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# **Promoting ectopic pancreatic fates: pancreas development and future diabetes therapies**

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## **Abstract**

Diabetes is a disease which could be treated more effectively with a better understanding of pancreas development. This review examines the role of master regulator genes driving crucial steps in pancreas development, from foregut specification to differentiation of the five endocrine cell types. The roles of *Pdx1*, *Ptf1a*, and *Ngn3* are particularly examined as they are both necessary and sufficient for promoting pancreatic cell fates (*Pdx1*, *Ptf1a*) and endocrine cell development (*Ngn3*). The roles of *Arx* and *Pax4* are studied as they compose part of the regulatory mechanism balancing development of different types of endocrine cells within the iselts and promote the development of  $\alpha$ /PP and  $\beta$ /δ cell progenitors, respectively. The roles of the aforementioned genes, and the consequences of misexpression of them for functionality of the pancreas, are examined through recent studies in model organisms, particularly *Xenopus* and zebrafish. Recent developments in cell replacement therapy research are also covered, concentrating on stem cell research (coaxing both adult and embryonic stem cells towards a β cell fate) and transdifferentiation (generating β cells from other differentiated cell types).

#### **Keywords**

cell replacement therapy; Ngn3; Pancreas; Pdx1; Ptf1a; stem cells; transdifferentiation; *Xenopus*; zebrafish

## **Diabetes and the importance of basic research**

Diabetes is a serious disease that could be treated more effectively with a better understanding of pancreas development. The discovery of insulin in 1921 and the first insulin treatment of a patient in 1922 has changed diabetes from an outright lethal disease

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into a chronic condition (1). Diabetes can be split into three main types. First, Type 1 diabetes, which includes insulin-dependent diabetes, involving autoimmune destruction of the insulin-producing β-cells, and neonatal insulin production deficiencies. Second, Type 2 diabetes, a form of the disease whereby people become resistant to insulin, often associated with obesity. Third, gestational diabetes, which develops during pregnancy and most often resolves itself after the child is born.

Insulin replacement therapy has long been the treatment for type 1 diabetes and despite the fact that this regimen has changed diabetes from a fatal to a chronic disease, complications associated with inappropriate control of glucose levels still endure. Poorly managed diabetes can lead to blindness, kidney damage, and amputations among other things. Pancreatic transplants and injections of islet cells from cadavers are new therapies, but the shortage of donor tissue and the long term effects of lifetime immunosupressive regimens means that this approach is not available nor suitable for all diabetics. In fact pancreatic transplants are mainly reserved for those in whom regular insulin treatments are not working or those with many or advanced complications. Alternative treatments need to be developed, but this requires a better understanding of the molecular pathways underlying normal and disturbed pancreas development. To this end, basic research in model organisms will lead to a better understanding of how individual pancreatic cell fates are specified and help elucidate the molecular mechanisms that break down in disrupted pancreas development. This review will examine the genetic regulation of pancreas development focusing on genes that are not only essential, but also sufficient to promote ectopic pancreatic cell fates, as these are most likely to form the basis of future diabetes therapies. Many reviews covering other aspects of pancreas development in more detail are available (2-6).

Several model organisms have been informative in pancreatic developmental studies. Mouse and chick are the traditional models, while recently *Xenopus* and zebrafish have also been utilized (7-13). The two aquatic species, *Xenopus* and zebrafish, are cheaper to work with, grow faster than mice, and have a shorter generation time allowing experiments with higher throughput. Knock down and overexpression experiments can be performed initially in *Xenopus*, for example, to confirm the involvement of genes of interest (such as those implicated by genome-wide association studies or a microarray experiment) before more expensive and time-consuming mouse knock-outs are made. In addition, *Xenopus* and zebrafish can be used for *de novo* discoveries. Indeed, one of the most important genes in pancreatic development, *Pdx1*, was first discovered in *Xenopus* (14) years before the homologue was found in mice (15-18).

The pancreas develops from the endodermal germ layer, initially as two ventral buds and a single dorsal bud. These buds arise from distinct locations and are specified by different molecular mechanisms. In *Xenopus* the two ventral pancreatic buds fuse initially with each other, and shortly thereafter with the dorsal pancreas, such that by 3 days post-fertilization the tadpole has a single pancreas (5). In mammals however, one of the ventral buds regresses and fusion with the dorsal pancreas only occurs at E12.5 in mice (reviewed in (6)) and the sixth week of fetal development in humans (reviewed in (19)). Defects in development at these early stages can lead to clinically recognisable pancreatic anomalies inappropriate development of the ventral pancreas can lead to annular pancreas or pancreas

divisum, whereas agenesis of the dorsal pancreas can occur (reviewed in (4)). Given that defects in development can lead to disease, a more thorough understanding of pancreas development from the earliest stages is important to understanding diabetes and other pancreatic diseases.

#### **Foregut regional specification**

The developing gut is divided into three regions, foregut, midgut, and hindgut; with the pancreas arising in the posterior part of the foregut. Several growth factor families, including bone morphogenetic protein (BMP) and Wnt, play important roles in patterning the endoderm and creating these regions. Interestingly, it is the repression of Wnt and BMP signaling that is essential in establishing the foregut (20, 21). Promotion of Wnt signaling in the anterior endoderm with ectopic expression of β-catenin or wnt8 during gastrula and neurula stages inhibits normal development of the pancreas and liver (21). In contrast, inhibiting Wnt signaling in the posterior endoderm with gsk3β or Dkk1 results in ectopic development of liver and pancreas buds. Similarly, the Smad transcriptional corepressor TGIF2 is required for proper specification of the pancreas (20). In addition to BMP and Wnt, retinoic acid (RA) and sonic hedgehog (Shh) signaling play key roles in positioning the posterior foregut domain (22-27). RA signalling is not only important for regional induction of this domain, but it is also essential for dorsal pancreas development (28), perhaps by suppression of endodermal Shh (29). The absence of *Shh* expression is vital for pancreas specification in amniotes and *Xenopus* (30, 31). In zebrafish Shh is required very early in foregut development for pancreatic induction (32-34) but has inhibitory effects on development in later stages, similar to those seen in amniotes setting up the organ boundaries in the foregut (34). Once the posterior region of the foregut is specified, downstream transcription factors are activated that function to specify development of the entire pancreas, followed by the activation of lineage-specific factors in distinct regions within the pancreas.

Several genes are expressed in a broad domain encompassing the entire posterior foregut prior to initial specification of the pancreas. Two of the earliest markers of the foregut are the onecut transcription factor, hepatocyte nuclear factor 6 (HNF6), and the ParaHox transcription factor, pancreas and duodenal homeobox gene 1 (Pdx1). Expression of *HNF6* in the dorsal and ventral endoderm is evident as early as the eight somite stage in mice, prior to expression of *Pdx1* in the pancreatic and rostral duodenum region (35). In HNF6<sup>-/-</sup> mice, although *Pdx1* expression is delayed (resulting in pancreatic hypoplasia), endocrine cells develop, albeit abnormally (36). In *Pdx1* mutant mice a more severe pancreatic phenotype is seen; pancreatic tissue is absent (37-39). Interestingly, initial budding of the pancreatic epithelium does occur, and early glucagon and insulin cells can be detected, though they do not persist. In humans, two different cases of pancreatic agenesis have been attributed to point mutations in the human *Pdx1* homologue, *IPF1* (40, 41). Studies in zebrafish show that knockdown of *Pdx1* using morpholinos results in reduced pancreatic tissue at 2 days, although by day 5 the pancreas is normal (42). Although *Pdx1* was initially cloned in *Xenopus* the first report of a *Pdx1* knockdown in *Xenopus laevis* did not come until 2006 (13). Morpholino knockdown of *Pdx1* in *X. laevis* results in a complete absence of acinar cells, while endocrine β cells develop normally; effects on other endocrine cells were not

Downstream of *Pdx1*, one of the earliest markers specific to the developing dorsal and ventral pancreas is the basic helix-loop-helix (bHLH) transcription factor, pancreas transcription factor 1a (Ptf1a) (43). Similar to Pdx1, loss of Ptf1a results in pancreas agenesis (43, 44). The fact that loss of either Pdx1 or Ptf1a results in agenesis of the pancreas would suggest that these two proteins may interact to specify initial pancreas development, and several facts support this. First, although *Ptf1a* is expressed slightly later than *Pdx1* (a day later in mouse development), it has recently been shown to bind to the *Pdx1* promoter suggesting a role in maintenance of *Pdx1* expression (45). Second, it was recently shown that Ptf1a and Pdx1 function interdependently to specify early pancreatic multipotent progenitor cells (46). Third, progenitors lacking *Ptf1a* expression instead become intestinal (43). Perhaps cells expressing both *Pdx1* and *Ptf1a* become pancreatic, while those expressing only *Pdx1* give rise to intestinal tissue.

What has until recently been perplexing is how Ptf1a, originally isolated as an acinarspecific transcription factor, could also be involved in specification of general pancreatic progenitors. Several recent papers provide answers to this conundrum. First, it was shown that Ptf1a binds a specific region of the *Pdx1* promoter (area III) that mediates the early pancreas-wide expression of *Pdx1* (45). Second, Ptf1a binds this region in cooperation with RBPJ, which is essential for early pancreas development (47). Third, PTF1a function in acinar cells is dependent on RBPJL (47). Thus the function of Ptf1a in early pancreas development is dependent on RBPJ, while its function in acinar cell development is dependent on RBPJL, providing a mechanism to regulate these two different functions of Ptf1a.

In contrast to the situation with loss of Pdx1, specification of endocrine cells does occur in Ptf1a mutants, albeit at a significantly reduced rate (8, 44, 46, 48). In Ptf1a mutant mice these endocrine cells are present in the small dorsal pancreatic remnant, while in humans the location of the remaining insulin-expressing cells has not been determined (49). In *Xenopus*, initial specification of β cells does not occur in tadpoles lacking Ptf1a, whereas insulin expressing cells can be detected at later stages (9, 13). The exact opposite is seen in zebrafish where only a small population of late emerging endocrine cells are Ptf1adependent (8). These results suggest that there are two populations of endocrine cells, a Ptf1a-dependent (ptf1a+ngn3+ cells) and a Ptf1a-independent (present in *Ptf1a* null mice) population (44, 46). However, these Ptf1a-independent endocrine cells are insufficient to establish the normal number of endocrine cells (44, 46).

None of these studies however, address the sufficiency of Ptf1a or Pdx1 in promoting pancreatic cell fates. This is quite important because although a factor may be necessary for the development of a specific cell type, it does not follow that it will also be sufficient to promote that fate. It is also possible that a specific factor may promote different cell fates depending on the cell type in which it is expressed. Regarding Ptf1a and Pdx1, we have shown (using *Xenopus*) that both are sufficient to promote ectopic pancreatic cell fates in other organs (9, 10). The benefit of using *Xenopus* is that we can rapidly test the function of

specific pancreatic transcription factors in different contexts: either in mRNA injections into early cleavage stage embryos to target naïve endoderm prior to organogenesis, or in transgenics to overexpress in specific organs at later developmental stages. Overexpressing genes in early endoderm is similar to overexpressing the same genes in embryonic stem cells (ES cells). Our lab has shown that overexpression of an activated *Pdx1*, *Pdx1-VP16*, in the liver cells of tadpoles and *in vitro* in HepG2 cells promotes the development of both endocrine and exocrine cells (10). Similar results were obtained by other labs, most notably by the Ferber lab, using either Pdx1 or Pdx1-VP16 (50-52). Interestingly, persistent overexpression of *Pdx1* in the pancreas (in all cell types) results in acinar-ductal metaplasia (53). Therefore, the ability of *Pdx1* to promote specific pancreatic cell fates depends on the context in which it is overexpressed.

Initial results suggesting that Ptf1a may promote ectopic pancreatic cell fates in the stomach and duodenum came from results in Hes1 mutant mice. In these mice the patches of differentiated ectopic pancreatic tissue that develop in the stomach, duodenum and common bile duct re-express *Ptf1a* (54). Although suggestive, the data did not show that Ptf1a directly promotes ectopic pancreas formation. We used *Xenopus laevis* to directly test the ability of Ptf1a and an activated form, Ptf1a-VP16, to promote ectopic pancreatic cell fates. We found that each was sufficient to promote ectopic pancreatic cell fates in the posterior foregut, but found differences in their activities (9). While overexpression of *Ptf1a* was sufficient to promote both endocrine and exocrine cell fates in the stomach and duodenum (both in early endoderm and in transgenics), *Ptf1a-VP16* was only able to promote acinar fates. We also found differences in the activity of *Ptf1a-VP16* depending on when it was overexpressed. In early endoderm, we found that Ptf1a-VP16 was able to convert most posterior foregut derivatives into acinar cells, including prospective liver, stomach, duodenum and pancreas, whereas in transgenics (where expression was much later) Ptf1a-VP16 was only able to convert liver cells to an acinar cell fate (9). The ability of Ptf1a to promote both endocrine and acinar cell fates only in posterior foregut derivatives suggests that it requires other coactivators that are localized to the foregut, such as Pdx1 (13).

#### **Regulation of ductal, endocrine and acinar cell fates**

Once a general pancreatic fate has been determined, individual ductal, acinar and endocrine cell fates need to be established. Although all three lineages arise from a common progenitor pool, specification of these cells within the pancreas occurs in a temporal manner, such that ductal cell fates are determined prior to the commitment of endocrine and acinar cells (55, 56). By E12.5 a subset of  $Pdx1<sup>+</sup>$  cells have been specified as ductal cells; after this stage  $Pdx_1^+$  cells will only give rise to endocrine and acinar cells (55, 56). Pancreatic progenitor cells that express *Pdx1* also express *Sox9*, a homeobox gene shown to be essential for maintenance of the pancreatic progenitor cells (57). Conditional inactivation of *Sox9* in the pancreas leads to pancreatic hypoplasia, reminiscent of that seen in Notch signaling pathway mutants. In agreement with this, expression of the downsteam Notch effector, *Hes-1*, is severely reduced in Sox9 mutants (57). Furthermore, Sox9 and several other pancreatic progenitor transcription factors, including FoxA2, Tcf2 and HNF6, interact to directly regulate each other's expression (58). Subsequently, these factors activate the expression of the endocrine progenitor marker, *neurogenin3* (*Ngn3*), to specifiy the endocrine lineage.

The bHLH transcription factor Ngn3 is the earliest marker of endocrine progenitor cells, both in the embryo and the adult (55, 59). Expression of *Ngn3* is transient in the progenitor cell population, and it is not expressed in differentiated cells (60); this allows tight regulation ensuring a balance between islet cell differentiation and progenitor cell proliferation. Ngn3 is essential for endocrine cell development, as demonstrated in Ngn3 knockout mice where no endocrine cells develop (60). One of the first genes Ngn3 activates is the zinc finger transcription factor *insulinoma associated protein 1* (*IA1*) (61). Much like *Ngn3*, *IA1* is only expressed in the progenitor cell population, and is required for the differentiation of all endocrine cells (62). The localized expression of both of these factors in endocrine progenitors coupled with the fact that they are indispensable for endocrine cell development would suggest that they ought to be sufficient for promoting endocrine cell fates. Indeed, overexpression of *Ngn3* in the pancreas is sufficient to promote differentiation of all endocrine cells (see Fig. 1), but this effect is context dependent (63). When expressed in early embryonic pancreas, *Ngn3* promotes differentiation of only the alpha cell population, but when expressed at progressively later stages it is also able to promote differentiation of three other endocrine lineages (64). In contrast to *Ngn3*, overexpression of *IA1* does not lead to any obvious changes in pancreas development (Horb ME, unpublished data). Thus, although Ngn3 is both necessary and sufficient for endocrine cell development, its ability to promote endocrine cell fates is context dependent.

Downstream of the Ngn3 pan-endocrine progenitor population there appear to be separate α/PP and β/δ lineages that are specified by the opposing actions of two transcription factors, aristaless related homeobox gene (Arx) and paired box 4 (Pax4), respectively (Fig. 1). In Arx mutants the α cell population does not develop, and there is an increase in the numbers of β and δ cells (65). Interestingly, overexpression of *Arx* is sufficient to promote the differentiation of both α and PP cell populations at the expense of β and δ cells, even though only the α cell population is affected in Arx mutants (66). The exact opposite is seen with Pax4. In Pax4 mutant mice the β and δ cell lineages do not develop, and there is an increase in the α cell lineage (67). Interestingly, the phenotype of the Arx/Pax4 double mutant mice is not simply additive of each single mutant – in these mice the  $\alpha$  and  $\beta$  cell populations are absent as expected but there are excessive numbers of δ and PP cells (68). These results would seem to indicate that there is a relationship between the δ and PP cell populations. This is supported by the recent results obtained in Rfx3 mutant mice; in these mice the α and  $\beta$  cell lineages do not develop, and while the  $\delta$  cell lineage is normal there is a large increase in the PP cell population (69). These results suggest a relationship whereby the  $\delta$ and PP cells arise from the same progenitor population and the  $\beta$  and  $\delta$  cells arise from a common progenitor.

In contrast to the four endocrine lineages described above, the factors responsible for promoting development of the fifth endocrine cell lineage, ε cells which produce ghrelin, have yet to be identified (70, 71). Several reports however have shown that loss of Nkx2.2, Pax4 or Pax6 leads to an increase in the ghrelin cell population (72, 73). Although several other transcription factors, such as Pax6, are required for proper development of the different endocrine lineages, it is unclear whether they are able to promote the development of ectopic pancreatic tissue. It is also important to remember that there are further

transcription factors responsible for the final maturation of the different cell types. As we do not have the space to discuss these factors in detail here the reader is recommended to several excellent recent reviews (2, 3, 5-7, 74, 75).

#### **Future therapies based on current research**

Current research into diabetes treatment is focused on generating replacement cells that can mimic the exquisite glucose-responsiveness of the normal pancreatic β cell (76). Two main sources of cells that can be used to produce ectopic  $\beta$  cells for cell replacement therapy are stem cells and differentiated cells (Fig. 2). In the first instance both embryonic (ES) and adult stem cells are possible sources. Recent studies using ES cells have demonstrated that these cells can be directed towards a pancreatic lineage, although these studies are still in their infancy (77-79). It is interesting to note that much of the information required to guide the differentiation of ES cells into a pancreatic lineage came from earlier developmental biology studies (80). Although adult stem cells do not possess the same pluripotency of ES cells, they are multipotent, and several recent reports have demonstrated their potential usefulness for diabetes therapy. Bone marrow derived stem cells have been examined most frequently, and can be used to either directly generate islet cells or to initiate endogenous regeneration of the pancreas (81-86). Other adult stem cell populations that may be used include umbilical cord, intestinal, liver, adipose and spleen (87-90). Although their existence remains controversial, pancreatic stem cells may also provide a rich source of cells (87, 91, 92). The pluripotent nature of ES cells would seem to favor their use, but questions surrounding their tumorigenic potential need to be answered (92). Adult stem cells provide less of an ethical dilemma, although it is unclear how competent they are to produce (or induce) fully functional β cells.

An alternative strategy is to generate pancreatic tissue from differentiated cells, known as transdifferentiation. (reviewed in (93, 94)). Transdifferentiation of liver tissue is the most promising since liver and pancreatic cells arise from common progenitors in the posterior foregut coupled with the fact that the liver has the ability to regenerate (9, 13, 50, 95, 96). The ability to alter a small population of a patient's own liver cells to become insulinproducing pancreatic cells would eliminate the problems of tissue shortage and rejection associated with islet cell or whole pancreas transplants. Transdifferentiation amongst different cell types in the pancreas is also possible as both ductal and acinar cells have been successfully transdifferentiated into  $\beta$ -cells (97, 98). In order for this to become a legitimate therapy a better understanding of the molecular control of transdifferentiation is required. *Xenopus laevis* is an excellent model organism in which to study the transdifferentiation process as liver-to-pancreas transdifferentiation been shown to occur in *Xenopus* (9, 10, 13). Furthermore, gene overexpression and knock down studies are easily, cheaply and quickly performed in *Xenopus* compared to other model organisms such as the mouse, enabling faster elucidation of the molecular networks regulating the process. Understanding the regulation of the transdifferentiation process in a model organism is the first step towards understanding it in humans and eventually being able to control the process in human therapies.

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#### **Figure 1. From pre-pancreatic endoderm to pancreas**

A schematic diagram outlining the major developmental steps involved in creating different pancreatic cell types. Important progenitors are inlcuded along with genes important in key steps in pancreas development.



#### **Figure 2. Creating a new pancreas, the future of diabetes therapy**

Many future diabetes therapies revolve around the idea of creating new pancreas cells. There are two major ways to do this. Transdifferentiation involves changing a differentiated cell type into β cells by turning on pancreatic transcription factors in non-β cells. The other method is guiding stem cells (either from adult or embyronic tissue) to become pancreatic β cells utilizing combinations of growth factors and chemicals.