Asymmetric positioning of visceral organs is determined by the left-right axis. Left-right determination is most critical to cardiovascular development, where precise alignment along the left-right axis is required for proper circulation and viability. Development fails if the heart does not loop from its initial midline orientation. Complete reversal of organ position, designated situs inversus, is compatible with normal development and viability. However, defects in consistently positioning organs along the left-right axis (situs ambiguous) are more clinically relevant and can lead to polysplenia, asplenia, cardiac and/or circulatory defects (Casey, 1998).

The mechanism that generates adult left-right asymmetry from a bilaterally symmetric embryo may involve a stepwise process of (1) generation of an initial asymmetric signal; (2) propagation and spatial maintenance of asymmetric information; and (3) transformation of these signals into morphological asymmetries. Based on the presence of a left-right phenotype and/or left-right asymmetrical expression, several genes have been identified that either act at early, middle or late steps in this pathway.

The Oak Ridge Polycystic Kidney (orpk) disease gene is required for left-right axis determination

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SUMMARY

Analysis of several mutations in the mouse is providing useful insights into the nature of the genes required for the establishment of the left-right axis during early development. Here we describe a new targeted allele of the mouse Tg737 gene, Tg737\textsuperscript{D2-3}Gal, which causes defects in left-right asymmetry and other abnormalities during embryogenesis. The Tg737 gene was originally identified based on its association with the mouse Oak Ridge Polycystic Kidney (orpk) insertional mutation, which causes polycystic kidney disease and other defects. Complementation tests between the original orpk mutation and the new targeted knock-out mutation demonstrate that Tg737\textsuperscript{D2-3}Gal behaves as an allele of Tg737. The differences in the phenotype between the two mutations suggest that the orpk mutation is a hypomorphic allele of the Tg737 gene. Unlike the orpk allele, where all homozygotes survive to birth, embryos homozygous for the Tg737\textsuperscript{D2-3}Gal mutation arrest in development at mid-gestation and exhibit neural tube defects, enlargement of the pericardial sac and, most notably, left-right asymmetry defects. At mid-gestation the direction of heart looping is randomized, and at earlier stages in development lefty-2 and nodal, which are normally expressed asymmetrically, exhibit symmetrical expression in the mutant embryos. Additionally, we determined that the ventral node cells in mutant embryos fail to express the central cilium, which is a characteristic and potentially functional feature of these cells. The expression of both Shh and Hnf3β is downregulated in the midline at E8.0, indicating that there are significant alterations in midline development in the Tg737\textsuperscript{D2-3}Gal homozygous embryos. We propose that the failure of ventral node cells to fully mature alters their ability to undergo differentiation as they migrate out of the node to contribute to the developing midline structures. Analysis of this new knockout allele allows us to define a critical role for the Tg737 gene during early embryogenesis. We have named the product of the Tg737 gene Polaris, which is based on the various polarity related defects associated with the different alleles of the Tg737 gene.

Key words: Situs inversus, Neural tube defect, Left-right asymmetry, Ventral node cilia, Targeted mutation, Insertional mutation, Complementation, Tg737, ORPK, Polaris
dynein appear to be involved in early steps of the left-right determination (Supp et al., 1997; Mochizuki et al., 1998; Morgan et al., 1998). Clues as to how a signal may be asymmetrically localized have emerged with the analysis of KIF3B mutants, and the finding that cilia on ventral node cells appear to generate an asymmetric flow across the node surface of primitive streak–stage embryos (Nonaka et al., 1998). This flow may create an asymmetric distribution of signaling molecules, establishing a left-right gradient across the node. Propagation and maintenance of initial asymmetry may be mediated through the actions of lefty-1 at the midline, and lefty-2 and nodal in lateral plate mesoder (Meno et al., 1998). Interpretation of molecular asymmetries into physical asymmetries may involve transcription factors such as Pitx2 (Ryan et al., 1998).

Many aspects relating to the establishment of left-right asymmetry during development are unknown. It would be useful to have a better understanding of the nature of the molecular signals that initiate this process. Access to additional mouse mutants that exhibit an early stage phenotype in the establishment of the left-right axis would be useful in this regard. Here we describe a new mutation, which appears to affect the early stages of left-right specification during embryogenesis. Utilizing targeted mutagenesis, we created a new allele of an existing gene, Tg737, which was originally identified by its association with the Oak Ridge Polycystic Kidney (orpk) mouse model of autosomal recessive polycystic kidney disease (ARPKD) (Moyer et al., 1994). Analysis of the phenotype associated with this new allele places the orpk gene early in the pathway of left-right determination.

MATERIALS AND METHODS

Generation of the Tg737Δ2-3]/Gal allele

The Tg737Δ2-3]/Gal allele of the Tg737 gene was generated by homologous recombination in embryonic stem cells. Briefly, 1 x 10⁶ ESCS cells (a gift from Dr Colin Stewart) were electroporated with 25 µg of NolI linearized targeting plasmid in a BioRad gene pulsar (320 V, 500 µF) and placed under G418 selection as previously described (Hogan et al., 1994). Genomic DNA from G418 resistant colonies was screened for recombinants by Southern blotting analysis as described below. Seven out of 196 clones were found to contain a targeted mutation in the Tg737 gene (Fig. 1B). Targeted clones were injected into C57BL/6J blastocysts. Chimeric males were bred to FVB/N females to establish germline transmission of the Tg737Δ2-3]/Gal allele.

Construction of the targeting vector

The targeting construct used for the homologous recombination experiments was produced utilizing the pSAβ-Gal plasmid (a gift from Dr P. Soriano). A genomic clone containing the 5’ region of the Tg737 gene was isolated from a 129/Sv genomic lambda library using probes corresponding to exons 1 and 2 of the Tg737 gene. A 6.4 kb NolI/ClaI genomic fragment containing exon 1 was subcloned between the NolI and Smal sites (after blunt-ending the ClaI overhang) upstream of the SAβ-Gal/pgk-neo cassette. Additionally, a 2.1 kb PCR fragment containing intron 3 and part of the flanking exons was amplified using standard PCR conditions from 129/Sv genomic DNA using primers that introduced SalI sites into the ends of the amplified product (primers: RW416 5’-tga ggt gta cac ggg ttt tca gca age a-3’ forward and RW415 5’-cct gtt gca cag tgc tgg tta-3’ reverse). After digestion with SalI, this 2.1 kb PCR-derived fragment was cloned into the SalI site downstream of the SAβ-Gal/pgk-neo cassette. All cloning steps followed standard methodology (Sambrook et al., 1989).

Genotyping and animals and embryos

A 1 kb intron 4-specific probe, which is outside the targeting construct, was utilized to identify the targeted allele at the molecular level. This intron 4 probe was generated by standard PCR amplification from genomic DNA (primers: RW436 5’-gca gcc cca tag cta ctt cgt ga-3’ forward and RW239 5’-ctt ccc att gat gat gtc ag-3’ reverse). In genomic DNA samples digested with BamHI, the intron 4 probe hybridizes to a 7 kb band from the mutant allele and to a 20 kb fragment on the wild-type allele (Fig. 1B). The orpk insertional mutation was identified as previously described and is depicted in Fig. 1A (Moyer et al., 1994). Embryos from Tg737Δ2-3]/Gal heterozygous parents were routinely analyzed by PCR using standard conditions and primers specific for the targeted mutant allele (primers: RW472 5’-agc aga agc ctg ctt c-3’ forward and RW473 5’-gta agc cga ttc att ggc ac-3’ reverse) and primers specific for the wild-type allele (primers: RW597 5’-agt gat atc cgg tac aaa tga taa ttc a-3’ forward and RW598 5’-gag tga tt tct cag tat cat agg ctg gtt gtt a-3’ reverse). These reactions amplify a targeted specific product of 270 bp and a wild-type product of 170 bp.

RT-PCR analysis

Embryonic day (E)9.5 embryos were isolated from Tg737Δ2-3]/Gal heterozygous intercrosses and genotyped to identify wild-type, heterozygous intercrosses and genotypes, as described above. Embryos of the same genotype were pooled and processed for total RNA isolation using RNA STAT-60 (TEL-TEST ‘B’, INC.). cDNA was synthesized following standard protocols (Sambrook et al., 1989). cDNAs were amplified using standard PCR conditions and primers that amplify from exon 1 to exon 11 (primers: RW117 5’-gga tca ggc gtc gct tct c-3’ forward and RW92 5’-act taa ggc gct tga gtg tga-3’ reverse, producing a 851 bp product), exon 2 (RW597 5’-agt gat atc cgg tac aaa tga taa ttc a-3’ forward and RW92 5’-act taa ggc gct tga gtg tga-3’ reverse, producing a 851 bp product), exon 2 to exon 26 of the Tg737 cDNA (primers: RW71 5’-agt gat atc cgg taa ttc a-3’ forward and RW53 5’-gag tga ttc ctt cag cat cat agg ctg gtt gtt a-3’ reverse, producing a 1020 bp product). β-Actin mRNA was amplified as a positive control (primers: RW51 5’-agt ggt cag aag tgc tgc tgc a-3’ forward and RW53 5’-gag tga ttc ctt cag cat cat agg ctg gtt gtt a-3’ reverse, producing a 1020 bp product).

Comparison experiments

Compound heterozygotes were generated by crossing mice heterozygous for the Tg737Δ2-3]/Gal allele on the mixed FVB/N/Sv genetic background with orpk heterozygotes on a uniform FVB/N genetic background. Individual animals in the offspring from these crosses were genotyped as described above. As a control for genetic background in evaluating the phenotype, FVB/N orpk heterozygotes were crossed with wild-type 129/Sv partners and the resulting F1 heterozygotes were crossed to FVB/N orpk heterozygotes to obtain orpk homozygotes in a mixed FVB/N/Sv genetic background.

Histological and skeletal analysis

For histological examination, tissues were fixed in 10% buffered formalin, embedded in paraffin and cut into 8 µm sections following standard procedures. Tissue sections were stained with Hematoxylin and Eosin, examined and photographed under light microscopy. Skeletal examinations were performed as previously described (Hogan et al., 1994).

Scanning electron microscopy (SEM)

Embryos for SEM analysis were prepared as previously described by Sulik et al. (1994), with slight modifications. Samples were fixed in 2.5% glutaraldehyde, 0.1 M cacodylate buffer overnight, washed twice
in 0.1 M cacodylate, dehydrated through an ethanol series and washed twice in 100% ethanol. Embryos were dried from liquid CO2, mounted, sputter-coated and viewed using a JEOL scanning electron microscope.

**β-Gal reporter gene analysis and mRNA in situ hybridization**

Primitive streak-stage (E7.5) and early headfold-stage (E8.0) embryos were collected from timed matings of Tg737Δ2-3bGal heterozygous intercrosses and were genotyped as described above. For β-Gal reporter analysis, embryos were processed as previously described (Hogan et al., 1994). Whole-mount mRNA in situ hybridizations with anti-sense digoxigenin-labelled riboprobes were performed as previously described (Henrique et al., 1995). Sections of whole-mount stained embryos were obtained as previously described (Hogan et al., 1994). *Lefty-2*, *nodal*, *Shh*, Hnf3β and Brachyury probes were kindly provided by Drs H. Hamada, M. Kuehn, T. Magnuson and R. Conlon.

**RESULTS**

**Production of the targeted allele, Tg737Δ2-3Gal**

The Tg737 gene is directly associated with the recessive insertional mutation in the mouse called orpk. This mutation causes polycystic kidney disease and other disorders (Moyer et al., 1994). Northern blot analysis demonstrated that the orpk mutation alters, but does not completely abolish, all mRNA expression from the Tg737 gene (Moyer et al., 1994; Yoder et al., 1995). This finding suggested that the orpk insertional mutation created a unique allele that does not necessarily completely inactivate the function of the Tg737 gene. Therefore, to further investigate the function of Tg737, we generated a knock-out allele (Tg737Δ2-3bGal) by homologous recombination in embryonic stem (ES) cells. This new allele was engineered to delete the initial coding exons (exon 2 and part of exon 3) of Tg737. This deleted region of Tg737 was replaced with the β-Galactosidase (β-Gal) reporter gene (Fig. 1A). We reasoned that this structural configuration would both inactive the expression of the gene and simultaneously allow the β-Gal reporter gene to be expressed in place of the normal Tg737 mRNA.

Seven correctly targeted clones were identified from the 196 clones analyzed, indicating that the targeting efficiency was 3.6% (Fig. 1B). Chimeric males were derived from C57BL/6 blastocysts injected with targeted 129/Sv ES cells, and germline transmission of the Tg737Δ2-3Gal allele was obtained by breeding the chimeras to wild-type FVB/N mice. The FVB/N strain was chosen since the orpk insertional mutation was generated on this strain. Unless otherwise indicated, most analyses were conducted after six generations inbred into the FVB/N background.

Expression of Tg737 mRNA transcripts derived from the Tg737Δ2-3Gal allele was tested by RT-PCR with total RNA isolated from embryonic day 9.5 (E9.5) wild-type, heterozygous and homozygous Tg737Δ2-3Gal embryos. Three different regions of the Tg737 gene were evaluated for expression using primers that amplify exons 1-11, exon 2 and exons 23-24. Tg737 transcripts were detected in RNA isolated from wild-type and heterozygous embryos; however, no amplification products were obtained with RNA from homozygous mutants (Fig. 1C). These experiments demonstrate that the Tg737Δ2-3Gal allele completely eliminates expression of the Tg737 gene.

**Targeted mutation Tg737Δ2-3Gal and the orpk insertional mutation are allelic**

As a first step in characterizing the new Tg737Δ2-3Gal allele, we conducted a series of complementation experiments with the original orpk insertional mutation. This was an important experiment because the original orpk insertional allele arose by random insertion of a transgene and many of these mutants contain structural rearrangements that affect more than one gene. Mice heterozygous for the Tg737Δ2-3Gal targeted allele and the orpk insertional mutation were crossed to generate offspring that were heterozygous for the Tg737Δ2-3Gal or orpk, or both, mutations (Δ2-3Gal/orpk). Littermates that were heterozygous for either allele had a normal phenotype. However, the compound heterozygotes developed cystic lesions in their kidneys, along with the liver and pancreatic lesions that are typical of the orpk mutation on a mixed genetic background (Fig. 2A-I). Additionally, analysis of the skeleton of the compound heterozygotes revealed preaxial polyactyly on all four limbs, which is also a feature of orpk homozygotes (Fig. 2J-K) (Moyer et al., 1994). Therefore, our new targeted mutation genetically functions as a second allele of the Tg737 gene.

**Tg737Δ2-3Gal homozygotes undergo developmental arrest**

As a follow-up to our complementation experiments, we intercrossed Tg737Δ2-3Gal heterozygotes in order to produce individual animals that were homozygous for the Tg737Δ2-3Gal mutation. Unlike the orpk allele of Tg737, where homozygotes could be detected in Mendelian ratios at birth (Moyer et al., 1994), we were unable to detect any Tg737Δ2-3Gal homozygotes that survived to birth. This result indicated that homozygosity of the Tg737Δ2-3Gal allele causes prenatal lethality. To begin characterizing the lethality we systematically genotyped embryos from heterozygous Tg737Δ2-3Gal matings at different stages of development. Between E18.5 and E12.5 no homozygous mutants were obtained (45/139 +/+ and 94/139 Δ2-3Gal/+); at E11.5 homozygotes were obtained, but these embryos exhibited neural tube defects (NTDs) and were not viable (16/56 +/+, 29/56 Δ2-3Gal/+, 11/56 Δ2-3Gal/Δ2-3Gal). Viable homozygous mutants were obtained at normal Mendelian ratios up to E10.5 (29/109 +/+, 56/109 Δ2-3Gal/+); at E10.5 homozygous mutants were obtained, but these embryos exhibited neural tube defects (NTDs) and were not viable (16/56 +/+, 29/56 Δ2-3Gal/+, 11/56 Δ2-3Gal/Δ2-3Gal). Analysis of Tg737Δ2-3Gal homozygotes at E9.5 revealed that they were runted and exhibited NTDs, including poor differentiation of the forebrain, midbrain, hindbrain, branchial arches, neural tube kinks and undulations of the neural tube (Fig. 3A). At midgestation (E9.5 and E10.5) these embryos exhibited an enlargement of the pericardial sac, indicating that cardiac insufficiency is the most likely cause of lethality in these mutants (Fig. 3A). These embryos also possessed broadened limb buds, a trait that is also characteristic of the embryonic phenotype of orpk homozygous mutants (data not shown). All of the embryos used for these experiments were derived from parents that were ten generations inbred in the FVB/N background.

**Tg737 is expressed during early post-implantation development in the murine node**

In an attempt to identify the earlier stage defects that are likely to give rise to the abnormalities apparent in the mid-gestation...
mutant embryos (Fig. 3A), we were interested in analyzing the temporal/spatial patterns of expression of the Tg737 gene during early post-implantation development. Utilizing the β-Gal reporter function of the Tg737Δ2-3βGal allele, we analyzed the expression of Tg737 in heterozygous embryos during the egg cylinder, primitive streak and early somite stages of development (E6.5-E8.5). Although a low level of reporter expression was observed throughout E6.5-E8.5 embryos, high-level reporter expression was evident only in the ventral layer of the node of primitive streak-stage embryos (Fig. 3B,C). We utilized mRNA whole-mount in situ hybridization with Tg737 antisense RNA probes to verify that the βGal reporter on the Tg737Δ2-3βGal allele faithfully recapitulates the endogenous pattern of Tg737 expression (data not shown).

Defects in the node of Tg737Δ2-3βGal mutant embryos

In addition to studying patterns of Tg737 expression, we carefully analyzed embryos at early post-implantation stages of development for cellular and morphological defects, particularly at sites where the Tg737 gene is normally expressed. Embryos at E9.5 were slightly runted and exhibited neural tube defects (Fig. 3A). At earlier gestational ages (E6.5-E8.5), mutants were morphologically indistinguishable from their heterozygous and wild-type littermates when inspected by light microscopy.

To improve our sensitivity for detecting cellular defects in the mutant embryos, we imaged E7.5 embryos, which express the Tg737 gene at relatively high levels in the node, with scanning electron microscopy (SEM). SEM analysis of whole embryos revealed that the individual cells on the surface of the node are different in embryos that are heterozygous from those observed with our light microscopy. Midgestational lethality and node abnormalities similar to those observed with our Tg737Δ2-3βGal mutants are also associated with the inactivation of the microtubule-dependent
motor protein KIF3B (Nonaka et al., 1998). The fact that the KIF3B mutants exhibit left-right asymmetry defects led us to test whether the Tg737Δ2-3βGal also exhibit left-right polarity abnormalities. Gross morphological comparisons between E9.5 Tg737Δ2-3βGal homozygous mutants revealed that the direction of heart looping was frequently reversed (Fig. 5G,H). Analysis of 25 E9.5 homozygous mutants revealed a random distribution of normal versus reversed heart looping, indicating that the Tg737 gene is required for left-right axis determination: for wild-type and heterozygous embryos, 36/36 showed situs solitus (100%) and 0/36 situs inversus; for homozygous mutants, 12/25 showed situs solitus (48%) and 13/25 situs inversus (52%).

To determine where Tg737 functions in the left-right pathway, whole-mount RNA in situ hybridization was utilized to analyze the expression patterns of known left-right marker genes in Tg737Δ2-3βGal homozygous mutants. Lefty-2 and nodal are members of the TGF-β superfamily of secreted polypeptide factors that are normally asymmetrically expressed along the L-R axis and function early in the left-right pathway (Meno et al., 1998; Collignon et al., 1996; Lowe et al., 1996). We evaluated the expression of Lefty-2 and nodal in both wild-type and mutant embryos at E8.0. Normally lefty-2 is expressed in the left lateral plate mesoderm (Fig. 5A left embryo, B), and nodal expression overlaps with lefty-2 in the left lateral plate mesoderm and is also expressed in an asymmetric pattern around the murine node (Fig. 5D left embryo, E-I). In Tg737Δ2-3βGal homozygous mutants, we observed bilateral expression of the lefty-2 and nodal genes in
Tg737Δ2-3Gal homozygotes exhibit neural tube defects in addition to left-right axis defects. To better understand the molecular nature of the neural tube defects we analyzed the expression of Shh and Hnf3β by whole-mount mRNA in situ hybridization. We focused our analysis on E8.0 embryos in order to correlate early neural tube development with the transient expression of the left-right marker genes lefty-2 and nodal. Wild-type E8.0 embryos normally expressed Shh in the presumptive floorplate and headfolds (Fig. 6A, left embryo). In E8.0 Tg737Δ2-3Gal homozygotes Shh expression remains confined to the presumptive floorplate and headfolds, although a slightly reduced level of Shh signal is reproducibly observed (Fig. 6A, right embryo). Hnf3β is normally expressed in the node, presumptive floorplate and headfolds of E8.0 wild-type embryos (Fig. 6B, left embryo). In Tg737Δ2-3Gal homozygotes Hnf3β expression is dramatically altered. Expression in the node is maintained, expression in the developing headfolds is qualitatively reduced and the presumptive floorplate does not appear to express significant levels of Hnf3β mRNA (Fig. 6B, right embryo). Brachyury (T) is expressed along the midline of primitive streak-stage embryos and it is required for mesoderm and notochord formation (Wilkinson et al., 1990). To rule out any major defects during mesoderm or notochord formation, we analyzed T expression in E8.0 Tg737Δ2-3Gal homozygotes. No abnormalities in T expression were found, indicating that Tg737 is not required for T expression and, that mesoderm and notochord form normally in Tg737Δ2-3Gal homozygous mutants (Fig. 6C,D).

### DISCUSSION

**Tg737Δ2-3Gal and orpk are allelic**

Previously we described the orpk insertional mutation, which represents a useful mouse model for ARPKD (Moyer et al., 1994; Yoder et al., 1995). Characterization of the orpk mutant locus led to the identification of the Tg737 gene, which is directly associated with the phenotype in this model (Moyer et al., 1994). Here we describe another allele of the Tg737 gene, Tg737Δ2-3Gal, which replaces the first and part of the second coding exons with a combination splice acceptor-βGal/gk-geo expression cassette (Fig. 1A). This mutation disrupts transcription across the Tg737 locus (Fig. 1C) and places the β-Gal reporter gene under the control of endogenous Tg737 regulatory elements. This new mutation completely inactivates the activity of the gene. The fact that animals homozygous for the Tg737Δ2-3Gal allele exhibit left-right symmetry defects and arrest in development at about E10.5 defines a new and critical function for the Tg737 gene during embryogenesis.

Our finding that knocking out the Tg737 gene causes a more severe phenotype than the orpk allele suggests that the original insertional mutation is a hypomorphic allele of Tg737. This is compatible with our previous finding that, although the primary transcript of 3.2 kb is not expressed from the orpk locus, other low-abundance higher-molecular mass transcripts can still be detected on a northern blot using RNA from the orpk mutants (Moyer et al., 1994). These residual transcripts may represent low abundance and normal alternatively spliced forms of mRNA that are not affected by the inserted transgene, or they may represent aberrant transcripts that arise from the unique configuration of the DNA at the mutant locus. These residual transcripts must still produce a functional gene product associated with the orpk allele. Whether any gene product arising from the mutant locus is normal or abnormal is not clear. Further analysis of the transcripts arising from the orpk allele will help to resolve this issue.

Also, in the process of characterizing the new Tg737Δ2-3Gal targeted allele we resolved an issue that arose in our earlier gene rescue experiments. Expression of a full-length Tg737 cDNA as a transgene rescued the kidney, but not the liver and pancreatic defects, in orpk homozygotes (Yoder et al., 1996). This raised the possibility that a disruption of a second closely linked gene could be contributing to the pleiotropy associated with the orpk allele, particularly in the liver and pancreas (Yoder et al., 1997). Here we demonstrate that this is unlikely to be the case. Although Tg737Δ2-3Gal homozygotes and orpk homozygotes exhibit dramatically different phenotypes, it is noteworthy that compound heterozygotes (Δ2-3Gal/orpk) are phenotypically identical to orpk homozygotes (Fig. 2). This
Node and L-R defects in Tg737\textsuperscript{D\,2-3b\,Gal} mutants

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non-complementation strongly suggests that Tg737 is the one and only gene associated with the mutant phenotype in the orpk mutant animals.

The role of Tg737 in left-right asymmetry

Analysis of the Tg737\textsuperscript{D\,2-3b\,Gal} homozygotes revealed that the ventral node is the site where we detect the first apparent structural abnormalities in the embryo. The murine node is a bilayer composed dorsally of ectoderm and ventrally of small, polarized cells, which express a single cilium on their apical

Fig. 6. Evidence for a midline defect in Tg737\textsuperscript{D\,2-3b\,Gal} homozygotes.

(A,B) Whole-mount mRNA in situ analysis in E8.0 embryos reveals defects in midline development. (A) Anterior view of Shh expression in heterozygous and homozygous Tg737\textsuperscript{D\,2-3b\,Gal} embryos reveals normal Shh expression in heterozygotes (A, left embryo) and reduced Shh expression in homozygous mutants (right embryo). More posterior sections through the node reveal asymmetrical nodal expression in heterozygotes and symmetrical expression of nodal in homozygous mutants (A and B, respectively). (C,D) Brachyury expression was utilized as a control for mesoderm development. In both heterozygous and homozygous Tg737\textsuperscript{D\,2-3b\,Gal} embryos (C and D, respectively), staining is apparent in the primitive streak and node, with faint staining along the notochord.
Evidence from several reports suggests that node function is required for left-right axis determination. In vitro culture experiments helped to define the window during which left-right axis determination occurs. Specification of left-right asymmetry is not sensitive to in vitro culture after early headfold stages (E8.0; Fujinaga and Baden, 1991; McCarthy and Mangold, 1924; Shih and Fraser, 1996). Node ablation experiments where the node is physically removed from the primitive streak-staged embryo increase left-right defects during in vitro culture, implicating node function or node-derived tissues in left-right axis determination (Davidson et al., 1999).

Additional data suggests that ventral node cells may function early in the left-right pathway. Nonaka et al. (1998) discovered that a targeted disruption of KIF3B causes a loss of cilia on ventral node cells and left-right defects in the embryo. They hypothesized that synchronized movement of ventral node cilia creates a ‘nodal flow’ across the node surface that causes a relative difference in the concentration of factors over the surface of the node. These relative differences in factor concentration are thought to cause differential signaling in the left and right sides of the node, and this in turn could be the basis for establishing the left-right axis in the embryo. Mutations that eliminate the cilia from the surface of ventral node cells would block nodal flow and block the development of any differential concentrations of signaling factors on the left and right sides of the node. This is potentially one possible explanation for the left-right polarity defects exhibited by both the KIF3B and Tg737 mutant embryos.

Alternatively, the fact that Tg737Δ2-3βGal and KIF3B mutants also exhibit neural tube defects (NTDs) may indicate that these mutants possess a midline defect, which causes both the left-right alterations and NTDs. Mutations in the development of the notochord and/or floorplate may cause NTDs and affect left-right development by disrupting the midline barrier (Meno et al., 1998).

In Tg737Δ2-3βGal homozygous mutants we have evidence for a midline defect. In E8.0 homozygotes, Shh mRNA is reduced and Hnf3β mRNA is dramatically absent in the developing floorplate and notochord (Fig. 6). Altered expression of these genes indicates that the floorplate and/or notochord in Tg737Δ2-3βGal homozygous mutants may not function properly. Therefore, independent of cilia defects in the node (Fig. 4), left-right development may be compromised by an abnormal midline in Tg737Δ2-3βGal homozygous mutants.

The loss of ventral node cilia and an abnormal midline in Tg737Δ2-3βGal homozygous mutants may be developmentally linked. As the primitive streak-staged embryo grows and elongates, ventral node cells migrate out of the node and contribute to the midline. Although the ventral node and notochord are contiguous in primitive streak-staged embryos, theoretically there must be a boundary where the migrating cells from the ventral node become committed to midline structures, such as the notochord and/or floorplate. In E8.0 wild-type and Tg737Δ2-3βGal heterozygous embryos, Hnf3β is expressed in both node and notochord and does not reveal any boundary between these structures. In E8.0 Tg737Δ2-3βGal homozygous mutant embryos, node cells express Hnf3β, however, notochord cells fail to express Hnf3β (Fig. 6B). This dramatic loss of Hnf3β expression at the anterior edge of the node in E8.0 Tg737Δ2-3βGal homozygous mutant embryos appears to delineate the boundary between the ventral node and the developing notochord and floorplate. Primitive streak-staged Tg737Δ2-3βGal homozygous mutants do not appear to be able to maintain Hnf3β expression during the transition from node to notochord/floorplate. This loss of Hnf3β expression in the developing midline indicates that these mutants have a midline defect, which appears to be derived from abnormal or incomplete differentiation of the ventral node epithelium.

The polarity connection

We have now analyzed the kidney phenotype of the orpk allele and the node and early embryonic defects associated with the Tg737Δ2-3βGal targeted mutation. In both mutations there are changes in polarized epithelial cells that appear to underlie the mutant phenotype. In Tg737Δ2-3βGal homozygotes, the polarized epithelial cells of the ventral node are affected. In the orpk homozygotes, cystic lesions develop as a consequence of the ectopic expansion of a population of polarized epithelial cells of the collecting duct, called principal cells (Sweeney and Avner, 1998). Both cell types have a central cilium. Additionally, we have recently determined that the cellular defect in the collecting duct involves abnormal polarity of the EGFR receptor (EGFR). Normally the EGFR is localized strictly on the basolateral surface of epithelial cells in collecting duct, but it is mislocalized to the apical surface of epithelial cells (principal cells) which line the lumen of collecting duct cysts (Richards et al., 1998).

Although it is presently unclear whether there are also polarity defects associated with the positioning of molecules like the EGFR on the node, it is noteworthy that the node defects predispose the embryos to develop left-right polarity defects during early embryogenesis. Therefore, polarity defects at both the cellular and multicellular level are associated with mutations in the Tg737 gene. Our best estimation is that the Tg737 gene plays a critical role in the development and maintenance of polarized epithelium in the embryo and the kidney, and changes in the epithelium in mutant animals are responsible for the phenotypes that we observe.

Polaris, the protein product of the Tg737 gene

The sequence of the Tg737 cDNA clone predicts a novel 824 amino acid protein. This protein contains ten copies of the tetratricopeptide repeat, a motif that was originally defined based on its conservation in several cell-cycle control genes (Goebl and Yanagida, 1991; Lamb et al., 1994). The presence of TPRs in many diverse proteins appears to point toward a protein structure that may mediate diverse protein-protein interactions (Groves and Barford, 1999). We originally named the Tg737 gene because it arose in the 737th transgenic line that was screened for insertional mutations at the Oak Ridge National Laboratory. Here we propose to name the Tg737 gene product Polaris, which refers to both the polarity defects in the
positioning of the EGFR and to the left-right polarity defects in the early embryo. We believe that this name for the gene product better reflects our current understanding of the underlying functions of the Tg737 gene at both the cellular and multi-cellular levels.

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