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, nhsl1b, required for FBM neuron migration. nhsl1b encodes a WAVE-homology domain-containing protein related to 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. Nhsl1b 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 Nhsl1b 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 Nhsl1b 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 in 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, and also required for 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. In our screen, a single allele of nhsl1b (nhsl1b<sub>NH</sub>) was identified. Two further non-complementing alleles, nhsl1b<sub>NH1</sub> and nhsl1b<sub>NH2</sub>, 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: Nhsl1b: (MO E414 5'-CTAAAGATT- TAACTTCTCACCCGTG-3'; MO exon1 ATG 5'-CGGGAAA-CGCCATTATACACATG-3'), 5 ng; Hoxb1a: (Cooper et al., 2003), 2 ng; Fkh1: 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 scrb gene and the pod5 gene (Meyer et al., 2005; Wada et al., 2005) were subcloned into pCS2 expression vectors as GST- or GFP-N-terminal fusion proteins using the gateway system (Villerflanc et al., 2007). 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-Nhsl1b antibody is a rabbit polyclonal antibody directed against the C-terminus of zebrafish Nhsl1b (1:200, AnaSpec).

**Cell culture, transfections and immunoprecipitations**

For protein-protein interaction studies, HEK293T cells were grown in MEM (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 neurons have an alternative, collective mode of migration that requires interactions between migrating FBM neurons themselves and occurs independently of Nhsl1b 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.
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-lsp70l:mrFP)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 a novel mutant allele of known PCP components in which the migration of FBM neurons is perturbed, including scrib (Wada et al., 2005) and fz3a (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., 1997; 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. 1B). 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, J 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 holder (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*<sup>fh280</sup> (Q408X) and *nhsl1b*<sup>fh281</sup> (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*<sup>fh131</sup>.

**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 WAVE homology domain (WHD) found in WAVE (Wiskott-Aldrich syndrome protein family Verprolin-homologous) 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<sup>r468</sup>*, with *nhsl1b<sup>fh131</sup>* heterozygous together to create double heterozygous embryos. We observed that 62% (*n* = 88) of double heterozygous *scrib<sup>r468</sup>*/*nhsl1b<sup>fh131</sup>* 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<sup>fh131</sup>* or single *scrib<sup>r468</sup>* heterozygotes, respectively (Fig. 3A-C). This strong genetic interaction was not observed in double heterozygotes with *nhsl1b<sup>fh131</sup>* and *vangl2<sup>29209</sup>* or *fz3a<sup>29509</sup>* or *celr<sup>r468</sup>* (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 Nhs1b, 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). Nhs1b 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, nhs1lb was expressed weakly throughout the neuroepithelium but was specifically upregulated in branchiomotor neurons, including FBM neurons (Fig. 4C-E). The nhs1lb paralog nhs1la 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).

Using an antibody directed against the C-terminus of zebrafish Nhs1lb, we observed, similar to our RNA in situ results, that Nhs1lb 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 nhs1lb mutant embryos, as mutant Nhs1lb(E1219X) protein is predicted to have a C-terminal truncation due to the premature stop codon (E1219X), demonstrating the specificity of the antibody for Nhs1lb (Fig. 4H). To confirm that the Nhs1lb immunolocalization was motorneuron-derived, we generated primary neuronal cultures from Tg(isl1:GFP)rw0 transgenic zebrafish (Fassier et al., 2010). We found that Nhs1lb colocalized with GFP-expressing motorneurons (Fig. 4J). Membrane localization of Nhs1lb was confirmed by staining Tg(isl1CREST-hsp70:mRFP)fh1 transgenic embryos, in which mRFP localizes to membranes of FBM neurons (Fig. 4K). Nhs1lb was similarly localized on trigeminal motorneurons, the segmental homologs of the FBM neurons in hindbrain r2 that do not undergo posterior migration, and on the unmigrated FBM neurons in scrib−/− mutant (Fig. 4I; data not shown), indicating that Nhs1lb is required but not sufficient for posterior-directed migration, and that Scrib is not required for the membrane localization of Nhs1lb.

**Nhs1lb 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, \(\chi^2\) 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 chimera analysis (Jessen et al., 2002; Wada et al., 2005; Wada et al., 2006). By contrast, nhs1lb mutants had normal neuroepithelial and floor plate planar polarity (Fig. 5D,F-H). Apicobasal polarity of progenitor cells was also normal in nhs1lb mutants (see Fig. S5 in the supplementary material). Together with the localization of Nhs1lb protein described above, these results indicate that Nhs1lb functions in the FBM neurons and not in their environment.

We confirmed a cell-autonomous function for Nhs1lb by chimera analysis. We transplanted Cascade 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)rw0 transgene and host embryos expressed the Tg(is1CREST-hsp70:mRFP)fh1 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 nhs1lb 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<sup>fh131</sup> mutant host could rescue the migration of a subset of nhsl1b mutant motorneurons (19/20 nhsl1b<sup>fh131</sup> hosts exhibit rescue by wild-type donor cells) (Fig. 6J).

The fact that FBM neurons lacking scrib and vangl2 failed to migrate in a pk1b morphant host, which has the environmental cues to support wild-type FBM neuron migration, reveals an essential cell-autonomous requirement for these core PCP components in addition to their function in the polarized environment. This cell-autonomous function was obscured by collective migration in previous studies (Jessen et al., 2002; Wada et al., 2005). A cell-autonomous role for Scrib is consistent with its physical and genetic interaction with Nhsl1b, as we discuss further below.

**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 Suetugu, 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; Wada et al., 2006). 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 the presence of other normally migrated neurons (E). The incomplete migration of donor-derived neurons observed in D or E when only one of these two mechanisms is available indicates that both mechanisms are functioning during normal migration.

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

Fig. 7. A model for facial branchiomotor (FBM) neuron migration. (A-C) FBM neuron migration requires the planar polarization of both the neurons and the surrounding neuroepithelium. Neurons fail to migrate either owing to lack of neuroepithelial polarity, e.g. in a vangl2 or scrib mutant (B) or owing to the inability of the neurons to be polarized in response to this environment, e.g. in an nhsl1b or pk1b mutant (C). (D, E) Chimeric analysis reveals that FBM neurons can migrate by one of two distinct mechanisms: one which requires the function of PCP proteins both within FBM neurons and the neuroepithelium (D), or collectively, independent of these functions in the ‘rescued’ neurons but requiring the presence of other normally migrated neurons (E). The incomplete migration of donor-derived neurons observed in D or E when only one of these two mechanisms is available indicates that both mechanisms are functioning during normal migration.

Fig. 6. A cell-autonomous role for Nhsl1b, Scrib and Vangl2 in migration. (A-J) Live confocal images at 48 hours post-fertilization (hpf) of chimeric zebrafish embryos with anterior to the top. Cascade blue marks donor-derived cells (blue), Tg isl1CREST-hsp70l:mRFP/fh1 marks host motorneurons (red) and Tg isl1::GFP marks donor-derived motorneurons (green). Histograms on the right indicate the percent of donor-derived FBM neurons in rhombomere (r)4 (unmigrated), r5 and r6 (fully migrated) under the transplantation conditions indicated on the far left, which are written as Donor>Host. n refers to the total number of FBM neurons scored in each condition. Pk1b MOs were used in D, E, G and I to prevent host FBM neurons from migrating by a cell-autonomous mechanism. J shows the rescue of host nhsl1b mutant FBM neurons expressing Tg isl1::GFP (green) (arrow) by wild-type donor FBM neurons expressing Tg isl1CREST-hsp70l:mRFP/fh1 (red). Scale bar: 50 μm.
Nhs1b regulates neuronal migration in vivo

in a PCP-dependent manner (Strutt and Warrington, 2008). The cell-autonomous function of Nhs1b 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 Nhs1b 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 nhs1lb 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 chemokin 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 sibo 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 nhs1lb 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-Nhs1b-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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