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Dynamic regulation of Pdx1 enhancers by Foxa1 and Foxa2 is essential for pancreas development

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The onset of pancreas development in the foregut endoderm is marked by activation of the homeobox gene Pdx1 (IPF1). Pdx1 is essential for the expansion of the pancreatic primordium and the development of endocrine islets. The control of Pdx1 expression has been only partially elucidated. We demonstrate here that the winged-helix transcription factors Foxa1 and Foxa2 co-occupy multiple regulatory domains in the Pdx1 gene. Compound conditional ablation of both Foxa1 and Foxa2 in the pancreatic primordium results in complete loss of Pdx1 expression and severe pancreatic hypoplasia. Mutant mice exhibit hyperglycemia with severely disrupted acinar and islet development, and die shortly after birth. Assessment of developmental markers in the mutant pancreas revealed a failure in the expansion of the pancreatic anlage, a blockage of exocrine and endocrine cell differentiation, and an arrest at the primitive duct stage. Comparing their relative developmental activity, we find that Foxa2 is the major regulator in promoting pancreas development and cell differentiation. Using chromatin immunoprecipitations (ChIP) and ChIP sequencing (ChIPSeq) of fetal pancreas and islet chromatin, we demonstrate that Foxa1 and Foxa2 predominantly occupy a distal enhancer at −6.4 kb relative to the transcriptional start site in the Pdx1 gene. In addition, occupancy of the well-characterized proximal Pdx1 enhancer by Foxa1 and Foxa2 is developmental stage-dependent. Thus, the regulation of Pdx1 expression by Foxa1 and Foxa2 is a key early event controlling the expansion and differentiation of the pancreatic primordia.

[Keywords: Pancreas; development; Pdx1; Foxa1; Foxa2; conditional gene ablation]

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described above and the previously reported Foxa2loxPloxP (Sund et al. 2000) and Pdx1CreERT2 mice (referred to as Pdx1CreE throughout) [Gu et al. 2002; Heiser et al. 2006]. Surprisingly, Foxa1loxPloxP,Pdx1CreE mice \( n = 20 \) and Foxa2loxPloxP,Foxa1loxPloxP,Pdx1CreE mice \( n = 61 \) were not only viable and fertile, but also euglycemic [Supplemental Fig. 2D]. Given that the Pdx1CreE transgene mediates gene ablation in the entire endocrine pancreas including α cells [Gu et al. 2002], this finding demonstrates that the neonatal lethality of Foxa1−/− mice is the consequence of nonpancreatic defects [Kaestner et al. 1999; Behr et al. 2004]. In contrast, Foxa1loxPloxP,Foxa2loxPloxP,Pdx1CreE mice \( n = 37 \) were severely hyperglycemic [Supplemental Fig. 2D] and died within the first 2 d of life. Interestingly, Foxa1loxPloxP,Foxa2loxPloxP,Pdx1CreE mice \( n = 8 \) also died before postnatal day 5.

In Foxa1loxPloxP,Foxa2loxPloxP,Pdx1CreE mice (referred to as “compound mutants” below), Cre recombinase initiated deletion of both genes on E9.0. When we analyzed embryos at late gestation (E18.5), only minimal pancreatic tissue remained in the compound mutant mice, in contrast to their control littermates [Fig. 1A–D]. This dramatic phenotype exhibited variable penetrance in mutant mice, affecting either the ventral or dorsal pancreas [Fig. 1B,C], or both [Fig. 1D]. This severe pancreatic hypoplasia explains the early postnatal death of Foxa1/Foxa2 compound mutant mice. As expected, no Foxa1 or Foxa2 protein was detected by immunohistochemistry in the remaining pancreatic tissue recovered from compound mutants at E18.5 [Fig. 1E,G], while a concomitant loss of Pdx1 protein in these mutant tissues was revealed in adjacent sections [Fig. 1F,H]. In contrast to the pancreas, the duodenum developed normally in compound mutants. Equivalent levels of Foxa1/Foxa2 proteins were detected by immunohistochemistry in control and mutant duodenal epithelia using an antibody that recognizes both Foxa1 and Foxa2, and the distribution of Foxa1/Foxa2+ cells within the duodenal epithelium was also identical [Fig. 1I,J]. Because Pdx1CreE expression in the duodenum is mosaic, this is either because the transgene did not result in Foxa1/Foxa2 deletion in this tissue or because Foxa1/Foxa2-null cells were replaced by wild-type cells.

**Decreased Pdx1 in the pancreatic buds of Foxa1/Foxa2 compound mutants**

Even though Pdx1 is a master regulator of pancreas formation, and Pdx1 mutant mice or people lack a mature pancreas [Jonsson et al. 1994; Stoffers et al. 1997], pancreas development is initiated in Pdx1−/− mice, and a small pancreatic rudiment is present [Offield et al. 1996]. We examined pancreatic bud formation in Foxa1/Foxa2 compound mutant animals utilizing the Rosa26R reporter line, which marks those cells in which the Pdx1CreE has been active. Both dorsal and ventral pancreatic buds formed [Fig. 2A–D, E9.5] and initially expanded [Fig. 2E–H, E10.5] in compound mutant mice. Sections of these β-gal-stained embryos were analyzed by immunohistochemistry for Foxa1/2. In contrast to control pancreatic buds [Fig. 2I], where nuclear Foxa1/Foxa2 was detected in both the foregut epithelium and the growing tips of the pancreatic primordia at E9.5 [Fig. 2J,K], a vast majority of the cells in the compound mutant pancreas were Foxa1/Foxa2-negative [Fig. 2L], except for a few scattered cells in the pancreatic anlage that retained nuclear staining [Fig. 2L, arrow]. The gut epithelium of the mutant embryos was clearly Foxa1/Foxa2-positive [Fig. 2J].

Pdx1 expression was reduced in compound mutant pancreatic anlagen compared with control sections as early as E9.5 [Supplemental Fig. 3A,B]. At E10.5, the growing pancreatic epithelial buds in control mice strongly expressed Pdx1 [Fig. 2M–P], while Pdx1 expression in the mutant epithelial cords was almost completely extinguished [Fig. 2O–T]. Thus, early pancreatic primordia in compound mutant mice formed with a normal number of Pdx1+ precursor cells in which Foxa1 and Foxa2 had not yet been deleted, but by E10.5 the Pdx1CreE transgene efficiently removed both Foxa genes, resulting in a loss of Pdx1 expression in the developing pancreas.

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**Figure 1.** Conditional ablation of Foxa1 and Foxa2 in the pancreatic primordia causes pancreatic hypoplasia. [A] Control E18.5 pancreas, outlined by the dotted line, is located between the stomach and duodenum. [B–D] Foxa1 and Foxa2 compound mutant pancreata were severely hypoplastic, with variable penetrance of the affected pancreatic lobes. Asterisks indicate the complete absence of the ventral pancreas. [E–H] Adjacent sections of control and compound mutant pancreas [E18.5] were stained for Foxa1/2 and Pdx1, with all three proteins being absent in the mutant pancreas. [I,J] Foxa1/Foxa2 expression in duodenal epithelia of the compound mutants was unaffected.
Pancreatic precursor cells fail to expand in Foxa1/Foxa2-deficient buds

During early pancreas development, Pdx1-expressing precursor cells expand to form a branched system of epithelial cords. Outgrowth and differentiation of exocrine and endocrine progenitors from these primitive cords initiates around E13.5. We observed near normal amounts of pancreas tissue, as indicated by β-galactosidase activity, in Foxa1loxP/+,Foxa2loxP/+,Pdx1CreE,Rosa26R mice at E13.5 (Fig. 3A,B). Interestingly, mice with only one remaining wild-type Foxa2 allele (Foxa1loxP/loxP,Foxa2loxP/+,Pdx1CreE) developed normal dorsal and ventral pancreata (Fig. 3C,D). In contrast, the pancreas anlage of compound mutant mice failed to expand (Fig. 3E,F). At E13.5, the control pancreas formed a ductal tree (Fig. 3G) concomitant with epithelial cell differentiation and proliferation. In contrast, the compound mutant pancreas contained epithelial cords without clear exocrine structure (Fig. 3H). This lack of morphological transformation in mutant tissue was supported by the scarcity of immature endocrine and exocrine cells marked by glucagon (Fig. 3J) and amylase (Fig. 3L) antibodies, while an abundance of glucagon+ and amylase+ cells were detected in the control pancreas (Fig. 3I,K). In addition, Cpa1+ cells, which form the multipotent progenitor domains at the tips of the ductal tree at this stage (Fig. 3M; Zhou et al. 2007), were very rare in the compound mutant pancreas (Fig. 3N). Using antibodies against Ngn3 and Ptf1a, known lineage determinants for endocrine and exocrine cells, respectively, we observed abundant Ngn3+ and Ptf1a+ cells in emerging acini (Fig. 3O,Q). In sharp contrast, compound mutant pancreata contained only a few cells expressing either factor (Fig. 3P,R). To quantify this reduction, we counted Ngn3+ and Ptf1a+ cells that were colabeled by β-gal staining in the control and mutant pancreas (Supplemental Fig. 3). This analysis revealed an 84% and 93% reduction of Ngn3+ and Ptf1a+ cells, respectively, in compound mutants (Supplemental Fig. 3M). Thus, the compound...
mutant pancreatic epithelial cords failed to elaborate sufficient numbers of endocrine and exocrine progenitors, resulting in severely reduced numbers of glucagon+ and amylase+ cells.

**Foxa1 and Foxa2 are not equivalent in promoting pancreas development**

In order to determine whether Foxa1 and Foxa2 are completely interchangeable in pancreas formation, we analyzed E14.5 mouse embryos with various combinations of Foxa1 and Foxa2 alleles. Interestingly, when one or both Foxa2 wild-type alleles were present (Fig. 4A,B), the number of wild-type Foxa1 alleles did not have an impact on pancreatic size. In other words, one copy of the Foxa2 gene was sufficient to induce pancreas formation. When both Foxa2 alleles were removed, however, a clear reduction in pancreatic mass was seen (Fig. 4C–F). Importantly, in this scenario, Foxa1 gene copy number became a determinant of the size of pancreatic lobes (Fig. 4, cf. C and E, and D and F). This was reflected by the relative area of the pancreas: 31% of control in Foxa1loxP/loxP,Foxa2loxP/+,Pdx1CreE mice, compared with 19% in compound mutant mice (Fig. 4G). While these data demonstrate that Foxa2 is more potent in promoting pancreas growth than Foxa1, Foxa1 is also a positive regulator of pancreas development. In addition, although both pancreatic lobes were affected in these mutant mice, the ventral pancreas was more sensitive to Foxa deficiency than the dorsal pancreas (Fig. 4D,F).

The notion of differential competency of the two Foxa genes was supported by our analysis of late gestation pancreata. E17.5 mice with only one remaining wild-type Foxa2 allele (Foxa1loxP/loxP,Foxa2loxP/loxP,Pdx1CreE) specified similar numbers of exocrine and endocrine cells as control pancreata (Fig. 5A,B). In contrast, a dramatic reduction in both cell types was seen in the Foxa1loxP/loxP,Foxa2loxP/loxP,Pdx1CreE pancreas (Fig. 5C).

**Figure 3.** Pancreatic precursors fail to expand in Foxa1 and Foxa2 compound mutants. (A–F) Whole-mount gut tissues were dissected from E13.5 embryos of the indicated genotypes. Dorsal and ventral pancreata developed in Foxa2loxP/+,Foxa2loxP/loxP,Pdx1CreE and Foxa2loxP/loxP,Foxa2loxP/loxP,Pdx1CreE mice as indicated by β-galactosidase activity, but failed to grow in compound mutant mice (dotted lines). (G,H) E13.5 control pancreas formed a ductal epithelial tree with abundant exocrine structures visible at the ductal tips. Compound mutant pancreata consisted primarily of ducts. (I–R) Control and compound mutant sections were stained with glucagon ([I,J], amylase ([K,L], CPA1 ([M,N]), Ngn3 ([O,P]), and Ptf1a ([Q,R]) antibodies in red, and counterstained for E-cadherin (blue) or DNA (green). Bars, 25 μm.
tants, some double-positive (amylase+/glucagon+) cells occupying the central core (Fig. 5E,F), in pancreas, where amylase+ or glucagon+ cells were rarely seen (Fig. 5G,H; Supplemental Fig. 4). However, when compared with the Foxa1/Foxa2-devoid pancreas, as marked by $\beta$-galactosidase activity of the Rosa26R reporter present in all embryos, was quantified in mice with various combinations of Foxa1 and Foxa2 alleles, in mice with introgressed Rosa26R reporter allele. (A–D) Pancreas development in E14.5 mice with one copy of Foxa2loxP/+,Foxa2loxP/loxP,Pdx1CreE mice (Fig. 5K,O). Very few $\beta$ cells were present in compound Foxa1/Foxa2 mutant pancreata from E17.5 (Fig. 5L, arrow) through postnatal day 1 (data not shown). Accompanying the reduced endocrine cell mass, we noted a loss of total epithelial tissue in compound mutant pancreata (Fig. 5O,P), as indicated by E-cadherin staining (Fig. 5M–P). In fact, the remaining epithelial cells in the compound mutant pancreas were almost exclusively ductal, as they were strongly positive for DBA lectin (Fig. 5R). We detected only scattered single $\delta$ cells and $\epsilon$ cells in sections of compound mutant pancreas, demonstrating that $\alpha$ and $\beta$ cells had not been reallocated to other lineages in Foxa1/Foxa2-deficient pancreas (data not shown). Finally, we found that the spaces between the remaining ductal epithelia in the compound mutant pancreas were filled with stromal tissue, including fibroblasts and smooth muscle cells, as identified by vimentin (Fig. 5S,T) and smooth muscle actin (data not shown) staining. Thus, compound loss of Foxa1 and Foxa2 arrested pancreas growth at the early pancreatic cord stage.

Likewise, one copy of Foxa2 was sufficient to specify a nearly normal complement of insulin$^+$ $\beta$ cells as compared with control mice (Fig. 5L). In contrast, the number of $\beta$ cells was greatly reduced in Foxa1loxP/+,Foxa2loxP/loxP,Pdx1CreE mice (Fig. 5K,O). Very few $\beta$ cells were present in compound Foxa1/Foxa2 mutant pancreata from E17.5 (Fig. 5L, arrow) through postnatal day 1 (data not shown). Accompanying the reduced endocrine cell mass, we noted a loss of total epithelial tissue in compound mutant pancreata (Fig. 5O,P), as indicated by E-cadherin staining (Fig. 5M–P). In fact, the remaining epithelial cells in the compound mutant pancreas were almost exclusively ductal, as they were strongly positive for DBA lectin (Fig. 5R). We detected only scattered single $\delta$ cells and $\epsilon$ cells in sections of compound mutant pancreas, demonstrating that $\alpha$ and $\beta$ cells had not been reallocated to other lineages in Foxa1/Foxa2-deficient pancreas (data not shown). Finally, we found that the spaces between the remaining ductal epithelia in the compound mutant pancreas were filled with stromal tissue, including fibroblasts and smooth muscle cells, as identified by vimentin (Fig. 5S,T) and smooth muscle actin (data not shown) staining. Thus, compound loss of Foxa1 and Foxa2 arrested pancreas growth at the early pancreatic cord stage.

Foxa1/Foxa2 are required for the expression of several endocrine transcriptional regulators

Disrupting either Nkx6.1 or Nkx2.2 affects $\beta$-cell development (Sussel et al. 1998; Sander et al. 2000; Wang et al. 2004), while abolishing Pax6 primarily inhibits $\alpha$-cell differentiation (Sander et al. 1997). None of these mutants demonstrates a phenotype with a severity comparable with that of Pdx1-null (Jonsson et al. 1994; Offield et al. 1996), or Foxa1/2 compound mutant pancreata. We examined the impact of Foxa1 and Foxa2 compound mutation on several early transcription factors shown to be critical for islet development. Although these key regulators were present in control endocrine compartments with expression patterns consistent with the literature (Fig. 6A–D,I–L), they were largely depleted in the Foxa1/Foxa2 compound mutant pancreas (Fig. 6E–H, M–P). This was illustrated by costaining for these factors with Foxa1/2, which were expressed in all control pancreatic epithelial cells (Fig. 6A,K) but only in scattered compound mutant cells (Fig. 6E,O, arrows). These single Foxa1/2-positive cells had apparently escaped Cre-mediated gene excision, and coexpressed Nkx6.1 (Fig. 6F), Pdx1 (Fig. 6G), Pax6 (Fig. 6M), and Nkx2.2 (Fig. 6N). In addition, we analyzed the expression of Isl1, which has been shown to be essential for formation of the dorsal pancreas (Ahlgren et al. 1997). In contrast to controls (Fig. 6Q,R), we found a dramatic reduction in the number of Isl1-expressing cells in compound mutant tissues (Fig. 5O,P), where the majority of the remaining Isl1-positive cells coexpressed Foxa1/2 protein in their nuclei. Thus, disruption of Foxa1 and Foxa2 caused pancreatic tissue loss with a concomitant reduction of cells expressing key transcriptional regulators.

![Image](genesdev.cshlp.orgownloadedsfromonJanuary13,2010-PublishedbyColdSpringHarborLaboratoryPress)
Foxa occupancy of the distal and proximal Pdx1 enhancers

Both Foxa1 and Foxa2 bind to the proximal enhancer Area I–II–III, in the Pdx1 gene in mature pancreatic islets (Supplemental Fig. 1). When Area I–II–III is deleted by gene targeting, the resulting mice display severe pancreatic hypoplasia; however, they develop a larger pancreas than our Foxa1/Foxa2 compound mutants, with ample exocrine tissue and even some endocrine cells remaining [Fujitani et al. 2006]. Combined with our finding that Foxa1/Foxa2-deficient cells extinguish Pdx1 expression completely, we hypothesized that Foxa1 and Foxa2 may bind to additional enhancer elements in the regulatory regions of Pdx1 that were not deleted by Fujitani et al. [2006]. To address this question, we performed ChIP sequencing (ChIPseq) experiments using a Foxa2-specific antibody on chromatin isolated from E14.5 wild-type fetal pancreas and primary islets, respectively. We chose E14.5 pancreas, since at this stage all acinar cells continue to express Pdx1, and Pdx1-expressing progenitor cells are still present in large numbers in the central epithelial cords. Alignment of the sequence tags obtained to the Pdx1 locus revealed that in the fetal pancreas, Foxa2 does not bind effectively to the well-characterized Area I–II–III enhancer, but rather predominately to Area IV farther upstream (Fig. 7A,B). This enhancer element, located 6.4 kb upstream of the transcription start site, is highly conserved among different animal species [Fig. 7B; Gerrish et al. 2004]. Notably, the binding of Foxa2 to Area IV or Area I–II–III is significantly enhanced in pancreatic islets compared with fetal pancreas [Fig. 7B].

Real-time PCR with primers specific for Area IV confirmed our ChIPseq data, demonstrating an average enrichment of 13-fold and 56-fold in Foxa2 immunoprecipitated DNA compared with input DNA in E14.5 pancreas and adult pancreatic islets, respectively [Fig. 7C]. In contrast, the average ChIP enrichments for Area I–II were only 2.3-fold and 6.4-fold in E14.5 pancreas and
islet, respectively (Fig. 7C). Foxa2 ChIP of pancreatic chromatin samples from various developmental stages demonstrated that Foxa2 occupancy of Area I–II increases with age (Fig. 7C). Although the binding of Foxa2 to Area IV is always greater than to Area I–II (Fig. 7C), it is important to note that the Foxa2 ChIP enrichment for Area I–II is statistically significant compared with input throughout all fetal stages tested ($P < 0.05$).

ChIP assay using a Foxa1-specific antibody revealed that the binding affinity of this protein for Area IV is also greater than that for Area I–II, with maximal occupancy in mature islets (Fig. 7C). In contrast, Foxa1 shows near constant binding to Area I–II throughout pancreas development (Fig. 7C). An overall lower ChIP enrichment was seen from Foxa1ChIP experiment compared with Foxa2 ChIP, which could either reflect the relative abundance or intrinsic affinity of the two proteins, or differences in the efficacy of the two antibodies used. Thus, while we are able to analyze the developmental time course of enhancer occupancy for each factor individually during pancreatic development, we cannot assess which of the two proteins occupies more binding sites in vivo.

The strong binding of both Foxa1 and Foxa2 to the Area IV enhancer in early pancreas development supports the observation that this enhancer alone is capable of directing $Pdx1$ expression (Sharma et al. 1997; Gerrish et al. 2004). This finding also explains why the phenotype of the Area I–II–III enhancer mutant described by Fujitani et al. (2006) is milder than the one we describe in our compound mutants. Our data demonstrate that differential occupancy of various $cis$-regulatory elements in the $Pdx1$ gene by Foxa1 and Foxa2 is dependent on developmental time, adding a further dimension to the regulatory properties of these transcription factors.

**Discussion**

Signals from the adjacent mesoderm initiate pancreas formation (Moriya et al. 2000; Stafford and Prince 2002; Chen et al. 2004; Martin et al. 2005; Molotkov et al. 2008; Watanabe et al. 2008; Fujitani et al. 2009). The strong binding of both Foxa1 and Foxa2 to the Area IV enhancer in early pancreas development supports the observation that this enhancer alone is capable of directing $Pdx1$ expression (Sharma et al. 1997; Gerrish et al. 2004). This finding also explains why the phenotype of the Area I–II–III enhancer mutant described by Fujitani et al. (2006) is milder than the one we describe in our compound mutants. Our data demonstrate that differential occupancy of various $cis$-regulatory elements in the $Pdx1$ gene by Foxa1 and Foxa2 is dependent on developmental time, adding a further dimension to the regulatory properties of these transcription factors.
2005), while signals from endothelial cells promote pancreatic expansion (Lammert et al. 2001, 2003). In addition to these extrinsic signals, we demonstrated here that the involvement of early intrinsic lineage determinants, inherited by the pancreas from early endoderm, is essential in orchestrating pancreatic organogenesis. Our data extend and complement the finding that targeted deletion of the proximal Pdx1 enhancer (Area I–II–III) causes pancreatic hypoplasia (Fujitani et al. 2006). We demonstrate that Foxa1 and Foxa2 are the essential transcription factors required for Pdx1 expression and pancreas growth in vivo.

**Foxa proteins regulate Pdx1 expression and pancreas development**

We used the Pdx1CreE mouse line to inactivate Foxa genes in early pancreatic primordia. The endogenous Pdx1 gene is initially activated along with the Cre transgene in the prospective pancreatic domains of Foxa1loxP/loxP, Foxa2loxP/loxP, Pdx1CreE mice. This was evident, as both ventral and dorsal pancreatic buds formed in the compound mutant mice and transiently expressed Pdx1. During the primary transition these precursor cells gave rise to daughter cells in the primitive pancreatic ducts. The remaining Pdx1 protein in these early ductal epithelia likely reflects the time required for the deletion of the four Foxa1/2 gene alleles, the degradation of Foxa1/2 proteins carried over from the endoderm parental cells, the loss of Pdx1 gene transcription, and the decay of existing Pdx1 protein. Thus, the variable penetrance of the mutant phenotype described above may reflect slight variations in the timing of Foxa1/Foxa2 deletion. Nevertheless, Pdx1 expression in exocrine and endocrine cells, as well as the differentiation of these tissues from the ductal epithelia, was completely dependent on Foxa1 and Foxa2. This conclusion is supported by the overall disruption of acinar and endocrine differentiation in Foxa1/Foxa2 compound mutant mice. The immediate consequences of this disrupted differentiation program are the severely reduced exocrine and endocrine progenitor cell populations [Ngn3+ and Ptf1+ cells], which determine the ultimate pancreatic mass. The attenuation of the multipotent progenitor domain was pronounced, consis-
tent with the drastically reduced ductal tip outgrowth and differentiation in the mutant pancreas. Our results are summarized schematically in Figure 8. The near total absence of β cells and other mature exocrine and endocrine cell types [Fig. 8A] represents the cumulative blockage of pancreatic differentiation at multiple transitional steps where Foxa1 and Foxa2 are needed [Fig. 8B]. These changes are consistent with the decrease in cells expressing various endocrine transcriptional regulators. Further, the expression of these factors, including Nkx6.1, Nkx2.2, Pax6, Is11, and Pdx1, in the few cells that retained Foxa1/2 in the mutant pancreas is consistent with a cell-autonomous regulatory effect of the Foxa factors in pancreas differentiation.

Developmental occupancy of Pdx1 enhancers

Foxa1/Foxa2 compound mutants display a more severe phenotype in exocrine pancreas development than Pdx1	extsuperscript{+/−} mice, as acinar cells are abundantly present the latter model [Fujitani et al. 2006]. This discrepancy is explained by our discovery that throughout early pancreas development, Foxa1 and Foxa2 predominantly bind to Area IV, a region left intact in the Pdx1	extsuperscript{+/−} model. Previous experiments have shown that key pancreatic transcription factors, including Foxa2, Pdx1, and Nkx2.2 are capable of transactivating this enhancer region in vitro [Gerrish et al. 2004]. Furthermore, this distal enhancer can independently direct Pdx1 expression and potentiate proximal enhancer activity [Sharma et al. 1997; Gerrish et al. 2004]. Thus, in the absence of Area I–II–III, Area IV plus Foxa1/Foxa2 are sufficient to specify some acinar development, while endocrine differentiation is blocked [Fig. 8C; Fujitani et al. 2006].

Although Foxa1 and Foxa2 bind to Area I–II–III with relatively low affinity, both factors occupy this core enhancer element throughout pancreas development and in mature islets. Our data support the importance of Foxa1/Foxa2 occupancy of the Area I–II–III enhancer, as
previously demonstrated by in vitro experiments [Gerrish et al. 2000]. The transactivation of Area I–II–III by Foxa1/Foxa2 and other factors such as Ptf1a [Wiebe et al. 2007] is sufficient for some level of Pdx1 expression, since a Pdx1 transgene driven by Area I–II–III alone rescued the Pdx1–/− pancreas phenotype [Fig. 8C; Boyer et al. 2006]. Our data and previous work [Fujitani et al. 2006] further suggest that endocrine differentiation requires higher levels of Pdx1 expression than acinar development.

**Differential contributions of Foxa factors to pancreas development**

Our study, utilizing a novel Foxa conditional allele, overcomes a major drawback of experiments using Foxa1–/− mice that, in addition to endoderm defects, have neurological and renal phenotypes as well [Behr et al. 2004; Ferri et al. 2007]. Unexpectedly, Foxa1loxP/loxP, Foxa2loxP/+, Pdx1CreE mice did not demonstrate major defects in pancreas development. Most strikingly, Foxa1loxP/loxP, Foxa2loxP/+, Foxa1loxP−/+ Pdx1CreE mice, with only one copy of wild-type Foxa2, developed a relatively normal pancreas with all mature cell types, and were metabolically healthy. In contrast, mice with one allele of wild-type Foxa1 alone failed to thrive. Thus, one allele of Foxa2, but not Foxa1, was sufficient for normal pancreas development and function, suggesting that the previously reported postnatal death of Foxa1–/− mice [Kaestner et al. 1999; Shih et al. 1999] is due to nonpancreatic defects.

The notion that Foxa1 is a positive regulator of pancreas development is supported by the findings that [1] in the absence of both Foxa1 and Foxa2 genes, very few amylase+ or glucagon+ cells, and no β cells were specified; [2] in the absence of Foxa2, one allele of Foxa1 specified more amylase+, glucagon+, and β cells than no Foxa1 alleles; and [3] in the absence of Foxa2, two alleles of Foxa1 specified a pancreas with exocrine and endocrine compartments, albeit with reduced α-cell number [Lee et al. 2005].

We were also able to directly compare the “developmental potency” of Foxa1 and Foxa2 in vivo. While both Foxa proteins can occupy the Pdx1 enhancers, binding by Foxa2 appears to predominate, if one assumes that the efficacy of ChIP with both antibodies is equivalent. This relative comparison to a large extent agrees with our in vivo data as well as previous observations that two copies of the Foxa1 [as in Foxa2loxP/loxP,Foxa3Cre mice] [Lee et al. 2005] promote pancreatic development with fewer α cells than one copy of the Foxa2 gene alone (in Foxa1loxP/loxP, Foxa2loxP/+,Pdx1CreE mice). We conclude that the dynamic regulation of Pdx1 enhancers by Foxa2 and Foxa1 plays a critical role in pancreas development.

**Materials and methods**

**Mice**

The Foxa1loxP targeting vector was constructed by retrieval of a 7.9-kb genomic DNA sequence encompassing the Foxa1 gene from a bacterial artificial chromosome [University of California at Santa Cruz], followed by insertion of a loxP sequence 273 bp upstream, and a FRT-PGKneo-FRT-loxP fragment immediately downstream from exon 2. Homologous recombination in the R1 ES cell line was screened by Southern blot with a 5′-external probe. Wild-type and targeted alleles were identified as 7.4-kb HindIII and 4.0-kb HindIII/SpeI fragments, respectively. Targeted ES cells were injected into C57/BL6 blastocysts, and one of the resulting chimeric males transmitted the loxp allele through the germ line. The offspring were bred to Flp1 deleter mice [Rodriguez et al. 2000] for removal of the FRT-flanked PGKneo cassette, resulting in Foxa1loxP−/− mice identified by genomic PCR with the following primers: forward, 5′-CTGTG GATTATGTTCCTGAT-3′; and reverse, 5′-GTGTCAGAGT CCTATCTGGT-GT-3′. Foxa2loxP−/− [Sund et al. 2001], Pdx1CreE [Gu et al. 2002], Heiser et al. 2006], and Rosa26R [Soriano 1999] mice have been described previously. Blood glucose levels were measured as previously described [Gao et al. 2007].

**β-galactosidase staining and immunohistochemistry**

Embryos or whole-mount pancreata were dissected into fresh PBS, fixed for 1 h in PBS with 1% formaldehyde, 0.2% gluteraldehyde, 2 mM MgCl2, 5 mM EGTA, 0.2% NP-40, and washed in PBS with 0.2% NP-40 three times. Embryos or tissues were then stained overnight at 37°C in a solution containing 5 mM potassium ferrocyanide, 5 mM potassium ferricyanide, 2 mM MgCl2, 0.01% sodium deoxycholate, 0.02% NP-40, and 1 mg/mL X-gal. Embryos were washed three times in PBS with 0.02% NP-40 and post-fixed in 4% paraformaldehyde. Whole embryos or tissues were imaged using a Leica dissecting microscope. To quantify the pancreatic tissue, one representative image was taken for each β-galactosidase-stained whole-mount tissue, and two-dimensional areas of β-galactosidase-positive pancreases were measured by ImageJ 1.38x (National Institutes of Health).

For immunohistochemistry after β-galactosidase staining, embryos or tissues were incubated in 30% sucrose in PBS overnight, embedded in OCT, and cryosectioned. Immunohistochemistry was performed using the Vectastain Elite ABC kit (Vector Laboratories). Primary antibodies used in immunohistochemistry included mouse anti-Ngn3 (1:1000), Developmental Studies Hybridoma Bank at the University of Iowa, F25A1B3), rabbit anti-Ptf1a (1:50000; gift from C. Wright, Vanderbilt University), guinea pig anti-Pdx1 (1:10000; gift from C. Wright), goat anti-Foxa1/2 (1:1000), Santa Cruz Biotechnologies, sc-6553), rabbit anti-carboxypeptidase A (1:1500, AbD Serotec, 1810-0006), rabbit anti-glucagon [predilute; Invitrogen, 800064], and rabbit anti-amylase [1:1000, Sigma, A8273]. For quantification, Ngn3+ or Ptf1a+ cells from one section of each five control and five compound mutant embryos were manually counted under a light microscope.

**Immunofluorescent analysis**

Procedures of confocal immunofluorescent analysis have been described previously [Gao et al. 2007]. Primary antibodies not mentioned above included guinea pig anti-insulin [1:1000], Linco), mouse anti-E-cadherin [1:500; BD Biosciences], biotinylated donkey biotin algalin conjugated (1:1000; Vector Laboratories), rabbit anti-Pax6 [1:500], Covance, PRB-278P), mouse anti-Nkx2.2 (1:50; Developmental Studies Hybridoma Bank), mouse anti-Nkx6.1 (1:500; Developmental Studies Hybridoma Bank), and mouse anti-lsl1 (1:50, Developmental Studies Hybridoma Bank).
ChIP
FoxA1 and FoxA2 ChIP were performed as described [Friedman et al. 2004], using antibodies against FoxA1 [Santa Cruz Biotechnologies, sc-22841] and FoxA2 [Santa Cruz Biotechnologies, sc-6554], or FoxA1-specific antisera [kind gift of G. Schütz, Heidelberg, Germany], and FoxA2-specific antisera [kind gift of J.A. Whitsett]. The ChIP PCR primers spanned the FoxA2-binding sites within Area I–II and IV of the mouse Pdx1 3′ upstream sequence (Wu et al. 1997; Gerrish et al. 2000, 2004) Area1F, TGGCCTGCAAAACACACTAAGA; Area1R, GAG GTACCCCTGGCTCCTCTC; Area2F, ATGAAAGCTCGAGAT GGAAG; Area2R, CACACCGAGATGTTGGCTTA; Area 4F; TGGCCTAGTGCCCTTTACTC; Area 4R, CTAAAGAGTGCT CTGGGCTCTG.

ChIPSeq
Each biological sample was generated from pooled pancreata isolated from 10–15 E14.5 CD1 embryos, or 3000–5000 pancreatic islets. The dissected tissues were cross-linked as described previously [Tuteja et al. 2008]. After washing in PBS to remove excess formaldehyde and glycine, the fixed tissues were homogenized in 200 µL of cold whole-cell lysis buffer (10 mM Tris-HCl at pH 8.0, 10 mM NaCl, 3 mM MgCl2, 1% NP-40, 0.1% SDS, 0.5% deoxycholic acid) and protease inhibitors. After incubating on ice for 10 min, lysates were sonicated using a Diagenode Bioruptor (30-sec on/off pulses for 10 min, on high setting). Debris was removed by centrifugation at 13,000 for 10 min, and the supernatant was collected and snap frozen in liquid nitrogen. As input, 10 µL of sonicated chromatin was incubated in PBS with 200 mM NaCl overnight at 65°C, treated with proteinase K and purified with the QIAquick PCR Purification Kit (Qiagen). Immunoprecipitations were performed as previously described [Tuteja et al. 2008], except that the herring sperm DNA was excluded from the agarose bead-blocking step. For ChIPSeq experiments, the immunoprecipitated DNA was modified for sequencing following the manufacturer’s protocol [Illumina]. Briefly, DNAs were blunted with a combination of T4 DNA polymerase, Klenow polymerase, and T4 PNK, then a single 3′-end “A” base was added using Klenow exo (3′-to-5′ exo minus). Adapters provided by Illumina were then ligated to the ends of the modified DNA before size selection of ~200-bp fragments via PAGE extraction. The isolated DNA samples were used as the template for amplification by 16 cycles of PCR. Amplified products were column purified with the QiAquick PCR Purification Kit [Qiagen] and assayed for quantity and quality with the Agilent 2100 Bioanalyzer [Agilent Technologies]. Cluster generation and sequence alignment to the mouse genome [mm8] following processing procedures were performed following Illumina’s protocol. Only sequence tags uniquely mapping to the Pdx1 locus were considered for this analysis.

Immunoprecipitated DNA was also used to confirm enrichment of target DNA fragments via qPCR. PCR reactions were assembled in triplicate with SYBR Green qPCR Supermix [Invitrogen] and run using the SYBR Green [with dissociation curve] program on the MX3000 Multiplex Quantitative PCR System [Stratagene]. The enrichment of target sequences in ChIP material was calculated relative to the myelin basic protein (MBP) locus as a reference for nonspecific binding, and normalized to their relative amplification in input DNA.

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References


