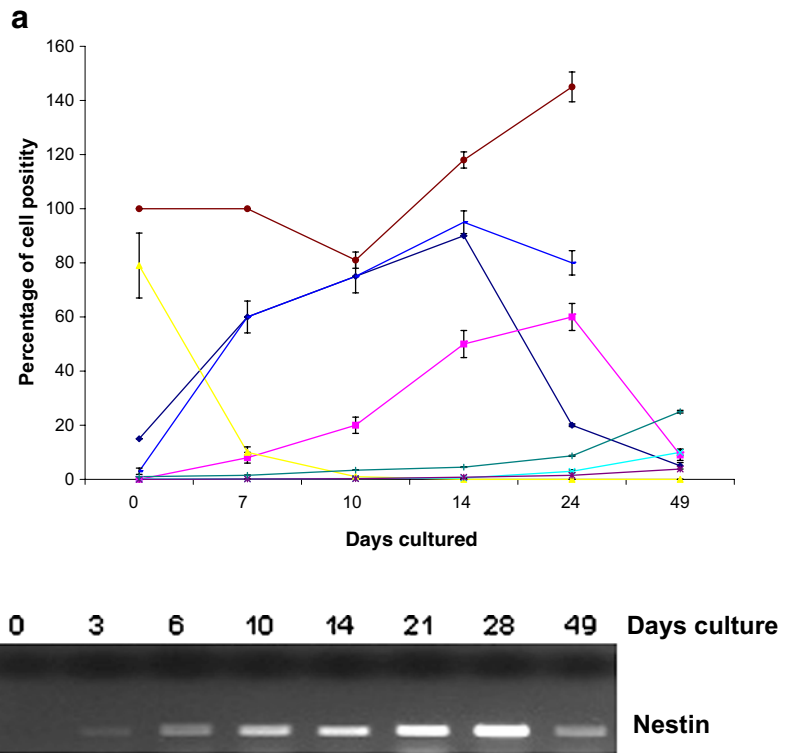
During 7 weeks of monolayer culture at  $\sim 70\%$  confluence, there was a rapid decrease in amylase-positive cells. The cell proliferation rate was low until 3 weeks in culture, as determined by the proliferation marker Ki67, BrdU incorporation and cell counting (Fig. 2a). As the initial proliferation rate was low (Fig. 2a), the cell number at day 7 was used as the starting cell number. The cell number decreased to 80% after the first trypsinisation. After the second week in culture, most cells adapted to the culture conditions and appeared healthy, with no microscopic evidence of cell death. Compared with the cell number at 7 days, the fold change in cell number by the end of the second, third and fourth weeks was  $0.81 \pm 0.03$ ,  $1.18 \pm 0.03$  and  $1.45 \pm 0.055$  ( $n=4$ ), respectively. The percentage of fibroblast cells in the initial cell preparations was  $< 1\%$  and there was no evidence of rapid proliferation, as there were fewer than 10% fibroblast cells during the 4-week cultures (Fig. 2a). The cells underwent rapid transdifferentiation in vitro. Expression of CK19 increased transiently, with a maximum of 90% of cells expressing CK19 after 2 weeks (Fig. 2a), declining thereafter. The cells expressing CK19 were not the typical duct cells as most of the CK19<sup>+</sup> cells also co-expressed vimentin, a marker of mesenchymal cells. Vimentin was not expressed in duct cells in human pancreas tissues (data not shown). Vimentin-expressing cells increased from 3% in the cell preparations to 95% after 2 weeks in monolayer culture (Fig. 2a). The number of CK19-expressing cells decreased rapidly, while vimentin-expressing cells declined relatively slowly and there were still more than 50% of vimentin-expressing cells by 4 weeks (Fig. 2a). Nestin expression (absent from the initial



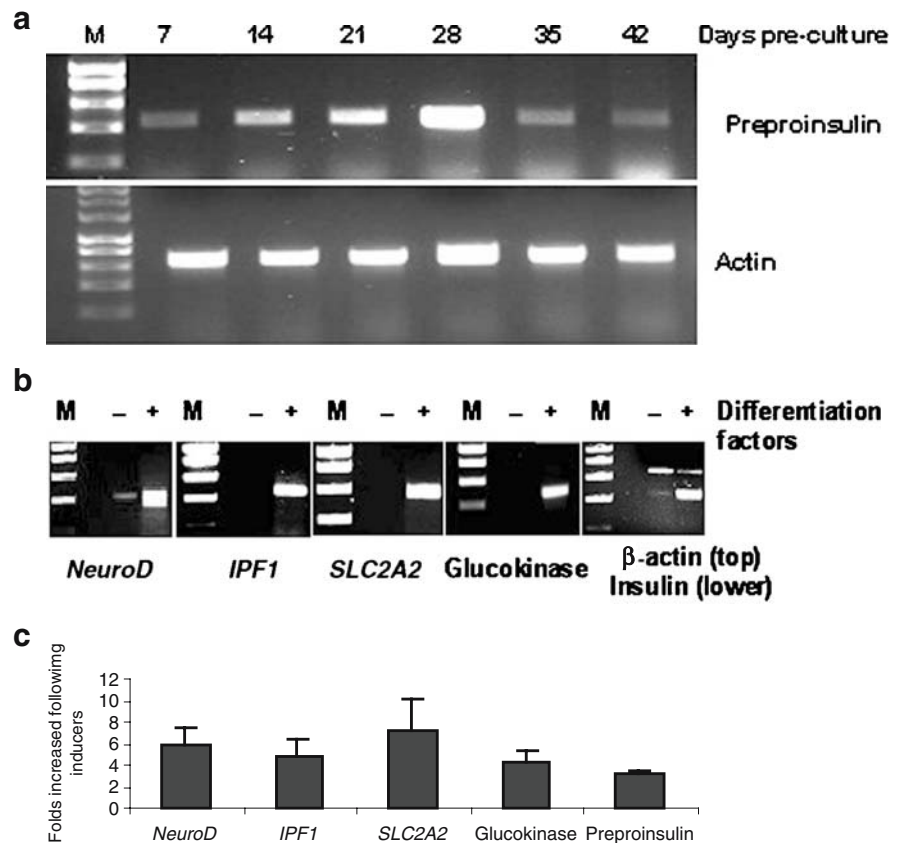
**Fig. 1** Removal of beta cells from exocrine cell preparations. **a** Typical low-power microscopic image of a routine preparation of human exocrine-cell-enriched cells following dithizone staining, showing the presence of <math><0.3\%</math> of dithizone-positive cells (arrows), with boxed area enlarged (inset). **b** Semiquantitative RT-PCR showing reduction in expression of preproinsulin in the cells following streptozotocin (STZ) treatment. **c** Relative quantitative RT-PCR, confirming the reduction in expression of preproinsulin in exocrine cell preparation following STZ treatment ( $n=12$ );  $**p<0.01$ . **d** Reduction of genomic DNA during STZ

treatment, indicating that cell loss is more obvious during the initial period of STZ treatment ( $n=4$ ). **e** Insulin content in the cells after STZ treatment, showing no difference from the lysate of MCF-7, a cancer cell line that does not express insulin. **f** Typical microscopic image of a graft of STZ-treated cells 6 weeks after transplantation within the kidney of an SCID mouse. It shows <math><0.01\%</math> cells positive for insulin (violet, arrow; nuclei counterstained with methyl green), which is a 30-fold decrease in beta cells compared with untreated cells (**a**), indicating that STZ treatment removed most beta cells

**Fig. 2** Phenotypic changes in cells cultured in monolayers for up to 49 days. **a** Phenotype changes during culture. Incorporation of amylose (yellow, *n*=8); CK19 (dark blue, *n*=8), nestin (pink, *n*=8), fibroblasts (green, *n*=4), vimentin (mid-blue, *n*=6), Ki67 (light blue, *n*=5) and BrdU (purple, *n*=5), assessed by immunocytochemical staining and cell number changes (brown, *n*=6) by counting. **b** Expression of nestin mRNA analysed by RT-PCR of cells maintained in monolayer culture



**Fig. 3** **a** RT-PCR showing the expression of preproinsulin and actin mRNA from cells that had been reverted to cluster culture for 8 days in the presence of ABNG differentiation inducers. **b** Beta cell marker analysis of cells precultured for 28 days in monolayer and subsequently cultured as clusters for 8 days in the absence (-) or presence (+) of differentiation factors of ABNG. **c** Relative quantitative RT-PCR confirming changes in expression after induction of differentiation



cell preparations) was first detected after 3 days of culture and increased to 60% after 4 weeks of culture, declining thereafter (Fig. 2a). The expression of nestin protein was simultaneous with its mRNA expression (Fig. 2b).

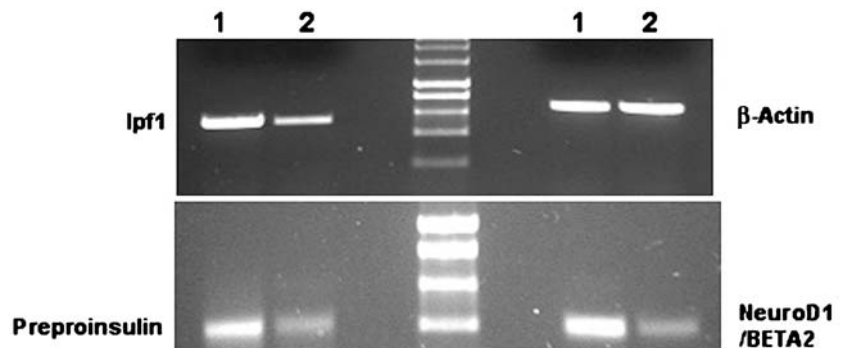
#### Plasticity of pancreatic non-endocrine cells

Cells in monolayer culture, without a phase of differentiation induction, did not express any mRNA specific for beta cells. We examined the existence of plasticity in the monolayer-cultured cells at various time points by converting them to cluster culture in the presence of differentiation inducers. After cluster culture with the differentiation cocktail ABNG, preproinsulin mRNA was detected in the cells, with maximal expression (Fig. 3a) in the cells following 4 weeks of monolayer culture, coincident with the highest percentage of cells expressing nestin protein (Fig. 2a). These cells also expressed other phenotypic markers of beta cells, including the products of *NeuroD1*, *IPF1*, *SLC2A2* and glucokinase (Fig. 3b), confirmed by relative quantitative RT-PCR analyses (Fig. 3c,  $n=4$ ). The best effect was seen after 8 days' incubation with ABNG. However, insulin protein was not detected. After transplanting these cells into diabetic SCID mice, a small percentage ( $3\pm 2.3\%$ ,  $n=6$ ) of insulin-producing cells was detected by immunohistochemistry 6 weeks later, but there was no significant reduction in hyperglycaemia in the mice (data not shown).

#### Effect of transfection with *IPF1*

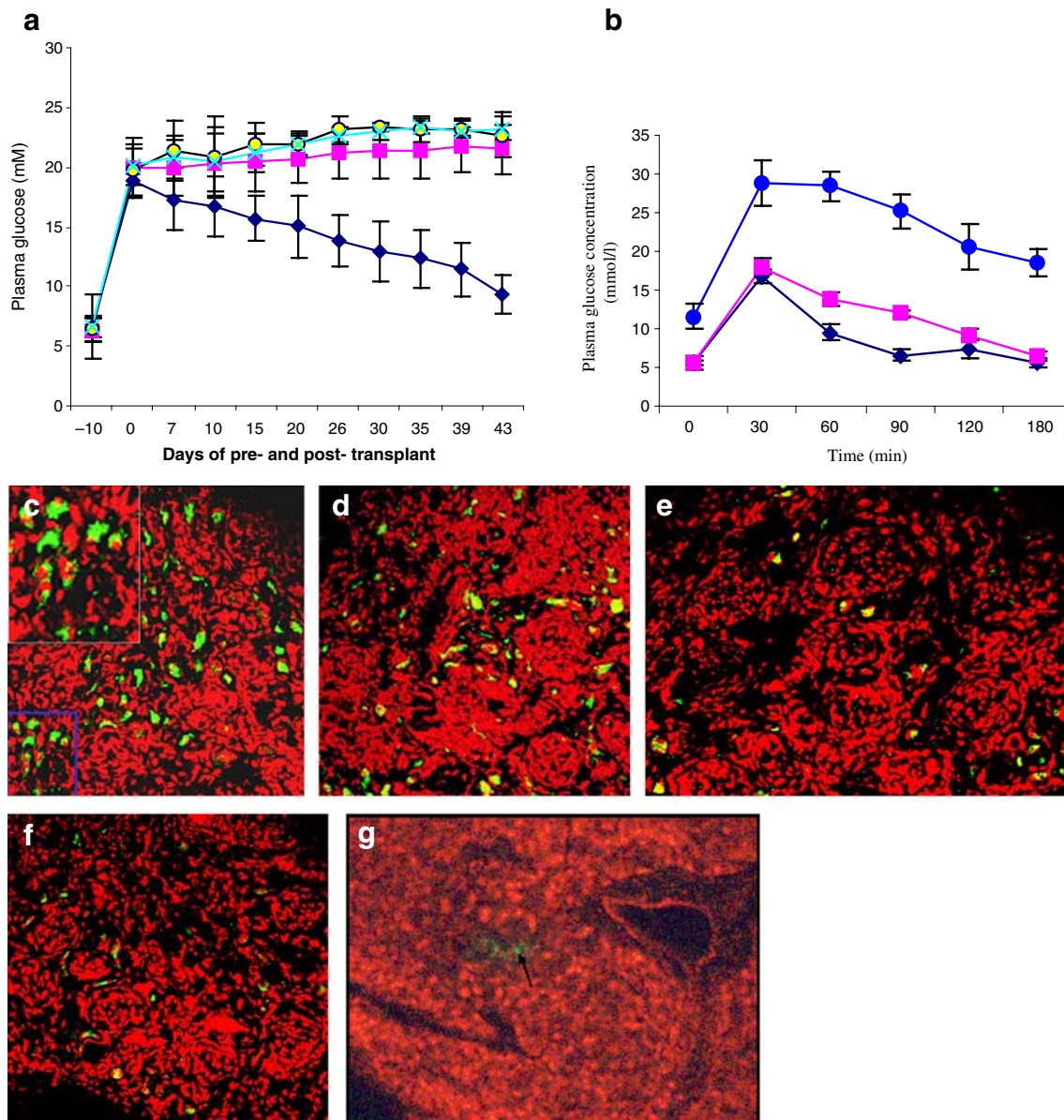
The cells that had been cultured for 4 weeks were transfected with *IPF1* for 48 h and then converted to cluster culture for 8 days in the presence of ABNG as described above. Q-PCR showed a  $2.15\pm 0.21$ - and  $3\pm 0.5$ -fold increase in the expression of preproinsulin and *NeuroD1* mRNA, respectively in the *IPF1*-transfected cells compared with the vector control cells (Fig. 4,  $n=6$ ). *SLC2A2* and glucokinase did not show significant changes (data not shown). Again, despite the increased expression of preproinsulin mRNA, the cells did not contain detectable insulin protein ( $n=6$ , data not shown).

**Fig. 4** RT-PCR analysis of the expression of preproinsulin, *IPF1* and *NeuroD1* in cells precultured for 28 days in monolayer and subsequently transfected with *IPF1* (lanes 1) or the empty vector (lanes 2) after treatment with differentiation factors for 8 days, corrected to the expression of  $\beta$ -actin. The RT-PCR was amplified for 22 cycles in order to distinguish the differential expression level



#### Effect of transplantation into STZ-induced diabetic mice

All of the 42 mice that received cells transfected with *IPF1* prior to incubation with ABNG showed a progressive reduction in plasma glucose concentrations over a period of 6 weeks (Fig. 5a). Forty per cent of the mice achieved non-fasting blood glucose levels within the non-diabetic range ( $<9$  mmol/l) and all of these showed measurable human C-peptide in their sera, as described below. In contrast, mice transplanted with cells transfected with empty vector remained hyperglycaemic, as did sham-operated mice and mice transplanted with cells isolated from the original STZ-treated pancreatic cells (Fig. 5a). Figure 5b shows the results of intraperitoneal glucose tolerance testing in six of 17 mice that had regained normoglycaemia after implantation with *IPF1* transfected cells, together with four sham-operated mice and four normal mice. The active implantation restored glucose tolerance to a near-normal level. The fasted human C-peptide value in mice that had regained normoglycaemia was  $0.63\pm 0.31$  ng/ml ( $n=11$ ) and  $1.05\pm 0.25$  ng/ml ( $n=6$ ) following the intraperitoneal glucose tolerance test, indicative of graft function, while human-specific C-peptide was undetectable in sham-operated and normal mice. Immunohistochemical analysis of kidney sections of the mice that had returned to normoglycaemia showed healthy grafts that contained  $15\pm 6.7\%$  insulin-positive cells (Fig. 5c),  $8\pm 2.3\%$  glucagon-positive cells (Fig. 5d) and  $3\pm 0.85\%$  somatostatin-positive cells (Fig. 5e). The grafts of the mice transplanted with vector-transfected cells contained  $3\pm 1.85\%$  insulin-positive cells (Fig. 5f;  $n=6$ ), similar to those without *IPF1* transfected cells (data not shown). There were no amylase-positive cells in the grafts, while  $4\pm 0.85\%$  fibroblasts,  $2.5\pm 0.5\%$  CK19-positive cells and  $15.6\pm 3.5\%$  vimentin-positive cells were observed in the grafts. No gross tumour formation was seen in the animals and no tumour-like structures were observed among the grafts. Only  $1.5\pm 0.5\%$  ( $n=8$ )  $Ki67^+$  cells were found in the grafts, suggesting no significant cell proliferation in the grafts. Approximately 50% grafted cells were unidentifiable with the antibodies used. The pancreases of all STZ-treated groups showed numerous sites of damaged islets and only a few residual beta cells (Fig. 5g;  $n=6$ ) remained, with no significant differences between trans-



**Fig. 5** **a** Non-fasted plasma glucose level over time in SCID mice rendered diabetic with STZ. Values are shown from 10 days before and after transplantation, either with *IPF1* ( $n=42$ ), or with empty vector-transfected-cells (pink,  $n=12$ ) treated with differentiation factors as in Fig. 3b and Fig. 4, and cells that had received 5 days of STZ treatment (light blue,  $n=4$ ). Sham-operated mice (yellow,  $n=8$ ) were used as controls. **b** Intraperitoneal glucose tolerance tests on the 6/17 mice that regained normoglycaemia (pink,  $n=6$ ) with diabetic mice (mid-blue,  $n=4$ ) and normal mice (dark blue,  $n=4$ ) as control. **c–e** The typical immunohistochemical images (green fluores-

cence) of kidney grafts of STZ-induced diabetic SCID mice 6 weeks after transplantation with *IPF1* gene-transfected human pancreatic non-endocrine cells and stained for insulin (**c**), glucagon (**d**) or somatostatin (**e**) in mice that had regained normoglycaemia, in comparison with insulin-expressing cells (green fluorescence) derived from cells that had been transfected with empty vector (**f**). Insulin-positive cells (**c**) are boxed and enlarged (inset). **g**. Typical section of pancreas of STZ-induced diabetic SCID mouse that had regained normoglycaemia, showing residual beta cells (green fluorescence, arrow) in the damaged islets (arrowhead). The nuclei are counterstained with propidium iodide

planted and sham-operated groups. There was no evidence of beta-cell proliferation (Ki67-positive cells) in the pancreatic islets (data not shown).

## Discussion

In this study, we explored the potential of human pancreatic non-endocrine cells from normal human pancreas donors

as a source of glucose-responsive insulin-producing cells. We developed a three-step protocol: (1) *in vitro* partial de-differentiation of pancreatic non-endocrine cells; (2) ectopic expression of *IPF1* in the partially de-differentiated cells followed by differentiation induction *in vitro*; and (3) transplantation to allow further differentiation into mature insulin-producing cells *in vivo*. This protocol produced cells that reversed moderate hyperglycaemia in 40% of diabetic mice and improved glucose control in the re-



maintaining 60%. It should be noted that the organ donors covered a broad range of ages and both genders.

The source material for this study was human pancreas donated for islet isolation. To prove the principle, it was important to remove pre-existing beta cells from the cell preparations, thereby ensuring that the insulin-producing cells identified were newly developed. The first step was to take the cell fractions from the pancreatic digests that were depleted of islets. There were no effective ways to remove human beta cells from the cell preparations. Therefore, the cell preparations were treated with STZ, an effective beta-cell toxin in rodents. Human beta cells are relatively resistant to STZ [24]. Nevertheless, STZ has been successfully used in combination with other drugs in treating tumours of beta-cell origin in man [25–27], although beta-cell tumours may react to STZ differently from non-tumour cells. We used a high concentration of STZ (0.95 mmol/l), a concentration that is lethal to mice, in four consecutive treatments. This removed all dithizone-positive cells from our preparations. It remains possible that endocrine cells in the final transplants may have come from undetected residual beta cells, but the numbers make this unlikely. Even after transplantation of the STZ-treated cells, a mere 0.01% of cells were insulin positive and the mice remained hyperglycaemic (Fig. 5a), making it unlikely that the 15.6% insulin-producing cells identified in the fully redifferentiated transplanted cells were carryover beta cells.

Nestin, observed in our de-differentiated cells, is an intermediate filament protein originally described as a neuronal stem cell marker [28]. The association of nestin with pancreatic endocrine cells is not clear [29–32]. The conversion of mouse embryonic stem cells to insulin-secreting cells *in vitro* involves an intermediate stage when nestin is expressed [33]. It is thought that the expression of nestin may be a marker of a transient cell state intermediate between differentiated and undifferentiated. In addition, we observed that when cell cultures contained a high proportion of nestin-expressing cells, the cells showed a greater capacity to express markers of beta cells following differentiation induction. Therefore, the expression of nestin was taken as a phenotypic marker for transdifferentiation induction in this study.

The molecular mechanisms underlying the transdifferentiation are not clear. We speculate that during culture the non-endocrine cells change their differentiation status and may gain some transient elements, yet to be identified, that allow them to respond better to differentiation induction. The ability to express beta cell markers was closely related to the length of time cells were in monolayer culture, supporting this hypothesis. The transient expression of duct-cell marker is interesting, as cells with duct-cell phenotype have been shown to be capable of expressing markers of beta cells *in vitro* without [13, 14] or with the ectopic expression of *NEUROG3* [15]. More interestingly, the CK19-positive cells in this system were not typical duct cells as they also co-expressed vimentin, a marker of mesenchymal cells, probably connected with epithelial-to-mesenchymal transition [34]. As mentioned earlier, Pdx-1 is one of the most important transcription factors determining

pancreatic development and maintenance of the beta-cell phenotype [12, 35–37]. More importantly, forcing the expression of *Ipf1* in liver cells in diabetic mice induces the expression of insulin [38], converting the liver into a pancreas in *Xenopus* tadpoles [39] and hepatocytes to cells with phenotypes of pancreatic cell in mice [40]. *Ipf1* has also been shown to facilitate the expression of insulin in liver cells in mice with damaged islets when their liver cells are undergoing active regeneration [41]. Together with the differentiation inducers, Pdx-1 seems to play a synergistic role in forcing cells with transient plasticity into low-level differentiation towards endocrine cells by functioning as a switch [42], driving a change in the gene expression profile of cells. For example, the transcription factor *CEBPB* has been used to convert exocrine cell line AR42J into liver cells [43].

The timing of the introduction of *IPF1* was also important in our study as the cells from the 28-day monolayer culture showed the greatest ability to express beta cell markers, indicative of cooperation between transient plasticity and the induction of differentiation. The differentiation factors in ABNG [44–46] may also work by altering the gene expression profile. The composition of ABNG was the result of extensive analysis of the redifferentiation of partially de-differentiated human islet cells [18] and the combination was essential in our system. The ABNG cocktail probably provides a balance between survival and stress signals to the cells. A similar phenomenon of environmental factors determining phenotype was observed in rat exocrine cells, as they could express markers of hepatocytes [47] or beta cells [16] under different conditions. Our protocol depended heavily on the *in vivo* environment, as no insulin protein was detectable until the cells were implanted into the diabetic mice. The hyperglycaemic *in vivo* environment and close contact with host cells may have contributed to the differentiation of cells into mature beta cells, although the exact mechanism is not yet fully understood. The slow reduction in plasma glucose in the diabetic mice following transplantation suggests the presence of a maturation process before the cells became fully glucose-responsive. Thus, the transdifferentiation of pancreatic non-endocrine cells into endocrine cells required interplay among complex factors, including transient plasticity, the ectopic expression of *Ipf1*, and the *in vitro* and *in vivo* environments. The origin of insulin-producing cells remains uncertain as the rapid phenotypic changes during culture made it difficult to identify the origin of the insulin-producing cells in our system. We have therefore attributed it to the non-endocrine cells as a whole. For reasons discussed above, we do not think the insulin-secreting cells came from a residuum of beta cells in the original cell preparation, although we cannot discount this absolutely.

Ultimately, as shown by the human C-peptide data and the glucose profiles in the intraperitoneal glucose tolerance tests, our protocol resulted in cells that were glucose-responsive, an important criterion for insulin-secreting cells for eventual human use. The culture system we describe is therefore a useful model in which to analyse the underlying molecular mechanisms of the transdifferentiation of human

non-endocrine cells to mature, functional endocrine cells, including beta cells, and has the potential to be developed further to generate glucose-responsive insulin-producing cells in large quantity for clinical use.

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#### Duality of Interest

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