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INTERPLAY BETWEEN IMMUNITY AND AMYOTROPHIC LATERAL SCLEROSIS: CLINICAL IMPACT

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Abstract

Amyotrophic lateral sclerosis (ALS) is a debilitating and rapidly fatal neurodegenerative disease. Despite decades of research and many new insights into disease biology over the 150 years since the disease was first described, causative pathogenic mechanisms in ALS remain poorly understood, especially in sporadic cases. Our understanding of the role of the immune system in ALS pathophysiology, however, is rapidly expanding. The aim of this manuscript is to summarize the recent advances regarding the immune system involvement in ALS, with particular attention to clinical translation. We focus on the potential pathophysiologic mechanism of the immune system in ALS, discussing local and systemic factors (blood, cerebrospinal fluid, and microbiota) that influence ALS onset and progression in animal models and people. We also explore the potential of Positron Emission Tomography to detect neuroinflammation in vivo, and discuss ongoing clinical trials of therapies targeting the immune system. With validation in human patients, new

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DECLARATIONS

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evidence in this emerging field will serve to identify novel therapeutic targets and provide realistic hope for personalized treatment strategies.

Keywords

immunity; inflammation; amyotrophic lateral sclerosis; biomarkers; targeted therapies; target

Introduction

Amyotrophic lateral sclerosis (ALS), the most common form of motor neuron disease (MND), is a debilitating and rapidly fatal neurodegenerative disease. It is characterized by progressive degeneration of upper and lower motor neurons with severe functional impairment (Hardiman et al., 2017). While marked phenotypic variability exists, ALS commonly begins insidiously with focal weakness and spreads to involve most skeletal muscles, including the diaphragm (Goutman, 2017). The incidence of ALS is between 0.6 and 3.8 per 100, 000 person-years, and the prevalence is between 4.1 and 8.4 per 100 ,000 persons (Chiò et al., 2013; Longinetti and Fang, 2019; Nelson et al., 2018). Incidence increases with age. Most cases of ALS are adult-onset (median age between 51 and 66 years) and sporadic, with proven evidence of familial disease in less than 20% of cases (Hardiman et al., 2017). Effective treatments remain elusive, and there is no available treatment capable of stopping the neurodegeneration or clinical progression of ALS. In the European Union (EU), only riluzole is currently approved for ALS disease modification, and in the United States of America (USA), only riluzole and edaravone are approved. Other candidates have failed to show efficacy in prior trials, though a number of candidate drugs are currently in clinical trials (Chiò et al., 2020).

Jean-Martin Charcot first described ALS in 1869, but exploration of the pathogenesis of ALS made a leap forward in 1993 with the discovery of ALS-causative mutations in the copper/zinc superoxide dismutase (SOD1) gene and the generation of reliable transgenic animal models (Gurney et al., 1994; Rosen et al., 1993). Nowadays, it is well established that some pathogenic mechanisms, such as protein misfolding, oxidative stress, impaired axonal transport, alterations in RNA metabolism and protein homeostasis, mitochondrial and cytoskeletal dysfunction, and defects in nucleocytoplasmic transport are central mechanisms underlying ALS. As with other neurodegenerative diseases, ALS pathogenesis is at least partially non-cell-autonomous, involving astrocytes, oligodendrocytes, microglia, and various peripheral immune cells (Mejzini et al., 2019; Taylor et al., 2016).

In recent years, considerable evidence has begun to support the hypothesis of an important role of neuroinflammation in ALS pathophysiology. Overall, the data from human studies suggest that we can detect imbalances in components of the immune system that allow: 1) differentiation of people with ALS from controls, 2) identification of subsets of patients with specific genotype/phenotype features, 3) improved prognostication, and 4) monitoring of disease progression (Beers and Appel, 2019). The role of the immune response in ALS has been demonstrated on several levels, from *in vivo* imaging studies in mouse ALS models to ex vivo analyses that revealed changes in activation of astrocytes and microglia already

in presymptomatic phases, as well as to recent discoveries showing involvement of several genes directly linked to the immune response (Béland et al., 2020; Cirulli et al., 2015; Freischmidt et al., 2015; Lai and Ichida, 2019; Maruyama et al., 2010). Early evidence of neuroinflammatory responses in human ALS brain has also been reported in autopsy studies for both sporadic and chromosome 9 open reading frame 72 gene (C9orf72) mutated patients (Brettschneider et al., 2013; Kawamata et al., 1992; Sasaki, 2011). Likewise, neuroimaging studies utilizing Positron Emission Tomography (PET) with 18 kDa translocator protein (TSPO) tracers have allowed the identification of in vivo neuroinflammatory responses and microglial activation (Turner et al., 2004; Zürcher et al., 2015).

A better understanding of the role of immunity and inflammation in ALS pathogenesis can have several positive repercussions. Not only can it support the identification of new biomarkers for diagnosis and for the precise tracking of immune responses from preclinical to clinical disease stages, but it can also offer an innovative avenue to identify therapeutic drugs and precision medicine opportunities. This paper is based on an extensive review of the literature and our multidisciplinary knowledge on this topic. Herein, we summarize the molecular mechanisms of immune dysregulation in ALS, the role of the major immune cell players, and the insights from in vivo modulators of inflammation and in vivo biomarkers of immune activation. We finally present an overview of emerging immune-targeted emerging drugs and cellular therapies for ALS.

Molecular mechanisms of immune dysregulation in ALS

The biological mechanisms underpinning immune dysregulation in ALS are still being elucidated. Of particular interest is the unresolved chicken-egg dilemma of the link between neurodegeneration and neuroinflammation. The predominant understanding is that neuroinflammation is secondary to neurodegeneration. Neuroinflammation then in turn serves to amplify damage, particularly at advanced disease stages when proinflammatory factors prevail (Chiot et al., 2019). Indeed, the evidence from >25 ALS-linked genes supports the idea that the aforementioned pathogenic mechanisms, such as dysfunction in proteostasis, axonal transport, RNA metabolism, mitochondria, the cytoskeleton, and nucleocytoplasmic transport, originate in neurons (Brown and Al-Chalabi, 2017; Hardiman et al., 2017). Subsequently, neuronal pathology, even at the very early stages of the disease, serves to activate the immune system. For example, damaged neurons or their products such as aggregated TAR DNA-binding protein 43 (TDP-43), a pathological hallmark in >95% of ALS cases irrespective of genetic background, and aggregated SOD1, found in ALS patients carrying mutated SOD1, induce microglial activation, which can become neurotoxic by itself (Boillée et al., 2006; Swarup et al., 2011; Roberts et al. 2013).

The second hypothesis that dysregulated immune and/or inflammatory responses could in some cases be an initial trigger and precede neurodegeneration has only recently begun to be explored in greater detail. This is particularly due to the fact that several recently researched ALS-linked genes have been shown to be direct immunomodulators. These include genes that encode for C9orf72, cylindromatosis protein (CYLD), TANK-binding kinase 1 (*TBK-1*), and optineurin (*OPTN*) (Cirulli et al., 2015; Freischmidt et al., 2015; Maruyama et al., 2010; Renton et al., 2011).

Similarly, an interleukin (IL)-6 receptor (IL-6R) polymorphism (Asp358Ala), has been linked with higher IL-6 and IL-6R levels, potentially acting as a disease modifier (Wosiski-Kuhn et al., 2019). It is notable that both excessive and ineffective immune responses have been linked with these genes, and that most of them also participate in some other cellular pathways such as autophagy, so it is still difficult to discern which of their functions is most important for ALS pathogenesis. A more detailed discussion of the dilemma on primary or secondary role of immune system dysfunction in ALS is out of the scope of this review, but can be found in our previous article (Béland et al., 2020). Here it is important to emphatize that the evidence on the involvement of the immune system in ALS exists at multiple levels: 1) protein aggregates associated with ALS can directly activate innate immune damage sensors, 2) most ALS-linked genes encode for multifunctional proteins, and some of their functions affect immune pathways, 3) there is a strong positive feedback between various ALS-linked pathogenic processes and inflammation, including mitochondrial damage, ER stress, and lack of proteasomal and/or autophagic degradation, 4) inflammaging, one of the most important ALS risk factors linked to advanced age, contributes to proinflammatory skewing, 5) gut microbiota influence immunity and subsequently the neurodegenerative process, and finally, 6) some of the newly discovered ALS-linked genes are direct modulators of innate immune responses and are expressed at the highest levels in myeloid cells (Beers and Appel, 2019; Béland et al., 2020; Franceschi et al., 2018; Lyon et al., 2019; McCauley and Baloh, 2019). Therefore, although it is sometimes difficult to unequivocally pinpoint immune dysfunction as primary, secondary or concomitant to neuronal damage, it is evident that it occurs at multiple levels and early in the pathogenic process, thus opening potentially important therapeutic avenues.

Key immune cell players

A large body of evidence in ALS patients and animal models demonstrates a prominent role of innate and adaptive immunity in modulating the course of the disease (Beers and Appel, 2019; Béland et al., 2020; Lyon et al., 2019; McCauley and Baloh, 2019). The principal immune cells in the central nervous system (CNS) are microglia - the only resident parenchymal immune cells (Kettenmann et al., 2011). Microglia arise from yolk-sack hematopoietic progenitors, rely on signaling through colony stimulating factor 1 receptor (CSFR1) for their development, maintenance, and renewal, and are not exchanged by bloodderived monocytes in healthy CNS (Askew et al., 2017; Elmore et al., 2014; Ginhoux et al., 2010; Weimer et al., 2019). Microglia are usually described in two states – resting and activated. The resting microglia, contrarily to their name, are highly active in screening the microenvironment and participating in synaptic pruning, neurogenesis, and modulation of neuronal networks, which do not induce inflammatory responses (Nimmerjahn et al., 2005). Microglial activation and subsequent inflammatory responses are triggered in response to CNS damage (neuronal debris, extracellular ATP, and/or aggregated proteins) detected through numerous damage sensors, such as Toll-like receptors (TLRs), cytosolic DNA/RNA sensors, triggering receptor expressed on myeloid cells 2 (TREM2), receptor for advanced glycation endproducts (RAGE), P2 purinergic receptors, or complement and scavenger receptors. Activation includes shortening of protrusions, an increase in cell body size, proliferation, and higher phagocytic ability, a state collectively known as microgliosis. Microgliosis is mediated through nuclear factor κB (NF- κB), interferon regulatory factor

(IRF3), mammalian target of rapamycin (mTOR), and other signaling pathways. Depending on the extent and duration of damage, microglia get polarized to predominantly a proinflammatory or anti-inflammatory phenotype. Pro-inflammatory microglia, traditionally known as M1, secrete cytokines, such as tumor necrosis factor (TNF), IL-1β and IL-6, interferon-β (IFN-β), and chemokines CCL2 and IL-8 (chemoattractants for monocytes and neutrophils), upregulate damage sensors, and produce reactive oxygen species (ROS) and nitric oxide (NO) (Beers and Appel, 2019; Béland et al., 2020). In contrast, antiinflammatory microglia, also known as M2, suppress inflammation, downregulate some damage sensors, promote tissue regeneration via cytokines IL-4, IL-13, and IL-10, and phagocytose cell debris and aggregated proteins, in part due to upregulation of scavenger receptors YM1 and CD206 (Gravel et al., 2016). Apart from microglia, several other macrophage populations populate meninges, perivascular spaces, and the choroid plexus (Goldmann et al., 2016). Meninges and abluminal perivascular spaces also harbor mast cells, whose number increases in ALS (Graves et al., 2004). Due to their granules prepacked with histamine, serotonin, and other mediators, and their ability to rapidly secrete cytokines, mast cells represent the early sentinel cells in the CNS that crosstalk with microglia to orchestrate an inflammatory response (Jones et al., 2019). While the fine role that would distinguish macrophages and mast cells from microglia in CNS tissue during ALS is still unclear, macrophages and mast cells clearly exert more prominent roles in peripheral nerves, as they are located in close proximity to axons and nerve terminals (Gupta and Harvima, 2018).

Although not immune cells per se, astrocytes and blood brain barrier (BBB) endothelial cells also represent an important source of immunologically relevant factors. Microglia have been shown to influence the functions of reactive astrocytes, driving astrocyte phenotype from neuroprotective to neurotoxic (Ferraiuolo et al., 2011; Filipi et al., 2020; Johann, 2017; Liddelow and Barres, 2017; Pehar et al., 2017; Sofroniew, 2015). Conversely, astrocytes release molecules (including TGF-β) that regulate microglial functions. Specifically, in response to activated microglia, astrocytes downregulate neuroprotective growth factor production, decrease glutamate excitatory amino acid transporter 2 (EAAT2), decrease lactate supply, and secrete proinflammatory cytokines, chemokines, and components of the complement pathway, thus amplifying pathological inflammatory signalling. This leads to astrogliosis and triggers excitotoxicity and disease progression. As homeostatic cells in the CNS, astrocytes are also involved in the modulation of oxidative stress, which is pivotal for inducing or perpetuating astrocyte-mediated inflammation (Filipi et al., 2020; Johann, 2017; Lee et al., 2016). Therefore, the bidirectional crosstalk between microglia and astrocytes has been shown to be crucial for the maintenance of a pro-inflammatory environment under pathological conditions (Burda and Sofroniew, 2017; Jha et al., 2019; Liddelow and Barres, 2017; Vainchtein and Molofsky, 2020). However, despite the attention given to the pro-inflammatory roles for astrocytes, there is mounting evidence supporting their ability to mediate a wide range of compensatory (protective) responses, including those aimed at mitigating inflammation (anti-inflammatory response), protecting against redox stress (antioxidant response), increasing small heat shock protein expression, and promoting protective and repair processes (Apolloni et al., 2017; Brambilla et al., 2016; Filipi et al., 2020; Gorter et al., 2019; Johann, 2017). Astrocytes form the BBB together with CNS endothelial cells, and astrocyte-derived growth factors, cytokines, and extracellular vesicles

directly influence endothelial cells. Endothelial cells are the source of various angiogenic factors, adhesion molecules, and chemokines important for regulating CNS oxygen and nutrient delivery, as well as selective entrance of blood-derived cells. In response to proinflammatory cytokines derived from astrocytes and microglia during ALS progression, endothelial cells upregulate adhesion molecules, such as intercellular adhesion molecule-1 (ICAM-1), vascular adhesion molecule (VCAM), and E-selectin, and expose chemokines at their surface, thus facilitating peripheral cell infiltration (Alexianu et al., 2001; Evans et al., 2013). ALS is also marked by damage to the BBB and/or brain spinal cord barrier (BSCB), as evidenced by endothelial cell degeneration, loss of tight junction proteins, astrocyte endfeet swelling, microhemorrhages, and increased permeability, with some reports suggesting that this precedes motor neuron damage (Garbuzova-Davis et al., 2019, 2007; Zhong et al., 2008).

The damage encountered in chronic neurodegenerative disorders exceeds the capacity to be repaired by the resident CNS cells. Therefore, during the neurodegenerative process, microglia and astrocytes orchestrate a network of peripheral immune cells (Beers and Appel, 2019; Béland et al., 2020). Some of these cells then infiltrate the CNS, such as T cells and natural killer (NK) cells, although the infiltration in ALS is limited in comparison to autoimmune CNS diseases, such as multiple sclerosis, and predominantly occurs late in the disease course. NK cells eliminate stressed cells via cytotoxic granules or Fas ligand (Orr and Lanier, 2010). Furthermore, by producing IFN-γ, they can influence microglia and macrophage polarization toward a proinflammatory phenotype, and suppress regulatory T cells (Tregs), thus influencing both innate and adaptive immunity. NK cells, which are absent from healthy CNS, in ALS accumulate in motor cortex, spinal cord, and muscles, contributing to disease progression (Garofalo et al., 2020). Other notable immune subsets that take part in ALS pathogenesis, such as monocytes, neutrophils, and dendritic cells (DCs), have no access to the CNS in health and have limited access during ALS. In contrast, they exert important roles in peripheral nerves and meninges. The role of DCs in ALS is perhaps less clear due to difficulties in telling them apart from other myeloid lineage cells, especially macrophages, given their shared origin from blood monocytes. DCs are also absent from healthy CNS parenchyma, but can be found in meninges. Some reports suggested that DC numbers decrease in peripheral blood and increase in ALS lesions (Henkel et al., 2004; Rusconi et al., 2017; Sta et al., 2011), but this needs to be confirmed by fate-mapping studies.

In the adaptive immune system, specific roles in ALS pathogenesis have been ascribed to several T cell subsets. Usually, T cells have limited access to healthy CNS, so it was initially presumed that they are invariably noxious in ALS. However, when mouse ALS models were rendered T cell-deficient, this led to accelerated disease, demonstrating their overall protective role (Beers et al., 2008a; Chiu et al., 2008). It is notable though that individual T cell subsets have distinct functions. Neuroprotective functions have been ascribed to $CD4+CD25+Tregs$ and $CD4+Th2$ subsets, whereas $CD4+Th1$, $CD4+Th17$, and $CD8+$ cytotoxic T cell subsets are linked to an accelerated disease course (Russo and McGavern, 2016; Schwartz and Shechter, 2010). It is clear now that, in contrast to microglia that get activated in the earliest stages of ALS, infiltrating T cells contribute to later stages, with CD8+ T cells being linked exclusively to end stage disease. It is still uncertain if T cells

in ALS can exhibit some of their effects without crossing the BBB, as was previously described for protective effects of CD4+ T cells in cognitive performance (Kipnis et al., 2012). Protective effects of Tregs and Th2 T cells are at least in part due to promoting the differentiation of anti-inflammatory microglia through IL-4 and IL-10 (Appel et al., 2010). In contrast, a direct neurotoxic role of $CD8⁺$ T cells, executed by classical cytotoxic mechanisms via granzymes, Fas ligand, and IFN-γ, has been recently demonstrated in co-cultures of motor neurons with CD8+ T cells taken from a mouse ALS model at a late disease stage (Coque et al., 2019). However, in the face of a toxic effect of CD8⁺ T cells on motor neurons at late stage, these cells as well as macrophages may exert protective effect in the peripheral nerves at the early stage of the disease (Chiu et al., 2009; Nardo et al., 2018, 2016) as discussed in next section. B cells do not appear to contribute to CNS homeostasis, and their role in ALS is still puzzling. Lack of B cells does not affect progression in mouse ALS models (Naor et al., 2009). Intriguingly, immunoglobulin G (IgG) has been reported to accumulate in and/or around motor neurons (Donnenfeld et al., 1984; Engelhardt and Appel, 1990). Moreover, administration of IgG from ALS patients can be taken up and/or stimulate motor neurons, astrocytes, and microglia, increase serum and spinal cord cytokine levels, and elicit motor neuron degeneration (Appel et al., 1991; Bataveljic et al., 2014; Miloševi et al., 2017; Obál et al., 2016; Pagani et al., 2011; Pullen et al., 2004). Some of the antibodies recognize aggregated proteins and neurofilaments, but their exact pathogenic mechanism is unclear (Malaspina et al., 2015; May et al., 2014).

Effector functions of antibodies are commonly linked to activation of complement, and depositions of activated complement components are present together with antibodies in the motor cortex of ALS patients (Donnenfeld et al., 1984; Sta et al., 2011). In healthy CNS, complement proteins are tightly linked to CNS homeostasis by participating in microglia-mediated synapse pruning and other remodeling, which represent non-immune functions of the complement system (Schafer et al., 2012; Stevens et al., 2007). Whereas peripheral complement system proteins are primarily produced by liver, in the CNS neurons, reactive microglia, and astrocytes are the main source of various complement proteins in the CNS (Lee et al., 2013; Luchena et al., 2018). Complement activation, antibodydependent or independent, amplifies microglial activation, and contributes to a broad scope of neurodegenerative diseases, including ALS (Dalakas et al., 2020). Many of the immune cells and factors listed here will be further discussed in the upcoming sections as potential therapeutic targets and diagnostic biomarkers.

Immunity insights from animal models

Due to the inaccessibility of the CNS in patients, animal ALS models continue to be crucial for understanding the real timing of immune cell activation, its causal relation to neuropathology, and potential for therapeutic targeting. Among available animal ALS models (De Giorgio et al., 2019; Picher-Martel et al., 2016), those that best recapitulate most of the features of human pathology are the transgenic rodents overexpressing human SOD1 mutations (mSOD1), most commonly SOD1^{G93A}. The multiple facets of immune cell activation, from the presymptomatic to end stage of ALS, in mSOD1 mouse models at three key locations – CNS, peripheral nerves and muscle – are summarized in Figure 1.

In brief, the first immune hallmark in the spinal cord of mSOD1 mice, which precedes symptom appearance, is microglial activation, occurring in concomitance with the upregulation of chemokines (Nardo et al.2013) and release of danger stimuli (misfolded mSOD1, HMGB1 and ATP) from damaged neurons (Lo Coco et al., 2007; Urushitani et al., 2006; Volonté et al., 2003); this is followed shortly thereafter by astroglial activation (Gandelman et al., 2010). The initial predominantly anti-inflammatory microglial phenotype advances into a proinflammatory phenotype as the disease progresses (Beers et al., 2011), leading to a self-propagating hyperinflammatory and neurotoxic environment that accelerates motor neuron loss and precipitates death (Appel et al., 2010). Notably, during the disease course there is a coexistence of a continuum of the aforementioned opposite microglial fingerprints $- M1$ and $M2$ – and their prevalence depends on the surrounding cytokine milieu, which is modulated by astrocytes (Endo et al., 2015), and/or the interaction with infiltrating T cells, NK cells, and eventually monocytes and DCs (Appel et al., 2010; Chiot et al., 2020; Garofalo et al., 2020; Henkel et al., 2004).

The resulting neuroprotective or neurotoxic immune functions can be manipulated in animal models. For example, CNS delivery of IL-4 or IL-10 via viral vectors in mSOD1 mice at the presymptomatic stage enhanced the M2 phenotype in the spinal cord and delayed disease onset (Rossi et al. 2018; Beland et al. 2016). On the other hand, the deletion of TLR4, known to promote the M1 phenotype and induce motor neuron death (De Paola et al., 2016), extended survival in SOD1G93A mice (Lee et al., 2015). Transplantation of astroglial precursor cells into the spinal cord of mSOD1 mice attenuated motor neuron loss, improved motor function, and extended survival of these mice (Lepore et al., 2008). The real role of monocytes within the CNS is still unclear due to difficulties in distinguishing them from microglia and other myeloid cells. However, a progressive monocyte infiltration and their differentiation to macrophages has been consistently demonstrated within peripheral motor axons and at the neuromuscular junctions of mSOD1 mice from an early disease stage, due to the release of chemoattractants (CCL2/monocyte chemoattractant protein-1 (MCP-1)), complement (C3)-mediated opsonization of motor axons, and immunoglobulins (IgM) deposition (Chiu et al. 2009; Kano et al. 2012; Nardo et al. 2013; 2016; Wang et al. 2017). This correlated with a significant delay of symptom onset and slower disease progression in $SOD1^{G93A}$ mice (Nardo et al., 2018, 2016), and is consistent with the association between peripheral nervous system (PNS) inflammation and longer disease duration in ALS patients carrying SOD1 mutations (Schreiber et al., 2019). According to the hypothesis that muscle denervation precedes motor neuron death and disease symptoms (Fischer et al., 2004), it is believed that the initial axonal-muscle immune infiltration facilitates the removal of the degenerating axonal debris to allow a compensatory reinnervation of the muscles (Chiu et al., 2009; Nardo et al., 2018, 2016). In addition to denervation, skeletal muscle might also play an active role in NMJ dismantling and the ensuing inflammation in ALS in line with the dying back hypothesis. For example, the complement activation products C3/C3b and C1q may precedes end-plate denervation in human ALS and mSOD1 mice (Bahia El Idrissi et al., 2016; Heurich et al., 2011). On the other hand, an early immune infiltration and a macrophage skewing from a proinflammatory (M1) to anti-inflammatory (M2) in the denervated/damaged muscle might trigger an initial regenerative stage through the activation, expansion and differentiation of satellite cells (Forcina et al., 2020).

If inflammatory mSOD1 macrophages are replaced with those overexpressing wild type SOD1 at symptom onset, disease progression is further slowed down, leading to a prolonged mouse survival (Chiot et al., 2020). Similarly, deletion or pharmacological inhibition of C5a complement receptor C5aR1 after disease onset attenuated overall inflammation in the CNS, blood, and muscle of SOD1^{G93A} mice, and extended their lifespan (Lee et al., 2017; Wang et al., 2017). Mast cells and neutrophils have also been shown to progressively infiltrate and exacerbate inflammation around degenerating motor nerve endings and in skeletal muscle of ALS patients and the SOD1^{G93A} rat model after the onset of paralysis (Trias et al., 2018). Interestingly, the inhibition of mast cell degranulation induced by the pluripotent tyrosine kinase inhibitor masitinib (Trias et al., 2018, 2017), or by the mast cell stabilizer cromolyn (Granucci et al., 2019), ameliorated the clinical phenotype and CNS pathology and reduced the immune cell-mediated inflammatory response within axons and skeletal muscles of mSOD1 rodent models. Therefore, while an efficient immune response in the periphery is crucial to maintain axonal integrity and maximize connectivity with the muscle during early disease, at the later disease stages this response needs to be suppressed.

T cells have gained particular attention in ALS, as they comprise a significant proportion of the immune cells infiltrating the CNS and PNS of ALS patients and animal models (Beers et al., 2008b; Chiu et al., 2008; Coque et al., 2019; Henkel et al., 2013; Nardo et al., 2018). Tregs proved to be the most attractive T cell subset for therapeutic manipulation since their declining effector functions over the disease course affect both adaptive and innate immune responses, hampering immune tolerance and stimulating a proinflammatory phenotype that, in a vicious circle, induces further Treg dysfunction and rapid disease progression (Beers et al., 2018). Lower Treg numbers are in fact a recognized immunological fingerprint in rapidly progressing ALS patients (Beers et al., 2017; Henkel et al., 2013). Interestingly, adoptive transfer of Tregs in SOD1G93A mice (Banerjee et al., 2008) or their expansion following treatment with IL-2/anti-IL-2 monoclonal antibody complexes (IL-2c) with rapamycin, induces M2 microglia in the spinal cord and prolongs mouse survival (Sheean et al., 2018). Presymptomatic depletion of NK cells using an antibody against NK1.1 delayed the onset of paralysis and increased survival of mSOD1 mice through the activation of Treg cells (Garofalo et al., 2020). However, the same procedure applied at symptom onset was ineffective, suggesting a narrow temporal window of intervention in targeting these cells. Cytotoxic CD8+ T cell infiltrations have been reported in both ALS patients (Holmøy, 2008; Sta et al., 2011) and mSOD1 mice (Coque et al., 2019; Nardo et al., 2018), although the systemic alterations in circulating CD8+ T cells were inconsistent in ALS patients, indicating either a decrease (Mantovani et al., 2009), increase (Gustafson et al., 2017; Jin et al., 2020), or no changes (Zhang et al. 2005). Notably, the depletion of CD8+ T cells and diminished major histocompatibility complex class I expression in ALS mice reduced inflammation and motor neuron loss in the CNS (Coque et al., 2019; Nardo et al., 2018), but in the periphery exacerbated the denervation-mediated atrophy, accelerating symptom onset. These data strengthen the hypothesis that activating the immune response in the PNS in the early phase is crucial for maintaining muscle innervation and delaying disease progression (Chiu et al., 2009; Nardo et al., 2018, 2016).

The immune system has been studied in a limited number of other animal ALS models as well; however, a major caveat is the paucity of neurologic symptoms in many models.

Particularly, among the mouse models carrying ALS mutant genes associated with the immune response, including TARDBP (encoding for TDP-43), C9orf72, TBK1, and OPTN, only the TDP-43 or C9orf72 transgenic models exhibit some neurologic symptoms, and often to a variable degree (De Giorgio et al., 2019; Hayes and Rothstein, 2016). Notable similarities to SOD1^{G93A} mice were reported in transgenic mice carrying the patient TDP-43Q331K mutation under a mouse prion protein promoter (Lee et al. 2018). These mice show microgliosis, astrocytosis, and functional and morphological neuromuscular junction abnormalities well before the loss of spinal motor neurons (Chand et al., 2018; Lee et al., 2018). Importantly, like SOD1 G^{93A} mice, they also exhibit an upregulation of complement C5a-C5aR1 in the spinal cord and tibialis muscle during disease progression, validating the C5aR1 as a potential therapeutic target for ALS. Interestingly, in a reversible neuron-specific model carrying a TDP-43 deletion in the nuclear localization signal, the neuroprotective role of microglia was unleashed only upon suppression of transgene expression, whereas prior to that, neuronal TDP-43 expression inhibited microglial functions and proliferation (Spiller et al., 2018). In accordance with the newly discovered role of STING in ALS, genetic deletion or pharmacological inhibition of the STING pathway in transgenic TDP43A315T mice led to a marked reduction of proinflammatory cytokines in the spinal cord and cortex, ameliorated symptoms, and increased survival (Yu et al., 2020).

An immunologic phenotype is practically absent in unmanipulated $TBK1$ (Tbk1^{+/-}) and OPTN models (knockouts and loss-of-function mutants) (Brenner et al., 2019; Dermentzaki et al., 2019; Gerbino et al., 2020; Markovinovic et al., 2018; Munitic et al., 2013; Slowicka et al., 2016), whereas complete loss of C9orf72 leads to an autoimmune disease marked by splenomegaly, lymphadenopathy, and widespread peripheral myeloid and lymphoid immune cell activation in the absence of neurodegeneration (O'Rourke et al. 2016; Atanasio et al. 2016; Burberry et al. 2016). Instead, mice expressing 500 G4C2 repeats in bacterial artificial chromosomes, which more accurately mimic potential gain-of-function patient C9orf72 mutations (BAC-C9orf72), were initially reported to exhibit motor abnormalities and decreased survival associated with motor neuron loss, without reactive gliosis, in about 30% of females (Liu et al., 2016). However, this ALS phenotype was not confirmed by other groups (Mordes et al., 2020) and was not observed in other BAC-C9orf72 mice (Jiang et al., 2016; O'Rourke et al., 2015; Peters et al., 2015). An elevated type I interferon response mediated by the STING pathway has also been found in myeloid cells from C9orf72 knockout mice and blood macrophages and brain tissue from ALS/frontotemporal dementia patients carrying C9orf72 G4C2 hexanucleotide repeats (McCauley et al., 2020). Mice haploinsufficient for TBK1 do not develop clinical or histological signs of motor neuron degeneration up to 2 years of age (Bruno et al., 2020; Gerbino et al., 2020). However, TBK1 haploinsufficiency in SOD1G93A mice led to an acceleration of symptom onset and muscle denervation, but surprisingly in later disease stages decelerated disease progression and increased life span (Brenner et al., 2019; Gerbino et al., 2020). Overall, these data further support the hypothesis that altered function of immune cells, while not directly starting neurodegenerative processes, may substantially contribute to disease pathogenesis and progression, and/or act in synergy with other ALS risk factors.

In conclusion, studies from animal models have identified key aspects of immune system involvement in the progressive damage of the neuromuscular system in ALS. Although these

models do not fully recapitulate human disease, they have advanced our understanding of the temporal and regional impact of both local and systemic immune changes in modulating neuroimmune interactions in the CNS and PNS. Such investigations hold promise in characterizing the immune response at different disease stages, not only for the development of the right therapy at the right moment, but also to identify diagnostic and prognostic biomarkers to improve clinical trials.

Immunity insight from neuropathology in ALS

Most of the earliest observations regarding inflammatory changes in ALS are based on studies of patient autopsy material. Several studies in the early 1990s immunohistochemically analyzed the cellular composition of inflammatory infiltrate in cases of sporadic ALS, showing scattered T cell infiltration (mainly represented by a cytotoxic $CD8⁺ T$ cell subset) associated with an abundant presence of reactive microglia/ macrophages, as well as reactive astrocytes throughout the degenerating areas (Troost, Van den Oord, and Jong 1990; Smitt et al. 1992; Engelhardt, Tajti, and Appel 1993; Schiffer et al. 1996; Kawamata et al. 1992). Besides T lymphocytes, DCs and NK cells involved in the crosstalk between innate and adaptive immunity have been identified in human ALS tissues (Garofalo et al., 2020; Sta et al., 2011). Additional studies confirmed the persistent and prominent activation of both innate and adaptive immunity in human ALS spinal cord and motor cortex samples, documenting the activation of the complement system, TLR signaling, and TNF-α related pathways (Brambilla et al., 2016; Casula et al., 2011; Gorter et al., 2019; Henkel et al., 2004; Sta et al., 2011; Tortarolo et al., 2017). These and other studies have also highlighted the role of astrocytes as emerging key regulators of the inflammatory responses in several human CNS diseases, including ALS (Johann, 2017; Pehar et al., 2017; Sofroniew, 2015).

Further supporting the relationship between inflammation and ALS, several transcriptomic studies in human ALS samples have been performed to study the molecular changes associated with motor neuron degeneration in ALS spinal cord and motor cortex (Aronica et al., 2015; Dols-Icardo et al., 2020; Krokidis and Vlamos, 2018; Morello et al., 2017). A recent study using machine learning algorithms stratified the transcriptomes of a large cohort of ALS post-mortem cortex samples into three distinct molecular subgroups, including one with a predominant signature of glial activation (Tam et al., 2019). The use of recently developed spatial transcriptomic techniques further allows the study of single-cell gene expression in situ (Gregory et al., 2020; Maniatis et al., 2019). Moreover, single nucleus RNA sequencing (snRNASeq) using droplet technology can be applied to frozen brain tissue to elucidate cellular heterogeneity in human tissue (Habib et al., 2017), offering the possibility to achieve a more detailed understanding of the heterogeneous and dynamic glial phenotypes and other cellular components contributing to the inflammatory/immune response in ALS. Finally, given the rapid advances in genetic technology and knowledge in ALS, recent studies describing the glial pathology associated with specific genetic mutations emphasize aberrant interglial communication as a contributor to immune activation and related clinical phenotype (McCauley and Baloh, 2019; Rojas et al., 2014; Thangavelu et al., 2011; Velebit et al., 2020; Wallis et al., 2018).

Ex vivo analysis of immune profiles as marker of disease course variability

Clinical heterogeneity in ALS is exemplified by the significant difference in survival from symptoms onset, with a percentage of ALS individuals reaching end stage disease in less than a year and others progressing over more than a decade (Ravits and La Spada, 2009). The complexity of clinical heterogeneity is also seen in the way different outcomes can be linked to the disease phenotype at onset. For example, bulbar onset ALS is more common in women with cognitive impairment and in elderly patients and is associated with a rapidly progressive disease course (Watanabe et al., 2015), while longer survival is seen in limb onset patients (Benjaminsen et al., 2018; Longinetti and Fang, 2019; Watanabe et al., 2015). The rate of progression from disease onset is possibly the feature of ALS that has more bearing on the inflammatory response observed systemically and at a tissue level in this condition. In fact, it has been shown that the immune response has a significant influence in governing the severity in the disease progression (Beers et al., 2018; Choi et al., 2020; Murdock et al., 2016). As described above, a key point of neuroinflammation is glial activation and associations with increased levels of inflammatory mediators. Several ILs have been found elevated in CSF and/or blood of ALS patients compared to controls and/or patients with other non-inflammatory neurological disorders.

- Systemic biomarkers—Blood is an excellent biofluid for the discovery and validation of disease biomarkers. First, blood biomarkers are easily accessible, and blood analyses are repeatable over time, in contrast with CSF and imaging biomarkers due to invasiveness and high costs. In addition, the ethical implications of collecting blood samples are minor relative to CSF collection. These features further allow consideration of blood biomarkers as an excellent tool for monitoring disease-related changes. Several immunological pathways can be investigated at the serum level, and differences in the immunological asset between ALS patients and healthy controls and among ALS patients in different disease stages have been reported. However, the agreement between blood and CSF biomarkers is still debated. Overall, some studies showed a significant correlation between blood and CSF for some biomarkers, such as for growth factors, IFN-γ (Guo et al., 2017), and neurofilaments (Gagliardi et al., 2019; Wilke et al., 2019), while other works failed to detect blood biomarker changes corresponding to those in CSF (Steinacker et al., 2008). Furthermore, some blood biomarkers are generated only peripherally, and thus are not detectable in CSF.

TGF-β1 is a pleiotropic cytokine able to regulate proliferation, survival, and differentiation of many types of cells. TGF-β1 and related pathways are one of the most studied inflammatory mechanism in ALS, but the role of this cytokine during the progressive degeneration of motor neurons, and in glutamate-mediated excitotoxicity, is debated (Katsuno et al., 2011). It seems that a chronically upregulated TGF-β1 system may promote disease progression by inducing an imbalance between neurogenesis and neurodegeneration (Peters et al. 2017). Independent studies showed higher plasma levels of TGF- β1 in ALS compared to controls, and a positive correlation between TGF-β1 levels and disease duration (Houi et al. 2002; Peters et al. 2017). Coherently, the group of De Carvalho (Duque et al., 2020) observed that TGF-β1 and TGF-β3 levels had a significant negative correlation with ALS Functional Rating Scale-Revised (ALSFRS-R) scores, a marker of disease severity. Likewise, an early and progressive increase of TGF-β1 and TGF-β3 mRNA was found in the

skeletal muscle of ALS patients and mSOD mice in correlation with disease severity (Si et al., 2015). However, other studies using proteomics simultaneously in brain and blood failed to detect changes in blood TGF-β1 levels between fast and slow progressing ALS patients (Zubiri et al., 2018).

In ALS, the dysregulation of plasma inflammatory biomarkers may involve several ILs, with both pro- and anti-inflammatory functions. Ehrhart and colleagues showed significant downregulation of IL-5 and upregulation of IL-6 in blood samples of ALS patients compared to controls when collected at the first evaluation, while at the follow-up evaluation, a normalization of IL-5 and IL-6 levels associated with a decrement in IL-2 and increase in IL-8 levels (Ehrhart et al., 2015). This finding showing correlation with disease duration suggests an evolving system where specific humoral factors represent specific inflammatory and oxidative stress responses during disease progression.

Another interesting study showed significantly increased IL-6 levels, along with other ILs such as TNF-α, IL-4, IL-13, in ALS patients when compared with controls at baseline (Lu et al., 2016). In the longitudinal analysis, IL-6 increased in some subgroups of patients, including the slow progressors (showing less functional impairment), males, patients with spinal onset, and patients treated with riluzole (Lu et al., 2016).

On the contrary, another report showed that serum IL6 levels, in most patients carried the IL6R358Ala variant, negatively correlate both with the patient's functional (ALSFRS-R and subscores), and with respiratory function as measured by the percent predicted forced vital capacity (FVC) (Wosiski-Kuhn et al., 2021).

The role of TNF-α can be more controversial. Indeed, other studies showed normal or lower levels in ALS patients when compared with controls (Andrés-Benito et al., 2017; Martinez-Merino et al., 2018). These inconsistent results may be explained by the pleiotropic role of TNF-α, which can act in both pro- and anti-inflammatory responses. Contrasting results have been reported also regarding IFN- γ , which can participate in both innate and adaptive immunity. Lu and colleagues documented that $IFN-\gamma$ was significantly decreased in plasma of ALS patients compared with controls. On the contrary, other studies highlighted elevated IFN-γ in ALS blood compared to controls, showing association also with faster progression and shorter survival (Guo et al., 2017; Liu et al., 2015; Saresella et al., 2013). Finally, IL-13, a profibrotic cytokine responsible for Th2 responses in humans, has been related to worse functional performances in ALS patients, showing a negative correlation with functional abilities measured by ALRFSR-R and a significant positive correlation with the disease progression rate (Shi et al., 2007).

To date, despite the large number of cytokines that participate in the interplay of neuroinflammation in ALS pathogenesis, there is no definitive biomarker that can be singularly used in clinical evaluation. However, blood-based biomarkers have the potential to improve diagnosis and monitoring of disease progression, by increasing convenience, offering ease of testing, and reducing costs.

As previously reported in ALS animal models, modulation of specific leukocyte or myeloid populations can be involved in disease progression, making blood leukocytes attractive as

biomarkers and targets for ALS drug development. Several alterations in T lymphocyte populations have been described in ALS patients as compared with controls. While differences on the percentage of different lymphocyte populations between patients and controls are discrepant among studies, changes in Tregs are more consistent and their levels inversely correlate with the rate of disease progression. Specifically, patients with minor disease severity have higher levels of Tregs, supporting a model where Tregs actively contribute to neuroprotection through their interactions with microglia (Beers et al., 2017, 2011; Henkel et al., 2017; Thonhoff et al., 2018b). Thus, the percentage of CD4+ T lymphocytes and Tregs in the blood of patients with ALS was proposed as a biomarker for differentiating slowly progressing from rapidly progressing patients (Beers et al., 2011; Henkel et al., 2013). However, a reduction of Tregs and CD14⁺ monocytes levels in ALS patients with a less severe disease has been also reported, suggesting a possible early recruitment of these cells in the damaged regions (Mantovani et al., 2009).

The complexity of peripheral immune responses may be supported by the shift from an anti-inflammatory phenotype (Th2 and Treg) to a pro-inflammatory profile (Th1 and Th17), as revealed by several studies investigating T cell changes in ALS patients (Beers et al., 2011; Henkel et al., 2013; Saresella et al., 2013). Jin and colleagues recently confirmed this pro-inflammatory shift, showing negative correlations between Th1 and Th17 with the ALSFRS-R score and FVC (Jin et al., 2020). Murdock and colleagues analyzed peripheral blood leukocytes from ALS patients, observing a significant increase in the percentage of neutrophils and a significant decrease in the percentage of CD4+ T cells and CD16 monocytes in the blood of patients compared to controls. However, only CD16- monocyte levels positively correlated with the disease progression (Murdock et al., 2016). The same group showed increased mean counts of total leukocytes per millimeter of blood, with a prevalence of neutrophils, CD16+ and CD16− monocytes, and NK cells, and further reported that early changes in immune cell numbers (neutrophils and CD4+ T cells) had a significant direct correlation with disease progression measured by the change in ALSFRS-R score (Murdock et al., 2017). A recent study on the quantification of myeloid cell populations showed that patients with greater disease severity had a reduction in non-classical monocytes, and patients with greater bulbar involvement had a reduction in the proportions of classical, intermediate, and non-classical monocyte populations (McGill et al., 2020). Finally, the Choi group (Choi et al., 2020), hypothesizing that the neutrophil-to-lymphocyte ratio can reflect the degree of neuroinflammation in patients with ALS, confirmed a shorter survival duration in subjects with higher baseline neutrophil-to-lymphocyte ratio.

- CSF markers—CSF is considered the most dependable fluid for biological ALS markers due to its anatomical contiguity with the CNS. Several CSF biomarkers have been proposed for ALS diagnosis and monitoring disease progression, but currently, it is not entirely clear the exact added diagnostic and/or prognostic value of these markers.

In CSF, as was already shown in blood, the overall trend is an imbalance between proand anti- inflammatory cytokines, chemokines, and other mediators of the inflammatory response. Among them, the most investigated immunological biomarkers are IFN- γ , IL-6, granulocyte-macrophage colony-stimulating factor (GM-CSF), MCP-1, and IL-8 showing an increased level, and IL-10, angiogenin, and follistatin showing a decreased level (Guo

et al., 2017; Kuhle et al., 2009; Lind et al., 2016; Mitchell et al., 2009). In support of this, Mishra et al. measured various inflammatory markers in rat astroglial cultures exposed to ALS-CSF and compared with the diseased or normal controls. The ALS-CSF enhanced the production and release of inflammatory cytokines, such as IL-6, TNF-α, COX-2, and PGE-2, and induced a down-regulation of anti-inflammatory cytokines, such as IL-10, vascular endothelial growth factor (VEGF), and glial cell-derived neurotrophic factor (GDNF) (Mishra et al., 2016). Other interesting factors are IL-17, basic fibroblast growth factor (bFGF), macrophage inflammatory proteins (MIP)-1β and −1α, MCP-1β (Guo et al., 2017), IL-1α, follistatin, and kallikrein-5 (Lind et al., 2016).

Only a few studies have investigated a possible prognostic value for these biomarkers. Higher levels of IL-4, IL-10, bFGF, VEGF, and MIP-1α have been reported to associate with slower disease progression (Furukawa et al., 2015; Guo et al., 2017), and IL-4 and IL-10 were also higher in patients with prevalent lower motor neuron phenotype (Furukawa et al., 2015). Alternatively, both CSF and serum IFN-γ levels were reported to be increased in ALS patients relative to controls (Guo et al., 2017; Tateishi et al., 2010) and to directly correlate with disease duration (> 12 months) (Liu et al., 2015), with higher IFN- γ levels directly correlating with the interval from the disease onset to diagnosis, disease progression rate (Liu et al., 2015), and shorter survival (Guo et al., 2017). Likewise, higher MCP-1 levels were associated with worse disease severity and faster progression (Zhang et al., 2017). A recent study by Yang et al. described the role of the milk fat globule-EGF factor 8 (MFG-E8), an inflammatory modulator, in ALS, reporting a relatively higher MFG-E8 level in ALS patients compared to healthy controls and a negative correlation between MFG-E8 and the ALSFRS-R score (Yang et al., 2020). The group of Tateishi (Tateishi et al., 2010) discovered, among cytokines/chemokines elevated in ALS, that CCL2 and CXCL8 levels were also negatively correlated with the ALSFRS-R score, while CCL4 and CXCL10 showed a positive correlation. Additionally, CCL4 and CXCL10 showed negative correlations with disease progression rate. The concentration of TGF-β1 in CSF, however, is still debated. One previous report indicated that the TGF-β1 concentration was significantly higher in the CSF of patients with a long disease duration compared to patients with a short duration of ALS, and that there was a significant positive correlation between CSF TGF-β1 and ALS duration (Iłzecka et al., 2002). Conversely, Masuda et al. found that TGF-β1 levels in the CSF were not significantly different between ALS patients and normal controls (Masuda et al., 2017) and did not correlate with the disease course or stages. Finally, elevated IL-6 levels in CSF and serum seemingly correlate with respiratory clinical severity and hypoxia, suggesting that the cytokine levels are dependent on oxygenation and highlighting a link between hypoxia and inflammation in ALS (Moreau et al., 2005).

Recently, several researchers have focused on chitinase levels in patients with ALS. Indeed, the level of macrophage-derived chitinases, as a signal of microglia/macrophage activation, seems to be clearly increased in ALS patients, gaining interest as potential disease biomarker (Swash, 2020). In 2013, Varghese et al. first reported chitinases in the context of ALS, showing that CSF levels of chitotriosidase-1 (CHIT1), chitinase-3-like protein 1 (CHI3L1/ YKL40), and chitinase-3-like protein 2 (CHI3L2) were significantly elevated in ALS patients relative to healthy controls (Varghese et al., 2013). Increased levels of YKL40 in CSF, expressed in inflammatory astrocytes, apart from a significant increase in the

CSF of patients compared to healthy controls, correlated with disease progression (Andrés-Benito et al., 2017; Gille et al., 2019) and degree of cognitive dysfunction (Thompson et al., 2019). Similarly, the levels of CHIT1 and CHIT3L2 were elevated in patients compared to controls and to ALS-mimics, and correlated with disease progression (Gille et al., 2019; Thompson et al., 2019). However, Gille et al. reported that elevated CSF chitinases were only weakly specific to ALS compared to a control group of patients with other neurological diseases (Gille et al., 2019). CHIT1 and YKL40 are also correlated with phosphorylated neurofilament heavy chain, considered a strong marker of axonal neurodegeneration, confirming the link between neuroinflammation and neurodegeneration. Importantly, all chitinase levels are longitudinally stable and do not change over time (Thompson et al., 2019). However, a flaw of these biomarkers is the absence of correlation with blood markers, due to limited elevation in blood.

Although these studies, even with a different list of inflammatory markers tested, have individually demonstrated the potential role of a combination of fluid biomarkers for diagnosis and progression of ALS, to date we cannot conclude which represents the best one, nor we can hypothesize that a unique CSF biomarker can capture all the pathogenic processes involved in the disease. However, we contend that the idea of hypothesizing a panel of immune markers should be considered for use in both clinical practice and as a common outcome in clinical trials.

- Imaging inflammation—PET allows for imaging of neuroinflammation in vivo by administration of radioligands targeting activated glial cells. The majority of these radioligands designed to visualize neuroinflammation target TSPO (Narayanaswami et al., 2018), a protein located in the outer mitochondrial membrane that is upregulated on activated glial cells. In ALS, a temporal pattern of TSPO expression on glial cells has been suggested, with TSPO expression mainly located on microglia during early disease stages and shifting to astrocytes in a later phase (Guilarte, 2019). A multitude of TSPO radioligands have been developed and will be briefly explained in the next paragraphs.

 $[$ ¹¹C]PK11195 is the first generation TSPO radioligand and has been adopted in sporadic and familial ALS patients (Turner et al. 2004; Tondo et al. 2020). In sporadic ALS patients, increased [11C]PK11195 binding was apparent in the motor cortex, pons, frontal cortex, and thalamus (Turner et al., 2004). Similarly, in symptomatic and asymptomatic patients with SOD1 mutations, higher $\lceil {^{11}C} \rceil PK11195$ binding was observed in the motor cortex, supplementary motor area, thalamus, medulla oblongata, and the occipital and temporal lobes (Tondo et al. 2020). The latter demonstrates that neuroinflammation can be discerned during the presymptomatic stage, important for future therapeutic studies. Despite these significant findings, $[11C]PK11195$ is hampered by a low signal-to-noise ratio and low brain extraction (Best et al., 2019). These limitations led to the development of second-generation TSPO radioligands; however, while the second generation radioligands have a higher signalto-noise ratio, they are hindered by their sensitivity to a polymorphism (rs 6971, Alanine/ Threonine) (Best et al., 2019). This polymorphism divides the human population into high (approx. 50%), medium (approx. 40%) and low (approx. 10%) binding affinity groups. Recently, it has also been shown that the first-generation TSPO radioligand $\lceil {}^{11}C|PK1195$ is influenced by this polymorphism, although in a more limited manner (Fujita et al., 2017).

 $[$ ¹¹C]PBR28 and $[$ ¹⁸F]DPA714, two second-generation TSPO radioligands, have been successfully applied in ALS studies to detect glial activation in the primary motor cortex, supplementary motor area, and frontotemporal lobes (Albrecht et al. 2018; Alshikho et al. 2018; Ratai et al. 2018; Corcia et al. 2012; Van Weehaeghe et al. 2020; Van Weehaeghe et al. 2020; Zürcher et al. 2015). Glial activation in the primary motor cortices correlated with clinical parameters of functional decline, such as ALSFRS-R, and structural and metabolic measures of neurodegeneration and axon loss, such as motor cortical thickness, fractional anisotropy, and spectroscopy changes (myoinositol/ creatinine and N-acetyl-aspartate/creatinine ratios) (Alshikho et al., 2018; Ratai et al., 2018). Longitudinal evaluation of glial activation by $[11C]$ PBR28 uptake in ten ALS patients over a 6-month time window revealed a stable glial activation (Alshikho et al., 2018). However, the authors acknowledged that this longitudinal evaluation was performed in a biased selection of slow progressors (decline of 0.5 points on the ALSFRS-R scale/month), which might obscure a significant difference in this limited timeframe (Alshikho et al., 2018). Future studies including fast progressors and over longer time periods are needed to answer this clinically relevant question. Importantly, the feasibility of pooling multicenter multitracer and multiscanner TSPO scans has been demonstrated for two second generation radioligands, $[11C]PBR28$ and $[18F]DPA714$ (Van Weehaeghe et al., 2020a). Pooling data is crucial to facilitate the multicenter therapeutic studies needed to boost sample size in future therapeutic neuroinflammation studies.

Ideally, a TSPO radioligand without the need for genotyping is required. Therefore, two recent third generation TSPO radioligands, $[{}^{18}F]GE180$ and $[{}^{11}C]ER176$, have been developed (Best et al., 2019). A head-to-head comparison study of $[11C]$ PBR28 and [18 F]GE180 disclosed low brain penetration of [18 F]GE180 in 4 healthy volunteers and one ALS patient (Zanotti-Fregonara et al., 2018). Therefore, [¹¹C]PBR28 is preferred to $[{}^{18}F]$ GE180 for TSPO imaging in the brain. In contrast, a head-to-head comparison study of $[11C]$ PBR28 and $[11C]ER176$ in seven healthy volunteers demonstrated that $[11C]ER176$ had a smaller intersubject variability compared to $[^{11}C]$ PBR28, and that specific binding of $\lceil 11 \text{C} \rceil$ in low affinity binders exceeds the specific binding of $\lceil 11 \text{C} \rceil$ PBR28 in high affinity binders (Zanotti-Fregonara et al., 2019). Accordingly, $[$ ¹¹C $]ER176$ studies would need fewer subjects to obtain a similar statistical power and obviate the need for genotyping prior to scanning, as all subjects can be included. Currently, no $[{}^{11}C]ER176$ studies have been performed in ALS patients.

Aside from the two previously described drawbacks of TSPO radioligands, they also have measurable endothelial binding which complicates quantification (Best et al., 2019). These downsides encouraged researchers to explore other promising neuroinflammation targets. At present, to our knowledge, two other neuroinflammatory markers have been examined in ALS: monoamine oxidase B (MAOB) and the P2X7 receptor (P2X7R). MAOB is an enzyme located on the outer mitochondrial membrane and is mainly located in astrocytes. Therefore, in contrast to TSPO radioligands that visualize both activated microglia and astrocytes, MAOB radioligands detect activated astrocytes (Narayanaswami et al., 2018). $L-[11]C$ deprenyl, an irreversible MAOB inhibitor, was increased in the pons, white matter, spinal cord, and motor cortex of ALS patients (Johansson et al., 2007).

The P2X7R is an ATP-activated ion-channel, and is predominantly expressed on the cell membrane of activated microglia (Narayanaswami et al., 2018). Nonetheless, neurons, astrocytes, and oligodendrocytes also express P2X7R, as the P2X7R mRNA signal dropped by only 83% in hippocampal slice cultures depleted of microglia (Masuch et al., 2016). A head-to-head comparison between $[{}^{11}C$ JNJ717, a P2X7R radioligand, and TSPO ligand [¹⁸F]DPA714 in vitro and in vivo in symptomatic ALS patients demonstrated increased [¹⁸F]DPA714 binding in the motor cortex on an individual level, whereas no increased $[$ ¹¹C]JNJ717 binding was discernible (Van Weehaeghe et al. 2020). Moreover, this study suggested that frontotemporal dysfunction in ALS patients is associated with increased glial activation in the frontal cortex (Van Weehaeghe et al., 2020c). Notably, the lack of increased P2X7R expression in this head-to-head study could be attributed to limited or even lack of P2X7R upregulation in symptomatic stages, as the P2X7R initiates microglial activation (Monif et al., 2010). It has also been hypothesized that the P2X7R is important around the switch from M2 neuroprotective neuroinflammation to M1 neurotoxic neuroinflammation (Cie lak et al., 2019). Future studies in presymptomatic ALS patients are required to clarify whether P2X7R radioligands may have value as a biomarker in ALS.

To this point, no studies have investigated *in vivo* neuroinflammation in the spinal cord; however, hypermetabolism suggested to be caused by neuroinflammation has been observed (Marini et al. 2016; 2018; Van Weehaeghe et al. 2020). Spinal cord imaging has been hindered by the small structure, although a recent study in chronic radicular pain patients demonstrated the feasibility of TSPO quantification in the spinal cord.

Altogether, these studies demonstrate the biomarker potential of neuroinflammation PET scans. First, they may allow patient stratification based on the amount and pattern of glial activation (Albrecht et al. 2018; Alshikho et al. 2018; Ratai et al. 2018; Zürcher et al. 2015; Corcia et al. 2012; Van Weehaeghe et al. 2020; Van Weehaeghe et al. 2020). Second, they may provide prognostic information, as glial activation in the frontotemporal regions is associated with frontotemporal dementia (Zhang 2015; Van Weehaeghe et al. 2020). Finally, they can enable direct therapeutic response monitoring (Dupont et al., 2018; Werry et al., 2019).

- Microbiota-immunity axis—An important modulator of the immune responses is the gut microbiota. Increasing data document that, in addition to circulating neuropeptides and other immune cells playing in concert through the gut-brain axis, the gut microbiota work by forming immune tolerance and controlling Treg number and suppressive activity. Therefore, the gut and brain are connected and mutually regulated through microbiotaimmune system crosstalk, and the alteration of the normal gut microbial composition (dysbiosis) may contribute to the onset and exacerbation of various neurodegenerative disorders. Previous mouse models and recent human data have shown an altered enteric flora in early-stage ALS, pointing to a possible gut microbiota role in ALS pathogenesis. First, the Sun group examined the gut of SOD1^{G93A} transgenic mice, a common ALS model, proposing a link between gut microbiota and ALS onset; the transgenic mice showed a leaky gut, increased number of intestinal Paneth cells, and a dysbiotic flora before ALS onset, suggesting the gut microbiota had a role in ALS pathogenesis (Wu et al., 2015). Interestingly, the administration of butyrate in these mice restored the

intestinal microbial homeostasis, reduced Paneth cell number, improved gut integrity, and prolonged mouse life span compared to control mice (Zhang et al. 2017). In addition, Blacher et al. observed a distinct microbiota profile in pre-symptomatic SOD1G93A mice, observing a vivarium-dependent gut microbiota composition, suggesting that a combination of genetic susceptibility and environmental factors driving early pre-clinical dysbiosis potentially contribute to ALS modulation (Blacher et al., 2019). Moreover, antibiotic treatment exacerbates the disease course in mice, and distinct commensal bacteria have been correlated with ALS severity. In particular, Akkermansia muciniphila ameliorates ALS symptoms (possibly due to nicotinamide production), whereas Ruminococcus torques and Parabacteroides distasonis exacerbate ALS symptoms. The authors identified distinct microbiome and metabolite configurations also in a cohort of 37 ALS patients compared with household controls. Additionally, Figueroa-Romero et al. confirmed the alterations in the gut microbiota composition early in the life of $SOD1^{G93A}$ mice, looking also at immune response changes and at the temporal evolution relative to symptom onset (Figueroa-Romero et al., 2020). Specifically, immune cell expansion and activation, particularly in the spinal cord, and global brain cytosine hydroxymethylation were noted in transgenic mice at disease end stage compared to control mice. The correlation analysis confirmed the microbiomeimmune system interplay, suggesting that gut flora could influence the epigenome by secreting metabolites and modulating the immune system.

Very recently, Burberry et al. tried to enhance current knowledge on the microbiota contribution to motor neuron degeneration, studying a mouse model of ALS carrying a mutant version of the C9orf72 gene (Burberry et al., 2020). In particular, the authors analyzed two vivariums of C9ort72 mice, housed in different facilities, which display discrepancy in ALS progression and severity. They demonstrated that the animals in the two facilities showed distinct microbial profiles, and that the alterations in the gut microbiota modulated how ALS-related symptoms manifested. More interestingly, they found that inflammation and autoimmune responses were attenuated by reducing the microbial burden in mutant mice with broad-spectrum antibiotic treatment, or by transplanting gut microflora from a healthy environment, even after their onset, suggesting that microbial modulation of inflammation outside the brain regulates the disease course.

Regarding human ALS research, few studies have compared the fecal microbiota of ALS patients to healthy subjects and have led to different and controversial conclusions, probably due to study limitations, such as the number of patients and other confounding factors (diet, secondary disease effects, dysphagia, etc.). Different groups comparing the fecal microbiota of a few ALS patients to controls have observed differences of some bacteria genera abundances (in particular Ruminococcus) and documented a lower Firmicutes/Bacteroidetes (F/B) ratio (a dysbiotic indicator) in ALS patients (Fang et al., 2016; Rowin et al., 2017; Zhai et al., 2019). Brenner and colleagues, comparing the fecal microbiota of 25 ALS patients with 32 healthy subjects, did not find substantial taxonomic or metagenomics differences, apart from different proportions of Ruminococcaceae (Brenner et al., 2018). Likewise, Ngo et al. have more recently confirmed, enrolling a wider number of patients, that the fecal microbiota of ALS patients does not differ significantly from healthy subjects. The authors did however find increased risk of earlier death in ALS patients with higher microbiome richness and diversity, and in those with a greater F/B ratio. Given the well-

known heterogeneity of ALS disease, they suggest that larger studies are needed to explore the correlation between microbiota and ALS progression/prognosis. Nevertheless, there are manifold recent evidence of intestinal dysbiosis in ALS patients (Di Gioia et al., 2020; Nicholson et al., 2020; Zeng et al., 2020). Zeng and colleagues have shown a marked change in microbial structure in 20 ALS patients, where the Bacteroidetes phylum and several bacterial genera were up-regulated and the Firmicutes and Megamonas genus were downregulated compared to healthy controls. Overall, ALS patients seem to be characterized by the reduction of butyrate-producing bacteria (Di Gioia et al., 2020; Nicholson et al., 2020), which are important for gut integrity and regulation of inflammation. In particular, since butyrate favors the expression of Foxp3 gene and regulates Treg/Th17 balances (Zhang et al., 2016), this observation provides additional proof of the microbiota and immune dysfunction link in ALS.

As such, the ascertained gut microbiota role in ALS pathogenesis could open innovative therapeutic opportunities to shape the microbiota composition to favorably modulate its functionality. Of relevance to this concept is the prospective longitudinal study addressing the impact of 6 months of probiotic supplementation on the gut microbiota on ALS progression. Fifty ALS patients and 50 matched controls were enrolled, with the former randomized to receive probiotic treatment or placebo. The results demonstrated that the gut microbiota composition of patients differed compared to controls, and that the gut microbiota changes during disease progression (Di Gioia et al., 2020). Additionally, while the probiotic treatment influenced the gut microbiota composition, it did not bring the biodiversity of intestinal microbiota of ALS patients closer to that of control subjects, nor did it affect the progression of the disease as measured by ALSFRS-R.

Since fecal microbial transplantation (FMT) seems to be the most efficacious therapeutic intervention to restore entire microbial communities and their metabolic products to modulate systemic immunity, a multicenter randomized double-blind clinical trial employing FMT as a therapeutic intervention for ALS is underway [\(ClinicalTrials.gov](http://ClinicalTrials.gov) identifier: [NCT03766321\)](https://clinicaltrials.gov/ct2/show/NCT03766321). The study will evaluate the effect of FMT on immunological features, in particular Treg numbers and the Th17/Treg ratio, and on the clinical response, in terms of safety and efficacy. Ultimately, detailed study of immune cell populations, levels of cytokines, and microbiota has potential to shed light on early processes that may lead to degenerative ALS (Mandrioli et al. 2019).

Finally, there are various theoretical reasons supporting the role of the microbiota-immunity axis in ALS pathogenesis that are supported by evidence in animal and human studies. In some cases, human studies have limitations due to the small number of enrolled patients or to the large genetic and phenotypical heterogeneity displayed in ALS. Moreover, it must be clarified whether the gut microbiota alterations observed in ALS patients precedes the disease or is a consequence of dietary changes due to dysphagia and anorexia that typically occur in during ALS progression. Larger, well-conducted clinical trials will be required to provide important information on the pathogenic mechanisms underlying ALS, and to define the effectiveness of therapies targeting the microbiota-immunity axis.

Clinical trials and therapeutic options

The recent pathogenic insights presented in this review are providing several therapeutic opportunities. Briefly, immune cells in both the CNS and the periphery have an inflammatory phenotype in ALS (Beers et al., 2017; Murdock et al., 2015; Zhao et al., 2017, 2013). Immune cell populations such as microglia are both more activated and cytotoxic during ALS (Zhao et al., 2010, 2004), and as the disease progresses, cytokine production in the CNS becomes increasingly pro-inflammatory (Beers et al., 2011; Henkel et al., 2006). In ALS mouse models, however, targeting populations of immune cells has induced both positive and negative effects on disease progression (Beers et al. 2006; Butovsky et al. 2012; Finkelstein et al. 2011; Beers et al. 2008), supporting the contention that the immune response in ALS is not purely destructive to CNS motor neurons. This likely explains why clinical trials utilizing global immune suppression have failed or accelerated disease (Cudkowicz et al. 2006; Gordon et al. 2007; V Meininger et al. 2006; Meininger et al. 2009): beneficial cells are being suppressed along with detrimental cells. These realizations have prompted development and translation of both pharmacologic and cell-based strategies that target specific immune populations and pro-inflammatory immune polarization in disease progression.

- Emerging drug therapies—Numerous drugs that modulate the immune system have been developed. Yet, several therapies targeting immune cell types, pathways, and regulatory factors that have shown promise in preclinical ALS studies ultimately had limited success in human studies (Crisafulli et al., 2018; Filipi et al., 2020; Khalid et al., 2017). While this lack of clinical efficacy may be explained by advanced disease progression in enrolled patients beyond a point where targeting neuroinflammation or immune activation could be effective, recently completed and ongoing studies, as well as novel drug repurposing strategies, are continuing to provide insight regarding the utility of immunomodulatory therapeutic strategies.

In one recently completed clinical trial, the NIPALS2013 study [\(NCT01884571](https://clinicaltrials.gov/ct2/show/NCT01884571); (Fournier et al., 2018)), 31 ALS subjects received a 6-month combination immunosuppression regimen consisting of basiliximab, tacrolimus, mycophenylate, and prednisone. This regimen mirrored that administered in a previous first-in-human trial of a stem cell transplantation therapy in ALS subjects where unanticipated improvement was seen in one subject (Feldman et al., 2014; Glass et al., 2016; Goutman et al., 2018). No subjects receiving the immunosuppression regimen in the NIPALS2013 trial, however, met the predefined criteria of a 6-point ALSFRS-R increase over 6 months. These findings are not surprising given the previously mentioned fact that global immune suppression studies have failed or accelerated disease (Cudkowicz et al. 2006; Gordon et al. 2007; V Meininger et al. 2006; Meininger et al. 2009), but additional studies are required to tease out how related immunomodulatory paradigms may affect ALS progression.

Another recently completed study, the TCZALS-001 study ([NCT0246896\)](https://clinicaltrials.gov/ct2/show/NCT0246896), assessed the safety and tolerability of tocilizumab in 22 ALS subjects across 5 Northeast ALS Consortium (NEALS) study sites in the USA. The intravenously-administered drug prevents immune cell stimulation by blocking IL-6 (Sebba, 2008). The primary study outcomes were

safety and tolerability of administration every 4 weeks for 8 weeks, and secondary endpoints included assessment of proinflammatory genes in peripheral blood mononuclear cells and CSF, evaluation of cytokines in CSF, and MRI-PET in a subset of subjects to examine immunomodulatory efficacy and CNS penetration. Results were posted to ClinicalTrials.gov in late 2019, but published reports are not yet available.

The Modifying Immune Response and OutComes in ALS (MIROCALS) study [\(NCT03039673](https://clinicaltrials.gov/ct2/show/NCT03039673)), a Phase II, placebo-controlled, double-blind, parallel group study based in the United Kingdom and France, assessed the efficacy and safety of Treg enhancement using low-dose (ld)-IL-2 (Tang et al., 2008; Zorn et al., 2006) in 304 subjects treated for 18 months. Secondary objectives included validation of a new Phase II study design, with the addition of exploratory assessments of immune and inflammatory phenotype, brain biomarkers, and genomics and transcriptomics. Recruiting has completed but results are not yet reported; however, this trial is a follow-on study of the earlier Immuno-modulation in ALS (IMODALS) trial where the safety, dosing, and activity of ld-IL-2 was assessed in 36 subjects randomized to placebo or one of two treatment doses [\(NCT02059759](https://clinicaltrials.gov/ct2/show/NCT02059759)). Results demonstrated that the treatment was well-tolerated and revealed a dose-dependent increase in Tregs (Camu et al., 2020), thus informing and supporting the ongoing MIROCALS trial.

Rapamycin is being evaluated in Italy in the Phase II RAP-ALS trial, where 63 ALS patients randomized to placebo or one of two rapamycin doses were treated for 18 months and followed for an additional 36 months [\(NCT03359538](https://clinicaltrials.gov/ct2/show/NCT03359538); (Mandrioli et al. 2018)). The orally-administered drug inhibits mTOR signaling, which enhances protein degradation and exerts immunomodulatory effects, thereby having multiple potential benefits in ALS (Barmada et al., 2014; Caccamo et al., 2009; Cheng et al., 2015). mTOR acts on the homeostasis of the naive CD4+ T cells, which can develop into Th1, Th2, or Th17 effectors using promoted by mTOR pathways. Conversely, mTOR inhibits the induction of Tregs. Rapamycin inhibits mTORC1, which targets regulatory proteins in cell signaling and regulates autophagy by inhibiting the unc-51-like kinase 1 complex. Inhibition of mTORC1 by the tested drug stimulates autophagy through the formation of autophagosome from the phagophore. Inhibition of mTORC1 by Rapamycin expands Tregs and, in a mouse model, increased Tregs and induction of M2 microglia, associated with a stable phase of the disease (Mandrioli et al., 2018). The primary outcome of the RAPALS study is enhanced Treg numbers, with secondary outcomes including safety, CNS penetrance, mTOR pathway inhibition, immune phenotyping, and other functional and survival assessments. Final follow-up is in progress, and results are anticipated in early 2021.

Another immunomodulatory treatment that is advancing through clinical trial stages is RNS60, a novel agent that upregulates Tregs and activates protective cells (Vallarola et al., 2018). Drug administration involves weekly infusions along with daily nebulization on remaining weekdays. A pilot study [\(NCT02525471](https://clinicaltrials.gov/ct2/show/NCT02525471)) in 24 ALS patients showed that a 23-week regimen was safe, tolerable, and capable of slowing disease progression (Paganoni et al., 2019), thus supporting a larger multicenter, randomized, double-blind, placebo-controlled, parallel group, add-on Phase II study designed to assess the effect of RNS60. ALS biomarkers, including Tregs and other pharmacodynamics markers, were the primary outcome, and ALSFRS-R scores, FVC, safety, quality of life, and survival were the

secondary outcomes. A total of 142 subjects received drug for 24 weeks, and an additional 24-week follow-up is in progress; anticipated study completion is targeted for mid-2021.

Immune-targeted therapies are also included in the recently launched Healey ALS Platform Trial. This innovative trial paradigm, the first of its kind in ALS, involves recruitment of subjects into a Master study protocol [\(NCT04297683](https://clinicaltrials.gov/ct2/show/NCT04297683)) that randomizes subjects into one of several treatment arms evaluating potential therapeutic compounds or into one placebo group which is shared across arms, thus increasing the percentage of subjects receiving a study drug while still maintaining power. At present, there are 3 drug regimens included in the platform trial, with the prospect for addition of new drugs as approved. Two of the three current drugs and one planned drug modulate immune mechanisms. Zilucoplan is a small-molecule inhibitor of complement protein C5 that has anti-inflammatory and cell protection properties through a mechanism that involves inhibition of membrane attack complex (MAC) assembly. The drug is administered by daily subcutaneous self-injection and had a favorable safety profile in trials for myasthenia gravis (Beecher et al., 2019; Howard et al., 2020). Verdiperstat, alternatively, is an orally-administered drug, but it also has a favorable safety profile and is well tolerated. Its antioxidative properties, potential to reduce microglial activation, and effects on mitigating brain inflammation are driven by inhibition of myeloperoxidase, a pro-oxidant enzyme present in activated microglia and other immune cells (Beecher et al., 2019; Howard et al., 2020; Jucaite et al., 2015). Finally, one of the planned therapies for this trial is IC14 immunotherapy. Initially screened in a Phase I pilot study ([NCT03487263\)](https://clinicaltrials.gov/ct2/show/NCT03487263), this treatment targets CD14, a master regulator of the immune response, particularly microglia, and is proposed as a strategy to "rebalance" the immune response in ALS. Recruiting for this platform trial commenced in late 2020, and results are highly anticipated.

In a similar mechanism to one of the platform trial drugs, the Phase III CHAMPION-ALS trial evaluating the safety and efficacy of ravulizumab (Lee et al. 2019), a complement C5 inhibitor, has recently commenced ([NCT04248465\)](https://clinicaltrials.gov/ct2/show/NCT04248465). This multi-site study involving 49 worldwide sites is designed to include 354 subjects who will receive a single intravenous loading dose followed by regular maintenance dosing of ravulizumab or placebo for 50 weeks, with a planned open-label extension period for all subjects. ALSFRS-R is the primary outcome measure, and survival, change in FVC, muscle strength, and serum neurofilament, as well as safety are secondary outcomes. Likewise, an open-label, adaptive design Phase II study of BLZ945 [\(NCT04066244](https://clinicaltrials.gov/ct2/show/NCT04066244)), a compound that impacts microglia (Wies Mancini et al., 2019), also began within the past year in the USA, Finland, and Sweden to evaluate safety, repeated dosing, and microglial response, as measured by PET imaging for TSPO binding, to inform future study planning. The study will include 20 subjects and completion is targeted for 2021.

A Phase III trial is also in the planning phases in Germany to evaluate two ascending dose titrations of masitinib, an oral tyrosine kinase inhibitor that exerts effects via CNS and PNS microglia, macrophages, and mast cells (Harrison and Rafuse, 2020; Trias et al., 2018), as an add-on therapy to riluzole [\(NCT03127267](https://clinicaltrials.gov/ct2/show/NCT03127267)). The estimated enrollment for the study is 495 participants, with ALSFRS-R over the 48-week evaluation period as the primary outcome and muscle strength, FVC, quality of life, and progression-free survival

as secondary outcomes. This trial is based on promising results following a previous doubleblind, randomized study that demonstrated safety and beneficial effects of masitinib versus placebo in 394 ALS subjects (Mora et al., 2020). Interestingly, palmitoylethanolamide, an endocannabinoid and potent inhibitor of mast cell activation (Skaper et al., 2013), was also reported to clinically improve pulmonary function in ALS patients (Palma et al., 2016).

Finally, there are several emerging immune-based strategies in development, including evaluation of compounds that modulate glial cells and repurposing drugs utilized in other disorders with immune components (Filipi et al., 2020; Khalid et al., 2017). One example includes recently developed inhibitors of the JAK/STAT pathway, a signaling pathway crucial to initiating inflammatory responses. These drugs inhibit Janus kinase (JAK) and thus alter immune polarization, preventing pro-inflammatory Th1 responses while preserving regulatory function (Kubo et al., 2014; Maeshima et al., 2012; Sonomoto et al., 2014). A Phase I study in renal transplant patients demonstrated that pharmacologically targeting JAK/STAT signaling can reduce peripheral NK cell levels in a dose-dependent manner (Van Gurp et al., 2008), and we have unpublished *in vitro* data showing that inhibiting JAK/STAT signaling can also reduce NK cell activity and cytotoxicity. Importantly, JAK/STAT inhibitors that have passed Phase III clinical trials to treat multiple diseases (Azevedo and Torres, 2018; Gladman et al., 2017; Sandborn et al., 2017) are commercially available, and others are already under development (He et al., 2017; Thorarensen et al., 2017). Repurposing such inhibitors therefore represents a novel approach to reduce peripheral NK cell levels and NK cell activity in ALS patients that is amenable to rapid clinical translation.

- Emerging cell-based therapies—The maturation of cell-based therapeutic approaches provides a new opportunity to reduce abnormal inflammation with cell-based therapies. Across medicine, cell therapy applications are expanding rapidly, with more and more cell types being employed for their therapeutic potential. Research in ALS has focused primarily, if not exclusively, on four types of cells: 1) neural stem cells (NSCs) and glial progenitor cells (GPCs), 2) induced-pluripotent stem cells (iPSCs), 3) mesenchymal stromal cells (MSCs), and 4) Tregs. The first three are progenitor cells whose actions are predicted to be broad, including neurotrophic factor elaboration, preservation of neuromuscular function, and (importantly) reduction in neuroinflammation. The last are immune cells, aimed at reducing both systemic inflammation and neuroinflammation.

Neural stem cells (NSCs) and glial progenitor cells (GPCs): NSCs have been investigated not for their potential to replace motor neurons, but rather for their ability to exert their influence to protect existing motor neurons. Their benefit in a variety of animal models of neurologic disease, from spinal cord injury (Teng et al., 2002) to models of Parkinson's and Huntington's disease (Cho et al., 2007; Redmond et al., 2007), have acted as the basis for critical early work examining their effect in ALS. In addition, non-neuronal cells in chimeric mice have long been demonstrated to have a beneficial impact on mSOD1 ALS neurons (Clement et al., 2003). A multi-center consortium of investigators examining the effect of NSCs on SOD1^{G93A} mice demonstrated engraftment of transplanted cells, reduced astrogliosis and neuroinflammation, and even improved survival and function (Teng et al.,

2012). The experiments suggested that broader spread of the cells met with better outcomes, as did a higher number of non-neuronal NSC-derived cells engrafted in close proximity to motor neurons. There was, however, variability in the functional and survival benefit of the cells. Other studies recapitulated the beneficial effect of GPCs in SOD1^{G93A} ALS rats (Lepore et al., 2008). However, again, not all research in GPCs demonstrated the same benefit in murine models. One study in $SOD1^{G93A}$ mice failed to demonstrate a functional or survival benefit with transplanted human GPCs (Lepore et al., 2011). These results could be providing important insight into limitations of GPCs as a therapy, or experimental design issues, such as problems with the immune suppression regimens used to dosage or spread of cells within the CNS, may have hampered the results.

The first FDA-approved clinical trial to treat ALS with allogenic human spinal cord-derived neural progenitor cells used a purpose-built catheter system for delivery into the ventral horn of the spinal cord (Glass et al., 2016). The trial demonstrated safety, albeit with a few notable adverse events of sensory disturbance and pain attributed to the surgical procedure. Fluorescence in-situ hybridization identified cells surviving up to 2.5 years later, with some differentiating into neurons and others remaining stem cells (Tadesse et al., 2014). Post-hoc long-term analysis of this small open-label cohort relative to historical controls suggested a potential slowing of functional decline, but no effect on survival (Goutman et al., 2018). Further trials are not yet underway. A trial of human GPCs is indexed on ClinicalTrials.gov, but has not begun startup activities or enrollment [\(NCT02478450](https://clinicaltrials.gov/ct2/show/NCT02478450)).

Mesenchymal Stromal Cells (MSCs): In vitro work using MSCs suggests an antiinflammatory effect in primary motor neuron cultures (Sun et al., 2013), providing evidence that therapy with MSCs may have an anti-inflammatory, and thus beneficial, effect on motor neurons. In ALS murine models, treatments with human MSCs intramuscularly or intrathecally have been safe and paved the way for clinical trials (Gothelf et al., 2014; Kim et al., 2010). Mesenchymal stromal cells have a robust ability to secrete neurotrophic factors and reduce the inflammatory milieu in the CNS, as measured by cytokine levels in the CSF (Kwon et al., 2014). Although MSC survival in animal models has been shown to be limited to weeks, their effect has frequently outlived the cells themselves (Sadan et al., 2009). Furthermore, human MSCs appeared to induce Tregs and anti-inflammatory cytokines in the blood of treated SOD1^{G93A} mice (Kwon et al., 2014), suggesting that the effect they exert is both anti-inflammatory and systemic. Subsequently, numerous trials have explored the effect of MSC in people with ALS.

An open label trial of autologous intrathecal transplantation of bone marrow-derived MSCs in ten participants in India demonstrated safety, but failed to show any statistical or clinically meaningful reduction in post-transplant rate of decline compared to baseline decline on the ALSFRS-R (Prabhakar et al., 2012). Additionally, a Phase I trial of bonemarrow derived MSCs (Neuronata-R) transplanted intrathecally demonstrated safety with longitudinal injections (Oh et al. 2015). Preliminary responder analyses have suggested that people whose MSCs secreted higher levels of neurotrophic factors and were more robustly anti-inflammatory had better clinical responses in one of these early trials (Kim et al. 2014). The Phase II trial demonstrated a slowing of decline of the ALSFRS-R in the treated group at four (2.98 points) and six months (3.38 points) post-treatment, without a difference in

long-term survival. TGF-β1 was increased in those reaching a threshold for benefit (Oh et al. 2018).

Phase I and IIa trials of MSC-NTF (NurOwn) in humans delivered intramuscularly and/or intrathecally demonstrated safety and suggested hints of possible efficacy (Berry et al., 2019; Petrou et al., 2016). In the subsequent Phase IIa trial, only a pre-specified subgroup analysis excluding slow progressors demonstrated a significant slowing of ALSFRS-R decline at four- and eight-weeks following treatment with MSC-NTF. Importantly, the pro-inflammatory biomarker MCP-1 was significantly reduced in CSF in the MSC-NTF group. The top-line Phase III trial [\(NCT03280056](https://clinicaltrials.gov/ct2/show/NCT03280056)) results were recently reported in a pressrelease ([https://ir.brainstorm-cell.com/2020-11-17-BrainStorm-Announces-Topline-Results](https://ir.brainstorm-cell.com/2020-11-17-BrainStorm-Announces-Topline-Results-from-NurOwn-R-Phase-3-ALS-Study)[from-NurOwn-R-Phase-3-ALS-Study\)](https://ir.brainstorm-cell.com/2020-11-17-BrainStorm-Announces-Topline-Results-from-NurOwn-R-Phase-3-ALS-Study). According to the release, the trial demonstrated no statistically significant effect in the overall trial population, though reportedly showed statistically significant increases in neurotrophic factors and decreases in inflammatory markers in the CSF of those treated with MSC-NTF. Future analysis will likely focus on determining any correlations of the biomarker response with clinical response.

Additional ongoing trials may shed further light on the ability of MSCs to reduce neuroinflammation and improve clinical outcomes for people with ALS. A Phase I trial of adipose-derived MSCs expanded ex vivo and delivered intrathecally demonstrated safety (Staff et al., 2016), and a Phase II trial is currently underway [\(NCT03268603](https://clinicaltrials.gov/ct2/show/NCT03268603)). A multicenter Phase I/II trial is also underway in Spain [\(NCT02290886](https://clinicaltrials.gov/ct2/show/NCT02290886)). More recently, a casecontrol study in 67 patients that received three intrathecal injections of human umbilical MSCs (hUC-MSCs) every two months at a dose of 30×10^6 cells showed reduction in the rate of disease progression and a two-fold extension of survival without adverse reactions, compared with 67 paired matched reference patients from the PRO-ACT database (Barczewska et al., 2020). Interestingly, the same cells injected into the cerebral ventricles of SOD1G93A mice protected lumbar motor neurons and upregulated anti-inflammatory and neurotrophic factors in the spinal cord, although this response was insufficient to prevent muscle denervation and prolong survival (Sironi et al., 2017). Even beyond the well-recognized glial activation, broad immune dysregulation and motor neuron loss, stem cell therapies have been shown to have beneficial effects on lesser-studied potential disease pathologies, such as endothelial cell damage (Garbuzova-Davis et al., 2021; Garbuzova-Davis and Borlongan, 2021) and microvasculature damage to lung tissue seen in SOD1 mouse models, both of which were shown to improve with intravenous delivery of human bone marrow-derived stem cells (Garbuzova-Davis et al., 2020a). Even cell-free extracellular vesicles derived from bone marrow endothelial progenitor cells have been shown to exert a beneficial effect on the microvasculature in ALS and could be shown to be of therapeutic value in the future (Garbuzova-Davis et al., 2020b).

Induced Pluripotent Stem Cells (iPSCs): In the SOD1^{G93A} rat model of ALS, neural progenitor cells transfected with lentivirus to secrete high levels of human GDNF were used to explore glial replacement in the spinal cord (Klein et al., 2005). While the primary focus of these experiments was on delivery of neurotrophic factors, the successes in cell survival and integration, and neurotrophic factor secretion, were a step forward for the field and have

led both directly and indirectly to more cell-based therapies in ALS. The Phase I human trial is now complete [\(NCT02943850](https://clinicaltrials.gov/ct2/show/NCT02943850)), though results have not been published yet.

Regulatory T Cells (Tregs): Under normal circumstances, Tregs exhibit an antiinflammatory effect when the immune system is activated, leading to the eventual diminution of the inflammatory response. In ALS, a reduction in Treg suppressive function correlates with more rapid disease progression (Henkel et al., 2013). Furthermore, monocytes are more pro-inflammatory in people with ALS than controls (Butovsky et al., 2012; Zhao et al., 2017), providing more rationale for seeking therapeutic strategies, like boosting Treg function, that can reduce the inflammatory state in people with ALS to slow disease progression. In an open-label Phase I trial, three people with ALS were treated with autologous Tregs harvested by leukapheresis, expanded ex vivo, and given as weekly intravenous infusions alongside concomitant ld-IL-2 therapy aimed at maintaining Treg phenotype (Thonhoff et al., 2018a). The Treg infusions appeared to slow decline of the Appel ALS scale, and Treg suppressive function increased in parallel. A Phase IIa trial is presently underway to further characterize these clinical and biomarker effects in the setting of a small randomized controlled trial ([NCT04055623\)](https://clinicaltrials.gov/ct2/show/NCT04055623). In addition, a Phase I trial of autologous Tregs with slightly different derivation is set to begin enrollment soon [\(NCT04220190](https://clinicaltrials.gov/ct2/show/NCT04220190)) and will extend the evidence from the first trials of autologous Tregs in people with ALS. And, while not a trial of cell therapy, per se, the MICROALS multicenter trial of ld-IL-2 mentioned above ([NCT03039673\)](https://clinicaltrials.gov/ct2/show/NCT03039673) is likewise aimed at bolstering the number and function of circulating Tregs in ALS patients and will provide additional insight.

Certainly, one of the benefits of cell therapies is that they can target multiple dysregulated pathways at the same time. Yet, these four categories of cell therapies are just beginning to generate data that will drive a rich understanding of novel ways to reduce neuroinflammation and protect motor neurons in people with ALS.

Future prospective and conclusions

The recent developments in understanding ALS pathophysiology have focused on the role of the immune system, and this field of research is rapidly expanding. This review summarizes many of the recent advances regarding immune involvement in ALS, with particular attention to clinical translation. With validation in human patients, the knowledge from this expanding field will serve to identify novel therapeutic targets.

Importantly, there is clear evidence of an extensive overlap in immune system activation in ALS patients and animal models of disease (Figure 2), providing important molecular insight into potential therapeutic targets and diagnostic biomarkers. Recent results have pinpointed T cells and NK cells, as well as other peripheral cells, such as monocytes, in disease pathology. Moreover, several ALS risk genes have been identified that directly modulate the immune system, and the immune system itself is also profoundly affected by gut microbiota, providing a broad array of potential therapeutic targets.

Given that the immune system has both harmful and beneficial effects, there is a need to focus research efforts on enhancing the beneficial effects of protective immunity. It also remains to be clarified if inflammation is of similar importance in all forms of ALS.

Taking into account the heterogeneity of the disease, not necessarily all individuals with ALS exhibit the same degree of neuroinflammation, or at all time points in the course of the disease. Hence, patients need to be stratified into subgroups based on the importance of inflammatory pathways to pathogenesis. PET might aid in patient stratification, as it provides in vivo information about neuroinflammation. This will facilitate identifying patients who may benefit most from anti-inflammatory and/or other immunomodulatory interventions. Improving our knowledge on the immune and inflammatory biomarkers, including but not limited to soluble factors, peripheral monocytes/macrophages, Tregs, and other T cells, and the composition of microbiota in relation with ALS phenotypes and progression may improve diagnosis and speed the development of immune-modulating treatments. An exciting novel and realistic route for the diagnosis and monitoring of the progression of neuroinflammation in ALS is represented by advanced neuroimaging techniques, and particularly PET, of the brain and spinal cord. However, some technological boundaries of imaging, particularly for the spinal cord, and the lack of specific ligands that can differentiate anti-inflammatory from proinflammatory microglia still limit the use of these methodologies in clinical practice.

The developments in understanding the role of immunity in the pathophysiology of ALS, however, have already encouraged new treatment approaches. Clinical trials using both pharmacologic and cell-based strategies that target specific immune cell subsets, pro-inflammatory mediators, and polarization in disease progression have been concluded and others are still ongoing. Although the initial broad-scope anti-inflammatory therapies were generally disappointing due to the incomplete understanding of the complexity of the immune response in ALS, the ongoing and upcoming selective and/or timely therapies provide a realistic hope for prospective, more specific personalized treatment strategies. To this end, both basic and clinical researchers must focus on understanding the interplay between innate and adaptive immunity that leads to immune disbalance and/or hyperinflammation. This is relevant at all stages of ALS progression in the different clinical phenotypes and genotypes for designing the best treatment trials.

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Highlights

- **•** Evidence regarding the role of the immune system in ALS is rapidly expanding
- **•** ALS involves a complex interplay between innate and adaptive immunity
- **•** Animal model and patient data reveal a multi-phased immune response
- **•** Several cell types contribute to immune mechanisms in ALS pathogenesis
- **•** PET provides neuroinflammatory response monitoring and possible ALS biomarkers
- **•** Clinical trials of emerging immune-targeted therapies provide hope in ALS

(A) Spinal cord: At the presymptomatic stage, CCL2 is activated by motor neurons and microglia to recruit neuroprotective CD4+ T cells (Th2 and Tregs), which together with microglia in an M2-activate state and with mildly activated astrocytes release neurotrophic (NTFs) and anti-inflammatory factors to preserve motor neurons. However, this phenomenon appears to be counterbalanced by infiltrating NK cells that injure motor neurons while inhibiting Tregs and M2 microglia through the expression of IFN-γ. During the disease course, a massive release of CCL2 enhances the recruitment of DCs alongside

with $CD8⁺$ and $CD4⁺$ T cells (Th1). Proinflammatory T cells influence the activation status of astrocytes, which release pro-inflammatory factors and TGF-β1, which polarize microglia to a M1 phenotype. M1 microglia in turn release ROS and pro-inflammatory factors (IL-1β, TNF-α) detrimental to motor neurons. Peripheral monocyte infiltration in the spinal cord of $SOD1^{G93A}$ rodent models is still controversial. (B) Sciatic nerve: At the presymptomatic stage, early production of CCL2 along with the complement-mediated opsonization of motor axons and IgM, IgG deposition elicit the infiltration of macrophages and mast cells. At onset, increased permeability of the blood-nerve barrier together with CCL2 overexpression and a massive IgM/IgG deposition promotes a further infiltration of mast cells, neutrophils, macrophages, and CD8+ T cells, which contribute to the massive degradation of peripheral motor axons and myelinating Schwann cells. (C) Skeletal muscle: At the presymptomatic stage, peripheral macrophages infiltrate the skeletal muscle of transgenic rodents alongside the increased expression of proinflammatory response initiator (Caspase1; C1q/C3) and byproducts (IL-1β). This likely is the response to neuromuscular junction (NMJ) alterations/denervation which precedes the motor neuron death according to the "dying back" hypothesis. Whether this response is an attempt to protect the myofibers or has a pathogenic role is still unknown. During disease progression, macrophages massively infiltrate the skeletal muscle together with mast cells, neutrophils, and T cells. This event is accompanied by increased inflammation due to IL-6, TNF-α, TGF-β1, TGF-β3, and C5a expression.

Abbreviations: C-C Motif Chemokine Ligand 2 (CCL2), T helper (Th), regulatory T cell (Treg), neurotrophic factors (NTFs), natural killer (NK), interferon gamma (IFN-γ), dendritic cell (DC), transforming growth factor (TGF), reactive oxygen species (ROS), Interleukin (IL), tumor necrosis factor-α (TNF-α), immunoglobulin (Ig). Image created in Biorender.com

Figure 2. The timeline of immune system involvement in ALS: evidence from animal models and patients.

The progression of the immune response in animal models (top) and human ALS patients (bottom) is depicted over time. Horizontal arrows mark the conversion of immune biomarkers when applicable, while vertical arrows mark non-immune milestones of disease. Monocyte infiltration is still controversial (*). Current studies reported no progression in PET tracing of microgliosis and astrogliosis but studies need to be expanded to include more patients. Abbreviations: cerebrospinal fluid (CSF), regulatory T cell (Treg), blood– brain barrier (BBB), central nervous system (CNS), natural killer (NK), peripheral blood mononuclear cell (PBMC), positron emission tomography (PET).