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Requirement for Foxd3 in the maintenance of neural crest progenitors

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Understanding the molecular mechanisms of stem cell maintenance is crucial for the ultimate goal of manipulating stem cells for the treatment of disease. Foxd3 is required early in mouse embryogenesis; *Foxd3*$^{-/-}$ embryos fail around the time of implantation, cells of the inner cell mass cannot be maintained in vitro, and blastocyst-derived stem cell lines cannot be established. Here, we report that Foxd3 is required for maintenance of the multipotent mammalian neural crest. Using tissue-specific deletion of *Foxd3* in the neural crest, we show that *Foxd3*$^{flox/-}$; *Wnt1-Cre* mice die perinatally with a catastrophic loss of neural crest-derived structures. Cranial neural crest tissues are either missing or severely reduced in size, the peripheral nervous system consists of reduced dorsal root ganglia and cranial nerves, and the entire gastrointestinal tract is devoid of neural crest derivatives. These results demonstrate a global role for this transcriptional repressor in all aspects of neural crest maintenance along the anterior-posterior axis, and establish an unprecedented molecular link between multiple divergent progenitor lineages of the mammalian embryo.

KEY WORDS: Neural crest, Foxd3, Mouse embryo, Stem cell maintenance

INTRODUCTION

Neural crest (NC) cells are multipotent progenitors that possess the unique ability to contribute to a variety of disparate adult derivatives: the entire peripheral and enteric nervous systems (PNS and ENS), bones and connective tissue of the head and neck, and the outflow tract of the developing heart, among others. NC cells emigrate from the dorsal neural tube during early embryogenesis and migrate to final sites of differentiation. Their fate depends on their rostral-caudal position of origin in the neural tube, their route of migration and final destination (reviewed by Le Douarin and Kalcheim, 1999). Many of the cellular mechanisms crucial to the development of an embryo are represented within this extraordinary tissue: specification of cell type, maintenance of multipotency of progenitor cells, directed migration of cells to their final destination and terminal differentiation of cells. Members of the PDGF, BMP and Wnt families of secreted molecules are important for the initial specification and subsequent maintenance of the NC (reviewed by Steventon et al., 2005). Many transcription factors are activated in NC in response to these signaling cascades; these include Foxd3, Sox8, 9 and 10 (Cheung and Briscoe, 2003; Southard-Smith et al., 1998), Ap2 (Tcfap2a – Mouse Genome Informatics) (Schorle et al., 1996) and Pax3 (Epstein et al., 1991). It is not yet clear how these factors work together to induce and then maintain this unique cell type.

Foxd3 encodes a transcriptional repressor of the winged helix or Forkhead family of proteins (Labosky and Kaestner, 1998; Sutton et al., 1996). This large family of proteins is characterized by a 100 amino acid DNA-binding domain and transcriptional activation or repression domains (reviewed by Wijchers et al., 2006). *Foxd3* was first characterized by its expression in embryonic stem (ES) cells and multipotent cells of the NC (Labosky and Kaestner, 1998). Our previous work demonstrated that Foxd3 is required early in mouse embryogenesis; *Foxd3*$^{-/-}$ embryos fail around the time of implantation, cells of the inner cell mass cannot be maintained in vitro, and ES cell and trophoblast stem cell lines cannot be established (Hanna et al., 2002; Tompers et al., 2005). In vivo, the pool of both embryonic and trophoblast progenitors is not maintained without Foxd3; embryonic progenitor cells die, while trophoblast progenitors give rise to an excess of trophoblast giant cells at the expense of the remaining trophoblast lineage. However, the ultimate effect in both cases is that the progenitor pool is not maintained and the cell lineage is lost.

Foxd3 is one of the earliest molecular markers of the NC lineage, it is expressed in many organisms in premigratory and migrating NC and expression is downregulated as the cells differentiate into most derivatives (Dottori et al., 2001; Labosky and Kaestner, 1998). Ectopic expression of Foxd3 in chick neural tube and *Xenopus* embryos can specify NC cell fate as measured by upregulation of HNK1 and Slug (Dottori et al., 2001; Kos et al., 2001; Sasai et al., 2001). In addition, maintained expression of Foxd3 in migrating NC interferes with differentiation and retains NC in an undifferentiated state, evidence that points to a potential role for Foxd3 in the control of stem cell self-renewal (Dottori et al., 2001). Morpholino knockdown of zebrafish *foxd3* and mutations that affect Foxd3 expression in the zebrafish NC have deleterious effects on maintenance of the NC (Lister et al., 2006; Montero-Balaguer et al., 2006; Stewart et al., 2006).

Because the deletion of *Foxd3* results in embryonic lethality around the time of implantation, we employed Cre-loxP technology to delete the Foxd3 coding region specifically in NC. Here we demonstrate that without this transcriptional regulator the NC lineage fails to be maintained, resulting in catastrophic loss of most NC derivatives. Mutant mice perish at birth with a cleft face, the PNS is severely reduced and the ENS is not formed. Surprisingly, although the cardiac NC is greatly reduced early in embryogenesis, by midgestation most cardiac NC derivatives are normal, with subtle defects in a small percentage of mutant embryos. We show that the mechanism of cellular loss of most of the NC is by a failure to maintain the progenitor pool, as much of the premigratory and early

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migrating NC undergoes cell death. Cells that survive are able to migrate and differentiate normally but cannot completely compensate for the early loss of progenitors. Our data demonstrate that Foxd3 is required for maintenance of NC progenitor cells and, taken together with our previous work, place Foxd3 in the unique role of maintaining the undifferentiated multipotent state of three completely divergent progenitor populations of the early mammalian embryo.

MATERIALS AND METHODS

Construction of *Foxd3 floxP* targeting vector

A 1.2 kb fragment of the *Foxd3* locus was inserted into the *Eco*RI site of pPNT4 downstream of the Frt-flanked *Neo* gene to serve as the 3′ homology arm. An oligonucleotide containing the loxP recognition sequence (ATAACTTCGTATAGCATACATTATACGAAGTTAT) was inserted 5′ of the *Foxd3* coding region. Upstream, a 4.2 kb fragment of the *Foxd3* locus was inserted to complete the 5′ homology arm to generate the final targeting vector shown in Fig. 1A.

ES cell electroporation and generation of mice

TL1 ES cells were electroporated as described (Tompers and Labosky, 2004). ES cell DNA was analyzed by Southern blot as shown in Fig. 1A,B. Lines were screened by PCR for the presence of the 5′ loxP site. We identified three correctly recombined cell lines out of 337 (0.9% frequency). Chimeras were generated by blastocyst injection and offspring of chimeras were genotyped to identify heterozygous founders. Two independent cell lines transmitted through the germ line and because both showed the identical phenotype we restricted our studies to one cell line. Mice were genotyped either by Southern blot or PCR with the following primers: 5′-CGGCTTTCTTTCGGGGGAC-3′ and 5′-ACATATCGCTGGCGCT-GCCG-3′ to give a 130 bp band for the wild-type allele and a 220 bp band for the floxed allele.

Mouse strains

Foxd3$^{tm2.Lby}$ is a null mutation of *Foxd3* generated previously (Hanna et al., 2002) and is referred to as *Foxd3*$^{-}$ throughout. *Wnt1-Cre* mice were a generous gift of Drs Andrew McMahon and David Rowitch (Harvard University, Cambridge, MA). In the reporter strain *Gt(ROSA)26Sor*^{tm1Sor} (referred to as *ROSA26R*), *Cre* expression results in removal of a *loxP*-flanked DNA segment that prevents expression of a *lacZ* gene. After *Cre* activation, *lacZ* is detected in cells/tissues where *Cre* is expressed. The transgenic line EIIaCre [Tg(EIIa-cre)C5379Lmgd, from The Jackson Laboratories] carries a *Cre* transgene under control of the adenovirus EIIa promoter that targets expression of *Cre* to the early mouse embryo and acts as a ubiquitous deletor strain for our purposes. The presence of *Cre* was detected with primers 5′-TGATGAGGTTCGCAAGAACC-3′ and 5′-CCATGAGTGAACGAACCTGG-3′, producing a band of 400 bp. All mouse strains were maintained on an outbred mixed genetic background that was primarily CD-1 and C57BL/6. Animals were maintained in accordance with the rules of the University of Pennsylvania and Vanderbilt University Institutional Animal Care and Use Committee (IACUC).

Histology and whole-mount in situ hybridization

Histology was performed using standard procedures (Presnell and Schreibman, 1997). For whole-mount LysoTracker staining, embryos were dissected in Hanks buffer, and incubated in 5 μM LysoTracker (Molecular Probes) at 37°C for 1 hour. Embryos were then washed in Hanks buffer and fixed in 4% paraformaldehyde (PFA) in PBS overnight, washed in PBS and dehydrated in methanol before imaging with a fluorescent stereoscope. TUNEL assay was performed in paraffin sections using the In Situ Cell Death Detection Kit (Roche). Whole-mount immunostaining was performed as described (Wall et al., 1992). Skeletal preparations and 5-bromo-4-chloro-3-indolyl-β-D-galactoside (X-Gal) staining followed standard techniques (Nagy et al., 2003). For histological analysis, paraffin sections (7-12 μm) were counterstained with Eosin or Nuclear Fast Red.

The following antibodies were used: rabbit anti-Foxd3 at 1:1000 (Tompers et al., 2005); mouse anti-PGP9.5 at 1:100 (Biogenesis); mouse anti-neurofilament (2H3 monoclonal) at 1:1000 (Developmental Studies Hybridoma Bank); mouse anti-β III tubulin (Tuj1; Tubb3) at 1:100 (Chemicon); rabbit anti-phosphohistone H3 at 1:200 (Upstate Biotechnology); goat anti-Fabp7 (also known as B-FABP) at 1:20 (R&D Systems); goat anti-rabbit Cy3, goat anti-mouse Cy3 and donkey anti-goat Cy2 (Jackson ImmunoResearch Laboratories). The Vectastain ABC Kit (Vector Laboratories) was used to detect the non-fluorescent secondary antibodies and DAPI (1:5000, Molecular Probes) was used to highlight nuclei.

Whole-mount in situ hybridization was performed using Costar 12-well inserts following standard protocols (Hanna et al., 2002). Probes for *Crabp1* (Stoner and Gudas, 1989), *Dlx1* (Dolle et al., 1992), *Msx1* (Satokata and Maas, 1994), *Pdgfa* (Mercola et al., 1990), *Pdgfc* (Ding et al., 2000) and *Sox10* (Southard-Smith et al., 1998) were as described previously. Digoxigenin-labeled RNA probes were prepared using reagents from Roche Molecular Biochemicals.

Corrosion casting was performed as described (Feiner et al., 2001) by injecting the left ventricle of embryonic or newborn hearts first with PBS and then with polymer containing red pigment (Polysciences #07349) using gentle pressure. Polymer containing blue pigment was injected into the right ventricle to monitor for possible ventricular septal defects. The casts were cured overnight at 4°C and surrounding tissue was macerated (maceration solution: Polysciences #07359) at 50°C for 6-8 hours.

RESULTS

Conditional deletion of the *Foxd3* locus in NC

A targeting vector was designed so that after homologous recombination in ES cells, the *Foxd3* coding region (Fig. 1A, purple box) would be flanked with loxP sequences (Fig. 1A, orange triangles). Correctly targeted ES cells were used to generate mice carrying a *Foxd3*^{flox} allele. Mice carrying two *Foxd3*^{flox} alleles (*Foxd3*$^{flox/flox}$ mice) appeared normal and healthy. To test whether Cre-mediated deletion of the *Foxd3* locus produced a null allele efficiently, we crossed *Foxd3*$^{flox/flox}$ mice with *Foxd3*$^{flox/+}$; *EIIa-Cre* mice. Timed pregnant females from this cross were dissected at 6.5 days post-coitum (dpc) and 25% of the resulting embryos had a phenotype identical to the original loss-of-function allele (data not shown). There was no difference in the results obtained with or without the *neo* selection cassette (data not shown).

To selectively delete *Foxd3* in the NC, we used the well-characterized *Wnt1-Cre* transgenic mouse line in which Cre recombinase is expressed in migrating NC starting at 8.0-8.5 dpc (Danielian et al., 1998). We used reciprocal matings between *Foxd3*$^{flox/flox}$ and *Foxd3*$^{+/-}$; *Wnt1-Cre* mice to obtain *Foxd3*$^{flox/-}$; *Wnt1-Cre* (mutant) embryos. At the four-somite stage (~8.0 dpc), Foxd3 protein was detected in migrating NC in the head folds (Fig. 1D). By contrast, we saw a severe reduction in Foxd3 protein in head folds of mutant embryos, detecting only one or two cells that were weakly positive for Foxd3 protein expression (Fig. 1E, arrow). By 9.5 dpc, no Foxd3 protein was detected in the mutant dorsal neural tube or migratory path of NC (Fig. 1, compare F with G). Foxd3 expression was not maintained in the facial mesenchyme at 13.5 dpc; expression was limited to forming cranial ganglia (Fig. 1H) and this expression was missing in mutant embryos. In the ENS, Foxd3 protein was expressed in the gut coils at 13.5 dpc and was missing in mutant embryos (Fig. 1J,K). These results demonstrate that *Foxd3* is deleted specifically in the NC by *Wnt1-Cre*.

Maintenance of cranial NC is dependent on Foxd3

Initially, litters were allowed to progress to term and no mutant mice were found at weaning (21 days). However, we found one dead mutant newborn pup (Fig. 2A) and began monitoring litters before the mice were born (Table 1). Although the majority of 18.5 dpc littermates appeared normal and could survive being delivered by caesarian section, the mutant mice attempted to breathe several

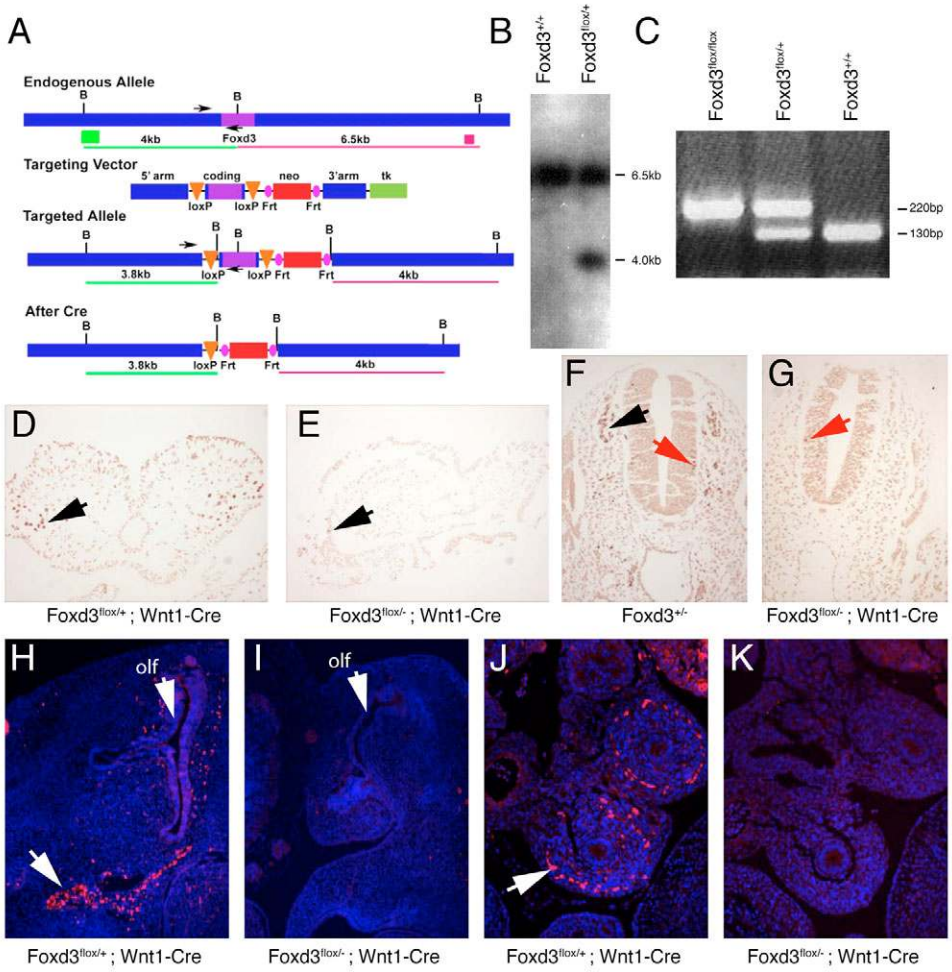

Fig. 1. Generation of a NC-specific deletion in *Foxd3*. (**A**) The mouse *Foxd3* locus, targeting vector and resulting alleles. Purple box indicates the single coding exon. (**B**) Southern blot analysis using the 3′ probe shown in A with *Bam*HI-digested genomic DNA; 6.5 kb wild-type band and correctly targeted 4 kb band are indicated. (**C**) Genotyping mice with PCR primers (black arrows in A). PCR product from *Foxd3* floxed allele is 220 bp, from wild-type allele 130 bp. (**D-K**) Foxd3 immunohistochemistry. In a control embryo, NC cells express Foxd3 at 8 dpc in the headfolds (D), at 9.5 dpc in migrating NC (F, black arrow), at 13.5 in cranial nerves (H, white arrow) and in the gut coils (J, white arrow). Foxd3 protein is detected in a few cells in headfolds of a mutant 8 dpc embryo (E, black arrow). By contrast, no Foxd3 expression is detected at 9.5 dpc in the trunk of a *Foxd3* mutant embryo (G) or in the cranial nerves (I) or gut coils (K) at 13.5 dpc. Foxd3-expressing ventral interneurons are detected in the neural tube of control and mutant embryos (red arrows in F,G). olf, olfactory epithelium.

times but then expired. Table 1 summarizes the number of offspring and embryos from both $Foxd3^{flox/+}\times Foxd3^{+/-}$; *Wnt1-Cre* and $Foxd3^{flox/flox}\times Foxd3^{+/-}$; *Wnt1-Cre* crosses. Embryos were found in the expected ratios at all times in development and no mutant mice survived more than a few hours.

All mutant mice had a severe cleft face and palate incompatible with survival and their inability to breathe was presumably the cause of their death immediately after birth. These defects occurred with 100% penetrance, although the width of the cleft sometimes varied in size. Nostrils and whisker pads were present but the facial midline never fused and the eyelids were partially open. Much of the skull vault is derived from cranial NC so we analyzed skeletons using Alcian Blue and Alizarin Red staining. Comparison of the control and mutant skulls in Fig. 2B revealed that the frontalnasal bone and nasal cartilage were missing in the mutants and the interparietal, parietal and basal occipital bones were greatly reduced in size. The maxilla and premaxila were shortened and the mandible was shortened and thickened. These cranial defects were obvious at midgestation stages (Fig. 2C).

To monitor NC cells and their derivatives, we introduced the *ROSA26R* (*R26R*) conditional reporter allele into the mutant background (Soriano, 1999). Upon expression of Cre protein, all cells and their descendants transcribe the *lacZ* gene, and therefore NC cell fate can be monitored directly with and without Foxd3 function. Note that we are comparing $Foxd3^{flox/-}$; *Wnt1-Cre*; *R26R* (mutant) embryos with $Foxd3^{flox/+}$; *Wnt1-Cre*; *R26R* (control) embryos so that the Cre protein will be recombining two sets of loxP sites; one to delete the *Foxd3* coding region and one to delete the stop sequence in the *ROSA26* locus. β-gal-positive tissue was observed in the frontalnasal mesenchyme in both control and mutant embryos, indicating that NC cells contribute to these tissues in the absence of Foxd3 (Fig. 2D and see Fig. S3 in the supplementary material).

Pharyngeal arch defects in *Foxd3* mutants

At 9.5 dpc, a comparison of lineage-mapped embryos revealed that NC cells have migrated into pharyngeal arches (PAs) 1 and 2 in both *Foxd3* mutants and controls (Fig. 3A). However, by 10.5 dpc, morphological differences in the PAs were apparent by scanning electron microscopy (Fig. 3B). The maxillary and the mandibular prominences of PA1 were present but reduced in size. There was a striking decrease of NC in PAs 3 and 4. Immunohistochemistry for neurofilament protein showed that all cranial ganglia and nerves are present but smaller than normal. Some cranial nerves were slightly misdirected (the glossopharyngeal nerve in Fig. 3C) or had not extended as far as in the control (the facial and vestibulocochlear nerves). Spinal nerves along the trunk of the mutant embryos were thinner. Examining expression of *Sox10*, a marker of early NC, revealed reduced expression in the developing trigeminal, facial and vestibulocochlear ganglia and no expression in the glossopharyngeal and vagus ganglia. *Sox10* expression was also reduced along the trunk of the embryo (Fig. 3D). Expression of other NC-specific genes in the PAs uniformly showed reduced expression in PAs 1 and 2 (see Fig. S1 in the supplementary material). Together, these data

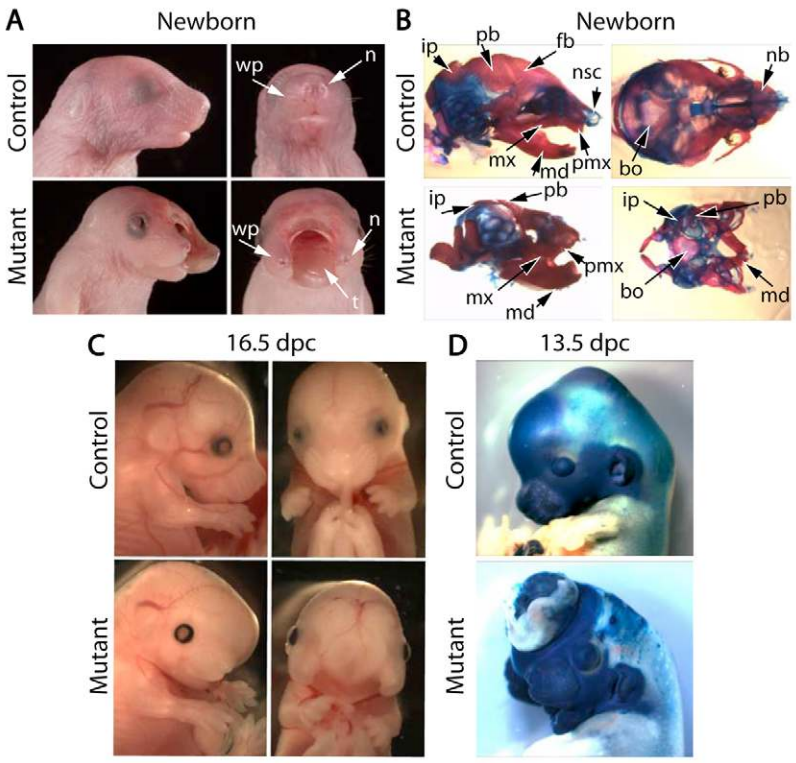

Fig. 2. Craniofacial dysmorphogenesis, skeletal abnormalities and PA malformations in *Foxd3*$^{flox/-}$; *Wnt1-Cre* mice and embryos. (**A**) Newborn *Foxd3* mutant mice were found with a severe cleft face and palate. (**B**) Alizarin Red and Alcian Blue staining of the head skeleton and cartilage, lateral and dorsal views. The frontal bone and nasal capsule are missing in mutants and the parietal and interparietal bones are greatly reduced in size. The basioccipital bone and premaxila are present but smaller, and the mandible is shortened and thickened. (**C**) Side and front views of embryos at 16.5 dpc show these defects at midgestation. (**D**) Side view of lineage-labeled (*R26R*) embryos showing the contribution of NC to the face at 13.5 dpc in control and *Foxd3* mutant embryos. bo, basioccipital bone; fb, frontal bone; ip, interparietal bone; md, mandible; mx, maxilla; n, nostrils; nb, nasal bone; nsc, nasal capsule; PA1md, mandibular prominence of pharyngeal arch 1; PA1mx, maxillary prominence of pharyngeal arch 1; PA2, pharyngeal arch 2; pb, parietal bone; pmx, premaxilla; t, tongue; wp, whisker pads.

suggest that the initial specification of NC occurs in *Foxd3* mutants, but there is an overall failure to maintain NC progenitors as demonstrated by a loss of PA-derived structures and a concomitant decrease in expression of NC-specific genes.

Reduction of peripheral nervous system and loss of enteric nervous system in *Foxd3* mutants

NC cells migrate into the limbs during development giving rise to neurons, Schwann cells and terminal glia cells. X-Gal lineage staining highlighted the cutaneous nerves and the developing sciatic nerve in a hindlimb from a 14.5 dpc control embryo (Fig. 4A). All of these NC-derived cells were missing in the *Foxd3* mutant embryos (Fig. 4B). A dorsal view of the same pair of embryos revealed the segmented pattern of spinal nerves exiting the dorsal root ganglia (DRG) and projecting ventrally in the control (Fig. 4C); the spinal nerves were absent in mutant embryos (Fig. 4D).

NC cells that migrate ventrally from the dorsal neural tube contribute to the ENS: the neurons and glia that innervate the entire gastrointestinal tract. Using the *ROSA26R* reporter allele, NC contribution to the ENS is easily visualized. In control midgestation embryos (14.5 dpc), the intestines were ensheathed in a plexus of NC-derived β-gal-positive cells, whereas in a *Foxd3* mutant littermate the gut was completely lacking these cells (Fig. 4E,F). When the gastrointestinal tract was dissected out of 17.5 dpc

Table 1. Genotypes of offspring and embryos from representative *Foxd3*$^{flox/+}$ × *Foxd3*$^{+/-}$; *Wnt1-Cre* and *Foxd3*$^{flox/flox}$ × *Foxd3*$^{+/-}$; *Wnt1-Cre* crosses

***Foxd3*$^{flox/+}$ × *Foxd3*$^{+/-}$; *Wnt1-Cre* crosses**

	Foxd3$^{flox/-}$; *Wnt1-Cre* (mutants)	*Foxd3*$^{flox/+}$; *Wnt1-Cre*	*Foxd3*$^{+/+}$ or *Foxd3*$^{+/-}$; *Wnt1-Cre*	*Foxd3*$^{flox/-}$	*Foxd3*$^{flox/+}$	*Foxd3*$^{+/+}$ or *Foxd3*$^{+/-}$	*n*
Expected frequency	12.5%	12.5%	25%	12.5%	12.5%	25%	
8.5 dpc	2 (18%)	0	4 (36%)	0	1 (9%)	4 (36%)	11
9.5 dpc	16 (12%)	17 (13%)	40 (30%)	11 (8%)	21 (16%)	30 (22%)	135
10.5 dpc	1 (6%)	3 (19%)	4 (25%)	3 (19%)	2 (12%)	3 (19%)	16
12.5 dpc	1 (8%)	1 (8%)	3 (25%)	3 (25%)	2 (17%)	2 (17%)	12
Newborn	1* (3%)	9 (24%)	7 (18%)	6 (16%)	4 (11%)	11 (29%)	38
Total	21 (10%)	30 (14%)	58 (27%)	23 (11%)	30 (14%)	50 (24%)	174

***Foxd3*$^{flox/flox}$ × *Foxd3*$^{+/-}$; *Wnt1-Cre* crosses**

	Foxd3$^{flox/-}$; *Wnt1-Cre* (mutants)	*Foxd3*$^{flox/+}$; *Wnt1-Cre*	*Foxd3*$^{flox/-}$	*Foxd3*$^{flox/+}$	*n*
Expected frequency	25%	25%	25%	25%	
9.5 dpc	19 (20%)	27 (29%)	23 (25%)	24 (26%)	93
16.5 dpc	4 (33%)	2 (17%)	3 (25%)	3 (25%)	12
Total	23 (22%)	29 (28%)	26 (25%)	27 (26%)	105

Percentages are rounded to the nearest whole number.
*One newborn pup was found dead in the third litter (Fig. 2A).

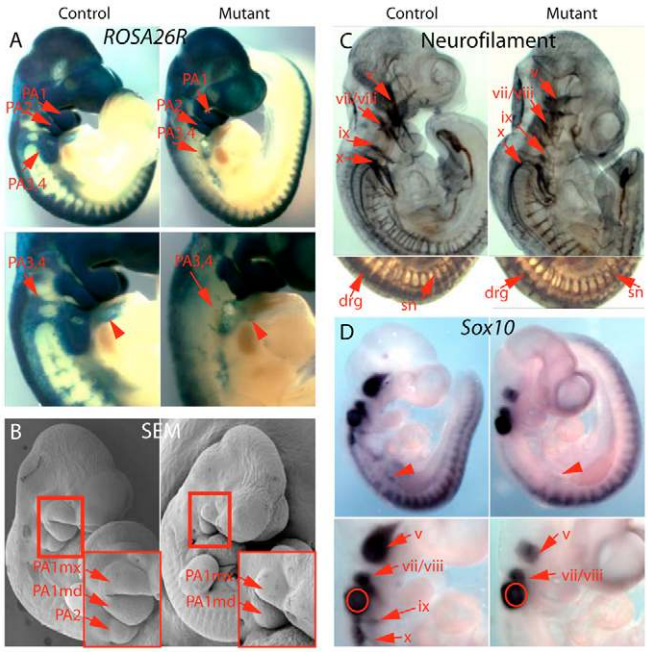

Fig. 3. Pharyngeal arch defects in *Foxd3*$^{flox/-}$; *Wnt1-Cre* embryos. (**A**) β-galactosidase activity as detected by X-Gal staining in control and mutant mouse embryos at 9.5 dpc. PA1 and PA2 are present but smaller in *Foxd3* mutants and there is a paucity of cells migrating into PAs 3-4 and into the developing cardiac region (arrowheads in enlarged view below). (**B**) Scanning electron micrographs of 10.5 dpc embryos showing PA deficiency. Embryos were matched for somite number. (**C**) Whole-mount antibody staining of neurofilament protein. Cranial nerves are present in mutants but smaller and slightly misdirected. In the trunk (lower panels), the mutant embryo has smaller dorsal root gangia (DRG) and thinner spinal nerves than the control. Note that these embryos have been cleared so that both left and right nerves are visible. (**D**) Whole-mount in situ hybridization of embryos for *Sox10*. In *Foxd3* mutant embryos, *Sox10* mRNA is not detected in the glossopharyngeal (IX) and vagus (X) ganglia, although it is detected at reduced levels in the trigeminal (V), facial (VII) and vestibulocochlear (VIII) ganglia. *Sox10* signal is also missing in the foregut of mutants (arrowheads); signal in the otic vesicle (circled) is background. drg, dorsal root ganglion; v, trigeminal ganglion; vii, facial ganglion; viii vestibulocochlear ganglion; ix, glossopharyngeal ganglion; x, vagus ganglion; PA, pharyngeal arch; sn, spinal nerves.

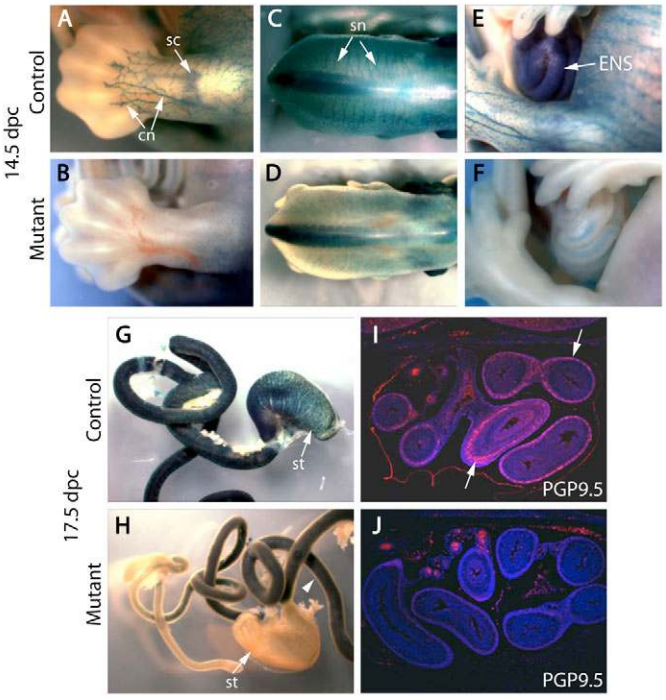

Fig. 4. Peripheral and enteric nervous system defects in *Foxd3*$^{flox/-}$; *Wnt1-Cre* embryos. (**A-H**) β-galactosidase activity detected by X-Gal staining in control and mutant mouse embryos. (A,B) Lateral view of hindlimbs of 14.5 dpc embryos. In control embryos, development of cutaneous nerves is obvious and the developing sciatic nerve is visible (A). None of these structures is seen in *Foxd3* mutant embryos (B). (C,D) Dorsal view of the trunk of a control embryo at 14.5 dpc shows the segmented development of spinal nerves radiating out from the developing spinal cord (C). This is not seen in mutant embryos (D). (E,F) Lateral view of a 14.5 dpc embryo shows coils of the developing gastrointestinal tract. In the control embryo, cells of the ENS stain blue on the outside of the gut coils (E). In the *Foxd3* mutant embryo, no blue staining of the ENS is visible and the absence of cutaneous peripheral nerves is apparent (F). (G,H) Dissected gastrointestinal tracts from 17.5 dpc embryos. In the control, the entire extent of the gut is ensheathed in NC-derived cells making up the ENS (G). In the mutant, there are no β-gal-positive cells around the outside of the gut (H). Blue staining inside the lumen is background (arrowhead). (**I**,**J**) Immunofluorescence for PGP9.5, a protein enriched in neurons, shows the location of the ENS neurons in cross-sections of the intestine in the control embryo (I), whereas no PGP9.5 signal is detected in the mutant (J). PGP9.5 signal is red; sections were counterstained with DAPI (blue) to reveal nuclei. cn, cutaneous nerves; ENS, enteric nervous system; sc, sciatic nerve; sn, spinal nerves; st, stomach.

embryos, the control sample was surrounded by β-gal-positive cells along the entire anterior to posterior axis, whereas the mutant sample had no NC-derived cells around the outside of the gut tube (Fig. 4G,H). Expression of PGP9.5 (Uchl1 – Mouse Genome Informatics) was readily detectable in neurons of the ENS in control embryos, whereas there were no PGP9.5-positive cells in *Foxd3* mutant embryos (Fig. 4I,J). Similar results were obtained with β III tubulin antiserum used to detect neurons, and with Fabp7 antiserum used to detect glia (data not shown).

Foxd3 mutants show subtle cardiac neural crest defects

NC cells from the mid-otic placode to somite 4 migrate through rhombomeres 6-8 into PAs 3, 4 and 6, contributing to the aortic arch arteries and the aorticopulmonary septum of the cardiac outflow tract. In control embryos, NC cells entered PAs 3, 4 and 6 (Fig. 3A) and the developing heart field by 9.5 dpc (Fig. 5A, arrows) and continued migrating at 10.5 dpc (Fig. 5B). We observed a striking decrease in the cardiac NC of *Foxd3* mutant embryos. Fewer cells entered the heart field at 9.5 dpc (Fig. 5C). At 10.5 dpc, there was a paucity of NC in mutant PAs (Fig. 5D, arrow) and a greatly reduced number of cells entering the heart (Fig. 5D, arrowhead).

To further investigate development of the cardiac NC, we examined patterning of vascular NC derivatives using corrosion casting (Fig. 5E-H). We observed normal patterning of the aortic arch in the majority of *Foxd3* mutants (13/17, 76%) between 15.5 dpc and birth. However, in three out of 17 *Foxd3* mutant embryos examined, we observed a duplication of the left common carotid artery (Fig. 5G,G′). One mutant embryo had severe cardiac NC defects,

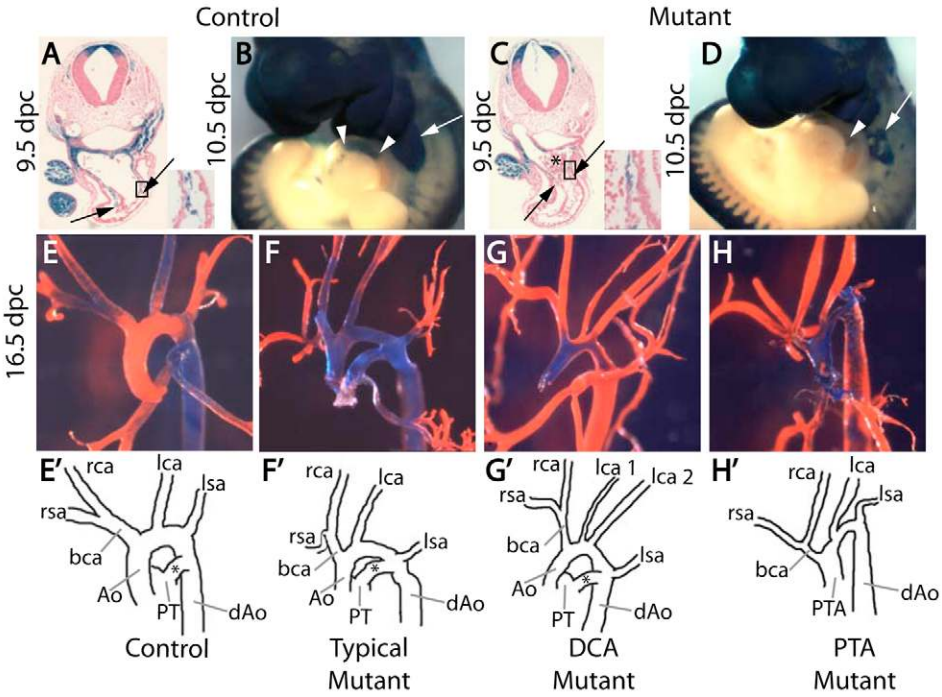

Fig. 5. Deletion of *Foxd3* in the NC has subtle infrequent effects on heart development. (**A**) A section through a lineage-labeled control mouse embryo at 9.5 dpc shows NC entering the developing heart (arrows). Box indicates area enlarged in inset. (**B**) In a control embryo at 10.5 dpc, NC cells are located in PAs 3 and 4 (arrow) and have migrated into the heart (between arrowheads). (**C**) At 9.5 dpc, a section through a *Foxd3* mutant embryo shows NC entering the developing heart (arrows). Asterisk marks blood inside the heart. (**D**) In a mutant embryo at 10.5 dpc, very few NC cells are migrating into the heart (arrowhead) and very little NC is detected in PAs 3 and 4 (arrow). (**E-H′**) Corrosion casts (E-H) and corresponding traces (E′-H′) of 16.5 dpc cardiac outflow tract and associated vessels. The majority of *Foxd3* mutants (13 of 17) are indistinguishable from controls (E,F). A few mutants had a duplicated left carotid artery (3 of 17) (G) and one mutant had a PTA (H). Ao, aorta; bca, brachiocephalic artery; dAo, dorsal aorta; DCA, duplicated carotid artery; lca, left carotid; lsa, left subclavian artery; PT, pulmonary trunk; PTA, persistent truncus arteriosus; rca, right carotid artery; rsc, right subclavian artery; *, ductus arteriosus.

including type A2 persistent truncus arteriosis (PTA) in which the septation of the outflow tract did not occur and the ductus arteriosis was absent (Fig. 5H,H′) (Van Praagh and Van Praagh, 1965). We examined the NC lineage in both control and mutant embryos with the *ROSA26R* reporter allele and saw no differences in NC contribution to the cardiovascular system at 17.5 dpc (n=7 mutants; see Fig. S2 in the supplementary material). Histological analysis of eight mutant and control littermates was performed and no septal defects were observed (see Fig. S2 in the supplementary material); however, while in the process of performing resin casts, 1/17 (the sample shown in Fig. 5H) displayed a ventricular septal defect.

NC cell migration, differentiation, death and proliferation

NC must maintain a delicate balance of proliferation and migration, and timing of differentiation is crucial for their final tissue contributions in the adult. Lineage tracing revealed that DRG were formed in *Foxd3* mutants (Fig. 6A,B) but were smaller than normal. The size of the DRG varies with the angle of section, but in whole-mount, mutant DRG were consistently smaller than controls (Fig. 3A). However, a more ventral field of the same region revealed that whereas control NC enter the foregut to eventually populate the ENS (Fig. 6C), mutant NC cells are fewer in number and halt their migration near the dorsal aorta in a position consistent with the final location of sympathetic ganglia (Fig. 6D). No mutant NC cells entered the developing gut anywhere along the anterior-posterior axis.

Terminal differentiation of NC occurs as cells reach their final destination. We detected expression of neural and glial markers in control and mutant DRG. At 9.5 and 14.5 dpc, the neural marker β III tubulin and the glial marker Fabp7 were expressed in both control and mutant DRG (Fig. 6E-H and data not shown).

We examined cell death in control and *Foxd3* mutant embryos and detected an increase in TUNEL-positive apoptotic cells in the dorsal spinal cord in the mutant, whereas there were few, if any, TUNEL-positive cells in the spinal cord of control embryos (Fig. 6I,J). Confirming this with LysoTracker Red dye, at 9.0 dpc mutant embryos showed increased apoptosis in the hindbrain, and by 10.5 dpc apoptosis was more pronounced in the posterior tail of the embryo (Fig. 6K-N). The absence of apoptosis in distal PAs of mutant embryos at 10.5 dpc (Fig. 6M) is likely to be due to the large deficit in NC cell numbers (note morphology of PAs in Fig. 6M and lineage label in Fig. 3B).

To more closely examine the curious recovery of most of the cardiac derivates, we analyzed cell proliferation in the cardiac NC using a combination of lineage labeling and immunohistochemistry for phosphorylated histone H3 (pH3), a marker for cells in mitosis. Septation is complete by 13.0 dpc so we chose to examine embryos at 12.5 dpc (Hiruma et al., 2002). Representative sections of 12.5 dpc control and mutant embryos are shown in Fig. 6O-R, clearly demonstrating the paucity of NC present in the outflow tract at the most rostral and caudal levels. The volume of the outflow tract in control and mutant embryos was calculated as 4 mm^3 and 0.7 mm^3, respectively. The proportion of pH3-positive NC cells was the

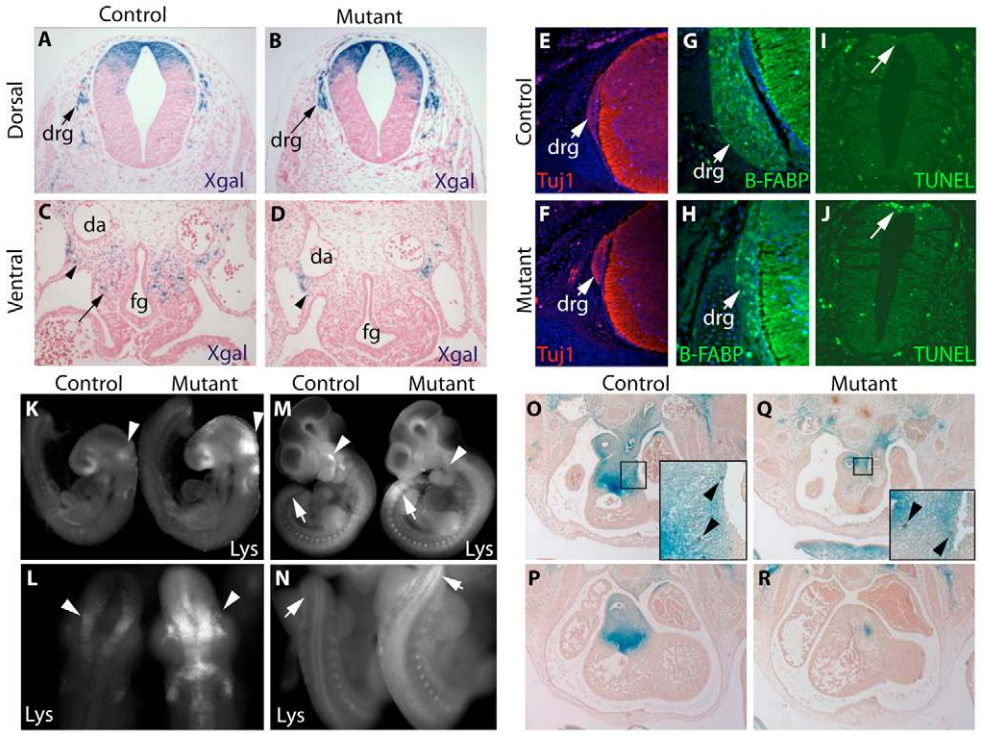

Fig. 6. Cell migration, survival and proliferation effects in *Foxd3* mutants. (**A**,**B**) Sections through lineage-labeled 9.5 dpc control and mutant mouse embryos show that NC cells have migrated ventrally to form the DRG. Samples stained as in Fig. 5. (**C**,**D**) A more ventral view of the same region pictured in A and B shows NC populating the foregut in the control embryo (arrow) but halting migration near the dorsal aorta in the *Foxd3* mutant (arrowhead). (**E-H**) Control and mutant DRG contain differentiated neurons and glia at 14.5 dpc as indicated by β III tubulin (Tuj1) and Fabp7 (B-FABP) expression. (**I**,**J**) Marked changes in cell death occur in the dorsal spinal cord of 9.5 dpc *Foxd3* mutant embryos (arrows). (**K-N**) Whole 9.0 dpc embryos incubated in LysoTracker Red to indicate dying cells. Note pronounced cell death in the mutant hindbrain and migrating NC (arrowheads). At 10.5 dpc (M,N), the mutant has fewer apoptotic cells in the distal region of the PAs (arrowheads), but increased apoptotic cells in the tail (arrows). The overall loss of PA tissue is apparent. (**O-R**) Matched sections from control and mutant rostral (O,Q) and caudal (P,R) outflow tracts with lineage label (blue) and pH3 immunostaining (brown) showing reduced NC in the *Foxd3* mutant outflow tract. Box indicates area enlarged in inset. Arrowheads in inset indicate pH3-positive NC cells.

same in controls and mutants (for details, see Fig. S3 in the supplementary material). These results suggest that although loss of Foxd3 reduces the number of cardiac NC, these cells are still able to pattern the outflow tract and give rise to smooth muscle cells.

DISCUSSION

NC specification

Previous data from several laboratories have demonstrated that ectopic expression of Foxd3 in the neural tube can change the fate of the neuroepithelium into NC (Cheung et al., 2005; Dottori et al., 2001; Kos et al., 2001; Sasai et al., 2001). However, our loss-of-function analysis suggests that Foxd3 is not required for the initial specification of the NC. In *Foxd3*$^{flox/-}$; *Wnt1-Cre* mutant embryos, we do not detect cells expressing Foxd3 at the earliest stages of NC specification (Fig. 1D-G), yet there is still NC present (Fig. 3). There remains the possibility that the *Wnt1-Cre* transgene does not produce Cre protein early enough and there might be a few Foxd3-expressing cells present, but if so, our data show that they are not maintained. It is more likely that the role of Foxd3 is in maintaining the NC, not in specifying this cell type.

Our findings do not completely agree with those of other model systems, highlighting differences between *Xenopus*, chick, zebrafish and mouse NC. Ectopic expression of a dominant-negative FoxD3 in *Xenopus* embryos suppresses NC specification as measured by the loss of NC marker expression (Sasai et al., 2001). Electroporation of antisense oligonucleotides specific to *Foxd3* in the chick bias the differentiation of NC towards the melanocyte lineage (Kos et al., 2001). There are three recent reports of mutations in the zebrafish *foxd3* locus or knockdown of *foxd3* using morpholinos (Lister et al., 2006; Montero-Balaguer et al., 2006; Stewart et al., 2006). These groups reported that NC was specified normally with a general downregulation of NC markers similar to what we have observed. Craniofacial defects were highlighted by jaw abnormalities in the fish, whereas defects in the mandible of our mice were minor. All three groups demonstrated a complete loss of DRG, whereas we see smaller DRG that contain neurons and glia. Similar to what we observe, in all cases the zebrafish ENS was lost and increased cell death in the NC lineage was observed along with defects in migration. Zebrafish are an ideal system to monitor changes in different types of NC melanocytes and all three groups described lineage-specific differences in these derivatives. For example, in the *mother superior* mutation, which is a mutation somewhere outside the coding region that affects only NC expression of *foxd3*, melanophores are delayed in their development but then recover, whereas iridophores remain greatly reduced (Montero-Balaguer et al., 2006). Zebrafish cardiac NC contributes primarily to the myocardial cell lineage (Li et al., 2003). Despite this, only one group reported a slight edema in the heart in *foxd3* mutants (Montero-Balaguer et al., 2006).

NC patterning

We did not detect anterior-posterior patterning defects in NC of *Foxd3* mutants, although caudal NC was most severely affected. All mutant embryos had severe facial clefting and were missing many NC-derived facial bones. However, the mandible was present in all mutants examined. It was shortened and thickened, similar to *Dlx5*$^{-/-}$ mice (Acampora et al., 1999), but its presence demonstrates that *Foxd3*$^{-/-}$ NC can differentiate into cartilage and bone and overt cranial patterning is unaltered. Similarly, trunk NC cells were present in reduced numbers, but those cells migrated away from the neural tube normally and formed small DRG that contained both neurons and glia.

By contrast, the vagal and sacral NC destined to contribute to the ENS did not migrate to the gut. There are several possibilities for the loss of this sub-lineage of NC. One hypothesis is that there may be expression of closely related Fox genes in the cranial and cardiac NC, but no such compensating family members expressed in the trunk NC caudal to somite 7. A second hypothesis is that ENS progenitors underwent selective cell death in the dorsal neural tube, whereas NC cells destined to populate the DRG were maintained. There are no molecular markers to distinguish these lineages prior to migration so we cannot test this hypothesis directly. A third possibility is that NC cells that underwent apoptosis in the dorsal neural tube were unspecified and the selective loss of the ENS NC is because this lineage must migrate farther than others. Therefore, a general loss in progenitor cell number might affect the ENS NC more severely. A fourth possibility is that *Foxd3*$^{-/-}$ NC might not be able to enter the foregut (Fig. 6, compare C with D). It has been demonstrated that vagal and sacral NC, unlike the rest of the trunk NC, possess a unique ability to enter the gut mesentery (Serbedzija et al., 1991). Recent studies suggest this difference might be at least partially explained by the expression of axon guidance molecules Slit and Robo on vagal NC (De Bellard et al., 2003). In contrast to our results, mice lacking members of the glial cell line-derived neurotrophic factor signaling pathway have enteric neurons in the anterior ENS (Cacalano et al., 1998; Pichel et al., 1996; Sanchez et al., 1996), whereas mutations in endothelin 3 or endothelin receptor type B cause the loss of ENS only in the distal colon (Baynash et al., 1994; Hosoda et al., 1994). In *Phox2b*$^{-/-}$ embryos, there is an initial migration of vagal NC into the proximal gut mesentery, but these progenitors are not maintained, leaving the entire gut without innervation (Pattyn et al., 1999). In fact, the only other mouse model lacking the entire ENS is *Sox10*$^{Dom/Dom}$ (Kapur, 1999; Southard-Smith et al., 1998) and it is interesting to note that *Sox10* is one of the genes severely downregulated in *Foxd3*$^{-/-}$ mutant embryos (Fig. 3C, arrowheads).

One final hypothesis, not mutually exclusive to those suggested above, is that although Foxd3 appears to be equally expressed throughout the early premigratory crest, it might be differentially required in specific subpopulations of the crest. Our surprising results showing the minimal phenotype of the mutant cardiac NC supports this last hypothesis. The cardiac crest normally migrates into PAs 3, 4 and 6, eventually contributing to the cardiac outflow tract and the aorticopulmonary septum. There is a striking reduction of cardiac NC in PAs 3, 4 and 6 in *Foxd3* mutant embryos compared with controls (Fig. 3A and Fig. 5A-D). However, this greatly reduced population of cardiac NC migrates into the heart field and even though there are far fewer cells (mutants contained 18% of the volume of NC of controls by lineage label), this reduced number can effectively septate the outflow tract in most cases. We did not observe alterations from the wild-type pattern of proliferation as monitored by phosphorylated histone H3 at 9.5 dpc. This suggests that the extent of migration of the cardiac NC, rather than the number of cardiac NC cells, is crucial for their ability to effectively septate the outflow tract. One of our future goals is to understand molecular differences between the cardiac NC, which can overcome the loss of Foxd3, and the rest of the NC lineage that is dependent on this transcription factor.

Conservation of Foxd3 function in progenitor cells

Development of all embryonic tissues relies on progenitor cells that are able to self-renew and differentiate appropriately. Our initial description of the *Foxd3*$^{-/-}$ phenotype demonstrated that this protein is required for maintenance of epiblast cells and therefore required for establishing ES cells (Hanna et al., 2002). Foxd3 is similarly required in the trophoblast progenitor lineage (Tompers et al., 2005), a lineage completely disparate from the embryonic one primarily affected in the null mutation. Therefore, the NC is the third multipotent lineage that requires Foxd3 for maintenance of progenitor cells, making an unprecedented molecular connection between these three distinct progenitor populations. These lineages are embryonically derived and we have yet to demonstrate that Foxd3 can play a similar role in adult-derived stem cells. However, our results support the premise that certain self-renewal mechanisms are likely to be conserved in very different progenitor lineages. There are several other proteins known to regulate multiple progenitor lineages. Bmi1 and other polycomb proteins repress genes that induce cell death in the hematopoetic lineages, neural stem cells, NC stem cells and cancer stem cells (reviewed by Pardal et al., 2005). Most recently, the transcription factor Zfx has been shown to be required for self-renewal of ES cells and maintenance of adult hematopoietic stem cells (Galan-Caridad et al., 2007). The proto-oncogene *c-Myc* has a well-documented role in cell proliferation; recent work in *Xenopus* suggests it might be involved in NC formation, whereas genetic studies in the mouse show that a NC deletion of *Myc* results in a relatively mild phenotype (Bellmeyer et al., 2003; Wei et al., 2007). In addition to its role in NC development, expression of Myc along with several other 'stem cell proteins' is sufficient to change the fate of somatic cells into pluripotent stem cells (Takahashi and Yamanaka, 2006). Finally, Sox2 is required in ES cells, TS cells and embryonic neural lineages (Avilion et al., 2003; Graham et al., 2003). Sox2 is also expressed in early migrating NC, in Schwann cells (Larysa Pevny, personal communication) and in the postnatal ENS (Vohra et al., 2006), all regions competent to give rise to NC stem cells. The role of Sox2 in the NC has not been investigated, and it is tempting to speculate that there might be a genetic interaction between Foxd3 and Sox2.

It is not clear how Foxd3 functions to maintain these progenitor pools. The protein can function as either an activator or a repressor in different contexts; in *Xenopus* mesoderm induction, FoxD3 recruits Groucho4 to repress target genes (Steiner et al., 2006; Yaklichkin et al., 2007), whereas in zebrafish somite maturation, Foxd3 activates *myf5* expression directly (Lee et al., 2006). We cannot rule out the possibility that Foxd3 might behave similarly to Foxa proteins in modifying chromatin structure to allow access of other co-repressors or activators to target genes (Cirillo et al., 2002). Our major challenges ahead are to identify Foxd3 target genes and to determine the signaling pathways in which the protein functions.

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Supplementary material

Supplementary material for this article is available at
http://dev.biologists.org/cgi/content/full/135/9/1615/DC1

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