



Review Article

Protein biomarkers for the diagnosis and prognosis of Amyotrophic Lateral Sclerosis

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ABSTRACT

Amyotrophic Lateral Sclerosis (ALS) is the most common motor neuron disease, still incurable. The disease is highly heterogenous both genetically and phenotypically. Therefore, developing efficacious treatments is challenging in many aspects because it is difficult to predict the rate of disease progression and stratify the patients to minimize statistical variability in clinical studies. Moreover, there is a lack of sensitive measures of therapeutic effect to assess whether a pharmacological intervention ameliorates the disease. There is also urgency of markers that reflect a molecular mechanism dysregulated by ALS pathology and can be rescued when a treatment relieves the condition. Here, we summarize and discuss biomarkers tested in multicentered studies and across different laboratories like neurofilaments, the most used marker in ALS clinical studies, neuroinflammatory-related proteins, p75^{ECD}, p-Tau/t-Tau, and UCHL1. We also explore the applicability of muscle proteins and extracellular vesicles as potential biomarkers.

1. Introduction

Motor neuron diseases designate a heterogeneous group of pathologies characterized by the selective and primary progressive involvement of motor neurons, a cell population that controls movement. Motor neurons are present in the primary motor cortex, brainstem, and the anterior horns of the spinal cord. Their progressive degeneration causes muscle cramps with fasciculations, atrophy, worsening paralysis with difficulties in walking and in the use of the upper limbs, leading to complete tetraplegia, dysarthria that evolves into anarthria, dysphagia which involves malnutrition, and respiratory failure-inducing death (Feldman et al., 2022; Goutman et al., 2022). Sensory symptoms are typically absent, while in a variable percentage of patients, there are clinical manifestations of cognitive involvement that can lead to a diagnosis of frontotemporal dementia (Feldman et al., 2022; van Es et al., 2017).

Motor neuron diseases are clinically variable: Amyotrophic Lateral Sclerosis is the most severe and is characterized by the involvement of both the upper and lower motor neurons (UMN and LMN); Primary Progressive Sclerosis with the exclusive participation of the upper motor

neuron; Progressive Muscular Atrophy shows an elective degeneration of the lower motor neurons; the loss of the brainstem motor neurons induces progressive bulbar palsy. This subdivision is usually valid at the early stages of the disease. In the more advanced phases, the different diseases manifest with the typical symptoms of ALS (van Es et al., 2017).

ALS is a rare disease, presenting an incidence of 2–3 new cases per year per 100,000 inhabitants and a prevalence of 10–12 cases per 100,000 inhabitants; the risk of developing the disease increases with age, with a peak incidence between 65 and 75 years, it prevails in males, especially in the younger age groups. The estimated cumulative lifetime risk for developing ALS is 1:350 in men and 1:400 in women. Most cases are sporadic (90%), while 10% account for familial origin (Masrori and Van Damme, 2020).

In sporadic cases, 60% of the disease's risk is attributed to genetic mechanisms and 40% to environmental factors (sports, injuries, pesticides) (Al-Chalabi and Hardiman, 2013). Approximately 70% of patients present with limb weakness at disease onset, typically insidiously, asymmetrically, and distally, with subsequent progression in the same anatomical region and spread to the contiguous areas (Ravits and La Spada, 2009). Bulbar symptoms (difficulty in articulating speech,

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chewing, or swallowing) are present in 25% of patients, while the onset with involvement of the respiratory muscles is much rarer. Of note, extraocular movements are usually spared until the very advanced stages of the disease (Ravits and La Spada, 2009).

Despite the clinical heterogeneity, pathologically, ALS is characterized by increased cytoplasmic localization of phosphorylated TDP-43 (TAR DNA-binding protein 43) (Neumann et al., 2006). TDP-43 is a DNA and RNA binding protein with multiple functions comprising pre-mRNA splicing and translational regulation (Cordts et al., 2023). TDP-43 binds to thousands of RNAs in the cell (Lagier-Tourenne et al., 2010). The loss of function in RNA processing and its propensity to aggregate and form protein inclusions are mainly studied to understand ALS pathogenesis (Shefner et al., 2020; Vucic et al., 2021) better. Notably, this protein is also observed in 57% of patients with frontotemporal dementia and 50% of cases with Alzheimer's disease. The accumulation of intracellular inclusions is called the TDP-43 pathology (Neumann et al., 2006).

A single diagnostic test for ALS is not available. Currently, the diagnosis is based on a combination of anamnestic data, objective findings, and neurophysiological characteristics and on the exclusion of other potential pathologies that may partially mimic the clinical picture (e.g., trunk neoplasms, compressive myelopathy). (Goutman et al., 2022). Clinical examination reveals a combination of the typical signs of involvement of upper (paralysis, spastic hypertension, osteotendinous hyperreflexia) and lower motor neurons (fasciculations, muscle atrophy, hypotonia, and areflexia). The original diagnostic criteria defined in 1990 in El Escorial and their revisions in 1998 in Airlie House (USA) and 2006 in Awaji-shima (Japan) were primarily based on the presence of signs of simultaneous involvement of UMN and LMN in one or more of the four body regions: bulbar, cervical, thoracic, and lumbosacral. From the various combinations, the following sub-categories were now identified: "suspected," "possible," "probable," "probable with laboratory support," and "definite" (van Es et al., 2017). However, using these criteria was insufficient for an early diagnosis or to meet the requirements for inclusion in therapeutic trials (Vucic et al., 2021). In September 2019, the most recent Gold Coast diagnostic criteria were defined, simplifying and allowing an earlier diagnosis of ALS. However, the diagnosis is still clinically based on (Shefner et al., 2020).

2. ALS protein biomarkers

Biological markers, also called biomarkers, are measurable variables that signal a normal, natural process, the presence of a disease state, or the pharmacologic response to therapy. Different types of biomarkers have been described, such as molecular, radiographic, or physiological markers (Califf, 2018). The NIH-FDA has identified seven categories of biomarkers related to BEST (Biomarkers, EndpointS, and other Tools) Resources, each with its specific application. The types of biomarkers are 1. susceptibility/risk, 2. diagnostic, 3. monitoring, 4. prognostic, and 5. predictive, 6. pharmacodynamic/response, and 7. safety (FDA-NIH Biomarker Working Group, 2016). All these classes have a critical role in the whole developmental process of new therapies.

In ALS, new biomarkers are warranted to diagnose the pathology early. Diagnosing a person with ALS takes an average of one year, and the disease is confirmed in its progression, excluding ALS mimic syndromes (Goutman et al., 2022). Biomarkers are needed to stratify patients for enrollment in clinical trials to evaluate the effects of treatment in a homogeneous population, particularly in a complex disorder like ALS, characterized by a spectrum of variable disease trajectories. It is also necessary to use biomarkers to predict the rate of disease progression and track biological responses to therapy (Brooks et al., 2000).

Nowadays, different types of biomarkers have been studied and proposed for ALS. Biochemical, imaging, and neurophysiological techniques are applied to study this pathology. Here, we will summarize the most discussed and validated molecular markers among different laboratories and measured in biofluids associated with ALS.

2.1. Neurofilaments

Neurofilaments are intermediate filaments with a diameter of approximately 10 nm that are found as exclusively cytoskeletal scaffolds of neurons in both the central nervous system (CNS) and peripheral nervous system (PNS) (Zucchi et al., 2020). They are major structural components of giant, myelinated axons but can also be present in cell bodies, dendrites, and synapses (Gürth et al., 2023). Four different subunits are the constituents of the neurofilaments' heteropolymers: light chain, medium chain, heavy chain, and α -internexin or peripherin, considering CNS or PNS, respectively (Benatar et al., 2022). Neurofilaments stabilize neuronal axons and their radial growth, enabling high-velocity nerve conduction (Khalil et al., 2018). Their turnover is poorly understood; the ubiquitin-proteasome system and autophagy have been proposed as mechanisms for their degradation (Rao et al., 2023). However, the mechanisms inducing their release into the bloodstream are not entirely uncovered; possibly, it is linked to axonal damage or degeneration. Other factors, such as an increased synthesis or turnover of the neurofilament proteins, an altered transport, or exosome release, have also been considered (Verde et al., 2023). As a result, neurofilament fractions can be detected in CSF and blood. It emerged that the measure of neurofilaments could be regarded as a non-specific marker of neuroaxonal injury, regardless of the causal pathway of neuronal degeneration (Verde et al., 2021).

Nevertheless, neurofilaments in biofluids, mainly CSF and blood, have been assessed in different diseases, including acute neurological conditions, infections, and neurodegenerative and neuroinflammatory diseases (Simrén et al., 2022). However, neurofilaments are considered the elective biomarkers for ALS for the surprisingly high levels observed in patients (Verde et al., 2021) (Table 1). The most vulnerable cell type in ALS is spinal motor neurons, which display large and long myelinated axons and are enriched in neurofilament fragments. Mutations in NFH and peripherin genes have been found in a few ALS patients (Verde et al., 2021), although it is unknown if their presence correlates with increased neurofilament levels (Figlewicz et al., 1994; Gros-Louis et al., 2004).

Many studies have been conducted to assess the robustness of neurofilament fragment measures in biofluids in ALS, considering both the neurofilament light chain (NfL) and phosphorylated neurofilament heavy chain (pNfH) as diagnostic, prognostic biomarkers and potentially also as pharmacodynamic biomarkers (Benatar et al., 2020; Poesen and Van Damme, 2019). Initially, the detection of neurofilament fragments was confirmed in the CSF, where the concentration of both NfL and pNfH can be easily quantified, and their levels are significantly higher in ALS patients than in controls (Abu-Rumeileh et al., 2020; Wilke et al., 2019). NfL is considered less specific to ALS than pNfH, which was proposed as the best biomarker for ALS in CSF by Poesen et al., 2017 (Poesen et al., 2017). At the same time, NfL correlates with the ALSFRS score, suggesting NfL in the CSF is a marker of ALS severity (Brodovitch et al., 2021).

Since lumbar puncture is an invasive procedure and is not part of the standard clinical practice, the possibility of translating the neurofilament fragments measurement from CSF to blood has been investigated with the observation that NfL is forty times less present in the bloodstream compared to the CSF (Verde et al., 2021). Nevertheless, the advent of sensitive techniques, like Simoa, allowed for examining the NF concentration in blood in longitudinal studies (Khalil et al., 2018; Zucchi et al., 2020). Notably, a moderately strong correlation exists between CSF and serum NfL levels (Alagaratnam et al., 2021; Gille et al., 2019). In contrast, such a correlation was not confirmed for pNfH levels (Benatar et al., 2019). The latter result is probably caused by the low dynamic range of the ELISA used to measure serum pNfH concentrations. ELISA methodological limitations resulted in more than 50% of the samples being outside the analytical curve, performed in a small cohort of patients (ten ALS, ten FTD, and ten control subjects) (Wilke et al., 2019).

Moreover, serum pNfH was reported not to add prognostic value to

Table 1

Summary of studies in which neurofilaments have been measured since 2016. Abbreviations: IPN=Inflammatory Peripheral Neuropathy, NHC=Neurologically Healthy Controls, eGFR=estimated Glomerular Filtration, PLS=Primary Lateral Sclerosis, MN=motor neurons, MND=motor neuron disease, OND=other neurodegenerative diseases.

Reference	Biofluid	Cohort of patients	Methodology	Take home message
Oeckl et al. (2016)	CSF	75 ALS 75 controls	ELISA	CSF NfL and pNfH are increased in ALS patients from fifteen centers
De Schaepdryver et al. (2018)	CSF Blood	85 ALS 31 ALS mimics 215 disease control	ELISA Optimized ELISA with biotin/streptavidin	CSF pNfH is higher in ALS patients and correlates with survival Serum pNfH correlates with CSF pNfH Serum pNfH ALS patients significantly overlap with levels of disease controls and ALS mimics pNfH does not associate with upper/lower MN dysfunction Serum pNfH has a weak but significant correlation with disease progression and survival pNfH is a diagnostic biomarker pNfH and NfL levels correlate with the extent of UMN and LMN involvement.
Poesen et al., 2017	CSF	220 ALS 316 OND 50 ALS mimics	pNfH (Biovendor, Brno, CzechRepublic; RD191138300R) NfL (UmanDiagnostics AB, Umea, Sweden; UD51001)	pNfH is a diagnostic biomarker pNfH and NfL levels correlate with the extent of UMN and LMN involvement.
Benatar et al. (2018)	CSF Blood	17 ALS 84 individuals at risk for ALS 10 phenoconverters 34 HC	Electrochemiluminescence immunoassay Electrochemiluminescence immunoassay	CSF NfL levels are higher in ALS patients than in controls and at-risk individuals and remain stable over time. Levels increase over HC in phenoconverters twelve months before symptoms onset Serum NfL levels are higher in ALS patients than in controls and at-risk individuals and remain stable over time Levels increase over HC in phenoconverters 12 months before symptoms onset
Gille et al. (2019)	Blood	149 ALS 19 ALS mimics 82 disease control	CSF NfL levels: enzyme-linked immunosorbent kit (UmanDiagnostics, Umea) Sweden Serum NfL levels: electrochemiluminescent assay Simoa	Strong correlation between serum NfL and CSF NfL levels Serum NfL correlates with UMN degeneration and disease progression rate
Verde et al. (2019)	Blood	124 ALS 44 disease control 50 controls 65 OND	Simoa	Serum NfL is higher in ALS than all other conditions (cut-off 62 pg/mL, 85.8% sensitivity, 81.8% specificity), except for Creutzfeldt-Jakob disease Serum NfL correlates with disease progression; higher levels are associated with shorter survival NfL remains stable over the disease course
Benatar et al. (2019)	CSF Blood	22 ALS 79 individuals at risk for ALS 14 phenoconverters 34 controls	Enzyme-linked immunosorbent assay Enzyme-linked immunosorbent assay	Longitudinal study, analysis of pNfH before and after phenoconversion CSF NfL and pNfH can discriminate against ALS patients CSF and serum pNfH levels are poorly correlated Serum NfL increases longitudinally before symptoms onset, and this has also been seen for pNfH In both serum and CSF: 6–12 months prior in SOD1 A4V mutation carriers, 2 and 3.5 years in FUS c.521del6 mutation and C9orf72 HRE, respectively Serum NfL distinguish between ALS and HC controls and at-risk individuals; pNfH levels overlap between the three groups Serum NfL is higher in ALS patients; levels > 15 pm/mL discriminate ALS patients and control (94% severity, 100% specificity)
Thouvenot et al. (2020)	Blood	207 ALS 21 HC	Simoa	Serum NfL is a strong and independent prognostic factor of death in ALS at the diagnosis and positively correlates with the ALSFRS-R rate of decline
Wilke et al. (2019)	CSF Blood	10 ALS 10 FTD 14 controls	Homebrew Simoa, commercially available Simoa, and ELISA Homebrew Simoa, commercially available Simoa, and ELISA	In CSF, pNfH concentrations are strongly correlated between the three analytical approaches CSF pNfH levels can differentiate ALS patients from controls Serum pNfH has a strong correlation between the two Simoa assays but not between Simoa and ELISA Serum pNfH correlates with CSF pNfH if measured by the two Simoa approaches
Abu-Rumeileh et al. (2020)	CSF	80 ALS 46 ALS mimics 43 HC	Enzyme-linked immunosorbent assay kits	CSF NfL levels are higher in ALS than in ALS mimics and control There is a positive correlation between NfL levels and the extent of LMN involvement; there is no significant correlation with UMN
Benatar et al. (2020)	Blood	229 ALS 20 PLS 11 progressive muscular atrophy	Simoa	Baseline serum NfL, but not pNfH, predicts the future ALSFRS-R slope and survival: clinically validated biomarker Serum NfL, and perhaps pNfH, potential pharmacodynamic biomarkers
De Schaepdryver et al. (2020)	Blood	383 ALS	-	Serum NfL is higher in women Serum NfL shows a weak significant correlation with disease progression rate; high serum NfL is associated with shorter survival
Dorst et al. (2020)	Blood	100 ALS	Simoa	Serum NfL positively associates with progression rate Fast progressors have higher NfL median levels and prognostic biomarkers
Falzone et al. (2020)	Blood	219 MND	ELISA	Serum pNfH is a negative independent prognostic factor of survival Pyramidal, bulbar, and classic phenotypes have higher pNfH

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Table 1 (continued)

Reference	Biofluid	Cohort of patients	Methodology	Take home message
				than LMN and UMN involvement Higher serum pNfH levels in C9orf72 MND patients compared to non-C9orf72 MND Higher levels but not significant in MND patients with cognitive dysfunction CSF NfL and pNfH levels are significantly higher in ALS patients and negatively correlated with survival Plasma NfL is significantly higher in ALS patients than controls Plasma NfL is significantly higher in ALS patients with bulbar onset than spinal onset Plasma NfL is significantly higher in patients with C9orf72HRE mutation than in patients with SOD1 mutation and worse survival Plasma NfL negatively correlates with survival and can differentiate between short and extended survival CSF NfL is the best marker of ALS severity CSF NfL + CSF ICAM-1 + serum IFN-gamma: improved diagnostic performance Serum NfL marker of disease progression rate
Behzadi et al. (2021)	CSF Blood	234 ALS 44 ALS mimics 9 controls	NfL: validated ELISA pNfH: in-house-developed ELISA Simoa	
Brodovitch et al. (2021)	CSF Blood	20 ALS 17 IPN 60 ALS 94 HC 43 IPN	R-PLEX Human Neurofilament L Antibody Set from MesoScale Discovery R-PLEX Human Neurofilament L Antibody Set from MesoScale Discovery	
Kläppe et al. (2022)	CSF	150 ALS 28 ALS mimics 108 HC	UmanDiagnostics' sandwich enzyme-linked immunoassay (Umeå, Sweden; cat number 10-7001) Simoa	CSF NfL slowly decreases and becomes stable after that CSF NfL performs better than hs-cTnT as a diagnostic and prognostic biomarker CSF NfL is higher in ALS patients, particularly in fast progressors than intermediate- and slow-progressors CSF NfL is a better diagnostic marker CSF NfL levels are associated with the number of body regions displaying UMN signs Plasma NfL is higher in ALS patients, particularly in fast progressors than intermediate- and slow-progressors Plasma NfL levels are associated with the number of body regions displaying UMN signs Longitudinally, plasma NfL levels remain stable CSF NfL does not provide any significant advantage over plasma NfL
Vacchiano et al. (2021)	CSF Blood	171 ALS 60 ALS mimics 171 ALS 60 ALS mimics	Simoa Simoa	
Thompson et al. (2022)	CSF Blood	258 ALS 80 OND 101 HC 258 ALS 80 OND 101 HC	Meso Scale Discovery R-PLEX electrochemiluminescence platform Meso Scale Discovery R-PLEX electrochemiluminescence platform	Plasma NfL is associated with survival Plasma NfL increases the power in clinical trials
Verde et al. (2023)	Blood	209 ALS 46 NHC	Simoa SR-X platform (Quanterix, Lexington, MA, United States)	Serum NfL levels can discriminate between ALS and NHC Females have higher serum NfL levels Serum NfL levels are higher with both UMN and LMN involvement, showing a predominance of UMN Negative correlation between serum NfL and eGFR

NfL (Benatar et al., 2020). As a cautionary note, blood NfL shows significant inter-individual variability (Simrén et al., 2022) and correlates with age (Benatar et al., 2018). This correlation is less pronounced but still present in ALS patients (Verde et al., 2023), with higher values in female ALS patients than males (De Schaepdryver et al., 2019; Thouvenot et al., 2020; Verde et al., 2023).

Concerning the involvement of UMN and LMN, both pNfH and NfL measured in the CSF correlate with the extension of the CNS regions involved in the degeneration (Abu-Rumeileh et al., 2020; Poesen et al., 2017). Peripherally, serum NfL levels are higher in patients displaying both UMN and LMN degeneration (20), even though serum NfL concentration exhibits a stronger correlation with clinical signs of UMN involvement (Gille et al., 2019; Verde et al., 2023). UMN and LMN's specific contribution to the neurofilament fractions detectable in biofluids is still under investigation.

From a prognostic point of view, NFs were measured in carriers of ALS genes in a longitudinal study and compared to sporadic patients and controls. NfL levels did not differ between patients with familial and sporadic ALS (Verde et al., 2023) but from the pre- to the symptomatic phase. ALS patients show significantly higher serum and CSF NfL levels than at-risk individuals and control (Benatar et al., 2018). Nevertheless, a progressive increase of NF levels in both CSF and serum in at-risk individuals carrying ALS mutation was also reported; for instance, in SOD1 mutation carriers, the increase was observed twelve months

before the onset of the symptoms, while in patients with FUS c.521del6 mutation or C9orf72 hexanucleotide repeat expansion (HRE) carriers up to 3.5 years before phenoconversion (Benatar et al., 2019). Further studies will be needed to determine if the length of the presymptomatic phase is proportional to that of the symptomatic stage. Finally, fast-progressor patients show higher median NfL levels at baseline than slow-progressors (Dorst et al., 2020).

Neurofilaments are nowadays quantified in clinical trials. One of the best examples of their use in clinical settings is the study of patients treated with Tofersen, an antisense oligonucleotide against SOD1. NfL levels were reduced in the plasma of treated patients (Miller et al., 2022).

2.2. (Neuro)Inflammation-related biomarkers

Nowadays, neuroinflammation is recognized as a pathological feature of ALS (De Marchi et al., 2023), even if it is still unclear whether it emerges because of neurodegeneration or as a pathogenic trigger that precedes neuronal loss. At the early stages of the disease, neuroinflammation may be involved in maintaining brain homeostasis through anti-inflammatory responses. Specifically, this phase is characterized by the presence of reactive CNS microglia and by the infiltration of immune cells from the periphery. There is an increase in regulatory T cells, upregulation of anti-inflammatory cytokines, and

activation of neuroprotective microglia cells. Subsequently, a proinflammatory response is elicited, with more effector T cells and cytokines and activated neurotoxic microglia cells (Vucic, 2019). Inflammatory biomarkers may be of great interest in predicting disease progression, stratifying patients, and monitoring drug responsiveness in clinical trials, even though they are not specific to ALS. The most studied inflammatory markers will be briefly presented.

2.2.1. Chitinases

Chitinases are a family of enzymes in the innate immunity cells; their expression is increased by inflammatory states (Kumar and Zhang, 2019). Chitotriosidase 1 (CHIT1) and chitinase-like proteins, namely chitinase-3-like protein 1 (YKL-40) and chitinase-3-like protein 2 (CHI3L2), exhibit high CSF levels in ALS patients, discriminating from healthy control subjects and patients affected by other neurodegenerative diseases (Dreger et al., 2022; Thompson et al., 2018; Thompson and Turner, 2019; Vu et al., 2020). CHIT1 and YKL-40 levels correlate with the disease progression rate and severity, and they are more abundant in fast than slow progressors (Andrés-Benito et al., 2018; Gille et al., 2019; Steinacker et al., 2018; Varghese et al., 2020; Vu et al., 2020). Finally, CSF CHIT1 displays the strongest correlation with NF levels, while YKL-40 ameliorates the prediction power of NFs in the survival of ALS patients (Masrori et al., 2022; Steinacker et al., 2021). In longitudinal studies, CHIT1 and YKL-40 levels are comparable to control groups at the asymptomatic stage of carriers of ALS-causing genetic mutation, with a rapid increase at symptom onset (Gray et al., 2020; Oeckl et al., 2019, 2018).

CHIT1 and YKL-40 levels were also investigated in serum and plasma. Still, no significant differences were observed among ALS patients and control (Gille et al., 2019; Steinacker et al., 2018), making the diagnostic accuracy of chitinases alone inferior to that of neurofilaments. However, in some studies, combining all three chitinases improves their diagnostic performance (Thompson et al., 2018).

Notably, one-third of Europeans manifest a duplication of the *CHIT1* gene that results in lower levels and activity of CHIT1 (Thompson and Turner, 2019). Particularly, homozygous carriers of *CHIT1* 24-bp duplication polymorphism have undetectable CHIT1 levels that result in a complete enzyme activity deficiency, while heterozygous and wild-type carriers have similar CHIT1 levels in CSF (Steinacker et al., 2021). This polymorphism has been proven to not correlate with axonal degeneration and disease severity in ALS patient studies (Oeckl et al., 2019). Still, it may be relevant to assess the presence of the polymorphism in future studies based on this neuroinflammation marker as a potential confounding factor.

2.2.2. GFAP

Glial fibrillary acidic protein (GFAP) is another protein linked to neuroinflammation, specifically astrogliosis, a feature observed in ALS patients (Vargas and Johnson, 2010). GFAP is also the most abundant astrocyte cytoskeletal protein. Conflicting results have been reported until now regarding its performance as a biomarker. In one study, the concentration of GFAP in CSF was higher in ALS patients than in other neurological conditions, suggesting a trend between its levels and the disease duration (Benninger et al., 2016). Oppositely, Oeckl reported no significant increase in GFAP levels in CSF of ALS patients (Oeckl et al., 2019). Considering GFAP concentration in serum instead, a significant increase was noted in ALS patients, with a weak or no diagnostic performance in discriminating ALS patients from controls (Falzone et al., 2022; Verde et al., 2023). Its serum levels are linked to cognitive and behavioral impairment in ALS patients (Falzone et al., 2022), with higher values in females (Verde et al., 2023). Further studies are needed to define its use as a biomarker for ALS.

2.2.3. Cytokines

Chitinases and GFAP are not the only candidate biomarkers of inflammation studied in biofluids of ALS patients; indeed, type I

interferons (IFNs), interleukins (ILs), and tumor necrosis factor (TNF) have gained attention. These innate immune system components highlight the importance of neuroinflammation, but more in general, of a systemic inflammatory response.

In recent years, several studies have analyzed many soluble factors in a multiplexing setting, obtaining a different combination of significantly altered cytokines in the biofluids of ALS patients (Dreger et al., 2022; Staats et al., 2022). Notably, cytokines cannot outperform the solid prognostic value for survival obtained by the analysis of neurofilaments, mainly due to the high inter-subject variability and the different pathways regulating cytokines release (Huang et al., 2020a). Cytokine levels correlate with age, which could result from ALS's pathogenic mechanism and the aging process (Olesen et al., 2020). In patients with a hexanucleotide repeat expansion in the *C9orf72* gene, there is a correlation between higher IL-1 β plasma levels and survival (Olesen et al., 2020). Patients with a short survival exhibit higher levels of TNF- α and IL-1 β in plasma and higher levels of TNF- α in CSF (Olesen et al., 2020). Another study found a significant increase of the proinflammatory cytokines MCP-1, MIP-1 α , and IL-18 in CSF and MCP-1 and IL-18 in the blood of ALS patients. Finally, a significant correlation was not observed between central and peripheral cytokine levels (Huang et al., 2020b).

Because of proinflammatory cytokines releases, such as IL-6, IL-1 β , and TNF- α , hepatocytes produce acute phase proteins (APPs). APPs include soluble CD14 (sCD14), lipopolysaccharide-binding protein (LBP), and C-reactive protein (CRP). All these three proteins have been reported to be elevated in the serum of ALS patients (Beers et al., 2020). sCD14 was also increased in the CSF and urine of ALS patients (Beers et al., 2020). Ferritin, creatine kinase (CK), complement C3, and complement C4 were also analyzed with an increase for plasma CK, serum ferritin, and C3 (Thompson et al., 2022), but further validations are needed.

2.2.4. Neopterin

Another marker of systemic proinflammation is neopterin, a small molecule released in response to IFN- γ from monocytic cells, such as macrophages and dendritic cells in the periphery and microglia cells in the CNS (Shepherd et al., 2022). Neopterin is, therefore, a marker of cell-mediated inflammation, and its release correlates with reactive oxygen species production (Sucher et al., 2010).

Neopterin urinary levels at baseline are higher among ALS patients than healthy controls and other neurological disease patients and inversely correlate with ALSFRS-R scores (Lunetta et al., 2020; Shepherd et al., 2022). Neopterin levels progressively increase during the disease (Shepherd et al., 2022), suggesting it is a potentially valuable marker for monitoring the effects of drugs targeting the immune system.

2.3. Other biomarkers

2.3.1. p75^{ECD}

The neurotrophin receptor (p75^{NTR}) is a member of the superfamily of tumor necrosis factor receptors that bind neurotrophins (and their respective pro-neurotrophins), a family of closely related proteins composed, among others, by nerve growth factor (NGF), brain-derived neurotrophic factor (BDNF), neurotrophin-3 (NT3), and neurotrophin-4 (NT4) (Chao, 1994). It mediates opposite functions, such as neuronal growth, synapse plasticity, and apoptosis (Sankorrakul et al., 2021). P75 is highly expressed postnatally during development, with a drastic downregulation (Chen et al., 2017). Its expression is restored after injury or in motor neurons and Schwann cells in postmortem tissue of ALS patients (Shepherd et al., 2017). The soluble extracellular domain of the neurotrophin receptor (p75^{ECD}) is cleaved after injury and excreted in urine; its urinary detection is indicative of motor neuron degeneration (Shepherd et al., 2014). Urinary p75^{ECD} levels are significantly higher in ALS than in patients affected by other neurological diseases and healthy controls, with a negative correlation between urinary p75^{ECD} and baseline ALSFRS-R (Jia et al., 2017). Its levels are

significantly higher in fast-progressing ALS patients than in slow-progressing patients (Jia et al., 2017), and it increases following disease progression and motor function decline (Shepherd et al., 2017).

These characteristics make p75^{ECD} a valuable marker for monitoring disease progression. Evaluating its levels in urine has clear advantages, considering that it is a biofluid that is readily accessible, non-invasive, easy to collect, and allows frequent sampling (Shepherd et al., 2017). This evidence must be validated in more extensive independent studies because p75^{ECD} is not highly specific for ALS. It would also be interesting to monitor its levels in FTD and ALS mimics patients (Jia et al., 2017).

2.3.2. p-Tau/t-Tau

Tau is a microtubule-associated protein stabilizing neuronal microtubules and promoting nerve growth (Wang and Mandelkow, 2016). A subset of neurodegenerative diseases, called tauopathies, are characterized by aggregates of hyperphosphorylated tau, mainly in paired helical filaments and neurofibrillary tangles (Wang and Mandelkow, 2016). In recent years, both total tau (t-tau) and phosphorylated tau (p-tau) have gained attention as biomarkers mainly for Alzheimer's disease (AD) and other tauopathies, and the ratio p-tau/t-tau is considered an established marker in frontotemporal dementia (FTD) spectrum (Abu-Rumeileh et al., 2020).

Tau protein has also been investigated in biofluids of ALS patients, and surprisingly, its levels were found to be altered compared to controls. In CSF, t-tau levels have been reported to be higher in ALS patients than in controls and ALS mimics (Abu-Rumeileh et al., 2020). Higher t-tau levels were found in ALS patients with bulbar onset (Petrozziello et al., 2022). Among the multiple phosphorylation sites present in the protein, tau phosphorylated at threonine 181 (p-tau181) is the predominant one. Even though no difference was detected in CSF p-tau181, the ratio p-tau181/t-tau is reduced in ALS patients (Scarafino et al., 2018). Notably, a correlation between the increased t-tau and decreased p-tau181/t-tau ratio and ALS progression rate was assessed with the ALSFRS-R, suggesting that they may be used as predictive biomarkers (Petrozziello et al., 2022).

Serum t-tau levels are significantly lower in the patients than in the healthy control (Falzone et al., 2022). Instead, plasma p-tau181 levels were significantly higher in ALS patients than in controls but still lower than in AD patients (Vacchiano et al., 2023), poorly discriminating between these neurodegenerative diseases (Cousins et al., 2022). Plasma p-tau181 levels correlate with lower motor neuron (LMN) signs in cervical, thoracic, and lumbosacral regions (Cousins et al., 2022). The absence of a correlation between p-tau181 levels in CSF and plasma-/serum may underline the peripheral origin of its increased amount (Gong et al., 2022; Vacchiano et al., 2023). Longitudinally, increased plasma p-tau181 levels have been reported over time, with a marked trend in fast progressors (Vacchiano et al., 2023).

In conclusion, tau protein does not outperform the predictive value of survival and the diagnostic performance of neurofilaments; anyway, it may be considered a valuable biomarker to integrate into the monitoring procedure as a complement of neurofilaments.

2.3.3. UCHL1

Ubiquitin carboxyl-terminal hydrolase isozyme L1 (UCHL1) is expressed in the cytoplasm of neurons and is involved in the ubiquitin-proteasome system (Falzone et al., 2022). It is a multifunctional protein with hydrolase and ligase activity (Barschke et al., 2020).

CSF levels of UCHL1 are significantly higher in ALS patients than in other neurodegenerative disorders patients (Li et al., 2020). CSF UCHL1 levels increase in fast-progressor ALS patients (Zhu et al., 2019) and discriminate between C9orf72 gene mutation (C9-ALS) carriers and C9-ALS patients with behavior variant FTD signs from C9-FTD and controls (Barschke et al., 2020).

The serum concentration of UCHL1 does not differentiate ALS from other neurological disorders and ALS mimics (Falzone et al., 2022). Still, it shows a significant difference with healthy controls, even if conflicted

results have also been reported (Li et al., 2020).

2.4. Muscle biomarkers

Cardiac troponin T (cTnT) is a component of the sarcomere of striated muscles in the heart that regulates excitation-contraction coupling and is released by disintegrated myocytes (Mueller et al., 2013). The expression of cTnT and cardiac troponin I (cTnI) is highly tissue-specific, and their detection in serum is commonly used as an indicator of myocardial infarction (Mueller et al., 2013). Surprisingly, cTnT levels were found elevated in the peripheral blood of more than half of ALS patients in a cohort of subjects without evidence of cardiac diseases (Mach et al., 2016). It has been reported that cTnT concentration correlates with disease progression (Mach et al., 2016) and increases longitudinally (Casmiro and Graziani, 2019; Kläppe et al., 2022). ALS had higher values than ALS mimics patients and healthy controls, with maximum concentration in non-bulbar ALS patients (Kläppe et al., 2022). There was no correlation between cTnT in serum/plasma and NfL (Kläppe et al., 2022) CSF levels and pNfH (Castro-Gomez et al., 2021). Considering this evidence and that cTnI serum levels remain stable in ALS patients, peripheral skeletal muscle is believed to be a possible source of cTnT (Castro-Gomez et al., 2021).

Regarding the exact nature of measured cTnT, it has been hypothesized that its re-expression in diseased skeletal muscle (Castro-Gomez et al., 2021). However, it has also been proved that there could be a cross-reaction of the immunoassay for cTnT with skeletal TnT (Schmid et al., 2018). Considering that the role of cTnT in ALS and its origin are still unclear, it would be interesting to better investigate this marker in ALS patients, considering its increasing levels over time and potential utility in monitoring the disease.

Interestingly, cTnT levels also correlate with another marker of muscle cell damage that can be measured in the serum of ALS patients: creatine kinase isoenzyme MB (CK-MB) (Kittipeerapat et al., 2023). CK is an enzyme involved in energy metabolism; the isoenzyme CK-MB is mainly expressed in the myocardium and minimally in skeletal muscles (Kittipeerapat et al., 2023). As cTnT, CK-MB was also elevated in more than half of ALS patients in the analyzed cohort, with higher levels recorded in patients with spinal onset (Kittipeerapat et al., 2023). Other studies also measured total CK in the blood of ALS patients, which is broadly expressed by various cell types. ALS patients reported higher concentrations, particularly spinal-onset patients (Ceccanti et al., 2020). The increased CK levels in ALS patients have been linked to lower motor neuron loss and muscle denervation (Tai et al., 2018).

2.5. Extracellular vesicles

Extracellular vesicles (EVs) are small membranous nanoparticles ubiquitously released from the cell. They are a heterogeneous group of stable particles carrying nucleic acids, lipids, and proteins of different sizes and origins (Hill, 2019). EVs mediate intercellular communication; they reach and fuse with neighboring or distant cells (Basso and Bonetto, 2016), even though the exact up-take mechanisms in the receiving cells have yet to be completely elucidated. EVs have been isolated from different biofluids, such as blood, CSF, saliva, urine, and milk. The possibility of detecting them in biofluids and that EV cargo reflects the parental cell composition favors EV applicability as a biomarker (Ferrara et al., 2018).

As ALS is a multisystem disease, circulating EVs may be very informative about the pathological state of the patients. Moreover, they could mirror early pathological events (Barbo and Ravník-Glavač, 2023). Plasma EVs themselves have been proposed as biomarkers for disease diagnosis and prognosis. Combining their biophysical parameters and the presence of two specific proteins in their cargo, namely HSP90 and cyclophilin A, and exploiting machine learning techniques, it was possible to propose EVs as diagnostic and prognostic biomarkers discriminating fast- and slow-ALS progressors (Pasetto et al., 2021).

Moreover, the leukocyte-derived microvesicles are over-represented in the blood of ALS patients and enriched in misfolded SOD1 protein (Sproviero et al., 2019). A few studies analyzed EVs isolated from CSF of ALS patients. Being CSF physically close to the cells of the central nervous system, we can speculate that its EV content is representative of alterations occurring when neuronal degeneration starts. Considering the size distribution of CSF EVs, no differences were reported between ALS patients and controls.

Still, the proteomic analysis revealed a defect in the proteostasis (Thompson et al., 2020). Similarly, in another study investigating the mRNA content of CSF EVs, several genes were deregulated in ALS patients compared to healthy controls, mainly involved in the ubiquitin-proteasome pathway, oxidative stress response, and unfolded protein response (Otake et al., 2019). Moreover, the transcriptomic analysis of blood EVs revealed a difference between the mRNA composition of small and large EVs in ALS patients (Sproviero et al., 2022). Among microRNAs in ALS patients, miR-15a-5p and miR-193a-5p showed a diagnostic potential and were associated with disability progression (Saucier et al., 2019). miRNAs have also been analyzed in neuron-derived EVs, a subpopulation of plasma EVs

immunoprecipitated with L1CAM/CD171 showing thirty deregulated molecules between ALS patients and healthy controls (Katsu et al., 2019). In another study, the comparison between EVs from the frontal cortex, spinal cord, and blood of ALS patients and healthy controls revealed miR-342-3p as increased and miR-1254 as decreased in ALS (Lo et al., 2021). Of note, there has yet to be a consensus on specific RNA, messengers, or microRNAs as biomarkers to measure to follow the disease progression. Although EVs are an attractive source of biomarkers, many challenges are still open in the EV field. The lack of consensus and standardization on protocols for the isolation and analysis of EVs makes inter-laboratory data comparison difficult (Théry et al., 2018).

3. Conclusions

Nowadays, many different molecules have been proposed as candidate biomarkers (Fig. 1). Although various studies have been conducted to validate them as promising diagnostic or prognostic markers, none are currently used in clinics. It is reasonable that a single marker would not be able to address the whole complexity of this pathology. Therefore,

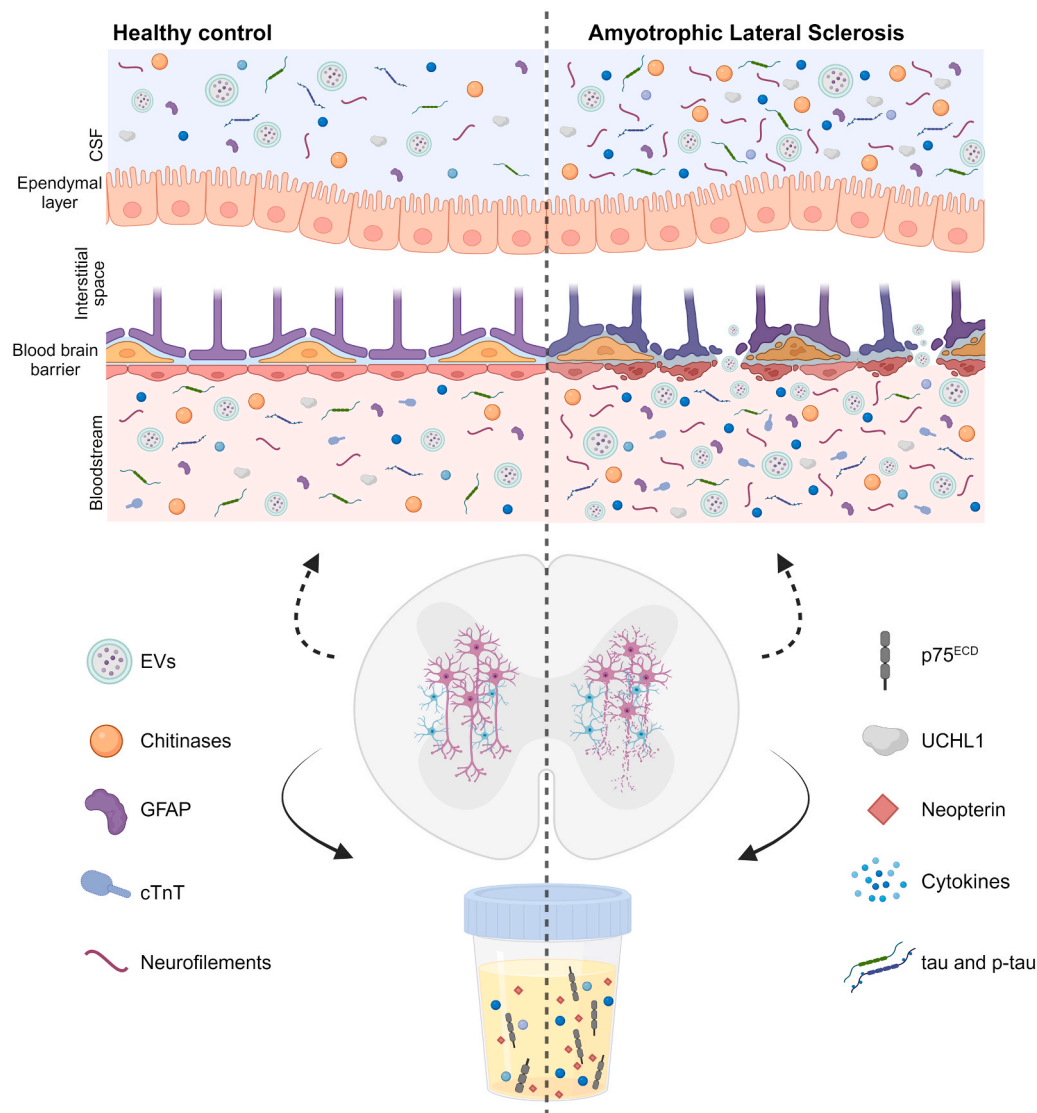


Fig. 1. Biochemical biomarkers for ALS. Schematic representation of the different biomarkers measured in ALS patients' biofluids (CSF, blood, and urine) with varying proportions in the pathology and healthy control context. EVs=extracellular vesicles; cTnT= cardiac troponin T; UCHL1 = ubiquitin carboxyl-terminal hydrolase isozyme L1; GFAP = glial fibrillary acidic protein; p75^{ECD} = extracellular domain of the neurotrophin receptor. Created with Biorender.com.

there is a joint interest in combining different biomarkers in a multiplexing system to obtain information deriving from other mechanisms involved in the neurodegenerative process. Among those proposed, blood- and urine-based biomarkers are favored, requiring less or non-invasive sampling and may be arranged in biochemical assays usable in clinical practice and repeated routinely.

Currently, neurofilaments are the most promising biomarkers for ALS. Many different groups and centers have validated them, and their measurement is reproducible and standardized. However, it is crucial to consider that its release is the outcome of motor neuron degeneration. In this review, we have listed several additional molecules investigated as candidate biomarkers. The joint effort to arrange multicenter studies for their final validation is notable for all of these. For any candidate marker, it is essential to be validated in many patients, in multiple centers, with a fixed sampling procedure, analysis, and the definition of standard endpoints.

For the future, it is auspicious to define biomarkers that recapitulate early changes happening in the presymptomatic stage when no apparent symptoms or signs of the disease are manifest.

Declaration of Competing Interest

The authors declare no conflict of interest.

Data Availability

No data was used for the research described in the article.

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