Calmodulin (CaM) is a multifunctional calcium ion sensor that transduces much of the signal. To better understand the role of Ca\(^{2+}\)-CaM in neuronal migration, we investigated mouse precerebellar neurons (PCNs), which undergo stereotyped, long-distance migration to reach their final position in the developing hindbrain. In mammals, CaM is encoded by three non-allelic CaM (Calm) genes (Calm1, Calm2 and Calm3), which produce an identical protein with no amino acid substitutions. We found that these CaM genes are expressed in migrating PCNs. When the expression of CaM from this multigene family was inhibited by RNAi-mediated acute knockdown, inhibition of migrating PCNs. We focused on the migration of hindbrain precerebellar neurons (PCNs). PCN migration is a suitable model owing to its long, highly stereotyped migratory path and the genetic tractability of this path (Kawauchi et al., 2006; Okada et al., 2007). PCNs refer to neurons constituting a collection of discrete medullary and pontine nuclei that provides input to the cerebellum (Altman and Bayer, 1987a,b, 1997). These neurons originate from the dorsal margin of the hindbrain, known as the lower rhombic lip (LRL), and diverge into three discrete tangential migratory streams: the anterior extramural stream (AEMS), which gives rise to the pontine nuclei (PN) in the pons; the posterior extramural stream (PEMS), which gives rise to the external cuneate nucleus (ECN) and the lateral reticular nucleus (LRN) in the medulla; and the intramural circumferential pathway, which gives rise to the inferior olivary nucleus (ION) in the medulla. After reaching the appropriate circumferential position via tangential migration, PCNs comprising the AEMS and PEMS then invade into the depth of the hindbrain to form nuclei by radial migration along radial glial fibers (Kawauchi et al., 2006). Therefore, this system allows us to study both tangential and radial modes of migration.

To genetically manipulate CaM function in PCNs, we utilized an RNAi-mediated acute knockdown approach. Intriguingly, in mammals CaM is encoded by a family of three non-allelic genes (Calm1, Calm2 and Calm3) that produce an identical protein with no amino acid substitutions (Toutenhoofd and Strehler, 2000). It is hypothesized that these three CaM transcripts provide distinct local pools of CaM protein through post-transcriptional regulation to meet various demands for its cellular functions (Toutenhoofd and Strehler, 2000; Palfi et al., 2002). On the basis of this genomic organization, we conducted RNAi-mediated acute knockdown of each of the three CaM genes.

Here, we show that all three CaM genes are expressed in migrating PCNs. Using shRNAs specific to each member of the CaM gene family, we demonstrated that Calm1 plays a dominant and crucial role in PCN migration. Many PCNs treated with Calm1 shRNA failed to reach the appropriate circumferential position by E17.5 and were still located in the migratory pathway. Those that reached the prospective target region did not invade the depth of the prospective nucleus through the required radial migration and were confined superficially. These results uncovered an essential role of Calm1 in tangential migration and possibly also in radial migration along the radial glia.

### RESULTS

#### Expression of all three CaM genes in migrating PCNs

We first examined which of the three CaM genes are expressed by migrating PCNs (Fig. 1). PCNs were identified by in situ
expressed in the floor plate (FP) (Fig. 1C-E,H-J). Calm1 genes was similar, with slight differences. For example, only migratory pathway of PCNs and in most hindbrain areas, with PCNs are actively migrating. LRN neurons in the PEMS have no sequence similarities are found. Transcripts from the three CaM genes were distinguished by cRNA probes of 600-800 nucleotide sequences within their 3′UTR, where no sequence similarities are found.

First, we examined expression at E14.5, when the majority of PCNs are actively migrating. LRN neurons in the PEMS have crossed the midline and reached the contralateral prospective LRN region (Fig. 1B), while PN neurons have just reached the ipsilateral prospective PN region (Fig. 1G) (Watanabe and Murakami, 2009; Shinohara et al., 2013). All three CaM genes were expressed in the migratory pathway of PCNs and in most hindbrain areas, with relatively strong expression in the brainstem motor nuclei (Xth and Xthl motor nuclei). The overall spatial expression of the three CaM genes was similar, with slight differences. For example, only Calm1 was expressed in the floor plate (FP) (Fig. 1C-E,H-J). Calm1 expression in the LRN region was relatively high compared with its surroundings, whereas Calm2 and Calm3 appeared low (Fig. 1C-E). Expression of all three CaM genes was also detected in the AEMS (Fig. 1H-J). We also examined expression at E17.5, when the majority of PCNs have settled at their final position (Kawauchi et al., 2006; Shinohara et al., 2013). We found that all three CaM genes were expressed in the ECN (Fig. 1M-O), LRN (Fig. 1Q-S) and PN (Fig. 1U-W).

To directly quantify relative expression, we performed real-time quantitative PCR using PN neuron-specific cDNA. For this purpose, the LRL was electroporated with plasmids expressing GFP at E12.5. In mice, the peak of LRN/ECN neuron generation is around E12, that of PN neurons is around E12-14, and that of ION neurons is earlier at around E10 (Taber Pierce, 1966, 1973; Kawauchi et al., 2006; Shinohara et al., 2013). Therefore, electroporation at E12.5 can simultaneously label PN and LRN/ECN neurons, but avoids labeling ION neurons. The resulting fluorescent PN neurons were dissected. GFP-labeled PN neurons were then dissociated and sorted by FACS. (Y) Relative copy numbers of the three CaM transcripts expressed in PN neurons (means±s.d.). The amount of each CaM transcript in the cDNAs generated from the FACS-sorted PN neurons was measured by real-time quantitative PCR. n=10 measurements from three independent cDNAs, each of which was derived from 8-9 embryos.
By performing fluorescent *in situ* hybridization (FISH), we directly examined the simultaneous expression of a pair of CaM gene family members and their subcellular localization at higher spatial resolution. Fig. 2F shows an example of the proximal region of the leading process probed for *Calm1* and *Calm2*. This PCN clearly expressed both *Calm1* and *Calm2* transcripts, although the signals rarely overlapped (Fig. 2F). All PCNs examined for the expression of *Calm1* and *Calm2* expressed both transcripts (n=88 cells), as was also the case for *Calm1* and *Calm3* (Fig. 2G; n=35 cells). From these results, we concluded that each PCN expresses all three CaM genes simultaneously, although the localization of each CaM transcript differs.

**Gene-specific knockdown of CaM gene family members by shRNA**

To reveal the role of the CaM genes in PCN migration, we generated a series of plasmids that produce shRNAs that specifically target each gene. When expressed in COS7 cells along with a YFP-tagged CaM reporter, each shRNA suppressed the expression of the reporter carrying its target CaM gene but not that of reporters carrying non-target CaM genes (Fig. 3A). For example, *Calm1*sh361, which targets *Calm1* mRNA, suppressed the expression of YFP-Calm1 but not that of YFP-Calm2 or YFP-Calm3. The efficiency and the specificity of the knockdown exerted by the three shRNAs are summarized in Fig. 3B. *Calm1*sh361 inhibited the expression of YFP-Calm1 to 7.1±2.5% of the control plasmid, *Calm2*sh414 inhibited YFP-Calm2 to 10.3±1.9%, and *Calm3*sh384 inhibited YFP-Calm3 to 11.8±2.2%.

We then examined the effectiveness of these shRNAs on endogenous CaM mRNAs expressed in migrating PCNs *in vivo*. The LRL was electroporated at E12.5 with plasmids expressing GFP and shRNA, then the GFP-labeled PN neurons were dissected and FACS sorted at E15.5, and cDNA was generated. Real-time quantitative PCR was performed and the percentage CaM gene expression in shRNA-treated PN neurons relative to that in untreated control PN neurons was calculated. Knockdown by *Calm1*sh361 suppressed the expression of endogenous *Calm1* mRNA to 18.9±3.2% of control. Similarly, *Calm2*sh414 and *Calm3*sh384 reduced...
the expression of *Calm2* and *Calm3* to 32.1±10.2% and 27.8±5.4%, respectively (n=4 measurements from pooled cDNAs, each derived from of 8-21 embryos). Persistent reduction of endogenous *Calm1* expression by *Calm1*sh361 was observed at E17.5 by ISH (data not shown).

**Calm1 is essential for the migration of PCNs**

We then examined the effect of the shRNAs on the migration of PCNs. We electroporated plasmids expressing GFP and shRNAs into PCNs residing in the LRL of E12.5 mouse embryos. The embryos were analyzed at E17.5, when the majority of PCNs had arrived at their target regions (Kawauchi et al., 2006; Okada et al., 2007; Kobayashi et al., 2013; Shinohara et al., 2013). Fig. 4 shows a ventral view of whole-mount hindbrain in which the PN and the LRN are discernible. The majority of PCNs treated with control shRNA had arrived at the target region by E17.5, and few neurons remained in the migrating paths (Fig. 4B,C; n=6). By contrast, a substantial number of *Calm1*sh361-treated PCNs failed to reach their targets, remaining in the path to the PN (Fig. 4D, arrowhead; n=7/7) or LRN (Fig. 4E, arrowhead) and between the LRN and ECN (Fig. 4E, arrow). Similar tangential migration defects were observed with another shRNA targeted to the *Calm1* gene, *Calm1*sh427. The defect caused by *Calm1*sh427 was even more severe than that of *Calm1*sh361, as fewer PN neurons reached the prospective PN region, while more PN neurons lingered in the migratory pathway (Fig. 4F, arrowhead). In the PEMS, many LRN/ECN neurons were stuck at the midline, failing to cross it (Fig. 4G, arrow). This defect in tangential migration was not observed with *Calm2*sh414 (n=0/6) or with *Calm3*sh384 (n=0/13) (Fig. 4H-K).

PCNs first arrive at the prospective target region by tangential migration, then migrate radially along the radial glial fibers, and finally invade into and populate the depth of the nucleus (Kawauchi et al., 2006; Watanabe and Murakami, 2009; Shinohara et al., 2013). To analyze this radial migration, transverse sections of the PN were examined at E17.5 (Fig. 5). Normally by this stage, many PN neurons have entered and populated the dorsal region of the nucleus, forming the outline of the mature PN, although they were still motile, adjusting their final position within the nucleus (Fig. 5A, control shRNA) (Shinohara et al., 2013). In clear contrast, most *Calm1*sh361-treated PN neurons failed to migrate into the dorsal PN. Instead, they tended to remain superficial and accumulated in the ventral PN (Fig. 5A). Furthermore, *Calm1*sh361-treated PN neurons also accumulated at the midline, which was rarely observed in the control at this stage (Fig. 5A). In accordance with the tangential migration defect observed in whole-mount preparations, this failure of radial migration within the PN was *Calm1*sh361 specific, as it was rarely seen in *Calm2*sh414- or *Calm3*sh384-treated PN neurons (Fig. 5A).

To analyze the extent of radial migration among shRNA-treated PN neurons, we quantified the ratio of the area occupied by fluorescently labeled neurons that had entered the dorsal PN to that in the entire nucleus (Fig. 5B,C). Whereas 36.2±11.4% of control PN neurons were distributed in the dorsal region, only 8.6±5.1% of *Calm1*sh361-treated PN neurons did (Fig. 5C; Mann–Whitney U-test, P=0.0004). *Calm1*sh427 caused similar defects, with 17.3±3.8% of *Calm1*sh427-treated PN neurons found in the dorsal region (Fig. 5C; Mann–Whitney U-test, P=0.0007). However, for *Calm2*sh414-, *Calm2*sh285-, *Calm3*sh384- and *Calm3*sh408-treated PN neurons, 34.5±4.5%, 41.5±5.0%, 37.5±12.8% and 46.7±16.1% reached the dorsal region, respectively – results not statistically different from the control (Fig. 5C). The substantial accumulation of *Calm1*-deficient PN neurons in the migratory path to the PN observed in whole-mount specimens (Fig. 4D,F) was also evident in transverse sections. We calculated the ratio of the area occupied by fluorescently labeled cells in the path to that observed in the entire section (Fig. 5D,E). Whereas only 7.5±4.8% of control PN neurons were found in the path, 22.7±9.8% of *Calm1*sh361-treated PN neurons remained there (Fig. 5E; Mann–Whitney U-test, P=0.0067).

Based on the findings of *Calm1* participation in PCN migration, we then examined the temporal profile of the migration defects caused by *Calm1*sh361 in more detail. We first examined the migration of PCNs at E15.5. There was no discernible difference between control and *Calm1*sh361-treated PCNs when PCN distribution in the hindbrain was examined in whole-mount configurations. In both the control and *Calm1*sh361 treatment, the leading PEMS population had similarly crossed the midline and entered the contralateral side, and the leading AEMS population had similarly reached the prospective PN regions at the ventral midline (data not shown). Upon examining transverse sections of the hindbrain, the first indications of migration defects were seen. In control preparations, the leading AEMS population that had reached the midline started to invade the prospective PN region along radial glial fibers (Fig. 6A,B). By contrast, only a few *Calm1*sh361-treated PN neurons associated with these fibers (Fig. 6D,E). Similarly, whereas the control PEMS population at the prospective LRN region frequently associated with radial glial fibers, *Calm1*sh361-treated PCNs did so rarely (Fig. 6C,F). We quantified the ratio of PN neurons that were engaged in radial migration at E15.5. Since radially migrating PN neurons were easily distinguishable from tangentially oriented neuronal mass at E15.5, we divided these two populations at the sharp dorsal border of the tangentially migrating mass (Fig. 6G) and calculated the ratio of PN neurons in the radially migrating area (Fig. 6H). Whereas 24.0±11.8% of control PN neurons were engaged in radial migration, only 4.2±2.5% of...
Calm1sh361-treated PN neurons were (Fig. 6G; Mann–Whitney U-test, \(P=0.0079\)). We then visualized the morphology of each PN neuron at E16.5 by a sparse labeling method using the Cre-loxP system (Kanegae et al., 1995; Kobayashi et al., 2013). We did not observe a morphological difference between tangentially migrating PN neurons treated with control shRNA or with Calm1sh361. In both cases, PN neurons exhibited bipolar morphology, extending a long leading process toward the midline (Fig. 7B,C, arrowheads). In the control, radially migrating neurons were frequently observed (Fig. 7B, arrows). These neurons oriented a short, thick leading process in the radial direction, sometimes making branches (Fig. 7D-F). In the case of Calm1sh361 treatment, radially migrating PN neurons were rarely observed at this labeling density. However, when found in the radially deviated population (Fig. 7C, arrow), they tended to extend multiple fine processes instead of a single thick leading process (Fig. 7G-I).

We also examined whether there was an increase in cell death at E17.5 caused by the reduced CaM expression. Fragmented DNA in dying cells was detected by anti-single-stranded DNA (ssDNA) antibody. The ssDNA signal was occasionally detected among the GFP-labeled PN neurons treated with control shRNA or Calm1sh361 (Fig. 7K-N). We did not observe a pronounced increase in the ssDNA signal caused by Calm1sh361. The ssDNA signal was also observed in the contralateral hemisphere of Calm1sh361-treated brain where untreated PN neurons resided, suggesting that the signal was independent of shRNAs.

Lastly, we analyzed the distribution of PCNs at E18.5, when the majority of PN neurons are stationary and PN nucleogenesis appears complete (Shinohara et al., 2013), to assess whether the migration defect caused by Calm1sh361 is a delay or a halt to migration. PCNs treated with Calm1sh361 still remained in the path when examined in whole-mount configuration (Fig. 8E,F, arrowheads). They failed to properly populate the prospective PN or LRN regions. Instead, they remained superficially in their respective nucleus: most PN neurons accumulated in ventral PN (Fig. 8G), while many LRN neurons remained in the tangential migratory pathway (Fig. 8H, arrowheads). We quantified the ratio of dorsally located PN neurons by measuring their occupation area (Fig. 8I). Whereas 49.4±13.7% of control PN neurons were distributed in the dorsal region, only 12.6±5.1% of Calm1sh361-treated PN neurons were (Fig. 8I; Mann–Whitney U-test, \(P=0.0079\)). These results suggest that the observed phenotypes are more likely to be caused by a cessation of migration, rather than by a delay to migration.

**DISCUSSION**

To reveal the role of Ca\(^{2+}\)-CaM signaling in migrating PCNs, we examined the tissue and subcellular expression of three CaM
transcripts in these neurons and found that multiple CaM genes are expressed in the proximal regions of their leading processes and in the trailing processes. RNAi with shRNA targeted to the Calm1 transcript caused both tangential and radial migration defects, which prevented arrival at the prospective nucleus regions. By contrast, shRNAs targeted to the two other CaM genes did not cause apparent migration defects.

The role of Ca²⁺-CaM signaling in the migration of PCNs
We have shown that CaM is essential for the proper migration of PCNs. Two types of migration defect were observed: (1) incomplete tangential migration with failure to reach the appropriate circumferential position; and (2) a failure of radial migration to invade the depth of the prospective nucleus regions. By contrast, shRNAs targeted to the two other CaM genes did not cause apparent migration defects.

A possible mechanism for the incomplete tangential migration phenotype is a failure to recognize guidance cues at the midline. PCNs treated with Calm1sh361 took the correct ventriculo-pial position and migrated abutting the pial meninges. PN neurons migrated anteriorly toward the trigeminal nerve roots, and finally turned medially toward the midline FP, while LRN/ECN neurons took the separate posterior pathway. No PCNs treated with Calm1sh361 were observed to deviate from the stereotyped pathway. However, fewer PN neurons migrated medially to reach the prospective PN, and those that reached the midline remained in the FP, a property rarely observed in the control at E17.5. LRN/ECN neurons treated with Calm1sh427 also remained at the midline. These observations suggest that the guidance toward/away from the midline might be defective in PCNs treated with Calm1sh361 or Calm1sh427. Previous reports that showed that the action of midline guidance cues, such as netrin 1 or slit, is regulated by calcium signaling (Hong et al., 2000; Xu et al., 2004; Guan et al., 2007) are consistent with this interpretation.
Alternatively, the failure to reach the target region could be explained by defective neuronal motility, since Ca^{2+} signaling has been implicated in somal translocation. Ca^{2+} imaging and pharmacological perturbation studies have revealed a correlation between Ca^{2+} fluctuations in the soma and the rate of somal translocation in cerebellar granule cells (Komuro and Rakic, 1996, 1998; Kumada and Komuro, 2004). At the molecular level, nuclear translocation requires microtubule-based motors at the proximal region of the leading process and acto-myosin contraction at the trailing process (reviewed by Marín et al., 2006; Bellion et al., 2005; Martini and Valdeolmillos, 2010). Some proteins involved in this process, such as IQGAP1 and myosin light chain kinase, are regulated by CaM (Bagchi et al., 1992; Kholmanskikh et al., 2006; Marín et al., 2006). In accordance with these reports, we observed that Calm1 transcripts are expressed at high levels at the proximal region of the leading process, and in the trailing process. Therefore, it is conceivable that nucleokinesis is affected in PCNs treated with Calm1sh361. It will be necessary to study the motility of these neurons to confirm this theory.

The absence of a clear nucleus structure at the target region suggests the possible involvement of Calm1 in radial migration, although the defective neuronal motility discussed above might also have contributed to the failed radial migration. Radial migration is initiated by a turning or de novo formation of the leading process in the radial direction (Watanabe and Murakami, 2009). PCNs then radially migrate in close association with radial glial fibers (Kawauchi et al., 2006). We found that, with Calm1sh361 treatment, the leading population of PN neurons that had reached the midline at E15.5 rarely oriented along the radial glial fibers (Fig. 7D,J). The majority of PN neurons remained at the pial side of the prospective nucleus until E17.5, while the number of PN neurons that arrived gradually increased. Recently, it was shown that the radial migration of cortical neurons along the radial glia requires the gap junction subunit connexin 43 (Cx43; also known as Gja1), which is expressed at the contact points of migrating neurons and glial fibers and has a binding site for CaM (Elias et al., 2007; Zou et al., 2014). Therefore, the ability of PN neurons treated with Calm1sh361 to recognize radial glia should be investigated in future studies.

In summary, the present study has suggested a role of Calm1 in several aspects of neuronal migration. It has been reported that Calm1 is required for the migration of neuroblasts in the rostral migratory stream (Khodosevich et al., 2009). Neuroblasts originate in the subventricular zone of the lateral ventricles and migrate to the olfactory bulb, where they mature into granule and periglomerular cells. Silencing the expression of Calm1 results in retarded migration and a decrease in the ratio of radial versus tangential migration in the target olfactory bulb (Khodosevich et al., 2009), similar to the defects observed in the present study. Together, these findings suggest that Calm1 is essential for the migration of many neuronal types.

Relative contribution of the three CaM genes in PCN migration

The physiological significance of the existence of multiple CaM genes that each encode the exact same protein remains unknown. Since CaM has to interact with a diverse array of targets in a temporally and spatially regulated manner within a single cell, a plausible hypothesis is that each CaM transcript is differentially processed through post-transcriptional regulation and provides
distinct intracellular local CaM pools to ensure independent localization and size of the pools (Toutenhoofd and Strehler, 2000). This hypothesis postulates that all three CaM genes are expressed in the same cell and implies that they can have different cellular functions.

The simultaneous expression of multiple CaM genes in a cell has been deduced from their similar tissue expression profiles (Fig. 1) (Ikeshima et al., 1993; Solé et al., 1996; Palﬁ et al., 1999). In fact, the expression of all three CaM genes in a single cell type was shown previously in PC12 pheochromocytoma and IMR-32 neuroblastoma cell lines (Zhang et al., 1993; Toutenhoofd and Strehler, 2002). The present study has, for the ﬁrst time, revealed that a single neuron simultaneously expresses multiple CaM genes. This expression pattern raises the possibility that the three CaM genes are not used in a cell type-speciﬁc or temporally segregated manner, but are simultaneously used in the same cell, supporting the CaM local pool hypothesis discussed above.

Different cellular functions attributed to the three CaM genes have been deduced from their differential subcellular mRNA localizations. In hippocampal neurons, dentritic targeting of Calm1 and Calm3 but not Calm2 transcripts was shown, suggesting their differential usage (Palﬁ et al., 1999, 2005). In our study, mRNAs of all three CaM genes were localized in the proximal region of the leading process. However, the transcripts rarely colocalized, raising the possibility that their processing is differentially regulated by functionally distinct RNA processing machinery, such as RNA granules or P-bodies (Kriechevsky and Kosik, 2001; Kiebler and Bassell, 2006; Zeitelhofer et al., 2008). Our ﬁnding that the functional contribution of CaM gene family members in neuronal migration is not equal, but dominated by Calm1, supports this idea. However, to conﬁrm this theory a more accurate evaluation of the amount of protein translated from each CaM gene is necessary in future studies.

In conclusion, the current study demonstrates that Ca2+-CaM signaling is essential for neuronal migration. The involvement of CaM in transducing midline guidance signals and in somal translocation implied by this study is in accordance with previous reports suggesting that Ca2+ signaling regulates these events. Our study also suggested the involvement of CaM in the radial migration along radial glial ﬁbers. Further studies on the dynamics of Calm1sh361-treated PCNs are needed to conﬁrm these interpretations, and future work on the interaction with radial glia should shed light on the molecular mechanism that regulates radial migration.

**MATERIALS AND METHODS**

**Animals**

For all experiments, we used inbred ICR mouse strains obtained from Japan SLC (Hamamatsu, Japan). Noon of the day of vaginal plug detection was considered embryonic day (E) 0.5. For ex utero and in utero electroporation, pregnant mice were anesthetized by intraperitoneal injection of sodium pentobarbital (50 mg/kg body weight). All animal procedures were performed according to the guidelines of the Osaka University Animal Care Committee.

**In situ hybridization**

Complementary DNA sequences corresponding to the 3′UTR (500-700 nt in length) of each Calm family member were cloned into a pGem-T Easy plasmid (Promega) using the following primers (5′-3′): Calm1Forward, CTCCTGTCACACACACAAAG; Calm1Reverse, TTGTGGTTGTGC-TCAAGTCC; Calm2Forward, TTATTTGTTTTCTCTTTTGTG; Calm2Reverse, TGAACTGGACTCTTTTTTCT; Calm3Forward, CCAAAAGATTGTCCCAACAG; and Calm3Reverse, GCATGGGATGTTAGCACCAG. DIG-labeled antisense cRNA probes were transcribed using a linear template of the above plasmids and used to distinguish the three Calm genes.

ISH on 20 µm- or 30 µm-thick cryosections was performed as previously described (Kobayashi et al., 2013). ISH on cultured PCNs was performed as described (Kobayashi et al., 2005), with some minor modiﬁcations. Before hybridization, PCNs were acetylated at 0.25% acetic anhydride in 0.1 M triethanolamine and were ﬁxed in 1% paraformaldehyde. Hybridization was performed at 55°C for 42 h. After the detection of bound cRNA probes, anti-MAP2 staining and nuclear staining with DAPI were performed.

Double ISH on cultured PCNs was carried out essentially as above, except that ﬂuorescein-labeled cRNA probes were used along with DIG-labeled probes. The detection of each cRNA probe was carried out sequentially as follows. The culture was ﬁrst reacted with anti-ﬂuorescein-POD (Roche) and then FITC-tyramide (PerkinElmer). After inactivation of POD with 0.3% H2O2 for 30 min and extensive washes, the culture was reacted with anti-DIG-POD (Roche), followed by Cy3-tyramide (PerkinElmer), and the culture was then processed for nuclear staining with DAPI.

**Immunohistochemistry**

Primary antibodies used were: rabbit anti-nestin antibody (1:2000; rat 401, kind gift from Dr Arimatsu), rabbit anti-ssDNA polyclonal (1:100; IBL 18731), mouse anti-MAP2 monoclonal (1:200; Chemicon, MAB3418), rabbit anti-GFP polyclonal (1:500; MBL, M048-3), rat anti-GFP monoclonal (1:1000; Nacalai Tesque, clone GF090R) and chick anti-GFP polyclonal (1:1000; Abcam, ab13970). Secondary antibodies used were: Cy3-conjugated goat anti-rabbit IgG (1:200; Jackson ImmunoResearch, 111-165-144), Cy3-conjugated goat anti-mouse IgG (1:200; Jackson ImmunoResearch, 115-165-020), Alexa 488-conjugated goat anti-rabbit IgG (1:200; Invitrogen, A11008), Alexa 488-conjugated goat anti-rat IgG (1:200; Invitrogen, A11006) and Alexa 488-conjugated goat anti-chick IgG (1:200; Jackson ImmunoResearch, 103-545-155). For nuclear staining, cultured PCNs were reacted with 0.5 µg/ml DAPI solution. Mounting medium consists of 9.6% MOWIOL 4-88 (Calbiochem) containing 2.5% 1,4-diazobicyclo-(2,2,2)-octane (DABCO) (Sigma) to reduce fading.

**Plasmid construction**

The construction of shRNA-producing plasmids was carried out following the manufacturer’s instructions (pSuper vector, OligoEngine). Brieﬂy, a double-stranded DNA consisting of a sense target sequence followed by a hairpin and an antisense target sequence was ligated into the BglII/HindIII site of a pSUPER vector (OligoEngine). Target sequences for each Calm shRNA were (5′-3′): Calm1sh361, GAAGT-AGATGAAATGATCA; Calm1sh427, GTACA-GATGATGACTGCAA; Calm2sh414, CTACGA-AAGTTGTTGACAA; Calm2sh285, GGATG-GCAATGGCTATATT; Calm3sh384, GGCGCGC-ATTGATGGAGAT; and Calm3sh408, GTGTC-AATTAGAAGATTT. Numbering of shRNAs refers to the nucleotide numbers in the CaM-coding sequence (the ﬁrst nucleotide in the coding sequence was deﬁned as +1).

**Cell culture**

COS7 cell culture, and the assessment of knockdown efﬁciency and speciﬁcity of shRNAs, were performed as previously described (Kobayashi et al., 2013). In brief, equal volumes of plasmid DNA solution [containing 1 µg/ml EYFP-CaM, 1 µg/ml mCherry and 8 µg/ml shRNA in OPTI-MEM (Life Technologies)] and Lipofectamine (Life Technologies) solution (20 µl/ml in OPTI-MEM) were mixed, and 50 µl shRNA in OPTI-MEM (Life Technologies) and Lipofectamine ([sh361, GGTC-ATTGATGGAGAT; and sh384, GGCGCGC-ATTGATGGAGAT]; and Calm3sh408, GTGTC-AATTAGAAGATTT). Numbering of shRNAs refers to the nucleotide numbers in the CaM-coding sequence (the ﬁrst nucleotide in the coding sequence was deﬁned as +1).
To culture PCNs, the LRL of E12.5 hindbrain was excised and placed on 15-mm round coverslips pre-coated with poly-L-lysine solution (1 mg/ml). The explants were overlaid with 20 µl Matrigel (Matrigel Basement Membrane Matrix, BD) and cultured with DMEM/F12 supplemented with 10% FBS and 2% N2 supplement (Gibco). After 3 days in vitro, the culture was fixed and processed for ISH.

Real-time quantitative PCR

The LRL was electroporated with GFP-expressing plasmids at E12.5, and the prospective PN regions containing GFP-labeled PN neurons were dissected from E15.5 embryos. Tissues from six to ten embryos were pooled and dissociated by trypsinization and by pipetting through the narrow tip of a fire-polished Pasteur pipette. GFP-positive PCNs were then collected using a fluorescence-assisted cell sorter (FACSCalibur Flow Cytometry System, BD). About 500-5000 GFP-labeled PCNs were collected for each experimental condition. RNAs were extracted from these cells using the RNeasy Micro Kit (Qiagen) following the manufacturer’s instructions and converted to cDNA using SuperScript III reverse transcriptase (Life Technologies). CaM mRNA content was quantified by real-time quantitative PCR with SYBR Green I on a LightCycler (Roche). To measure the absolute copy number of each CaM mRNA in a cDNA sample, standard curves were generated from quantifiable CaM cDNA cloned into plasmids. Normalization of cDNA content between samples was achieved by measuring internal control genes Ppia and Actb.

Electroporation

Exo utero electroporation and in utero electroporation were performed as previously described (Kawauchi et al., 2006; Kobayashi et al., 2013). In brief, plasmid solution (final concentration of 1 µg/µl pCAG-EGFP, 1.5 µg/µl pSUPER-shRNA plasmid) containing 0.01% Fast Green was injected into the fourth ventricle of E12.5 mouse embryos, and DNA was electroporated into the LRL. The embryos were then allowed to continue normal development in utero.

For the sparse labeling, we co-introduced pCALNL-EGFP and pCAG-Cre. In this system, the expression of EGFP is prevented by an upstream neomycin resistance gene flanked byloxP sequences. EGFP expression is achieved by excision of the neomycin sequence by Cre recombimase (Kanegae et al., 1995). We combined 1 ng/µl pCAG-Cre and 1 µg/µl pCALNL-EGFP for appropriate labeling density.

Image analysis

Fluorescence images were taken with a digital camera (AxioCaM, Zeiss) and analyzed with Metamorph software (Universal Imaging). To quantify the dorsalventral distribution of PCNs in the E17.5 PN, a 667 µm×667 µm square and its dorsal two-thirds were delineated. Total pixel area showing EGFP fluorescence above threshold was measured for each square, and the ratio of the fluorescent area in the dorsal two-thirds to that of the entire square was calculated. For quantification in the E18.5 PN, a 800 µm×800 µm square and its dorsal two-thirds were used. To quantify the ratio of radially migrating PN neurons at E15.5, fluorescent cells within 435 µm of the midline were analyzed. The percentage of radially migrating neuronal area among the entire fluorescent area was calculated. To quantify PN neurons in the migratory pathway, the ratio of the fluorescent cell area located farther than 640 µm from the midline to that of the entire section was calculated. Three to four sections 80-90 µm apart were chosen and analyzed for each brain. Data were analyzed statistically with the Mann-Whitney U-test for comparisons between the control and each shRNA-treated group. P<0.01 was considered significant.

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Competing interests

The authors declare no competing financial interests.

Author contributions

H.K. and F.M. designed the study. H.K., S.S., A.N. and K.I. performed the experiments. H.K. and A.N. performed the expression analysis. H.K., S.S. and K.I. performed functional assays. D.K. established the foundation of the experimental system. H.K. and F.M. wrote the paper.

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