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belladonna/lhx2 is required for neural patterning and midline axon guidance in the zebrafish forebrain.

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Summary

Some of the earliest axon pathways to form in the vertebrate forebrain are established as commissural and retinal axons cross the midline of the diencephalon and telencephalon. To better understand axon guidance in the forebrain, we characterized the zebrafish *belladonna (bel)* mutation, which disrupts commissural and retinal axon guidance in the forebrain. Using a positional cloning strategy we determined that the *bel* locus encodes zebrafish Lhx2, a lim-homeodomain transcription factor expressed in the brain, eye, and fin buds. We show that *bel(lhx2)* function is required for patterning in the ventral forebrain and eye and that loss of *bel* function leads to alterations in regulatory gene expression, perturbations in axon guidance factors, and the absence of an optic chiasm and forebrain commissures. Our analysis reveals new roles for *lhx2* in midline axon guidance, forebrain patterning, and eye morphogenesis.

Introduction

The anterior commissure (AC), post-optic commissure (POC) and the optic chiasm are the first major axon pathways to cross the midline of the vertebrate forebrain during embryonic development. The POC is formed as neurons in the lateral diencephalon extend axons anteriorly and across the midline (reviewed in Bak and Fraser, 2003), while the AC forms as lateral telencephalic neurons extend axons anteriorly across the midline of the ventral/anterior telencephalon (reviewed in Chitnis and Kuwada, 1990; Wilson et al., 1990). Soon after formation of these forebrain commissures, retinal ganglion cell (RGC) axons from the eye cross the midline of the diencephalon near the POC to form the optic nerve, optic chiasm, and optic tract (Burrill and Easter, 1995). In monocular organisms such as zebrafish, all retinal axons cross the ventral midline, whereas in binocular organisms some retinal axons turn ipsilaterally at the midline and innervate ipsilateral targets in the brain (reviewed in Williams et al., 2004). In humans, congenital defects in chiasm formation lead to visual defects including nystagmus and loss of depth perception (Apkarian and Bour, 2001).

The cellular and molecular cues that guide midline-crossing axons in the forebrain are poorly understood. Glial cells may provide the cellular substrate for midline crossing axons and help establish the position of commissures, as glial structures have been found associated with many brain commissures including the corpus callosum (Shu et al., 2003), chiasm (Marcus et al., 1995), AC and POC (Barresi et al., 2005). This role in guiding commissural axons may be conserved through evolution, as midline glial cells are known to help guide axons toward the midline in the *Drosophila* CNS (Chotard and Salecker, 2004; Hidalgo and Booth, 2000).

Compared to these cellular cues, more is known about the molecular guidance cues that influence commissure formation. In the vertebrate spinal cord a combination of attractive and repulsive cues regulates commissural axon crossing (Dickson, 2002). Netrin and Sonic hedgehog (Shh) act as attractants for spinal commissural axons (Salinas, 2003), while Slit molecules prevent non-commissural axons from crossing the midline (Brose et al., 1999). In the vertebrate forebrain, *netrin* expression in the telencephalon is consistent with a possible role in AC formation, however the lack of *netrin* expression in the diencephalon suggests it does not play a role in POC or chiasm formation (Lauderdale et al., 1997). *slit* genes are expressed in bands across the midline of both the telencephalon and diencephalon, and these proteins act to channel Robo expressing retinal axons during chiasm formation (reviewed in Rasband et al., 2003; Richards, 2002). This repellent function also helps position glial cells and axons in the POC region (Barresi et al., 2005). The transcription factor Zic2 is expressed in a subset of retinal axons that grow ipsilaterally in binocular organisms, and Zic2 may regulate EphB1 receptors that receive the repulsive EphrinB2 cues from the midline, thus preventing these axons from crossing the midline (Herrera et al., 2003).

The precise expression of axon guidance cues in the eye and forebrain depends on complex cellular differentiation events that lead to an exquisitely patterned neural tube. A large number of transcription factors interact to help pattern the forebrain (Dodd et al., 1988; Herrera et al., 2004; Shimamura et al., 1997). These include several members of the Lim-HomeoDomain (LHD) transcription factor family that are involved in the related processes of neural patterning, cell fate determination, and axon pathfinding (reviewed in Sockanathan, 2003). Among these, Lhx2 is required for mouse forebrain patterning and eye formation, with *Lhx2* knock-out (KO) mice having a highly reduced telencephalon and no eyes (Porter et al., 1997). While the telencephalic and eye phenotypes in *Lhx2* KO are well documented, little information is available about the role of Lhx2 in forebrain axon

guidance or in the formation of the diencephalon, a region where it is also strongly expressed.

Here we show that the zebrafish axon guidance mutant *belladonna* (*bel*) encodes Lhx2. In *bel* mutants, both POC and RGC axons fail to cross the midline of the forebrain and no optic chiasm forms. *bel(lhx2)* mutant embryos have subtle eye defects, but have no other morphological defects and can grow to adulthood (Karlstrom et al., 1996). *bel(lhx2)* mutants also have a reversed optokinetic response, similar to defects in human achiasmats (Rick et al., 2000). We show that *bel(lhx2)* mutants have subtle forebrain patterning defects that are restricted to regions of the forebrain where the AC, POC and optic chiasm form. Our detailed analysis of forebrain defects in *bel*(*lhx2*) mutants indicates that disorganization of midline glia and the mis-expression of a subset of known axon guidance molecules accompany retinal and commissural axon guidance defects. These results demonstrate a role for *bel*(*lhx2)* in forebrain axon guidance and in the patterning of the diencephalon and eye, and help characterize the guidance substrate for commissural and retinal axons in the forebrain.

Methods

Fish lines and genetic mapping

bel^{tv42} was isolated in a screen for retinotectal axon guidance mutants (Karlstrom et al., 1996) while *bel*^{b700} was isolated in a genetic screen for forebrain patterning mutations (Z. Varga, unpublished data). For genetic mapping, *bel*^{tv42} heterozygotes in the Tü background were crossed into polymorphic TL and WIK strains (Rauch et al., 1997). Mutant embryos were identified by axon guidance defects or visible eye defects at 5 dpf. PCR was performed on embryonic DNA using simple sequence repeat (SSR) markers (Knapik et al., 1998). Polymorphisms were visualized on 2.5 % agarose gels or by single strand conformation polymorphism (SSCP) analysis (Karlstrom et al., 1999).

In situ hybridization and immunohistochemistry

Embryos were maintained at 28.5°C and 0.003% 1-phenyl-2-thiourea (PTU) was added to block melanin biosynthesis (Westerfield, 1993). Embryos were staged (Kimmel et al., 1995) and ages designated as hours post fertilization (hpf) or days post fertilization (dpf). In situ labeling was performed as previously described (Karlstrom et al., 1999). Probes used were: *dlx2* (Akimenko et al., 1994), *erm* (Munchberg et al., 1999), *fgf8* (Furthauer et al., 1997), *netrin1* (Lauderdale et al., 1997), *nk2.1b* (Rohr et al., 2001), *nk2.2* (Barth and Wilson, 1995), *pax2.1* (Krauss et al., 1991), *sema3D* (Halloran et al., 1998), *slit2* (Yeo et al., 2001), *vax2* (Take-uchi et al., 2003), and *zic2.1* (Grinblat and Sive, 2001). Antisense *lhx2* probes were generated against the full length cDNA cloned into the pCR4TOPO vector (see below).

Immunohistochemistry was performed as described for whole mount embryos (Karlstrom et al., 1999) and frozen sections (Devoto et al., 1996). Antibodies used were: ZN-5 (1:25) to label RGCs (University of Oregon Monoclonal Antibody Facility) (Laessing et al., 1994), anti-acetylated tubulin (1:1000, Sigma) to label axons (Wilson et al., 1990), anti-GFAP (1:400) to label glial cells (Nona et al., 1989), and anti-phosphohistone H3 (pH3) (1:100, Sigma) to label mitotic cells (Nechiporuk and Keating, 2002). Individual pH3 labeled cells were counted in the telencephalon (dorsal to the optic recess and first ventricle) and preoptic area of the diencephalon. Cell numbers were compared between wild type and *bel* mutants using a student's paired t-test. 7 μM sections of 5 dpf larvae and adult eyes were embedded in epon/araldite (Mollenhauer, 1964) and counterstained with toluidine blue.

Positional cloning of the bel locus

The zebrafish CHORI-211 BAC library (RZPD, Germany) was screened by PCR using closely linked zMarkers according to manufacturer's instructions. BAC ends were sequenced directly or obtained from the Sanger zebrafish genome database (http://www.sanger.ac.uk/Projects/D_rerio/). PCR primers were designed using these sequenced ends and the library was re-screened until a BAC was identified that spanned the *bel* genetic interval (zC142I8). Genescan analysis (http://genes.mit.edu/GENSCAN.html) of the zC142I8 sequence revealed a single coding sequence encoding Lhx2.

The *lhx2* coding region was amplified from first strand cDNA (Clonetech RT-PCR kit) using 5'UTR and 3'UTR PCR primers (lhx2.5Fw: 5'-GGGTTGCAGATCTGACGG, lhx2.21Rv-5'-GCAGTGGGTAAAATGATGG). Gel purified 1191bp PCR product was cloned into the pCR4TOPO cloning vector (Invitrogen) and sequenced (Genbank accession 725255). The predicted Lhx2 protein sequence was compared with Lhx2 sequences from other species using ClustalW analysis (Biology

Workbench, http://workbench.sdsc.edu/). To sequence the *lhx2* gene in the two *bel* alleles, primers flanking each of the five *lhx2* exons were used to amplify genomic DNA from *bel*^{tv42} siblings, *bel*^{tv42} mutants, *bel*^{b700} siblings and *bel*^{b700} mutants.

For genotyping *bel* carriers, fin clip or embryo DNA was amplified using allele specific primers. *bel*^{tv42} genotyping primers (tv42.GT.Fw-5'-, GCTGCAACATAAGAGAG, and tv42.GT.BsmAI.Rv: 5'-CTCAGACTCCAGGTTCAGTTTACAGTC) amplify a 248 bp fragment with the mutant sequence containing a restriction site for BsmAI. *bel*^{b700} genotyping primers (lhx2.37Fw: 5'-CAATCACACGGATGTAGC and lhx2.18Rv. 5'-CAGTTAACCAGCAGCAAC) flank the 22 bp deletion. DNA fragments were resolved on 3.5% Metaphor (Cambrex) or 4% agarose (Sigma) gels.

Anti-sense oligonucleotide injections and cell transplantation

Phosphorothioated anti-sense oligonucleotides (S-oligos) (Stenkamp and Frey, 2003) were generated against three different regions in zebrafish *lhx2* coding sequence. S-oligo sequences were: CCTgtaggacgcgcttGGTg, GCAtgtgccattgcttGTCc, and CGCctccaggcagaccGTGg (Sigma-Genosys). An *lhx2* splice blocking morpholino (MO) (GeneTools) (5'-CTTTTCTCCTACCGTCTCTGTTTCC) (8-15ng), an unrelated mismatch control MO (10ng), or a cocktail of the three S-oligos (1-1.5 pg each) was injected into 1-2 cell embryos. Embryos were incubated at 28.5^{0}C until the desired time points, fixed in 4% paraformaldehyde, and processed for in situ labeling.

For cell transplantation, wild type or *bel* embryos were injected with rhodamine-dextran (2.5%) at the 1-2 cell stage and used as donors. 10 to 20 cells were transplanted from the donor animal pole at the dome stage to the same region of unlabeled wild type or mutant hosts. Donor and host embryos were maintained as pairs in 24-well dishes in Danieau's solution (1x Danieau: 58 mM NaCl, 0.7 mM KCl, 0.4 mM $MgSO_4$, 0.6 mM $Ca(NO_3)_{2)}$) containing penicillin and streptomycin (1% each). At the Prim-5 stage (24 hpf), donors and hosts were analyzed for *dlx2* expression by in situ hybridization. Genotypes were determined by *dlx2* expression or by PCR based genotyping of tail tissue as described above.

FGF signaling inhibition

To block Fgf signaling, embryos were treated with 20μM SU5402 (Calbiochem) diluted in embryos raising medium for described time intervals at 28.5^{0}C. Control embryos were treated with DMSO (SU5402 carrier). Embryos were placed in 12-well plates (30 embryos per well) with 0.5 ml of medium. After treatments, embryos were fixed and processed for in situ hybridization. As a control for SU5402 efficacy, we examined expression of the Fgf regulated gene *erm* (Raible and Brand, 2001) in similarly treated embryos.

Results:

belladonna mutations affect midline axon guidance in the forebrain

We initially identified *belladonna* in a large-scale screen for mutations that affect axon guidance in the zebrafish retino-tectal system. In 5 day old *bel* mutants, retinal axons fail to cross the midline and instead project to the ipsilateral tectal lobe where they find their correct topographical target (Karlstrom et al., 1996) (Fig. 1A,B). To understand the nature and onset of *bel* axon guidance defects, we examined retinal axon growth at earlier time-points. As retinal axons grew toward the midline (32-36 hpf) two distinct phenotypes were seen in *bel* mutants; retinal axons either projected ipsilaterally immediately after leaving the eye (16/39 optic nerves (ONs) examined), or projected toward the midline (23/39 ONs) (Fig. 1D, D inset). When examined at 38-48 hpf of development, RGC axons failed to cross the midline in 88% of *bel* mutants (n = 276 embryos) (Fig. 1F) and almost no midline growth was seen. Thus, in *bel* mutants RGC axons often approached the midline at early stages of development, but subsequently axons failed to cross the midline and instead projected ipsilaterally.

We next examined the formation of the forebrain commissures in *bel* mutants (Chitnis and Kuwada, 1990; Wilson et al., 1990). In 28 hpf wild type embryos axons from the nucleus of the tract of the post-optic commissure (ntPOC) and axons of the nucleus of the tract of the AC (ntAC) have crossed the midline to form the POC and the AC, respectively (Fig. 1G, Bak and Fraser, 2003). In *bel* mutants, both ntPOC and ntAC axons were present but failed to extend axons across the midline and no forebrain commissures were formed (Fig. 1H). All other major axon pathways appeared normal in *bel* mutants. These include the posterior commissure, hindbrain commissures, Mauthner cells, spinal cord commissures, and peripheral axons (data not shown). Thus mutation of *bel* affects midline axon crossing only in the forebrain.

bel mutations disrupt zebrafish *lhx2*

To understand the molecular mechanisms underlying the *bel* phenotype we next identified the gene encoded by the *bel* locus. Using simple sequence repeat (SSR or Z) markers we linked *bel* to chromosome 8. Fine mapping using a mapping panel that represented more than 2500 meioses identified two Z markers closely linked to *bel* on either side of the *bel* locus, z44909 (0.6 cM) and z24272 (0.3cM) (Fig. 2A). A chromosomal walk identified two overlapping clones (zC142I8 and zC95F8) that spanned the *bel* locus (Fig. 2A). Genescan analysis of zC142I8 sequence identified only one potential gene with high sequence homology to chick Lh-2A and mouse and human Lhx2 (Fig. 2B,C). Similar to other LHD family members, the predicted Lhx2 sequence contains two LIM domains followed by a highly conserved homeobox domain (Fig. 2E). Based on the sequence homology and expression analysis (see below), we concluded that *bel* is more closely related to Lhx2 than the closely related family member Lhx9.

A single nucleotide polymorphism (SNP) in the first intron of the predicted *lhx2* sequence co-segregated with the *bel* locus (0 recombination events in 2500 meioses). We therefore sequenced the *lhx2* gene in two *bel* alleles and found genetic lesions leading to severe protein truncations in both cases. In *bel*^{tv42}, a point mutation (C to A) in the second exon introduces a premature stop codon that would truncate the Lhx2 protein in the first LIM domain (Fig.2E). In *bel*^{b700}, a 22 bp deletion in the third exon results in a frame-shift that leads to a stop codon after the second LIM domain (Fig. 2E).

To verify that *lhx2* is the gene mutated in *bel* embryos, we used antisense thio-ester oligos (S-oligos) and a splice blocking morpholino (MOs) to reduce Lhx2 function in wild type embryos.

Injection of the MO or of a cocktail of three S-oligos (SO) led to reduced *dlx2* (Fig. 5A inset, Table I) and *sema3D* (Fig. 6D inset) expression in the ventral forebrain that was very similar to that seen in homozygous *bel* mutants. These results further support the idea that *bel* disrupts *lhx2* and suggest that these two *bel* alleles result in a loss of Lhx2 function. These antisense injections also led to subtle and variable axon defects, including POC defasciculation and RGC guidance errors at the midline (data not shown). Ipsilateral projections were not seen, suggesting antisense injections may not reduce Lhx2 function as completely as the *bel* mutations.

Expression of lhx2 and regulation by FGF signaling

To determine whether *lhx2* is expressed in regions disrupted by *bel(lhx2)* mutations, we analyzed the expression pattern of *lhx2* during zebrafish embryonic development. *lhx2* mRNA was first detectable at shield stage, with no maternal message detectable by RT-PCR at the 4 cell stage (data not shown). At tailbud stage (10 hpf), *lhx2* expression was seen in the anterior CNS corresponding to the forebrain including the eye fields (Fig. 3A, inset). By 23 hpf, *lhx2* was strongly expressed in the forebrain, including in the epiphysis (Fig. 3A). At 26 hpf, *lhx2* expression was seen in two bands in telencephalon, in the preoptic area and in the hypothalamus (Fig. 3B). In *bel(lhx2)* mutants *lhx2* expression was severely reduced in the preoptic area but was unaffected elsewhere in the embryo (Fig. 3B, inset). At 32 and 48 hpf, *lhx2* was also expressed in the tectum, midbrain-hindbrain boundary and was more discrete in the hindbrain (Fig. 3C-E). In the hindbrain, *lhx2* expression was seen in distinct cells at the rhombomere boundaries at 48 hpf (Fig. 3F). In the eyes, *lhx2* was initially expressed globally in the eye fields from 15 hpf (Fig. 3G) to 21 hpf (Fig. 3H) then became restricted to the amacrine cells in the inner nuclear layer by 32 hpf (Fig. 3I), and further restricted to ventral amacrine cells at 3 dpf (Fig. 3J). *lhx2* expression was also seen in entire fin buds at 26 hpf and this expression became restricted to the posterior half of the fin bud by 48 hpf (Fig. 3K,L).

Because of the timing of *lhx2* expression and the known role of Hedgehog (Hh) and Fibroblast growth factor (Fgf) signaling in regulating forebrain patterning, we next examined whether Fgf and/or Hh signaling regulate lhx2 expression. We first blocked all Fgf signaling using the small molecule SU5402 (Mohammadi et al., 1997), starting prior to the onset of *lhx2* expression (6 hpf). This SU5402 treatment nearly eliminated *lhx2* expression in the forebrain at 10 hpf, with expression remaining in only a few ventral cells (Fig. 4A,B). Treating embryos with SU5402 starting at 10 hpf led to a major reduction of *lhx2* expression at 24 hpf, showing a continued role for Fgf in the expression of *lhx2* (Fig. 4C,D). In contrast to these results, elimination of Hh signaling either in Shh pathway mutants or using the alkaloid Hh signal blocker CyA had little affect on *lhx2* expression (data not shown). These results show that Fgf signaling is required for both the onset and maintenance of *lhx2* gene expression.

zebrafish *lhx2* function is required cell autonomously for forebrain patterning

The identification of *bel* as a LHD forebrain transcription factor led us to look for forebrain patterning defects that might underlie the observed axon guidance defects, focusing on the regions where commissural and retinal axons cross the midline. The distal-less related transcription factor *dlx2* is expressed in the ventral telencephalon adjacent to the AC, and in the preoptic area of the diencephalon adjacent to the POC and chiasm prior to commissure formation (Fig. 5A) (Akimenko et al., 1994; Ellies et al., 1997). In *bel* mutants, *dlx2* expression is absent from the diencephalon in the preoptic area (Fig. 5B). The homeodomain transcription factor *nk2.1b* is also expressed in the anterior telencephalon and diencephalon (Fig. 5C) (Rohr et al., 2001). In *bel* mutants, *nk2.1b* expression is subtly disrupted in the preoptic area, with a small region adjacent to the optic recess ectopically expressing *nk2.1b* and a small region in lateral diencephalon adjacent to the tract of the POC lacking *nk2.1b* expression (Fig. 5D). In

the telencephalon, expression of *dlx2* is slightly reduced in the AC region (Fig. 5B), while expression of *nk2.1b* appears unaffected (Fig. 5D), indicating that *lhx2* is also required for ventral telencephalon formation. These forebrain patterning defects are apparent starting at 24 hpf, as POC axons are crossing the midline, suggesting that *bel(lhx2)* is required for patterning the neural growth substrate that provides guidance cues for retinal and commissural axons.

Mutations affecting the Hh and Fgf signaling pathways lead to forebrain patterning defects and axon guidance defects similar to those seen in *bel* mutants (Barresi et al., 2005; Culverwell and Karlstrom, 2002; Karlstrom et al., 1999; Karlstrom et al., 2003; Shanmugalingam et al., 2000; Tyurina et al., 2005; Walshe and Mason, 2003). Further, it was previously suggested that *bel* might mediate FGF and Hh signaling in the regulation of *vax* expression in the preoptic area (Take-uchi et al., 2003). To determine whether the forebrain defects seen in *bel* may be due to defects in Hh or Fgf signaling, we examined the expression of Hh and FGF signaling molecules or their downstream targets in *bel* mutants. *fgf8* expression is lost in the preoptic area of *bel* mutants (Fig. 5). In contrast, preoptic expression of the Hh target genes *ptc1* and *nk2.2* was unaffected in *bel* mutants (data not shown), suggesting loss of Lhx2 function does not affect Hh signaling in the POA. Thus *bel(lhx2)* might affect forebrain patterning and axon guidance at least partially via Fgf8 signaling.

We next examined optic stalk expression of *vax2, zic2.1* and *pax2.1*. As previously documented, we showed that *bel* mutants lack *vax2* expression only in preoptic area and medial optic stalk (data not shown, Take-uchi et al., 2003). *pax2.1* is expressed prior to *vax2* expression in the optic stalk and eye (Krauss et al., 1991). Similar to *vax2*, *pax2.1* was missing in *bel* mutants in the medial regions, but was unaffected in more lateral regions and the ventral retina (Fig. 5G,H). Another transcription factor involved in establishing retinal projections in mice is Zic2, acting both in the retina (Herrera et al., 2003) and ventral diencephalon (Williams et al., 2004). In zebrafish, *zic2.1* is expressed in the optic stalk but not in RGCs. Similar to *pax2.1*, *bel* mutants lack expression of *zic2.1* in the optic stalk (Fig. 5I,J).

Given the multiple roles for *lhx* genes in cell differentiation and axon guidance, we next wondered whether *lhx2* affected cell differentiation cell autonomously in the brain. When transplanted into a wild type forebrain, *bel* mutant cells were unable to correctly express *dlx2* (Fig. 5S,U). Conversely, wild type cells were able to express *dlx2* appropriately when transplanted into a *bel* mutant forebrain (Fig. 5R,T). These results indicate that *lhx2* function is cell-autonomously required for cell differentiation in the forebrain.

Reduced cell proliferation in *bel(lhx2)* mutants

Loss of *lhx2* function in mouse leads to a highly reduced cortex and reduced cell proliferation in the telencephalon (Porter et al., 1997). We therefore examined *bel* mutants to determine whether zebrafish *lhx2* similarly affects cell proliferation in the forebrain. Labeling mitotic cells with the anti-phosphohistone3 antibody revealed that *bel* mutants have regionally reduced cell proliferation in the ventral forebrain (Fig. 5K,L). In the diencephalon, *bel* mutants had less than half the number of proliferating cells when compared to the wild type siblings. However, in the telencephalon, there was no statistical difference in the number of proliferating cells (Fig. 5M). No differences were seen in cell death in the forebrain (data not shown). Thus defects in ventral forebrain patterning, including loss of *dlx2*, *vax2* and *pax2.1,* may at least partially result from the failure of precursor cells to proliferate in the preoptic area of the forebrain.

***bel(lhx2)* is required for the formation of forebrain glial bridges and for proper expression of axon guidance molecules**

Given the restricted forebrain patterning defects documented above and the lack of midline axon crossing in *bel(lhx2)* mutants, we wondered how *bel(lhx2)* affects the cellular substrate for commissural and retinal axon growth. GFAP expressing glial cells span the midline forming a glial bridge prior to commissure formation and may thus be the cellular substrate for midline growth of AC, POC and RGC axons (Barresi et al., 2005). At 21hpf, prior to axonogenesis in the forebrain, these midline glial cells are present but highly disorganized in *bel* mutants, spreading dorsally to fill the preoptic area (Fig. 6A,B). The disorganization of GFAP expressing cells was also observed at later ages and AC and POC axons appear to grow in association with the mis-placed glial cells (Fig. 6A,B insets).

To further link *bel* forebrain defects to the observed axon guidance defects, we analyzed the expression pattern of several axon guidance molecules that are expressed in the ventral forebrain near the AC, POC and/or chiasm. *Semaphorin3D* (*Sema3D)* is expressed at the midline of the diencephalon immediately ventral to the POC and chiasm (Fig. 4C, Halloran et al., 1998). In *bel* mutants, *sema3D* expression is absent in the diencephalon, while expression is unaffected in the midbrain (Fig. 6D). *netrin1a* is normally absent in the diencephalon where the POC and optic chiasm form (Fig. 6E) (Lauderdale et al., 1997). In *bel* mutants, *netrin1a* expression was unaffected in the telencephalon but was expanded across the optic recess into the preoptic area of the diencephalon (Fig. 6F). *Slit2* is normally expressed in domains that surround the optic nerve, tract, and POC (Erskine et al., 2000; Nguyen-Ba-Charvet and Chedotal, 2002; Plump et al., 2002; Rasband et al., 2003; Richards, 2002). In *bel* mutants, *slit2* expression is expanded in the region where RGC axons across the ventral midline (Fig. 6G,H). While Ephrin and Eph receptors are known to influence ipsilateral retinal axon growth (Nakagawa et al., 2000; Williams et al., 2003) their role in guiding axons toward or across the midline is not known. In *bel* mutants EphB2 expression was reduced in parts of the diencephalon, but was largely unaffected in the chiasm region. (Fig. 6I,J). Similarly, *EphB3*, *ephrinA4* and *sdf-1A, and sdf-1B* expression appeared normal at the midline (data not shown).

In summary, *sema3D* expression is reduced in the chiasm region in *bel* mutants. In contrast, *netrin1a* and *slit2* expression is expanded across the commissure region where axons fail to cross the midline in *bel* mutants. Several other guidance molecules were not mis-expressed in *bel* mutants, indicating that *bel(lhx2)* affects only some but not all axon guidance molecules in the forebrain.

***bel(lhx2)* is required for eye development**

belladonna mutants have a 'dilated pupil' phenotype at 5 dpf (Karlstrom et al., 1996) and thus they were named after the plant whose extract causes pupil dilation in humans (Duncan and Collison, 2003; Feinsod, 2000). To understand the eye defects in *bel* mutants we sectioned 5 dpf wild type and mutant eyes. This analysis showed that the pigmented epithelium (PE) fails to contact the lens in mutants, leaving a gap between PE and the lens (Fig. 7A,B). *bel* mutant eyes are also shorter in the dorsal-ventral axis and wider in the medial-lateral axis than wild type eyes; the ratio of eye width (medial-lateral axis) to eye height (dorsal-ventral axis) is 15% greater in *bel* mutants than in wild types. Finally, in nearly all *bel* eyes we observed an acellular aggregate near a normal looking lens that was labeled with the lens protein specific Zl-1 antibody (Fig. 7A,B insets).

While all cell layers appear to be present in *bel* mutant eyes, labeling with the *apoE* (Babin et al., 1997) revealed that amacrine cells are mostly absent with only a few cells remaining in the ventral retina (Fig. 7C,D). Labeling of Müller glial cells showed that these cells are disorganized (data not shown). These subtle eye morphogenesis defects become more severe in those *bel* mutants that survived into adulthood. *bel* mutant eyes are much smaller than in wild type, with highly disorganized retinal layers

athat appear to fold over on themselves, most likely due to the failure of fluid filled posterior compartment to form (Fig. 7E,F). In some adults, vascularized retinal tissue protrudes from the eye adjacent to the lens (Fig. 7F, left inset).

Discussion

We have identified a zebrafish lim-homeodomain protein that appears to be orthologous to Lhx2 based both on sequence similarity and embryonic expression pattern (Bachy et al., 2001; Nohno et al., 1997). Our analyses show that *lhx2* is disrupted in *bel* mutants and that two *bel* alleles encode severely truncated Lhx2 proteins that lack the highly conserved homeodomain. Both alleles appear to be loss of function based on two criteria; first, neither allele appears to have any dominant activity, and second *bel* forebrain patterning defects are similar to those seen following MO or S-oligo induced loss of Lhx2 function. Analysis of the *bel* phenotype reveals that zebrafish Lhx2 function is required for proper patterning of the anterior forebrain and eye, and for proper expression of a several axon guidance molecules in the preoptic area of the diencephalon. Coincident with these localized gene expression defects, retinal axons fail to cross the midline and instead project ipsilaterally and forebrain commissural neurons fail to cross the midline.

Lhx2 and neural patterning

Our analysis shows that, similar to mouse, Lhx2 is required for both proper gene expression and for cell proliferation in the forebrain (Fig. 5). *fgf8*, one of the genes down-regulated in the forebrain of *bel* mutants, is known to regulate cell proliferation (Xu et al., 1993). Thus, reduced *fgf8* signaling may account for reduced proliferation in *bel* (Fig.5 K,L). However, since the loss of the optic stalk marker *pax2.1* occurs prior to the loss of *fgf8* expression in this region (data not shown), it appears that cell differentiation defects may precede these cell proliferation defects. Further, while it is possible that regional reductions in cell proliferation could account for the observed losses in forebrain gene expression (Fig. 5), we show that the ventral telencephalic markers *nk2.1b* and *netrin1* are expanded into the preoptic area of the diencephalon. Thus, *lhx2* may directly regulate cell specification and regional identity. This is consistent with the model for Lhx2 function in the mouse cortex, in which Lhx2 is initially thought to function in the specification of cortical cells as distinct from the cortical hem and later is required for proliferation of cortical precursors (Bulchand et al., 2001). Whether *lhx2* and other forebrain patterning genes regulate neural patterning primarily by affecting precursor cell differentiation or by selectively regulating precursor proliferation, or both, is an important issue that remains to be determined.

In the spinal cord, combinatorial expression of LHD and Lim Domain Binding (LDB) proteins generates a 'LIM code' that determines motor neuron identity (Allan and Thor, 2003; Bach, 2000 ; Gill, 2003; Lumsden, 1995; Sockanathan, 2003). Similarly, overlapping expression of a large number of LHD and lim domain only (LMO) genes in the forebrain helps define prosomeric boundaries (Rubenstein and Beachy, 1998) and combinatorial Lhx function may control the specification of post mitotic thalamic neurons as well as thalamocortical axon projections (Nakagawa and O'Leary, 2001). Overlapping expression may also result in overlapping functionality. In fact, although zebrafish *lhx2* is expressed in the midbrain, hindbrain, epiphysis and fin buds, we did not observe any early developmental defects in these structures. This is similar to the situation in mice, where it has been speculated that the highly related LHD gene *lhx9* may compensate for the loss of *lhx2* function in tissues that express both genes (Bachy et al., 2001; Retaux et al., 1999). Consistent with this idea, our search of the zebrafish genome sequence database uncovered a zebrafish expressed sequence tag (EST) on chromosome 22 that is highly similar to *lhx9* (Fig. 2) and may compensate for loss of *lhx2* function in regions of overlapping expression.

Lhx2 and diencephalon development

We show that the optic stalk and preoptic area of the diencephalon are major targets of Lhx2 function in zebrafish. Expression of several patterning and axon guidance molecules is disrupted in this region (Figs. 5,6), glial cells are disorganized (Fig. 6), and commissural and retinal axons are unable to cross the midline (Fig. 1). *lhx2* is expressed throughout this region in all vertebrates examined, including mice (Bachy et al., 2001; Nohno et al., 1997), but no gene expression or axon guidance defects have yet been reported in *lhx2* mutant mice (Bulchand et al., 2003; Vyas et al., 2003). While development of the anterior diencephalon and optic stalk have not yet been explicitly described in mouse *lhx2* mutants, published reports show disrupted *dlx2* expression in more posterior regions of the diencephalon (Vyas et al., 2003), suggesting *lhx2* function is likely to be conserved in this region.

Some aspects of zebrafish Hh (Culverwell and Karlstrom, 2002) and Fgf (Shanmugalingam et al., 2000) pathway mutant phenotypes resemble those seen in *bel* mutants. Further, previous studies suggested that *bel* might act downstream of Hh and in parallel to Fgf signaling (Take-uchi et al., 2003). We thus examined whether *lhx2* is regulated by, or regulates, Fgf and Hh signaling in the diencephalon. *lhx2* expression is largely unaffected in *yot* and *dtr* mutations that block Hh signaling (Karlstrom et al., 2003), and *bel* mutants have normal expression of the Hh regulated genes *nk2.2* and *ptc1* (data not shown). This indicates that *lhx2* is not regulated by Hh and strongly suggests that defects seen in *bel* mutants are not due to defects in Hh signaling. In contrast, we show that Fgf signaling is required for both the induction and maintenance of *lhx2* expression.

Lhx2 and telencephalon development

Lhx2 function is best studied in the mammalian cortex, where loss of *lhx2* function leads to a general reduction in the dorsal telencephalon (neocortex or pallium) but not more medial and ventral telencephalic structures (paleocortex or subpallium) (Vyas et al., 2003). Loss of cortical tissue in mouse *lhx2* mutants was originally attributed to a general reduction in telencephalic cell proliferation (Porter et al., 1997). More recent work showed that the cortical hem is expanded at the expense of cortex in *lhx2* mutant mice, suggesting that Lhx2 may also pattern the cortex through selectively influencing precursor cell proliferation (Bulchand et al., 2003). It was also suggested that Lhx2 influences cell fate decisions at later times (Porter et al., 1997). In zebrafish, loss of Lhx2 function subtly disrupts ventral telencephalon patterning but does not grossly affect the telencephalon. However, since teleosts lack a cortex, this difference likely reflects the structural differences between species.

More ventrally, our analysis of *bel* mutants revealed a slight reduction in *dlx2* expression in the subpallium (Fig. 5) that precedes the failure of AC axons to cross this region of the forebrain (Fig. 1). This suggests that patterning defects may underlie axon guidance defects in the telencephalon, and shows that Lhx2 is required for normal development of this tissue. In mouse, this region includes the medial and lateral ganglionic eminences (MGE and LGE) that are just ventral to the pallium/subpallium border (PSB). Similar to *bel(lhx2)* mutants, *dlx2* expression appears subtly disrupted in the MGE and LGE of mouse *lhx2* mutants (Vyas et al., 2003), although this phenotype has not been described in detail. A more detailed analysis of ventral forebrain development in *lhx2* mutant mice may thus reveal a conserved role for Lhx2 in neural patterning in this region.

Lhx2 and eye development

Lhx2 is one of the six known eye field transcription factors (EFTFs) that establish the presumptive eye field and can induce ectopic eyes in Xenopus (Zuber et al., 2003). Mice lacking *lhx2* completely lack eyes at birth (Porter et al., 1997). However, this phenotype does not represent a complete loss of eye development, as *pax6* expressing optic vesicles are formed in these embryos. Eye

development arrests before the optic cup forms, at which time the defective eye tissue is reabsorbed (Porter et al., 1997). In contrast *bel* mutants have relatively well developed, functional eyes (Karlstrom et al., 1996; Rick et al., 2000) (Fig. 7). While this seemingly large phenotypic difference may represent a divergence in Lhx2 function between species, it is more likely explained by the fact that zebrafish embryos do not reabsorb defective tissue, as is the case for mouse embryos.

Our analysis of *bel* mutants has thus allowed us to identify new roles for *lhx2* in vertebrate eye development. While most cell layers form normally in *bel(lhx2)* mutants, amacrine cells are extremely reduced (Fig. 7D). The most obvious defect in *bel* mutant adults is the small size of the eye and disorganization of the retinal layers (Fig. 7). In teleosts, the eye grows throughout life, with new cells being added at the ciliary marginal zone (CMZ). We did not observe major cell proliferation defects in the eye using the phospo-histone antibody (data not shown) and at 5 dpf *bel* mutant eyes are normal in size (Fig. 7), suggesting the small size of *bel* eyes at later ages is not due to proliferation defects but is due to the failure of the posterior compartment to form. The posterior compartment is filled with vitreous humor, which is produced by cells of the CMZ (reviewed in Bishop et al., 2002). CMZ cells appear to differentiate appropriately based on *α-collagen* expression in *bel* mutants (data not shown), however this region of the eye is clearly disrupted as evidenced by the gap between the PE and the lens and the presence of ectopic lens proteins (Fig. 7B). Thus, failure of the posterior chamber to form in *bel* may result from defects in CMZ cell function, and/or from defects in formation of a barrier to contain the vitreous humor in the eye.

Lhx2 and forebrain axon guidance

Despite the fact that numerous guidance systems are affected by mutations in *bel*, the observed axon guidance defects are remarkably specific. Axon defects are limited to the midline, with retinal axon pathways forming normally on the ipsilateral side of the brain. This indicates that dorsal guidance systems are unaffected by defects in midline axon crossing and is in contrast to other mutations affecting single axon guidance systems in the forebrain. In mutants affecting only Robo/Slit mediated repulsion, defects in axon crossing are accompanied by axon wandering in the rostral/caudal axis and formation of ectopic chiasm (Plump et al., 2002; Richards, 2002). Loss of Netrin results in lack of the hippocampal commissure, the corpus callosum and the anterior commissure in the forebrain (Mitchell et al., 1996). Similarly, mice with disrupted ephrin function show a wide range of defects including guidance errors, incorrect mapping in the tectum or lateral geniculate nucleus, and defasciculation (O'Leary and McLaughlin, 2005).

Despite extensive work on LHD proteins and forebrain patterning, little is known about how LHD mediated forebrain specification affects neural connectivity. LHD transcription factors have been shown to regulate the expression of the axon guidance molecule receptor EphA in motoneurons, thus directly affecting the response to the guidance molecule EphrinA (Kania and Jessell, 2003). While it is possible that cell fate changes or changes in guidance receptors in commissural and retinal neurons could account for the lack of midline crossing in *bel(lhx2)* mutants, RGCs appear to be specified correctly in *bel* mutants and can form functional projections on the incorrect tectal lobe (Rick et al., 2000) (Fig. 1). Combined with the observed gene expression defects in the preoptic area, this strongly suggests that forebrain patterning defects underlie the observed axon defects in *bel(lhx2)* mutants.

The midline defects seen in *bel* mutants are in fact surprisingly similar to those seen in the hedgehog pathway mutant *you-too (yot)* (Barresi et al., 2005). Both mutants have similar defects in midline-spanning glial bridges that provide the cellular substrate for commissural and retinal axons (Barresi et al., 2005). In addition, *slit* guidance molecule expression is expanded across the commissure

regions in both *yot* and *bel* mutants. Slit2 and Slit3 have been shown to directly influence the position of the forebrain commissures (Barresi et al., 2005) and the optic chiasm (Rasband et al., 2003) by a surround/repulsion mechanism. Expanded *slit* expression appears to be the major cause of axon defects in *yot*, as reducing Slit function in *yot* mutants largely rescues commissure formation (Barresi et al., 2005). Since Slit repulsion also helps position the glial bridges (Barresi et al., 2005), the expansion of *slit* genes across the midline in *bel* mutants could affect midline crossing by disrupting the cellular substrate for axon growth and/or by directly repelling midline crossing axons. Finally, mis-expression of the axon guidance genes *sema3D* and *netrin-1* in *bel* mutants may also contribute to the observed axon guidance defects. Further analysis of the causes of axon guidance defects in *bel* thus promises to shed light on the relative importance of multiple guidance systems in the vertebrate forebrain.

Table I. Phenocopy of *bel* forebrain defects following *lhx2* anti-sense oligonucleotide injections. *dlx2* expression was assayed in embryos injected with either a cocktail of three *lhx2* S-oligos or a *lhx2* splice-blocking MO.

Antisense oligo injection	*dlx2* reduced* in POA (%)	wild type *dlx2*	# embryos
lhx2 S-oligo cocktail (4.5 pg total)	100 (91%)	10	110
lhx2 S-oligo cocktail (3 pg total)	12 (44%)	15	27
lhx2 MO (15 ng)	81 (86%)	5	86
lhx2 MO (8 ng)	13 (61%)	16	29
control MO	0 (0%)	11	11
uninjected	0 (0%)	70	70

*; similar to *bel* mutants, POA; preoptic area of the diencephalon.

Acknowledgements

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Figure Legends

Figure 1: Retinal and commissural axon defects in *bel*. (A) Schematic showing that all retinal axons cross the wild type midline (arrowhead) and project topographically on the contralateral tectal lobe (anterior/dorsal retina (green) to posterior/ventral tectum, posterior/ventral retina (red) to anterior/dorsal tectum). (B) In *bel* mutants retinal axons fail to cross the midline (arrowhead) and instead project to the ipsilateral tectal lobe in a topographically correct manner (see Karlstrom et al., 1996). (C) At 36 hpf, wild type RGC axons have reached the midline (arrowhead). (D) In most *bel* mutants, RGC axons have grown towards the midline (arrowhead) but in some mutants axons project ipsilaterally immediately after leaving the eye (inset, arrowheads). (E) At 38 hpf, wild type RGC axons have crossed the midline (arrowhead). (F) In *bel* mutants, all RGCs project ipsilaterally at 38 hpf. (G) Both the AC (arrow) and POC (arrowhead) are fully formed in wild type embryo by 28 hpf. (H) In *bel* mutants, both forebrain commissures fail to form. (A, B) Schematic dorsal views of the head, anterior left (adapted from Culverwell and Karlstrom, 2002). (C-H) Ventral views of the forebrain, eyes on either side of each panel, anterior up.

Figure 2: *bel* mutations disrupt zebrafish *lhx2*. (A) Map of the *bel* genetic region on chromosome 8. The number of recombinants for each marker is shown. BAC clones linked to *bel* are shown below the line. (B) Sequence comparison of Lhx2 protein sequence from zebrafish, chick, and mouse. Underlined sequence represents the two Lim domains; boxed sequence is the conserved homeobox domain. (C) Cladogram showing sequence divergence of Lhx2 and the closely related family member (Lhx9, genbank #NM001017710) in zebrafish, chick and mouse. (D) Sequence defects lead to premature stop codons in both *bel* alleles. In bel^{tv42} a transversion (C to A) introduces a premature stop codon at position 243. In bel^{b700} a 22bp deletion starting at position 664 (underlined in wild type sequence) leads to a frame-shift and introduces a premature stop codon following 4 novel amino acids. (E) Schematic of the Lhx2 protein showing LIM domains (green), the homeobox domain (blue), intron/exon borders (black lines), and the position of premature stop codons encoded by the two *bel* alleles.

Figure 3: Embryonic expression of zebrafish *lhx2*. (A) At 23 hpf, *lhx2* is expressed in most of the telencephalon, anterior diencephalon and in the epiphysis. Inset shows *lhx2* expression in the anterior CNS at the tailbud stage (arrowhead). (B) At 26 hpf, *lhx2* is regionally expressed in the telencephalon and diencephalon and epiphysis. Inset shows reduced *lhx2* expression only in the dorsal/anterior diencephalon in a *bel* mutant (arrowhead). (C,D) *lhx2* continues to be regionally expressed in the forebrain, midbrain, and hindbrain at 32 and 48 hpf. By 48 h, *lhx2* expression is reduced at the chiasm region and also in the telencephalon. (E) Lateral view shows *lhx2* expression in the midbrain/hindbrain border and hindbrain at 32 hrs (arrowheads). (F) Dorsal view shows *lhx2* expression at rhombomere boundaries (arrowheads) at 48 hpf. (G) *lhx2* expression throughout the eye field (arrowhead) at 15hpf. Initial expression in the eye field is low relative to that in the forebrain. (H) At 21 hpf *lhx2* is expressed throughout the optic vesicle with higher levels of expression in the dorso-nasal region (arrowhead). (I) At 32 hpf and 48 hpf (inset), *lhx2* is expressed in the marginal zones (arrowheads) and in the amacrine cell layer (arrow) of the eye. (I) By 3 dpf, expression in the amacrine layer becomes restricted ventrally (arrow). (K,L) *lhx2* is expressed in most of the fin bud at 26 hpf and becomes restricted to the posterior bud at 48 hpf (arrowheads). (A-E) lateral views, anterior to the left. (F,G,J and K) dorsal views. (H,I) 7μm sections of the eye. Black dots mark the position of the optic recess. e: epiphysis, di: diencephalon, hb: hindbrain, mb: midbrain, mhb: midbrain-hindbrain boundary, t: telencephalon.

Figure 4: Regulation of *lhx2* expression. (A,B) Wild type embryos were treated with SU5402 (B) or DMSO carrier (A) from 6 hpf to 10 hpf and labeled to show *lhx2* expression. Blocking Fgf signaling during the onset of *lhx2* expression nearly eliminated *lhx2* expression in the embryo (B, arrowhead).

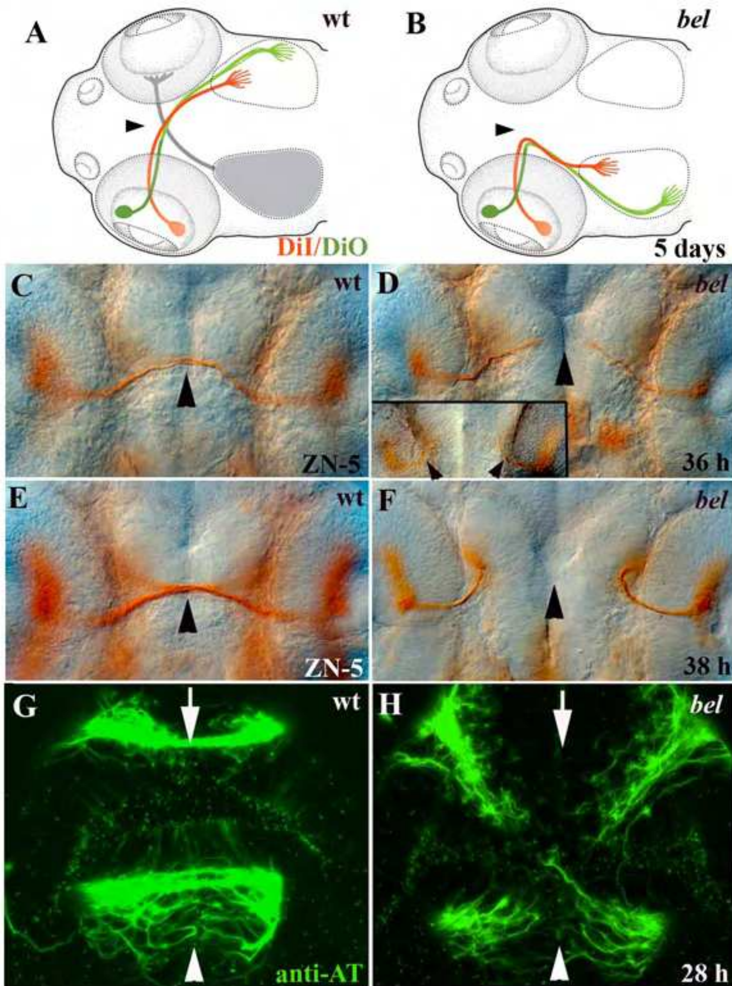
Insets show complete loss of the Fgf regulated gene *erm* in the forebrain and hindbrain of identically treated embryos (arrows). (C,D) Treating embryos with SU5402 from 10 hpf to 24 hpf reduced *lhx2* expression in the telencephalon (arrowheads) and diencephalon (arrow). All panels show lateral views of the head, anterior to the left. Eyes were removed in C and D.

Figure 5: Forebrain patterning defects in *bel* mutants. (A,B) In *bel* mutants, *dlx2* expression is extremely reduced in anterior/dorsal diencephalon (arrows) and is slightly reduced in the telencephalon (brackets). Inset shows similar loss of *dlx2* expression in the anterior diencephalon after injection of *lhx2* anti-sense MO into a wild type embryo. (C,D) In *bel* mutants, *nk2.1b* expression is regionally disrupted in the diencephalon (arrows) and expanded at a small region at the optic recess (arrowhead). (E,F) *fgf8* expression is extremely reduced in the optic stalk region (arrowheads). Insets show anterior views of the head, with *fgf8* expression absent at the midline (arrowheads) in *bel*. (G,H) In *bel* mutants, *pax2.1* expression is absent in the medial optic stalk (arrowheads) but remains laterally. (I,J) *zic2.1* expression is similarly absent across the midline (arrowheads). (K,L) The number of phospho-histone labeled mitotic cells is reduced in the dorsal/anterior diencephalon of *bel* mutant (brackets). (M) Graph showing a significant reduction in the number of proliferating cells in the mutant diencephalon (asterisk, $p< 0.01$). (N,O) Anterior views showing the loss of *dlx2* expression in the anterior diencephalon of *bel* mutants (arrows, compare to lateral views in A,B). (P-U) Fluorescein dextran labeled cells (red/brown) were transplanted between wild type and *bel* mutant embryos. (P, R,T) Transplanted wild type cells express *dlx2* (blue) in a wild type (P) and *bel* mutant (R,T) background (7 embryos). (Q) Transplanted *bel* mutant cells do not express *dlx2* in the ventral midline in *bel* mutants. (S,U) In a wild type background (19 embryos), *bel* mutant cell clones do not express *dlx2,* but populate the midline and are intermingled with wild type cell clones. (T, U) Higher magnification of transplanted cells in the diencephalon. (T) *dlx2* transcripts (blue) and lineage tracer (red) are present in wild type cells (purple arrowheads) in a *bel* mutant forebrain. (U) In contrast, alternating blue (*dlx2* positive wild type) and red (lineage tracer containing *dlx2* negative; *bel* mutant) cells occupy the ventral midline in a wild type background (red and blue arrowheads). (A-F,K,L) lateral views of the forebrain, anterior left, eyes removed, (G-J) Ventral views of the forebrain, anterior up, N-U) anterior views of the forebrain, dorsal up. (T,U) Black dots mark the position of the optic recess. Scale bar: 15 μm.

Figure 6: The axon growth substrate is disrupted in *bel* mutants. (A,B) Confocal images of ventral views of 21 hpf embryos labeled with anti-GFAP antibody, white line marks the optic recess. (A) GFAP expressing glial cells span the midline in the position of the AC (arrow) and POC (arrowhead). (B) In *bel* mutants, these glial bridges are disorganized and glial cell bodies are present between the commissures (arrows). Insets show similar disorganization of glial cells in the mutant at 28 hpf in embryos double labeled for axons (anti-AT, green) and glial cells (anti-GFAP, red). (C,D) *sema3D* is absent in the forebrain the *bel* mutants (arrowhead). Upper insets show ventral views. Lower insets show similar loss of *sema3D* expression in the anterior diencephalon after injection of *lhx2* anti-sense MO into a wild type embryo. (E,F) *netrin1a* expression is expanded ventrally into the diencephalon in *bel* mutants (arrowhead). (G,H) Expression of *slit2* in *bel* mutants is expanded across the chiasm region (arrows). Insets show ventral views, anterior up. (I,J) *EphB2* expression is reduced in the diencephalon and hypothalamus (arrows), but appears normal in the chiasm region (arrowheads). (K-N) Schematic lateral (K,L) and ventral (M,N) views showing expression of a subset of the genes described in this and the previous figure. AC; anterior commissure, OR; optic recess, POC; post optic commissure, black dots mark the position of the optic recess.

Figure 7: Larval and adult eye defects in *bel* mutants. (A,B) Toluidine blue stained sections from 5 dpf wild type and *bel* mutants. In *bel* mutants there is a gap between the PE and lens (arrows) and an

abnormal acellular mass is often present (arrowhead). Inset: In a different embryo, an acellular aggregate was labeled with the ZL-1 antibody, indicating it contains lens proteins (arrowhead). (C,D) At 4 dpf *bel* mutants lack most amacrine cells as determined by *apoE* in situ labeling (arrowhead). A few cells remain in the ventral retina. (E,F) Eyes of surviving *bel* adults are much smaller than wild type due to the lack of a posterior compartment (asterisk). Retinal layers are folded back on one another (arrowhead). Insets show lateral views of whole eyes. (E, left inset) In some adults, vascularized retinal tissue extends out of the eye. L; lens, pe; pigmented epithelium.



Seth et al., Figure 1

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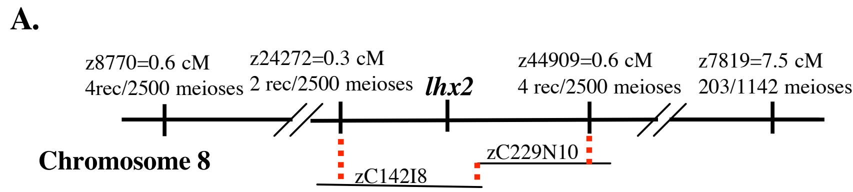

B.

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zfLhx2   1:MLFHGLPGGEMHGVMEEMERRGKSDSATISSAIDMGETETN-MPSISGDRVALCAGCGGK
ChLh-2a 1:....S.S.S.....ID..D..T.TEA.A......R.....QT.....S..A.........
Mu Lhx2 1:....S.S.P.V...ID..D..A..EAPA......R.D...-T.....S..A.........

zfLhx2    :ISDRYYLLAVDKQWHMRCLKCCECKLNLESELTCFSKDGSIYCKEDYYRRFSVQRCARCH
ChLhx2a   :............................................................
Mu Lhx2   :............................................................

zfLhx2    :LGISASEMVMRARDLVYHLNCFTCTTCNKMLTTGDHFGMKDSLVYCRLHFETLIQGDFPT
ChLh-2a   :.........................................N..............EYQV
Mu Lhx2   :...................................................A.L..EY.A

zfLhx2    :HFNHTDV-------APNK--GLS--STGPLGLSYYNGVNTVQKGRPRKRKSPGPGADLAA
ChLh-2a   :....S..-------.AG.GPA.GAG.ANT...P.....G.....................
Mu Lhx2   :....A..AAAAAAA.AA.SA..GSAGAN....P.....G.....................

zfLhx2    :YNAALSCNENDGDPMDRDSQYSSSQKTKRMRTSFKHHQLRTMKSYFAINHNPDAKDLKQL
ChLhx-a   :.............HL...Q..P.N....................................
Mu Lhx2   :...........AEHL...QP.P......................................

zfLhx2    :AQKTGLTKRVLQVWFQNARAKFRRNLLRQENTGVDKASDGSNLAGGTPSGPASEISNASM
ChLh-2a   :....................................T..-.T.QA...............
Mu Lhx2   :....................................T..-AT.QT.........L....L

zfLhx2    :SPSSTPTTLTDLTNPTMPTVTSVLTSVPGSLDVHECRSPSQSTLTSLF 396
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Mu Lhx2   :.............S..L............N.EG..PH....T...N.. 406
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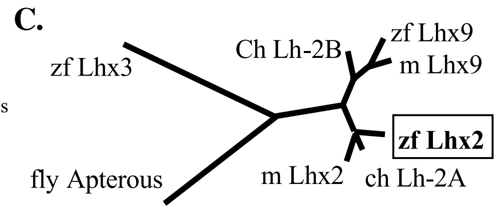
C.



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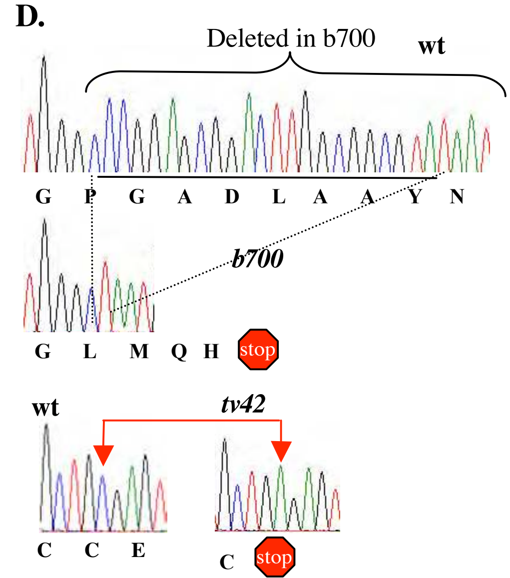

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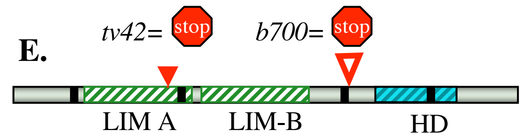

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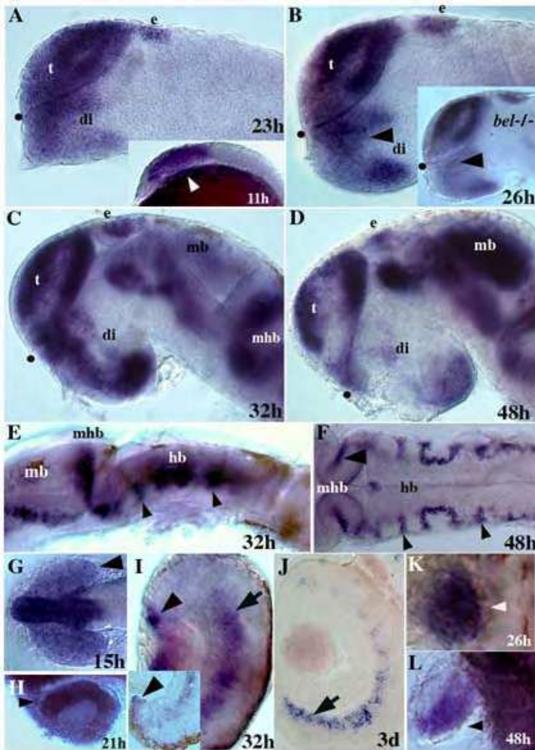

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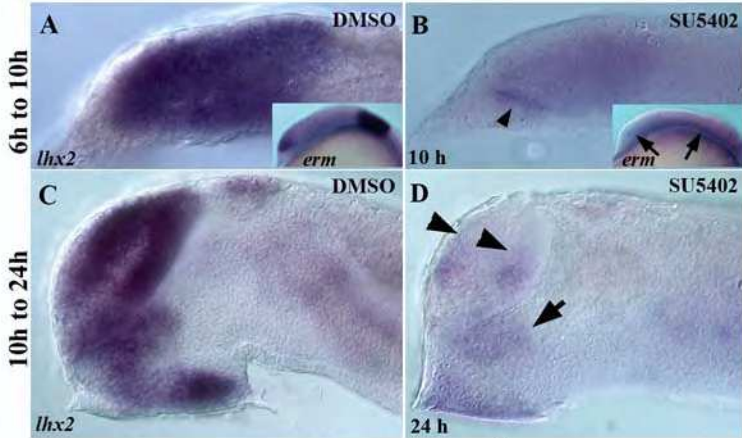

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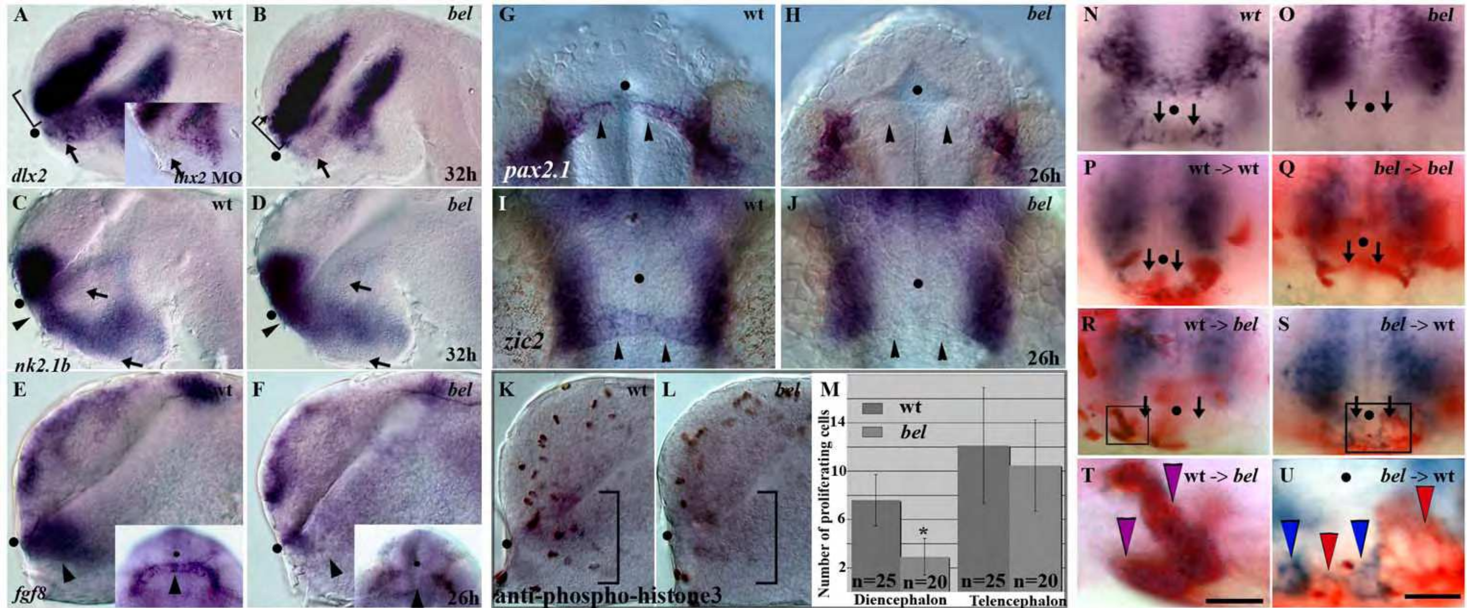

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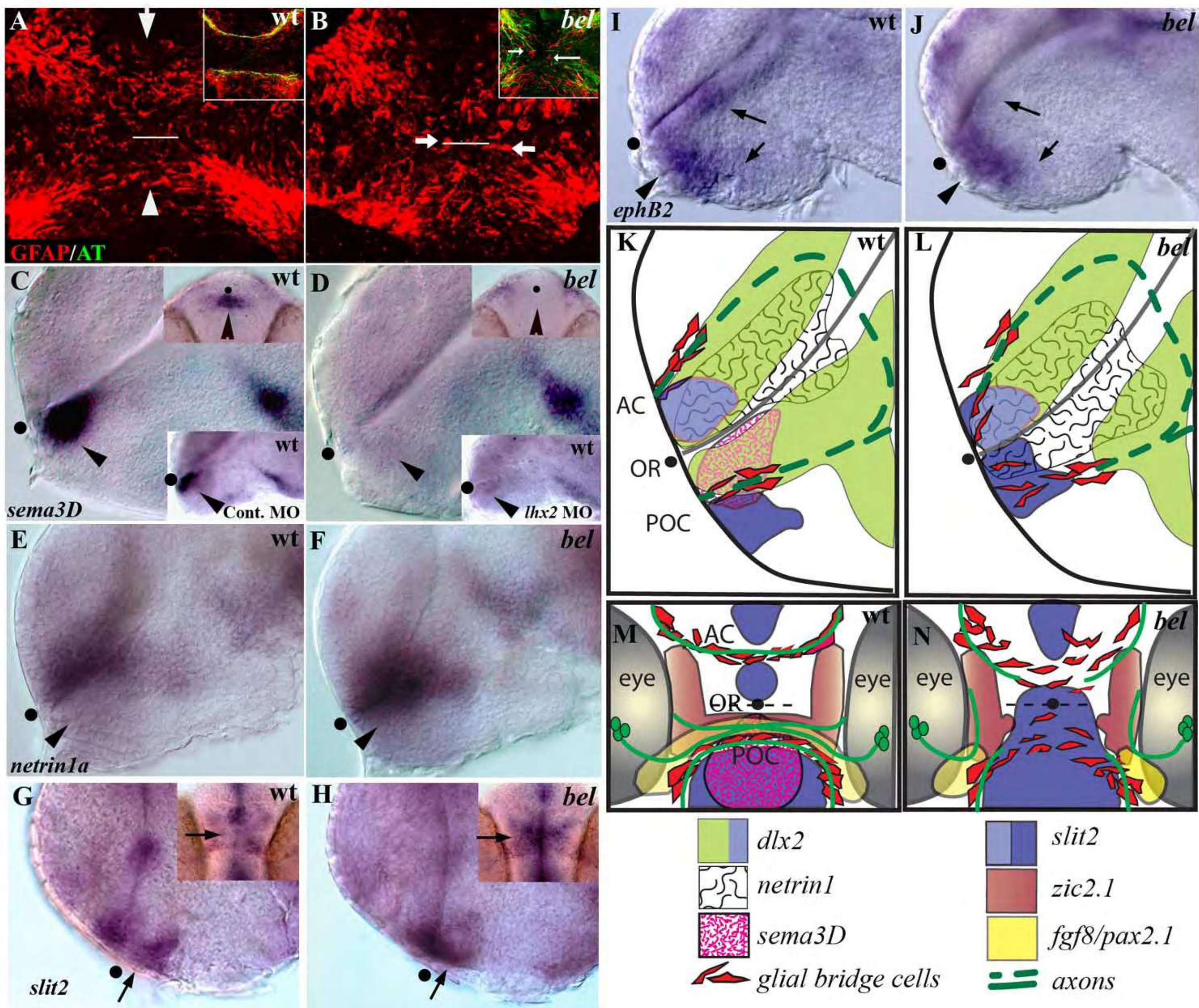

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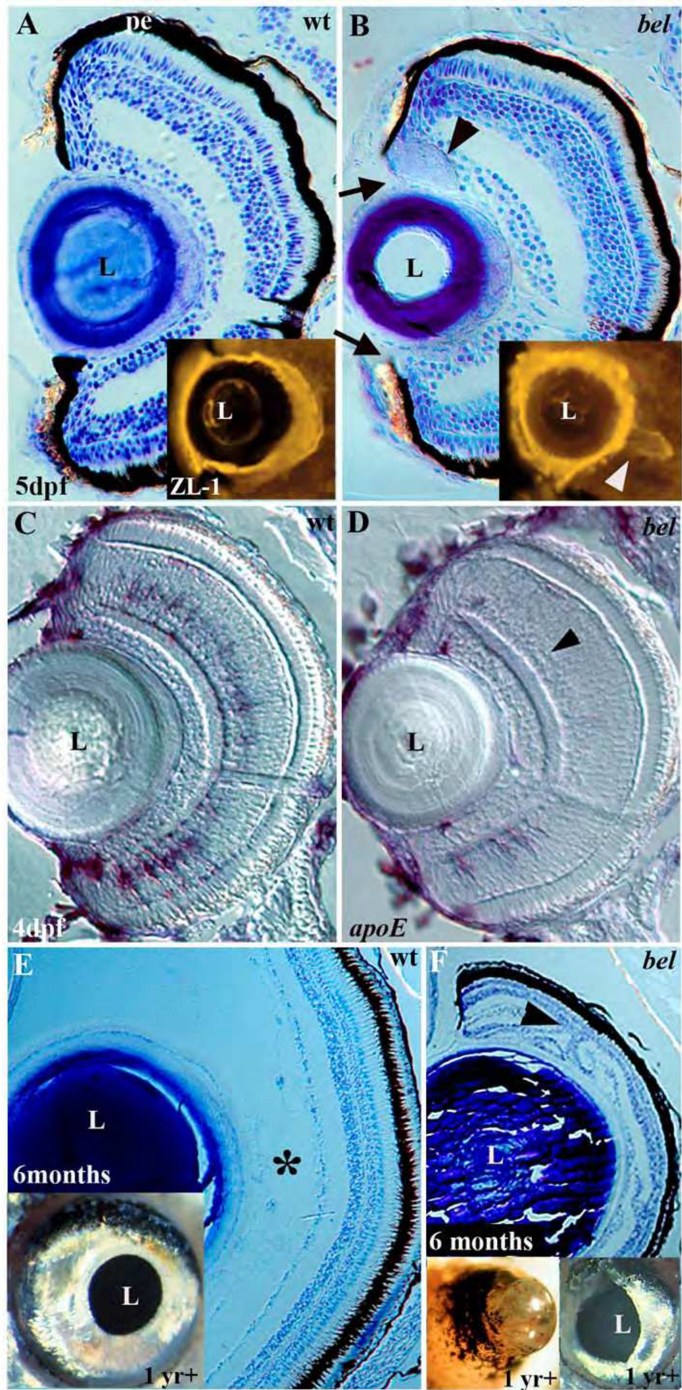

Seth et al, Figure 7

Literature Cited

Akimenko, M. A., Ekker, M., Wegner, J., Lin, W. and Westerfield, M. (1994). Combinatorial expression of three zebrafish genes related to distal-less: part of a homeobox gene code for the head. *J Neurosci* **14**, 3475-86.
Allan, D. W. and Thor, S. (2003). Together at last: bHLH and LIM-HD regulators cooperate to specify motor neurons. *Neuron* **38**, 675-7.
Apkarian, P. and Bour, L. J. (2001). See-saw nystagmus and congenital nystagmus identified in the non-decussating retinal-fugal fiber syndrome. *Strabismus* **9**, 143-63.
Babin, P. J., Thisse, C., Durliat, M., Andre, M., Akimenko, M. A. and Thisse, B. (1997). Both apolipoprotein E and A-I genes are present in a nonmammalian vertebrate and are highly expressed during embryonic development. *Proc Natl Acad Sci U S A* **94**, 8622-7.
Bach, I. (2000). The LIM domain: regulation by association. *Mech Dev* **91**, 5-17.
Bachy, I., Vernier, P. and Retaux, S. (2001). The LIM-homeodomain gene family in the developing Xenopus brain: conservation and divergences with the mouse related to the evolution of the forebrain. *J Neurosci* **21**, 7620-9.
Bak, M. and Fraser, S. E. (2003). Axon fasciculation and differences in midline kinetics between pioneer and follower axons within commissural fascicles. *Development* **130**, 4999-5008.
Barresi, M. J., Hutson, L. D., Chien, C. B. and Karlstrom, R. O. (2005). Hedgehog regulated Slit expression determines commissure and glial cell position in the zebrafish forebrain. *Development* **132**, 3643-56.
Barth, K. A. and Wilson, S. W. (1995). Expression of zebrafish nk2.2 is influenced by sonic hedgehog vertebrate hedgehog-1 and demarcates a zone of neuronal differentiation in the embryonic forebrain. *Development* **121**, 1755-1768.
Bishop, P. N., Takanosu, M., Le Goff, M. and Mayne, R. (2002). The role of the posterior ciliary body in the biosynthesis of vitreous humour. *Eye* **16**, 454-60.
Brose, K., Bland, K. S., Wang, K. H., Arnott, D., Henzel, W., Goodman, C. S., Tessier-Lavigne, M. and Kidd, T. (1999). Slit proteins bind Robo receptors and have an evolutionarily conserved role in repulsive axon guidance. *Cell* **96**, 795-806.
Bulchand, S., Grove, E. A., Porter, F. D. and Tole, S. (2001). LIM-homeodomain gene Lhx2 regulates the formation of the cortical hem. *Mech Dev* **100**, 165-75.
Bulchand, S., Subramanian, L. and Tole, S. (2003). Dynamic spatiotemporal expression of LIM genes and cofactors in the embryonic and postnatal cerebral cortex. *Dev Dyn* **226**, 460-9.
Burrill, J. D. and Easter, S. S. J. (1995). The first retinal axons and their micro-environment in zebrafish: cryptic pioneers and the pretract. **15**, 2935-2947.
Chitnis, A. B. and Kuwada, J. Y. (1990). Axonogenesis in the brain of zebrafish embryos. **10**, 1892-1905.
Chotard, C. and Salecker, I. (2004). Neurons and glia: team players in axon guidance. *Trends Neurosci* **27**, 655-61.
Culverwell, J. and Karlstrom, R. O. (2002). Making the connection: retinal axon guidance in the zebrafish. *Semin Cell Dev Biol* **13**, 497-506.
Devoto, S. H., Melancon, E., Eisen, J. S. and Westerfield, M. (1996). Identification of separate slow and fast muscle precursor cells in vivo, prior to somite formation. *Development* **122**, 3371-80.
Dickson, B. J. (2002). Molecular mechanisms of axon guidance. *Science* **298**, 1959-64.
Dodd, J., Morton, S. B., Karagogeos, D., Yamamoto, M. and Jessell, T. M. (1988). Spatial regulation of axonal glycoprotein expression on subsets of embryonic spinal neurons. **1**, 105-116.

Duncan, G. and Collison, D. J. (2003). Role of the non-neuronal cholinergic system in the eye: a review. *Life Sci* **72**, 2013-9.
Ellies, D. L., Stock, D. W., Hatch, G., Giroux, G., Weiss, K. M. and Ekker, M. (1997). Relationship between the genomic organization and the overlapping embryonic expression patterns of the zebrafish dlx genes. *Genomics* **45**, 580-90.
Erskine, L., Williams, S. E., Brose, K., Kidd, T., Rachel, R. A., Goodman, C. S., Tessier-Labinge, M. and Mason, C. A. (2000). Retinal ganglion cell axon guidance in the mouse optic chiasm: expression and function of robos and slits. *Journal of Neuroscience* **20**, 4975-4982.
Feinsod, M. (2000). The blind beautiful eye. *J Neuroophthalmol* **20**, 22-4.
Furthauer, M., Thisse, C. and Thisse, B. (1997). A role for FGF-8 in the dorsoventral patterning of the zebrafish gastrula. *Development* **124**, 4253-64.
Gill, G. N. (2003). Decoding the LIM development code. *Trans Am Clin Climatol Assoc.* **114**, 179-89.
Grinblat, Y. and Sive, H. (2001). zic Gene expression marks anteroposterior pattern in the presumptive neurectoderm of the zebrafish gastrula. *Dev Dyn* **222**, 688-93.
Halloran, M. C., Severance, S. M., Yee, C. S., Gemza, D. L. and Kuwada, J. Y. (1998). Molecular cloning and expression of two novel zebrafish semaphorins. *Mech Dev* **76**, 165-8.
Herrera, E., Brown, L., Aruga, J., Rachel, R. A., Dolen, G., Mikoshiba, K., Brown, S. and Mason, C. A. (2003). Zic2 patterns binocular vision by specifying the uncrossed retinal projection. *Cell* **114**, 545-57.
Herrera, E., Marcus, R., Li, S., Williams, S. E., Erskine, L., Lai, E. and Mason, C. (2004). Foxd1 is required for proper formation of the optic chiasm. *Development* **131**, 5727-39.
Hidalgo, A. and Booth, G. E. (2000). Glia dictate pioneer axon trajectories in the Drosophila embryonic CNS. *Development* **127**, 393-402.
Kania, A. and Jessell, T. M. (2003). Topographic motor projections in the limb imposed by LIM homeodomain protein regulation of ephrin-A:EphA interactions. *Neuron* **38**, 581-96.
Karlstrom, R. O., Talbot, W. S. and Schier, A. F. (1999). Comparative synteny cloning of zebrafish you-too: mutations in the Hedgehog target gli2 affect ventral forebrain patterning. *Genes Dev* **13**, 388-93.
Karlstrom, R. O., Trowe, T., Klostermann, S., Baier, H., Brand, M., Crawford, A. D., Grunewald, B., Haffter, P., Hoffmann, H., Meyer, S. U. et al. (1996). Zebrafish mutations affecting retinotectal axon pathfinding. *Development* **123**, 427-38.
Karlstrom, R. O., Tyurina, O. V., Kawakami, A., Nishioka, N., Talbot, W. S., Sasaki, H. and Schier, A. F. (2003). Genetic analysis of zebrafish gli1 and gli2 reveals divergent requirements for gli genes in vertebrate development. *Development* **130**, 1549-64.
Kimmel, C. B., Ballard, W. W., Kimmel, S. R., Ullmann, B. and Schilling, T. F. (1995). Stages of Embryonic Development of the Zebrafish. **203**, 253-310.
Knapik, E. W., Goodman, A., Ekker, M., Chevrette, M., Delgado, J., Neuhauss, S., Shimoda, N., Driever, W., Fishman, M. C. and Jacob, H. J. (1998). A microsatellite genetic linkage map for zebrafish (*Danio rerio*). *Nature Genet.* **18**, 338-343.
Krauss, S., Johansen, T., Korzh, V. and Fjose, A. (1991). Expression pattern of zebrafish pax genes suggests a role in early brain regionalization. *Nature* **353**, 267-70.
Laessing, U., Giordano, S., Stecher, B., Lottspeich, F. and Stuermer, C. A. O. (1994). Molecular characterization of fish neurolin: a growth-associated cell surface protein and memeber of the immunoglobulin superfamily in the fish retinotectal system with similarities to chick protein DM-GRASP/SC-1/BEN. *Differentiation* **56**, 21-29.
Lauderdale, J. D., Davis, N. M. and Kuwada, J. Y. (1997). Axon tracts correlate with netrin-1a expression in the zebrafish embryo. *Mol Cell Neurosci* **9**, 293-313.
Lumsden, A. (1995). Neural development. A 'LIM code' for motor neurons? *Curr Biol* **5**, 491-5.

Marcus, R. C., Blazeski, R., Godement, P. and Mason, C. A. (1995). Retinal axon divergence in the optic chiasm: uncrossed axons diverge from crossed axons within a midline glial specialization. **15**, 3716-3729.
Mitchell, K. J., Doyle, J. L., Serafini, T., Kennedy, T. E., Tessier-Lavigne, M., Goodman, C. S. and Dickson, B. J. (1996). Genetic analysis of Netrin genes in Drosophila: Netrins guide CNS commissural axons and peripheral motor axons. *Neuron* **17**, 203-15.
Mohammadi, M., McMahon, G., Sun, L., Tang, C., Hirth, P., Yeh, B. K., Hubbard, S. R. and Schlessinger, J. (1997). Structures of the tyrosine kinase domain of fibroblast growth factor receptor in complex with inhibitors. *Science* **276**, 955-60.
Mollenhauer, H. H. (1964). Plastic Embedding Mixtures for Use in Electron Microscopy. *Stain Technology* **39**, 111-114.
Munchberg, S. R., Ober, E. A. and Steinbeisser, H. (1999). Expression of the Ets transcription factors erm and pea3 in early zebrafish development. *Mech Dev* **88**, 233-6.
Nakagawa, S., Brennan, C., Johnson, K. G., Shewan, D., Harris, W. A. and Holt, C. E. (2000). Ephrin-B regulates the Ipsilateral routing of retinal axons at the optic chiasm. *Neuron* **25**, 599-610.
Nakagawa, Y. and O'Leary, D. D. (2001). Combinatorial expression patterns of LIM-homeodomain and other regulatory genes parcellate developing thalamus. *J Neurosci* **21**, 2711-25.
Nechiporuk, A. and Keating, M. T. (2002). A proliferation gradient between proximal and msxb-expressing distal blastema directs zebrafish fin regeneration. *Development* **129**, 2607-17.
Nguyen-Ba-Charvet, K. T. and Chedotal, A. (2002). Role of Slit proteins in the vertebrate brain. *J Physiol Paris* **96**, 91-8.
Nohno, T., Kawakami, Y., Wada, N., Ishikawa, T., Ohuchi, H. and Noji, S. (1997). Differential expression of the two closely related LIM-class homeobox genes LH-2A and LH-2B during limb development. *Biochem Biophys Res Commun* **238**, 506-11.
Nona, S. N., Shehab, S. A., Stafford, C. A. and Cronly-Dillon, J. R. (1989). Glial fibrillary acidic protein (GFAP) from goldfish: its localisation in visual pathway. *Glia* **2**, 189-200.
O'Leary, D. D. and McLaughlin, T. (2005). Mechanisms of retinotopic map development: Ephs, ephrins, and spontaneous correlated retinal activity. *Prog Brain Res* **147**, 43-65.
Plump, A. S., Erskine, L., Sabatier, C., Brose, K., Epstein, C. J., Goodman, C. S., Mason, C. A. and Tessier-Lavigne, M. (2002). Slit1 and Slit2 cooperate to prevent premature midline crossing of retinal axons in the mouse visual system. *Neuron* **33**, 219-32.
Porter, F. D., Drago, J., Xu, Y., Cheema, S. S., Wassif, C., Huang, S. P., Lee, E., Grinberg, A., Massalas, J. S., Bodine, D. et al. (1997). Lhx2, a LIM homeobox gene, is required for eye, forebrain, and definitive erythrocyte development. *Development* **124**, 2935-44.
Raible, F. and Brand, M. (2001). Tight transcriptional control of the ETS domain factors Erm and Pea3 by Fgf signaling during early zebrafish development. *Mech Dev* **107**, 105-17.
Rasband, K., Hardy, M. and Chien, C. B. (2003). Generating X: formation of the optic chiasm. *Neuron* **39**, 885-8.
Rauch, G. J., Granato, M. and Haffter, P. (1997). A polymorphic zebrafish line for genetic mapping using SSLPs on high percentage agarose gels. *Trends Tech. Tips Online.*
Retaux, S., Rogard, M., Bach, I., Failli, V. and Besson, M. J. (1999). Lhx9: a novel LIM-homeodomain gene expressed in the developing forebrain. *J Neurosci* **19**, 783-93.
Richards, L. J. (2002). Surrounded by Slit--how forebrain commissural axons can be led astray. *Neuron* **33**, 153-5.
Rick, J. M., Horschke, I. and Neuhauss, S. C. (2000). Optokinetic behavior is reversed in achiasmatic mutant zebrafish larvae. *Curr Biol* **10**, 595-8.
Rohr, K. B., Barth, K. A., Varga, Z. M. and Wilson, S. W. (2001). The nodal pathway acts upstream of hedgehog signaling to specify ventral telencephalic identity. *Neuron* **29**, 341-51.

Rubenstein, J. L. and Beachy, P. A. (1998). Patterning of the embryonic forebrain. *Curr Opin Neurobiol* **8**, 18-26.
Salinas, P. C. (2003). The morphogen sonic hedgehog collaborates with netrin-1 to guide axons in the spinal cord. *Trends Neurosci* **26**, 641-3.
Shanmugalingam, S., Houart, C., Picker, A., Reifers, F., Macdonald, R., Barth, A., Griffin, K., Brand, M. and Wilson, S. W. (2000). Ace/Fgf8 is required for forebrain commissure formation and patterning of the telencephalon. *Development* **127**, 2549-2561.
Shimamura, K., Martinez, S., Puelles, L. and Rubenstein, J. L. (1997). Patterns of gene expression in the neural plate and neural tube subdivide the embryonic forebrain into transverse and longitudinal domains. *Dev Neurosci* **19**, 88-96.
Shu, T., Sundaresan, V., McCarthy, M. M. and Richards, L. J. (2003). Slit2 guides both precrossing and postcrossing callosal axons at the midline in vivo. *J Neurosci* **23**, 8176-84.
Sockanathan, S. (2003). Towards cracking the code: LIM protein complexes in the spinal cord. *Trends Neurosci* **26**, 57-9.
Stenkamp, D. L. and Frey, R. A. (2003). Extraretinal and retinal hedgehog signaling sequentially regulate retinal differentiation in zebrafish. *Dev Biol* **258**, 349-63.
Take-uchi, M., Clarke, J. D. and Wilson, S. W. (2003). Hedgehog signalling maintains the optic stalk-retinal interface through the regulation of Vax gene activity. *Development* **130**, 955-68.
Tyurina, O. V., Guner, B., Popova, E., Feng, J., Schier, A. F., Kohtz, J. D. and Karlstrom, R. O. (2005). Zebrafish Gli3 functions as both an activator and a repressor in Hedgehog signaling. *Dev Biol* **277**, 537-56.
Vyas, A., Saha, B., Lai, E. and Tole, S. (2003). Paleocortex is specified in mice in which dorsal telencephalic patterning is severely disrupted. *J Comp Neurol* **466**, 545-53.
Walshe, J. and Mason, I. (2003). Unique and combinatorial functions of Fgf3 and Fgf8 during zebrafish forebrain development. *Development* **130**, 4337-49.
Westerfield, M. (1993). The Zebrafish Book. Eugene: University of Oregon Press.
Williams, S. E., Mann, F., Erskine, L., Sakurai, T., Wei, S., Rossi, D. J., Gale, N. W., Holt, C. E., Mason, C. A. and Henkemeyer, M. (2003). Ephrin-B2 and EphB1 mediate retinal axon divergence at the optic chiasm. *Neuron* **39**, 919-35.
Williams, S. E., Mason, C. A. and Herrera, E. (2004). The optic chiasm as a midline choice point. *Curr Opin Neurobiol* **14**, 51-60.
Wilson, S. W., Ross, L. S., Parrett, T. and Easter, S. S. J. (1990). The development of a simple scaffold of axon tracts in the brain of the embryonic zebrafish, Brachydanio rerio. **108**, 121-145.
Xu, Y., Baldassare, M., Fisher, P., Rathbun, G., Oltz, E. M., Yancopoulos, G. D., Jessell, T. M. and Alt, F. W. (1993). LH-2: a LIM/homeodomain gene expressed in developing lymphocytes and neural cells. *Proc Natl Acad Sci U S A* **90**, 227-31.
Yeo, S. Y., Little, M. H., Yamada, T., Miyashita, T., Halloran, M. C., Kuwada, J. Y., Huh, T. L. and Okamoto, H. (2001). Overexpression of a slit homologue impairs convergent extension of the mesoderm and causes cyclopia in embryonic zebrafish. *Dev Biol* **230**, 1-17.
Zuber, M. E., Gestri, G., Viczian, A. S., Barsacchi, G. and Harris, W. A. (2003). Specification of the vertebrate eye by a network of eye field transcription factors. *Development* **130**, 5155-67.