**Zebrafish no isthmus reveals a role for pax2.1 in tubule differentiation and patterning events in the pronephric primordia**

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**SUMMARY**

Pax genes are important developmental regulators and function at multiple stages of vertebrate kidney organogenesis. In this report, we have used the zebrafish pax2.1 mutant no isthmus to investigate the role for pax2.1 in development of the pronephros. We demonstrate a requirement for pax2.1 in multiple aspects of pronephric development including tubule and duct epithelial differentiation and cloaca morphogenesis. Morphological analysis demonstrates that noi− larvae specifically lack pronephric tubules while glomerular cell differentiation is unaffected. In addition, pax2.1 expression in the lateral cells of the pronephric primordium is required to restrict the domains of Wilms’ tumor suppressor (wt1) and vascular endothelial growth factor (VEGF) gene expression to medial podocyte progenitors. Ectopic podocyte-specific marker expression in pronephric duct cells correlates with loss of expression of the pronephric tubule and duct-specific markers mAb 3G8 and a Na+/K+ ATPase α1 subunit. The results suggest that the failure in pronephric tubule differentiation in noi arises from a patterning defect during differentiation of the pronephric primordium and that mutually inhibitory regulatory interactions play an important role in defining the boundary between glomerular and tubule progenitors in the forming nephron.

Key words: Zebrafish, no isthmus, noi, Pronephros, pax2.1, wt1, Tubulogenesis

**INTRODUCTION**

Kidney organogenesis in vertebrates can be viewed as occurring in four general stages or developmental events. The early patterning of the mesoderm during gastrulation to generate nephrogenic cell populations in the intermediate mesoderm is followed by the formation of a nephric primordium during somitogenesis and the caudal growth of the pronephric or Wolffian duct, which will form the future collecting system of the kidney. Induction of nephron development from nephrogenic mesenchyme and the patterning of nephron primordia into glomerular and tubule domains is closely followed by vascularization of the glomerulus and the onset of blood filtration. Genetic studies have identified a number of regulatory genes that play important roles in nephric development (Lechner and Dressler, 1997; Vize et al., 1997). While a variety of mutants have provided insights into the developmental signals controlling ureteric bud growth and metanephric induction, the molecular mechanisms underlying nephron patterning are still not known.

The pax2 gene is expressed during multiple stages of vertebrate nephrogenesis and is mutated in human genetic diseases of the genitourinary system (Dressler et al., 1990, 1993; Krauss et al., 1991; Puschel et al., 1992; Sanyanusin et al., 1996; Dressler and Woolf, 1999). In vertebrates, the pax2, pax5 and pax8 genes have been grouped into a common subfamily based on their sequence similarity and expression pattern. pax2/pax5/pax8 members share in common the paired domain, an octapeptide motif, and a partial homeodomain. Mice homozygous for a null mutation in pax2 display severe defects in genitourinary development (Torres et al., 1995). Specifically, the Wolffian, or pronephric, duct degenerates before it is completely formed, resulting in kidney agenesis thus demonstrating a critical role for this gene in early stages of nephrogenesis.

In addition to its role in pronephric duct growth, pax2 is likely to function later in kidney development during nephron differentiation. During metanephric development, pax2 is expressed strongly in the branching ureteric bud and in comma- and S-shaped mesenchymal condensations, suggesting a role for pax2 during nephron differentiation and morphogenesis (Dressler et al., 1990; Ryan et al., 1995). Derepressed expression of pax2 in transgenic mice impedes tubular and glomerular differentiation and results in kidney cysts, implying that temporal and spatial control of pax2 expression is important for proper renal epithelial differentiation (Dressler et al., 1993). In addition, antisense oligonucleotides directed against pax2 interfere with nephron differentiation in organ culture (Rothenpieler and Dressler, 1993). In mouse embryos
pronephric development. suggesting an additional role for this transcription factor in gene, the observed absence homozygous for a disrupted pax2 gene, the observed absence of mesonephric tubule differentiation indicates a role for pax2 in mesenchyme-to-epithelial transitions in forming nephrons (Torres et al., 1995). However, the failure of the pronephric duct to grow to the level of the metanephric mesenchyme removes the normal inductive signal for nephron development (the ureteric bud) and precludes a complete analysis of the role of pax2 during later stages of nephrogenesis. The function of pax2 in nephron differentiation and patterning is therefore not known.

The Wilms’ Tumor Suppressor gene (wt1), like pax2, is a key regulator of kidney development and knock out of the wt1 locus in mouse results in degeneration of the metanephric mesenchyme and failed kidney organogenesis (Pelletier et al., 1991; Armstrong et al., 1993; Kreidberg et al., 1993). The wt1 gene may also function later during nephrogenesis during nephron patterning events. Following metanephric induction, pax2 and wt1 are expressed in spatially complementary patterns in S-shaped bodies during nephron patterning (Ryan et al., 1995). pax2 is transiently expressed in regions of the S-shaped body adjacent to the branched ureteric bud while high levels of wt1 are observed in a crescent region of the S-shaped body where podocytes will differentiate. Potential molecular interactions between pax2 and wt1 have been explored in cell culture transfection assays where wt1 was shown to act as a repressor of pax2 expression (Ryan et al., 1995). These results suggest that interactions between pax2 and wt1 are likely to play an important role in regulating the differentiation of cell types within the nephron.

Pronephric development in zebrafish and Xenopus has been recently reviewed (Vize et al., 1997; Brandli, 1999; Drummond, 2000). Compared with the metanephric kidney, the zebrafish larval kidney, the pronephros, is a simple structure composed of just two nephrons joined at the embryo midline where they receive vascular input through capillaries from the overlying dorsal aorta. Each nephron is composed of glomerular and pronephric tubule segments and contains the typical cell types found in nephrons from higher vertebrates (Drummond et al., 1998). Mutagenesis screens have produced a large collection of mutants affecting various organ systems, including the pronephros (Brand et al., 1996; Driever et al., 1996; Haffter et al., 1996; Drummond et al., 1998). The zebrafish no isthmus (noi) mutant has been isolated as a loss-of-function allelic series in pax2.1 based on a failure to properly form a midbrain-hindbrain boundary (MHB) (Brand et al., 1996; Lun and Brand, 1998). noi embryos have also been shown to exhibit a defect in optic tract formation (Macdonald et al., 1995; Brand et al., 1996; Lun and Brand, 1998), pax2.1 functions, together with wt1 and fgf8 signals, in the formation of the MHB organizer (Lun and Brand, 1998; Reifers et al., 1998). Zebrafish have two pax2 genes, pax2.1 and pax2.2, with pax2.1 more closely resembling the mammalian pax2 based on it expression pattern (Pfeffer et al., 1998). pax2.1 and pax2.2 are both expressed in the MHB, neural tube, ears and optic tracts, but only pax2.1 is expressed in the pronephros suggesting an additional role for this transcription factor in pronephric development.

In this report, we have used the zebrafish pax2.1 mutant no isthmus (noi) to investigate the role for pax2 in pronephric differentiation. The initial analysis of noi suggested a defect in pronephric duct epithelial cell differentiation; however, the full extent of pax2.1 function in the pronephros has not been described (Brand et al., 1996). We find that pax2.1 expression in the lateral cells of the pronephric nephron primordia is required for pronephric tubule development and for restricting the domain of the Wilms’ tumor suppressor gene expression to medial cells. pax2.1 is required for tubule cell fate and, in its absence, presumptive tubule and duct cells express podocyte-specific markers. In addition, pax2.1 is required in the pronephric ducts for complete epithelial differentiation and cloaca morphogenesis.

**MATERIALS AND METHODS**

**Zebrafish stocks**

Zebrafish were grown and mated at 28.5°C (Westerfield, 1993). The noi<sup>p21</sup> allele behaves as a hypomorphic mutation in pax2.1 and is associated with deletion of amino acids 263-303 (Lun and Brand, 1998). The noi<sup>p21</sup> allele gives rise to a truncated protein detectable on western blots (data not shown). The noi<sup>p29e</sup> allele is an RNA and protein null allele of pax2.1 resulting from a stop codon mutation at amino acid 139 (Brand et al., 1996; Lun and Brand, 1998). In this work, the null allele noi<sup>p29e</sup> homozygotes are referred to as noi-. noi mutant embryos were phenotypically identified under the dissecting microscope based on the absence of a midbrain-hindbrain boundary and reduced or absent tectum.

**Histological sections**

Zebrafish embryos were fixed in BT fix (Westerfield, 1993), dehydrated and embedded in JB-4 (Polysciences) for plastic sectioning. Sections of 4 μm thickness were cut and stained using methylene blue/azure II (Humphrey and Pittman, 1974; Drummond et al., 1998) and Permum (SIGMA) mounted for light microscopy. Photographs were taken on Kodak Ektachrome 160T film on a Zeiss Axiosplan microscope.

**In situ hybridization and immunocytochemistry**

Whole-mount in situ hybridization was performed as described using digoxigenin-labeled antisense RNA probes and anti-digoxigenin alkaline phosphatase-conjugated antibodies (Boehringer Mannheim (Otxoby and Jowett, 1993). Hybridized embryos were cleared in benzyl benzoate/benzyl alcohol 2:1 and photographed on Kodak 160 Tungsten film. Tissue sections, made by embedding embryos in JB-4 plastic and sectioning at 4 μm, were photographed using DIC optics. The following templates were linearized and transcribed with RNAP (Boehringer Mannheim) to make antisense probes: pax2.1 BamHI/T7, Wilms’ Tumor Suppressor gene (wt1) NotI/T7, vascular endothelial growth factor (VEGF) EcoRI/T3, α1-subunit Na<sup>+</sup>/K<sup>+</sup> ATPase BamHI/T7, and ret1 EcoRI/T7.

Wheat Germ Agglutinin (WGA, Molecular Probes) was used at 1:10 dilution to stain in situ hybridized embryos in PBDT (1× PBS, 1% BSA, 1% DMSO, 1% dry milk, 0.1% Tween-20) and all washes were done in PBDT. Embryos were processed for sectioning as described above.

Whole-mount antibody staining was performed following the BT fixation (Westerfield, 1993) method or the Dent’s fixation method (Dent et al., 1989) depending upon the sensitivity of the 1<sup>st</sup> antibodies. Embryos were Dent’s fixed and stained with α-6F antibody as described in Drummond et al. (1989). Alternatively, embryos were BT fixed and stained with a 1:2 dilution of mAb 3G8 (Vize et al., 1995) and staining was visualized with goat anti-mouse Cy3 conjugated 2<sup>nd</sup> antibody (Jackson Labs).

**Electron microscopy**

Zebrafish embryos were processed for electron microscopic analysis as described (Majumdar and Drummond, 1999).
RESULTS

noi mutants show defects in multiple aspects of pronephric development.

pax2.1 is sequentially expressed during different stages of pronephric development and its expression patterns are summarized in Fig. 1 (Krauss et al., 1991; Puschel et al., 1992). During somitogenesis stages, pax2.1 is initially expressed in the intermediate mesoderm which includes the nephrogenic cells (Fig. 1A). Afterwards, at the pharyngula stage (24 hours postfertilization (hpf)), strongest pax2.1 expression is seen in the anterior and posterior pronephric duct cells, with lower levels of expression in between (Fig. 1B). At 30 hpf, pax2.1 is transiently expressed in the nephron primordia while expression remains strong in anterior duct cells (Fig. 1C).

During normal zebrafish development, glomerular filtration of blood begins between 40 and 48 hpf (Drummond et al., 1998; Majumdar and Drummond, 1999). no isthmus (noi) homozygotes display severe edema by 48 hpf indicating a failure in osmoregulation and a possible defect in pronephric function (Brand et al., 1996). To investigate the role of pax2.1 in zebrafish pronephric development, we examined the pronephros histologically in two alleles of no isthmus representing the extremes of allele strength; noi29a (noi−/−; null allele) and noi29b, a hypomorphic exon 7 deletion allele showing reduced expression of pax2.1 mRNA and protein (A. M., unpublished observations; Lun and Brand, 1998).

In wild-type pronephroi, tubules extend laterally off of the medial glomerulus and connect with the caudally extending ducts (Fig. 1D). Importantly, noi mutants lack differentiated pronephric tubules while still retaining a midline glomerulus (Fig. 1G). The tubule-loss phenotype is equally severe in the noi29b and null noi− alleles. The noi glomerulus is complete with podocytes and surrounding parietal epithelium (Bowman’s capsule), suggesting glomerular differentiation and morphogenesis does not require pax2.1. Unlike the mouse or human pax2 mutations, which behave haploinsufficiently, noi heterozygotes do not display edema or show a histological pronephric phenotype, suggesting that one copy of the pax2.1 gene is sufficient for normal development.

In order to determine whether the pronephric phenotype in noi mutants resulted from a developmental defect, we followed the differentiation of noi pronephroi with tubule and duct molecular markers. mAb 3G8 has been described as a marker for visualizing zebrafish and Xenopus pronephric development where it labels pronephric tubules and ducts (Vize et al., 1995; Drummond et al., 1998). In zebrafish, mAb 3G8 stains tubules and ducts at 3 days post fertilization (dpf) and is restricted to the tubules by 3.5 dpf (Fig. 2A and data not shown). The pronephric tubules and ducts also express the Na+/K+ ATPase α1 subunit which can be visualized with the monoclonal antibody α6F (Fig. 2B). In 3 dpf noi29b mutants, tubule and anterior duct mAb 3G8 expression is not seen, demonstrating a defect in the differentiation of these pronephric structures (Fig. 2C). Furthermore, in noi29b Na+/K+ ATPase expression can not be detected in tubule or anterior duct, again pointing to a failure in pronephric tubule and duct epithelial differentiation (Fig. 2D).

noi mutants show defects in nephric patterning

We sought to identify the earliest stage when the pronephric defects in noi embryos were detectable. During wild-type development, the glomerular and tubular pronephric components arise from a common nephron primordium
Prior to overt morphological differentiation, \textit{pax2.1} is transiently expressed in the lateral cells of the nephron primordium between 30 and 32 hpf and is the earliest known marker of tubule differentiation and nephron patterning (Fig. 4A; refer to Fig. 3 for details on plane of section). In the hypomorphic \textit{noi tb21} allele, \textit{pax2.1} mRNA expression can be detected in several tissues during pharyngula stages where \textit{pax2.1} is normally expressed including the optic tracts, spinal cord and anterior pronephric duct cells (Fig. 4H). However, \textit{pax2.1} mRNA expression is specifically lost in the lateral cells of the nephron primordium at 30 hpf where expression would normally occur (Fig. 4B). The loss of \textit{pax2.1} expression in the primordium indicates that the absence of pronephric tubules at later stages is due to a defect at the earliest stages of tubule differentiation. Furthermore, the result indicates that \textit{pax2.1} positively regulates its own expression. In \textit{noi} homozygotes, pronephric primordia cells can be seen histologically (Fig. 4B, D) and by pronephric molecular marker expression (see below and Fig. 5) demonstrating that the lack of \textit{pax2.1} expression is due to the absence of a functional \textit{pax2.1} gene rather than a loss of lateral cells altogether. In addition, expression of earlier markers of pronephric development like \textit{lim-1} and \textit{ret1} were unaffected in \textit{noi} mutants at the 12-somite stage (data not shown). We were not able to detect any cell death in the pronephros using acridine orange while apoptosis in the MHB was easily detected suggesting that cell death was not the basis for the loss of pronephric tubule differentiation (data not shown; Brand et al., 1996).

We next asked whether loss of tubule differentiation might affect the development of glomerular progenitor cells in \textit{noi}. The Wilms’ tumor suppressor gene (\textit{wt1}) is expressed in the nephron primordia reflecting the morphological events associated with patterning the pronephric nephron (Drummond et al., 1998). \textit{wt1} is initially expressed in the intermediate mesoderm and then becomes restricted to the nephron primordia cells which lie adjacent to the anterior tips of the pronephric ducts (Fig. 4C; Drummond et al., 1998). Coincident with tubular differentiation, \textit{wt1} expression is downregulated in lateral primordium cells. \textit{wt1} expression is later maintained only in differentiated glomerular podocytes. The Na\textsuperscript{+}/K\textsuperscript{+} ATPase \textalpha{}1 subunit is another marker of nephron patterning and is expressed in the pronephric duct. At 25 hpf, the Na\textsuperscript{+}/K\textsuperscript{+} ATPase \textalpha{}1 shows a complementary pattern of expression compared to \textit{wt1}, being expressed in the pronephric duct but not in the pronephric primordia (Fig. 4E).

In both \textit{noi} and \textit{noi tb21} mutants, the \textit{wt1} expression domain is expanded caudally at 25 hpf implying that \textit{pax2.1} restricts the spatial domain of \textit{wt1} expression (Fig. 4D). No rostral expansion was detected. In situ hybridization during the 12-somite stage on embryos from \textit{noi} crosses did not reveal any differences in \textit{wt1} expression demonstrating that the posterior restriction occurs after this time (data not shown). Expanded \textit{wt1} expression was also observed at later stages (36 hpf) with the onset of podocyte differentiation (data not shown).

\textbf{Fig. 3.} Diagram of the zebrafish pronephros. The nephric primordia (np), pronephric duct (pd) and cloaca (cl) are shown for a 25-32 hpf embryo. The dashed lines A and B mark the anteroposterior level of histological sections made and correspond to the schematized transverse cross sections to the right. (A) Sections are made at the level of the nephric primordia. (B) Sections are made through the anterior pronephric duct, immediately behind the nephric primordia.
Correlating spatially with an expansion of wt1 expression, we observed a loss of Na+/K+ ATPase α1 subunit expression in the anterior duct cells, demonstrating that duct epithelial cell differentiation is altered in noi−/− mutants (Fig. 4F). wt1 has been shown to repress pax2.1 transcription in vitro (Ryan et al., 1995). Ectopic wt1 expression in noi could result in repression of pax2.1 in the anterior pronephric duct. pax2.1 expression persists in noi anterior ducts indicating the ectopic wt1 expression is not repressing pax2.1 transcription (Fig. 4H).

In order to determine whether the duct cells that lost Na+/K+ ATPase α1 subunit expression were the same cells ectopically expressing wt1, we carried out a double labeling experiment with wheat germ agglutinin (WGA), a lectin that stains basement membrane and allows the morphological identification of the pronephric tubules and ducts in cross section. In wild type, anterior duct cells express the Na+/K+ ATPase α1 subunit but not wt1 (Fig. 5A,E; refer to Fig. 3 for details on plane of section). In noi mutants, cells in the position of the anterior duct lose Na+/K+ ATPase α1 subunit expression and instead ectopically express wt1 confirming that anterior duct cell differentiation is affected in noi (Fig. 5C,G).

We next asked whether the expression of other podocyte cell fate markers is also expanded in noi. The vascular endothelial growth factor (VEGF) gene is expressed in differentiating podocytes but not in tubules or duct cells (Fig. 5I,J; (Liang et al., 1998). In noi−/−, VEGF is ectopically expressed in cells in the position of the anterior ducts (Fig. 5K). These results demonstrate that pax2.1 restricts the domain of wt1 and VEGF expression to the future glomerulus and that in the absence of pax2.1 function, presumptive tubule cells and anterior duct cells ectopically express podocyte-specific markers.

**Pronephric duct differentiation is abnormal in noi mutants**

Epithelial cells of the pronephric tubules and ducts form a polarized epithelium with well-defined apical and basal surfaces and a central lumen. The ducts can be visualized histologically in sections (Fig. 1E). In noi−/− 36 hpf mutants, the ducts appear dilated and the epithelia have a flattened appearance suggesting a defect in duct epithelial morphogenesis (Fig. 1H). These defects are observed prior to vascularization of the glomerulus and are therefore not due to abnormally high filtration pressure.

The Na+/K+ ATPase protein is localized to the basolateral surface of wild-type tubule and duct epithelial cells (Fig. 6A). In noi−/− mutants, Na+/K+ ATPase is not localized to the basolateral surface of duct cells, instead appearing diffusely throughout the cytoplasm (Fig. 6B). In addition, transverse sections reveal duct cells where no Na+/K+ ATPase expression is detectable adjacent to cells that express Na+/K+ ATPase in a delocalized manner. In contrast to the pronephric ducts, Na+/K+ ATPase basolateral subcellular localization in the gut is unaffected in noi, demonstrating the organ-specific nature of the defect (data not shown).

In order to assess the extent of epithelial differentiation in noi pronephroi, we examined noi pronephric duct epithelium by electron microscopy. In wild-type embryos at 2.5 dpf, pronephric duct columnar epithelial cells extend apical microvilli and cilia into the central lumen to form a dense brush border while basally, a basement membrane is visible (Fig. 6C). Duct epithelial cells display well-formed apical cell-cell
junctions. Mitochondria are found basally and laterally, but are excluded from the terminal web region beneath the microvilli. Ciliated and non-ciliated cells are found throughout the anterior posterior length of the duct. In noi mutants, an apical brush border is absent and, unlike wild-type cells, mitochondria can be found at the apical poles of the cells (Fig. 6D). Duct epithelia are not columnar and appear flattened while the duct lumen is greatly distended along its entire length. However, apical cell-cell junctions and basement membranes are visible suggesting that these epithelia do retain some apicobasal polarity. No evidence of nuclear fragmentation or cell death was observed.

**Posterior pronephric duct development**

The pronephros opens to the environment at the cloaca where the posterior pronephric ducts have fused to form a single tubule. In wild-type 3 dpf embryos, histological sagittal sections at the cloaca reveal the organization of the pronephric duct with cuboidal epithelial cells surrounding a central lumen (Fig. 1F). In noi mutants, the posterior pronephric duct at the cloaca appears cystic with a significantly enlarged lumen and severely flattened epithelial cells (Fig. 1I). The retl tyrosine kinase receptor is known to play an important role in pronephric duct growth and ureteric bud branching during mouse kidney development (Pachnis et al., 1993; Schuchardt et al., 1994). In zebrafish, retl is first detected at the caudal end of the growing pronephric duct and, later, retl is expressed in a discrete group of cells at the caudal end of the pronephric duct (Marcos-Gutierrez et al., 1997; Fig. 6E). This later phase of retl expression is completely missing in noi embryos, demonstrating a correlation between the cloaca defect and missing retl expression (Fig. 6F). The result also suggests that pax2.1 may positively regulate retl during cloaca formation.

**DISCUSSION**

**pax2.1 functions in nephron patterning**

We demonstrate here a requirement for the transcription factor pax2.1 in multiple aspects of pronephric development including tubule and duct epithelial differentiation and cloaca morphogenesis. Zebrafish have two pax2 genes, pax2.1 and pax2.2, but only pax2.1 is expressed in the pronephros. The phenotypic analysis of noi mutants demonstrates that defects in tubule, duct and cloaca development correlate with the expression of pax2.1 in these parts of the pronephros. A related gene, pax8, is expressed at the 1-somite stage in the intermediate mesoderm and its expression is later maintained by pax2.1 (Pfeffer et al., 1998). However, pax8 expression has not been observed during nephron patterning events making pax2.1 the only pax member thus far to be expressed during tubule differentiation (A. M. unpublished observations). The observation of a fully penetrant pronephric tubule phenotype in noi may therefore mean that pax2.1 is the only member of the pax2/5/8 genes active in tubule development with no redundant function to compensate for loss of pax2.1.

During zebrafish pronephric development, nephron primordia are patterned to give rise to the glomerular and tubular epithelial components. Medial primordia cells express the wtl gene while lateral cells express pax2.1. In the noi mutant, the pronephric primordia are present, but subsequent nephron patterning events are abnormal. Presumptive tubule
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...presumptive tubule cells follow an alternative developmental pathway in pax2.1 mutants (Fig. 7). The result suggests that pax2.1 expression serves as an instructive signal for lateral cells to assume a different fate from neighboring cells in the primordium and may function, at least in part, by repressing podocyte-specific gene expression.

Phenotypic analyses of pax mutants in Caenorhabditis elegans, Drosophila and mouse suggest requirements for pax2 homologs in specific cell fate decisions and patterning events in a variety of developmental contexts. During C. elegans vulval development, the pax2/pax5/pax8 homolog egl-38 is needed to specify the uterine cell fate and, in its absence, presumptive uterine cells adopt an alternative cell fate resulting in a vulval morphogenesis defect (Chamberlin et al., 1997). In Drosophila, the pax2 homolog, D-pax2, similarly functions in multiple cell fate decisions. During ommatidial development, D-pax2 is required for the differentiation of non-neuronal cone and primary pigment cells (Fu and Noll, 1997). In the pupal notum, D-pax2 is needed for shaft cell differentiation during bristle sensory organ development (Kavaler et al., 1999). Our analysis of noi raises the possibility that pax2.1 may function in a similar way in nephron patterning by repressing podocyte-specific gene expression in the lateral primordial cells to promote the tubule cell fate.

Alternatively, pax2.1 could function in lateral pronephric primordium cells as a proliferative signal. In this scenario, a lack of cell divisions in noi nephron primordia would underlie the failure to elaborate pronephric tubules. While proliferation may play a role during normal tubule development, several
observations argue that \textit{pax2.1} is not simply regulating cell proliferation. First, \textit{pax2.1} is expressed throughout the pronephric ducts, yet we do not see a decrease in the number of duct cells in comparing \textit{noi} mutant and wild-type embryos (data not shown). In addition, in BrdU-labeling experiments, we observe S-phase cells in pronephric primordia from \textit{noi} mutants (data not shown). Furthermore, no evidence of increased apoptosis was seen in the pronephros of \textit{noi} mutants. Together, these results suggest presumptive tubule and anterior duct cells follow an alternative developmental pathway in the absence of \textit{pax2.1} function.

\textbf{\textit{pax2.1} also functions in renal epithelial differentiation}

In addition to a role for \textit{pax2.1} in nephron patterning, the ultrastructural and immunohistochemical studies presented here suggest a more general requirement for \textit{pax2.1} in pronephric terminal epithelial differentiation, consistent with previous morphological analyses (Brand et al., 1996). While \textit{noi} mutant duct cells do have morphologically distinct apical and basal cell surfaces and cellular junctions, they lack apical microvilli and mis-localize the Na$^+/K^+$ ATPase, reflecting a defect in terminal differentiation. This phenotype is not limited to the region affected by ectopic \textit{wt1} expression and occurs along the entire length of the duct, demonstrating that the abnormal membrane protein targeting results from a loss of \textit{pax2.1} function and not from ectopic \textit{wt1} expression. Delocalized Na$^+/K^+$ ATPase has been observed in other zebrafish pronephric mutants where it correlates with the presence of pronephric cysts and dilated duct lumens (Drummond et al., 1998). We suggest that the epithelial defects in \textit{noi} may reflect the persistence of an immature developmental state. Consistent with this interpretation, previous studies on explanted mouse kidneys have demonstrated that antisense oligonucleotides directed against \textit{pax2} can interfere with the conversion of mesenchyme to epithelium in the process of nephron development (Rothenpieler and Dressler, 1993).

\textit{pax2.1} is also required for formation of the cloaca. In \textit{Xenopus} pronephric development, the rectal diverticulum, an anterior outgrowth of the proctodeum, establishes a continuity between the duct and the cloaca (Heller and Brandli, 1997; Brandli, 1999). The existence of a rectal diverticulum in zebrafish is not known. Electron microscopic sections of \textit{noi} mutant ducts (Fig. 6D and data not shown) show that the pronephric duct lumen is continuous with the cloaca suggesting that morphogenesis of the intermediate mesoderm to form a continuous duct tube occurs in \textit{noi}. Furthermore, the early pattern of \textit{c-ret} expression suggests posterior migration of duct cells occurs successfully in \textit{noi}. Together, these data suggest cloacal defects result from a problem in differentiation of the cloacal epithelium rather than a morphogenetic defect.

\textbf{Regulatory relationships between \textit{pax2} and \textit{wt1} genes}

Our analysis suggests \textit{pax2.1/}wt1 regulatory interactions are important for proper nephric development. Similar patterns of \textit{pax2} and \textit{wt1} gene expression are observed during \textit{Xenopus} pronephric development with \textit{pax2} transcripts found in more lateral and \textit{wt1} transcripts found in more medial pronephric analage cells (Carroll et al., 1999). During mouse metanephric development, tubular and podocyte epithelia arise from a common renal vesicle where \textit{pax2} and \textit{wt1} are expressed in mutually exclusive domains of the forming nephrons. \textit{wt1} is expressed in visceral glomerular epithelium while \textit{pax2} is expressed throughout the mesenchymal condensates and comma shaped body but is dramatically downregulated in regions of \textit{wt1} expression (Ryan et al., 1995). The relative expression patterns of \textit{pax2.1} and \textit{wt1} during nephron development are evolutionarily conserved between zebrafish nephron primordia and nephron formation in other vertebrates implying a common mechanism underlying nephron patterning.

The expression analysis in mouse, together with in vitro binding studies demonstrating that \textit{wt1} protein can bind to the \textit{pax2} upstream regulatory region to repress \textit{pax2} transcription, have led to the idea that \textit{wt1} is a direct negative regulator of \textit{pax2} expression (Ryan et al., 1995). This idea has received further support from analysis of \textit{pax2} and \textit{wt1} expression in kidney tissue from Denys-Drash syndrome (DDS) patients (Yang et al., 1999). DDS is a rare human urogenital disorder caused by dominant negative mutations in \textit{wt1} that abolish its ability to bind to its downstream targets (Pelletier et al., 1991; Hastie, 1992). Kidney tissue from Denys-Drash patients show a loss of \textit{wt1} podocyte nuclear localization and display an upregulation of \textit{pax2} in podocytes, suggesting that in normal tissue, \textit{wt1} functions to repress \textit{pax2} expression in podocytes. In the absence of a functional \textit{wt1} gene, the ectopic expression of \textit{pax2} in podocytes may account for some aspects of the glomerulopathy phenotype observed in DDS since glomerular dysgenesis is also observed when \textit{pax2} is constitutively overexpressed in transgenic mice kidneys (Dressler et al., 1993).

Our results suggest a complementary in vivo role for \textit{pax2} in repressing, either directly or indirectly, \textit{wt1} transcription in the pronephric primordium and anterior pronephric ducts during zebrafish development. These results are in contrast to a previous report showing \textit{pax2} transactivation of a \textit{wt1} promoter reporter construct in cell culture transient transfection assays (Dehbi et al., 1996). This apparent discrepancy may reflect differences in experimental systems rather than inherent differences in the function of mouse and zebrafish \textit{pax2} genes. The context in which \textit{pax2} is functioning is different in our experiments compared to the erythroleukemia cell line employed in Dehbi et al. (1996). Also, the target \textit{wt1} reporter plasmid used their experiments may not contain the complete set of \textit{cis}-regulatory elements controlling \textit{wt1} expression. In the case of the zebrafish pronephros, \textit{pax2.1} is not expressed in the forming nephron primordium at 24 hpf when \textit{wt1} is highly expressed, indicating that \textit{wt1} expression is independent of \textit{pax2.1} at this stage (Toyama and Dawid, 1997).

It is also possible that \textit{pax2} function may vary depending on which mRNA splice forms are present in a given tissue. Although at present it is not known which of the twelve \textit{pax2.1} splice forms are expressed in the pronephros, our results demonstrate that inclusion of exon 7 is essential for \textit{pax2.1} function in the pronephros given that the \textit{noi$^{b21}$} allele is essentially an exon 7 deletion (Lun and Brand, 1998). \textit{noi$^{b21}$} has been characterized as a hypomorphic allele based on the partial development of brain structures (the optic tectum), which are completely missing in embryos homozygous for the
null allele. This characterization of the noi allele series holds true for the pronephros with regard to pax2.1 transcript expression (A. M., unpublished observations). However, our studies on the pronephros show that the null and exon 7 deletion noi alleles result in similar phenotypic outcomes, i.e. a complete absence of pronephric tubules and expansion of podocyte marker gene expression. The exon 7 sequence of pax2.1 has been shown to encode amino acids adjacent to the C-terminal transactivation domain (Dorfler and Busslinger, 1996; Lechner and Dressler, 1996). While the function of this domain is currently unknown, its absence may result in a reduction in the transactivation potential of pax2.1. Whether or not pax2.1 acts directly or indirectly to inhibit wt1 expression in the pronephros, our results along with the observations in DDS glomeruli suggest that during nephron differentiation, pax2 and wt1 act in a mutually antagonistic fashion to limit their respective expression domains (summarized in Fig. 7). This relationship is likely to be important for proper demarcation of podocyte versus tubule regions of the nephron.

Are the nephron patterning defects in noi a result of loss of pax2.1 function or the ectopic expression of wt1 in nephron primordia? In noi embryos, pax2.1 function is missing in all cells of the embryo while the expression of the pronephric markers mAb 3G8 and Na+/K+ ATPase is specifically missing in the presumptive tubules and anterior pronephric ducts where wt1 is ectopically expressed. From this observation, we would argue that in the absence of a functional pax2.1 gene, ectopic expression of wt1 (or other podocyte-specific regulatory factors) in the pronephric duct is likely to account for the downregulation of tubule and duct-specific gene expression. This interpretation is consistent with observations by Wallingford et al. (1998) who show that ectopic expression of Xenopus wt1 is sufficient to inhibit pronephric tubule differentiation. However since, in noiM21 embryos, pax2.1 mRNA is detectable in the anterior duct cells, which ectopically express wt1, it would appear that wt1 is not sufficient by itself to repress pax2.1.

pax2.1 may function in regulating its own expression since only barely detectable levels of pax2.1 mRNA are found in noiM21 lateral primordia cells while expression in other tissues is less affected. A similar requirement for pax2.1 in maintaining its own expression is observed in the midbrain-hindbrain boundary (Brand et al., 1996; Lun and Brand, 1998). The fact that pax2.1 mRNA is observed in pronephric duct epithelial cells argues against the idea that pax2.1 M21 mRNA may be generally unstable in the pronephros. The anterior pronephric duct cells could be the source of a signal that induces pax2.1 expression in the primordium or alternatively, pax2.1 protein expressed at a low level earlier during pronephric development may be needed for upregulation of pax2.1 expression at 30 hpf in the lateral primordium.

In summary, our results suggest that pax2.1 expression is critical for proper nephron patterning in zebrafish and plays an important role in defining the border between different cell types during pronephric development. Further experiments in higher vertebrates, for example using conditional knockout alleles of pax2, may reveal new roles for pax2 in nephron patterning during metanephric development.

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REFERENCES


Humphrey, C. and Pittman, F. (1974). A simple methylene blue-azure II-
basic fuchsin stain for epoxy-embedded tissue sections. Stain Technol. 49, 9-14.