Planar polarity pathway and Nance-Horan syndrome-like 1b have essential cell-autonomous functions in neuronal migration

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SUMMARY
Components of the planar cell polarity (PCP) pathway are required for the caudal tangential migration of facial branchiomotor (FBM) neurons, but how PCP signaling regulates this migration is not understood. In a forward genetic screen, we identified a new gene, nhs1b, required for FBM neuron migration. nhs1b encodes a WAVE-homology domain-containing protein related to the human Nance-Horan syndrome (NHS) protein and Drosophila GUK-holder (Gukh), which have been shown to interact with components of the WAVE regulatory complex that controls cytoskeletal dynamics and with the polarity protein Scribble, respectively. Nhs1b localizes to FBM neuron membrane protrusions and interacts physically and genetically with Scrib to control FBM neuron migration. Using chimeric analysis, we show that FBM neurons have two modes of migration: one involving interactions between the neurons and their planar-polarized environment, and an alternative, collective mode involving interactions between the neurons themselves. We demonstrate that the first mode of migration requires the cell-autonomous functions of Nhs1b and the PCP components Scrib and Vangl2 in addition to the non-autonomous functions of Scrib and Vangl2, which serve to polarize the epithelial cells in the environment of the migrating neurons. These results define a role for Nhs1b as a neuronal effector of PCP signaling and indicate that proper FBM neuron migration is directly controlled by PCP signaling between the epithelium and the migrating neurons.

KEY WORDS: Facial branchiomotor neuron, Nance-Horan syndrome-like 1b, Planar cell polarity, Neuron migration, Zebrafish

INTRODUCTION
In the developing vertebrate brain, neurons frequently migrate considerable distances from the proliferative zone where they are born to the location where they carry out their specialized functions. Cell migration in general involves complex interactions between the migrating cell and its environment. Examples of such interactions within the central nervous system are those between migrating cortical neurons and their radial glia substrates (Marin and Rubenstein, 2003) and between neurons of the rostral migratory stream and the astrocytic tubes through which they migrate to the olfactory bulb (Kaneko et al., 2010). An in vivo genetic approach is required to understand the interactions between migrating neurons and their environment and to identify the genes involved in these interactions.

Accumulating evidence has indicated that directed cell migration is impacted by activity of the non-canonical Wnt/planar cell polarity (PCP) signaling pathway. In vertebrates, as in Drosophila, PCP signaling coordinates the orientation of cellular structures within the plane of an epithelium, such as the orientation of stereocilia bundles in the inner ear (Kelly and Chen, 2007) and the asymmetric localization of motile cilia in epithelia (Park et al., 2008; Borovina et al., 2010). The PCP pathway is also known to be active in controlling directed cell motility in convergent extension (CE) movements during gastrulation and the polarized cell behaviors required for neural tube closure (Heisenberg and Tada, 2002; Wallingford, 2006), neural crest migration (De Calisto et al., 2005; Carmona-Fontaine et al., 2008) and epidermal wound healing (Caddy et al., 2010). The involvement of PCP genes in neuronal migration comes from the study of facial branchiomotor (FBM) neurons in the segmented hindbrain of vertebrates. FBM neurons are a subset of cranial branchiomotor neurons that are generated ventrally in rhombomere (r)4 and undergo a highly stereotyped caudal migration into r6 and r7 in the zebrafish. There, they form the facial motor nucleus from which axons exit the hindbrain in r4 and innervate muscles in the head derived from the second branchial arch (Chandrasekhar, 2004). During this migration, FBM neurons move through the neuroepithelium adjacent to the floor plate, in contact both with the basement membrane and with other migrating FBM neurons (Grant and Moens, 2010). Zygotic loss-of-function of the core PCP components Vang-like 2 (Vangl2), Prickle (Pk1a and Pk1b), Frizzled (Fzd3a) and Celsr (Celsr2) in zebrafish all lead to a specific failure of FBM neuron migration (Bingham et al., 2002; Jessen et al., 2002; Carreira-Barbosa et al., 2003; Wada et al., 2005; Wada et al., 2006; Rohrschneider et al., 2007). This role for PCP in directing FBM neuron migration is evolutionarily conserved, as similar phenotypes are observed in mouse mutants for Vangl2, Fzd3 and Celsr (Vivancos et al., 2009; Qu et al., 2010).

Although this genetic evidence implicates the PCP pathway in FBM migration, it is unclear how PCP components regulate migration. In epithelia, PCP core components function to...
communicate subcellular differences in polarized information between neighboring cells in a cell-cell contact-dependent manner (Vladar et al., 2009). This molecular polarity is then transferred into context-dependent morphological asymmetries through the activity of cell type-specific downstream effector molecules that link polarity information to changes in the actin cytoskeleton (Strutt et al., 1997; Lee and Adler, 2002; Strutt and Warrington, 2008). In FBM neuron migration, previous chimeric analyses have suggested that the PCP components Vangl2, Fzd3a and Celsr2 act primarily non cell-autonomously, as wild-type neurons fail to migrate through a mutant neuroepithelium and mutant neurons do migrate through a wild-type environment, albeit incompletely (Jessen et al., 2002; Wada et al., 2005; Wada et al., 2006). Because the neuroepithelium through which FBM neurons migrate displays aspects of planar polarity and expresses PCP components (Ciruna et al., 2006; Borovina et al., 2010), it has been suggested that this environment shapes the trajectory of FBM neuron migration indirectly, by providing a permissive route for migration. However, other evidence suggests a more direct role for PCP signaling, as the core component Pk1b is required cell-autonomously for FBM neuron migration (Rohrschneider et al., 2007; Mapp et al., 2011). Importantly for this work, no PCP effectors for migration have been identified to date that could help to elucidate how the PCP pathway regulates neuronal migration in vivo.

The large PDZ-domain containing protein Scribble (Scrib) is also required for FBM neuron migration (Wada et al., 2005; Vivancos et al., 2009). Scrib has diverse functions in cell polarity and migration. In addition to its well known function in defining apico-basal polarity in epithelial cells in Drosophila together with Discs large (Dlg;Dlg1 – FlyBase) and Lethal giant larvae ([Lgl;L(2)gl – FlyBase] (Bilder et al., 2000; Bilder and Perrimon, 2000), Scrib functions as a PCP component in vertebrates, where it interacts with Vangl2 to control the orientation of ear sensory cells, convergent extension and neural tube closure (Montcouquiol et al., 2003; Murdoch et al., 2003; Wada et al., 2005; Montcouquiol et al., 2006). In migratory cells in culture, Scrib is localized to the leading edge, where it promotes cell protrusions by locally modulating the activity and localization of Rac and Cdc42 as a complex with the exchange factors βPIX and GIT1 (Osmani et al., 2006; Dow et al., 2007; Nola et al., 2008). Thus, Scrib represents a polarity protein with well characterized cell-autonomous functions in migration; however, until now, its function in FBM neuron migration, like that of other PCP components, has been described as largely non-autonomous (Wada et al., 2005).

In a zebrafish forward genetic screen for mutants with defective FBM neuron migration, we identified a mutation in Nance-Horan syndrome-like 1b (nhs1l1b

\[\text{nhs1l1b}^{\text{nhsl1bfh131}}\]). Nhs1lb is related to the human Nance-Horan syndrome (NHS) protein and to the Drosophila Scrib-interacting protein Guk-holder (Gukh). We show that nhs1lb

is required cell-autonomously in FBM neuron migration and show that Nhs1lb protein localizes to the edge of membrane protrusions in FBM neurons in vivo. In cell transplantation experiments, we show that scrib and vangl2 have a previously unappreciated cell-autonomous role in FBM neuron migration in addition to their non-cell-autonomous role, and that nhs1lb

interacts genetically with scrib in this process. We hypothesize that Nhs1lb is a neuronal PCP effector, the first in this system, which functions in migrating neurons to execute directed cell movements. Our results thus support a model whereby PCP signaling between FBM neurons and their environment functions to control directly the trajectory of migration. Furthermore, our chimeric analyses revealed that FBM neurons have an alternative, collective mode of migration that requires interactions between migrating FBM neurons themselves and occurs independently of Nhs1lb or PCP proteins in the migrating neurons. We propose a model in which PCP-dependent and collective modes together drive directed migration of FBM neurons in vivo.

**MATERIALS AND METHODS**

Zebrafish husbandry, screening and positional cloning

Zebrafish (*Danio rerio*) were maintained according to standard procedures and staged as previously described (Kimmel et al., 1995). The Isl1:GFP transgenic line, registered as Tg(isl1:GFP)pw0 at The Zebrafish International Resource Center (ZIRC) (Higashijima et al., 2000) was maintained in the *AB background. The isl1:membRFP transgenic line, designated Tg(isl1:CREST-hsp70:mRFP);fh1, was described previously (Grant and Moens, 2010). The WIK strain was used for positional cloning (Shimoda et al., 1999). The *scrib* mutant was originally described as landlocked, *llk*\(^{w668}\) (Wada et al., 2005). The *vangl2*\(^{rilobite}\) mutant was originally described as *re*\(^{p209}\) (Jessen et al., 2002).

To induce point mutations in premeiotic germ cells, male Isl1-GFP fish were treated with the chemical mutagen N-ethyl-N-nitrosourea (ENU, Sigma) according to standard methods (van Eeden et al., 1999). Mutants with defects in the migration of FBM neurons were isolated by screening gynogenetic diploid zebrafish embryos produced using the early pressure method (Beattie et al., 1999; Walker et al., 2009). Putative mutants were outcrossed to the wild-type (WT) WIK strain and mutants and carriers identified by random crosses between siblings. Bulk segregant analysis was performed on mutant progeny and phenotypically WT animals collected from crosses (Bahary et al., 2004).

In our screen, a single allele of *nhsl1b* (*nhsl1b*\(^{nhsl1bfh131}\)) was identified. Two further non-complementing alleles, *nhsl1b*\(^{d260}\) and *nhsl1b*\(^{d261}\), were identified by screening *nhsl1b* exon 6 (1923 bp) on a library of 8600 F1 ENU-mutagenized fish by TILLING (Draper et al., 2004).

**Morpholino injections**

Antisense morpholinos (MO) were injected at the 1-cell stage. Morpholinos were as follows: Nhs1lb: (MO E4I4 5'-CTAAAGTT-TAACCTTCAACCGTG-3'; MO exon1 ATG 5'-CGGAAA-CGCCATTTAAATCTGCT-3'), 5 ng; Hoxb1a: (Cooper et al., 2003), 2 ng; Pk1b: MO1 + MO2 (Rohrschneider et al., 2007), 2 ng each; Scrib MO: (Wada et al., 2005), 5 ng; Vangl2 MO (Park et al., 2008), 3 ng.

**Plasmids and mRNA injections**

Plasmids encoding the *scrib* gene and the *psd95* gene (Meyer et al., 2005; Wada et al., 2005) were subcloned into pcRS2 expression vectors as GST- or GFP- N-terminal fusion proteins using the gateway system (Villefranc et al., 2010). GFP-prickle mRNA was used as described (Ciruna et al., 2006). Sense-capped mRNA was synthesized using mMessage mMachine (Ambion). Approximately 1 nl of mRNA was injected into one-cell- or eight-cell-stage embryos at concentrations ranging from 0.1 to 0.5 ng/μl in nuclease-free water (Ambion).

**In situ hybridization and whole-mount immunohistochemistry**

RNA in situ hybridization was carried out as previously described (Feng et al., 2010; Moens et al., 1998). Whole-mount immunostaining was performed as described previously (Grant and Moens, 2010) with the following antibodies: anti-islet1 (1:50, Developmental Studies Hybridoma Bank); anti-GFP (1:200, gift from Z. Sun, Department of Genetics, Yale University School of Medicine). The anti-Nhs1lb antibody is a rabbit polyclonal antibody directed against the C-terminus of zebrafish Nhs1lb (1:200, AnaSpec).

**Cell culture, transfections and immunoprecipitations**

For protein-protein interaction studies, HEK293T cells were grown in DMEM (Gibco), 10% heat-inactivated fetal bovine serum, 2 mM L-glutamine, 100 U/ml penicillin and 100 μg/ml streptomycin (Gibco). Cells were transfected using Lipofectamine 2000 (Invitrogen) using standard
protocols. Cells were washed twice in cold PBS, and lysed in NP40 lysis buffer (50 mM Tris, pH 8.0, 150 mM NaCl, 1% NP40, 0.01 M EDTA) with complete protease cocktail inhibitor (Roche) and 1 mM PMSF. Lysates were cleared and incubated with anti-GST (Abcam), anti-myc (9E10) or anti-GFP (Torrey Pines) for 2 hours at 4°C. Immunocomplexes were precipitated by the addition of protein A-, or G-conjugated Dynabeads (Invitrogen) for 1 hour at 4°C. Beads were washed three times in NP40 lysis buffer and resuspended in 2× SDS sample buffer. Immunoprecipitates were separated by SDS-PAGE and analyzed by immunoblotting with the indicated antibodies.

Cell transplantation
Chimeric embryos were made by transplantation at the early gastrula stage as described (Carmany-Rampey and Moens, 2006; Kemp et al., 2009). To track transplanted cells, donor embryos carrying the isl1-GFP transgene were injected with cascade blue-dextran or rhodamine dextran (10,000 mw, Molecular Probes). In some experiments, host embryos carried the Tg(isl1CREST-hsp70:mlRFP)fh1 transgene so that host motorneurons could be visualized in live embryos. Alternatively, the position of host motorneurons was visualized by immunostaining with anti-islet1 antibody. Embryos were imaged on a Zeiss Pascal or Zeiss 510 confocal microscope.

RESULTS
A forward genetic screen yields a mutant with specific disruption in migration of facial branchiomotor neurons
To identify novel genes required for the tangential caudal migration of facial branchiomotor (FBM) neurons, we conducted a forward genetic screen using Tg(isl1-GFP)rw0 transgenic zebrafish, which express GFP in branchiomotor neurons (Fig. 1A) (Higashijima et al., 2000). We screened clutches from 355 independent F1 females using the early pressure method (Beattie et al., 1999; Walker et al., 2009). From this screen, we identified new mutant alleles of known PCP components in which the migration of FBM neurons is perturbed, including scrib (Wada et al., 2005) and fzd3a (Wada et al., 2006) (data not shown). We also isolated a novel mutant, designated as fh131, which displays a specific impairment in the migration of FBM neurons previously seen in other zebrafish mutants for PCP components (Fig. 1B,C). Experiments in this study explore the basis of the neuronal migration defect in the fh131 mutant.

In wild-type embryos, FBM neurons begin to differentiate and can first be visualized by GFP fluorescence in rhombomere (r)4 at 16 hours post-fertilization (hpf; Fig. 1E). Almost immediately, FBM neurons begin to migrate ventrally and posteriorly, reaching the basement membrane near the r4-r5 boundary, at which point they accelerate and migrate posteriorly to r6 (Chandrasekhar et al., 1996; Higashijima et al., 2000; Wada et al., 2005; Grant and Moens, 2010). A subset of earliest-born FBM neurons migrate to r7 (P.K.G. and C.B.M., unpublished). The first FBM neurons reach their target by 24 hpf (Fig. 1G) and the migration of later-born FBM neurons is complete by 48 hpf (Fig. 1H). In fh131 mutants, GFP-expressing neurons appear normally beginning at 16 hpf in r4 (Fig. 1F); however, none of the r4-derived GFP-expressing neurons migrate posteriorly and they instead remain in r4 (Fig. 1C,F,H). The location of other branchiomotor neurons in the hindbrain is normal, including neurons of the trigeminal, glossopharyngeal and vagal nucleus (Fig. 1A-C). Despite their abnormal positioning in r4, FBM neurons in fh131 mutant embryos extend axons to the correct target muscles in the second branchial arch (see Fig. S1 in the supplementary material). Therefore, fh131 mutant embryos have a specific impairment in the caudal migration of FBM neurons.

fh131 mutant embryos are morphologically normal, and adult homozygous mutants are viable and fertile (Fig. 1B,C). Because the maternal functions of other genes involved in FBM neuron migration such as vangl2 and scrib are required for convergent extension movements and neural tube morphogenesis, we tested whether fh131 functions more broadly in PCP processes by generating embryos that lack both maternal and zygotic fh131 function (mz mutants). mz-fh131 were identical to zygotic fh131 mutant embryos, indicating that its role in neuronal migration is the earliest detectable function for this gene (Fig. 1D,D').

Correct segmental patterning of r4 is required for FBM neuron migration (Studer et al., 1996; Cooper et al., 2003). We determined that segmental patterning is normal in fh131 mutants, as is the expression of genes required to initiate a migratory transcriptional program in FBM neurons (see Fig. S2A-H in the supplementary material) (Coppola et al., 2005; Song et al., 2006). Expression of tag-1 (cntn2 – Zebrafish Information Network), which encodes a cell adhesion molecule specifically expressed by FBM neurons, was also normal (see Fig. S2I in the supplementary material) (Sittaramane et al., 2009). Taken together, these results suggest that the overall patterning of the hindbrain and differentiation of FBM neurons was unaffected by the mutation in fh131 embryos, and that fh131 functions more directly in the migratory process.
Using high-resolution mapping and positional cloning, we found that the fh131 mutation disrupts the Nance-Horan syndrome-like 1b (nhsl1b) gene. Briefly, we used standard positional cloning and recombination mapping to place the fh131 mutation within a defined interval on chromosome 20 (Fig. 2A). This interval contained 13 genes, including nhsl1b, a member of the Nance-Horan syndrome (NHS) family of genes, which in mammals includes NHS, NHSL1 and NHSL2 (Brooks et al., 2004; Brooks et al., 2010). In humans, mutations in the founding member of this family, NHS, cause X-linked cataracts, dental anomalies and partially penetrant mental retardation (Brooks et al., 2004). The zebrafish genome encodes four NHS-related genes, two orthologs of NHS (nhsa and nhsb) and two orthologs of NHSL1 (nhsl1a and nhsl1b) (Fig. 2D). No NHSL2 orthologs have been identified to date. Using a bioinformatics approach, Katoh (Katoh, 2004) suggested that vertebrate NHS genes are orthologs of Drosophila guanylate kinase homolog (GukH), which was isolated based on its physical interaction with the polarity proteins Discs large (Dlg) and Scribble (Mathew et al., 2002). Given the known requirement for zebrafish Scrib in FBM neuron migration, we pursued nhsl1b as a likely candidate.

Sequence analysis of nhsl1b exons revealed that the fh131 allele carries a nonsense mutation (E1219X) resulting in a premature stop codon in exon 6 (Fig. 2C) that co-segregated with the fh131 mutant phenotype (n=72/72). Injection of an antisense morpholino oligonucleotide (MO) targeted to the exon 4-intron 4 splice junction caused a mis-splicing of the nhsl1b transcript leading to the retention of intron 4 and resulted in a strong block in FBM neuron migration (Fig. 2E and see Fig. S3 in the supplementary material). Furthermore, two additional nonsense alleles, nhsl1b\(^{Q408X}\) (Q408X) and nhsl1b\(^{E1219X}\) (L454X), identified by TILLING (Draper et al., 2004), failed to complement the fh131 allele originally found in our forward genetic screen (Fig. 2G-I). Taken together, these findings demonstrate that Nhsl1b function is necessary for the caudal migration of FBM neurons. Hereafter, we refer to the fh131 mutant as nhsl1b\(^{fh131}\).

race (3′ and 5′ rapid amplification of cDNA ends) indicate that nhsl1b is composed of eight exons, with an alternatively spliced fifth exon and four alternative translational start sites encoded from four alternative first exons (exon 1, exon 1a, exon 1b and exon 1c) (Fig. 2B). Exon 1 is the largest of these first exons and is located 132 kb upstream of exon 2, a genomic structure that is highly conserved in human NHSL1 (Brooks et al., 2010). Similar to the human NHS homologs, exon 1 of zebrafish nhsl1b encodes an N-terminal WASH homology domain (WHD) found in WASH (Wiskott-Aldrich syndrome protein family) proteins (Brooks et al., 2010). Injection of a translation-blocking morpholino targeted specifically to the ATG of exon 1 also caused a complete block in FBM neuron migration indicating that the exon 1-encoded WHD domain is essential for the function in migration of Nhsl1b (Fig. 2F).

**Nhsl1b interacts genetically and physically with Scrib to regulate FBM neuron migration**

We crossed scrib\(^{rw468}\) with nhsl1b\(^{fh131}\) heterozygotes together to create double heterozygous embryos. We observed that 62% (n=88) of double heterozygous scrib\(^{rw468}\); nhsl1b\(^{fh131}\) embryos exhibited an almost complete loss of FBM migration, compared with much milder migration defects in only 8% (n=85) and 18% (n=69) of single nhsl1b\(^{fh131}\) or single scrib\(^{rw468}\) heterozygotes, respectively (Fig. 3A-C). This strong genetic interaction was not observed in double heterozygotes with nhsl1b\(^{fh131}\); vangl2\(^{m209}\), f2a\(^{m260}\) or celer\(^{m71}\) (data not shown).

Guanylate-kinase homolog (gukh), the single Drosophila homolog of the vertebrate NHS family, encodes a scaffold protein bridging Dlg and Scrib at the neuromuscular synapse (Mathew et al., 2002). Our genetic studies linking Nhsl1b and Scrib in FBM migration prompted us to investigate whether the zebrafish proteins interact biochemically. We observed that immunoprecipitation of Myc-tagged Nhsl1b, but not the Myc epitope alone, co-precipitated GFP-Scrib and vice versa when the two proteins were expressed in HEK293T cells (Fig. 3D,E). Nhsl1b also co-immunoprecipitated with a zebrafish ortholog of Dlg, PSD95 (Dlg4) (Fig. 3F,G). These findings indicate that, like Drosophila GukH, vertebrate Nhsl1b can exist in a protein complex with both Scrib and PSD95.

**Nhsl1b is expressed in FBM neurons and Nhsl1b protein localizes to membrane protrusions during migration.**

Nhsl1b is expressed at low levels maternally and at higher levels zygotically (Fig. 4A). RNA in situ hybridization revealed that nhsl1b is expressed in somitic mesoderm as well as weakly in...
progenitor cells throughout the nervous system at 14 hpf (Fig. 4B). At 24 hpf, when FBM neurons are migrating, nhsl1b was expressed weakly throughout the neuroepithelium but was specifically upregulated in branchiomotor neurons, including FBM neurons (Fig. 4C-E). The nhsl1b paralog nhsl1a and the more distantly related nhsa gene were also expressed in neural progenitors and somitic mesoderm; however, neither were expressed in migrating FBM neurons (see Fig. S4 in the supplementary material).

Fig. 3. Nhsl1b interacts genetically and physically with Scrib in the regulation of facial branchiomotor (FBM) neuron migration. (A, B) Wild-type (A) and double heterozygous nhsl1b<sup>h131/</sup> x scrib<sup>+</sup> embryos (B) at 48 hours post-fertilization (hpf). Double heterozygotes have unmigrated FBM neurons in rhombomere (r)4, indicative of a strong genetic interaction between the two genes. (C) Histogram of phenotypes in the genotypic classes arising from a nhsl1b<sup>h131/+</sup> x scrib<sup>+/+</sup> cross. (D-G) Nhsl1b associates with Scrib and Pkd95 (Dlg4). cDNA constructs were transfected into HEK293T cells as indicated. Whole cell lysates were immunoprecipitated (IP) and western-blotted (WB) with the indicated antibodies. Scale bar: 20 μm.

Nhsl1b regulates neuronal migration in vivo

Using an antibody directed against the C-terminus of zebrafish Nhsl1b, we observed, similar to our RNA in situ results, that Nhsl1b protein was detectable at low levels in neuroepithelial progenitors and more strongly in migrating FBM neurons, where it localized as foci at the membrane and was abundant at the edges of membrane protrusions (Fig. 4F,G). This immunolocalization was absent in nhsl1b mutant embryos, as mutant Nhsl1b<sup>E1219X</sup> protein is predicted to have a C-terminal truncation due to the premature stop codon (E1219X), demonstrating the specificity of the antibody for Nhsl1b (Fig. 4H). To confirm that the Nhsl1b immunolocalization was motorneuron-derived, we generated primary neuronal cultures from Tg(isl1:GFP)<sub>rw0</sub> transgenic zebrafish (Fassier et al., 2010). We found that Nhsl1b colocalized with GFP-expressing motoneurons (Fig. 4J). Membrane localization of Nhsl1b was confirmed by staining Tg(isl1CREST-hsp70l:mRFP)<sub>fh1</sub> transgenic embryos, in which mRFP localizes to membranes of FBM neurons (Fig. 4K). Nhsl1b was similarly localized on trigeminal motoneurons, the segmental homologs of the FBM neurons in hindbrain r2 that do not undergo posterior migration, and on the unmigrated FBM neurons in scrib<sup>+/+</sup> mutants (Fig. 4J; data not shown), indicating that Nhsl1b is required but not sufficient for posterior-directed migration, and that Scrib is not required for the membrane localization of Nhsl1b.

Nhsl1b functions cell-autonomously in migrating FBM neurons

FBM neurons migrate through a complex cellular milieu in the ventral neural tube, amongst neural progenitors and adjacent to floorplate cells (Grant and Moens, 2010; Mapp et al., 2010). Neuroepithelial cells are polarized along the anterior-posterior axis in a PCP-dependent manner. For instance, maternal and zygotic vangl2 function is required for the anterior membrane localization of GFP-tagged Prickle (GFP-Pk) on neuroepithelial progenitors (Ciruna et al., 2006) and the asymmetric positioning of cilia and basal body at the posterior surface of floorplate cells (Borovina et al., 2010). We observed that in zygotic mutants of both vangl2 and scrib, which lack motorneuron migration but have milder convergent extension defects than the maternal-zygotic mutants, planar polarity of neuroepithelial progenitor and floorplate was disrupted (compare Fig. 5B,C with 5A and 5F, χ² test, P<0.0001; data not shown). This is consistent with a function for core PCP components in the migratory environment, as suggested by previous chimeric analysis (Jessen et al., 2002; Wada et al., 2005; Wada et al., 2006). By contrast, nhsl1b mutants had normal neuroepithelial and floor plate planar polarity (Fig. 5D,F-H). Apicobasal polarity of progenitor cells was also normal in nhsl1b mutants (see Fig. S5 in the supplementary material). Together with the localization of Nhsl1b protein described above, these results indicate that Nhsl1b functions in the FBM neurons and not in their environment.

We confirmed a cell-autonomous function for Nhsl1b by chimera analysis. We transplantedCascade Blue-dextran (CB)-labeled cells from donor embryos into the presumptive ventral hindbrain territory of gastrula stage hosts, such that donor-derived cells contributed mosaically to FBM neurons as well as to other ventral hindbrain cells (Cooper et al., 2003). In these experiments, donor embryos expressed the Tg(isl1:GFP)<sub>rw0</sub> transgene and host embryos expressed the Tg(isl1CREST-hsp70l:mRFP)<sub>fh1</sub> transgene, both marking FBM neurons. In control experiments, 90% of wild-type FBM neurons migrated normally from r4 into r6 in a wild-type environment (Fig. 6A). 60% of wild-type FBM neurons were similarly capable of migrating into r6 in an nhsl1b morphant or...
nhsl1b mutant environment, albeit not as well as in a wild-type environment (Fig. 6B). This observation is consistent with a cell-autonomous function for nhsl1b and is similar to the behavior of wild-type cells in a pk1b or hoxb1a morphant environment (61% and 64%, respectively; Fig. 6D and see Fig. S6B in the supplementary material), both of which are known to act cell-autonomously in FBM neuron migration (Cooper et al., 2003; Rohrschneider et al., 2007). This is different from the complete failure of wild-type FBM neurons to migrate in vangl2 or scrib mutant hosts (Jessen et al., 2002; Wada et al., 2005), consistent with a non-cell-autonomous role for these PCP proteins in polarizing the environment.

In reciprocal transplants with nhsl1b, vangl2 or scrib FBM neurons transplanted into wild-type hosts, the majority of mutant FBM neurons migrated out of r4 (65% for nhsl1b, 61% for scrib and 63% for vangl2; Fig. 6C,F,H). This result has been interpreted as proof of a non-autonomous function for vangl2 and scrib (Jessen et al., 2002; Wada et al., 2005); however, observing it for nhsl1b, which otherwise appeared to function cell-autonomously, led us to explore this finding further.

In addition to neuroepithelial progenitor cells and floorplate cells, FBM neurons contact one another during migration, and we considered the possibility that mutant FBM neurons might be rescued in their migration via interactions with neighboring wild-type FBM neurons. To test this, we made use of the fact that the PCP component Prickle1b (Pk1b) is expressed specifically in FBM neurons and is required strictly cell-autonomously for their migration (Rohrschneider et al., 2007). We reasoned that if nhsl1b, vangl2 or scrib mutant FBM neurons fail to migrate in pk1b-depleted hosts, this would mean that the rescue of their migration that we observed in a wild-type environment was mediated by the host FBM neurons themselves. First, we confirmed that planar polarity was normal in the pk1b morphant neuroepithelium and that wild-type FBM neurons could successfully migrate into r6 in a pk1b morphant environment, indicating that the environmental cues to support FBM neuron migration were present even though the host neurons failed to migrate (Fig. 5E,F and Fig. 6D). In this pk1b-morphant environment, the vast majority of mutant neurons failed to migrate out of r4 (84% for nhsl1b, 91% for scrib, 97% for vangl2; Fig. 6E,G,I). Identical results were observed when nhsl1b and scrib mutant cells were placed into a host lacking hoxb1a, which is also required cell-autonomously for FBM neuron migration (Cooper et al., 2003) (see Figs S6 and S7 in the supplementary material). Thus, FBM neurons that lack nhsl1b, scrib or vangl2 can be ‘rescued’ in their migration by an...
alternative, collective mode that depends on the presence of wild-type migrating neurons. Indeed, we found that transplantation of a small number of wild-type FBM neurons into an nhsl1b mutants (B) could rescue the migration of a subset of nhsl1b mutant motorneurons (19/20 nhsl1b hosts exhibit rescue by wild-type donor cells) (Fig. 6J).

**DISCUSSION**

We have identified a new gene, nhsl1b, required for FBM neuron migration. Nhsl1b encodes one of four zebrafish NHS family proteins, all of which have an N-terminal WAVE homology domain (WHD) encoded by an alternatively spliced first exon (Brooks et al., 2010). WAVE proteins, members of the larger Wiskott-Aldrich syndrome protein (WASP) family, exist in an inhibitory heteropentameric WAVE complex that is activated by Rac to promote actin polymerization in protrusive membrane structures via interaction with the Arp2/3 complex (Takenawa and Suetsugu, 2007; Insall and Machesky, 2009; Derivery and Gautreau, 2010). Human NHS binds components of the hetero-pentameric WAVE complex, but lacks the other domains required for interaction with actin and Arp2/3, suggesting a model in which NHS family proteins regulate actin polymerization by controlling the assembly of the WAVE complex (Brooks et al., 2010). We find that Nhsl1b protein is localized at the membrane and is often abundant in protrusive structures of migrating FBM neurons in vivo, consistent with a role for Nhsl1b in modulating cytoskeletal-membrane rearrangements in migrating cells, downstream of PCP signaling.

In *Drosophila*, the single NHS family homolog Gukh interacts physically with Scribble and is required for Scribble localization at the neuromuscular junction (Mathew et al., 2002). Consistent with this, we observed that, in zebrafish, Nhsl1b and Scrib interact physically and exhibit a strong genetic interaction. Interestingly, Scrib has also been implicated in directed migration in other cellular contexts. Scrib is required for polarization and migration of astrocytes and mammary epithelial cells in an in vitro scratch ‘wound healing’ assay and in transwell cultures (Osmani et al., 2006; Dow et al., 2007; Nola et al., 2008). In these cells, Scrib is recruited to the leading edge where it is required for the localized activation of Rac and Cdc42 via a direct interaction with the Rac/Cdc42 GEF, βPIX (Audebert et al., 2004; Osmani et al., 2006; Dow et al., 2007; Nola et al., 2008). Given that Rac is known to activate the WAVE complex (Derivery and Gautreau, 2010), our finding that Nhsl1b and Scrib physically and genetically interact raises the possibility that Scrib could function as a scaffold that brings together components that regulate assembly (via Nhsl1b) and activation (via Rac) of the WAVE complex in migrating FBM neurons.

Previous work has shown that the PCP components Scrib and Vangl2 function non-cell-autonomously in FBM neuron migration, and suggested that a planar polarized epithelium shapes the trajectory of this migration (Jessen et al., 2002; Wada et al., 2005). Consistent with this idea, we have shown that the zygotic functions of Scrib and Vangl2 are required for planar polarization of neuroepithelial progenitors and floorplate cells across the anterior-posterior axis of the neural tube at a time when FBM neurons are migrating (see also Borovina et al., 2010). By contrast, our investigation of Nhsl1b function supports a cell-autonomous role for Nhsl1b within migrating FBM neurons: (1) Nhsl1b is not required for planar polarity in the surrounding...
neuroepithelial progenitors or in the nearby floorplate, (2) wild-type neurons can migrate in an nhsl1b mutant environment, and (3) nhsl1b mutant neurons fail to migrate through a wild-type environment if host neurons are unmigrated. Importantly, our chimeric analysis also uncovered essential cell-autonomous functions for the PCP components Scrib and Vangl2 in this migration. Taken together, our data support a model in which FBM neuron migration depends both on planar polarization of the epithelium/floorplate, which requires Vangl2 and Scrib (Fig. 7B), and on the ability of FBM neurons to be polarized in response to it, which requires Vangl2, Scrib, Nhsl1b as well as Pk1b (Mapp et al., 2011) in the neurons themselves (Fig. 7C). In this scenario, extrinsic planar polarity in neuroepithelial cells is translated into intrinsic neuronal polarity to control the direction of migration. The dual requirement for PCP components in the FBM neurons and their environment is reminiscent of the cell-autonomous and non-cell-autonomous functions of core PCP components in the fly wing (Lawrence et al., 2007; Wu and Mlodzik, 2009) and suggests the intriguing possibility that FBM neuron migration involves direct PCP signaling between the planar polarized neuroepithelium/floorplate and the migrating neurons. We refer to this as ‘PCP-dependent migration’ (Fig. 7D). The precise molecular mechanism by which polarity is communicated in this context remains to be determined.

PCP effectors are cell type-specific proteins that function cell-autonomously downstream of PCP signals to link planar polarity to changes in cytoskeletal networks (Strutt et al., 1997; Lee and Adler, 2002; Strutt and Warrington, 2008). For example, the most downstream PCP effector Multiple Wing Hairs was recently shown to encode a Formin Homology 3-domain containing protein that regulates actin polymerization at the apical surface of fly wing cells.
in a PCP-dependent manner (Strutt and Warrington, 2008). The cell-autonomous function of Nhsl1b specifically in FBM neuron migration and not in other PCP-dependent processes, its localization to cell protrusions, and the known role of NHS family members in regulating WAVE complex activity (Brooks et al., 2010) together argue that Nhsl1b functions as a neuron-specific PCP effector, the first in this system.

Analysis of our transplantation experiments also distinguishes an alternate form of migration that depends on interactions between FBM neurons themselves. We observed that vangl2, scrib and nhsl1b mutant FBM neurons, which are unable to migrate using the ‘PCP-dependent’ mode of migration, can be ‘rescued’ in their migration if they are in the presence of neighboring wild-type FBM neurons. We refer to this as ‘collective migration’ (Fig. 7E). This is analogous to the collective migration of cells in the zebrafish lateral line primordium, where cells lacking the receptor for the chemokine Sdf1 (Cxcl12a — Zebrafish Information Network) are nevertheless able to migrate if they are in the presence of wild-type cells that can detect the signal, or to the fly egg chamber where border cells lacking the transcription factor slbo can migrate in the presence of wild-type border cells (Rorth et al., 2000; Haas and Gilmour, 2006). A collective mode of FBM neuron migration, demonstrated in this paper, can explain previous observations that not all wild-type neurons efficiently migrate in environments where host neurons are unmigrated but epithelial polarity is normal (Cooper et al., 2003; Rohrschneider et al., 2007). The ability of one FBM neuron to direct the migration of another is presumably mediated through cell-cell contact-mediated signaling. Although the molecular mechanism of collective migration remains to be explored, our data argue that it is genetically distinguishable from PCP-dependent migration because it does not require the function of vangl2, scrib or nhsl1b in the ‘rescued’ neurons.

PCP-dependent and collective modes of migration are likely to both be active during wild-type FBM neuron migration, as neither mode alone is sufficient for complete migration. We hypothesize that initial migration out of r4 might predominantly be driven by the first, PCP-and-Nhsl1b-dependent mode, whereas later migrating cells might use the collective mode. However, the same neuron might use the two modes at different times during their migration, or the two modes might even be active in different parts of a cell at the same time. High-resolution live imaging of chimeric embryos in which one or the other mode is unavailable will help to elucidate the relative contributions of PCP-dependent and collective modes of FBM neuron migration.

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Competing interests statement

The authors declare no competing financial interests.

Supplementary material

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