

The blood biomarker puzzle – A review of protein biomarkers in neurodegenerative diseases

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Highlights

- Fluid biomarkers for neurodegenerative conditions are an urgent unmet need
- Technical advances enable a highly sensitive detection of biomarkers in blood
- Each biomarker is reflecting different aspects of CNS pathology
- Biomarkers can stratify patients based on biology rather than clinical phenotype

Abstract

Neurodegenerative diseases are heterogeneous in their cause and clinical presentation making clinical assessment and disease monitoring challenging. Because of this, there is an urgent need for objective tools such as fluid biomarkers able to quantitate different aspects of the disease. In the last decade, technological improvements and awareness of the importance of biorepositories led to the discovery of an evolving number of fluid biomarkers covering the main characteristics of neurodegenerative diseases such as neurodegeneration, protein aggregates and inflammation. The ability to quantitate each aspect of the disease at a high definition enables a more precise stratification of the patients at inclusion in clinical trials, hence reducing the noise that may hamper the detection of therapeutical efficacy and allowing for smaller but likewise powered studies, which particularly improves the ability to start clinical trials for rare neurological diseases. Moreover, the use of fluid biomarkers has the potential to support a targeted therapeutical intervention, as it is now emerging for the treatment of amyloid-beta deposition in patients suffering from Alzheimer's disease. Here we review the knowledge that evolved from the measurement of fluid biomarker proteins in neurodegenerative conditions.

Abbreviations

AD	Alzheimer's disease
ALS	Amyotrophic lateral sclerosis
BBB	Blood-brain barrier
CIS	Clinically isolated syndrome
CNS	Central nervous system
CSF	Cerebrospinal fluid
CXCL13	C-X-C Motif Chemokine Ligand 13
ECL	Electrochemiluminescence
ELISA	Enzyme-linked immunosorbent assay
FTD	Frontotemporal dementia
GFAP	Glial fibrillary acidic protein
HD	Huntington's disease
IMR	Immunomagnetic reduction
MCI	Mild cognitive impairment
MMP9	Matrix metalloproteinase 9
MRI	Magnetic resonance imaging
MS	Multiple sclerosis
NfL	Neurofilament light chain
(p)NfH	(phosphorylated) Neurofilament heavy chain
PD	Parkinson's disease

PEA	Proximity extension assay
PET	Positron emission tomography
PCR	Polymerase chain reaction
pwMS	Patients with multiple sclerosis
qPCR	Quantitative PCR
RT-QuIC	Real-time quaking-induced conversion
SMA	Spinal muscular atrophy
Simoa	Single molecule array
TDP-43	Transactive response DNA-binding protein 43

1. Introduction

Neurodegenerative diseases are caused by a wide spectrum of biological dysfunctions. The clinical manifestation, the disease course and the therapeutical response is therefore heterogeneous. Biomarkers are tools that enable the detection of pathological processes responsible for these dysfunctions. Sometimes we measure biomarkers that are a byproduct of the disease, other times we measure biomarkers that reflect the damage caused by the disease. In the last few decades, an improvement of immunoassays and mass spectrometry-based methods enabled the robust detection of a number of blood biomarkers that are now initiating a revolution in the way that neurological patients are monitored. Biomarkers originating from the central nervous system (CNS) are present at a higher concentration in the cerebrospinal fluid (CSF) and at multiple fold lower concentration in the blood. Thus, the initial process of biomarker discovery took advantage of CSF biospecimen, particularly from patients suffering from Alzheimer's disease (AD) and amyotrophic lateral sclerosis (Rosengren et al., 1996). These positive findings set a fertile ground for the further development of immunoassays. We may think of them as first generation assays as immunoblot, second generation assays as the enzyme-linked immunosorbent assay (ELISA), third generation using electrochemiluminescence (ECL) technology and the latest fourth generation based on Single molecule array technology (Simoa) (Khalil et al., 2018). The translation of CSF assays into blood was particularly successful with the fourth generation of assays. This category expanded over the last years and now, besides the Simoa (Rissin et al., 2010), it encompasses also proximity extension assays (PEA) (Chitnis et al., 2019), Single Molecule Counting (SMC) (Fischer et al., 2015), immunomagnetic reduction (IMR) (Lue et al., 2019), the Ella platform based on microfluidic channels (Dysinger et al., 2017), and ongoing developments on platforms already used in clinical routine as the ADVIA Centaur and Atellica (Plavina et al., 2019). What was known from the CSF was strengthened and expanded by blood analysis. This exciting new horizon for the biomarker field opens new challenges, including which biomarker suits which disease the best, and what does a fluid biomarker concentration reflect in terms of tissue pathology/pathophysiology and how should it be interpreted. Here we want

to help achieving answers to these questions by reviewing the knowledge pertaining to the use of protein biomarkers in blood for neurodegenerative diseases (**Table 1**).

2. Highly sensitive platforms

Technological advances have made it possible to quantify CNS proteins in the blood (**Figure 1 and Table 2**). This mostly started with the third generation of immunoassays based on ECL (Khalil et al., 2018), which is a kind of luminescence produced during electrochemical reactions in solutions. This technology builds on the sandwich immunoassay principle in which one antibody captures the analyte and another antibody detects it, but instead of an enzymatic reaction producing the detection signal, electrochemiluminescent labels are conjugated to detection antibodies. At the reading phase an electrical stimulus activates the labels that emit a quantifiable signal. The use of an electrical instead of optical signal (as in the ELISA) conferred to the ECL a higher sensitivity (Kuhle et al., 2016).

The advent of the fourth-generation assays characterized by a deeper sensitivity began with the Simoa technology. One of the core characteristics is the formation of immunocomplexes on paramagnetic beads instead of the bottom of a well. This allows to separate the immunocomplexes at the reading stage in spatially distant micro-wells. Hence, the signal originating from one immunocomplex is not spilling into the signal originating from other immune complexes. It allows for the optical detection of signal emitted from the single beads. The ratio between the wells with and wells without signal plotted against a calibrator curve results in the concentration of the targeted protein (Rissin et al., 2010). Most of the current literature on blood biomarkers for neurodegenerative diseases have been produced by using this technology.

A more recent fourth-generation platform is Ella. The platform is based on the use of microfluidic circuits. The sample loaded in a cartridge flows through the microfluidic channels presenting a pre-coating capture antibody that binds the target protein. The antibody is coated on three separate areas, thus allowing for three technical replicates. A system of pumps allows

the flow of the detector antibody, wash solution and the fluorescent dye through the channels. The level of fluorescence is compared to pre-analyzed calibrator curve (Dysinger et al., 2017).

A different concept is brought by the PEA. Two antibodies used to recognize the targeted protein present a specific sequence of oligonucleotide (a DNA “barcode”). The DNA barcodes have specific annealing sites that hybridize if in close proximity, *i.e.*, bound to the same protein, this is followed by an extension and initial amplification by PCR. The PCR is per se non-quantitative. The quantitative read-out is obtained by qPCR or by sequencing. The specificity of the DNA barcodes allows for an incredible number of simultaneously measured proteins (multiplex) and the amplification cycles at the qPCR stage allow for the detection of low abundant proteins (Assarsson et al., 2014).

SMC is a fourth-generation assay characterized by a spatially defined excitation area. More precisely, the sample is first incubated with capture and fluorescently labelled detector antibodies; unbound antibodies are removed by washing. The sample is scanned by a laser able to excite the fluorophore present on the immune complex. The concentration of the target protein is calculated by comparing the count of excitations in the sample and the count in the calibrators (Todd et al., 2007).

The measurement of proteins by IMR could be seen as the equivalent of doing a magnetic resonance imaging (MRI) scan of the samples. Paramagnetic beads coated with an antibody specific to the targeted protein are incubated with the sample and stimulated by alternate magnetic field. The device detects the magnetic pulse originating by the rotating beads. The presence of immunocomplexes on the bead causes a decrease in the rotation speed of the bead, which reflects the quantity of targeted protein present in the sample (Lue et al., 2019).

A further approach is the real-time quaking-induced conversion (RT-QuIC) that is employed for the quantification of prion-like protein seeds. Aggregation-prone proteins, like prion protein and α -synuclein, can adopt a certain conformation that can stimulate further misfolding and aggregation of normally folded proteins. Tissue extracts have been found to contain such seeds and recently they have been found in cerebrospinal fluid (CSF) from patients with, *e.g.*,

prion disease or Parkinson's disease. The assay principle is surprisingly simple: to detect misfolded seeds, recombinant protein (e.g., prion protein) is added into the sample that is incubated over days with regular shaking. Seeded misfolding is detected with fluorescent thioflavin T sensitive to the β -sheet folding of the target protein. The fluorescence is measured over time and compared with reference material of positive and negative controls and the final output is a qualitative result (Cramm et al., 2016; Scialò et al., 2020). An RT-QuIC assay for prion inclusions uses recombinant prion protein, an assay for α -synuclein inclusions uses recombinant α -synuclein, etc. The technique does not work for blood yet.

Finally, mass spectrometry-based techniques for protein concentration determination in blood are getting increasingly common. For example, immunoprecipitation mass spectrometry (IP-MS) is the assay type that results in the most reliable quantification of amyloid β ($A\beta$) peptides in plasma to date.

Regarding inter-platform comparisons, a practical example was brought by Gauthier and colleagues who showed how the blood levels of neurofilament light chain (NfL) measured by Simoa (NfL advantage kit) and Ella are highly correlated (Gauthier et al., 2021), hence the findings obtained by Ella translate to Simoa and vice versa. However, the absolute NfL level was almost half in the Simoa measurements, despite the fact that both use the same pair of antibodies. The main reason for differences in absolute concentration in such cases is that the assays use different calibrators that have not been standardized to each other. A certified reference material that can be used by assay manufacturers to “calibrate their calibrators” can result in standardization of biomarker assays.

3. Alzheimer's disease (AD)

The marvelous success of biomarkers in this disease shaped the landscape of biomarker discovery in neurologic diseases. Analysis of postmortem tissue and later PET scans evidenced the presence of aggregates of beta amyloid and neurofibrillary tangles in the brain

of AD patients (Masters et al., 2015). In chronological order, the disease appears to start with an overproduction of an amyloid beta isoform that is 42 amino acids long (A β 42, A) followed by an accumulation of neurofibrillary tangles rich in truncated and phosphorylated tau (T), which results in neurodegeneration (N) (Masters et al., 2015). From a biomarker perspective, these three domains are part of the ATN biomarker classification for neurologic diseases (Jack et al., 2016).

A. Presence or absence of A β pathology in the brain can be estimated through the analysis of the levels of A β peptides in the CSF (Blennow and Zetterberg, 2018). The fluid biomarker gold standard has become the ratio of 42 (aggregation-prone) to 40 (more soluble) amino acid-long A β in the CSF (A β 42/A β 40 ratio) (Schindler et al., 2019). The quantification of A β 42 in CSF showed a high agreement with the A β deposition seen on PET scan (Blennow et al., 2015; Palmqvist et al., 2014). Biological limitations hampered the translation of the A β assays in the blood (Janelidze et al., 2016); the levels are low, A β sticks to other plasma proteins and there is also peripheral production in, e.g., blood platelets, which leads to noise in the assays (Citron et al., 1994). Anyhow, new mass spectrometry-, Simoa- and ECL-based techniques are now making it possible to reproduce the well-established CSF A β 42/A β 40 reduction in individuals who are A β -positive according to amyloid positron emission tomography (PET) also in blood (Nakamura et al., 2018; Ovod et al., 2017; Palmqvist et al., 2019). The reduction of the A β 42/A β 40 ratio is around 50% in CSF but only about 10-15% in blood since it occurs on the background of non-CNS A β .

T. It is fascinating that the presence of tau in the CSF/blood of AD patients may not only be a consequence of neuronal damage, but an active release from the neurons in response to the accumulation of A β (Kanmert et al., 2015; Maia et al., 2013; Sato et al., 2018). This hypothesis is further supported by the higher magnitude of increase in CSF tau seen in AD patients compared to patients suffering from other tauopathies (diseases with both neurodegeneration and neurofibrillary tangles) (Skillbäck et al., 2015; Zetterberg, 2017a). The quantification of total-tau (t-tau; measured using assays directed at the N-terminal and mid-regions of the

protein, which do not discriminate between different isoforms) in the blood remains challenging, but with Simoa and some other techniques it is now possible to quantify different phosphorylation states of tau and fragments of tau in the blood. Specifically, blood pTau181 discriminated with an accuracy of 100% AD patients from A β - conditions like frontotemporal dementia patients (FTD), and discriminated with an accuracy of more than 80% AD patients from patients with mild cognitive impairment (MCI), progressive supranuclear palsy, corticobasal syndrome, vascular dementia, primary progressive aphasia, Parkinson's disease and multiple systems atrophy (Karikari et al., 2020). Even more strikingly, blood pTau181 was able to discriminate asymptomatic A β + individuals from asymptomatic A β - individuals (Karikari et al., 2020). These findings were extended and strengthened by two parallel seminal works from Thijssen and colleagues (Advancing Research and Treatment for Frontotemporal Lobar Degeneration (ARTFL) investigators et al., 2020) and Janelidze and colleagues (Janelidze et al., 2020). Strikingly, blood pTau231, another phosphorylation state of tau, showed an even greater performance by detecting the pathology at earlier stages (Braak 0 and 1 stadium)(Ashton et al., 2021). To top up this, a third phosphorylation state of pTau with a phosphorylation at threonine-217 is emerging as promising blood biomarker (Mattsson-Carlgren et al., 2020; Palmqvist et al., 2020). Hence, pTau meritedly gained the stage by being a blood biomarker with a diagnostic specificity comparable to the accepted CSF AD-biomarkers. Moreover, promising evidence shows that the quantification of a N-terminal segment of tau may also serve as AD specific blood biomarker (Mengel et al., 2020) and already at the early disease stages (Chhatwal et al., 2020).

N. Neurodegeneration can be quantified by the levels of neurofilaments or tau. The CSF levels of tau and NfL showed an association with both neurocognitive impairment and imaging measures of disease progression (Olsson et al., 2016). The stability of neurofilaments enabled the translation of these findings to blood measurements. The deposition of A β and neurofibrillary tangles starts decades prior symptom onset with the prodromal phase of the disease (Masters et al., 2015). Consistently with this, an increase in NfL was detected years prior to symptom onset in retrospective studies involving patients with a familial form of the

disease (Preische et al., 2019; Quiroz et al., 2020; Weston et al., 2019, 2017). Blood NfL entails the ability of monitor disease activity over time (Lewczuk et al., 2018; Lin et al., 2018; Mattsson et al., 2017; Pereira et al., 2017; Preische et al., 2019; Sánchez-Valle et al., 2018; Weston et al., 2017); however it lacks diagnostic specificity as shown in the comparison with pTau181 (Advancing Research and Treatment for Frontotemporal Lobar Degeneration (ARTFL) investigators et al., 2020).

Moreover, the presence of ongoing brain damage is reflected by increased activation of microglia cells in AD patients (Butovsky and Weiner, 2018): the levels of a soluble fragment of TREM2 (sTREM2, that is a membrane protein present on microglia) were increased in AD patients (Bekris et al., 2018; Heslegrave et al., 2016; Ohara et al., 2019; Piccio et al., 2016) and proportional to the level of tau pathology as measured by CSF t-tau and pTau181 (Suárez-Calvet et al., 2016). However, the presence of sTREM2 also in peripheral cells (outside the CNS) from the myeloid compartment hampers its translation into a blood measurement (Zetterberg, 2017b). Further novel biomarkers are being explored, such as flotillin, an exosomal protein found by western blot to be decreased in the CSF and blood of AD patients (Abdullah et al., 2019).

Interestingly, it was unclear whether the Amyloid-Tau-Neurodegeneration (ATN) temporal profile seen on PET scans were mirrored by the same temporal sequence of A β followed by pTau and by NfL in the blood. A recent study shed some light on this, the NfL levels of 198 patients from the ADNI study and 116 patients from the TRIAD study with different grades of cognitive impairment were analyzed and associated with PET measures of amyloid and tau (Benedet et al., 2020). Interestingly, in pre-symptomatic individuals elevated blood NfL was associated with the presence of A β plaques (^{18}F -florbetapir), whereas at the symptomatic stage NfL was associated with the load of tau (^{18}F -MK6240) (Benedet et al., 2020). Hence, the combination of these biomarkers may allow both a correct diagnosis and disease staging. A practical application can be the stratification of patients for clinical trials of drugs that may be targeting the A β deposition (A) or the neurofibrillary tangles (T) or the prevention of

neurodegeneration (N). In fact, there are undergoing clinical trials exploring monoclonal antibodies able to remove A β (Selkoe, 2020) and other targeting tau are under early phase of development. Depending on the targeted disease stage and the targeted protein each blood biomarker could play a significant role. This was explored in an animal model of APP/PS1 mice where the decrease of A β corresponded to a decrease in NfL levels (Bacioglu et al., 2016). Finally, the clinical implementation of these biomarkers may succeed by a two-step approach with an initial screening with a blood test, that if positive will be followed by deeper investigations through CSF biomarkers and PET scan.

4. Multiple sclerosis (MS)

MS is a chronic autoimmune disease where an inflammatory and neurodegenerative process leads to an accrual in disability (Trapp and Nave, 2008). Most of the patients undergo an initial inflammatory phase with acute bouts of disease activity that is followed by a subtle phase of slow accrual in disability (Baecher-Allan et al., 2018).

Well-established clinical and MRI criteria enabled an accurate diagnosis (A. J. Thompson et al., 2018). On the other hand, the monitoring of the disease activity is challenged by the heterogeneity of the disease. In order to address this need and to reach an even earlier diagnosis, several fluid biomarkers have been explored with the most promising being structural components of the brain parenchyma that are disrupted and released upon disease activity (e.g., NfL, glial fibrillary acidic protein - GFAP) or cytokines (e.g., CXCL13) and enzymes (e.g., metalloproteinases or chitinases) released by the activated immune system (Huang et al., 2020; Pinteac et al., 2021).

Neurodegeneration. Back in 1998 in Sweden Jan Lycke showed that CSF NfL levels in relapsing remitting (RRMS) patients were increased compared to controls, they were associated with disability and increased with higher relapse rate during the previous 2 years (Lycke et al., 1998). Further studies from independent laboratories confirmed and broaden

these findings supporting CSF NfL as marker of disease activity in MS (Burman et al., 2014; Khalil et al., 2013; Kuhle et al., 2013; Malmestrom et al., 2003; Martinez et al., 2015; Modvig et al., 2015; Norgren et al., 2004; Novakova et al., 2017; Romme et al., 2013; Teunissen et al., 2009; Trentini et al., 2014; Villar et al., 2014) and as prognostic marker (Arrambide et al., 2016). Increased CSF NfL reflected suboptimal treatment response in patients treated with first versus second line treatment (Novakova et al., 2017). Moreover, patients beginning treatment with rituximab, natalizumab and fingolimod showed a decrease in CSF NfL levels associated with less clinical and MRI disease activity over one year (de Flon et al., 2016; Gunnarsson et al., 2011; Kuhle et al., 2015). A translation of the NfL assay in blood created an unprecedented situation: tens of thousands of frozen blood samples collected over decades of observational cohorts and clinical trials became a Rosetta stone that gave the field an immense knowledge over the time course, causes and preventive measures of neurodegeneration in MS. Blood NfL measurements supported the idea of a prodromal stage of MS with neurodegeneration occurring years prior to symptom onset (Bjornevik et al., 2020). Moreover, it demonstrated that a blood measurement does not only reflect clinical and MRI disease activity (Disanto et al., 2017; Barro et al., 2018; Cantó et al., 2019; Chitnis et al., 2018; Håkansson et al., 2018; Jens Kuhle et al., 2019; J. Kuhle et al., 2019a; Kuhle et al., 2017; Manouchehrinia et al., 2020; Siller et al., 2019; Varhaug et al., 2018; Bittner et al., 2020) but it also reflects response to treatment (Calabresi et al., 2020; Delcoigne et al., 2020; Kuhle et al., 2018; J. Kuhle et al., 2019a; Sejbaek et al., 2019) or presence of subclinical disease activity (Yaldizli et al., 2018). Notably, an unexpected lack of decrease in NfL levels was seen after treatment with ibudilast in progressive MS patients (Fox et al., 2021) despite the treatment successfully improved the disease outcome in the respective clinical trial (Fox et al., 2018). The inclusion of progressive MS patients, that are more affected by comorbidities than RRMS, may have reduced the sensitivity of NfL in detecting a treatment effect. There is compelling evidence that blood NfL may be used for monitoring disease activity in patients with MS. Nevertheless, its application relies on a careful consideration of biological confounders (extensively reviewed in (Barro et al., 2020)).

Astrocytic dysfunction and damage. The early stages of the disease – RRMS – present acute inflammatory events characterized by disruption of the blood brain barrier (BBB) and migration of peripheral immune cells in the CNS (Chitnis and Weiner, 2017). The natural history of the disease results in a transition to a more subtle process compartmentalized to the CNS where plasma cells and innate immune systems are believed to be the main players (Baecher-Allan et al., 2018). At this later stage, the neurodegeneration is the result of a chronic continuous damage rather than pulses of peripheral immune activation. Consistently, this biological change was reflected by a lower magnitude of blood NfL increase upon acute disease activity (Rosso et al., 2021). Resident cells as astrocytes are also affected by this process. Astrocytes are not only damaged but they also increase their expression of glial fibrillary acidic protein (GFAP), an astrocyte specific cytoskeletal protein (Liddel et al., 2017; Sofroniew and Vinters, 2010). Like most of the biomarkers, GFAP was initially studied in CSF and only recently translated to blood. Astrocytes are integral components of the BBB (Sofroniew and Vinters, 2010), it would therefore be expected that a disruption of the BBB seen in acute episodes of disease activity would result in an increased release of GFAP. Astonishingly, there is not such clear increase in GFAP levels with contrasting findings showing increased (Malmeström et al., 2003; Noppe et al., 1986; Watanabe et al., 2019) or normal (Ayrygnac et al., 2020; Mane-Martinez et al., 2016; Norgren et al., 2004; Novakova et al., 2017; Rosengren et al., 1995) GFAP levels during an MS relapse. One speculation is that the GFAP released with a damage of the BBB is released in the blood where the half-life of the protein may be too short for remaining detectable. This can actually be a good thing. The relative stability of GFAP levels upon relapse constitute a unique property of this biomarker contrasting with the more dynamic profile of NfL. Thus, the combination of NfL and GFAP results in increased and not overlapping information. The load of astrocytic activation seen in the progressive stage of the disease was reflected by increased GFAP levels in progressive MS patients (PMS) compared to RRMS and healthy individuals (Abdelhak et al., 2018; Ayrygnac et al., 2020; Gunnarsson et al., 2011; Högel et al., 2020; Huss et al., 2020; Mane-Martinez et al., 2016; Novakova et al., 2018). Moreover, in contrast to neurofilament levels, patients treated

with natalizumab or rituximab/mitoxantrone did not show a decrease in GFAP levels (Axelsson et al., 2014; Gunnarsson et al., 2011), hence this biomarker appear to be consistently influenced only by the underlying astrocytic pathology that is not targeted by any of the currently available treatments. Nonetheless, based on the data of the EXPAND study of Siponimod (J. Kuhle et al., 2019b), it might be fair to speculate that the lack of increase in GFAP levels seen in the active arm indicates that effective treatment may prevent pathologic astrocytic activation, thus disease progression.

Inflammation. Several cytokines or enzymes are secreted during an inflammatory process, the main hurdle in validating secreted molecules as CNS biomarkers is the confounding effect of a secretion from peripheral sources, hence the vast majority of the studies has focused on CSF samples. The effectivity of B-Cell therapies in MS has attracted attention to the role of the B-cells compartment with the most investigated cytokine being the chemokine ligand 13 (CXCL13) that targets B-cells (Alvarez et al., 2013). Indeed, CSF CXCL13 was found to be elevated in MS patients compared to healthy controls in a great number of studies, for instance (Alvarez et al., 2013; Axelsson et al., 2014; Brettschneider et al., 2010; Hakansson et al., 2017; Puthenparampil et al., 2017; Sellebjerg et al., 2017, 2009), although this difference was not detectable in blood (Alvarez et al., 2013). A decrease of CSF CXCL13 levels after 12-24 months of rituximab or mitoxantrone treatment suggested a possible role of CXCL13 in detecting treatment efficacy (Axelsson et al., 2014). Of note, increased levels of CSF CXCL13 appeared to be prognostic of conversion from CIS to clinically definite multiple sclerosis (Brettschneider et al., 2010; Khademi et al., 2011). It is technically important to mention that the studies around this cytokine faced an unsatisfactory sensitivity of the ELISA assay used with only a part of the samples in the detectable range (Axelsson et al., 2014; Hakansson et al., 2017). In a different category we find the chitinases, hydrolytic enzymes with the peculiarity of being more specific for the myeloid compartment of immune cells with their levels reflecting the activation of macrophages and microglia (Pinteac et al., 2021). In this family the most promising biomarker candidate is chitinase 3 like 1 (CHI3L1). Its CSF levels were shown to be increased in 48 clinically isolated syndrome (CIS) patients that converted to clinically defined

MS compared to 36 CIS that did not convert and CHI3L1 levels were associated with the presence of active and chronic MRI lesions (Comabella et al., 2010). This was confirmed in two larger studies involving more than 800 CIS patients (Canto et al., 2015; Martinez et al., 2015). Further studies found consistently that CSF CHI3L1 levels were increased in patients with MS (pwMS) compared to healthy individuals (Cantó et al., 2012; Gil-Perotin et al., 2019; Hakansson et al., 2017; Hinsinger et al., 2015; Huss et al., 2020; Malmeström et al., 2014; Mane-Martinez et al., 2016; Novakova et al., 2017; Sellebjerg et al., 2017; Thouvenot et al., 2019), although the association with MRI and clinical disease activity was less clear (Canto et al., 2015; Cantó et al., 2012; Comabella et al., 2010; Hakansson et al., 2017, p. 201; Novakova et al., 2017; Oldoni et al., 2020; Quintana et al., 2018; Thouvenot et al., 2019). The blood levels of CHI3L1 despite not being prognostic for CIS patients (Comabella et al., 2010), held promising results by being elevated in pwMS (Cantó et al., 2012; Hinsinger et al., 2015) and associated with the expanded disability status score (Cantó et al., 2012; Huss et al., 2020). The potential role of chitinases as biomarkers was reviewed to a great extent in (Pinteac et al., 2021). Of interest is also the family of metalloproteinases, catalytic enzymes, of which matrix metalloproteinase 9 (MMP9) has been the most studied for its possible role as MS biomarker of inflammation (Leppert et al., 2001). Its levels were in fact increased in the presence of either clinical or MRI inflammatory activity (Avolio et al., 2005, 2003; Fainardi et al., 2006; Leppert et al., 1996; Sellebjerg et al., 2017, 2003; Waubant et al., 2003).

There are further undergoing efforts to identify additional biomarkers for MS. For instance, Huang and colleagues applied a highly sensitive proteomic approach to identify biomarkers in the CSF of a discovery cohort of 136 pwMS and 49 healthy controls (HCs) and found 11 CSF proteins that were significantly more represented in pwMS than HC, 10 of which were validated on a replication cohort of 95 pwMS and 47 HCs (Huang et al., 2020). Nevertheless, these findings were not confirmed in plasma samples of the same patients, and this might be because of insufficient sensitivity of the methodic, hence it might be worth to investigate those proteins with highly sensitive immunoassays in blood.

The clinical utility of blood biomarkers at the individual patient level is currently unclear. Nonetheless, a prospective observational multicentre study was initiated in July 2018 by a net of German university hospitals with the goal of investigating the utility of blood biomarkers in MS, hopefully this and more prospective studies will shed a light on this aspect (Abdelhak et al., 2020). We reference also further interesting reviews on fluid biomarkers in MS (Barro et al., 2017; Varhaug et al., 2019; Kapoor et al., 2020; Williams et al., 2020; Thebault et al., 2021).

5. Amyotrophic lateral sclerosis (ALS)

ALS is a neurodegenerative disease of the upper and lower motoneurons with a poor prognosis (Hardiman et al., 2011). A precise diagnosis for patients with ALS is of utmost importance for evaluating potential treatments (Turner et al., 2013). Thus, biomarkers may have a fundamental role in correctly stratifying the patients for clinical trials and to monitor treatment efficacy and disease progression (Bakkar et al., 2015).

Neurodegeneration. The majority of ALS patients present cytoplasmic aggregates of transactive response DNA-binding protein 43 (TDP-43) (De Marco et al., 2017; Emily Feneberg et al., 2018). As extensively reviewed by Feneberg and colleagues the investigation of TDP-43 revealed to be technically challenging by the lack of specific antibodies and the presence in blood of TDP-43 derived from peripheral tissues (Emily Feneberg et al., 2018). Very recent data suggest that seeds of misfolded TDP-43 can be detected in lumbar CSF from patients with ALS and FTD using a real-time quaking-induced conversion (RT-QuIC) reaction (Scialò et al., 2020). This is a very promising technology that potentially could make an *in vivo* biomarker for TDP-43 pathology come real. Neurofilaments are an established biomarker of neurodegeneration, in ALS both the light (NfL) and the heavy isoform (NfH) have been explored. NfH was studied in both its native and hyperphosphorylated isoform as NfH and pNfH, respectively (Lu et al., 2012). Because NfH formed aggregates in the blood matrix (hook effect), the translation of the NfH assay from CSF to blood was challenging, however this was elegantly solved by the group of Petzold by pre-incubating the samples in a urea-based buffer

(Lu et al., 2011). The levels of both NfL and NfH in CSF and blood were prognostic for survival (Brettschneider et al., 2006; De Schaepdryver et al., 2020; Gille et al., 2019; Lu et al., 2015; Rosengren et al., 1996; Thouvenot et al., 2020; Verde et al., 2019b; Weydt et al., 2016; Zetterberg et al., 2007) and shown a diagnostic value when discriminating ALS from other motoneuron diseases (De Schaepdryver et al., 2018; E. Feneberg et al., 2018; Gille et al., 2019; Verde et al., 2019b). Interestingly, the concentration of neurofilaments appears stable over the course of the disease (Benatar et al., 2018; Gille et al., 2019; Lu et al., 2015), hence NfL/NfH may not be suitable for monitoring ALS progression. Despite this, a recent clinical trial of tofersen found a decrease in NfL/NfH levels in the treated arm compared to the placebo arm (Miller et al., 2020). A technical note - similarly to NfL, the quantification of NfH in blood benefited from the higher sensitivity of fourth generation assays as shown in a work from Wilke and colleagues (Wilke et al., 2019) and a second work from Gray and colleagues (Gray et al., 2020a). Interestingly, the performances of both Simoa assays were excellent, however the quality of the antibodies kept playing a role in achieving a better sensitivity in a homebrew compared to the commercial assay (Wilke et al., 2019).

Inflammation. The immune system appear to have a role in the pathology (Butovsky et al., 2012), even if it is unclear whether its activation is a mere consequence or a contributor to the disease (Béland et al., 2020). Biomarkers as cytokines may be helpful in quantifying the level of immune system activation and possibly help in disease staging. Notably, the production of these molecules occurs also in the periphery, hence their use is limited to CSF samples. Recent studies in CSF found that interleukin-6 (IL-6) and tumor necrosis factor alfa (TNF- α) were particularly elevated in ALS patients (Hu et al., 2017; Tortelli et al., 2020). Chitinases were also explored as CSF biomarkers of inflammation and their levels were found increased in ALS patients compared to healthy controls (Oeckl et al., 2019; Thompson et al., 2019), prognostic for survival (A. G. Thompson et al., 2018) and stable over the course of the disease (Gray et al., 2020b; Thompson et al., 2019), similarly to what was observed with neurofilaments. However, the levels were not increased in the pre-symptomatic phase of the disease as observed in patient with the familial form of the disease (Oeckl et al., 2019). Further

interesting reviews that focused at biomarkers in ALS are for example (Bakkar et al., 2015; Ryberg and Bowser, 2008; Turner et al., 2009; Verde et al., 2019a).

6. Frontotemporal dementia (FTD)

FTD is a neurodegenerative disease with both a sporadic and genetic origin (Bang et al., 2015). Forty percent of patients suffer from a genetic form of the disease caused in 60% of cases by *GRN* or *MAPT* mutations or *C9orf72* expansion (Bang et al., 2015).

Neurodegeneration. Patients with a *MAPT* mutation present, similarly to other neurodegenerative diseases, tau aggregates in neurons (Bang et al., 2015). The recent development of assays against phosphorylated states of tau enabled the discrimination of FTD from AD (Advancing Research and Treatment for Frontotemporal Lobar Degeneration (ARTFL) investigators et al., 2020; Karikari et al., 2020). The levels of the protein progranulin (encoded by the *GRN* gene) was found to be lower in FTD patients carrying the *GRN* mutation linked to FTD compared to healthy controls (Meeter et al., 2016). This had set the basis to the use of progranulin levels for detecting treatment efficacy – increase in progranulin levels may be interpreted as therapeutical success (Meeter et al., 2016; Swift et al., 2021). Most tau-negative FTD patients have TDP-43 inclusions. As described above (in an ALS context), this pathology is hard to detect using biomarkers, but a recent RT-QuIC assay has given promising results in both ALS and FTD (Scialò et al., 2020). Neurofilaments, a more universal marker of neuronal damage, were increased in FTD patients in the pre-symptomatic (van der Ende et al., 2019) and symptomatic stage (Al Shweiki et al., 2019; Katisko et al., 2020; Wilke et al., 2016). Thus, offering a measure on the progression of the disease.

Astrocytic dysfunction and damage Notably, the presence of astrogliosis in patients harboring the *GRN* mutation was reflected by an increase in blood GFAP levels compared to the other forms of FTD (Heller et al., 2020).

Inflammation. Increased levels of various cytokines, most notably the highly pro-inflammatory IL-6, TNF- α has been detected in CSF and blood (Bossù et al., 2011; Sjogren et al., 2004). The presence of pro-inflammatory cytokines was matched by elevated chitinases in the CSF reflecting activated microglia, astrocytes and macrophages in the CNS (Abu-Rumeileh et al., 2019; Woollacott et al., 2020).

In such a heterogeneous disease, it is critical to achieve methods that enable a precise stratification of patients for clinical trials and fluid biomarkers may play a prominent role in this. Further interesting reviews on fluid biomarkers in FTD are (Zetterberg et al., 2019; Swift et al., 2021).

7. Parkinson's disease (PD)

The loss of dopaminergic neurons in the substantia nigra associated with the presence of α -synuclein aggregates constitutes a hallmark of this pathology (Poewe et al., 2017). It was a natural step to explore α -synuclein as PD biomarker. The levels of α -synuclein in CSF were found to be consistently lower in PD patients compared to healthy controls (Mollenhauer et al., 2017; Parnetti et al., 2008), nevertheless this was overlapping with other α -synucleinopathies. The presence of high levels of α -synuclein in red blood cells poses a technical challenge to the use of this biomarker and particularly to its translation to blood measurements (Barkovits et al., 2020). On a similar fashion to what we saw in AD, a higher specificity for the biology of PD might be achieved by measuring a specific phosphorylation state of α -synuclein phosphorylated at the serine in position 129. This was detected by mass spectrometry in the CSF of PD patients (Wang et al., 2012) but could not be confirmed by using immunoassays (Cariulo et al., 2019). Hence, it is fair to speculate that technical improvements may lead to one or more biomarkers able to discriminate the biology of PD compared to other α -synucleinopathies. Similar to TDP-43, but more advanced and well-replicated, RT-QuIC-based assays to detect α -synuclein seeds in lumbar CSF have been developed (Fairfoul et al., 2016; Shahnawaz et al., 2017; Rossi et al., 2020; Iranzo et al., 2021). The assays reproducibly detect

α -synuclein pathology in PD, dementia with Lewy bodies, multiple system atrophy and PD-associated REM-sleep disorders with diagnostic accuracies exceeding 90%. Furthermore, the level of neurodegeneration occurring in PD patients can be quantified as level of NfL in the CSF or blood. The NfL levels are very mildly increased in PD compared to other neurological conditions (Bridel et al., 2019), and this increase was found associated with the severity of the motor impairment defined with the Hoehn and Yahr scale (Lin et al., 2019). Thus, blood NfL could help in monitoring disease progression, particularly at the late stages of PD when motor impairment is manifested. Moreover, the mild increase in NfL levels contrasts with the more pronounced increase detected in atypical parkinsonian disorders (disorders with a similar initial clinical presentation as PD); hence NfL may be helpful in differentiating patients with PD from those with progressive supranuclear palsy, cortical basal syndrome or multiple system atrophy (Hansson et al., 2017; Marques et al., 2019).

8. Spinal muscular atrophy (SMA)

SMA is an autosomal recessive neurodegenerative condition that affects the second motor neuron and manifest with muscular weakness (Talbot and Tizzano, 2017). Increased CSF pNfH levels were observed in the pre-symptomatic phase (De Vivo et al., 2019). Moreover, higher blood pNfH levels were associated with earlier disease onset and worse clinical presentation (Darras et al., 2019), though this association differed in the different phenotypes of the disease (the MND-Net et al., 2020; Walter et al., 2019; Wurster et al., 2019). Nusinersen, a first therapy based on an anti-sense oligonucleotide, became recently available (Finkel et al., 2017; Mercuri et al., 2018). The efficacy of this treatment was reflected by a decrease in blood pNfH (Darras et al., 2019; De Vivo et al., 2019), CSF pNfH (Winter et al., 2019) and CSF NfL levels (Olsson et al., 2019; Winter et al., 2019). Thus, the quantification of neurofilaments can be an important tool in identifying the best time to treat and monitoring the response to treatment.

9. Huntington's disease (HD)

HD is a neurodegenerative disease caused by an autosomal dominant mutation with expansion of CAG trinucleotide repeats that affect the correct production of a protein named huntingtin (Bates et al., 2015). Similarly, to other neurodegenerative diseases the neuronal damage occurs years prior to the first clinical manifestation (Tabrizi et al., 2012). Indeed, NfL in both CSF and blood was already increased in the pre-symptomatic stage of the disease and kept increasing during the course of the disease (Byrne et al., 2017; Vinther-Jensen et al., 2016; Rodrigues et al., 2020). The levels of CSF NfL were associated with the disease progression measured by clinical assessment (Constantinescu et al., 2009; Niemelä et al., 2017; Rodrigues et al., 2020; Vinther-Jensen et al., 2016). An increased level of neuronal damage - increased NfL – was prognostic for progression to the symptomatic stage (Byrne et al., 2017; Niemelä et al., 2017). In symptomatic patients, blood NfL levels were associated with measures of brain atrophy (Byrne et al., 2017; Johnson et al., 2018; Rodrigues et al., 2020), cognitive decline (Byrne et al., 2017; Rodrigues et al., 2020). These promising results underscore the potential role of NfL in both monitoring and supporting treatment trials in this disease. A new avenue for a diagnostic and monitoring tool emerged with the development of a single-molecule-count assay able to quantify huntingtin in the CSF (Wild et al., 2015). From what we learnt from NfL, the quantification of blood biomarkers may detect treatment efficacy already 3 months after treatment start (Hauser et al., 2019; Sejbaek et al., 2019). Sensitivity limitations are still challenging the detection of huntingtin in blood. Nonetheless, the translation of the huntingtin assay to blood could offer an unprecedented opportunity to quickly detect treatment efficacy in ongoing clinical trials.

10. Conclusion

The discovery of protein biomarkers able to objectively quantitate pathological processes of neurons, astrocytes and inflammation gave us an amazing tool to deepen our understanding of the disease, follow the disease progression over time and predict its course in presence or

absence of treatments. Discovery that was possible because of an improvement in the detection methods of which both the availability of high quality monoclonal antibodies and highly sensitive platforms were critical parts (Gisslen et al., 2016; Kuhle et al., 2016). A further step was achieved in the AD biomarkers by looking at post-translational modifications of a protein: tau. Different phosphorylation states of tau revealed to be an incredibly specific blood signature of AD (Teunissen et al., 2020). A universal neurological biomarker, NfL, is specifically detecting neuronal damage independently from the disease causing it. Hence, a cautious interpretation of this biomarker can have an immense impact in the clinical care of neurological patients (Barro et al., 2020; Barro and Zetterberg, 2021). The utility of neurofilaments, both NfL and pNfH, have been demonstrated also in mouse models of neurologic disease (Bacioglu et al., 2016; Wilke et al., 2020). Thus, blood biomarkers can assist preclinical studies and basic research. Moreover, the ability to quantitate each aspect of the disease at a high definition enables a more precise stratification of the patients during inclusion to clinical trials, hence reducing the noise that may hamper the detection of therapeutical efficacy and allowing for smaller but likewise powered studies. Ultimately, we are living in an amazing time in which an increasing number of biomarkers has the potential to support the best care for patients suffering from neurological conditions.

Contributions

CB, HZ did literature search, reviewed the manuscript, drafted the manuscript, and prepared the table. All authors read and approved the final version of the manuscript.

Conflict of interest

CB has nothing to disclose. HZ has served at scientific advisory boards for Eisai, Denali, Roche Diagnostics, Wave, Samumed, Siemens Healthineers, Pinteon Therapeutics, Nervgen, AZTherapies and CogRx, has given lectures in symposia sponsored by Cellectricon, Fujirebio,

Alzecure and Biogen, and is a co-founder of Brain Biomarker Solutions in Gothenburg AB (BBS), which is a part of the GU Ventures Incubator Program (outside submitted work).

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Figure 1. Overview of available and perspective blood biomarkers with a potential clinical utility for neurodegenerative diseases. In brackets perspective biomarkers.

Table 1. Blood biomarkers with their pathological interpretation and detection methods.

Blood biomarkers	Pathological process	Potential application	Detection methods	References
<i>Aβ42; Aβ42/ Aβ40</i>	Amyloid plaques	AD	ECL, IP-MS, Simoa	(Nakamura et al., 2018; Ovod et al., 2017; Palmqvist et al., 2019)
N-terminal segment of tau	Tau tangles	AD	Simoa	(Mengel et al., 2020)
pTau181	Phosphorylation in tau tangles	AD	ECL	(Advancing Research and Treatment for Frontotemporal Lobar Degeneration (ARTFL) investigators et al., 2020; Janelidze et al., 2020)
			Simoa	(Karikari et al., 2020)
pTau231			Simoa	(Ashton et al., 2021)
pTau217			ECL	(Mattsson-Carlgren et al., 2020; Palmqvist et al., 2020)
NfL	Neurodegeneration	All neurodegenerative conditions	Simoa, Ella, ECL, PEA, ADVIA Centaur and Atellica	(Barro et al., 2021; Chitnis et al., 2019; Gauthier et al., 2021; Kuhle et al., 2016; Plavina et al., 2019)
pNfH			ELISA	(Lu et al., 2011)

			Simoa	(Wilke et al., 2019)
GFAP	Astrogliosis and astrocytic activation	MS, FTD	Simoa	(Heller et al., 2020; Högel et al., 2020)
TDP-43	Formation of protein aggregates	ALS, FTD	RT-QuIC	(Scialò et al., 2020)
CHI3L1	Activation of the innate immune system	All neurodegenerative conditions	ELISA	(Cantó et al., 2012; Huss et al., 2020)
IL-6	Inflammation	All neurodegenerative conditions	Bio-Plex	(Tortelli et al., 2020)
TNF- α				

A β : beta-amyloid; AD: Alzheimer's disease; ALS: amyotrophic lateral sclerosis; ECL: electrochemiluminescence; FTD: frontotemporal dementia; GFAP: glial fibrillary acidic protein; IL-6: interleukin 6; IP-MS: immunoprecipitation mass spectrometry; MS: multiple sclerosis; NfL: neurofilament light chain; pNfH: phosphorylated neurofilament heavy chain; PEA: Proximity Extension Assay; pTau: phosphorylated tau; RT-QuIC: Real-time quaking-induced conversion; Simoa: single molecule array; SMC: Single Molecule Counting; TDP-43: transactive response DNA-binding protein 43; TNF- α : tumor necrosis factor alfa.

Table 2. Highly sensitive immunoassay platforms used for quantifying protein biomarkers in the blood.

Technology	Assay generation	Automated	Sample processing	Core characteristic	Advantages	Disadvantages	Ref
ECL	3 rd	No	Simultaneous	Electrochemical	<ul style="list-style-type: none"> - Cost - High flexibility for in-house development 	<ul style="list-style-type: none"> - Lower sensitivity than 4th generation technologies - Not automated - Long processing time 	(Kuhle et al., 2016; Limberg et al., 2016)
Simoa	4 th	Yes	Consecutive	Bead-based	<ul style="list-style-type: none"> - High flexibility for in-house development - High throughput 	<ul style="list-style-type: none"> - Cost - Consecutive sample processing 	(Rissin et al., 2010)
Ella		Yes	Simultaneous	Microfluidic	<ul style="list-style-type: none"> - Cost - Minimal hands-on time - Rapid measurement - Integrated calibrator curves 	<ul style="list-style-type: none"> - Limited flexibility for in-house development 	(Dysinger et al., 2017)
Proximity extension assay		Yes	Simultaneous	DNA barcode	<ul style="list-style-type: none"> - Low sample volume - High level of multiplexing - High throughput 	<ul style="list-style-type: none"> - Long processing time 	(Assarsson et al., 2014)

Single Molecule Counting		Yes	?	Focal excitation	?	?	(Todd et al., 2007)
Immunomagnetic Reduction		Yes	Simultaneous	Magnetic stimulus	?	?	(Lue et al., 2019)
Real-time quaking-induced conversion	-	No	Simultaneous	Quake of the sample	- Measures proteins that are otherwise aggregated	- Long processing time - May require an ultracentrifuge	(Scialò et al., 2020)

*range volume needed for a duplicate determination. ECL: electrochemiluminescence; CSF: cerebrospinal fluid; LLOQ: lowest limit of quantification;

Simoa: Single molecule array.