**Drosophila** homeodomain protein Nkx6 coordinates motoneuron subtype identity and axonogenesis

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**Summary**

The regulatory networks acting in individual neurons to control their stereotyped differentiation, connectivity, and function are not well understood. Here, we demonstrate that homeodomain protein Nkx6 is a key member of the genetic network of transcription factors that specifies neuronal fates in *Drosophila*. Nkx6 collaborates with the homeodomain protein Hb9 to specify ventrally projecting motoneuron fate and to repress dorsally projecting motoneuron fate. While *Nkx6* acts in parallel with *hb9* to regulate motoneuron fate, we find that *Nkx6* plays a distinct role to promote axonogenesis, as axon growth of Nkx6-positive motoneurons is severely compromised in *Nkx6* mutant embryos. Furthermore, *Nkx6* is necessary for the expression of the neural adhesion molecule Fasciclin III in Nkx6-positive motoneurons. Thus, this work demonstrates that *Nkx6* acts in a specific neuronal population to link neuronal subtype identity to neuronal morphology and connectivity.

Key words: *Drosophila melanogaster*, Neuronal fate specification, Motoneurons, Interneurons, Axon outgrowth, Nkx6, *hb9* (exex), *lim3*, *isle*, *eve*, *vnd"

**Introduction**

The development of neuromuscular circuits depends critically on the specification of distinct motoneuron (MN) subtypes during development. Conserved transcriptional regulators help establish MN subtype identity (see Jurata et al., 2000; Thor and Thomas, 2002). The expression of unique combinations of transcription factors in distinct MN subtypes probably regulates the differential expression of cell-surface receptors that translate guidance cues to downstream effectors of cytoskeletal changes (e.g. Kania and Jessell, 2003). Such cytoskeletal rearrangements enable motor axons of different MN subtypes to make strikingly distinct guidance choices in a common environment of guidance cues. However, the manner in which distinct transcription factor profiles are translated into unique patterns of motor axon projections remains an outstanding question.

In many model systems, MNs that extend axons along common trajectories express similar sets of transcriptional regulators – which in turn regulate key aspects of the differentiation of these MN subtypes (for a review, see Thor and Thomas, 2002). *Drosophila* MNs are classified by the location of the body wall muscles they innervate. MNs that innervate dorsal body wall muscles in *Drosophila* express the homeodomain (HD) transcription factor Even-skipped (Eve) (Doe et al., 1988). Furthermore, genetic analyses indicate that Eve is a key determinant of the fate of dorsally projecting MNs (Landgraf et al., 1999). Eve engages in a cross-repressive interaction with the HD protein Hb9, a determinant of ventrally projecting MNs (Broihier and Skeath, 2002). Ventrally projecting MNs also express the HD transcription factors Lim3 and Isl. Functional analyses have demonstrated that these three HD factors are required for proper axon guidance of ventrally projecting MNs (Broihier and Skeath, 2002; Odden et al., 2002; Thor and Thomas, 1997; Thor et al., 1999). The genetic hierarchy governing the fate of ventrally projecting neurons has, however, remained elusive as Lim3, Isl, and Hb9 are expressed independently of each other.

Lim3, Isl, and Hb9 are conserved regulators of MN cell fate whose vertebrate homologs – Lhx3/4, Isl1/2, and Hb9 – play key roles in vertebrate MN specification (Arber et al., 1999; Sharma et al., 1998; Thaler et al., 1999; Thaler et al., 1999; Tsuchida et al., 1994). In vertebrates, the genetic hierarchy linking the three transcription factors appears more linear than in *Drosophila*, as Hb9 regulates Lhx3/4 and Isl1/2 expression (Arber et al., 1999; Thaler et al., 1999). As in *Drosophila*, the vertebrate Eve homolog, Evx1, is expressed in a distinct population of neurons – in this case, a subset of vertebrate interneurons (Moran-Rivard et al., 2001).

In *Drosophila* and vertebrates, Hb9, Isl1/2, and Lhx3/4 are expressed almost exclusively by postmitotic neurons. In vertebrates, the expression of these factors in MNs depends on proper establishment of the MN progenitor domain by the coordinated action of upstream HD transcription factors (Briscoe et al., 2000). For example, the pair of Nkx-class HD proteins, Nkx6.1 and Nkx6.2 (Nkx6 proteins), have complementary expression patterns in MN and interneuron progenitors (Briscoe et al., 2000; Cai et al., 1999). Nkx6.1/Nkx6.2 compound mutants exhibit a near complete loss of somatic MNs, demonstrating that Nkx6 proteins are
essential for MN generation (Sander et al., 2000; Vallstedt et al., 2001). Expression of Nkx6 proteins persists in postmitotic MNs, where they regulate proper nuclear migration and axon guidance in visceral MNs in the hindbrain (Müller et al., 2003; Pattyn et al., 2003).

To explore further the genetic networks behind neuronal diversification in Drosophila, we investigated the role of the Drosophila Nkx6 homolog in regulating distinct MN fates. We characterized genetic interactions between Nkx6 and factors that promote axonogenesis of Nkx6-positive neurons. Consistent with a direct regulatory role in this process, Nkx6 activates the expression of the neural adhesion molecule Fasciclin III in ventrally projecting motoneurons. These data suggest that Nkx6 is a primary transcriptional regulator of molecules essential for axon growth and guidance in a specific neuronal population.

Materials and methods

Fly stocks

The following fly stocks were used: hb9(KK30), hb9(1114), hb9(GAL4), UAS-hb9 (Brouilier and Skeath, 2002), UAS-vnd (D. Mellercik), UAS-GAPGFP (A. Chiba), elavGAL4 (A. DiAntonio), UAS-eve (A. Brand), lim3-tmyc (S. Thor). Nkx6
dig was generated in an enhancer trap from the predicted start to the predicted stop codon. We cloned and sequenced the 1539 bp product, which matches the Nkx6 locus (Materials and methods). All other stocks were obtained from the Bloomington Stock Center.

Nkx6 cDNA and UAS-Nkx6

We isolated a full-length Nkx6 cDNA via RT-PCR from RNA prepared from a 0- to 20-hour collection of Oregon R embryos. pol3A RNA was prepared using the RNeasy midi kit and oligotex beads (Qiagen) and converted into cDNA using superscript II reverse transcriptase (Gibco BRL). Nkx6 cDNA was generated using primers that amplify from the predicted start to the predicted stop codon. We cloned and sequenced the 1539 bp product, which matches Nkx6 cloned from an embryonic library (Uhler et al., 2002) at the amino acid level. To create UAS-Nkx6, we inserted the Nkx6 cDNA into the NotI site of pUAST (Brand and Perrimon, 1993) and created germline transmigrants following standard methods.

Antibody production, immunofluorescent, and immunohistochemical studies

Amino acids 34-386 of Nkx6 were cloned into pET29a (Novagen) for protein expression and purification. This antigen was used to immunize rats at Pocono Rabbit Farm. Confirming antibody specificity, we failed to detect Nkx6 protein in embryos homozygous for Nkx6D25 or Df(3L)fz-D21 (data not shown). The following primary antibodies were used: rat anti-Islet, guinea pig anti-Lim3, rabbit anti-Hb9 (Brouilier and Skeath, 2002); rabbit anti-Odd (E. Ward); rabbit anti-Vnd (D. Mellercik); rabbit anti-EGFP (P. Silver); rabbit anti-Eve (M. Frasch); mouse anti-Eve (N. Patel); mouse anti-Myc (Sigma); rabbit anti-βgal (ICN; mouse anti-βgal (Promega); and mouse monoclonal 1D4/FaS2 and 7G10/FaS3 were generated by C. Goodman’s Laboratory and obtained from the Developmental Studies Hybridoma Bank. The anti-Lim3 antibody was affinity purified using the Ultralink Immobilization Kit (Pierce). We used the Vector ABC kit for immunohistochemistry and Alexa-488 and Alexa-594 with appropriate species specificity for immunofluorescence (Molecular Probes).

Results

Nkx6 expression and functional analysis

To identify additional regulators of neuronal fate determination in Drosophila, we conducted a computational search of the Drosophila genome for uncharacterized homologs of vertebrate genes with essential functions in neuronal fate specification (H.T.B. and J.B.S., unpublished). A detailed analysis of other regulators will be described elsewhere; here we describe our identification and characterization of Drosophila homeodomain protein Nkx6. We identified a single Drosophila Nkx6 homolog (Fig. 1A) (Uhler et al., 2002) located in the 70C-D region of chromosome 3L. RNA in situ hybridization analysis indicated that Nkx6 is expressed in the embryonic central nervous system (CNS) (data not shown).

To initiate a functional analysis of Nkx6, we identified a P element insertion, p{JG[LacZ]} inserted 4 KB downstream of the Nkx6 locus. p{JG[LacZ]} is an enhancer trap and a mutant allele of Nkx6 as Nkx6 protein levels are greatly reduced in p{JG[LacZ]} homozygotes (Fig. 1A; data not shown). Via imprecise excision of p{JG[LacZ]}, we generated a 25 KB deletion that removes the 3’ end of the Nkx6 locus (Nkx6D25; see Materials and methods; Fig. 1A). Nkx6D25 homozygous embryos do not express Nkx6 RNA or protein (data not shown), indicating that Nkx6D25 is a null allele of the Nkx6 locus. The deletion also removes CG13479, a predicted gene with a single 83 amino acid ORF situated 14 KB downstream of Nkx6. We attribute the CNS phenotypes observed in Nkx6D25 mutant embryos to the Nkx6 locus for four reasons. First, CG13479 is unlikely to be an embryonically-expressed transcript since we fail to detect CG13479 expression in wild-type embryos via RNA in situ hybridization (data not shown) and the Berkeley Drosophila Genome Project has not identified any embryonic ESTs for CG13479. Second, the axonal phenotypes in Nkx6 mutant embryos are largely rescued by Nkx6 expression in the CNS (see Fig. 4). Third, we were able to phenocopy the Eve phenotype that we observe in hb9(KK30) Nkx6D25 double mutant embryos by injection of Nkx6 RNA into hb9 mutant embryos (see below; see Fig. S1 in the supplementary material). Fourth, the cell fate and axonal outgrowth phenotypes we observe in Nkx6D25 embryos are reciprocal to those observed when Nkx6 is misexpressed via the GAL4/UAS system (see Fig. 5) (Brand and Perrimon, 1993).

To identify the neuronal cell types most likely to be affected by loss of Nkx6 function, we generated Nkx6-specific antibodies. We verified antibody specificity on embryos bearing deletions of the Nkx6 locus (Materials and methods). We find that Nkx6 exhibits a highly dynamic expression pattern...
Nkx6 and motoneuron identity

Within the embryonic CNS (Fig. 1B-D), Nkx6 is first expressed in CNS midline precursors at embryonic stage 9 (Fig. 1B); this expression is transient and is extinguished by stage 10. At stage 10, we observe relatively weak Nkx6 expression in neural precursors or neuroblasts (NBs). To identify the Nkx6-positive NBs, we assayed Nkx6 expression relative to Svp-LacZ and Deadpan – characterized markers of NB identity. These experiments illustrate that NBs 1-1, 1-2, 2-2, 3-1, 3-2, 4-2 and 5-2 express Nkx6 at low to moderate levels (Fig. 1E; data not shown). By stage 11, Nkx6 is expressed in medial clusters of approximately 15 cells (Fig. 1C). Based on their position and size, these cells appear to be a mixture of intermediate precursor cells called ganglion mother cells (GMCs) and postmitotic neurons. Beginning at stage 12, neurons in the intermediate and lateral regions of the CNS activate dNkx6 expression. By stage 14, Nkx6 is expressed in a complex pattern of 30-40 neurons in each hemisegment. Notably, Nkx6 expression levels vary dramatically and reproducibly between neurons in late-stage embryos (Fig. 1D,F,H). The dynamic pattern of Nkx6 expression in the CNS suggests Nkx6 may function in the development of specific CNS cell types.

To establish the identity of Nkx6-positive neurons, we compared Nkx6 expression to markers of defined neuronal subsets. We first investigated whether Nkx6 is expressed in MN and interneuron populations in Drosophila. We compared Nkx6 expression to that of Odd-skipped (Odd), and find that Nkx6 and Odd are co-expressed in the MP1 and dMP2 interneurons (data not shown). We then asked whether Nkx6 is present in distinct MN groups. To this end, we compared Nkx6 expression to that of Hb9 and Eve. Hb9 is expressed in ventrally and laterally projecting MNs while Eve is expressed in dorsally projecting MNs (Broihier and Skeath, 2002; Landgraf et al., 1999; Odden et al., 2002). Like Hb9 and Eve, Nkx6 and Eve are also expressed in complementary patterns (Fig. 1F). On the other hand, the majority of Nkx6-expressing cells express Hb9, although Nkx6 is expressed in slightly more neurons than Hb9 (Fig. 1H-J). The extensive co-expression of Nkx6 and Hb9 suggested that Nkx6 is also expressed in ventrally projecting MNs. Confirming this, we find that Nkx6 is co-expressed with a Lim3-tauymc transgene, a marker of RP 1,3,4,5 (RP MNs) – a group of well-characterized ventrally projecting MNs (arrowheads in Fig. 1G) (Thor et al., 1999). This analysis established that Nkx6 is expressed in both interneurons and ventrally projecting MNs.

The co-expression of Nkx6 and hb9 in ventrally projecting MNs raised the possibility that they act in a linear genetic pathway to control the development of these MNs. In addition, vertebrate Nkx6.1 is expressed in MN progenitors and is necessary for the activation of Hb9 in postmitotic MNs (Sander et al., 2000; Vallstedt et al., 2001). However, we find that Nkx6 and Hb9 are expressed independently of each other in the Drosophila CNS (data not shown). Thus, if Nkx6 regulates neuronal fate, it does so independently of regulating hb9 transcription. Instead, the independent regulation of Nkx6 and hb9 combined with their similar expression profiles suggests they may act in parallel to regulate neuronal fate.

Nkx6 and hb9 act in parallel to repress vnd

During early CNS development, Nkx6 is co-expressed with Ventral nervous system defective (Vnd) in a subset of medial column NBs (see Fig. S2 in the supplementary material), prompting us to investigate the genetic relationship between vnd and Nkx6. Vnd expression marks medial column CNS NBs and is required for the development of these cells (Chu et al., 1998; Jimenez and Campos-Ortega, 1990; Skeath et al., 1994). We first compared Nkx6 and Vnd expression in wild-type embryos. Surprisingly, while Nkx6 and Vnd are co-expressed in a subset of medial column NBs, their expression patterns are otherwise complementary (Fig. 2A-C). At stage 9, Nkx6 is expressed in CNS midline precursors, while Vnd is expressed
patterns of Nkx6 and Vnd arise due to their opposing activities, we asked if \(vnd\) misexpression represses \(Nkx6\). These analyses focus on the genetic relationship between \(Nkx6\) and \(vnd\) in postmitotic neurons since these genes exhibit mutually exclusive patterns in these cells. We used the elav-GAL4 driver to express \(vnd\) in postmitotic neurons and found this abolishes CNS expression of \(Nkx6\) (Fig. 2D,E). We were unable to obtain meaningful loss-of-function data for \(vnd\) because nearly all medial column NBs and their progeny, many of which are Nkx6-positive, fail to develop in \(vnd\) mutant embryos. The requirement of \(vnd\) to promote medial column NB formation inhibited our ability to assay the effect of removing \(vnd\) function on Nkx6. Nevertheless, the ability of \(vnd\) misexpression to abolish \(Nkx6\) expression supports the model that \(vnd\) represses \(Nkx6\) to help establish the complementary expression patterns of Nkx6 and Vnd.

In the reciprocal experiment, we found that postmitotic misexpression of \(Nkx6\) dramatically reduces the number of Vnd-positive neurons (compare Fig. 2F,G). Normally, 10.0±1.3 neurons express Vnd per hemisegment (\(n=30\)) whereas only 4.2±1.8 neurons express Vnd per hemisegment (\(n=53\)) in \(Nkx6\) misexpression embryos. However, Vnd expression is wild type in \(Nkx6\) mutant embryos (data not shown). Thus, \(Nkx6\) is sufficient but not necessary to repress \(vnd\) expression.

These data suggest that while high levels of Nkx6 and Vnd are cross-repressive in postmitotic neurons, these factors function in concert with other regulators during normal development to limit each other’s expression. Given the similar expression profiles of Nkx6 and Eve and their independent regulation we asked whether \(Nkx6\) and \(hb9\) act in parallel to repress \(vnd\) expression. As observed for \(Nkx6\), \(hb9\) misexpression in postmitotic neurons significantly reduces the number of \(vnd\)-positive CNS neurons (2.8±1.7 neurons per hemisegment; \(n=48\)), while \(hb9\) mutants exhibit wild-type \(vnd\) expression (data not shown). However, removal of both \(hb9\) and \(Nkx6\) leads to an overproduction of \(vnd\)-positive neurons as 13.6±2.1 \(vnd\)-positive neurons (\(n=41\)) develop in double mutant embryos relative to ten in wild type (compare Fig. 2F and 2I). These results show that \(hb9\) and \(Nkx6\) act in parallel to repress \(vnd\), and support the model that the complementary patterns of Nkx6 and \(vnd\) arise at least in part due to their opposing activities.

### Nkx6 and hb9 collaborate to regulate MN fate

We next explored the regulatory relationship between Nkx6 and \(hb9\) – both of which are expressed in ventrally projecting motoneurons – and the dorsal motoneuron determinant \(eve\). \(eve\) and \(hb9\) engage in a cross-repressive relationship to maintain their expression in distinct neuronal populations (Broihier and Skeath, 2002). Since Nkx6 and Eve are also expressed in non-overlapping populations of neurons (Fig. 1E), we asked whether they repress each other. We first asked whether \(eve\) is sufficient to repress \(Nkx6\) by misexpressing \(eve\) in all postmitotic neurons. \(Eve\) misexpression results in a near complete suppression of Nkx6 expression by embryonic stage 16 (compare Fig. 3A and 3B), demonstrating that \(eve\) is sufficient to repress Nkx6.

In a reciprocal manner, misexpression of Nkx6 in all postmitotic neurons severely reduces Eve expression in the U MNs and EL neurons, though Eve expression in RP2 and aCC/pCC appears grossly normal (compare Fig. 3D,E).
for Nkx6. Ectopic Stage 15 (C) wild-type, (D) elavGAL4:UAS-Nkx6 hb9 KK30 neurons relative to wild type (Broihier and Skeath, 2002).

3E). This number represents an increase of two Eve-positive neurons to repress eve.

19.4±2.0 Eve-positive neurons per hemisegment (n=50; Fig. 3F), representing an increase of six Eve-positive neurons relative to wild type. The ectopic Eve-positive neurons arise at multiple positions within the CNS, suggesting they develop from multiple NB lineages; however, a number are situated close to the midline (see Discussion). To confirm this phenotype is caused by loss of Nkx6 activity from an hb9 mutant background, we injected double-stranded Nkx6 RNA into hb9KK30 mutant embryos. We find an average of 24.8±5.9 Eve-positive neurons per hemisegment in these embryos (n=39; see Fig. S1 in the supplementary material), demonstrating that injection of Nkx6 RNA into hb9 mutants phenocopies the Eve phenotype observed in hb9KK30 Nkx6D25 mutants. The further increase of Eve-positive neurons in hb9 Nkx6 mutant embryos relative to hb9 mutant embryos demonstrates that Nkx6 and hb9 collaborate to repress Eve.

hb9 and Nkx6 thus act together to limit the expression of eve, a key determinant of dorsally projecting MN identity. We next investigated whether hb9 and Nkx6 coordinate the specification of ventrally projecting MN identity. RP1,3,4,5 MNs are large Nkx6-positive cells that lie close to the midline and project their axons contralaterally to ventral muscles within ISNb (Fig. 1F, Fig. 6A) (Sink and Whitington, 1991a; Sink and Whitington, 1991b; Schmid et al., 1999). Since both Nkx6 and Hb9 are expressed in RP1,3,4,5 (Fig. 1G) (Broihier and Skeath, 2002), we asked whether these neurons develop properly in hb9 Nkx6 double mutant embryos. Islet and Lim3 are markers of RP1,3,4,5 identity (Thor and Thomas, 1997; Thor et al., 1999) and are expressed in the these MNs in embryos singly mutant for Nkx6 or hb9 (data not shown) (Broihier and Skeath, 2002). However, expression of Islet and Lim3 in the RP1,3,4,5 MNs is strongly reduced in hb9 Nkx6 double mutant embryos (arrowheads in Fig. 3G-J). Interestingly, the requirement of Nkx6 and hb9 to promote Islet and Lim3 expression is relatively specific to these RP MNs, since Islet and Lim3 expression is otherwise grossly normal in these embryos. The absence of these early determinants of RP1,3,4,5 MN identity strongly suggests that RP MNs are specified incorrectly in the absence of these early determinants of RP1,3,4,5 MN identity. We find an average of 24.8±5.9 Eve-positive neurons per hemisegment in these embryos (n=39; see Fig. S1 in the supplementary material), demonstrating that injection of Nkx6 RNA into hb9 mutants phenocopies the Eve phenotype observed in hb9KK30 Nkx6D25 mutants. The further increase of Eve-positive neurons in hb9 Nkx6 mutant embryos relative to hb9 mutant embryos demonstrates that Nkx6 and hb9 collaborate to repress Eve.

**Nkx6 is necessary for axon outgrowth**

Nkx6 is co-expressed with Hb9, Lim3, and Islet in populations of ventrally projecting MNs. Since Hb9, Lim3, and Islet are known to be required for proper axon guidance of ventrally projecting axons (Broihier and Skeath, 2002; Odden et al., 2002; Thor and Thomas, 1997; Thor et al., 1999), we asked whether Nkx6 was also necessary for the axonal development of this MN population. Using Fas2 to label motor axon pathways (mAB 1D4) (Van Vactor et al., 1993), we find that two of the four major nerve branches that innervate ventral and lateral muscles exhibit highly penetrant phenotypes in Nkx6 mutants.
mutant embryos. Specifically, both secondary branches of the ISN, ISNb and ISNd, are absent in a significant proportion of Nkx6 mutant hemisegments (arrowheads in Fig. 4A-C). Notably, the Nkx6-positive RP1,3,4,5 MNs project within ISNb. We quantified the ISNb phenotype in four allelic combinations of Nkx6 (Fig. 4E), including embryos transheterozygous for Nkx6D25 and an unrelated deficiency of the region. We scored the ISN as completely absent if we failed to detect axon extension into the ventral muscle field (Fig. 4B). Likewise, we scored ISNb as reduced if any axons grew into the ventral muscle field, even if they initially bypassed their normal choicepoint (Fig. 4C). In all allelic combinations, we found defects in ISN outgrowth in at least half of all hemisegments. In fact, for dNkx6D25 homozygotes or Nkx6P[J] /Df(3L)fz-D21 transheterozygotes, the penetrance is greater than 90% (Fig. 4E). The penetrance of the ISNd phenotype is roughly equivalent to that of ISNb (Fig. 4A-C; data not shown). Hence, Nkx6 activity promotes proper axonal development of ISN and ISNd.

To ensure that loss of Nkx6 activity is responsible for the observed axonal phenotypes, we assayed whether Nkx6 misexpression in a Nkx6 mutant background rescues the ISNb outgrowth phenotype. We used targeted transposition to engineer an Nkx6GAL4 enhancer trap from the Nkx6P[J] (Materials and methods) (Sepp and Auld, 1999). We then used the Nkx6GAL4 driver to express Nkx6 in Nkx6P[J]/Nkx6D25 mutant embryos (Fig. 4E). We find that Nkx6 expression is sufficient to rescue ISNb outgrowth in 72% of hemisegments (n=154), compared to 27% in the absence of Nkx6 misexpression (n=166). The ability of Nkx6 expression to largely rescue the observed motor axon phenotypes provides strong evidence that loss of Nkx6 is responsible for the axonal phenotypes in Nkx6D25 mutant embryos.

Since Nkx6 and hb9 act in parallel to regulate neuronal fate (see above), we wondered whether they also act in parallel to regulate axon growth. However, the motor axon phenotypes in hb9 Nkx6 mutant embryos are nearly identical to those in Nkx6 mutants (Fig. 4E). Therefore, while Nkx6 and hb9 collaborate to regulate multiple neuronal fates, Nkx6 plays a specific non-redundant role to promote axonogenesis.

To examine the role of Nkx6 during axonogenesis in more detail, we focused on axon projections of HB9-positive neurons. Since HB9 and Nkx6 are normally expressed in largely overlapping neuronal subsets, this enriched for Nkx6-positive axons relative to Fas2, which labels all motor axons. In wild-type embryos, HB9-positive axons project in ISNb and synapse with their appropriate targets (Fig. 4F). However, we fail to detect HB9-positive axons in ISNb in Nkx6D25 homozygous mutant embryos (Fig. 4G). In fact, few HB9-positive axons are observed in the periphery of Nkx6 mutant embryos, suggesting these motor axons may remain in the nerve cords of Nkx6 mutants. To test this, we followed HB9-positive axons in the nerve cords of Nkx6 mutant embryos. In wild type, HB9-positive interneurons extend axons in multiple longitudinal fascicles in the CNS (Fig. 4H). In contrast, in Nkx6 mutant embryos, we observe very few HB9-positive axons projecting along longitudinal fascicles (Fig. 4I). Since all HB9-positive neurons appear to be specified in Nkx6 mutants, the motor axon phenotypes observed in Nkx6 mutants do not represent motoneuron to interneuron transformations. Rather, these data argue that Nkx6 potentiates axon growth of Nkx6-expressing neurons.

Fig. 4. Nkx6 is necessary for axon growth. Three hemisegments of Stage 16 dissected (A) wild-type (B) Nkx6D25/Nkx6D25 (C) Nkx6PJG/Nkx6D25, and (D) UAS-Nkx6+/Nkx6GAL4/Nkx6D25 embryos labeled with α-Fas2 to mark motor axon projections. Schematics summarizing the observed phenotype are shown below each panel. (A) In wild type, ISNb (arrowheads) and ISNd innervate the ventral muscle field. (B) In Nkx6D25 homozygous embryos, ISNb and ISNd do not innervate their muscle targets. Arrowheads indicate ventral muscle field. (C) In Nkx6PJG/Nkx6D25 mutants the ventral muscle field is not innervated, though presumptive ISNb axons extend along ISN (arrowheads). (D) In Nkx6 rescue embryos ISNb axons usually contact their appropriate target muscles. (E) Penetration of mutant phenotypes for different Nkx6 allelic combinations. See text for details. (F) Three hemisegments of wild-type and (G) UAS-GAPGFP+/; hbgGAL4 Nkx6D25/Nkx6D25 mutants labeled with α-GFP (green) to mark HB9-positive axons and α-MHC (red) to mark muscles. HB9-positive axons extend along ISN to contact ventral muscles in wild-type (F), but not mutant (G) embryos. (H) Three segments of wild-type and (I) UAS-GAPGFP+/; hbgGAL4 Nkx6D25/Nkx6D25 mutant nerve cords labeled with α-GFP to mark HB9-positive axons. In wild type (H), numerous HB9-positive longitudinal fascicles are visible, while in I very few HB9-positive axons are present. Anterior is up in all panels.
**Nkx6 overexpression leads to ISNb overgrowth**

The impaired axon extension observed in Nkx6 mutant embryos argues that Nkx6 is a positive mediator of axon growth. To test this model, we analyzed axon growth in embryos that over-expressed Nkx6 in all postmitotic neurons. To ensure high levels of Nkx6 expression in neurons, we used embryos carrying elavGAL4 and two copies of UAS-Nkx6 and again focused on ISNb. The overall pattern and thickness of ventral motor axon projections (including ISNb) is normal in these embryos suggesting that postmitotic overexpression of Nkx6 does not result in widespread transformations of neurons to the ventrally projecting MN fate (Fig. 5). In support of this, Hb9 expression is wild type in elavGAL4:2xUAS-Nkx6 embryos (data not shown). However, in this background a significant proportion of ISNb axons exhibit phenotypes consistent with overgrowth (Fig. 5). For example, we observed at least one ISNb branch with a clearly expanded terminal arbor in 28% of hemisegments (n=176; Fig. 5B) compared to 6% in wild type (n=155). We also observed two phenotypes in Nkx6 overexpression embryos that we never observed in wild type (n=155). Namely, we observed excessive axonal branching in ISNb in 14% of hemisegments (n=176; Fig. 5C). In 4% of hemisegments, ISNb axons from adjacent segments extend across the segment boundary and fuse together (n=176; Fig. 5D). These data support the conclusion that Nkx6 overexpression in ISNb-projecting neurons leads to axonal overgrowth, probably via the upregulation of molecules that promote axon growth and regulate guidance. Furthermore, the reciprocal effects of loss of function and overexpression of Nkx6 on axon growth argue that Nkx6 activates genes that promote axonogenesis.

**Nkx6 regulates axon development and gene expression of ventrally projecting RP MNs**

The preceding analysis indicates that Nkx6 promotes axon outgrowth of a subset of MNs. To investigate this possibility in more detail, we followed the well-characterized axon projections of the RP1,3,4,5 MNs in wild type and Nkx6 mutant backgrounds. We utilized a lim3-tau myc transgene (Thor et al., 1999) to follow RP motor axon projections in wild-type and Nkx6 mutant embryos (Fig. 6A-D). In wild type, we are able to detect RP motor axons exiting the CNS in 86% of hemisegments scored (n=160; arrowheads in Fig. 6A). In contrast, we could trace motor axons leaving the CNS in only 39% of hemisegments of Nkx6 mutant embryos (n=210; posterior hemisegments in Fig. 6C; anterior right hemisegment in Fig. 6D). In most mutant hemisegments, the motor axons appear thinner than in wild type (posterior hemisegments in Fig. 6C). Furthermore, in 61% of Nkx6 mutant hemisegments, RP motor axons remain within the CNS (n=210; all projections of four micron series from dissected stage 16 (A) wild-type and (B-D) Nkx6D25 nerve cords carrying a lim3-tau myc transgene. α-Myc marks axon projections of RP1,3,4,5. (A-D) An asterisk indicates the RP MN cell bodies and arrowheads mark the extent of the RP axon projection. (A) In wild type, RP motor axons leave the CNS. Nkx6D25 mutant embryos RP motor axons display various defects. (B) RP motor axons frequently truncate and exhibit aberrant morphology. (C) RP motor axons in the bottom left and both right hemisegments are markedly thinner than in wild-type embryos. (D) RP motor axons in the top left hemisegment diverge from their normal course and turn toward the midline. (E,F) Confocal projections of four micron series from dissected stage 16 nerve cords from (E) wild-type and (F) Nkx6D25 mutant embryos labeled with Fas3. (E) In wild type, the Nkx6-positive RP MNs express Fas3 (arrowheads) as do Nkx6-negative lateral neurons (arrows). (F) In Nkx6D25 mutant embryos, RP MNs lose Fas3 expression (arrowheads), while expression in more lateral Nkx6-negative neurons is unaffected (arrows). Anterior is up in all panels.
hemisegments in Fig. 6B), compared to 14% of wild type. The morphology of these truncated axons is often aberrant, suggesting their outgrowth has stalled. For example, we frequently observed enlarged growth cones with a club-like appearance (Fig. 6B). Finally, in 10% of mutant hemisegments, RP motor axons make dramatic guidance errors, often turning back inappropriately and extending toward the midline (n=210; anterior left hemisegment in Fig. 6D). These data demonstrate that Nkx6 activity is critical for proper growth and guidance of the RP1,3,4,5 MNs. Furthermore, the axon phenotypes exhibited by these MNs probably reflect a general requirement of Nkx6 in promoting axonogenesis of Nkx6-expressing neurons.

The Nkx6 axonal phenotypes strongly suggest that Nkx6 regulates – probably directly – molecules that control axonal outgrowth and guidance. Fasciclin III (Fas3), a cell adhesion molecule, is a possible target of Nkx6 action in MNs as it is expressed by the RP1,3,4,5 MNs and promotes target recognition by their motor axons (Fig. 6E) (Chiba et al., 1995; Patel et al., 1987). Notably, Fas3 expression is strongly reduced in the RP MNs in Nkx6 mutant embryos relative to wild type (arrowheads in Fig. 6E,F). Consistent with a specific role for Nkx6 in regulating Fas3 expression, more lateral neurons that express Fas3 (arrows, Fig. 6E,F) but not Nkx6 (data not shown) exhibit wild-type Fas3 expression in Nkx6 mutants (Fig. 6E,F).

Together, these data show that Nkx6 promotes proper RP motor axon growth, and indicate that Nkx6 controls RP motor axon growth by regulating the transcription of adhesion and guidance molecules – one of which is Fas3.

Discussion

The nervous system must precisely coordinate neuronal fate and morphology to establish functional neural circuits during development. In fact, neuronal identity is often intimately connected to cellular morphology – for example, MNs can be classified based on common patterns of axonal growth as well as by transcription factor expression profiles. Motor axons of distinct MN subtypes make joint guidance decisions as they navigate toward their muscle targets, suggesting that MN subtypes express related sets of receptor and signaling molecules. Despite this elegant model, little is known about the transcriptional mechanisms acting in populations of neurons to produce characteristic axonal trajectories. Here we present an analysis of Drosophila homeodomain protein Nkx6. We find that Nkx6 has roles in both the specification and differentiation of ventrally projecting MNs (Fig. 7). In particular, we find that Nkx6 plays a pivotal role in promoting axon growth of these MNs and regulates the expression of a key determinant of synaptic target selection. Hence Nkx6 activity links neuronal identity and cellular morphology.

Nkx6 and neuronal subtype identity

This work places Nkx6 in the regulatory circuit that specifies distinct postmitotic neuron fates in the Drosophila CNS (Fig. 7). In the mouse, Nkx6 protein function in MN progenitors regulates Hb9 expression in postmitotic MNs (Arber et al., 1999; Sander et al., 2000; Thaler et al., 1999; Vallstedt et al., 2001). We find that Drosophila Nkx6 is expressed in neural precursors and postmitotic neurons while Hb9 expression is nearly exclusive to postmitotic neurons (this work) (Broihier and Skeath, 2002; Odden et al., 2002). However, in contrast to the linear relationship of Nkx6.1/2 and Hb9 in vertebrates, our experiments establish that Nkx6 and hbb9 act in parallel to specify neuronal fate in Drosophila (Figs 2, 3, 7). Nkx6 and hbb9 act in concert both to repress expression of the dorsal MN determinant Eve and to promote expression of Lim3 and Islet (Fig. 7). In particular, we find that hbb9 Nkx6 double mutant embryos exhibit wild-type Nkx6 expression in ventrally and laterally projecting MNs, raising the possibility that they do so by repressing an unidentified repressor of ventrally projecting MN identity.

eve represents an appealing candidate for the unidentified repressor in this model (Fig. 7). Ectopic Eve expression in RP MNs in hbb9 Nkx6 double mutants may repress Lim3 and Islet. Consistent with this, though we were unable to unambiguously identify the ectopic Eve neurons in hbb9 Nkx6 mutants, many of them are situated close to the midline (Fig. 3F) – suggesting they may represent mis-specified RP MNs. Furthermore, pan-neuronal eve expression represses Lim3 and Islet expression in the RP MNs demonstrating that Eve can repress Lim3 and Islet (data not shown) (Landgraf et al., 1999). A direct test of this model will require resolving the identity of the ectopic Eve neurons in hbb9 Nkx6 mutant embryos.

While Nkx6 and hbb9 play conserved roles in MN specification in Drosophila and in vertebrates, the genetic network within which they act differs. In vertebrates, Nkx6 is upstream of dHb9, while in Drosophila, Nkx6 and hbb9 display a parallel requirement in MN generation. Why might the genetic relationship between Nkx6 and hbb9 vary between Drosophila and vertebrates? We propose that the reason may relate to the different relationship between regional identity and vertebrates?
and neuronal subtype identity in Drosophila relative to vertebrates. In vertebrates, a given neuronal population is generated at a distinct dorsoventral position in the spinal cord in response to graded Sonic hedgehog levels. Thus, gene expression in neural precursors can simultaneously promote both precursor and neuronal subtype identity. In Drosophila, no obvious link ties regional identity to neuronal subtype. For example, Drosophila NBs arise within three dorsoventral columns (for a review, see Skeath, 1999). However, the dorsoventral position of neural precursors does not regulate postmitotic neuronal identity. NBs at all dorsoventral positions give rise to diverse populations of neurons, and neurons of given subtypes develop at many dorsoventral positions. For example, MNs are generated from NBs across the dorsoventral axis (Schmidt et al., 1999). Therefore in Drosophila embryos, gene expression in NBs does not directly promote neuronal subtype identity.

A possible mechanism that might contribute to neuronal subtype identity in Drosophila is suggested by the temporal gene cascade in NBs (Isshiki et al., 2001; Kambadur et al., 1998). In this cascade, Hunchback (Hb) is expressed in the earliest-born one or two GMCs in a NB lineage followed by sequential expression of Kruppel, Pdm, and Castor in later-born GMCs. The majority of MNs arise from early-born GMCs (Schmidt et al., 1999), consistent with the idea that hb promotes MN identity. Thus while regional identity promotes postmitotic identity in vertebrates, temporal identity may play a similar role in Drosophila. However, many early-born GMCs do not produce MNs, indicating additional layers of complexity. Regional identity may interface with the temporal gene cascade to activate the proper combination of transcription factors to promote the MN fate in a subset of early-born GMCs. In this paradigm, MN specification occurs relatively late in development, suggesting that cells may need to rapidly activate and execute the genetic pathways leading to MN identity. As a result, near simultaneous activation of factors—such as Nkx6 and hb9—that act in parallel to promote MN identity, might be required.

Nkx6 and axonogenesis

While Nkx6 and hb9 exhibit parallel requirements in cell fate specification, Nkx6 plays a specific non-redundant role to promote axon growth and guidance in Nkx6-positive neurons. Nkx6 is, therefore, probably an element of the transcriptional code regulating the differential transcription of receptor and signal transduction molecules required to promote unique patterns of axon growth and guidance in distinct MN subsets. In support of this, Nkx6 activity is necessary for Fas3 expression in ventrally projecting RP MNs. Clearly, it will be necessary to elucidate the entire cassette of genes that Nkx6 activates to promote axonogenesis. In this regard, determining whether Nkx6 activates the same gene battery in all Nkx6-positive neurons or if Nkx6 regulation of such genes is cell-type-specific will be of interest. The singular requirement for Nkx6 in axon growth combined with the redundant functions of Nkx6 and hb9 in neuronal specification hints at the transcriptional complexity of neuronal specification and differentiation. It will be important to further distinguish the specification and differentiation functions of Nkx6—either by identifying additional interacting proteins, or by identifying protein domains within Nkx6 required specifically to promote either specification or differentiation. Precedence for the latter comes from the elucidation of distinct domains within the bHLH proteins Mash1 and Math1 required to promote neuronal differentiation and specification (Nakada et al., 2004).

Nkx6 is one of a number of transcription factors that have been implicated in controlling fundamental aspects of neuronal morphology. In Drosophila, several transcription factors have recently been shown to regulate dendritic morphogenesis (Brenman et al., 2001; Grueber et al., 2003; Moore et al., 2002). For example, different levels of the homeodomain protein Cut have been shown to regulate distinct dendritic branching patterns of peripheral nervous system (PNS) neurons, with higher Cut levels directing the development of more complex dendritic arbors (Grueber et al., 2003). Interestingly, we find that Nkx6 protein levels vary dramatically and reproducibly between CNS neurons (Fig. 1). This raises the possibility that Nkx6 directs distinct patterns of axon outgrowth as a function of expression level—potentially adding another layer of complexity to Nkx6-transcriptional output.

Our study also indicates that Nkx6 proteins have evolutionarily conserved functions in neuronal fate specification. In Drosophila, the role of Nkx6 in neuronal specification is uncovered in hb9 Nkx6 double mutants. The phenotype we observe in Nkx6 mutants is a dramatic block to axon growth of Nkx6-positive neurons. Is it possible that this activity of Nkx6 in postmitotic neurons is conserved? Similar to Nkx6, vertebrate Nkx6.1 is expressed in postmitotic neurons, consistent with a functional role in neuronal differentiation. Interestingly, Müller et al. show that hindbrain visceral MNs in Nkx6.1 mutant mice display aberrant axon guidance and ectopically express the Ret and Unc5h3 receptors (Müller et al., 2003). Hence, Nkx6-class proteins appear to play conserved roles in regulating axon growth and guidance. It will be critical to determine whether the downstream factors they regulate are conserved as well.

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We dedicate this paper to the memory of Nancy C. Tarczy.

Supplementary material

Supplementary material for this article is available at http://dev.biologists.org/cgi/content/full/131/21/5233/DC1

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