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## Axon growth and synaptic function: a balancing act for axonal regeneration and neuronal circuit formation in CNS trauma and disease

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### Abstract

Axons in the adult mammalian central nervous system (CNS) fail to regenerate inside out due to intrinsic and extrinsic neuronal determinants. During CNS development, axon growth, synapse formation and function are tightly regulated processes allowing immature neurons to effectively grow an axon, navigate towards target areas, form synaptic contacts and become part of information processing networks that control behavior in adulthood. Not only immature neurons are able to precisely control the expression of a plethora of genes necessary for axon extension and pathfinding, synapse formation and function, but also non-neuronal cells such as astrocytes and microglia actively participate in sculpting the nervous system through refinement, consolidation and elimination of synaptic contacts. Recent evidence indicates that a balancing act between axon regeneration and synaptic function may be crucial for rebuilding functional neuronal circuits after CNS trauma and disease in adulthood. Here we review the role of classical and new intrinsic and extrinsic neuronal determinants in the context of CNS development, injury and disease. Moreover, we discuss strategies targeting neuronal and non-neuronal cell behaviors, either alone or in combination, to promote axon regeneration and neuronal circuit formation in adulthood.

### Keywords

Axon growth and regeneration; branching and synapse formation; astrocyte; microglia

### INTRODUCTION

Axon regeneration failure following central nervous system (CNS) trauma and disease often leads to permanent functional disability. Promoting axon sprouting and regeneration of spared and injured axons as well as refinement of existing or de novo formation of neuronal circuits can attain neurological recovery (Hutson & Di Giovanni, 2019; Maier & Schwab,

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#### CONFLICT OF INTEREST

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2006). The development of neuronal circuits in the mammalian central nervous system (CNS) is a dynamic process that requires coordinated epigenetic regulation of gene expression (Henikoff, 2008; Jaenisch & Bird, 2003). Genome-wide remodeling of the epigenetic landscape allows axon elongation, membrane expansion and navigation towards target areas as well as axon branching, synapse formation and refinement to be spatially and temporally ordered (Kolodkin & Tessier-Lavigne, 2011; J. Li et al., 2020; Mahar & Cavalli, 2018; Palmisano et al., 2019; Venkatesh, Mehra, Wang, Califf, & Blackmore, 2018; Williams, de Wit, & Ghosh, 2010). Non-neuronal cells including astrocytes and microglia also actively participate in CNS development and function (Allen & Lyons, 2018; Barres, 2008; Nayak, Roth, & McGavern, 2014; Salter & Beggs, 2014). From worms to mammals, the ability to regenerate injured axons and rebuild functional neuronal circuits sharply declines with age (Byrne et al., 2014; Geoffroy, Hilton, Tetzlaff, & Zheng, 2016; Verdu, Ceballos, Vilches, & Navarro, 2000). Axon regeneration failure has been attributed to the presence of both neuronal intrinsic and extrinsic determinants (Fawcett & Verhaagen, 2018; He & Jin, 2016; Schwab & Strittmatter, 2014). Recent progress has furthered our understanding of the intrinsic molecular brakes to axon growth and regeneration (Barber et al., 2019; Bray et al., 2019; Chauhan et al., 2020; Koseki et al., 2017; Y. Liu et al., 2017; Sekine et al., 2018; Song et al., 2019; Tedeschi et al., 2016; Tedeschi & Popovich, 2019; C. Yang et al., 2020; Zhang et al., 2019). It is now possible to reprogram adult mammalian neurons into a growth-competent state by recapitulating, at least in part, developmental programs (Blackmore et al., 2012; Hilton & Bradke, 2017; K. Liu et al., 2010; Moore et al., 2009; O'Donovan et al., 2014). However, recapitulation of early developmental programs may proceed at the expense of synaptic specificity, synapse formation and functional connectivity (Carlin et al., 2018; Carlin, Halevi, Ewan, Moore, & Cavalli, 2019; Tedeschi & Bradke, 2017; Z. Wang, Reynolds, Kirry, Nienhaus, & Blackmore, 2015), negatively impacting formation and consolidation of neuronal circuits. Thus, intrinsic neuronal roadblocks must be overcome with temporal precision to maximize CNS repair strategies after trauma and disease. Here we discuss recent evidence that suggests that axon regeneration, synapse formation and function may be at odds with one another.

## 1. Neuronal intrinsic mechanisms of axon growth and synaptic targeting

The establishment of intricate connectivity patterns where functional modules are interlinked by hub regions enables complex nervous system function. How is such a complex wiring scheme achieved in the nervous system? During early stages of development, electrically silent immature neurons rapidly extend axons towards target areas (Figure 1). This initial phase of axon growth is characterized by axon elongation with no branching and the presence of a growth cone situated on the tip of the growing axon (Gribnau, de Kort, Dederen, & Nieuwenhuys, 1986; Mason & Gregory, 1984). On the one hand, the production of building blocks including newly synthesized lipids for membrane expansion that are anterogradely transported to the distal portion of the axon via vesicles, cholesterol- and sphingolipid-rich rafts enables rapid extension of growing axons (Maday, Twelvetrees, Moughamian, & Holzbaaur, 2014; Quiroga, Bisbal, & Caceres, 2018; Vance, Campenot, & Vance, 2000). On the other, cytoskeletal mechanisms, receptor arrays, cell adhesive molecules and transsynaptic signals allow growth cones to navigate with accuracy to appropriate target regions (Dickson, 2002; Giger, Hollis, & Tuszynski, 2010; Mosca, Hong,

Dani, Favaloro, & Luo, 2012; Roig-Puiggros et al., 2020; Xie et al., 2019; Zipursky & Sanes, 2010).

**1.1 Lipid metabolism and membrane resealing**—Large amount of lipids are also required during axon regeneration (Chauhan et al., 2020; de Chaves, Rusinol, Vance, Campenot, & Vance, 1997; Vance et al., 2000). Secretion and accumulation of apolipoprotein E (ApoE), a plasma protein acting as a ligand for low-density lipoprotein (LDL) receptors (Mahley, 1988), increases during regeneration of peripheral axons (Comley et al., 2011; Jimenez et al., 2005; F. Q. Li, Fowler, Neil, Colton, & Vitek, 2010; Rozenbaum et al., 2018). The tip of these regenerating axons contains high concentration of LDL receptors (Boyles et al., 1989), providing evidence for the presence of a cellular mechanism allowing cholesterol supply for membrane biogenesis during axon regeneration. By combining an axonal transection model with *ex vivo* postnatal day (P)1 cortical explants, another study has found that cerebral cortices from ApoE null mice show reduced axonal growth and regeneration when compared to the control condition (Yin, Guo, He, Wang, & Sun, 2019). Exogenous application of ApoE is sufficient to rescue regeneration defects in ApoE null cortices (Yin et al., 2019). Of particular interest, a recent study has shown that fatty acid synthesis in satellite glial cells actively participates in axon elongation during peripheral nerve regeneration presumably by paracrine lipid transfer to dorsal root ganglia (DRG) neurons (Avraham et al., 2019). Adult neuronal membranes are composed by a variety of lipids, but the lipids that may be necessary for membrane insertion during axon elongation and regeneration are not known. A recent study has reported that neuronal depletion of the phosphatidic acid phosphatase enzyme lipin 1 promotes axon regeneration after optic nerve injury in mice by regulating glycerolipid metabolism and, more specifically, triglyceride hydrolysis and phospholipid synthesis (C. Yang et al., 2020). Of note, lipin 1 catalyzes the conversion of phosphatidic acid to diglycerides (Carman & Han, 2019). Triglyceride hydrolysis is also required during regeneration of peripheral nerves (C. Yang et al., 2020), further suggesting triglycerides may provide lipid precursors for phospholipid synthesis necessary for membrane biosynthesis during nerve regeneration. Understanding the impact of specific classes of lipids and their metabolism on early versus late stages of neuronal maturation as well as axon regeneration versus functional connectivity will be an important topic for future investigation.

Mechanical damage to plasma membranes occurs following CNS trauma and disease. Therefore, promoting membrane resealing represents a crucial step in re-equilibrating the concentration of ions and small molecules in neurons and along axons for growth cone formation and axon regeneration to occur (Bradke, Fawcett, & Spira, 2012). A large screening for genes with growth-promoting or –inhibiting functions in *Caenorhabditis elegans* has identified annexins, calcium sensitive phospholipid-binding proteins (Draeger, Monastyrskaya, & Babychuk, 2011), as plasma membrane repair factors for axon regeneration. Indeed, axon regeneration is reduced in annexin *nex-1* mutants compared to wild-type worms (Nix et al., 2014). Although a growth cone may form after axotomy in *nex-1* mutants, it collapses or fails to extend (Nix et al., 2014), suggesting damaged membranes that fail to reseal may interfere with growth cone formation and dynamics.

**1.2 Actin dynamics and axon branching**—Growth cone motility and protrusion rely on actin dynamics. Specifically, the assembly of actin filaments at the leading edge of the growth cone and disassembly at its central domain, as well as actin treadmilling and retrograde flow enable growth cone exploration, integration of directional cues and protrusion (Lowery & Van Vactor, 2009; Van Goor, Hyland, Schaefer, & Forscher, 2012). Actin depolymerizing factor (ADF)/cofilin (AC) controls actin turnover through its actin-severing activity (Bamburg & Wiggan, 2002; Pollard, Blanchoin, & Mullins, 2000). Overexpression of the transcription factor serum response factor promotes axon regeneration through cytoplasmic localization and cofilin-mediated reactivation of actin dynamics in stalled retraction bulbs (Stern et al., 2013). By genetic loss- and gain-of-function, we have recently demonstrated that elevated actin turnover fuels regeneration of sensory axons after spinal cord injury (SCI) in adult mice (Tedeschi et al., 2019). Strategies engineering neuronal growth cones by pharmacological inhibition or genetic silencing of nonmuscle myosin II have proven similarly effective in promoting axon regeneration over growth-inhibitory substrates including chondroitin sulfate proteoglycans and myelin-associated inhibitors (Hur et al., 2011). Calcium influences growth cone motility through remodeling of the actin cytoskeleton (Henley & Poo, 2004; Kater, Mattson, Cohan, & Connor, 1988; Rehder & Kater, 1992; Welnhof, Zhao, & Cohan, 1999). Extracellular guidance cues including proteoglycans, cell adhesion molecules and myelin-associated proteins use calcium to transduce cell surface signals that affect growth cone exploratory behavior (Bandtlow, Schmidt, Hassinger, Schwab, & Kater, 1993; Nicol, Hong, & Spitzer, 2011; Snow, Atkinson, Hassinger, Letourneau, & Kater, 1994). Interestingly, the frequency of intracellular calcium transients at the growth cone has been shown to inversely correlate with the rate of axon outgrowth in the embryonic *Xenopus* spinal cord (Gomez & Spitzer, 1999). In particular, high frequencies of calcium transients associate with growth-cone stalling and axon retraction, also known as hallmarks of axon regeneration failure (Gomez & Spitzer, 1999). Whereas mimicking transients with photorelease of calcium slows rapid axonal extension, suppression of calcium transients effectively accelerates axon extension (Gomez & Spitzer, 1999). Mechanistically, calcium transients inhibit axon extension via the calcium-dependent phosphatase calcineurin acting on the growth cone actin cytoskeleton in *Xenopus* spinal neurons (Lautermilch & Spitzer, 2000).

As axons approach target areas in late development, axon elongation halts and extensive axon branching and formation of collaterals take place (Gallo, 2011; Gibson & Ma, 2011) (Figure 1), thereby maximizing terminal surface area for synaptic transmission and synapse formation. At this time, electrically silent neurons switch to a transmitting phase. In rats, the outgrowth of the pioneer axon of the corticospinal tract (CST) is completed by postnatal day (P)9 and later developing CST axon branches and collaterals are continuously added beyond P9 (Gribnau et al., 1986). During axon branching, plasmalemma expansion is thought to primarily occur via exocytosis (Futerman & Banker, 1996; Pfenninger, 2009; Pfenninger & Friedman, 1993). Not only does exocytosis promote secretion of signaling molecules and enzymes, but also the insertion of lipids and membrane proteins into the plasma membrane. Membrane fusion is a universal process in eukaryotic cells. The soluble N-ethylmaleimide-sensitive factor attachment protein receptor (SNARE) and Sec1/Munc18-like (SM) proteins mediate membrane fusion of vesicles in a constitutive manner for cargos delivery or for

neurotransmitter release upon calcium influx (Sudhof & Rothman, 2009). At synapses, synaptotagmin as well as Munc13 and RIM proteins localize at the active zone to control the membrane fusion machinery (Sudhof & Rizo, 2011). The SNARE proteins were first identified as targets of neurotoxins (e.g., clostridial botulinum and tetanus toxins), proteases that selectively block presynaptic membrane fusion (Link et al., 1992; Schiavo et al., 1992). The SNARE complex is constituted by three or four SNARE proteins including syntaxin, VAMP (synaptobrevin) and SNAP-25 homologs (Poirier et al., 1998; Sollner, Bennett, Whiteheart, Scheller, & Rothman, 1993; Sollner, Whiteheart, et al., 1993; Sutton, Fasshauer, Jahn, & Brunger, 1998). In humans, 35 SNARE proteins have been identified (Bock, Matern, Peden, & Scheller, 2001). SNARE proteins localize to vesicle (also called v-SNARE) and target (also called t-SNARE) membranes. To avoid inappropriate fusion events, SNARE proteins are maintained in inactive conformations. Only upon proper stimulation are SNARE proteins released to bind to each other. Axon branching requires constitutive SNARE-mediated exocytosis (Winkle et al., 2014). By taking advantage of computer vision software for automated detection of VAMP-mediated exocytosis, Urbina et al. has described spatiotemporal changes in exocytosis and membrane expansion in developing neurons (Urbina, Gomez, & Gupton, 2018). Interestingly, VAMP2-mediated vesicle fusion occurs near the site of a growing branch process (Urbina et al., 2018), thereby supplying excess material for plasma membrane expansion during morphogenesis.

Actin dynamic is critical for axon branching. In filopodia and lamellipodia, the balance between actin polymerization and depolymerization determines the rate of membrane protrusion and withdrawal for branching control (Kalil & Dent, 2014). In order to stabilize axon branches, dynamic microtubules enter into filopodia (Dent, Callaway, Szebenyi, Baas, & Kalil, 1999; Kornack & Giger, 2005). Actin associated proteins including enabled/vasodilator-stimulated phosphoprotein (ENA/VASP), diaphanous related formin 3 (DIAPH3) and actin-related proteins-2/3 (ARP2/3) regulate formation of actin arrays and branches (Campellone & Welch, 2010). The ENA/VASP family of proteins enhances actin filament elongation by counteracting the capping proteins that inhibit F-actin elongation (M. Krause, Dent, Bear, Loureiro, & Gertler, 2003). Depletion of ENA/VASP proteins by sequestering them to the mitochondria surface results in a reduction of filopodia formation and branching in frog retinotectal axons (Dwivedy, Gertler, Miller, Holt, & Lebrand, 2007). Moreover, all cortical tracts including major forebrain commissures and the internal capsule in the brain of ENA/VASP null mice are lost (Kwiatkowski et al., 2007). *In vitro*, the vast majority of cortical neurons from null mice lack filopodia and fail to extend an axon (Kwiatkowski et al., 2007). Filopodia formation can be restored in these neurons by ectopic expression of the formin DIAPH3 (Dent et al., 2007). ARP2/3 is required for the formation of lamellipodia and branched actin networks (Korobova & Svitkina, 2008; Q. Yang, Zhang, Pollard, & Forscher, 2012). Whereas Arp2/3 blockade using N-WASP CA or Wave-1 VCA peptides in cultured primary neurons significantly enhances axon elongation, it causes defects in growth cone guidance (Strasser, Rahim, VanderWaal, Gertler, & Lanier, 2004). Arp2/3 inhibition using small molecules causes a reduction in barbed end actin assembly at the leading edge, actin veils disruption and retraction (Q. Yang et al., 2012). Depletion of Arp2/3 complex in primary neurons by RNA interfering leads to formation of multiple neurites, aberrant pattern of neurite extension and excessive formation of focal adhesions

(Korobova & Svitkina, 2008). Terminal branching and neuronal wiring is also controlled by activity dependent mechanisms. In mice, expression of the inwardly rectifying potassium channel Kir2.1 in callosal projection neurons reduces firing rate of cortical neurons and suppresses their branching pattern (Mizuno, Hirano, & Tagawa, 2007). Whereas suppression of spontaneous neuron firing or synaptic activity decreased axon branching, increased spontaneous neuronal activity parallels branch formation of thalamocortical projections in organotypic cocultures of the thalamus and cortex (Uesaka, Hayano, Yamada, & Yamamoto, 2007). *In vivo* time-lapse imaging of *Xenopus* retinal axons shows how visual experience directly controls axon branch dynamics for the development of topographic maps (Ruthazer, Akerman, & Cline, 2003).

Looking at the variety of studies focused on axon elongation and branching during development, after CNS trauma and as a result of disease, it is clear that these complex mechanisms of axon growth and regeneration need to be controlled with precision to allow selection of appropriate pathways and specific targets for neurons to integrate and process information from different regions of the nervous system.

**1.3  $\alpha 2\delta$  subunits, synaptic transmission and function**—The transition from a dynamic growth cone to a presynaptic terminal specialized for neurotransmitter release may represent one of the first key steps in the gradual loss of axon growth and regeneration ability (Tedeschi & Bradke, 2017) (Figure 1). In search for putative gene switches controlling this transition, we have sequenced the whole transcriptome of mouse DRG neurons in both growth competent and incompetent states at different developmental stages, in diverse culture and *in vivo* experimental conditions. In these neurons, the developmental transition from a growth competent to a transmitting phase is associated with a marked increase in the expression of genes that control axon branching, synaptic transmission and synapse formation (Sudhof, 2018; Tedeschi et al., 2016). Similarly, a cell-surface proteomic profiling in the fly brain has discovered a global downregulation of neural development molecules and upregulation of synaptic transmission molecules in the transition from developing to mature olfactory projection neurons (J. Li et al., 2020). Our search has found *Cacna2d2*, the gene encoding the  $\alpha 2\delta 2$  subunit of voltage-gated calcium channels (VGCC) (Dolphin, 2018), which acts as a neuron intrinsic switch limiting axon growth during development and axon regeneration in adulthood (Sun et al., 2020; Tedeschi et al., 2016).  $\alpha 2\delta$  subunits positively regulate synaptic transmission by increasing plasma membrane expression of VGCC and vesicle release probability (Hoppa, Lana, Margas, Dolphin, & Ryan, 2012). However, these subunits may also play a pathological role during development and following injury. Presynaptic overexpression of  $\alpha 2\delta 2$  leads to aberrant wiring of glutamatergic presynaptic boutons with GABAergic postsynaptic positions (Geisler et al., 2019), contributing to an excitatory-inhibitory imbalance that is often associated with neuropsychiatric disorders. Expression of  $\alpha 2\delta 1$  increases following axonal injury, resulting in aberrant neuron activities associated with chronic pain and posttraumatic epilepsy (C. Y. Li et al., 2006; H. Li et al., 2012). Overexpression of *Cacna2d1*, the gene encoding  $\alpha 2\delta 1$ , potentiates presynaptic and postsynaptic N-methyl-D-aspartate receptor activity of spinal dorsal horn neurons to trigger pain hypersensitivity in mice (Chen et al., 2018). In rodent hippocampal neuron cultures, *Cacna2d1* overexpression enhances spontaneous neuronal

network activity (Bikbaev et al., 2020). Hence, increased pathological expression of  $\alpha 2\delta$  subunits may hijack the self-repair mechanisms of the CNS by forcing aberrant plasticity after trauma and disease. In adult DRG neurons, *Cacna2d2* forced expression leads to the formation of short and highly branched neurites *in vitro*. In contrast, genetic deletion or silencing of *Cacna2d2* promotes the formation of long and sparsely branched neurites (Tedeschi et al., 2016). Mechanistically, *Cacna2d2* forced expression in adult DRG neurons leads to an increase expression of Cav2.1 (Tedeschi et al., 2016), which is responsible for initiation of synaptic transmission (Catterall, 2011). By providing an entry point for calcium to trigger vesicle fusion, presynaptic VGCC clustered at the active zone play a crucial role in neurotransmitter exocytosis (Dolphin & Lee, 2020; Sudhof, 2013). Interestingly, recent studies have demonstrated that i) alternative splicing of Cav2.1 channels controls synapse-specific release probability (Heck et al., 2019) and ii) ultrastructural analysis of Cav2.1 and Munc13-1 shows strong synapses are comprised of synaptic vesicles that are tightly coupled (10 nm) to VGCC clusters (Rebola et al., 2019). Deletion of  $\alpha 2\delta 3$  in cultured spinal ganglion neurons leads to a reduction of P/Q-type current by 60% (Stephani et al., 2019). Axon growth defects in *Cacna2d2* overexpressing DRG neurons can be rescued by incubation with N- and P/Q-type channel blockers and by chelating calcium (Tedeschi et al., 2016). Interestingly, treating control neurons with the calcium-independent secretagogue Ruthenium Red and P/Q-type channel agonists can mimic similar defects in axon elongation (Tedeschi et al., 2016). This suggests that *Cacna2d2* inhibits axon elongation in adult neurons by forcing synaptic transmission and branching. Munc18/nSec1 interacts with monomeric syntaxin 1, preventing its interaction with SNAP-25 and VAMP (Pevsner et al., 1994). Calcium-dependent vesicle exocytosis is markedly reduced in mouse chromaffin cells lacking Munc18-1, (Voets et al., 2001). In the absence of UNC-18, the size of the readily releasable pool is severely reduced in *Caenorhabditis elegans* (Weimer et al., 2003). Given that SM proteins are key partners for SNARE proteins in vesicle fusion (Sudhof & Rothman, 2009), how is axon elongation, branching and nerve regeneration regulated in the absence of Munc18 and Munc13? More recently we have found that  $\alpha 2\delta 2$  also negatively regulates axon growth and regeneration of corticospinal neurons (Sun et al., 2020), the cells that originate the corticospinal tract (CST). There, upregulation of  $\alpha 2\delta 2$  expression parallels the increased spontaneous firing of corticospinal neurons at times when the CST growth program is near completion and synaptogenesis starts (Bregman, Kunkel-Bagden, McAtee, & O'Neill, 1989; Gribnau et al., 1986). Gabapentinoids (e.g., gabapentin and pregabalin), drugs used clinically to treat neurological disorders (Goodman & Brett, 2017), bind with high affinity and selectivity to  $\alpha 2\delta 1/2$  subunits (Gee et al., 1996; Gong, Hang, Kohler, Li, & Su, 2001). Pharmacological blockade of  $\alpha 2\delta 2$  through systemic administration of gabapentinoids dampens excitatory synaptic transmission and promotes structural plasticity and regeneration after SCI in adult mice (Sun et al., 2020; Tedeschi et al., 2016). Moreover, we have shown that mice administered gabapentinoids recover upper extremity function after cervical SCI (Sun et al., 2020) and a multi-center cohort study has found that motor recovery is improved in SCI individuals receiving gabapentinoids (Warner et al., 2017). Together, these data highlight the need to consider repurposing gabapentinoids as a novel treatment for CNS repair.

In addition to the strategies discussed above, a number of target gene manipulations that promote axon regeneration in the adult CNS by recapitulating early developmental programs have been recently developed (Carlin et al., 2018; K. Liu et al., 2010; Park et al., 2008; Romero et al., 2007; D. Wu et al., 2015). Despite promoting anatomical regeneration, many of these strategies impair synaptic function including learning deficits (Costa et al., 2002), reduction in synaptic transmission (Fraser, Bayazitov, Zakharenko, & Baker, 2008), dendritic spine deficits and synaptic impairments (Goorden, van Woerden, van der Weerd, Cheadle, & Elgersma, 2007; Nie et al., 2015; Sugiura et al., 2015; Yasuda et al., 2014).

Recent evidence suggests that a spared source of synaptic activity may be sufficient to harness the activation of intrinsic regenerative programs after injury. Using highly localized laser axotomy, Lorenzana et al. has demonstrated how sensory axons respond to injuries at different locations relative to the main bifurcation point in the spinal cord. Results clearly show that a surviving intact branch suppresses the regeneration of the damaged branch (Lorenzana, Lee, Mui, Chang, & Zheng, 2015). In *Caenorhabditis elegans*, axon branching also influences axon regeneration. Mechanosensory axons regenerate when severed proximal to their collateral synaptic branch, but not when severed distal to the branch point (Z. Wu et al., 2007), and dendrites actively suppress axon outgrowth of adult sensory neurons (Chung et al., 2016). Following dorsal root crush injury in adult mice, regenerating sensory axons are stabilized as they penetrate into the CNS territory by formation of synaptic-like contacts on non-neuronal cells (Di Maio et al., 2011), thereby contributing to axon regeneration failure. Similarly, dystrophic sensory endings intimately associate with nerve/glial antigen 2 (NG2) positive cells in the penumbra after injury to the spinal cord (Filous et al., 2014). When stabilized, dystrophic end bulbs may persist for decades in SCI individuals (Ruschel et al., 2015).

Thus, accumulating evidence suggests that axon regeneration, synaptic transmission and function may be at odds with one another. Further testing of the developmental-dependent and adult self-repair mechanisms that stabilize neuronal connectivity at the expense of axon elongation and nerve regeneration could help the development of novel strategies and therapeutic opportunities to treat a variety of CNS trauma and disease conditions.

**1.4 Lipid rafts, actin remodeling and exocytosis**—The plasma membrane features different subcompartments that differ in their composition and thus physical properties such as thickness, curvature or bending rigidity (McIntosh & Simon, 2006). Cholesterol and glycosphingolipids are important structural components of highly specialized subdomains (10-200 nm) of the plasma membrane called lipid rafts (Munro, 2003; Pike, 2006; Sezgin, Levental, Mayor, & Eggeling, 2017) (Figure 2). By recruiting other lipids and proteins, cholesterol-rich subdomains and glia-derived cholesterol play a crucial role in trafficking, signal transduction, presynaptic differentiation, evoked transmitter release and synapse formation (Goritz, Mauch, & Pfrieder, 2005; Lingwood & Simons, 2010; Mauch et al., 2001; Simons & Ikonen, 1997). Lipid rafts are decorated with a variety of signaling receptors and ion channels (Brown & London, 1998), serving as docking stations to integrate extracellular signals into intracellular pathways. The limited size (<200 nm) (Pralle, Keller, Florin, Simons, & Horber, 2000) makes lipid rafts difficult to resolve using conventional microscopy. With the development of super resolution microscopy and single



particle tracking, it is now possible to study nano-scale structures and dynamics of raft in cells (Owen, Williamson, Magenau, & Gaus, 2012; Saka et al., 2014). Thus far, the molecular code for selective incorporation of proteins into raft domains remains unknown. Whereas prenyl groups associate with non-raft regions, saturated lipid anchors including glycosphosphatidylinositol-anchored (GPI) proteins prefer ordered membranes (Goswami et al., 2008; Levental, Grzybek, & Simons, 2010). Trafficking and integration to raft domains is subjected to regulation through N- and O-linked glycosylation, transmembrane elements and GPI anchor (Hanzal-Bayer & Hancock, 2007). Indeed, protein N-glycosylation is one of the most abundant post-translational modifications, contributing to protein folding, stability, trafficking and localization (Freeze, Chong, Bamshad, & Ng, 2014). For example,  $\alpha 26$  subunits of VGCC are glycosylated extracellular proteins that localize within cholesterol-rich raft domains via GPI anchor (Dolphin, 2012). Interestingly, we have recently shown that  $\alpha 262$  glycosylation in corticospinal neurons positively correlates with increased spontaneous firing, network activity and synaptogenesis, but negatively with CST regeneration ability (Sun et al., 2020). Comprehensive analysis of rat synaptic membranes during postnatal development has shown remarkable lipidomic remodeling during the first 8 weeks with progressive accumulation of sphingolipids and cholesterol-rich raft domains to synaptic sites (Tulodziecka et al., 2016). Interestingly, blocking Neogenin raft association is sufficient to promote neuron survival and axon regeneration after both optic nerve crush and compression of the thoracic spinal cord in rats (Tassew et al., 2014). Similarly, cholesterol depletion favors axon growth *in vitro* and peripheral nerve regeneration *in vivo* by disrupting lipid raft (Rosello-Busquets et al., 2019). Of interest, the stemness-associated gene *Prom1* has been recently identified as positive regulator of peripheral regeneration in adulthood (Lee et al., 2020). *Prom1* encodes for the membrane glycoprotein Prominin-1. By inhibiting the expression of genes related to cholesterol biosynthesis, *Prom1* forced expression enhances axon regeneration via Smad2-dependent signaling (Lee et al., 2020). It is important to note that a reduction of membrane cholesterol has been shown to alter activity of transient receptor potential cation channels in trigeminal neurons (Saghy et al., 2015), synaptic vesicle biogenesis and increased transmitter packing (Rodrigues et al., 2013). Nanoscale organization at the synaptic active zone is highly heterogeneous. In fact, presynaptic VGCC and postsynaptic ligand-gated ion channels are confined to nanodomains of the plasma membrane where individual molecules are only transiently trapped (Heine & Holcman, 2020).

Cholesterol reduction inhibits exocytosis of synaptic vesicles in cultured hippocampal neurons (Linetti et al., 2010). This suggests that lipid rafts are key in the regulation of exocytosis. SNARE proteins localize at defined sites of the plasma membrane including raft domains (Lafont et al., 1999), thereby allowing exocytic proteins and protein complexes to be spatially regulated. Syntaxin 1A and SNAP-25 concentrate in cholesterol-dependent clusters in PC12 cells thereby restricting docking and fusion sites for exocytosis discrete clusters (Lang et al., 2001). Importantly, these clusters disperse following cholesterol extraction from the plasma membrane (Lang et al., 2001). In addition, about 20% of syntaxin 1A and SNAP-25 copurified with detergent resistant (e.g., sphingolipid/cholesterol-rich domains) raft membranes in PC12 cells (Chamberlain, Burgoyne, & Gould, 2001). To a variable degree, SNAP23 and 25 associations to rafts is directly linked to palmitoylation of

cysteine residues (Melkonian, Ostermeyer, Chen, Roth, & Brown, 1999; Salaun, Gould, & Chamberlain, 2005).

The interaction between membrane rafts and cytoskeletal components such as actin plays an important role for raft assembly and clustering (Gowrishankar et al., 2012; Head, Patel, & Insel, 2014; Kusumi, Koyama-Honda, & Suzuki, 2004; Ritchie, Iino, Fujiwara, Murase, & Kusumi, 2003; Simons & Gerl, 2010; Viola & Gupta, 2007; Whitehead, Gangaraju, Aylsworth, & Hou, 2012). Along this line, the cortical actin cytoskeleton has been shown to influence exocytosis, organization, diffusion and mechanical properties of cell membranes (Fritzsche, Erlenkamper, Moeendarbary, Charras, & Kruse, 2016; Koster & Mayor, 2016). Indeed, the integrity of actin filaments is crucial for the delivery of a variety of polypeptides to the apical membrane. Cytochalasin D, a cell permeable fungal toxin, binds to the barbed end of actin filaments inhibiting both the association and dissociation of subunits thereby disrupting the subcellular architecture of the actin network and consequently, the surface delivery of vesicles in polarized cells (Jacob, Heine, Alfalah, & Naim, 2003; Maples, Ruiz, & Apodaca, 1997; Ojakian & Schwimmer, 1988; Schliwa, 1982; Valentijn, Gumkowski, & Jamieson, 1999). The actin nucleation factors Arp2/3 are critical for the establishment of actin coats, also called ring structures, at the boundary between the vesicle and the plasma membranes (P. Li, Bademosi, Luo, & Meunier, 2018; Sokac, Co, Taunton, & Bement, 2003; Yu & Bement, 2007). As myosin II drives the contractility of the actin coats, inhibition of Myosin II causes defects in the final stages of exocytosis (Nightingale et al., 2011), more specifically a delay between vesicle fusion and release. In a reconstituted fluid bilayer, actomyosin dynamics drive local membrane component organization (Koster et al., 2016). In addition, changes in actin patterning are known to alter membrane architecture (Fritzsche et al., 2017).

Together, experimental evidence suggests that highly specialized membrane microdomains enriched in cholesterol and glycosphingolipids regulate signal transduction and pathways influencing the transition from a growing to a transmitting phase. Whether manipulating the expression and localization of regulators and components of the SNARE complex promotes axon elongation and regeneration remains to be determined.

## 2. Astrocyte-dependent mechanisms of circuit formation and refinement

Along with neurons, astrocytes participate in coordinating and sustaining electrical activity in the CNS. Astrocytes are widely recognized as one of the most ubiquitous glial cell type in the brain and spinal cord. Astrocytes derive their namesake when their star-shaped morphology was revealed by metal-impregnation techniques (Garcia-Marin, Garcia-Lopez, & Freire, 2007). It is now appreciated that the cellular structures of astrocytes are much more complex than when first characterized by Ramón y Cajal. Intracellular injection of fluorescent dye in rat hippocampal protoplasmic astrocytes reveals extensive ramification of fine processes that compose the majority of the astrocyte cellular domain, allowing the establishment of minimally overlapping territories among adjacent protoplasmic astrocytes (Bushong, Martone, Jones, & Ellisman, 2002). Such structural complexity is further expanded by heterogeneous morphology of astrocytes in other brain regions, such as velate astrocytes and Bergmann glia in the cerebellum and fibrous astrocytes in brain white matter.

These unique structures are even more intricate and complex in nonhuman primates where astrocytes possess varicose processes or processes that extend across multiple cortical layers, which are structural elements not seen in rodent astrocytes (Oberheim, Goldman, & Nedergaard, 2012).

Astrocytes perform a multitude of homeostatic functions like maintaining extracellular potassium levels, regulating extracellular pH, water transport, control of CNS blood circulation, and neurotransmitter clearance (Kimelberg, 2010). These fundamental capabilities astrocytes possess has led to the proposal that astrocytes are functionally defined as homeostatic cells and maintain CNS homeostasis (Verkhatskiĭ & Butt, 2013). However, the extent to which astrocytes control neuron function and participate in synaptic transmission remains controversial.

**2.1 Astroglial network and gap junctions**—Astrocytes possess a prominent characteristic in that they couple with neighboring astrocytes through gap junctional coupling to form extensive syncytial networks, which are also referred to as the astrocyte syncytium (Brightman & Reese, 1969; Giaume et al., 1991; Kuffler, Nicholls, & Orkand, 1966; Kuffler & Potter, 1964; Rash, Yasumura, Dudek, & Nagy, 2001). Astrocyte syncytial coupling mediates the exchange of ions, metabolites, and calcium that play critical roles in neuron homeostatic and signaling functions (Kuga, Sasaki, Takahara, Matsuki, & Ikegaya, 2011; Langer, Stephan, Theis, & Rose, 2012; Lin et al., 1998; Nagy & Rash, 2000; Orkand, Nicholls, & Kuffler, 1966; Rose & Ransom, 1997; Rouach, Koulakoff, Abudara, Willecke, & Giaume, 2008; Simard, Arcuino, Takano, Liu, & Nedergaard, 2003; F. Wang et al., 2012). The importance of this syncytial network is revealed when two major astrocytic gap junctions subunits, connexin 43 (Cx43) and 30 (Cx30) are genetically deleted from mice. The loss of syncytial coupling results in disruption of potassium homeostasis: potassium clearance decelerates and higher potassium accumulates during synchronized neuronal firing in 1-3 month old mice (Wallraff et al., 2006). Also, this results in altered neuronal function as shown by a decrease in synaptic long-term potentiation (LTP) in P16-25 mice (Pannasch et al., 2011) and aberrant hippocampal network activity in P17-25 *ex vivo* brain slices (Chever, Dossi, Pannasch, Derangeon, & Rouach, 2016). The loss of syncytial coupling also impairs spatial memory tasks in novel object recognition in 4 months old mice (Lutz et al., 2009). Altogether, the evidence indicates the importance of the astrocyte syncytial network to facilitate neuronal function and synaptic transmission. It is enticing to envision that the functional state of the astrocyte syncytial network may be involved in neural circuit formation, in particular, synaptogenesis and synaptic plasticity. A mouse model with astrocytic Cx43 and Cx30 deletion did not show any alterations in the expression of synaptic markers synaptophysin and PSD-95 (Pannasch et al., 2011). This suggests that postnatal synaptogenesis may be astrocyte network-independent, and may be governed at the single cell level. However, it isn't clear if the syncytial network plays any role in synaptic formation and plasticity in the adult CNS. For example, can astrocytes in one area of the brain or spinal cord influence astrocytes in another area via long-range astrocyte signaling through gap junctions thereby affecting synaptic formation and activity? Or is astrocytic influence constrained to spatiotemporal 'hotspots' within an astrocyte domain?

**2.2 Astrocyte heterogeneity across the CNS**—Astrocytes are not simply a homogenous class of glial cells, but heterogeneous and functionally specialized (Ben Haim & Rowitch, 2017; Farmer & Murai, 2017; Khakh & Deneen, 2019). Intrinsic variation and regional specificity may allow astrocytes to refine and optimize neuronal function locally. Evidence of astrocyte specialization to specific circuits is observed in a study where astrocytes were depleted in the ventral spinal cord. This resulted in altered motoneuron synaptogenesis that could not be resolved by tangential migration of neighboring astrocytes from adjacent regions (Tsai et al., 2012). This intriguing finding not only underscores critical interactions between astrocytes and neurons in synaptogenesis and circuit formation but also demonstrates that astrocytes are purposefully allocated to specific regions of the CNS. In addition, neuronal factors dictate astrocyte specialization to generate heterogeneous astrocyte populations. Sonic hedgehog (Shh) signaling from neurons is necessary to confer and maintain specialized functional astrocyte properties (Farmer et al., 2016). This was demonstrated first in the cerebellum that contained velate astrocytes and Bergmann glia, which are two types of astrocytes that are morphologically and functionally distinct from each other. The perturbation of the Shh pathway using viral-delivery of Cre to genetically delete Purkinje cell-derived Shh or its receptor Patched on Bergmann glia causes Bergmann glia to take on the functional phenotype of the neighboring velate astrocytes. Conversely, constitutive activation of Smoothened, a transmembrane protein immediately downstream from Shh/Patched signaling pathway, in velate astrocytes causes the acquisition of some molecular characteristics associated with Bergmann glia, such as higher expression of AMPA receptor GluA1 and annexin A7. Interestingly, the cellular morphology appears not to be affected, suggesting Shh signaling is not involved in the diversification of astrocyte cellular structures. An interesting point of this study is that persistent Shh signaling is necessary to maintain the functional profiles of these astrocytes. This has potential implications in scenarios where Shh signaling is disrupted such as after CNS injury (Allahyari, Clark, Shepard, & Garcia, 2019). It isn't known if the disruptions of such signaling pathways affect astrocyte contributions to synaptic formation and function as a result of an altered functional phenotype.

**2.3 Tripartite Synapse: astrocyte processes as the third component of a synapse**—It is increasingly recognized that astrocytes are important contributors to synapse formation and transmission. The active participation of astrocytes in synaptic function has led to its inclusion as the third component of a synapse to form the tripartite synapse (Araque, Parpura, Sanzgiri, & Haydon, 1999). The intricate cellular morphology enables a single astrocyte to cover over an estimated 100,000 synapses through its dense ramification of fine processes positioned next to synaptic terminals (Bushong et al., 2002). This direct association between presynaptic axons, postsynaptic dendritic spine, and perisynaptic astrocyte processes (PAPs) is visualized at the ultrastructural level using electron microscopy (Spacek, 1985; Ventura & Harris, 1999). Using electron microscopy to examine the association of hippocampal astrocytes with synaptic type, another study has found that PAPs preferentially associate with larger synapses and that these processes are typically less than 200 nm wide (Witcher, Kirov, & Harris, 2007). The ramification of these fine processes increases during development, which is seen in rat hippocampal protoplasmic astrocytes between 1-4 weeks of age (Bushong, Martone, & Ellisman, 2004). While these

studies reveal important ultrastructural details at the synaptic level, tissue samples require chemical fixation that negates the ability to observe these processes in a living astrocyte. To circumvent this, the activity of PAPs in living astrocytes can be observed using *in situ* or *in vivo* confocal or 2-photon microscopy. In acute brainstem slices from transgenic mice expressing GFP in astrocytes, PAPs display a high degree of motility (Hirrlinger, Hulsmann, & Kirchhoff, 2004). Another study has used hippocampal slice cultures from P4-5 mice and time-lapse 2-photon imaging to correlate PAP motility to lifetime and maturation of dendritic spines (Nishida & Okabe, 2007). This dynamic process is also seen *in vivo* in the adult mouse barrel cortex when a whisker is stimulated and motile PAPs increase dendritic spine coverage, suggesting neuronal activity controls PAP motility in a calcium-dependent manner (Bernardinelli et al., 2014). Thus, astrocytes are structurally active with motile processes that respond to synaptic transmission, emphasizing the significant crosstalk occurring between synapses and astrocyte processes. A recent study used innovative live-cell 3D-STED microscopy to obtain nanoscale details of the astrocyte spongiform domain that contains a meshwork of shafts, loops, and nodes. Interestingly, the majority of synaptic spines form stable contacts with nodes, and these nodes exhibit spatially-constrained calcium transients (Arizono et al., 2020). While PAPs are commonly referred to as the fine processes on an astrocyte, it isn't clear if the entire astrocyte can contribute to the same synaptic formation and function as the fine processes. In essence, are these mechanisms confined to the fine processes, or can the astrocyte soma and large processes contribute to synaptic formation and function as well? *In vivo* analysis should be in position to answer this question.

The importance of astrocytes in synaptogenesis, synapse maturation, and synaptic activity is evident in experiments where murine neurons cocultured with astrocytes exhibit an increased number of mature and functional synapses, whereas neurons cultured without astrocytes form only a few functionally immature synapses (Pfrieger & Barres, 1997; Ullian, Sapperstein, Christopherson, & Barres, 2001). The first study showing a connection between astrocytes and synaptic function was performed *in vitro* using retinal ganglion cells (RGC) and glia cocultures. When glial cells are present, RGC exhibit a large increase in the frequency and amplitude of postsynaptic currents. They also decrease the failure rate of evoked synaptic transmission (Pfrieger & Barres, 1997). This has been followed by another study using the same model *in vitro* system to show that astrocytes also increase the number of functional synapses between neurons using immunoblot and immunofluorescence imaging of synaptic markers synaptotagmin, synaptophysin, and SV2 (Ullian et al., 2001). These studies suggest that astrocytes are signaling to neurons to generate functional synapses. The notion that astrocytes facilitate synapse formation and maturation is underscored by the fact that synaptogenesis coincides with peak astrogenesis during development (Reemst, Noctor, Lucassen, & Hol, 2016) (Figure 3). This strongly suggests that astrocytes play a critical role in the formation and maturation of synapses during this developmental time window.

**2.4 Astrocyte-derived factors and synaptogenesis**—Astrocytes secrete substances that facilitate the formation and maturation of synapses (Figure 3). One of the first discovered astrocyte-derived soluble factors is cholesterol (Mauch et al., 2001). Of note,

cholesterol is an essential structural component of cell membranes that acts as a bidirectional regulator of membrane fluidity. Whereas cholesterol intercalation between the phospholipids prevents membrane stiffening at low temperatures, it stabilizes membranes and raises their melting point at high temperatures (M. R. Krause & Regen, 2014). This study used glial conditioned culture media and gel filtration chromatography and initially identified apolipoprotein E (ApoE). Afterwards, cholesterol was identified as the active substrate and ApoE as the cholesterol carrier. As synaptogenesis requires the production of new cell membranes, astrocytes provide cholesterol as building material to allow synapses to form.

Of the multiple classes of molecules that astrocytes release to induce synapse formation, matricellular protein thrombospondin has been identified in filtered astrocyte conditioned media to promote synaptogenesis (Christopherson et al., 2005). The addition of thrombospondin to RGC increases the number of synaptic puncta for synaptotagmin and PSD-95 (Christopherson et al., 2005). Thrombospondin synaptogenic effect is mediated via  $\alpha 2\delta 1$  (Eroglu et al., 2009). However, measurements of miniature excitatory post synaptic currents (mEPSC) show that thrombospondin only facilitates the formation of postsynaptically-silent synapses (Christopherson et al., 2005). Gene expression profiling of astrocytes has uncovered matricellular proteins hevin and SPARC as highly expressed genes that persist through adulthood (Kucukdereli et al., 2011). The addition of hevin to cultured RGC increases the number of synapses *in vitro*, while SPARC exhibits an antagonistic effect to hevin. A genetic knockout (KO) of hevin and SPARC in mice creates defects in synaptogenesis in the superior colliculus, whereas hevin KO resulted in a decrease of synapses and SPARC KO had an increase in synapses *in vivo*. Similarly to thrombospondin, the synapses formed by hevin are postsynaptically silent. This study identified hevin and SPARC as positive and negative regulators of synapse formation, respectively. Hevin was later determined to induce synaptogenesis by acting as a bridge between presynaptic neuroligin1 $\alpha$  and postsynaptic neuroligin1 (Singh et al., 2016). The formation of silent synapses suggests that there may be an astrocyte-derived signal to induce a silent synapse to become functionally active. Heparan sulfate proteoglycans glypicans 4 and 6 have been identified through biochemical fractionation of astrocyte conditioned media, and are sufficient to induce synaptic activity (Allen et al., 2012). The addition of glypicans to RGCs *in vitro* induces an increase in amplitude and frequency of mEPSC events. This regulation of synaptic activity by Glypican 4 and 6 is achieved by inducing increased surface level expression and clustering of AMPA glutamate receptor subunit GluA1 on postsynaptic terminals. Astrocyte-released cytokines such as transforming growth factor beta (TGF- $\beta$ ) is also necessary for synaptogenesis. In both human and murine astrocyte conditioned media, TGF- $\beta$  induces the formation of functional excitatory synapses in cortical neurons and increases levels of NMDA co-agonist D-serine *in vitro* (Diniz et al., 2012). Similarly, TGF- $\beta$  promotes inhibitory synaptic formation by activating calcium/calmodulin-dependent protein kinase II in neurons, which in turn assembles neuroligin 2 on inhibitory postsynaptic terminals (Diniz et al., 2014).

There are some studies that show direct astrocyte contact also plays a role in synaptogenesis. Astrocytic expression of  $\gamma$ -Protocadherin, a cell adhesion membrane protein, promotes both excitatory and inhibitory synapses in the neonatal mouse spinal cord and contact-dependency has been shown *in vitro* (Garrett & Weiner, 2009). Selective KO of membrane

protein neuroligin 2 in murine cortical astrocytes *in vivo* causes a reduction in synaptic puncta for excitatory synapses (Stogsdill et al., 2017).

**2.5 Astrocytic release of synaptogenic factors**—It is well established that astrocytes play an important role in building neuronal circuits. The body of evidence has revealed that astrocytes utilize an assortment of extrinsic factors to facilitate synaptogenesis during CNS development. The number of secreted- and contact-factors raises a number of intriguing questions about how astrocytes perform their role in forming a neural circuit. If astrocytes regulate these factors, through what mechanisms do they achieve this? One mechanism may be through sensing synaptic activity through astrocytic neurotransmitter receptors. A study using neuron-astrocyte feeder cultures reported increased production of SPARC in astrocytes when neuronal firing is increased using bicuculline. This astrocytic response acts through Group I Gq-linked metabotropic glutamate receptors (mGluR), which was determined using a Group I mGluR agonist 3,5-dihydroxyphenylglycine (DHPG), and elicits an astrocytic cytosolic calcium response and increased SPARC expression (Jones et al., 2011). Group I mGluRs consists of mGluR1 and 5, and astrocytes express only mGluR5 during early development that peaks at P7 in mice and drops rapidly thereafter at the transcript level (Cahoy et al., 2008). In adult mice, cortical astrocytes fail to elicit a calcium response to Group I agonists, which is in agreement with the transcriptional profile (Sun et al., 2013). This developmental timing coincides with synaptogenesis, which suggests one mechanism is that astrocytes sense synaptic activity and release synaptogenic factors through a calcium-dependent response (Figure 3). However, mGluR5 is downregulated by the end of the third postnatal week (Sun et al., 2013). This raises the question if mature astrocytes deliver synaptogenic factors by utilizing other calcium-responding mechanisms, such as transient receptor channels, purinergic P2X receptors, sodium/calcium exchangers and mitochondrial calcium efflux through its permeability transition pore (Agarwal et al., 2017; Palygin, Lalo, Verkhratsky, & Pankratov, 2010; Pankratov, Lalo, Krishtal, & Verkhratsky, 2009; Shigetomi, Tong, Kwan, Corey, & Khakh, 2011; Verkhratsky, Reyes, & Parpura, 2014; Verkhratsky, Rodriguez, & Parpura, 2012). Is there any spatiotemporal specificity in the release of astrocytic factors? The previous studies have performed the critical task of identifying the multitude of astrocyte factors involved in synaptic formation. It isn't clear how all these factors identified so far work together *in vivo* to form synapses. Does the astrocyte release a cocktail of factors at once, or are these factors segregated according to the specific signaling mechanisms regulating its release? In addition, are these secreted factors spatially targeted towards a single synapse, or is release more volumetric in nature?

While the physiological mechanisms remain to be fully elucidated, the ability of astrocytes to regulate synapse formation and function under injury and disease conditions is unclear. The role of astrocyte participation in forming neural circuits is generally considered in the context of CNS development. How are the astrocytes' roles in synaptic formation altered in the context of injury and disease? Astrocytes become reactive in response to injury and disease with morphological and molecular changes, such as the characteristic upregulation of glial fibrillary acidic protein (GFAP) (Sofroniew & Vinters, 2010). It is currently proposed that this astroglial reactivity is heterogeneous in nature that varies depending on

the context and severity of the insult, ranging from mild to severe reactive astrogliosis (Anderson, Ao, & Sofroniew, 2014). In certain insults such as SCI, newly proliferated elongated astrocytes intertwine to form an astrocyte scar border that surrounds the lesion area (Wanner et al., 2013). Scar-forming astrocytes have traditionally been viewed as a physical and chemical barrier to axon regeneration and functional recovery (Silver & Miller, 2004), though recent reports challenge that notion. Attenuation or ablation of scar-forming astrocytes resulted in exacerbation of neuronal loss and did not result in increased axon regrowth or recovery, suggesting a protective role of the glial scar in preserving the surrounding neural tissue (Anderson et al., 2016; Gu et al., 2019). It isn't clear what specific changes and functional consequences occur in facilitating synaptic formation and function, in particular during the initial and post-injury processes. Are astrocyte synaptogenic and homeostatic functions impacted as a result of astrocyte reactivity? Does the presence or absence of astrocyte synaptogenic factors contribute to failures in axon regeneration and synapse reformation? Astrocyte homeostatic functions and synaptogenic factors may represent an attractive target to manipulate for therapeutic purposes.

### 3. Microglia-dependent mechanisms of circuit formation and refinement

Microglia is another class of non-neuronal cells that are commonly described as the phagocytic immune cells of the CNS. These cells are mesodermal in origin that migrate into the brain parenchyma early during development (Ginhoux & Prinz, 2015). Many of the studies of microglial function have focused in the context of CNS injury and disease. However, recent work has shed light on microglial function in a healthy and uninjured CNS, in particular to microglia's role in synaptic refinement and elimination.

**3.1 Microglial actively monitor the neural environment**—The development of chronic *in vivo* imaging techniques and genetic strategies to observe microglia 'at play' has led to findings that microglial processes constantly extend and contract to actively inspect the brain parenchyma (Wake, Moorhouse, Jinno, Kohsaka, & Nabekura, 2009). Such dynamic process allows microglia to rapidly survey the cellular environment and physically contact other cellular structures such as axons and synapses (Davalos et al., 2005; Jung et al., 2000; Nimmerjahn, Kirchhoff, & Helmchen, 2005) (Figure 4). In the mouse somatosensory and visual cortex, microglia processes contact synapses about once per hour (Wake et al., 2009). Implementation of cutting edge super resolution microscopy combined with fluorescent labeling of the extracellular fluid has demonstrated microglia move rapidly in an amoeboid fashion across bundles of axons and displacing neural structures in living organotypic mouse brain slices. This restructuring of the extracellular space by motile microglia may also effect changes in extracellular matrix structures. In 2-photon induced lesion conditions, microglia move in a curved path towards and around the lesion area, while other microglia rips through the neuropil and leaving an empty space from its path (Tonnesen, Inavalli, & Nagerl, 2018). A number of studies has demonstrated that microglia motility is regulated by neuronal activity. *In vivo* time lapse calcium imaging in the optic tectum of larval zebrafish has found that neuronal activity instructs microglia motility and promote microglia contact with active neurons through activation of pannexin-1 hemichannels expressed in neurons (Y. Li, Du, Liu, Wen, & Du, 2012). Microglial motility and dendritic spine contacts are regulated by neuronal activity, and is increased in awake



mice compared to anesthetized mice *in vivo* (Nebeling et al., 2019). Conversely, dampening neuronal activity causes a decrease in the frequency of microglia contacts and motility (Nebeling et al., 2019; Wake et al., 2009), further underscoring a reciprocal regulation between microglia dynamics and neuronal activity *in vivo*. While synapses can be targeted for pruning, microglia requires a mechanism that enables a cellular response to changes in synaptic activity. Microglia accomplishes this through P2Y<sub>12</sub> purinergic signaling (Figure 4). By altering their morphology, motility, phagocytic behavior and interaction at synapses, microglia actively respond to monocular deprivation during the critical period in the visual system (Sipe et al., 2016). Monocular deprivation during a critical period of brain development leads to changes of neuronal firing (Wiesel & Hubel, 1963). Of note, P2Y<sub>12</sub> disruption causes alteration in microglia response following monocular deprivation in mice, effectively abrogating ocular dominance plasticity (Sipe et al., 2016).

**3.2 Microglia shape neural circuitry by pruning synapses**—During development and maturation of the CNS, neural circuits are sculpted and refined through elimination of synapses also known as synaptic pruning. It is now recognized that microglia plays a major role in synaptic pruning by engulfing synaptic structures (Paolicelli et al., 2011), and accomplishes this function through several mechanisms. C1q/C3 complement cascade signaling mediates microglia phagocytosis of synapses (Figure 4). C1q and C3 are members of the classical complement cascade that may be used as a molecular “eat me” tag for microglia, through its C3 receptor (CR3), to recognize and prune the synapse during development in the lateral geniculate nucleus (Schafer et al., 2012; Stevens et al., 2007). Whereas neurons express C1q during circuit refinement, the extracellular signals controlling C1q expression have remained obscure. Astrocyte-secreted transforming growth factor beta (TGF- $\beta$ ) has been found to regulate neuronal C1q expression, where genetic ablation of TGF- $\beta$  receptor II in retinal neurons reduces C1q expression and synaptic localization of complement, thereby causing defects in subsequent pruning (Bialas & Stevens, 2013). Advanced light-sheet microscopy and correlative light and electron microscopy have further characterized microglia behavior in association with synapses. Rather than eliminating the entire synaptic apparatus, microglia prune presynaptic structures via partial phagocytosis or trogocytosis in developing postnatal organotypic mouse hippocampal cultures (Weinhard et al., 2018). C1q tagging of a synapse requires specific alteration in the synaptic proteome. Along this line, a recent study has demonstrated the presence of apoptotic-like mechanisms underlying C1q tagging of synapses in the mouse cerebral cortex (Gyorffy et al., 2018). While the classical complement cascade is used to eliminate synapses, inhibition of the complement cascade can protect synapses against removal. Sushi domain protein SRPX2 is shown to bind directly to C1q, preventing the initiation and activation of the complement cascade, thereby preventing complement-mediated synapse elimination (Cong, Soteros, Wollet, Kim, & Sia, 2020).

Microglia production of C1q and C3 and regulation of lysosomal function are mediated by expression of progranulin. Deficiencies in progranulin in microglia lead to upregulation of complement and lysosomal genes, as well as excessive synaptic pruning (Lui et al., 2016). Another receptor essential for microglia-mediated synaptic refinement and pruning is triggering receptor expressed on myeloid cells 2 (TREM2). Hence, mice lacking *Trem2*

display neurodevelopmental defects due to microglia dysfunction. At P18-20, *Trem2* null hippocampal CA1 pyramidal neurons show higher frequency of miniature excitatory postsynaptic currents when compared to control littermates (Filipello et al., 2018). Similarly, an increase in synaptic contacts is also confirmed by the higher density of pre and postsynaptic specialization in *Trem2* null mice compared to the control condition (Filipello et al., 2018). The analysis of microglia morphology in the CA1 region of P18-20 *Trem2* null mice highlights a more complex, ramified structure (Filipello et al., 2018). TREM2 is required for synapse engulfment as microglia originating from null mice display reduced engulfment of synaptosomes compared to controls (Filipello et al., 2018), further supporting the relevance of the neuro-immune crosstalk for normal CNS development.

Microglial phagocytosis is also regulated by cytokine signaling transmitted from other cells. During CNS development, astrocyte-derived Interleukin-33 (IL-33) signals to microglia to promote synaptic pruning and circuit remodeling through synaptic engulfment in the thalamus and spinal cord (Vainchtein et al., 2018). Interestingly, neuron-derived IL-33 promotes microglial phagocytosis of the extracellular matrix in an activity-dependent manner in the adult brain. This clearance and remodeling of the extracellular matrix thereby promotes synaptic formation and dendritic spine plasticity (Nguyen et al., 2020).

Genetic regulations of microglia phagocytic function in healthy and uninjured CNS are beginning to be uncovered. A study has identified the TAR DNA-binding protein 43 (TDP-43) as a critical regulator of microglial phagocytic activity. TDP-43 is encoded by the *Tardbp* gene and acts as transcriptional repressor, splicing factor and mRNA binding protein (Buratti & Baralle, 2001; Lagier-Tourenne, Polymenidou, & Cleveland, 2010). Depletion of TDP-43 induces excessive phagocytosis and loss of synapses as shown by the decrease in the pre and postsynaptic markers Vglut1 and PSD95 in the cerebral cortex of null mice (Paolicelli et al., 2017).

The cumulative evidence demonstrates that microglia play an important role in refining synaptic circuitry, in particular through partial phagocytosis of synaptic structures. The aforementioned studies have taken place predominantly in the brain, where detailed connectivity maps have been characterized in select areas. In addition, brain structures such as the hippocampus and cortex are readily accessible for chronic *in vivo* imaging studies. While the role and mechanisms of microglia synaptic engulfment have been characterized in select brain regions, it remains unknown if these same mechanisms governing microglia synaptic engulfment are implicated in other unexplored brain regions and spinal cord of other species with different neuronal populations and connectivity. The development of new technologies, powerful algorithms and more specific genetic tools will reveal in more detail the microglia-synapse interactions and microglia's role in synapse refinement and elimination.

## DISCUSSION

Here we have presented and discussed recent evidence that suggests axon regeneration, synapse formation and function may be at odds with one another. The correct assembly, refinement and consolidation of intricate neuronal networks that constitute the mammalian

CNS represent an arduous task during development. The same task is far more challenging after injury and disease in adulthood where the chaotic and metabolically disrupted environment adds on to the age dependent decline in axon regeneration ability (Byrne et al., 2014; Geoffroy et al., 2016; Verdu et al., 2000). In adulthood, the gap that separates injured axons from their target field is significantly larger than what the very same axons are programmed to cover during early stages of development (He & Jin, 2016). Building functional neuronal circuits requires a coordinated series of steps including axon elongation, branching, formation and consolidation of synaptic contacts in specific target areas (Lewis, Courchet, & Polleux, 2013). Not only neurons, but also non-neuronal cells including astrocytes and microglia actively participate in synapse formation and remodeling (Allen & Eroglu, 2017; Clarke & Barres, 2013; Kettenmann, Kirchhoff, & Verkhratsky, 2013; Y. Wu, Dissing-Olesen, MacVicar, & Stevens, 2015). Such an ordered series of steps is accomplished through spatial and temporal dynamics of gene expression (Delile et al., 2019). Pioneer transcription factors are able to unmask chromatin domains during development to jump start different cellular programs in a timely fashion (Mayran & Drouin, 2018; Zaret & Carroll, 2011). Following trauma, however, epigenetic constraints prevent proper tuning of the transcriptional landscape (Cho, Sloutsky, Naegle, & Cavalli, 2015; Loh et al., 2017; Puttagunta et al., 2014; Tedeschi, 2011; Weng et al., 2017). Promoting axon regeneration and new circuit formation using uncoordinated strategies can have deleterious outcomes such as aberrant synaptogenesis, spasticity, hyperexcitability and excitation-inhibition imbalance of neuronal circuits, all of which obstruct functional recovery (Carlin et al., 2018; Ding & Hammarlund, 2018; Z. Wang et al., 2015). Further dissection of the cellular and molecular mechanisms controlling the transition from a growing to a transmitting phase as well as the role of the genetic background (Omura et al., 2015; Tedeschi, Omura, & Costigan, 2017) in coordinating non-neuronal cell behavior may pave the way for the development of novel treatment strategies for CNS repair.

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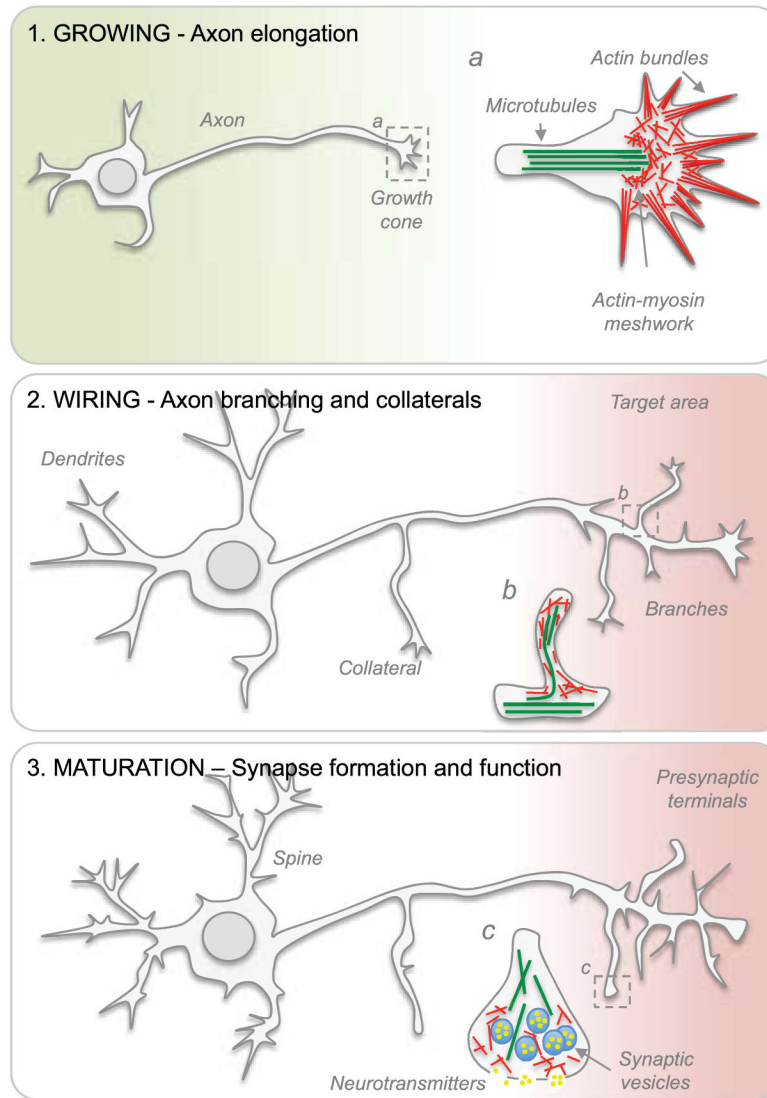
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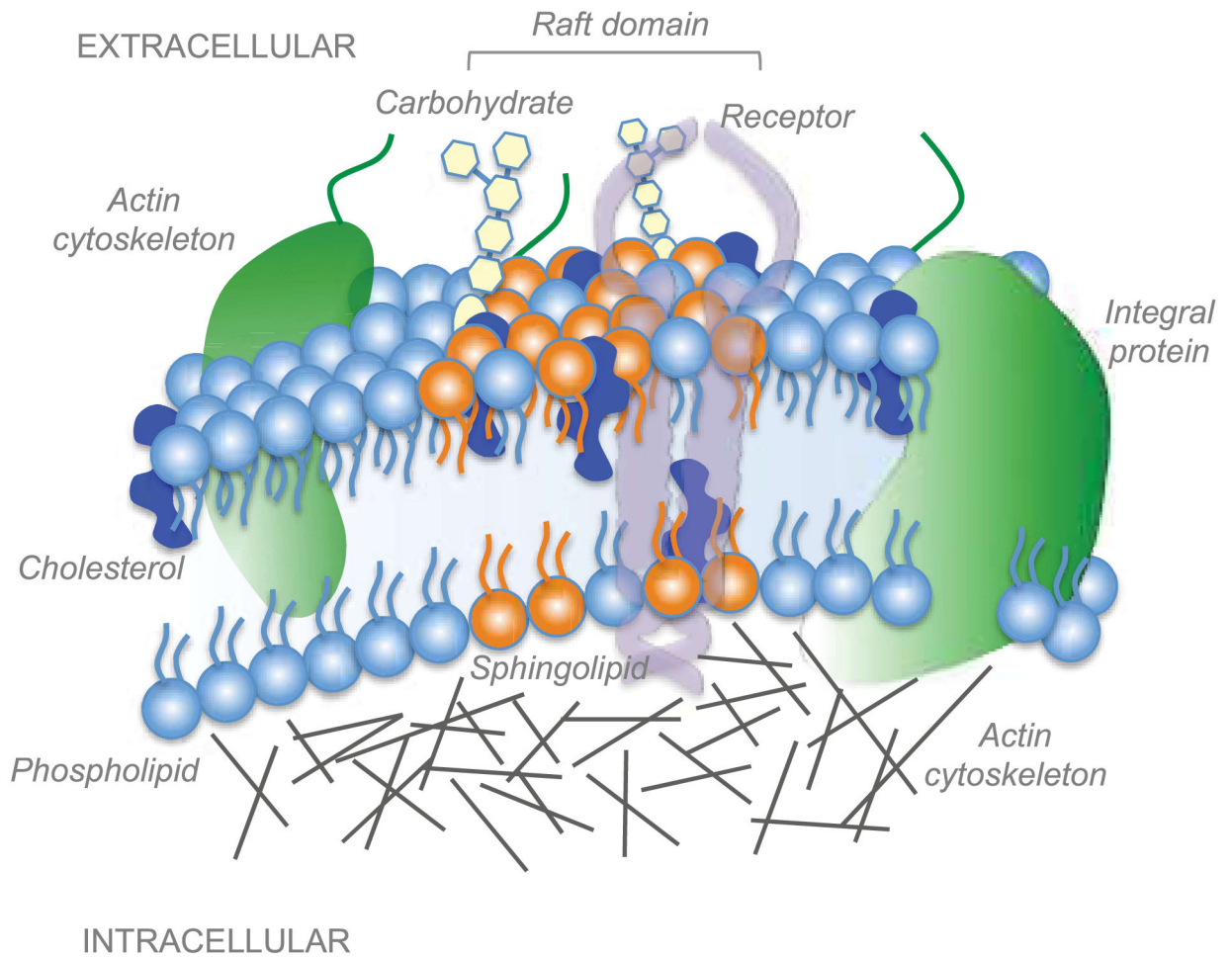
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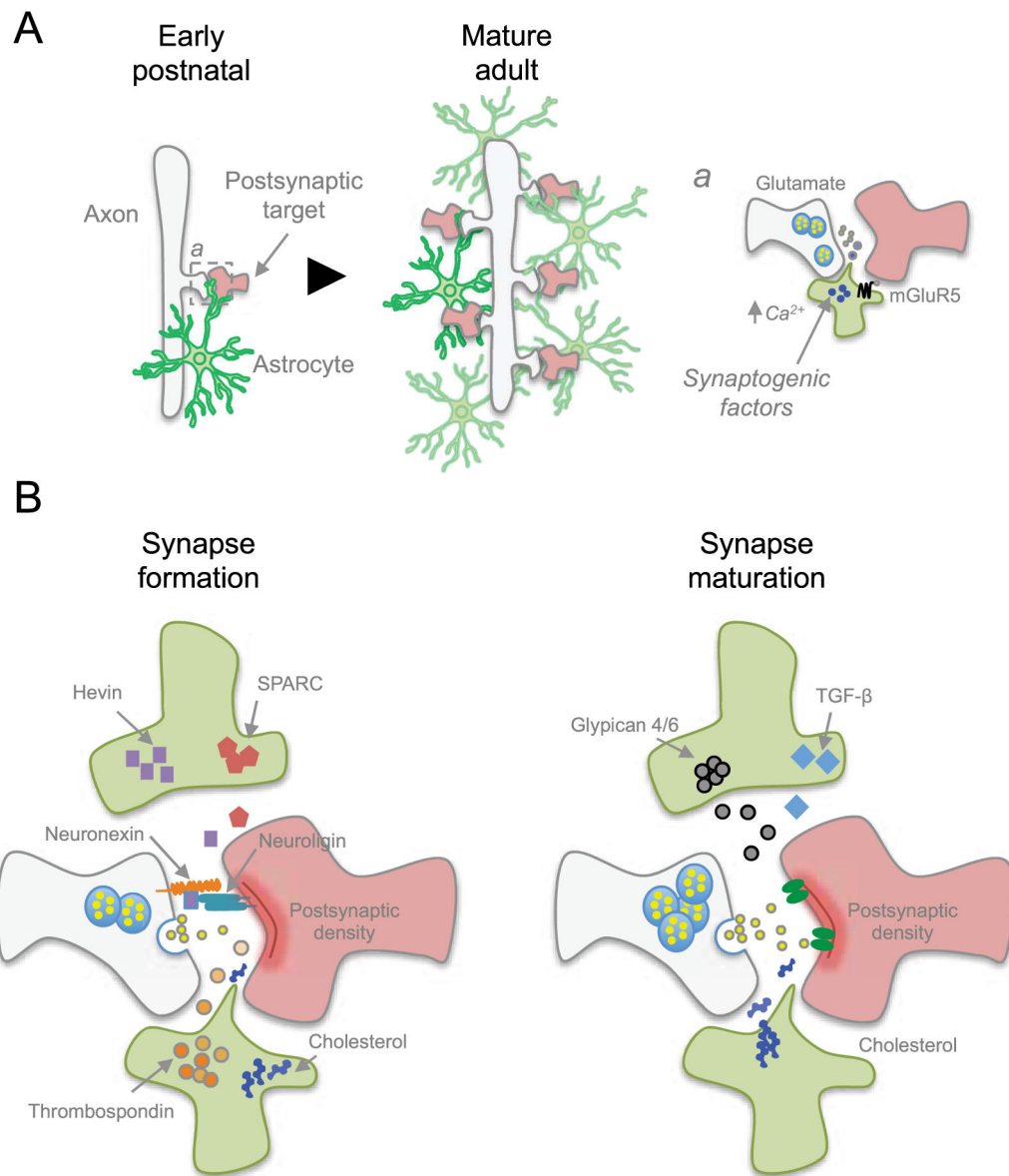


**Figure 1. The developmental transition from a growing to a transmitting phase.** Schematic representation of axon elongation, branching, synaptic transmission and synaptogenesis during neuronal maturation. Cytoskeletal arrangements present in (a) growth cones and (b) axon branches. (c) Detailed view of a few structural elements found within presynaptic terminals.



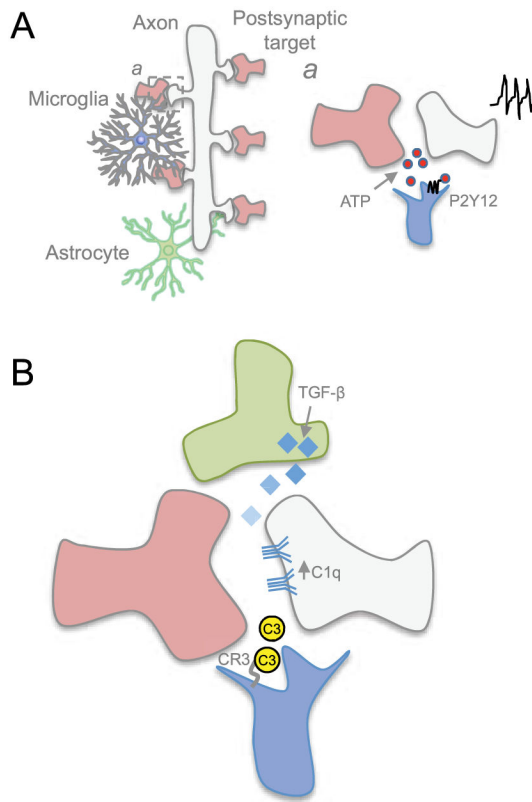
**Figure 2. Lipid raft microdomains of the plasma membrane.**

Lipid rafts are highly organized subdomains of the plasma membrane enriched in cholesterol and glycosphingolipids. Rafts serve as a platform for the recruitment, insertion and interaction of membrane receptors and biomolecules involved in a variety of cellular processes including signal transduction, membrane trafficking and cytoskeletal organization. Membrane proteins are either free to move or immobilized to the actin cytoskeleton.



**Figure 3. Astrocytes regulate formation and function of synapses.**

**A)** During early postnatal development, astrocytes begin participating in synaptogenesis while proliferating to expand the astrocyte network. This rapid expansion of astrocytes coincides with the increase in the number of synapses as the nervous system matures. *a)* Astrocytes control synaptogenesis by releasing synaptogenic factors in a calcium-dependent response after sensing neurotransmitters, such as through Gq-metabotropic glutamate receptor mGluR5. **B)** Astrocytes release factors to facilitate structural formation of synapses. Cholesterol provides building material for new membrane production, while other factors such as Hevin and Thrombospondins promote synapse formation, or opposing synapse formation via SPARC. Additional factors are involved in synapse maturation and function, such as Glypican 4/6 and TGF- $\beta$  that induces functional synapses.



**Figure 4. Microglia refines the circuit by eliminating synapses.**

**A)** Microglia constantly surveils the neural environment, and **a)** its motile processes respond to synaptic activity through P2Y12 receptor by sensing ATP released during neurotransmission. **B)** Microglia, through its C3 receptor, identifies synapses to be pruned through complement molecules C1q and C3. C1q expression on neurites may be regulated through astrocyte-secreted TGF- $\beta$ .