Protease nexin 1 and its receptor LRP modulate SHH signalling during cerebellar development

Catherine Vaillant1, Odysse Michos2, Slobodanka Orolicki1, Florence Brellier1, Sabrina Taieb1, Eliza Moreno1, Helene Te1, Rolf Zeller2 and Denis Monard1,*

Development of the postnatal cerebellum relies on the tight regulation of cell number by morphogens that control the balance between cell proliferation, survival and differentiation. Here, we analyze the role of the serine-protease inhibitor protease nexin 1 (PN-1; SERPINE2) in the proliferation and differentiation of cerebellar granule neuron precursors (CGNPs) via the modulation of their main mitogenic factor, sonic hedgehog (SHH). Our studies show that PN-1 interacts with low-density lipoprotein receptor-related proteins (LRPs) to antagonize SHH-induced CGNP proliferation and that it inhibits the activity of the SHH transcriptional target GLI1. The binding of PN-1 to LRPs with SHH-induced cyclin D1 expression. CGNPs isolated from Pn-1-deficient mice exhibit enhanced basal proliferation rates due to overactivation of the SHH pathway and show higher sensitivity to exogenous SHH. In vivo, the Pn-1 deficiency alters the expression of SHH target genes. In addition, the onset of CGNP differentiation is delayed, which results in an enlarged outer external granular layer. Furthermore, the Pn-1 deficiency leads to an overproduction of CGNPs and to enlargement of the internal granular layer in a subset of cerebellar lobes during late development and adulthood. We propose that PN-1 contributes to shaping the cerebellum by promoting cell cycle exit.

KEY WORDS: Protease nexin 1, Sonic hedgehog, Low density lipoprotein, Receptor-related protein (LRP), Proliferation, Cerebellum, Mouse

INTRODUCTION
Protease nexin 1 (PN-1; also known as SERPINE2 – Mouse Genome Informatics) is a 43 kDa member of the serpin superfamily and inhibits serine proteases (Baker et al., 1980; Gloor et al., 1986; Knauer et al., 2000). After secretion, PN-1 is complexed with its target proteases and binds to specific members of the low density lipoprotein receptor-related protein (LRP) family (Strickland and Ranganathan, 2003). The ligands are internalized in endosomes via clathrin-coated pits and are degraded in lysosomes. Simultaneously, the intracellular LRP domain signals, via coupling, to adaptor and scaffold proteins (Schneider and Nimpf, 2003). The role of PN-1 in the adult brain has been studied (Kvajo et al., 2004; Luthi et al., 1997), but possible functions during nervous system development remained elusive. During embryogenesis and in the postnatal brain, PN-1 is expressed prominently in areas of high remodelling, in which cell proliferation and fate specification are influenced by morphogens such as sonic hedgehog (SHH) (Kury et al., 1997; Mansuy et al., 1993). SHH is a key regulator of vertebrate morphogenesis (Ingham and McMahon, 2001) and its binding to the patched homolog 1 (PTC1; also known as PTCH1 – Mouse Genome Informatics) receptor causes the cessation of smoothened (SMO)-mediated inhibition of signal transduction and triggers the activation of the GLI family of transcriptional regulators (Ho and Scott, 2002). In the developing CNS, Shh and Pn-1 are co-expressed in the ventral part of the mesencephalon and myelencephalon, and in the mid-hindbrain junction, otic vesicles and cerebellum (Dahmane and Altaba, 1999; Mansuy et al., 1993; Wallace, 1999; Wechsler-Reya and Scott, 1999).

The developing cerebellum is a good model in which to study the regulatory pathways that coordinate cell proliferation with cell survival and differentiation. In rodents, this cortical structure is transiently enveloped by the external granular layer (EGL), which consists of cerebellar granule neuron precursors (CGNPs), which proliferate from birth until postnatal day 15 (P15). SHH is considered as the main proliferative signal of CGNPs (Dahmane and Altaba, 1999; Kenney and Rowitch, 2000; Wallace, 1999; Wechsler-Reya and Scott, 1999), a role that requires the extracellular modulation of SHH by heparan sulfates (Rubin et al., 2002) and the binding of the chemokine SDF-1 (also known as CXCL12 – Mouse Genome Informatics) to its receptor CXCR4 (Klein et al., 2001). By contrast, negative regulators of SHH signalling such as vitronectin (Pons et al., 2001), fibroblast growth factor 2 (FGF2) (Wechsler-Reya and Scott, 1999), BMPs (Rios et al., 2004) and PACAP (also known as ADCYAP1 – Mouse Genome Informatics) (Nicot et al., 2002) induce cell cycle exit and the differentiation of CGNPs.

Our results show that PN-1 modulates the signalling activity of SHH and promotes the differentiation of CGNPs and Bergmann glia. In particular, we establish that PN-1 antagonizes SHH-induced proliferation of CGNPs. In Pn-1-deficient mice, the expression of SHH targets is enhanced in the EGL and Bergmann glia, which correlates well with the delayed differentiation of CGNPs and altered maturation of Bergmann glia. In particular, the Pn-1 deficiency causes an increase in mature granular cells. We conclude that the interaction of PN-1 with SHH is important for shaping the cerebellum during its postnatal development.

MATERIALS AND METHODS
Materials
The 19 kDa N-terminal fragment of SHH was kindly provided by S. Pons [Instituto de Biologia Molecular de Barcelona (CSIC), Barcelona, Spain] and U. Mueller (Scripps Institute, San Diego, CA, USA), or from R&D Systems. FGF2 was purchased from R&D Systems, and KAAD-cyclopamine from Invitrogen. Rat recombinant PN-1 was purified and the P960 and P965 peptides produced as described previously (Knauer et al.,
Mice
Wild-type C57BL/6J mice were purchased from Charles River (France). Homozygous Pn-1 knockout (Luthi et al., 1997) and knock-in (Kvajo et al., 2004) mice were backcrossed in the C57BL/6J line for 11 generations. Heterozygous matings of Pn-1-deficient mice allowed the comparative analysis of littermates of all genotypes. All animal experiments were performed according to the Swiss laws governing animal experimentation and approved by the Swiss veterinary authorities.

Primary cultures of CGNs
CGNs were isolated from P5–P8 mice cerebella over a Percoll gradient, as described previously (Hatten, et al., 1988). Purified CGNs were resuspended in 10% horse-serum medium and 105 cells per well were plated in 24 well plates on glass coverslips coated with poly-L-lysine (10 or 500 μg/ml; Fluka). After overnight recovery, cells were cultured in serum-free medium containing 1% stripped BSA and I-1884 supplement (Sigma). Depending on the assay, the culture medium was supplemented with either 50, 100, 200 or 3000 ng/ml SHH, and/or 30 or 210 nM PN-1, and/or 1 μg/ml RAP for 48 hours. Bergmann glial cells were isolated and purified as described previously (Hatten, 1985). For proliferation studies, cells were incubated with 10 μg/ml BrdU for 16 hours. Mixed cultures from Pn-1-deficient mice were prepared from individually processed cerebella to compare proliferation rates among age-matched littermates. All coverslips were processed for BrdU immunostaining and were counterstained with Hoechst. Pictures were acquired using a Leica DMR microscope and a SPOT-1 digital camera. Fluorescent staining was analyzed using Image-Pro Plus (Media Cybernetics). For proliferation index determination, the ratio of BrdU-positive cells/Hoechst-labelled cells was calculated over ten fields per coverslip. The averages were calculated using four independent experiments.

Beta-galactosidase staining and activity assays
Beta-galactosidase-detection and activity assays were performed as described previously (Kvajo et al., 2004). CGNs were incubated overnight in serum-free medium with or without FGF2 (25 or 50 ng/ml) and/or SHH (3 μg/ml), lysed and processed using the Galacto-Star kit (Applied Biosystems), and analyzed using a microplate reader.

Immunohistochemistry and immunocytochemistry
Cells grown on coverslips were post-fixed in 4% paraformaldehyde and the antibodies used were: anti-beta-III-tubulin (1/200, Chemicon), 4B3 monoclonal anti-PN-1 (1/100; provided by D. Strickland, Department of Biochemistry, American Red Cross, MD, USA), anti-prominin 1 (1/300, Chemicon), anti-GFAP (1/1500, Sigma). P10 wild-type and Pn-1-deficient mice were injected intraperitoneally with BrdU (Sigma) at 100 μg/g of body weight, and brains isolated 1 hour later. Cryostat or paraffin sections (12 μm) were stained using: anti-PN-1 (1/100), anti-LRP1 (1/1000, BD Pharmingen), anti-GFAP (1/1000, Sigma), anti-p27 (1/100, BD Pharmingen), anti-MATH1 (also known as anti-ATOH1; 1/100; generous gift from J. Johnson, University of Texas Southwestern Medical Center, Dallas, TX, USA) and anti-doublecortin (1/100, Santa Cruz Biotechnology). The specificity of the PN-1 antiserum was established by the absence of staining in cerebella of Pn-1-deficient mice (data not shown). Alexa Fluor 488 or horseradish peroxidase (HRP)-coupled antibodies included anti-mouse (1/500, Molecular Probes; 1/1000, Amersham Bioscience) and anti-rabbit (1/500, Molecular Probes). PN-1, LRP1 and doublecortin immunostainings were performed using a Discovery XT automated stainer (Ventana Medical Systems) with Ventana DAB Map detection kit (Easwaran et al., 2003). Antigen retrieval was achieved in CC1 and CC2 buffers (Ventana). Secondary biotinylated antibodies were: donkey anti-goat (1/200, Jackson ImmunoResearch) and Ventana universal secondary antibody. Signals were amplified using the AmpMap kit with TSA (Ventana). Sections from wild-type and mutant mice were processed simultaneously. Quantification of BrdU labelling and p27-positive cells was performed on mid-sagittal sections in the region of the pre-culminate fissure of lobes III and IV. The average ratio of BrdU- or p27-positive to -negative CGNs was determined over 200 μm of EGL for each cerebellum.
CNS neurons. (B) Schematic representation of the Pn-1 receptor complex (G). (C) Glial cells were immunostained for GFAP. Scale bar: 20 μm. (D) Glial cells were immunostained for GFAP. Scale bar: 20 μm. (E) Glial cells were immunostained for GFAP. Scale bar: 20 μm. (F) Glial cells were immunostained for GFAP. Scale bar: 20 μm. (G) Glial cells were immunostained for GFAP. Scale bar: 20 μm. (H) Glial cells were immunostained for GFAP. Scale bar: 20 μm. (I) Glial cells were immunostained for GFAP. Scale bar: 20 μm. (J) Glial cells were immunostained for GFAP. Scale bar: 20 μm. (K) Glial cells were immunostained for GFAP. Scale bar: 20 μm. (L) Glial cells were immunostained for GFAP. Scale bar: 20 μm. (M) Glial cells were immunostained for GFAP. Scale bar: 20 μm. (N) Glial cells were immunostained for GFAP. Scale bar: 20 μm. (O) Glial cells were immunostained for GFAP. Scale bar: 20 μm. (P) Glial cells were immunostained for GFAP. Scale bar: 20 μm. (Q) Glial cells were immunostained for GFAP. Scale bar: 20 μm. (R) Glial cells were immunostained for GFAP. Scale bar: 20 μm. (S) Glial cells were immunostained for GFAP. Scale bar: 20 μm. (T) Glial cells were immunostained for GFAP. Scale bar: 20 μm. (U) Glial cells were immunostained for GFAP. Scale bar: 20 μm. (V) Glial cells were immunostained for GFAP. Scale bar: 20 μm. (W) Glial cells were immunostained for GFAP. Scale bar: 20 μm. (X) Glial cells were immunostained for GFAP. Scale bar: 20 μm. (Y) Glial cells were immunostained for GFAP. Scale bar: 20 μm. (Z) Glial cells were immunostained for GFAP. Scale bar: 20 μm.
Furthermore, the PN-1 protein was detected in cells of the forming Purkinje cell layer (PCL; Fig. 1G,H, red arrowheads), in Bergmann glial cells (Fig. 1H, black arrowheads), diffusely in the EGL (Fig. 1H) and in the dorsal anterior lobes (Fig. 1G, arrow). By P2, abundant Pn-1-expressing cells were detected in the PCL (Fig. 1C,D). The distribution of beta-galactosidase-positive cells was graded along the
anteposterior axis, being absent or weak in dorsal and ventral parts, but stronger in central lobes. Each of the positive lobes displayed lower beta-galactosidase activity in its invaginations (Fig. 1C). By contrast, the PN-1 protein was rather lower in central than in dorsal and ventral regions (Fig. 1L). These regional differences in PN-1 transcript and protein distributions could be due to secretion and internalization of the PN-1 protein by target cells (see below) and/or to additional post-transcriptional regulation. PN-1 distribution within the PCL is rather reminiscent of those of Shh and Gli1 transcripts at equivalent stages (Corrales et al., 2004; Lewis et al., 2004). In the EGL, a few PN-1-positive CGNPs were still scattered throughout the lobes (Fig. 1D, arrowheads). By P8, the overall level of beta-galactosidase activity had decreased (Fig. 1E), but remained in Purkinje and Bergmann glia cell bodies (Fig. 1F, arrowheads). PN-1 protein was detected in dorsal lobes and their invaginations (Fig. 1K, arrows), in Bergmann glia (Fig. 1L, arrowheads), in the PCL and in scattered progenitors of the EGL (Fig. 1M, red and green arrowheads).

In adults, Pn-1 expression was weak and rather homogeneous within the PCL (data not shown). The distribution of the major PN-1 receptor, LRP1, was rather ubiquitous, although was higher in the PCL of the dorsal and ventral regions (similar to PN-1, for details see Fig. S1 in the supplementary material).

**PN-1 is expressed by a subpopulation of cultured CGNPs and is internalized in an LRP1-dependent manner**

To further analyze Pn-1 expression and function, primary cerebellar cells were isolated from P5 reporter mice, cultured for 3 days, and characterized with respect to Pn-1 expression and their differentiation status (Fig. 2A and see Fig. S2 in the supplementary material). Less than 5% of all cells expressed Pn-1 (Fig. 2A). Approximately 70% of all PN-1-positive cells corresponded to GFAP-apositive astroglias (Fig. S2 in the supplementary material), which accounted for about 30% of all astroglial cells in the cerebellum. In addition, around 75% of all cerebellar stem cells (positive for prominin 1) (Lee et al., 2005) were PN-1 positive, whereas only few neuronal cell types expressed PN-1 (<3%; data not shown). FGF2 is known to antagonize SHH-mediated proliferation of cultured CGNPs (Wechsler-Reya and Scott, 1999). Interestingly, Pn-1 expression is upregulated by FGF2 in mid-/hind-brain-derived mesenchymal cells (Kury et al., 1997). To determine whether PN-1 could be a target of SHH and/or FGF2 signal transduction, CGNPs from P5 reporter mice were cultured in medium supplemented with either recombinant SHH or recombinant FGF2 (Fig. 2B). Pn-1 expression levels were elevated in a dose-dependent manner upon FGF2 addition (Fig. 2B). In particular, FGF2 induced a 30-70% increase in Pn-1-expressing astroglial cells (Fig. S2 in the supplementary material).

Free or complexed extracellular PN-1 binds to LRP1, which mediates its internalization (Knauer et al., 1997b). LRP1 was detected in the cell body and along neurites of all CGNPs (Fig. 2C) and receptor-associated protein (RAP; also known as LRPPAP1 – Mouse Genome Informatics)-mediated blocking of LRPs significantly inhibited PN-1 internalization into CGNPs (Fig. 2D-G). Because RAP has a high affinity for all LRPs (Herz et al., 1991), we used the 12 amino acid P960 peptide derived from the N-terminal region of PN-1 to characterize the involved LRP subtype further. This peptide has been shown to specifically interfere with LRP1-mediated PN-1 uptake (Knauer et al., 1997a). Indeed, P960 completely blocked the internalization of recombinant PN-1 (Fig. 2G), which indicates that LRP1 is required for PN-1 internalization by CGNPs.

**PN-1 antagonizes SHH signalling in cultured CGNPs**

In order to investigate the potential effects of PN-1 on SHH-induced cell proliferation, CGNPs were cultured for 48 hours in the presence of SHH and/or PN-1. Proliferating cells were labelled with BrdU during the last 16 hours to determine their proliferation rates (Fig. 3A,B). As previously reported (Wechsler-Reya and Scott, 1999), the addition of recombinant SHH stimulated CGNP proliferation (Fig. 3A,B, series 1). Such SHH-induced cell proliferation was significantly antagonized by PN-1 using SHH at 50 or 100 ng/ml (Fig. 3A,B, series 2 and 3). Higher SHH concentrations were able to significantly antagonize by PN-1 using SHH at 50 or 100 ng/ml (Fig. 3A,B, series 2 and 3). Higher SHH concentrations were able to overcome the inhibitory effect of PN-1, which is indicative of its limited modulation potential and/or saturation of the system. To determine whether the antagonistic effect of PN-1 is mediated by receptor competition or via an independent intracellular pathway,
cells were pre-treated with SHH for 5 hours prior to PN-1 addition (Fig. 3B). Pre-treatment with SHH did not significantly alter the inhibitory potential of PN-1, pointing to PN-1 having antagonistic effects on SHH signal transduction rather than on its direct competition for receptor binding.

Following this result, we also assessed the potential effects of PN-1 on cyclin D1, a known SHH target gene (Kenney and Rowitch, 2000). Indeed, cyclin D1 was detected at a high level in cells treated with SHH alone, and levels were lower by treatment with SHH and PN-1 (Fig. 3C). These results are consistent with the observed reduction in cell proliferation (compare Fig. 3C with Fig. 3A,B). Interestingly, cyclin D1 was also downregulated in cells treated with both SHH and RAP, thus indicating a possible requirement of LRPs for SHH-mediated stimulation of cell proliferation. The specificity of the antagonistic effects of PN-1 on SHH signal transduction was validated further by monitoring its ability to interfere with SHH-induced transcriptional activation. Gli1 transcription was used as a sensitive read-out of SHH pathway activity in CGNs cultured for 48 hours in the presence of SHH alone or with PN-1 (Fig. 3D). Whereas SHH alone upregulated Gli1 expression, the addition of PN-1 reduced Gli1 transcription to basal levels, as revealed by semi-quantitative reverse transcriptase (RT)-PCR analysis (Fig. 3D). To substantiate these results further, NIH3T3 cells, which are routinely used to assess SHH signal transduction (Yao et al., 2006), were transfected with a Gli1 reporter plasmid (Dai et al., 1999). Treatment of transfected cells with SHH alone caused an approximately fourfold increase in the expression of the Gli1 reporter gene within 24 hours, which could be blocked by PN-1 (Fig. 3E). Taken together, these results indicate that PN-1 antagonizes SHH signal transduction and/or the upregulation of the transcriptional target Gli1.

Next, the proliferation rates of mixed CGNs/glial cells (Fig. 3F) and enriched CGNs cultures (data not shown) isolated from wild-type and Pn-1-deficient mice were determined in response to SHH signalling. Indeed, mixed CGN cultures from Pn-1–/– mice displayed an almost twofold-higher basal proliferation rate and a higher sensitivity to SHH-induced stimulation of proliferation than wild-type controls. Addition of PN-1 antagonized SHH-induced proliferation of both mutant and wild-type cells (Fig. 3F). In particular, the addition of 210 nM of recombinant PN-1 reduced the proliferation of Pn-1-deficient CGN cultures to wild-type levels (Fig. 3F). The naturally occurring chemical cyclopamine (Cp), which blocks SHH signal reception, had little effect on the proliferation of wild-type cells, but reduced the proliferation of Pn-1-deficient cultures to wild-type levels (Fig. 3F). Enriched

Fig. 5. The Pn-1 gene deficiency delays the onset of CGNP differentiation in the EGL. (A-H) Sections from P10 wild-type (A,C,E,G) and Pn-1-deficient mice (B,D,F,H) were immunostained for MATH1 (green; Hoechst, blue). In both groups, MATH1 staining is detected in the oEGL. The zone of MATH1-positive cells is enlarged in Pn-1-deficient mice. In addition, the intensity of the MATH1 staining increases at the cellular level. (I-L) Sections from P10 wild-type and Pn-1-deficient mice were immunostained for p27 (green; Hoechst, dark blue; overlap, light blue). The wild-type EGL is divided into two zones: the oEGL, with few p27 expressing cells, and the iEGL, expressing p27 at high levels (L). In Pn-1-deficient cerebellum, the p27-negative oEGL is approximately twice the width of the iEGL (L). (M,N) Sections from P10 wild-type and Pn-1-deficient mice injected with BrdU 1 hour prior to sacrifice were immunostained (BrdU, green; Hoechst, blue). Analysis of the wild-type oEGL (M) reveals regularly dispersed BrdU-positive CGNs (arrowheads), whereas the proliferating CGNs of Pn-1-deficient mice are closer to the external pial border (N). (O) The ratio of BrdU positive versus negative CGNs is not significantly altered in mutants. (P) Mutant mice show a significant decrease in the fraction of p27-labelled CGNs. *P<0.05 (Student’s t-test). (Q,R) P10 cerebellar sections of Pn-1+/+ and Pn-1–/– mice immunostained for GFAP were analyzed by confocal microscopy. Pn-1–/– Bergmann glia display higher GFAP levels together with an increased thickness of and larger endfeet (R) in comparison to wild type (Q). iEGL, inner external granular layer; oEGL, outer external granular layer. Scale bars: 80 μm in B for A-D; 20 μm in F for E-H; 40 μm in I for I-J and in Q for Q,R; 15 μm in K for K-N and in inset in Q doe insets in Q,R.
CGNP cultures from Pn-1-deficient mice showed only a 28% increase in proliferation compared with the control (data not shown). This confirms that the glial population is the main source of PN-1 (also see Fig. S2 in the supplementary material) and provides evidence that the increased proliferation rates of Pn-1-deficient CGNPs could be due to overactivation of SHH signal transduction. These results indicate that PN-1 acts as a negative modulator of SHH signal transduction. Indeed, PN-1 inhibited SHH-induced differentiation of Bergmann glial cells (see Fig. S3 in the supplementary material). Taken together, these results show that PN-1 can antagonize both proliferation- and differentiation-inductive properties of SHH in culture.

**Pn-1 deficiency potentiates the expression of SHH target genes in vivo**

Given the higher SHH sensitivity of cultured Pn-1-deficient CGNPs, SHH signal transduction may be altered in Pn-1-deficient mice. Therefore, the expression of several SHH target genes was evaluated by in situ hybridization at P8 (Fig. 4 and see Fig. S4 in the supplementary material). Gli1 and Ptc1 are positive SHH targets and provide a sensitive read-out of SHH activity (Goodrich and Scott, 1998; Lee et al., 1997). Both genes were expressed in the EGL and by Bergmann glia in wild-type mice (Fig. 4A,C,G,H,J). In Pn-1–/– mice, the expression of both Gli1 and Ptc1 was increased in cells within the outer EGL (oEGL) [Fig. 4B,D,I,K; identified as MATH1 (also known as anti-ATOH1)-positive CGNPs: see Fig. 5F]. In addition, higher levels of Gli1 and Ptc1 expression were also detected in Bergmann glia in Pn-1-deficient mice (see Fig. S4 in the supplementary material).

Shh and Gli3 are expressed in rather complementary patterns and have been shown to functionally antagonize one another (Zeller, 2004). Gli3 was broadly expressed in the EGL and in the internal granular layer (IGL) of wild-type mice (Fig. 4E,L), whereas its expression was lower and more-restricted in Pn-1-deficient mice (Fig. 4F,M). Interestingly, Gli3 expression was normal in the external part of the cerebellum but significantly reduced in fissures (Fig. 4F). The changes are not due to altering Shh itself, because Shh was expressed at similar levels in both wild-type and mutant mice (predominantly in Purkinje cells; Fig. 4N,O). The results were confirmed by semi-quantitative RT-PCR analysis, which revealed that the expressions of Gli1 and Ptc1 were significantly increased while that of Gli3 was reduced in the cerebellum of Pn-1-deficient mice (see Fig. S5 in the supplementary material). Taken together, these studies corroborate the proposal that SHH signal transduction is potentiated in mice lacking Pn-1.

**CGNP differentiation is delayed in Pn-1-deficient mice**

In Pn-1-deficient mice, the overall thickness of the EGL was not altered at P5 and P10 (data not shown). By contrast, the Pn-1 deficiency resulted in a thickening of the oEGL and thinning of the inner EGL (iEGL; Fig. 5A-L). The bHLH transcription factor...
MATH1 identifies the early progenitors of the granular lineage (Ben Arie et al., 1997). The number of immature MATH1-positive CGNPs increased slightly at P5 (data not shown) and significantly at P10 in Pn-1-deficient mice (Fig. 5A-H), and MATH1 immunoreactivity was stronger in mutant CGNPs (Fig. 5E,F). To analyze the postmitotic zone of the EGL, the p27 cyclin-dependent kinase inhibitor, which accumulates in the nuclei of postmitotic CGNPs, was used to monitor differentiation (Miyazawa et al., 2000). In wild-type cerebella, overall p27 staining was weak in the oEGL and became more intense as CGNPs entered the iEGL (Fig. 5I,K). In Pn-1-deficient mice, the decrease in iEGL thickness was noticeable at P5 (data not shown) and obvious by P10 (Fig. 5J-L). The intensity of p27 staining was reduced in the expanded oEGL and was restricted to a limited region of the iEGL (Fig. 5L). In agreement, the ratio of p27-labelled to non-labelled cells was significantly reduced in Pn-1-deficient mice by P10 (Fig. 5P). This delay in CGNP differentiation was further evidenced by immunodetection of doublecortin, an early marker for neuronal differentiation (Gleeson et al., 1999), whose expression was decreased in Pn-1-deficient mice (see Fig. S6 in the supplementary material). These results show that the onset of differentiation is delayed in CGNPs of Pn-1-deficient mice. However, during the stages analyzed, this delay did not correlate with significantly altered proliferation rates (Fig. 5M-O and data not shown). Interestingly, the BrdU-labelled CGNPs remained located close to the pial surface in Pn-1−/− cerebella (Fig. 5N), whereas the proliferative CGNPs were spread throughout the oEGL in wild-type littermates (Fig. 5M, arrowheads). We also studied whether PN-1 modulates the SHH-mediated differentiation of Bergmann glial cells in vivo. Indeed, an overall increase in the thickness of GFAP-positive fibres was observed in Bergmann glial cells at P10 in Pn-1-deficient mice (Fig. 5R). The Bergmann glial fibres appeared irregular and contacted the pial surface with larger endfeet in comparison to wild-type (Fig. 5Q). These results indicate that the SHH-mediated effects on the proliferation of CGNPs and differentiation of Bergmann glia cells are potentiated in Pn-1-deficient mice. Finally, the in vivo levels of the cell cycle regulators cyclin D1 and cyclin D2, two SHH targets (Kenney and Rowitch, 2000), were evaluated. Immunoblot analysis was performed on cerebellar extracts from P10 wild-type and Pn-1-deficient mice. The levels of cyclin D1 and cyclin D2 were increased by 33 and 68%, respectively, in mutant cerebella (Fig. 6A,B).

**Pn-1 deficiency induces cerebellar overgrowth**

The differentiation impairments caused by Pn-1 deficiency during postnatal development prompted us to evaluate the overall morphology of the cerebellum. The thickness of the IGL was examined in Pn-1+/+ and Pn-1−/− mice at P5, P10 and in adults. The gross morphology of the P5 mutant cerebellum was similar to that of wild type (data not shown). By contrast, P10 mutant mice showed an increased thickness of the external IGL that was restricted to the anterior-central part of the cerebellum (see Fig. S7 in the supplementary material). In particular, the IGL of lobe VI showed a 67% increase in thickness compared with its wild-type counterpart (Fig. 7E). The IGL of the posterior lobes and zones facing the deep fissures were unaffected. The observed phenotype became more prominent in adult mutant mice (Fig. 7A-E); the width of the IGL in posterior lobe VIII showed a 40% increase and the IGL of lobe VI was 60% thicker in comparison to wild type. Thus, the Pn-1 deficiency probably resulted in an overproduction of mature granular cells, which caused the enlarged IGL. However, this difference in thickness may not necessarily reflect differences in the total volume of the IGL, because there may be compensation. Therefore, both wild-type and mutant cerebella (P10 and adults) were serially reconstructed (Fig. 8). The complete IGL in the cerebellum of three pairs of age-matched wild-type and Pn-1-deficient mice was measured. At P10, the mutant cerebellum showed a 6% increase in volume in comparison to wild type (data not shown), whereas the overall increase was 12.2% in adults. Potential regional differences were assessed by subdividing the cerebellum into three regions: anterior (lobes III-V), medial (lobes VI-VII) and posterior lobes (lobes VIII-X). At P10, the medial part was most affected (data not shown). In the adult, the anterior, medial and posterior regions of Pn-1-deficient mice showed an increase of 11.3, 9.3 and 15.4%, respectively. Moreover, the 3-D reconstruction of wild-type and mutant cerebella revealed an elongation of the anterior and posterior parts in comparison to wild type (Fig. 8B-D, red double arrows,). In particular, lobe IX protruded much more in Pn-1-deficient mice (Fig. 8D). Interestingly, these enlarged and elongated territories contained the highest levels of PN-1 protein during early development (Fig. 1). Taken together, this in vivo analysis suggests a modulatory role of PN-1 during cerebellar development.

**DISCUSSION**

The present study establishes PN-1 as a modulator of neuronal precursor proliferation and differentiation in the postnatal developing cerebellum. Pn-1 expression was high during the active phase of CGNP proliferation and was downregulated during differentiation. PN-1 inhibited SHH-induced CGNP proliferation...
and CGNPs isolated from Pn-1-deficient mice displayed higher proliferation rates. In vivo, an increased number of CGNPs expressed Gli1 and Ptc1 in the oEGL of mutant mice. The cerebellar development of Pn-1-deficient mice resulted in an enlarged oEGL and a reduced iEGL. SHH-regulated maturation of the Bergmann glia was potentiated in Pn-1-deficient mice. In addition, the SHH targets cyclin D1 and cyclin D2 were overexpressed in mutant cerebellum. Finally, the Pn-1 gene deficiency caused a regionalized increase of the IGL, which led to a localized size increase in the adult cerebellum. Thus, Pn-1 functions in combination with SHH to shape the adult cerebellum. SHH binds Megalin (also known as gp330 and LRP2) with high affinity and is endocytosed via LRP family members (McCarthy et al., 2002). Nybakken and Perrimon (Nybacken and Perrimon, 2002) proposed that the SHH-LRP interaction may allow the clustering of PTC1, SMO and SHH, thus causing internalization and potentiation of the signal. However, the biological relevance of LRP in SHH signal transduction remained unclear. Using RAP, we provide evidence that LRP accessibility is important for SHH-mediated stimulation of CGNP proliferation. Proteoglycans are crucial for binding to LRP and for the subsequent internalization of ligands, such as Pn-1 (Crisp et al., 2000). Interestingly, proteoglycans are also required for SHH-induced proliferation of progenitor cells in the postnatal developing cerebellum (Rubin et al., 2002). Because Pn-1 is known to bind to several LRP family members (Croy et al., 2003), it is possible that Pn-1 and SHH could share the same LRP receptors on CGNPs. In agreement with other studies, we demonstrate that Pn-1 uptake is mediated by LRP1. Moreover, microarray analysis indicates that, in the cerebellum, LRP1 transcripts are at least tenfold more abundant than any other LRP's (data not shown). Thus, LRP1 seems to be the best candidate for mediating the Pn-1 and SHH interactions during CGNP proliferation. The potential competition for LRP-binding sites may be mechanistically similar to what has been reported for dickkopf 1 (DKK1) and the Wnt modulator Wise (also known as SOSTDC1 – Mouse Genome Informatics), which inhibit Wnt signalling by interacting with LRP5 and/or LRP6 (Glinka et al., 1998). However, we cannot exclude that the interaction of Pn-1 with LRP5 also interferes with other ligands sharing this co-receptor, such as BMP4. In fact, BMP4 is present in the EGL (Rios et al., 2004) and interacts with LRP2, which induces its clearance (Spoelgen et al., 2005).

The cerebella phenotype of Pn-1-deficient mice corroborates the results obtained by the analysis of primary CGNP cultures. The Pn-1 deficiency results in increased expression of the SHH transcriptional targets Gli1 and Ptc1 in the oEGL, indicative of enhanced SHH signal transduction. Furthermore, the number of immature CGNPs and the initiation of their differentiation is enhanced in mutant mice, which is detrimental to the postmitotic iEGL. These changes in CGNP differentiation probably underlie the enlargement of the IGL from P10 onwards. The increase in IGL thickness follows an anteroposterior gradient: it initiates in lobe VI and affects more posterior lobes as differentiation progresses. It is interesting to note that these regions correspond to the territories with the highest Pn-1 protein levels during cerebellar development. Studies using gain- and loss-of-function approaches have established that the SHH-mediated, controlled local increase in the proliferation of CGNPs determines the extent of cerebellar foliation (Corrales et al., 2004; Corrales et al., 2006; Lewis et al., 2004). These authors postulate that regulation of the length and intensity of SHH signalling is crucial to lobule formation. We now identify the Pn-1 extracellular serine protease inhibitor as a valuable candidate modulator. Indeed, SHH overexpression in transgenic mice does not alter EGL thickness or CGNP proliferation in the oEGL between P5 and P10, but the IGL is expanded from P8 onwards (Corrales et al., 2004; Corrales et al., 2006). In adult transgenic mice, all cerebellar lobes exhibit a thickened IGL as also observed in Pn-1-deficient mice. Our study uncovers a role of Pn-1 in the cellular events that are controlled by morphogenetic SHH signalling during cerebellar development. Pn-1 may restrain SHH-mediated proliferation and thereby contribute to the regulation of the size and shape of the cerebellum via the fine-tuning of SHH-mediated foliation. This would explain the rather localized gross-morphological phenotype observed in Pn-1-deficient mice. Further investigation is necessary to understand how Pn-1 may participate in the formation and maintenance of an anteroposterior gradient of SHH signal transduction, and how Pn-1 may potentially impact the switch from proliferation to differentiation.

We are grateful to S. Arber and N. Hynes for critical reading of the manuscript. We also thank U. Mueller, S. Pons, S. Ishii, M. Eterodt, D. Strickland, J. Johnson and A. Zuniga for comments and reagents. We thank A. Weigel, M. Lino, F. Fischer and P. Schwarz for valuable technical assistance. This work was supported by the Novartis Research Foundation (to D.M.) and the Swiss National Science Foundation (to R.Z.).

Supplementary material
Supplementary material for this article is available at http://dev.biologists.org/cgi/content/full/134/9/1745/DC1

References
Crisp, R. J., Knauer, D. J. and Knauer, M. F. (2000). Roles of the heparin and low-density lipoprotein receptor-related protein-binding sites of protease nexin 1 (PN1) in urokinase-PN1 complex catabolism. The PN1 heparin-binding site mediates complex retention and degradation but not cell surface binding or internalization. J. Biol. Chem. 275, 19628-19637.
39-kDa protein modulates binding of ligands to low density lipoprotein receptor-related protein/alpha 2-macroglobulin receptor. J. Biol. Chem. 266, 21232-21238.


Knauper, M. F., Kriel, S. J., Hawley, S. B. and Knauper, D. J. (1997b). The efficient catabolism of thrombin-protease nexin 1 complexes is a synergistic mechanism that requires both the LDL receptor-related protein and cell surface heparins. J. Biol. Chem. 272, 29039-29045.


