



Zones and Stripes: Development of Cerebellar Topography

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Contents

The Architecture of the Adult Cerebellar Cortex	46
From Allocation to Rhombomere 1 to Two Germinal Epithelia	48
Purkinje Cell Birth Date, Phenotype, and Location	49
From Ventricular Zone to Clusters	49
Purkinje Cell Subtype Specification	50
From Embryonic Clusters to Adult Stripes	50
Afferent Topography	52
Climbing Fibers	52
Mossy Fibers	53
Interneurons	54

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Cerebellar Topography and Circuit Function	55
From Zones-And-Stripes to Complex Motor Behaviors	56
Conclusions	57
References	58

Abstract

Cerebellar architecture is organized around the Purkinje cell. Purkinje cells in the mouse cerebellum come in many different subtypes, organized first into four transverse zones and then further grouped into hundreds of reproducible topographical units – stripes. Stripes are identified by their functional properties, connectivity, and expression profiles. The molecular pattern of stripes is highly reproducible between individuals and is conserved through evolution. Pattern formation in the cerebellar cortex is a multistage process that begins with the generation of the Purkinje cells in the ventricular zone (VZ) of the fourth ventricle. During this stage, or shortly after, Purkinje cell subtypes are specified toward specific positions. Purkinje cells migrate from the VZ to form an array of clusters that form the framework for cerebellar topography. At around birth, these clusters begin to disperse, triggered by Reelin signaling pathway proteins, to form the adult stripe array.

The chapter will begin with a brief overview of adult cerebellar topography, primarily focusing on the mouse cerebellum, and then discuss the cellular and molecular mechanisms that establish these remarkable patterns. Considering how functionally diverse the cerebellum is despite its conserved organization of patterns, this chapter will end exploring how stripes might contribute to neuronal activity and the execution of cerebellar-dependent behaviors.

Keywords

Cerebellum · Purkinje cell · Patterning · Stripes · Zones · Topography

The Architecture of the Adult Cerebellar Cortex

The adult mouse cerebellum is shown in Fig. 1, immunoperoxidase stained for the antigen zebrin II (Brochu et al. 1990; zebrin II, aldolase C (AldoC) – Ahn et al. 1994). There are two subsets of Purkinje cells: zebrin II-immunopositive (zebrin II+) and zebrin II-immunonegative (zebrin II-). Purkinje cells in each subset are aligned to form an alternating array of parasagittal stripes (Brochu et al. 1990; Sillitoe and Hawkes 2002). Stripes are reproducible between individuals and symmetrically distributed about the midline (Hawkes et al. 1985; Hawkes and Leclerc 1987; Brochu et al. 1990). Zebrin II+ stripes are numbered as P1+ to P7+ starting from the midline and going laterally, and the intervening zebrin II- stripes are numbered with reference to the medial zebrin II+ stripe (i.e., P1- lies immediately lateral to P1+, etc.). In the vermis, four transverse domains in the anterior–posterior axis are identified by zebrin II expression: the striped anterior zone (AZ: ~lobules I–V), the

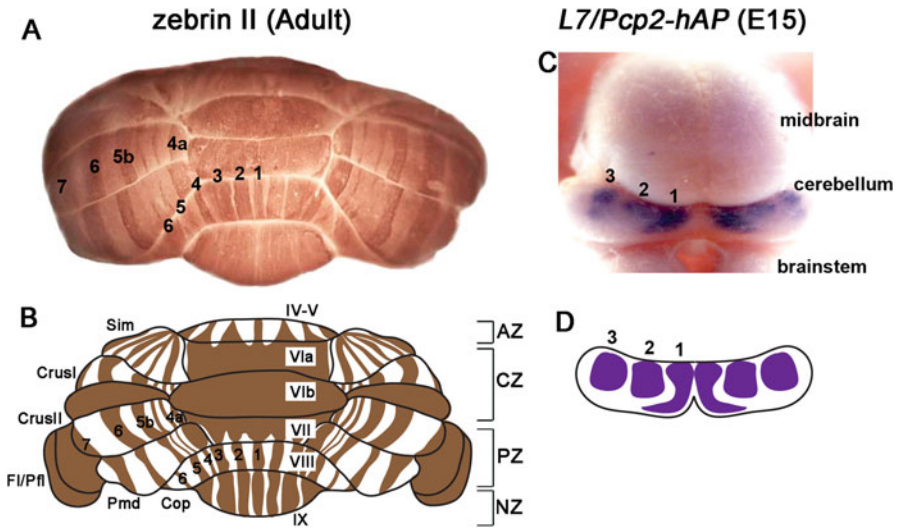


Fig. 1 The mouse cerebellum is organized into an array of transverse zones and parasagittal stripes. (a) Adult mouse cerebellum immunoperoxidase stained in whole mount with anti-zebrin II/aldolase C. (b) Schematic illustrating the pattern of zebrin II in the mouse cerebellum. (c) Embryonic day (E) 15 mouse cerebellum stained in whole mount for alkaline phosphatase (hAP) to detect the expression of an *L7/Pcp2-hAP* transgene (see Sillitoe et al. 2009 for details). (d) Schematic illustrating the pattern of embryonic Purkinje cell clusters as revealed by hAP staining in *L7/Pcp2-hAP* transgenic mice. Abbreviations: AZ anterior zone, CZ central zone, PZ posterior zone, NZ nodular zone, *Sim* simplex, *Fl/Pfl* flocculus/paraflocculus, *Pmd* paramedian, *Cop* copula pyramidis. Lobule numbers are indicated by Roman numerals, and stripes are labeled with Arabic numerals (panels C and D were adapted from Sillitoe et al. 2009)

uniformly zebrin II⁺ central zone (CZ: ~lobules VI–VII), the striped posterior zone (PZ: ~lobules VIII–dorsal IX), and the uniformly zebrin II⁺ nodular zone (NZ: ~lobules IX ventral and X: Ozol et al. 1999). A similar alternation of zones is seen in the hemispheres (Sarna et al. 2006).

Numerous molecular markers are co-localized with either the zebrin II⁺ or zebrin II⁻ Purkinje cells. For example, the GABA-B receptor is expressed in the zebrin II⁺ population (Chung et al. 2008a) and phospholipase C(PLC) β 4 in the zebrin II⁻ population (Sarna et al. 2006). However, detailed comparisons between zebrin II expression and other antigenic markers reveal that the parasagittal stripes are much more elaborate than the expression of any one antigen indicates. For example, comparisons between zebrin II and the glycoprotein epitope HNK1 reveal that although these two antigens are largely co-localized (Eisenman and Hawkes 1993), discrete Purkinje cell populations in several lobules can express these antigens separately (Marzban et al. 2004). Similarly, expression of the 25 kDa small heat shock protein (HSP) 25 reveals parasagittal Purkinje cell heterogeneity in both the CZ and NZ – areas in which zebrin II is homogeneously expressed in all Purkinje cells (Armstrong et al. 2000). As a result, the adult cerebellar cortex of the mouse can

reliably and reproducibly be subdivided into several hundred distinct regions, each typically comprising no more than a few hundred Purkinje cells (e.g., reviewed in Hawkes 1997; Sarna and Hawkes 2003; Apps and Hawkes 2009). Stripe and zone compartments influence all aspects of cerebellar biology. They are highly reproducible between individuals, conserved through evolution (AZ – Sillitoe et al. 2005; PZ – Marzban and Hawkes 2011), and insensitive to experimental manipulation (reviewed in Larouche et al. 2006). Afferent topography is also striped. Zone and stripe boundaries restrict afferent terminal fields (e.g., climbing fibers, spinocerebellar mossy fibers, and trigeminocerebellar mossy fibers that relay somatosensory signals terminate mainly in zebrin II- stripes throughout the AZ and into rostral lobule VI, where the AZ interdigitates with the CZ, e.g., reviewed in Voogd and Ruigrok 2004) into compartments that are reflected by functional cerebellar maps (e.g., Chockkan and Hawkes 1994; Hallem et al. 1999; Ebner et al. 2012).

Many cerebellar mutant phenotypes are restricted by zone and stripe boundaries. For example, *swaying* (Thomas et al. 1991), *rostral cerebellar malformation/Unc5h3* (Napieralski and Eisenman 1996), *cerebellar deficient folia* (Cook et al. 1997; Beierbach et al. 2001; Park et al. 2002), and *meander tail* (Ross et al. 1990) all exhibit deficits restricted primarily to the AZ; the gain of function $\delta 2$ glutamate receptor mutant *lurcher* (*Lc/+*) has a zebrin II expression domain during development that is restricted at the CZ/PZ boundary (Tano et al. 1992); and the *weaver* mouse exhibits a Purkinje cell ectopia that is primarily restricted to the CZ (Eisenman et al. 1998; Armstrong and Hawkes 2001). Finally, most examples of Purkinje cell death due to mutation or insult show restriction to parasagittal stripes (reviewed in Sarna and Hawkes 2003; Duffin et al. 2010; Armstrong et al. 2011; Williams et al. 2007; Ragagnin et al. 2017).

How does this remarkable zone-and-stripe pattern develop?

From Allocation to Rhombomere 1 to Two Germinal Epithelia

In mice, the cerebellar primordium arises between E8.5 and E9.5 entirely from within the metencephalon (Wassef and Joyner 1997; Zervas et al. 2004). The boundary between *Otx2* and *Gbx2* expression domains initially demarcates the border between mes- and metencephalon and the location of the isthmus organizer, a tissue patterning structure that promotes interactions between cerebellar patterning genes (reviewed in Zervas et al. 2005). Several studies have examined putative allocation events during this period, which generate the Purkinje cell population: the general conclusion is that the entire Purkinje cell population in the adult arises from ~100 to 150 precursors, likely specified at around E7–E8 (Baader et al. 1996; Mathis et al. 1997; Hawkes et al. 1998; Watson et al. 2005), although there is no evidence that these are restricted to a particular Purkinje cell subset. The early stages of cerebellar development are reviewed in detail in ► [Chap. 6, “Specification of Granule Cells and Purkinje Cells.”](#) This chapter will only consider mechanisms pertinent to the origin of stripe patterning (for other reviews, see Hawkes and Gravel 1991; Hawkes and Eisenman 1997; Herrup and Kuemerle 1997; Oberdick et al.

1998; Armstrong and Hawkes 2000; Larouche and Hawkes 2006; Sillitoe and Joyner 2007; White and Sillitoe 2013).

The cerebellum houses two distinct germinal matrices: the dorsally located rhombic lip and the ventrally located ventricular zone (VZ) of the fourth ventricle. Genetic fate mapping studies show that the rhombic lip gives rise to glutamatergic projection neurons of the cerebellar nuclei, cerebellar granule cells, and unipolar brush cells (Wingate 2001; Machold and Fishell 2005; Wang et al. 2005; Englund et al. 2006). The VZ gives rise to GABAergic components of the cerebellum including all GABAergic interneurons and all Purkinje cells: all cerebellar GABAergic neurons derive from progenitors expressing *Ptf1a*, which is required for their specification (Hoshino et al. 2005; Pascual et al. 2007). However, the VZ is not homogenous but divided by gene expression into numerous overlapping molecular domains (e.g., Chizhikov et al. 2006; Zordan et al. 2008). This issue is discussed in ► [Chap. 15, “Genes and Cell Type Specification in Cerebellar Development.”](#)

Purkinje Cell Birth Date, Phenotype, and Location

Purkinje cells undergo terminal mitosis in the VZ between E10 and E13 in the mouse (Miale and Sidman 1961; Hashimoto and Mikoshiba 2002). Birthdating studies, using incorporation of either adenovirus (Hashimoto and Mikoshiba 2002), bromodeoxyuridine (e.g., Feirabend et al. 1985; Karam et al. 2000; Larouche and Hawkes 2006), or genetic fate mapping (Sudarov et al. 2011), reveal a direct correlation between the birthdate of a Purkinje cell and its final mediolateral location, suggesting that Purkinje cells acquire positional information at or shortly after their terminal differentiation in the VZ. It is not known whether positional information and phenotype are specified at the same time. Postmitotic Purkinje cells migrate dorsally out of the VZ, presumably along radial glia processes (Morales and Hatten 2006), and stack in the cerebellar anlage with the earliest-born Purkinje cells located most dorsally.

From Ventricular Zone to Clusters

After migration from the VZ, the Purkinje cells undergo a complex and poorly understood reorganization (E14–E18), possibly involving cell-signaling molecules including cadherin (Redies et al. 2010) and Eph-ephrin (Karam et al. 2000), to yield a stereotyped array of early clusters with a range of molecular phenotypes. The Purkinje cell migration pathways are carefully described in Miyata et al. (2010) (see also ► [Chap. 9, “Purkinje Cell Migration and Differentiation”](#)). During this same period, Purkinje cell clusters begin to express a variety of early markers that reveal both rostrocaudal and mediolateral compartments (e.g., calbindin, Wassef et al. 1985; cyclic GMP-dependent protein kinase, Wassef and Sotelo 1984; HSP25, Armstrong et al. 2001; neurogranin, Larouche et al. 2006; cadherins, reviewed in Redies et al. 2010; homeobox genes, including *En1*, *En2*, *Pax2*, and *Wnt17b*,

Bally-Cuif et al. 1992; Millen et al. 1995; *L7/pcp2-LacZ*, Smeyne et al. 1991; Oberdick et al. 1993; Ozol et al. 1999; *OMP-LacZ*, Nunzi et al. 1999; *inositol 1,4,5-trisphosphate (IP3) receptor (IP3R)nls-LacZ*, Furutama et al. 2010; etc.). Detailed comparisons of various other early markers are not comprehensive but such data as are available suggest that they all fit into a common schema.

Purkinje Cell Subtype Specification

When is Purkinje cell stripe phenotype specified? In order to answer this, many attempts have been made to alter Purkinje cell phenotype, which have almost always been ineffective. First, surgical interventions in the neonate have no effect on the expression of compartmentation markers (e.g., zebrin I, Leclerc et al. 1988; *L7/pcp2-LacZ*, Oberdick et al. 1993; HSP25, Armstrong et al. 2001). Secondly, in cerebellar explants taken as early as E13 and placed either in slice culture (Oberdick et al. 1993; Seil et al. 1995; Rivkin and Herrup 2003; Furutama et al. 2010) or transplanted (Wassef et al. 1990), Purkinje cell subtypes apparently develop normally. Finally, ectopic Purkinje cells in various mouse mutants develop their normal adult phenotypes (e.g., *reeler*, Edwards et al. 1994; *disabled*, Gallagher et al. 1998; *weaver*, Armstrong and Hawkes 2001). These data suggest that cell autonomous mechanisms early in cerebellar development direct the specification of Purkinje cell phenotypes toward distinct subtypes.

The only experimental manipulation that is known to alter Purkinje cell subtype is deletion of *Early B-cell Factor 2 (Ebf2)*, Croci et al. 2006; Chung et al. 2008b). In the adult cerebellum, *Ebf2* expression is restricted to the zebrin II- Purkinje cell subset. When *Ebf2* is deleted, a complex cerebellar phenotype results, but in particular a prominent subset of zebrin II- Purkinje cells express zebrin II+ markers in addition to the normal zebrin II- ones (Croci et al. 2006; Chung et al. 2008b). This suggests that EBF2 is a repressor of the zebrin II+ phenotype. The role of *Ebf2* is discussed in detail in ► [Chap. 2, “Proneural Genes and Cerebellar Neurogenesis in the Ventricular Zone and Upper Rhombic Lip.”](#)

From Embryonic Clusters to Adult Stripes

Starting at around E18, the embryonic clusters begin to disperse. This occurs at the same time as cerebellar lobules begin to exhibit extensive morphogenetic changes (Sudarov and Joyner 2007). The two processes are coupled – if Purkinje cell dispersal is blocked, then lobulation is prevented, and the cerebellum is lissiform – but the mechanistic relationship is unknown. In contrast to the relationship between cluster dispersal and lobules, a recent genetic study demonstrated that Purkinje cell stripe patterning and foliation can be uncoupled and *En1/2* controls each process independently (Sillitoe et al. 2008b). Whether cluster dispersal is the passive concomitant of granular layer maturation and lobule formation or requires active Purkinje cell migration is not known. Whatever the case, because cluster dispersal

occurs primarily in the rostrocaudal plane – the rostrocaudal length of the mouse vermis increases ~25-fold from E17 to P30, while the width of the vermis increases only ~1.5× during the same time period (Gallagher et al. 1998) – the clusters elongate into long parasagittal stripes. About 50 embryonic clusters are thought to produce the adult pattern of stripes (Fujita et al. 2012). The transformation of embryonic Purkinje cell clusters into mature stripes is mediated by Reelin signaling (Tissir and Goffinet 2003). The external granular layer (EGL) secretes Reelin starting around E17 (D’Arcangelo et al. 1997; Jensen et al. 2002). Reelin binds two receptors on Purkinje cells – the apolipoprotein E receptor 2 (Apoer2) and the very low-density lipoprotein receptor (VLDLR, Trommsdorff et al. 1999). Binding induces receptor clustering (Strasser et al. 2004) and activates an intracellular protein kinase cascade leading to tyrosine phosphorylation of the docking protein Disabled-1 (mdab-1, Howell et al. 1997; Goldowitz et al. 1997; Sheldon et al. 1997).

Downstream of Disabled-1 are interactions with Src and Fyn cytoplasmic tyrosine kinases and with phosphatidylinositol 3-kinase (Bock and Herz 2003; Kuo et al. 2005). The cyclin-dependent kinase (cdk)5 signaling pathway has also been implicated in Reelin signaling as Purkinje cells in cdk5 pathway mutants phenocopy the *reeler* mouse (e.g., Ohshima and Mikoshiba 2002). The end result is thought to be a drop in Purkinje cell-cell adhesion, thereby allowing the early clusters to disperse.

Accordingly, mutations in the Reelin pathway affect all Purkinje cells and result in the complete failure of cluster dispersal and global Purkinje cell ectopia. However, deletion of either of the Reelin receptors, Apoer2 and Vldlr, results in selective, specific Purkinje cell ectopias (Larouche et al. 2008): in *Apoer2*^{-/-} mice, ectopic Purkinje cells are largely restricted to the zebrin II- population of the anterior vermis; in contrast, *Vldlr*^{-/-} mice have a much larger population of ectopic Purkinje cells that includes members from both zebrin II+/- phenotypes, and HSP25 immunoreactivity reveals that a large portion of ectopic zebrin II+ cells is destined to become stripes in lobules VI–VII. Finally, a small, very specific population of ectopic zebrin II- Purkinje cells is observed in animals heterozygous for both receptors (*Apoer2*^{+/-}; *Vldlr*^{+/-}: no ectopia is present in mice heterozygous for either receptor alone). Despite the known importance of the Reelin pathway in regulating Purkinje cell dispersal, other genetic cues are also likely required. For example, the HSP25+/zebrin II+ Purkinje cell subset in the CZ is selectively ectopic in *weaver* mutants (Armstrong and Hawkes 2001).

This model suggests a direct genealogical relationship between embryonic clusters and adult stripes. This is not straightforward to establish because the parasagittal pattern of early antigens tends to disappear perinatally, either because they are downregulated (e.g., neurogranin, Larouche et al. 2006) or because they become expressed uniformly by all Purkinje cells (e.g., calbindin, Wassef et al. 1985), while most adult stripe antigens are not expressed in the mature pattern of stripes until ~P15 (e.g., zebrin II, Lannoo et al. 1991; HSP25, Armstrong et al. 2001). While the basic cerebellar architecture seems to be laid down in the embryo, the maturation of stripe phenotypes is not complete until P15 or so. For example, zebrin II is first expressed at around P6, but by P10–P12 all Purkinje cells express zebrin II. From P12 to P15 zebrin II is downregulated in the zebrin II- population to reveal the

mature stripe array (Brochu et al. 1990; Lannoo et al. 1991; Rivkin and Herrup 2003). The molecular mechanism that mediates zebrin II downregulation is not known. However, recent studies have identified markers that bridge between clusters to stripes (e.g., Larouche et al. 2006; Marzban et al. 2007; Sillitoe et al. 2009; White and Sillitoe, 2013). The current hypothesis is that embryonic clusters are the precursors of the adult stripes. While the hypothesis implies a direct relationship, experimental evidence indicates that it is not at all simple. On the one hand, current maps suggest about 20 different clusters but 10 times as many stripes in the adult. Where does the additional complexity come from? While the apparent lack of complexity could merely be a reflection of an underdeveloped toolkit, the internal consistency of the different cluster antigens does not support this view: all known embryonic markers conform to a common schema with ~10 clusters on each side of the cerebellum. Therefore, there may be secondary patterning stages, perhaps associated with the transformation of clusters into stripes, which takes the embryonic broad-stroke pattern and elaborates it into a more complex adult form. Perhaps the 20 clusters are partitioned into 50 during postnatal development before these go on to form the adult stripes (Fujita et al. 2012). On the other hand, there is evidence that some stripes in the adult result from the coalescence of multiple clusters (e.g., the P1-stripe in the AZ is the fusion of three distinct clusters in the embryo, Ji and Hawkes 1994; Marzban et al. 2007). Finally, genetic fate mapping using an *L7/pcp2-CreER* allele supports the hypothesis that at least some embryonic clusters contribute Purkinje cells to multiple stripes in the adult cerebellum (Sillitoe et al. 2009).

Afferent Topography

It is generally believed that the Purkinje cell map serves as a scaffold around which other cerebellar structures are organized – both afferent projections (climbing fibers and mossy fibers, reviewed in Sotelo 2004) and interneurons including granule cells, Golgi cells, and unipolar brush cells (e.g., Chung et al. 2009; reviewed in Apps and Hawkes 2009).

Climbing Fibers

In the adult, climbing fibers project from neurons in the contralateral inferior olivary complex and terminate on Purkinje cell dendrites, with each Purkinje cell receiving input from a single climbing fiber. Each subnucleus in the inferior olive projects to a limited number of Purkinje cell stripes (e.g., Voogd and Ruigrok 2004; Sugihara and Quy 2007; Apps and Hawkes 2009). The cerebellar projection neurons of the inferior olive are born in the caudal rhombic lip and migrate ventrally in the submarginal stream (Sotelo and Chédotal 2005). Similar to their target Purkinje cells, the fate, survival, differentiation, and migration of inferior olivary neurons are dependent on the function of *Ptf1a* (Yamada et al. 2007). Climbing fibers enter the cerebellar anlage at ~E15 and immediately terminate within specific Purkinje cell clusters (e.g., Chédotal and Sotelo

1992; Paradies et al. 1996). During Purkinje cell cluster dispersal into stripes, the climbing fibers are presumably carried along with them, thereby creating parasagittal terminal fields that align with the Purkinje cell stripes (Gravel et al. 1987; Apps and Hawkes 2009). In the neonatal cerebellum, each Purkinje cell receives input from several climbing fibers. This is converted to the adult mono-innervation pattern by the elimination of all but one (reviewed in Cesa and Strata 2009; Carrillo et al. 2013). However, it appears that the sculpting of climbing fiber innervation does not contribute significantly to the refinement of cerebellar stripe topography (Crépel 1982; Sotelo et al. 1984).

Sotelo and colleagues have argued that matching gene expression domains between the cerebellum and inferior olive contain cues that guide the formation of a precise topographical projection map (Wassef et al. 1992; Chédotal et al. 1997; Sotelo and Chédotal 2005). In support of this model, Nishida et al. (2002) demonstrated that overexpression of Ephrin-A2 by using retroviral vectors disrupts the general topography of the olivocerebellar projection. Moreover, inferior olivary axons expressing high Eph receptor activity are prevented from entering into domains with ectopic Ephrin-A2 ligand expression (Nishida et al. 2002). Although the parasagittal band topography of climbing fibers was never examined, these experiments identify the Eph/Ephrin signaling pathway as likely to provide positional information during afferent/target matching.

Mossy Fibers

The other major afferents of the cerebellum are mossy fibers, which arise from multiple sources and terminate in synaptic glomeruli on the dendrites of granule cells. Mossy fibers are also restricted by transverse zone and parasagittal stripe boundaries (e.g., Gravel and Hawkes 1990; Ji and Hawkes 1994; Armstrong et al. 2009; Sillitoe et al. 2010; Ruigrok 2011; Gebre et al. 2012). In some cases, mossy fiber terminal fields align with specific subsets of stripes (e.g., Armstrong et al. 2009), and in others they split Purkinje cell stripes into smaller units (e.g., cuneocerebellar/spinocerebellar terminal fields in the P1- stripes of the AZ, Ji and Hawkes 1994). The major features of the development of mossy fiber topography are similar to that for climbing fibers. The earliest mossy fibers enter the cerebellar anlage by around E12 (rat, Ashwell and Zhang 1992, 1998). Mossy fiber topography is established before most granule cells are formed (Arsenio-Nunes and Sotelo 1985) and is accompanied by direct contacts between mossy fiber growth cones and Purkinje cells in embryonic and early postnatal clusters (Mason and Gregory 1984; Takeda and Maekawa 1989; Grishkat and Eisenman 1995; Kalinovsky et al. 2011; Sillitoe 2016). This model is consistent with observations from mutant animals with agranular cerebella, in which the spinocerebellar mossy fiber topography is organized into bands despite the absence of a normal mossy fiber-granule cell-Purkinje cell pathway (e.g., Arsenio-Nunes and Sotelo 1985; Arsenio-Nunes et al. 1988; Eisenman and Arlinghaus 1991), and with the data from neonatal lesion studies demonstrating that there does not seem to be a significant role for

competition between mossy fiber sources in sculpting terminal fields (Ji and Hawkes 1995). The molecular basis of mossy fiber terminal field restriction is not well understood, but deletion of either the retinoic acid receptor-related orphan receptor alpha (RORalpha: Arsenio-Nunes et al. 1988) or *En1/2* (Sillitoe et al. 2010) or overexpression of *En2* in Purkinje cells (Baader et al. 1999) results in mossy fiber targeting defects.

As for climbing fibers, mossy fiber terminals are presumed to disperse along with the Purkinje cells as embryonic clusters transform into stripes. Then postnatally, as granule cells are born in the external granular layer and descend past the Purkinje cells to the granular layer, the mossy fiber terminals displace from the Purkinje cells and synapse with differentiated granule cells. As a result, the mossy fiber terminal fields become aligned with the overlying Purkinje cell stripes. Although there is evidence that the process of establishing afferent compartmentation is genetically controlled (Sillitoe et al. 2010), the refinement of the map may be in part dependent on neuronal activity (Tolbert et al. 1994; White et al. 2014).

Interneurons

Several cerebellar inhibitory interneurons show evidence of restriction by the Purkinje cell scaffold. First, Golgi cell dendrites are restricted by Purkinje cell stripe boundaries (Sillitoe et al. 2008a). Second, subsets of unipolar brush cells are associated with particular adult stripes (Chung et al. 2009; Lee et al. 2015). Models have been proposed by which both patterns of restriction involve mechanisms similar to those that organize mossy fiber afferent growth cones. Both Golgi cells and unipolar brush cells are thought to intermingle with Purkinje cells at the embryonic cluster stage. Hence, as the Purkinje cell clusters disperse, the interneurons become restricted to a particular stripe. Next, and as the granule cells form, the Golgi cells displace from the Purkinje cells to the neighboring granule cell axons, and the unipolar brush cells displace to the underlying granular layer, where mossy fibers contact them and they in turn synapse with granule cells and other unipolar brush cells (Mugnaini et al. 2010).

Granule cells are born in the external granular layer (EGL), a germinal epithelium that forms from the rhombic lip and spreads to cover the cerebellar surface. Post-mitotic granule cells migrate into the cerebellar anlage, following Bergmann glial guides, for 20–30 days, to create the adult granular layer (reviewed in Sillitoe and Joyner 2007).

The EGL of the developing cerebellum and the granular layer of the adult cerebellum are subdivided by transverse boundaries revealed by lineage tracing, gene expression patterns, or through the consequences of genetic mutations. Several patterns of granular layer and/or EGL gene expression reveal transverse expression boundaries (e.g., reviewed in Hawkes et al. 1999), one aligned with the AZ/CZ boundary (~lobule V–VI) and another at the PZ/NZ boundary (in lobule IX: reviewed in Ozol and Hawkes 1997). In addition, mRNA analysis reveals a complex map of *Fgf* receptor and ligand expression in the EGL and granular layer (Yaguchi

et al. 2009). These zonal relationships may reflect either epigenetic interactions with Purkinje cells or distinct cell autonomous effects. It is likely that both occur. From the spatial distribution of genotypes in embryonic stem cell chimeras, it was concluded that the cerebellar granular layer derives from two distinct precursor pools on either side of a lineage boundary within the rhombic lip (Hawkes et al. 1999). This is consistent with previous chimera studies, which also suggested that granule cells across the AZ/CZ and PZ/NZ boundaries have separate developmental origins (e.g., Goldowitz 1989). Additional evidence for a multiple origin of the EGL comes from studies of *scrambler* (Goldowitz et al. 1997) and *disabled* (Gallagher et al. 1998) mutants in which there is an incomplete fusion of the anterior and posterior granular layers in lobule VI leaving distinct, overlapping anterior and posterior leaflets. Finally, by using a *Math1^{CreER}* allele, Machold and Fishell (2005) demonstrated by genetic fate mapping that granule cell progenitors are destined to populate specific anterior–posterior zones. For example, lineages marked at E12.5 selectively populate the AZ, whereas those marked at E15.5 populate all but the NZ. Together, these data suggest that the allocation of cells to specific EGL compartments may be dependent on spatial and temporal regulation of cellular movements and gene expression.

It is difficult to imagine that the striped expression patterns in the granular layer are generated by the differential migration of EGL lineages. For example, neuronal nitric oxide synthase (nNOS – or its surrogate nicotinamide adenine dinucleotide phosphate (NADPH)-diaphorase) is expressed in the adult granular layer in stripes that align with Purkinje cell stripes (Hawkes and Turner 1994). NADPHd/nNOS activity is first detected at P3. During the first postnatal week of development, the granular layer expresses nNOS uniformly (Schilling et al. 1994). Subsequently, clusters of granule cells begin to suppress their expression of nNOS, and from this, a new heterogeneous pattern of nNOS expression emerges that persists into adulthood (Yan et al. 1993; Schilling et al. 1994; Hawkes and Turner 1994). In such cases, it seems more plausible that differential gene expression is induced by the local Purkinje cell environment or by the input from mossy fiber stripes (Schilling et al. 1994). However, the migration of differentiated granule cells within parasagittal “raphes” could provide a physical mechanism that supports the segregation of granule cells into different topographic domains as they proceed toward the internal granular layer (Lin and Cepko 1998; Karam et al. 2001).

Cerebellar Topography and Circuit Function

It is evident that Purkinje cells are central to cerebellar topography. Purkinje cells contact or communicate with climbing fibers, mossy fibers, and granule cells throughout development to organize the cerebellar cortex into distinct domains. Given the structural role Purkinje cells have, it is not surprising that they are also vital for cerebellar function. Purkinje cells serve as the sole output of the cerebellar cortex and project directly to cerebellar nuclei neurons to control the rate and pattern of cerebellar output (Chaumont et al. 2013; Witter et al. 2013; White et al. 2014).

This cortico-nuclear projection is also compartmentalized (Hawkes and Leclerc 1986; Sugihara et al. 2009) raising the possibility that cerebellar function depends on an interplay between extrinsic and intrinsic Purkinje cell factors.

From Zones-And-Stripes to Complex Motor Behaviors

At first glance, the cerebellar circuit is organized rather simplistically: structurally identical circuits comprised of Purkinje cells, cerebellar nuclei neurons, afferent inputs, and interneurons are reiterated throughout its entirety. However, the presence of evolutionarily conserved zones-and-stripes raises the possibility that patterning is important for functional compartmentalization, information processing, and the execution of behaviors (Attwell et al. 1999; Horn et al. 2010; Mostofi et al. 2010; Graham and Wylie 2012). This hypothesis is especially intriguing since stripe and zone representations can vary with ecological niche (Corfield et al. 2016), which is perhaps a reflection of species-related functional specializations (tenrec, Sillitoe et al. 2003; star-nosed mole, Marzban et al. 2015). Moreover, severe motor deficits develop in disease models where zone formation is delayed or stripe boundaries are left unrefined (Sarna and Hawkes 2003; Strømme et al. 2011; White et al. 2014, 2016).

One reason for why stripes may drive cerebellar function is because Purkinje cells in different stripes have intrinsically different molecular profiles and synaptic properties, which in turn influence learning and behavior (Furuta et al. 1997; Nagao et al. 1997; Dehnes et al. 1998; Mateos et al. 2001; Wadiche and Jahr 2005; Kano et al. 2008; Paukert et al. 2010; Wang et al. 2011). For example, zebrin II⁺ Purkinje cells are enriched for mGluR1 at parallel fiber synapses and neuronal glutamate transporter (EAAT4) in their cell bodies, dendrites, and spines. Due to increased expression of mGluR1, upon parallel fiber and climbing fiber stimulation, “long latency patches,” or regions of increased Ca²⁺ release, form at zebrin II⁺ parallel fiber–Purkinje cell and zebrin II⁺ climbing fiber–Purkinje cell synapses. These molecular differences are thought to support the compartmental regulation of synaptic plasticity (Wadiche and Jahr 2005; Paukert et al. 2010; Wang et al. 2011). It is interesting that several proteins that are expressed in stripes are required for the expression of long-term depression at parallel fiber – Purkinje cells synapses (Hawkes 2014).

Despite these advances in understanding the heterogeneous expression of plasticity, it is only recently that we have begun to appreciate how cellular function might support these differences. Single unit extracellular recordings were used to show that zebrin II⁺ Purkinje cell cells fire at a relatively low rate and with a regular firing pattern and that zebrin II⁻ Purkinje cells fire at a much higher rate with a more irregular pattern (mouse, Zhou et al. 2014; rat, Xiao et al. 2014). Although the mechanism by which zebrin II⁺ Purkinje cells maintain lower baseline firing frequencies or more regular spike trains is unknown, an enrichment in VGLUT2 is thought to manifest in longer complex spikes, higher phase amplitudes, and more

spikelets per complex spike (Paukert et al. 2010; Xiao et al. 2014; Tang et al. 2017). This is because increased VGLUT2 expression has been shown to correlate with a larger ready-release vesicle pool, enhanced multivesicular release, and larger glutamate transients (Paukert et al. 2010). In contrast, zebrin II- Purkinje cells express more active transient receptor cation channels (TRPC3) downstream of mGluR1 than do zebrin II+ Purkinje cells (Hartmann et al. 2008; Zhou et al. 2014; Tang et al. 2017). Blocking TRPC3 results in decreased simple spike frequencies only in zebrin II- Purkinje cells, which supports its role in influencing basal activity (Zhou et al. 2014).

Perhaps the biggest unknown is how stripes contribute to motor behavior (Horn et al. 2010; Cerminara and Apps 2011). Among the questions are whether each stripe controls a specific behavior, or if not, how do stripes communicate and cooperate during a particular task? Synchronous activity might play a critical role in either scenario. Synchrony within zones is dependent on olivocerebellar connectivity (Welsh et al. 2002; Schultz et al. 2009). The presence of parallel fibers that disregard stripe boundaries and Purkinje cell collaterals that link neighboring cells and stripes are two possible anatomical substrates for how Purkinje cell activity might synchronize across zones-and-stripes (Tsutsumi et al. 2015; Witter et al. 2016). Parallel fibers span multiple zones and likely connect distant, molecularly heterogeneous Purkinje cells (Valera et al. 2016; Levy et al. 2017). Purkinje cell collaterals, on the other hand, directly connect Purkinje cells to other Purkinje cells, granule cells, interneurons, and Lugaro cells in select lobules. Such local connectivity could provide additional means to regulate cerebellar circuit activity and enhance processing capabilities (Watt et al. 2009; Witter et al. 2016; Guo et al. 2016). Whatever the mechanism, synchronizing Purkinje cells within and across stripes might dynamically control the cerebellar nuclei during motor behavior (Welsh et al. 1995; Gauck and Jaeger 2000; Yamamoto et al. 2001; De Zeeuw et al. 2011; Person and Raman 2012).

Conclusions

Every facet of cerebellar structure and function is built around the zone-and-stripe architecture. While the pattern formation process is complex, so is the operation of circuits that are located in the functional maps that ultimately form. Despite these challenges, a simple theme emerges – Purkinje cells are both the scaffold around which other structures organize and the control center from which different outputs are produced; disrupting them can lead to widespread abnormalities in cerebellar topography, function, and behavior.

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