

Review

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Review

# Cerebellar Abnormalities: A Component of Autism Pathophysiology

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## Abstract

Autism spectrum disorder (ASD) is a prevalent and largely idiopathic developmental disorder with relatively widespread etiology. Currently there are no validated diagnostic or screening biomarkers for ASD, besides addressing the associated comorbidities. ASD is primarily diagnosed based on behavioral motor and cognitive characteristics. Until recently, the cerebellum had been particularly implicated in motor control, and under-researched for its potential role in the development of ASD. However, cerebellar circuitry is altered in ASD, impacting its brain interconnections, affecting brain development, and social and behavioral outcomes associated with ASD. We review the potential role of the cerebellum in ASD, how its dysfunction during development or its early postnatal injury may impact the maturation of other connected circuits, and play a role in the development of core ASD symptoms. We address cerebellar changes that may alter synaptic pruning, immune cells' function, neurotransmitters, blood brain barrier permeability, and potential signaling pathways involved in ASD and how all these changes interplay may contribute to ASD pathophysiology. Understanding of these interactions, may provide novel therapeutic options specifically targeted to the cerebellum.

**Keywords:** autism; cerebellum; astroglia; autism linked genes; autism signaling pathways; neurodevelopmental disease

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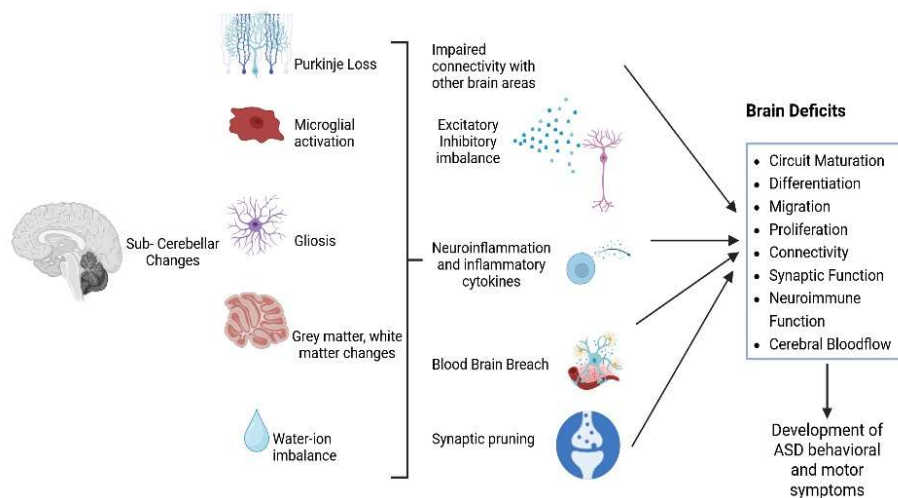
## Introduction

Autism Spectrum Disorders (ASD) are neurodevelopmental diseases of varying severity, resulting from complex genetic, environmental and immunological interactions. ASD is diagnosed by atypical social behavior and interactions, limited intellectual and interest skills, repetitive/stereotypic behaviors, and variable levels of cognitive and intellectual impairments [1]. Individuals with ASD may also present with other symptoms such as seizures, anxiety, apraxia of speech, sleep disorders, and gastrointestinal complications. According to CDC, about 1 in 44 children have been identified with ASD corresponding to estimates from CDC's Autism and Developmental Disabilities Monitoring (ADDM) network [2]. While most cases are idiopathic, multiple genetic mutations were identified in patients and are widely studied in animal models, also implicating immune dysregulation and environmental factors, as all these could interact to bring about ASD [1,3,4]. There are currently no validated biomarkers for diagnostic or screening for ASD, besides addressing the related comorbidities. Therefore, understanding the fundamental mechanisms of the disease is of utmost importance to develop ASD-specific targeted treatment strategies.

Most studies have focused on various neural networks associated with social behavior, language, and cognition. Post-mortem studies of ASD patients with genetic predisposition and showing clinical evidence, and of animal models have implicated cerebellar development and

dysfunction in ASD etiology [5–7]. The cerebellum, previously mostly associated with motor functions, is now recognized for its involvement in cognitive functions, due to its complex connections with other brain areas [8–11]. Cerebellar structural, functional and neurochemical abnormalities have been identified in ASD, and lesions in particular cerebellar sites yield effects all throughout the brain via network connections [1,9,12]. Cerebellar dysfunction during development may affect the maturation of other connected cerebral circuits that have been shown to regulate several ASD-relevant behaviors [7,10,13]. Multiple animal models of early life cerebellar damage display ASD behavioral symptoms. Indeed, cerebellar defects if they arise by birth or during early postnatal period are often sufficient to induce ASD behavioral symptoms [5].

This review article offers a comprehensive overview of different aspects of cerebellar involvement with respect to brain development and function, enabling the onset of ASD (Figure 1), highlighting earlier studies and new potential areas of research. Thorough understanding of the cerebellar function in ASD may lead to novel strategies regulating the underlying mechanisms to elaborate treatments that are more precisely aimed at cerebellar dysfunction in ASD individuals.



**Figure 1.** ASD-associated cerebellar alterations that may lead to ASD symptoms development. (Created with BioRender.com).

## 2. Cerebellum structure and function

The highly conserved brain structure and neuronal developmental trajectory of the vertebrate cerebellum develop following a conserved chronological sequence of neurogenesis, preserving its function and internal circuitry [14]. During the evolution, the size of the mammalian cerebellum has expanded when compared to the other areas of the brain, especially the cerebellar posterior lobe, which is important for the processing of cognitive as well as language skills [1,15–17]. While the cerebellum occupies just 10% of the total brain volume, it contains more neurons than the rest of the brain because of its substantial number of granule cells [18,19].

The orderly spaced parallel grooves of the cerebellar cortex are organized in three layers, the outer molecular layer (ML), Purkinje cell layer (PCL) and the inner granular layer (GL). The neuronal organization of Purkinje cells (PC) and granule cells (GC) brings about an immense and complex signal processing potential. However, the output signal from the cerebellar cortex goes out through a set of cells called cerebellar deep nuclei sitting in the white matter of the cerebellum [20]. Mossy fibers, climbing fibers and parallel fibers are the three types of axons playing a major role in the cerebellar circuit. The molecular layer, the outermost layer of the cerebellar cortex, is comprised of

PC dendritic branches and parallel fibers, which are the axons of the granule cells. The molecular layer contains two types of cells, the stellate cells and the basket cells, which are inhibitory interneurons forming GABAergic synapses with PC dendrites [19]. PC are unique neurons in the brain with large cell bodies arranged into a single cell layer of the cerebellar cortex. The PC dendrites receive inputs from parallel fibers, estimated around 200,000 dendritic spines on a single human PCs, and are inhibitory in nature [19]. Loss of PC, consistent with impaired cerebellar function is typically identified in ASD and may contribute to the excitatory/inhibitory imbalance that characterizes the disorder [13,21]. Thus, PC play a critical role in providing downstream cerebellar nuclei with efferent inhibitory output [22,23]. Granular cells are small and seen in large number in the human brain, estimated around 50 billion in total number and are mainly excitatory in nature as glutamate is their neurotransmitter [19]. Granular cells receive input from mossy fibers while PCs receive input from climbing fibers.

Cerebellar deep nuclei consist of three nuclei embedded within the white matter, the fastigial (medial) nucleus, the interposed nucleus, and the dentate (lateral) nucleus. These nuclei together form the exclusive output of the cerebellum, and it has been estimated that the total number of cerebellar deep nuclei neurons in cerebellum are about 50-100,000 [24] and include both excitatory projection neurons [25–27] and inhibitory projection neurons [28,29]. Therefore, disruption of GC/PC and cerebellar deep nuclei output may contribute to excitatory/inhibitory imbalance underlying ASD neuropathophysiology.

The cerebellar deep nuclei are closely associated with the cerebellar functions related to the sensorimotor region, limbic system etc., Besides their role in motor function, it has been reported that the cerebellar deep nuclei are also involved in cognitive and linguistic functions [30], as evidenced by neuropsychological, neurophysiological and imaging studies.

Evidence shows that the cerebellum may coordinate communication and contribute to sensory motor deficits in ASD [7,13,23,31]. For instance, while the primary cause of apraxia is damage to the cortex, cerebellar damage can also contribute to apraxia of speech [30,32]. A recent study from Milton S. Hershey Medical Center, recognizes apraxia as a common incidence in ASD, involving both speech and communication. Apraxia of speech affects children's brain pathways accountable for performing movement associated with speech production and their ability to align motor movements to deliver speech, despite having fully functional muscles [1]. In a previously reported study, 64% of the children with ASD diagnosis also exhibited apraxia of speech, and 37% of the children with an apraxia diagnosis also had ASD [33]. Because of the failure in coordinating tongue, lips, mouth and jaw, the same word would be pronounced differently every time it was spoken [33].

Localized lesions in the cerebellum yield effects throughout the brain via its network connections [1]. Patients with cerebellar damage failed to control their thought process, as the cerebellum plays a crucial role in regulating cognitive processes [8,34]. Although ASD is behaviorally defined, brain structural differences may be implicated. In neuroimaging and neuromodulation studies, specific sub-cerebellar regions differences have been associated with ASD, both in humans and animal studies [7,10,21,23]. Van Overwalle et al reported decreased cerebellar volume in the posterior vermis, bilateral Crus II and right VI and Crus I/II in children with autism, that correlated with social interaction and communication scores. Reduced gray matter volume has been found in the posterior vermis, Crus I/II, inferior cerebellar vermis (lobule IX), left lobule VIII B and right Crus I in autism. ASD children also displayed differences in cerebellar activation in lobule VII, including Crus I/II. Among other differences, cerebellar volume and reduced grey matter volume, white matter and activation in specific cerebellar regions have been observed in ASD patients compared to controls [7,10,35–37].

Studies also documented a significant reduction in Purkinje cells in the autistic brains [38–41]. Understanding how these cerebellar dysfunctions are associated with neuroinflammation and neuroimmune alterations seen in ASD, would contribute to targeted intervention strategies.

*Cerebellar astroglial involvement in ASD*

Reports from our laboratory and others, and postmortem and genomic studies, demonstrated neuroinflammation with increased pro-inflammatory cytokines, astrocytic and microglial activation in brains of animal ASD models and ASD patients [42–45].

#### *Cerebellar astrocytes involvement*

Astrocytes, the most numerous glial cell type and accounting for one third of brain mass, are involved in the maintenance of the blood–brain barrier (BBB), regulation of water, ion homeostasis and amino acid neurotransmitter metabolism, as well as energy and nutrient support of neurons. Neuron–glia bidirectional communication is associated with the proliferation, migration and differentiation of neural precursor cells and is essential for normal functioning of the brain during early neurodevelopment and throughout life. Altered expression of astroglial markers, such as GFAP, aquaporin-4 (AQP4), and connexin 43 (CX43) have been reported in postmortem studies of ASD patients [46–48]. During neuroinflammation, GFAP expression is upregulated when astrocytes are hypertrophic and proliferate. Other studies in animal models of ASD have also reported an upregulation of *GFAP* gene expression, and an increase in GFAP protein level in the cerebellum [44,46,47,49,50]. Mounting evidence has illustrated that glial cells have a key role in synaptic pruning through phagocytosis in health and disease [51–55]. To uncover the involvement of glial phagocytosis in synaptic pruning, Morizawa et al., created a genetic strategy for visualizing phagocytic events [56]. In naive healthy mouse cerebellar cortex, they found that Bergmann glia (BG) has a high phagocytic capacity and the BG engulfment of neuronal structures, spines and the dendrites were characterized by three-dimensional electron microscopy (3D-EM) analysis. Mice undergoing cerebellum-dependent motor learning, tissue examination revealed enhancement of nibbling of both presynaptic and postsynaptic structures by BG, including postsynaptic spine volume reduction [56].

CX43 is a major protein component in the astrocytic gap junctions and is primarily expressed in BG in the cerebellum. CX43 is responsible for regulating cellular growth and cell–cell adhesion, which also allow for gap junction intercellular communication between cells to regulate cell death, proliferation, and differentiation. Studies reported a higher expression level of CX43 in ASD patients [57], which could suggest enhancement of glial–neuronal communication in the brain. Cx43 on astrocytes can be involved in influencing neurotransmitter transport, thus inhibiting hyperactivation of the nervous system [58]. Cx43-mediated gap junction overactivation can trigger excitotoxicity, neuroinflammation and other pathological conditions [59,60]. Excitation/Inhibition (E/I) Imbalance has been observed in patients with ASD, generally there is less inhibition to balance the overexcitation [61,62]. Abnormal Cx43 expression causes (E/I) Imbalance and excitotoxicity which in turn can substantially hamper synaptic pruning through triggering synapse loss, disturbing neural connections, causing network dysfunction, and contributing to neurological disorders [63,64]. However, conflicting findings report that CX43 decreased as a result of AQP4 depletion [65]. Earlier findings enable us to assume that correcting the AQP4 changes in the brain could also lead to the normalized function and expression of CX43 in the gap junctions.

We hypothesize that reactive astrocytes and alterations in GFAP, AQP4 and CX43 expression in the cerebellum not only compromise the neuron–glia communication but also facilitate and aggravate the effects of neuro-inflammation, edematous condition and hinder synaptic sprouting during early development. Cerebellar abnormalities may also be responsible for dysfunctions within the motor system associated with autism. Understanding the effects of astrocytes and especially how the alterations in any of the GFAP, AQP4 or CX43 markers in the cerebellum may contribute to the development of therapeutic advances in ASD patients.

AQP4 is widely expressed in astrocyte terminal feet enwrapping blood vessels that constitute the blood brain barrier (BBB) and is the most abundant water channel in the CNS. AQP4 has many functions, especially in a developing brain, such as accelerating cell migration by facilitating the transmembrane water fluxes that mediate migrating cells rapid changes in shape and volume as they

move through a developing brain [66]. Decreased cerebellar AQP4 expression may mean that the cell structure, cell volume and ionic homeostasis are compromised.

In addition, AQP4 regulates the water transport in various organs such as the formation of cerebrospinal fluid in the brain, formation of urine and aqueous humor of the eye [67–69]. As reported, water accumulation was greater in AQP4 knockout mice than in wild type mice in brain tumor edema and vasogenic edema [70,71]. Bloch et al., 2006 [72] demonstrated that the brain swelling was accelerated in obstructive hydrocephalus condition in AQP4 null mice. Studies also report AQP4's involvement in seizures, as seizures duration and their intensity increased in AQP4 deficient mice [73]. This phenomenon is supported by studies showing that delayed K<sup>+</sup> reuptake by AQP4 deficient astrocytes leads to neuroexcitation [73,74]. In addition to synaptic alterations, dysregulation of AQP4 leads to compromised brain homeostasis and BBB development and BBB breach that have been associated with autism and Fragile X through overlapping pathways of neuroinflammation and synaptic dysfunction [75].

Furthermore, several studies support the hypothesis that AQP4 has a key role in regulating synaptic plasticity, including compelling data suggesting a promising link between defective long-term potentiation (LTP) and the downregulation of glutamate transporter-1 (GLT-1), with AQP4 and GLT-1 co-localized expression [76–83]. Zhang et al and others have evidenced that decreased GLT-1 expression in AQP4-null mice which lead to the reduced glutamate uptake by astrocytes [83,84].

Another potential mechanism that could be linked to synaptic plasticity and learning and memory impairment is that AQP4 deficiency promoted a decrease in BDNF signaling [85,86]. Studies found that the release of mature BDNF leads to LTP [87], and the inhibition of LTD [88], hence, the delayed LTP in AQP4<sup>-/-</sup> mice was a remarkable finding [76]. These data suggest a tight control of BDNF release for either LTP or LTD and that BDNF release in adaptable synaptic plasticity may be modified by AQP4.

Broad opportunities remain for the development of AQP4-based diagnostics and therapeutics. Several anti-epileptic drugs, including zonisamide, lamotrigine, phenytoin, and topiramate, were also found to inhibit AQP4 [89]. In addition, 2-(nicotinamide)-1,3,4-thiadiazole (TGN-020) appears to be a more selective inhibitor and has demonstrated promising results in preclinical studies [90]. Inhibitors of AQP4 and small molecule aquaporin modulators are predicted to reduce brain swelling in cytotoxic edema, potentially offering neuroprotection following brain injury, ischemic stroke, epilepsy, infection, neuroinflammation and thus could also alleviate ASD symptoms.

#### *Cerebellar microglia, macrophage, monocyte and neutrophil involvement*

Previous reports have documented increased microglia and Bergmann glia reactivity within the PC layer and accompanying white matter in ASD patients' brain. Activated microglia are detected in the vicinity of degenerating PCs and granule cells [44]. The microglia and astrocyte activation extends beyond the cerebellum to mid-frontal and cingulate gyrus as measured by the increased expression of cell surface major histocompatibility complex molecule HLA-DR and glial fibrillary acidic protein. Activated microglia and astrocytes are also accompanied by monocyte and macrophage accumulation. Such accumulation may underlie the phagocytic capacity of synaptosomes by human macrophages derived from peripheral blood monocytes, macrophage polarity [91]. Higher microglia activation in white matter is detected in ASD individuals with a history of epileptic seizures compared to non-epileptic ASD population. The microglia activation results in increased production of several cytokine and chemokines such as interleukin (IL-6), transforming growth factor beta 1 (TGFβ1), C-C motif ligand 2 (CCL2), and CCL17 [44,92–94]. Gene expression analysis from ASD patients further confirms a significantly increased and/or activated MET, NF-κB, IL-1 receptor, TOLL, and TNF receptor 2 immune system-related genetic pathways. Whether the altered immune activity is causal or in response to the neuronal damage induced during early onset of ASD is unknown [95]. Beyond cerebellum, the immune activation is also a hallmark factor that is compounded with elevated plasma cytokine levels (IL-1β, IL-6, IL-12, and TNFα), immunoglobulin levels, complement

proteins and chemokines (CCL2, CCL5, CCL11) within the periphery. The natural killer cells, monocytes and T cells that show higher activation in response to immunological challenges disrupt cellular functions in ASD patients in parallel to decreased production of regulatory cytokines such as TGF $\beta$ 1 and IL-10 implying a shift in inflammatory profile [96–99]. The high production of cytokines also correlates with higher activation of monocyte, macrophage, mast cells and microglia [100]. Applying CIBERSORT algorithm, Li et al., [101] showed that ASD patient group exhibit a significantly higher estimated proportion of resting/activated dendritic cells, M0/M2 macrophages, and monocytes in children and M0 macrophages, resting mast cells, and resting/activated NK cell group in adults with a higher percentage or increasing trend of apoptosis in monocytes [102]. Preclinical animal models support clinical studies especially with respect to monocyte infiltration [103] and neutrophil density [104]. We have previously shown increased microglial activation in the Sema3F-KO mouse model of autism [45]. The idiopathic BTBR autism mouse model that exhibits ASD phenotypes display increased IL-33, IL-18 and IL-6 cytokines [105]. More recent results show that the brain region specific knockout of PTEN that results in macrocephaly, motor coordination defects, cellular hypertrophy and autistic phenotype in mice show enhanced phagocytic capacity of microglia and aberrant microglia activation [106]. Beyond glial activation, children with ASD exhibit a higher neutrophil to lymphocyte ratio (NLR) primarily mediated by acute immune infections, autoimmune diseases [107] and superoxide dismutase mediated dysregulated enzymatic antioxidant network [108]. In summary, both human and mice with ASD phenotype show increased generalized and cerebellar microglia activation that leads to altered cytokine and chemokine levels, and enhanced monocyte and macrophage accumulation and higher neutrophil density.

Several immune-regulating compounds have demonstrated a potential effect decreasing some of the inflammatory ASD symptoms. Several anti-inflammatory compound such as a COX2 inhibitor (Celecoxib) and inflammatory cytokines inhibitor (Pentoxifyllin) have been shown to improve social deficits but have not yet been proven as significant therapies [109–112].

#### *Neurotransmitters and cerebellar connectivity association with ASD*

The neurobiological characteristic of ASD comprise abnormal synaptic connectivity, imbalances in excitatory inhibitory signaling, and alterations in neurotransmitters such as glutamate, gamma aminobutyric acid (GABA), dopamine and serotonin [113,114]. Thus far, accruing evidence points out to the hypothesis that fundamental features of ASD emerge from irregularities in the excitatory inhibitory balance within neural circuits [115–117]. Among the neurotransmitters involved, the abnormal signaling of Glutamate and GABA have been steadily reported to be the most affected in ASD [118–120]. A study by Purcell et al. reported a decrease in glutamatergic neurotransmission in ASD patients' cerebellum when compared to the neurotypical ones [49]. Both motor and cognitive impairment in ASD directs attention to an excitatory/inhibitory imbalance within the cerebellum [121].

#### *Cerebellar coordination of cerebral activity involvement in ASD.*

Among the main three layers of the cerebellar cortex, the outer molecular layer is composed of inhibitory neurons such as stellate cells and basket cells, and the Purkinje layer consists of inhibitory Purkinje cells. The inner granular layer is composed of both excitatory granule cells and inhibitory Golgi cells. The mossy fibers and the climbing fibers are the primary input pathways entering the cerebellum, where in the granular layer mossy fibers synapse on the dendrites of granular cells, whose axons lead to the molecular layer where they form parallel fibers [122,123]. Mossy fiber axons derive from multiple sources in the brain stem and spinal cord neurons, including pontine nuclei, vestibular nuclei, and reticular formation, providing main excitatory input to the cerebellum by synapsing onto granule cells. The granule cells then project parallel fibers, which go up to the molecular layer forming excitatory synapses onto Purkinje cells [124–128]. Parallel fibers and climbing fibers send excitatory signals to Purkinje cells projecting their neurons to deep cerebellar

nuclei neurons [129], which in turn give the cerebellar final output by incorporating both inhibitory and excitatory inputs from Purkinje cell axons, mossy fiber and climbing fibers [130].

Several anatomical studies have reported that cerebellum is interconnected with the cortex, hippocampus and amygdala, shaping cognitive, affective, and social behavior [12,37,131–134]. Coactivation of amygdala and cerebellum was reported during the demonstration of facial expressions in human subjects [135], and its connection with the cingulate cortex indicates the participation in motivational and emotional processing [136]. Studies have reported electrical stimulation of deep cerebellar nuclei in rodents to induce the release of dopamine in the medial prefrontal cortex [137–139]. Previous studies have shown that the cerebellum regulates the prefrontal cortical function and the disturbances in this cerebellar-prefrontal circuitry directs to deficits in executive functioning and social cognition in ASD individuals [37,140]. Overall, these reports show that the dysfunctions in the cerebellar cortical network, typically associated with ASD symptoms, could be linked to a compromised connectivity between the cerebellum and cortical social areas in the brain.

Earlier studies in ASD patients' cerebellum reported a decrease in PC of glutamic acid decarboxylase 67 (GAD67) mRNA, a basic enzyme converting glutamate to GABA [141,142]. On the other hand, in another study, Yip et al. found increased GAD67 mRNA expression in the cerebellar molecular layer interneurons, indicating the presence of an upregulation process to counterbalance the altered inhibition of Purkinje cells [143]. Studies have reported that deep cerebellar nuclei GABAergic neurons, which project precisely to the Inferior olive showed a decrease in GAD65 mRNA expression [144–146]. Hence, changes in GABAergic neurotransmission in the deep cerebellar nuclei could intensely disturb the Purkinje cell activity. Other studies have also reported that serotonin concentrations were altered in the cerebellum of ASD individuals [147,148]. Serotonin, an inhibitory neurotransmitter, has a significant role in neurodevelopment, neuronal survival, controlling cellular migration, proliferation, neurite outgrowth, and synaptogenesis [149–151]. Chugani et al. showed lowered serotonin levels in the thalamus and the frontal cortex accompanying with elevated serotonin concentration in the deep cerebellar nuclei using PET scanning with tracer for serotonin synthesis in ASD individuals [147,148]. Fatemi and colleagues reported that the reelin expression was decreased in the cerebellum of ASD individuals [141]. Reelin is a glycoprotein encoded by the RELN gene, that can regulate the development of inhibitory synapses, proper cortex lamination, neuronal migration during development in the cerebellum and adult life maintaining cell signaling and synaptic function [152–154]. RELN genetic alteration and single nucleotide polymorphisms (SNPs) have been reported to affect brain development and contribute to ASD [154]. Mutations in RELN gene have been found associated with individuals having ASD symptoms (SFARI Gene), as autistic postmortem brains show an impaired reelin signaling in the cortex and cerebellum [153]. RELN mouse mutants exhibit cerebellar hypoplasia, ataxia, reduced GC numbers, PC migration deficits, with motor coordination, and balance deficits, co-relating with human RELN mutations with intense cerebellar hypoplasia [155,156].

Multiple drugs modulating neurotransmitter's function are currently under study or at different stages of clinical trials. Baclofen and Arbaclofen, selective GABA-B agonists, appear to improve ASD-relevant behavior [157,158]. Serotonin receptors antagonists such as Risperidone and Aripiprazole or SSRI drugs such as Clomipramine and Fluoxetine are in clinical use and show improvement in aggression, anxiety and obsessive behavior [111]. Memantine, a noncompetitive NMDA antagonist, shows improvement in language function, social behavior, self-stimulatory behavior and hyperactivity [111,158]. Several metabotropic mGluR antagonists (Fenobam, JNJ16259685, MPEP) improve social behavior and reduce repetitive behavior [111,159]. In conclusion these findings spotlight the vital role of GABAergic neurotransmission, GAD enzymes, reelin and serotonin concentration in the cerebellum of ASD patients, however more studies are required to better assess the mechanisms underlying excitatory and inhibitory imbalance in ASD.

Taken together, these observations suggest that these cerebellar processes are the center of active chronic neural dysfunction in ASD. Elucidating potential cerebellar signaling pathways disrupted by ASD and affecting cerebellar circuitry, could provide promising therapeutic interventions.

#### *Cerebellar signaling involved in ASD pathogenesis.*

Studies highlight the cerebellum as a pathological brain area in ASD patients, as hundreds of identified and validated autism genes have been shown to have important functions in cerebellar development and could provide precise molecular targets for the treatment of ASD symptoms [13,160–163]. Multiple genes mutation can lead to dysregulation of signaling pathways that may affect cerebellar development, synapse function, elimination or plasticity, and could interact to lead to variable intensity of ASD symptoms. Manipulating these pathways may connect them more specifically to certain phenotypes and allow mitigation of ASD symptoms.

#### *Mammalian target of rapamycin (mTOR)*

The mammalian target of rapamycin (mTOR) signaling pathway is an important regulator with a critical role mediating various cellular processes involving protein synthesis and synaptic plasticity [164,165]. The PI3K/Akt/ mTOR pathway is expressed as two types of complexes, mTORC1, controlling cellular metabolism and autophagy, and mTORC2, controlled by TSC1/2 (tuberous sclerosis complex 1 and 2) and up-stream PI3K signaling. mTORC2 Akt phosphorylation results in mTORC1 activation. Pathogenic variants of genes of the PI-3K/Akt/mTOR signaling pathway, including FMR1, PTEN, TSC1, and TSC2, have been associated with ASD [112,166]. Reports on various neurodegenerative diseases show that overactivation of mTOR is associated with BBB disruption, enhanced ROS, superoxide and eNOS uncoupling, and exacerbate patients' vascular cognitive impairment and worsen the disease [167,168]. In a normal brain, mTOR regulates BBB integrity by inhibiting the downstream effector of mTOR, rpS6, reducing superoxide production and enhancing NO production [169]. We and others have previously reported increased BBB permeability, neuroinflammation, oxidative stress, and iNOS expression in the Sema3F KO and the BTBR pre-clinical models of ASD [45,170]. Multiple studies report that enhanced mTOR signaling may play a significant role in the pathophysiology of ASD and that pharmacological intervention with mTOR signaling could rescue behavioral ASD symptoms as well as some ASD-related brain morphological changes [171–173]. Mitigating mTOR with rapamycin in a mouse model of Alzheimer's disease (AD) improves cognitive function, cerebral blood flow and microvascular endothelial function [174–178]. Altogether, the neuroinflammatory response associated with BBB breach, mTOR activation and abnormal trafficking of BBB tight junction proteins could promote BBB dysfunction in ASD.

The level of cerebellar contribution to the pathogenesis of ASD still remains unclear. Tuberous Sclerosis Complex (TSC) is a genetic disorder with increased proportions of co-morbid ASD consequences of mutation of either *TSC1* or *TSC2*, whose protein products dimerize and negatively regulate mTOR signaling [179]. TSC mutation is an interesting model to study the cerebellar involvement in the underlying pathogenesis of ASD, as recent reports in TSC patients reveal cerebellar pathology and associate cerebellar pathology with increased ASD symptomatology [180–182]. Although, *Tsc1*'s roles and its dysfunction in the cerebellum have not been well explored, Tsai et al., show that both heterozygous and homozygous loss of *Tsc1* in mouse cerebellar PCs results in autistic-like behaviors, including abnormal social interaction, and repetitive behavior [183]. They also found that treatment of mutant mice with the mTOR inhibitor, rapamycin, reversed the pathological and behavioral deficits. Thus, PC *Tsc1* mutants can deliver a study model to explore the effects of PC dysfunction on neuronal networks and other mechanisms causative of ASD pathogenesis, to assess potential therapeutic strategies attenuating the effect of mTOR overactivation and BBB dysfunction and that could further be used to alleviate the cognitive dysfunction and behavioral impairment in children with ASD. However, mTOR inhibitors also depress autophagy and have some immunosuppressive effects, impairing Treg cells differentiation, therefore may not be applicable to

ASD populations unless some concomitant treatment alleviates this side effect [112]. It is important to study different ASD models using pharmacological mTOR inhibitor, rapamycin and /or a specific amino acid diet aimed at attenuating mTOR signaling pathway in the cerebellum.

#### *Additional ASD-linked genes associated with cerebellar development.*

Mutations of the gene encoding the chromatin remodeler chromodomain helicase DNA-binding protein 8 (CHD8) are substantial risk factors for ASD [184,185]. Patients with CHD8 mutations regularly display cognitive deficits, gastrointestinal illnesses, anxiety, macrocephaly, craniofacial abnormalities, in addition CHD8 also regulates the expression of ASD risk genes associated with synaptic function and neurodevelopment [186–188]. A study reported by Kawamura et al reveals CHD8 plays a critical role in cerebellar development, with its substantial associations of this brain area to manifest ASD symptoms [189]. The study shows that the removal of the CHD8 in neural precursor/stem cells or granular neuron progenitor (GNP) specific deletion of CHD8 in mice, results in cerebellar malformation and motor function defects. Additionally, they uncovered CHD8 regulation of local chromatin accessibility, thus activating the expression of several neuronal genes in GNPs. Engrailed homeobox 2 (EN2) has a crucial role in the early and late embryonic development of cerebellar neurons as mice deficient of EN2 exhibit abnormal cerebellar development [162,190]. A few studies have found a genetic correlation between the gene encoding the transcription factor EN2 and autism, as the EN2 knockout mice exhibit behavioral impairments that are related to autism, including social deficits and increased grooming [163,191–193].

Several studies have reported that transcription factors such as forkhead box 2 (Foxp2) and RAR-related orphan receptor alpha (ROR-alpha) are crucial for the cerebellar PC development [194,195]. Foxp2 gene deficient mice and mice model with language disorders show impairment in cerebellar cell development, migration, cell morphology and cerebellar synaptic deficits, impaired motor learning [196–198]. Foxp2 gene mutations in humans cause developmental speech and language deficits are associated with autism (SFARI Gene, Autism KB).

A study by Li et al., suggests that Jun proto-oncogene (JUN) and platelet derived growth factor receptor alpha (PDGFRA) are critical genes in the cerebellum of individuals with ASD [199]. They have indicated that the activation of cerebellar JUN and PDGFRA in ASD children may be significantly associated with the inflammatory response, as they have highlighted the role of the IL17 signaling pathway in the activation of the immune response in ASD. In addition, JUN plays an important role in the BBB integrity and function and with the release of a variety of inflammatory mediators including IL-6, IL-1 $\beta$ , TNF- $\alpha$  etc., as it regulates the transcription of proinflammatory genes [200,201].

Further investigations are needed to explore this area and provide more insights into the molecular mechanisms underlying these altered pathways in cerebellum, and how they relate to ASD, to enable novel therapeutic strategies.

## **Conclusion**

Several studies have reported that the cerebellum is an important brain area that affects ASD pathology [13,161,202]. Additionally, the concurrence of early behavioral defects in ASD, including motor, cognitive, and behavioral impairments, suggests that the cerebellar abnormalities are an important factor affecting individuals with ASD [202]. More studies need to be conducted to explore the cerebellum pathology and its impairment to the ability to coordinate the communication between neuronal groups in social, cognitive, and corticostriatal networks, thus the appearance of autistic behaviors in children with ASD. Molecular studies to evaluate the therapeutic efficacy of different compounds targeting interventions including both pharmacological and dietary aspects, may offer a new approach in the management of ASD.

Further investigations are needed to better understand the complex interactions between social brain areas, connectivity, frequency bands, and physiological aspects (i.e., roles of specific cell types, maturational processes, receptors) and how they relate to different cognitive processes.

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