Novel mutations affecting axon guidance in zebrafish and a role for plexin signalling in the guidance of trigeminal and facial nerve axons

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In zebrafish embryos, the axons of the posterior trigeminal (Vp) and facial (VII) motoneurons project stereotypically to a small number of target muscles derived from the first and second branchial arches (BA1, BA2). Use of the Islet1 (Isl1)-GFP transgenic line enabled precise real-time observations of the growth cone behaviour of the Vp and VII motoneurons within BA1 and BA2. Screening for N-ethyl-N-nitrosourea-induced mutants identified seven distinct mutations affecting different steps in the axonal pathfinding of these motoneurons. The class 1 mutations caused severe defasciculation and abnormal pathfinding in both Vp and VII motor axons before they reached their target muscles in BA1. The class 2 mutations caused impaired axonal outgrowth of the Vp motoneurons at the BA1-BA2 boundary. The class 3 mutation caused impaired axonal outgrowth of the Vp motoneurons within the target muscles derived from BA1 and BA2. The class 4 mutation caused retraction of the Vp motoneurons in BA1 and abnormal invasion of the VII motor axons in BA1 beyond the BA1-BA2 boundary. Time-lapse observations of the class 1 mutant, vermicelli (vmc), which has a defect in the plexin A3 (plxna3) gene, revealed that Plxna3 acts with its ligand Sema3a1 for fasciculation and correct target selection of the Vp and VII motor axons after separation from the common pathways shared with the sensory axons in BA1 and BA2, and for the proper exit and outgrowth of the axons of the primary motoneurons from the spinal cord.

KEY WORDS: Zebrafish, Trigeminal motoneuron, Facial motoneuron, Plexin A3 mutant, Axon pathfinding

INTRODUCTION

The neuromuscular connection is one of the simplest model systems available for analysis of the mechanisms underlying establishment of functional neural circuits. This system has been used in many studies in vertebrates and invertebrates. Gene knockdown analyses and tissue- and cell-transplantation studies in mouse, chick and zebrafish have revealed that the differentiation and specification of each motoneuron type that innervates target muscles is regulated by the combined temporal expression of transcription factors. These include the LIM-homeodomain-type transcription factors Isl1 (Isl1), Isl2 (Isl2) and Lhx3, and the bHLH-type transcription factors neurogenin 2 and Neuro-M (Appel et al., 1995; Eisen, 1991; Inoue et al., 1994; Landmesser, 2001; Lee and Pfaff, 2003; Segawa et al., 2001; Thaler et al., 2002; Tokumoto et al., 1995; Tsuchida et al., 1994; Uemura et al., 2005). In vertebrates, screening for Drosophila mutants showing defects in the axonal pathfinding of motoneurons to specific target muscles has led to the identification of specific ligands and receptors in the neuromuscular connection system, including Semaphorin (Sema)/Plexin (Plex), Slit/Robo, Netrin/Frazzled (a Drosophila homologue of mouse Dcc), and receptor protein tyrosine phosphatases (Desai et al., 1996; Johnson and Van Vactor, 2003; Kidd et al., 1999; Kolodkin et al., 1993; Kolodziej et al., 1996; Winberg et al., 1998). Cell adhesion molecules, extracellular matrix molecules, and glycosylated derivatives of these molecules, also participate in the axonal pathfinding process (Birely et al., 2005; Kantor et al., 2004; Keshishian et al., 1996; Schneider and Granato, 2006). The role of these molecules in the regulation of motoneuron axonal pathfinding, the temporal and spatial regulation of these molecules as an integrated system, and the mechanisms underlying their molecular interactions remain unclear.

The jaw muscles of zebrafish embryos are composed of a small number of identifiable muscles derived from the first and second branchial arches (BA1 and BA2) (Fig. 1A,B) (Higashijima et al., 1997; Higashijima et al., 2000; Schilling and Kimmel, 1994; Schilling and Kimmel, 1997). These muscles are innervated by the axons of the anterior and posterior trigeminal motoneurons (Va and Vp) that originate from rhombomeres 2, 3 (r2 and r3), and also by the axons of the facial motoneurons (VII) that originate from r4 (Fig. 1C). The present study shows the stereotypical stepwise outgrowth pattern of the Vp and VII motor axons to target muscles. This was achieved in the Isl1-GFP transgenic strain (Higashijima et al., 2000) using time-lapse observations of axonal pathfinding behaviour of the Vp and VII motoneurons in the lower jaw region of BA1 and BA2, together with laser-mediated cell ablation and

Accepted 12 June 2007

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single-cell labelling of the Vp motoneurons. The identification of the genetic loci regulating the stereotypical axonal pathfinding of the Vp and VII motoneurons was achieved by screening mutants. Seven distinct mutant loci leading to specific disruption of the different steps of the axonal pathfinding processes were identified. These mutants were classified into four groups according to the developmental stage in which the axons of the Vp and VII motoneurons began to show abnormal behaviour in the lower jaw region. In addition to abnormal motor axon pathfinding, some mutants displayed other neural defects. In the mutant vermicielli (vc), the thick bundle of the Vp and VII motor axons defasciculated into thin branches, with each axon behaving randomly after separation from the common pathway shared with sensory axons. We identified a defect in the gene encoding the zebrafish orthologue of plexa3 and demonstrated that Ptxna3-mediated Sema3a1 signalling is required for the outgrowth of the Vp and VII motoneurons.

### MATERIALS AND METHODS

#### Animals

Zebrafish (*Danio rerio*) were maintained according to standard procedures (Westerfield, 2000). The Isl1-GFP and α-actin-GFP lines, registered as Tg(CM-isl1:GFP)5179 and Tg(a-actin:GFP), respectively, in the Zebrafish National BioResource Center of Japan, http://www.shigen.nig.ac.jp/zebra/ (Hiyama et al., 1997; Hiyama et al., 2000), are derived from the RIKEN Wako (RW) wild-type strain. The WIK strain was used for genetic mapping. The embryos were staged according to Kimmel et al. (Kimmel et al., 1995). To prevent pigmentation, embryos were raised in fish water containing 0.0015% N-phenylthiourea (PTU; Nakara) from approximately 12 hours postfertilisation (hpf) (Burrill and Easter, 1994).

#### Mutagenesis

Mutagenesis was carried out as described previously (Solnica-Krezel et al., 1994; Wada et al., 2005). Mutations were induced in the male germ cells of Isl1-GFP fish using N-ethyl-N-nitrosourea (ENU; Sigma). To isolate the mutants showing defects in axonal pathfinding of the Vp and VII motoneurons, the embryos from the F2 pairwise crosses were fixed at 72 hpf using trichloroacetic acid (Wako) and stained with anti-acetylated α-tubulin antibody, as described below. The axonal projection patterns of the Vp and VII motoneurons were examined under a dissecting microscope (SMZ1500; Nikon). Of the 1816 haploid genomes (1171 families) screened, three alleles of the vermicielli locus (vmc<sup>206</sup>, vmc<sup>314</sup> and vmc<sup>415</sup>), one allele of the keep off locus (kof<sup>390</sup>), one allele of the mekong locus (mek<sup>656</sup>), one allele of the blue nile locus (bnv<sup>664</sup>), three alleles of the rio grande locus (rgd<sup>218</sup>, rgd<sup>395</sup> and rgd<sup>520</sup>), one allele of the loose end locus (loe<sup>215</sup>), and one allele of the trespassing locus (tps<sup>455</sup>) were identified. To confirm the allelic group, we performed complementation analysis within with phenotypically related mutations.

#### Genetic mapping of the mutation loci

Homozygous embryos (708 of vmc, 438 of kof, 474 of mkn, 1068 of bnl, 794 of rgd, 480 of loe and 460 of tps) were selected from the heterozygous parents, which themselves were made by crossing the heterozygous mutant fish with the wild-type WIK strain. Genomic DNA was extracted from individual embryos at 72 hpf, which were fixed and stained with anti-acetylated α-tubulin antibody as described below. To assign the locus of the mutation to a linkage group, we performed bulk segregant analysis. We then refined the mapping position by scoring meiotic recombination frequency using simple sequence-length polymorphism (SSLP) markers. The positions of SSLP markers were confirmed using the ENSEMBL genome assembly database. The genetic locus of each mutation is shown in Fig. 3. We also confirmed the positions of mutation loci by LN54 radiation hybrid panel using the closest (<0.1 CM) SSLP markers. The linkage group and the positions in the radiation hybrid map are indicated for each mutant in Table 2. By comparison with the known mutation loci registered in Zebrafish Information Network (ZFIN) database, we found that all our mutants were novel.

| Table 1. The antisense morpholino oligonucleotides (AMOs) used in this study |
|---------------------------------|-------------------------|
| **plexa3 AMO**                  | 5'-TACCGACGCGCCACAGGACCTAGT-3' |
| **plexa3 AMO-5mis**             | 5'-TCaGAgGACGACGAGGAgTCATG-3' |
| **sema3f1 AMO**                 | 5'-ACCGCAGAGATTTATGCACGTCTC-3' |
| **sema3f1 AMO-5mis**            | 5'-ACGGTAAAGAAATTATCTACGC-3' |
| **sema3f2 AMO**                 | 5'-CATGACCTGCTGACAAGGATGTC-3' |
| **sema3f2 AMO-5mis**            | 5'-CAACAGAGCAAACCCACACGATCC-3' |
| **nrp1b AMO**                   | 5'-ACAGAAAGCAAAAGCCATACATC-3' |
| **nrp1b AMO-5mis**              | 5'-CCTGATTGATAATACGAAATGGC-3' |
| **nrp2a AMO**                   | 5'-CCTGGTAGAGAAAGAAGCTGAAGTC-3' |
| **nrp2a AMO-5mis**              | 5'-CGGGTAGAGAAAGAAGCTGAAGTC-3' |
| **nrp2b AMO**                   | 5'-CGCCATACACCAAGAAGCTAATCC-3' |

Cloning and sequencing of plexa3 cDNA

To confirm the nucleotide substitution within the plexa3 gene, total RNA was extracted from homozygous vmc embryos at 72 hpf (vmc<sup>206</sup>, vmc<sup>314</sup> and vmc<sup>415</sup>) using the RNA Extraction Kit (Nippon Gene), and cDNA was synthesised using the SuperScript III One-Step RT-PCR System with Platinum Taq DNA Polymerase (Invitrogen). The primers used to synthesise full-length plexa3 cDNA were designed according to genomic sequences from the genome database of the Sanger Centre, Cambridge, UK: sense, 5'-CTCGGACCAACATGGCATTTCC-3' and antisense, 5'-TCAGCTGTCCAGAGCATCAG-3'.

#### Gene knockdown by antisense morpholino oligonucleotides

The antisense morpholino oligonucleotides (AMOs) were designed (by Gene Tools, LLC) to target the first initiation codon of each gene: for AMO sequences, see Table 1. plexa4, sema3a1, sema3a2 and nrp1A AMOs have been described previously (Miyashita et al., 2004; Sato-Maeda et al., 2006; Yu and Moens, 2005). Approximately 1 nl of AMO (2 mg/ml) was injected into one- to two-cell stage embryos, as described previously (Nasevicius and Ekker, 2000).

#### In situ hybridisation, immunohistochemistry and rhodamine-phalloidin staining

In situ hybridisation was performed essentially as described previously (Westerfield, 2000) using RNA probes for isl1, isl2, plexa3, plexa4, sema3a1, sema3a2, sema3f1, sema3f2, nrp1a, nrp1b, nrp2a and nrp2b. Immunohistochemistry, using a cocktail of znp-1 antibody and zn-1 monoclonal antibody that recognises primary motoneurons (Oregon Monoclonal Bank; 1:200 and 1:50, respectively), or anti-Kaele polyclonal antibody (MBL; 1:50), was performed according to standard procedures (Westerfield, 2000). For immunohistochemistry using anti-acetylated α-tubulin (Sigma; 1:2000), the embryos were fixed at 72 hpf for 2 hours at room temperature, according to the protocol kindly provided by Dr Stephen W. Wilson (University College London, UK), using 2% trichloroacetic acid in 0.1 M phosphate buffer (pH 7.3), followed by treatment as described above. For the secondary antibody, anti-mouse IgG conjugated to Alexa-488, anti-rabbit IgG conjugated to Alexa-532 (Invitrogen; 1:500) and Histofine Simple Stain MAX-PO (M) (Nichirei) were used. Rhodamine-phalloidin staining was performed according to a previously described procedure (Higashijima et al., 2000). Specimens were visualised by laser-scanning confocal microscopy (LSM 510; Zeiss).

#### Dial labelling

Anterograde and retrograde labelling of the Vp axons was performed using 2 mg/ml 1,1'-dioctadecyl-3,3,3'2-tetrachlorodihydrodicyanoborane perchlorate (Dil) dissolved in 100% dimethylformamide. Before labelling, embryos at 70 hpf were anesthetised and embedded in 1.2% low melting point agarose. Dil solution was then applied to the peripheral axons of the Vp motoneurons using a pressure injector (IM300; Narishige). Dil-injected embryos were incubated for 2 hours at 28°C, and labelled axons were observed by laser-scanning confocal microscopy.
Single-cell labelling by transient mosaic expression of GFP or Kaede

The CMICP-GFP plasmid (Higashijima et al., 2000) (for consistency with the name of the transgenic line, this is referred to here as the Isl1-GFP plasmid) was used to drive expression of GFP under the control of the enhancer of the isl1 gene in most cranial motoneurons. The HuC-Kaede plasmid (Sato et al., 2006) was used to drive expression of Kaede in most neurons under the control of the HuC (also known as elavl3 – ZFIN) promoter. The plasmid Isl1-GFP at 10 to 50 ng/μl, or the plasmid HuC-Kaede at 5 ng/μl, was pressure injected into one-cell stage zebrafish embryos. Kaede protein emits green fluorescence that can be converted to red fluorescence by the irradiation of ultraviolet (UV) or violet light (Ando et al., 2002). To observe stochastically Kaede-labelled motoneurons in the Isl1-GFP embryos, Kaede was photoinactivated by irradiation of the whole embryo with UV light for 1 to 2 seconds using an upright epifluorescence microscope (Axioplan; Zeiss) with an Achromplan 40× (NA 0.80) water-immersion objective. Selected embryos were fixed and stained with anti-Kaede antibody as described above. To observe GFP-labelled neurons, the embryos were anesthetised and embedded in 1.0% low melting point agarose. The axonal projection patterns of the labelled neurons were then examined using the laser-scanning confocal microscope.

Sequential time-lapse z-stack imaging of the multiple mutant embryos

Time-lapse z-stack imaging of multiple live mutant embryos was performed using a procedure we developed for sequential time-lapse observation of multiple samples with the laser-scanning confocal microscope equipped with an electric motor-driven stage (MCU28; Zeiss) (for details, see Fig. S3 in the supplementary material). Sequential z-stack images (1 μm intervals, 30 focal planes) of six embryos were collected automatically every 15 minutes for 12 to 24 hours using the software supplied with the LSM510 (Multi Time Series Rev. 3.2p). All images were obtained using a Plan-NEOFLUAR 20× (NA 0.50) objective.

Laser-mediated cell ablation

Isl1-GFP transgenic zebrafish embryos were used for laser-mediated cell ablation. Anesthetised 48-hpf embryos were embedded in 1.2% low melting point agarose. The cluster of the Vp motoneurons was then killed using a Micropoint dye laser-mediated cell-ablation system (VSL-337ND; Laser Science) with Coumarin440 nitrogen-pumped dye (peak wavelength 445 nm) attached to an upright epifluorescence microscope (Axioskop; Zeiss) with Achromplan 63× (NA 0.90) water-immersion objective. Irradiation of the Vp cluster with five or six laser pulses was performed until the GFP signals disappeared. After irradiation, we observed the axonal pathfinding behaviour of the intact Vp neurons on the non-operated contralateral side using the laser-scanning confocal microscope. Images were captured every 2 hours from 48 hpf to 62 hpf, and at 72 hpf.

RESULTS

The Vp and VII motoneuron axons project sequentially to target muscles within BA1 and BA2 in a stereotypic stepwise manner

Time-lapse observations of the growth of the Vp and VII motor axons were made using Isl1-GFP transgenic embryos expressing GFP in the cranial motoneurons under the control of the motoneuron-specific enhancer of the isl1 gene (Higashijima et al., 2000). Time-lapse observations were also made using the double-transgenic embryos for Isl1-GFP and α-actin-GFP, which expressed GFP in both motoneurons and muscles. By 52 hpf, the Vp motoneuron axons extended ventrally along the pathway in BA1 shared by the sensory trigeminal axons (Fig. 1B, thick black arrow), then separated from the common pathway before extending into the lower jaw region (Fig. 1Da,f,k). At about 54 hpf, the Vp motoneuron axons bifurcated (Fig. 1Db inset, 1D1) and reached the BA1-BA2 boundary, at which stage the growth cones of the axons extended along the boundary (Fig. 1Db,g, broken line).

Concomitantly, the precursors of the intermandibular anterior and the intermandibular posterior muscles started to differentiate around the midline in BA1 (Fig. 1Db,g,l). At 58 hpf, the growth cones of the Vp motoneurons crossed the midline and paused for about 4 hours (Fig. 1De,h,m). Then, at approximately 62 hpf, the growth cones on both sides again changed growth direction and extended posteriorly by crossing the BA1-BA2 boundary toward the interhyal muscles derived from BA2 (Fig. 1Dd,i,n). Around 72 hpf, the Vp motor axons completed the projection to the hyohyal muscles in the lower jaw region (Fig. 1De,j,o).

The growth cones of the VII motoneurons also detached from the common pathway shared with the sensory axons in BA2 at about 42 hpf (Fig. 1B, thick white arrow). At approximately 54 hpf, they were near the already differentiated hyohyal muscles derived from BA2 (Fig. 1Db,g,l). From 54 to 58 hpf, the growth cones of the VII motoneurons paused at this position and resumed growth only after 62 hpf (Fig. 1Db-d,g-i,l-n, arrowheads). At about 72 hpf, the VII motoneurons completed the projection to the hyohyal muscles in the lower jaw region (Fig. 1De,j,o).

These observations suggested that both Vp and VII motoneurons projected to their target muscles in a stepwise fashion. Initially, the Vp motoneurons projected to the muscles derived from BA1. During this period, the VII motoneurons did not project to target muscles derived from BA2, even though these muscles were already differentiated. When the initial projection to the BA1-derived muscles was complete, the Vp and VII motoneurons then projected to muscles derived from BA2.

The Vp motoneuron axons bifurcate and project to BA2-derived target muscles on both sides

Time-lapse observations revealed that the growth cones of the Vp motor axons from both sides crossed the midline of the lower jaw region. To examine whether correct axonal pathfinding of the Vp motoneurons from one side depends on interaction with axons from the other side at the ventral midline, the Vp motoneurons on the right side (Fig. 2Aa, arrowhead) were selectively removed at 48 hpf using laser ablation. The outgrowth of the Vp motor axons from the intact side was observed (Fig. 2A). To avoid damage to the Vp neurons on the left side, some of the Vp motoneurons on the right side close to the midline were left intact (Fig. 2Aa-e, brackets). The axons from the laser-irradiated Vp neurons completely degenerated, and the axons from the remaining Vp neurons on the right side did not reach the lower jaw by 72 hpf (Fig. 2Af-j, asterisks). Despite the absence of axons from the contralateral Vp motoneurons, the axons from the intact side showed normal pathfinding behaviour, and projected to the interhyal muscles on both sides in BA2 (Fig. 2Af-j). This result demonstrated that axonal outgrowth of the Vp motoneurons on each side proceeded independently.

We then investigated whether the same or different Vp motoneurons on one side of the hindbrain projected to both the ipsilateral and contralateral lower jaw muscles in BA2. DiI was applied to the common pathway of the Vp axons, and DiI-labelled axons were observed to transfer anterogradely to the interhyal muscles on both sides (Fig. 2Ba, arrowheads). DiI was then applied to the caudal end of the interhyal muscles on one side, which resulted in labelling of the ipsilateral and contralateral branches of the Vp axons innervating the interhyal muscles (Fig. 2Bb, arrowhead). Injection of the Isl1-GFP construct into one-cell stage embryos enabled the transient and stochastic GFP labelling of some of the cranial motoneurons (Fig. 2Ca,b). The GFP-positive axon from a single Vp motoneuron (Fig. 2Ca, arrowhead) was observed.
to bifurcate and project bilaterally to the interhyal muscles (Fig. 2C, arrowheads). These results showed that most of the Vp motoneurons bifurcated at the BA1-BA2 boundary and extended axons to the interhyal muscles on both sides in BA2.

**Mutant identification allowed genetic dissection of the stepwise outgrowth of the Vp and VII motor axons into the lower jaw region**

To identify the molecules regulating the axonal pathfinding behaviours of Vp and VII motoneurons in BA1 and BA2, we screened ENU-induced mutants with specific defects in these processes. Using complementation analysis, we identified 11 mutations disrupting seven different genes, each affecting the axonal pathfinding behaviour of the Vp and VII motoneurons in a distinctive manner (Fig. 3, Table 2). Each mutation locus was genetically mapped to a distinct location on the chromosome, and these loci did not coincide with any other mutation loci registered in the ZFIN database (Fig. 3). These results were also confirmed using a LN54 radiation hybrid panel (Table 2). Therefore, we concluded that each mutant allele had a novel, distinct mutation locus. These mutations were categorised into four groups according to the developmental stage in which the axons of the Vp and VII motoneurons begin to show abnormal behaviour.

The class 1 mutations included three *vermicelli* (*vmcrw260*, *vmcrw314* and *vmcrw413*) and one *keep off* (*kofrw309*) allele (Fig. 3B,C). The axons of both Vp and VII motoneurons (*vmc* mutants) or of Vp motoneurons alone (*kof* mutant) were defasciculated and extended randomly over target muscles (Fig. 3B,C). The class 2 mutations included one *mekong* (*mknrw656*), one *blue nile* (*bnlrw646*) and three *rio grande* (*rgdrw218*, *rgdrw395*, and *rgdrw520*) alleles (Fig. 3D-F). In contrast to the class 1 mutants, axons of the Vp and VII motoneurons (*vmc* mutants) or of Vp motoneurons alone (*kof* mutant) were defasciculated and extended randomly over target muscles (Fig. 3B,C). The class 2 mutations extended normally through BA1, with the outgrowth of the Vp axons ceasing when the growth extended just past the ventral midline. In these mutants, the axons of the Vp motoneurons did not project to the target muscles in BA2 on either side (Fig. 3D-F). The class 3 mutation included one *loose end* allele (*loerw357*) (Fig.
3G). Unlike the class 1 and 2 mutants, the axons of the Vp motoneurons in the loe mutant extended along the normal pathway until the BA1-BA2 boundary was crossed, then the growth cones stalled on the way to the caudal end of BA2 (Fig. 3G). The class 4 mutation included one trespassing allele (tpsrw453) (Fig. 3H). In this mutant, the axons of the Vp motoneurons extended initially to the intermandibularis posterior muscles in BA1, then retracted along the path they had grown. The axons of the VII motoneurons extended ectopically as far as the muscles in BA1, by crossing the BA1-BA2 boundary.

In addition to the defects in axonal pathfinding of the Vp motoneurons described above, the kof, bnl and rgd mutations caused defects in the axonal pathfinding of the retinal axons and in differentiation of neurons in the lateral part of the hindbrain and the spinal cord (see Fig. S1 in the supplementary material).

**The vmc mutation causes severe axonal pathfinding errors of the Vp and VII motoneurons after separation from the common pathways**

Time-lapse observations were performed to examine axonal outgrowth of the Vp and VII neurons in the vmc embryos (Fig. 4; see Movies S1-6 in the supplementary material). The axons of the VII motoneurons (Fig. 4A, red in the schemes) grew normally along the common pathway within BA1 that was shared with the trigeminal sensory axons (blue in the schemes). As observed for the VII motoneurons, the Vp motor axons also defasciculated into thin branches and grew randomly over the lower jaw region, whereas the outgrowth of the trigeminal sensory and facial sensory axons remained normal (Fig. 4B; see Movies S5-6 in the supplementary material). These observations suggested that the vmc mutation selectively affected the axons of the Vp and VII motoneurons only after they were separated from the common growth pathways and extended towards their target muscles.

**The vmc locus encodes the zebrafish orthologue of plxna3**

The mutated vmc gene was cloned to elucidate the role of the vmc gene product. The vmc locus was genetically mapped between the SSLP markers fj56g03 and z15045 on chromosome 8 (Fig. 5A). This locus encodes the zebrafish orthologue of plxna3. cDNA fragments of plxna3 were isolated from total RNA extracted from wild-type and vmc homozygous embryos by RT-PCR. A comparison of the cDNA nucleotide sequences of three vmc mutants (vmcrw260, vmcrw314 and vmcrw413) revealed missense mutations within the regions encoding the Sema domain (vmcrw260, E169D), the IPT Plexin repeat 3 domain (vmcrw314, C1090S) and the SP domain (vmcrw413, W1746R) of Plxna3 (Fig. 5B). In addition, one of the alleles (vmcrw260) had an additional nonsense mutation within the Sema-encoding region. There were no significant differences in phenotype between these alleles.

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**Fig. 2. No interaction is required between the left and right Vp motor axons for projection to the bilateral interhyal muscles in BA2.** (A) Time-lapse images from 48-72 hpf of the Vp motoneurons after laser irradiation to the lateral part of the Vp motoneurons on the right side (a-e, arrowheads). Dorsal (a-e) and ventral (f-j) views of the same operated zebrafish embryo. Anterior, top. Brackets indicate remaining cells on the right side (a-e). Asterisks indicate the nerve end of the operated motoneurons (f-j). (B) Anterograde (a) and retrograde (b) labelling of the Vp motor axons of 72-hpf wild-type embryos with Dil. Ventral view; anterior, top. Asterisks indicate the points of Dil application. Arrowheads indicate the ends of the labelled axons. (C) Stochastic expression of GFP using the isl1-GFP construct. Ventral (a) and dorsal (b) views; anterior, top. Arrowheads indicate a single Vp motoneuron labelled with the isl1-GFP construct (a) and the ends of the labelled axons (b).
**Plxna3 (vmc) may act as an essential component of the receptor for Sema3a1 signalling in axonal pathfinding of the Vp and VII motoneurons**

A previous study using *plxna3*/*plxna4* double-knockout mice demonstrated that in sensory and sympathetic neurons, Plxna3 is principally responsible for responses to Sema3f via neuropilin 2 (Nrp2), and Plxna4 is principally responsible for responses to Sema3a via Nrp1 (Yaron et al., 2005). However, there is significant cross association of Plxna3 with Nrp1 and of Plxna4 with Nrp2, which results in involvement of Plxna3 and Plxna4 in mediation of the Sema3a and Sema3f signals, respectively. Therefore, we examined the localisation of the expression of *plxna3*, *plxna4*, *isl1* and *nrp1a* in the cranial motoneurons (Fig. 6Aa-d). Expression of *plxna4* was not observed in the cranial motoneurons, but was possibly present in some interneurons located more dorsolaterally than the cranial motoneurons in the hindbrain (Fig. 6Ad). A previous report demonstrated that *nrp2a* is expressed in the medial part of r2, r3 and r6, which correspond in part to the locations of the Va, Vp and VII motoneurons, and also that *nrp2b* is expressed in a subset of hindbrain neurons in r4 to r6 that may correspond to the VII motoneurons (Yu et al., 2004). We found that *plxna3* and *nrp1a* were expressed at 36 hpf in the Va, Vp, and VII motoneurons, similarly to *isl1* (Fig. 6Aa-c). These expression patterns imply that Plxna3 forms a receptor complex with either Nrp1a, Nrp2a or Nrp2b in the cranial motoneurons (Yu et al., 2004). We found that *plxna3* and *nrp1a* were expressed at 36 hpf in the Va, Vp, and VII motoneurons, similarly to *isl1* (Fig. 6Aa-c). These expression patterns imply that Plxna3 forms a receptor complex with either Nrp1a, Nrp2a or Nrp2b in the cranial motoneurons (Yu et al., 2004).

Sema3a2 was expressed in the dorsal part of BA2 and in the boundary region between BA1 and BA2 at 36 and 48 hpf. Sema3f1 was expressed in the boundary region between BA1 and BA2 at 36 and 48 hpf. Sema3f2 was weakly expressed in the ventral part of BA2 at 36 and 48 hpf. Among these, the expression of *sema3a1* changed remarkably during development (Fig. 6Ba,e; Fig. 6C). At 36 hpf, expression of *sema3a1* was observed in the posterior margin of BA2 (Fig. 6Ba, arrow; Fig. 6C). By 48 hpf, an additional expression domain appeared in the regions around the adductor mandibulae muscles in BA1 (Fig. 6Be, arrows; Fig. 6C). The temporal expression pattern of *sema3a1* correlates with the timing of the separation of the axons of the Vp motoneurons from the common pathway in BA1 as described above. These findings raise the possibility that Sema3a1 signalling through the Plxna3-Nrp1a, Nrp2a or Nrp2b receptor complexes might be involved in regulation of the axonal growth of the Vp and VII motoneurons in BA1 and BA2.

To test this hypothesis, we examined the knockdown phenotypes using AMOs against all zebrafish paralogues of *plxna3*, *plxna4*, *nrp1*, *nrp2*, *sema3a* and *sema3f* (Fig. 7; see Table S1 in the supplementary material). The embryos injected with these AMOs at the one- or two-cell stage were stained with anti-acetylated α-tubulin antibody at 72 hpf. The embryos injected with the *nrp1a* AMO died early owing to angiogenesis defects, whereas the other morphants developed up to 72 hpf (Fig. 7; see Table S1 in the supplementary material). The *plxna3* and *sema3a1* morphants displayed similar defects in the axonal pathfinding behaviour of both the Vp and VII motoneurons as were observed in the *vmc* embryos (Fig. 7B,D, arrows; Fig. 7E). By contrast, the other morphants showed normal trajectories of the Vp and VII motoneurons (Fig. 7C,E; see Table S1 in the supplementary material). These results suggest that Plxna3 is likely to act as an essential component of the receptor for Sema3a1,
**Table 2. Mutations affecting the axonal pathfinding of the Vp and VII motoneurons**

<table>
<thead>
<tr>
<th>Genetic locus</th>
<th>LG (position*)</th>
<th>Alleles</th>
<th>Phenotypes</th>
<th>Other phenotypes</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Class 1</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><em>vermicelli</em> (vmc)</td>
<td>LG8 (117.9 cR)</td>
<td>rw260, rw314, rw413</td>
<td>The axons of both Vp and VII defasciculate and grow randomly on their target muscle regions</td>
<td></td>
</tr>
<tr>
<td><em>keep off</em> (kof)</td>
<td>LG4 (464.0 cR)</td>
<td>rw309</td>
<td>The axons of the Vp defasciculate and grow randomly on their target muscle regions</td>
<td>Abnormal formation of the optic chiasm; tail curl down</td>
</tr>
<tr>
<td><strong>Class 2</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><em>mekong</em> (mkn)</td>
<td>LG7 (22.7 cR)</td>
<td>rw656</td>
<td>Axonal growth of the Vp into BA2 is impaired</td>
<td></td>
</tr>
<tr>
<td><em>blue nile</em> (bnl)</td>
<td>LG14 (297.4 cR)</td>
<td>rw646</td>
<td>Axonal growth of the Vp into BA2 is impaired</td>
<td>Is1-GFP-positive neurons are ectopically induced in the dorsolateral part of r4 to r6 in the hindbrain and in the epibranchial region in BA2. The axons of secondary motoneurons show abnormal trajectory</td>
</tr>
<tr>
<td><em>rio grande</em> (rgd)</td>
<td>LG5 (25.5 cR)</td>
<td>rw218, rw395, rw520</td>
<td>Axonal growth of the Vp into BA2 is impaired</td>
<td></td>
</tr>
<tr>
<td><strong>Class 3</strong></td>
<td></td>
<td></td>
<td></td>
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<tr>
<td><em>loose end</em> (loe)</td>
<td>LG24 (156.0 cR)</td>
<td>rw357</td>
<td>Axonal growth of the Vp is impaired on their target muscles and projection of the VII to the hyohyal muscles is impaired</td>
<td></td>
</tr>
<tr>
<td><strong>Class 4</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><em>trespassing</em> (tps)</td>
<td>LG22 (92.9 cR)</td>
<td>rw453</td>
<td>The axons of the Vp retract along the growing pathway in BA1 and the axons of the VII ectopically grow to BA1 crossing the BA1-BA2 boundary</td>
<td></td>
</tr>
</tbody>
</table>

*Positions of each mutation locus were determined by LN54 radiation hybrid panel using the closest (<0.1 cM) SSLP markers of each mutation locus.

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**Fig. 4. Time-lapse observations of the axonal outgrowth of the Vp and VII motoneurons in vmc embryos.** (A) Time-lapse images of the axonal outgrowth of the VII motoneurons in wild-type (a-d) and vmc (e-h) zebrafish embryos. Lateral views; anterior, left. The axons of the VII motoneurons (red) and facial sensory (fs) neurons (blue) separated from each other at the points indicated by red asterisks (b-d,f-h). Arrows indicate the abnormal axons (f-h). (B) Time-lapse images of the axonal outgrowth of the Vp and VII motoneurons in wild-type (a-d) and vmc (e-h) embryos. Ventral views; anterior, top. The axons of the Vp and VII motoneurons (red) defasciculated into thin axons and grew abnormally (e-h). However, the axons of the trigeminal sensory (tg) and fs neurons (blue) grew normally (e-h).
although the involvement of Plxna3 in the Sema3a signal was reported to be rather minor in the axonal pathfinding of the sensory ganglia in mice (Yaron et al., 2005).

**Plxna3 (vmc) is required for correct axonal pathfinding of primary motoneurons**

We found defects in the axonal pathfinding of primary motoneurons in the vmc embryos (Fig. 8). The axons of primary motoneurons were visualised by immunohistochemistry, using a cocktail of the znp-1 and zn-1 monoclonal antibodies (Fig. 8A,Be). In the vmc embryos, some of the axons extended ventrally out of the spinal cord through the normal exit point (Fig. 8A, arrowheads) then displayed an abnormal trajectory at 28 hpf (Fig. 8Ab, blue arrow). Other axons extended out of the neural tube through ectopic exit points (Fig. 8Ab, red arrows). We also performed single-cell labelling by the transient and stochastic expression of Kaeede following injection of the HuC-Kaeede plasmid (Sato et al., 2006) into one-cell stage embryos (Fig. 8B). In the wild-type embryos, the axons of primary motoneurons initially grew posteriorly (rostral and middle primary motoneuron, Fig. 8Ba,b) or ventrally (caudal primary motoneuron, Fig. 8Bc) within the spinal cord and extended through the same exit point (Fig. 8B, arrowheads). By contrast, in the vmc embryos, some axons grew anteriorly within the spinal cord then extended out of the spinal cord through an abnormal exit point (Fig. 8Bd-f, arrows; see Fig. S2A,B, arrows, in the supplementary material). The expression profile of plxna3 and nrp1a overlapped in all primary motoneuron types (Fig. 8C, asterisks). These findings suggest that Plxna3-dependent signalling is required not only for axonal pathfinding of the Vp and VII motoneurons in the cranial region, but also for pathway selection by the primary motoneurons in the spinal region in zebrafish.

**DISCUSSION**

In this study, time-lapse observations of the axonal pathfinding of the Vp and VII motoneurons in BA1 and BA2 in the Isl1-GFP transgenic line, revealed that the motoneurons projected to their target muscles in a stepwise fashion. We showed that the axonal pathfinding behaviours of the Vp and VII motoneurons could be genetically dissected into seven distinct mutations. This is the first example of genetic dissection of the axonal pathfinding of the cranial motoneurons in a vertebrate. Among the mutations, we found that the vermicelli (vmc) locus encodes the zebrafish orthologue of plxna3. We also showed that Plxna3 is likely to act as an essential
component for Sema3a1 signalling for fasciculation and target selection of the extending axons of the Vp and VII motoneurons in zebrafish embryos.

**Axonal growth of the Vp and VII motoneurons before separation from the common pathways might be regulated redundantly**

The axonal pathfinding of the Vp and VII motoneurons can be divided into two stages. Initially, these motor axons grow along common pathways shared with sensory neuron axons. Subsequently, they separate to extend to their respective target muscles. In the present study, all mutants displayed defects in the later stage of the axonal outgrowth of the Vp and VII motoneurons, after separation from the common pathways. Several redundantly expressed receptor tyrosine phosphatases regulate the separation of the motor axons from the common pathway at the choice point, both in *Drosophila* and in vertebrates (Desai et al., 1996; Johnson and Van Vactor, 2003; Sun et al., 2001; Stepanek et al., 2005; Uetani et al., 2006). Therefore, it is possible that the axonal pathfinding along the common pathway might be regulated by such redundant cues as receptor tyrosine phosphatases.

**Class 2 mutant gene products may regulate the boundary crossing of the Vp motoneurons at the BA1-BA2 boundary**

The growth cones of the Vp motoneurons paused several hours before they crossed the BA1-BA2 boundary and extended to their target muscles. In the class 2 mutant embryos (*mkn*, *bnl* and *rgd* mutants), growth of the Vp motor axons ceased at the BA1-BA2 boundary and did not resume. The *bnl* and *rgd* mutant embryos also displayed defects in the spinal motoneurons (see Fig. S1 in the supplementary material), suggesting a common mechanism underlying regulation of axonal pathfinding of the Vp motoneurons at the BA1-BA2 boundary and the pathway decision of the spinal motoneurons at the choice point. The zebrafish *unplugged* (*unp*; also known as *musk*) and *diwanka* (*diw*; also known as *plod3*) mutant embryos display cessation of axonal growth of the primary motoneurons at the growth pathway choice point (Schneider and Granato, 2006; Zhang et al., 2004). The *unp* locus encodes muscle-specific kinase, which is implicated in the accumulation of chondroitin sulphate proteoglycans around the choice point (Zhang et al., 2004). The *diw* locus encodes Procollagen-Iysine 2-oxoglutarate 5-dioxygenase 3, which glycosylates Col18α1, in the extracellular matrix along the motor path (Schneider and Granato, 2006). Similarly, modification of the extracellular matrix around the choice point may be affected in the *bnl* and *rgd* embryos.

**Class 3 and class 4 gene products are required for extension of the Vp motor axons to the target muscles**

The class 3 mutant *loe* caused impairment of the axonal outgrowth of the Vp motoneurons on the target muscles in BA1 and BA2. Unlike the other classes of mutants, the growth cones of the Vp motoneurons in the *loe* mutant embryos behaved normally at the BA1-BA2 boundary. Growth was inhibited, but there was no deviation from the normal growth pathway. In the class 4 mutant *tps*, the axons of the Vp motoneurons, which normally grow to the BA1-BA2 boundary, retracted from the boundary region. Concurrently, the axons of the VII motoneurons, which normally never cross the BA1-BA2 boundary, extended to the muscles in BA1 beyond the BA1-BA2 boundary. This observation suggests that the affinity of the growth cones of the Vp and VII motoneurons for the boundary region had changed in the *tps* mutation. Therefore, the molecules encoded by the *loe* and *tps* loci are implicated in the molecular machinery required for the extension of axons to target muscles or in the maintenance of the extended axons, but not in the growth pathway decisions.

**Sema3a1/Plxna3 signalling is required for fasciculation and correct axonal pathfinding of the Vp, VII, and the primary motoneurons**

In the present study, we identified the *vmc* locus encoded by the zebrafish orthologue of *plxna3*. We also demonstrated that Sema3a1/Plxna3 signalling is necessary for correct axonal pathfinding of the Vp and VII motoneurons. Mice homozygous for a targeted mutation in *Sema3a* or *Nrp1* show severe abnormalities in the peripheral axon projections of cranial and spinal neurons (Kitsukawa et al., 1997; Taniguchi et al., 1997). The loss-of-function phenotype for *Sema3a* signalling causes severe defasciculation and aberrant axonal pathfinding of the lateral motor column motoneurons around the target muscles in mouse and chick (Huber et al., 2005). These phenotypes are similar to the defects in the
Fig. 8. Plxna3 (vmc) is required for correct axonal pathfinding of the primary motoneurons. (A) Axons of primary motoneurons of wild-type (a) and vmc (b) zebrafish embryos at 28 hpf. The blue arrow indicates an axon that showed abnormal pathfinding after extending from the normal exit point. Red arrows indicate axons that extended from the abnormal exit points. (B) Kaede-labelled primary motoneurons of wild-type and vmc Isl1-GFP embryos at 36 hpf (a-f, red). Arrows indicate the axons of RoP- or MiP-like neurons that extended out of the spinal cord through abnormal exit points (d-f). In e, all axons were visualised using a cocktail of znp-1 and zn-1 antibodies (green). Arrowheads in A and B indicate the normal exit points. (C) Expression ofplxna3, nrp1a, isl1, isl2 and plxna4 mRNA in the spinal cord at 24 hpf. Asterisks indicate expression ofplxna3 (a) and nrp1a (b) mRNA. Bracket (c-e) indicates Rohon-Beard sensory neurons (RB). In all images, dorsal is top, anterior is left. CaP, caudal primary motoneuron; MiP, middle primary motoneuron; RoP, rostral primary motoneuron.

We wish to thank the members of the mutant-screening team in the Okamoto laboratory for their expert technical assistance and fish care, and M. Granato and K. A. Palaisa for communication of unpublished data. This research was supported in part by a Grant-in-Aid from the Ministry of Education, Science, Technology, Sports and Culture of Japan, and grants for Core Research for Evolutional Science and Technology from the Japan Science and Technology Corporation.

Supplementary material
Supplementary material for this article is available at http://dev.biologists.org/cgi/content/full/134/18/3259/DC1

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Development 134 (18)


