

CSF in the dementias

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Abstract

Alzheimer's disease, vascular dementia, dementia with Lewy bodies and frontotemporal dementia are the most common central nervous system disorders that cause progressive neurocognitive dysfunction and ultimately dementia. Here, we give an overview of the current state of practice and research regarding CSF biomarkers for these disorders. The chapter discusses both established and upcoming biomarkers and details, wherever appropriate, clinical use and differential diagnostics aspects.

Abbreviations

AD	Alzheimer's disease
fAD	Familial AD
VaD	Vascular dementia
DLB	Dementia with Lewy bodies
FTD	Frontotemporal dementia
CJD	Creutzfeldt-Jakob disease
MCI	Mild cognitive impairment
APP	Amyloid precursor protein
sAPP α	Soluble APP alpha
sAPP β	Soluble APP beta
CNS	Central nervous system
CSF	Cerebrospinal fluid
T-tau	Total-tau
P-tau	Phospho-tau
A β 42	Amyloid β 42
NFL	Neurofilament light
CCL2	C-C chemokine ligand 2
TREM2	Triggering receptor expressed on myeloid cells 2
CV	Coefficient of variation
HIV	Human immunodeficiency virus
QC	Quality control
IFCC	International Federation of Clinical Chemistry and Laboratory Medicine
ELISA	Enzyme-linked immunosorbent assay

Introduction

Dementias constitute a broad category of brain diseases that cause a gradual decrease in cognitive functioning. The most common type of dementia is Alzheimer's disease (AD), which makes up 50% to 70% of cases (Winblad et al., 2016). Other common types include vascular dementia (VaD), dementia with Lewy bodies (DLB), and frontotemporal dementia (FTD). Less common causes include Parkinson's disease dementia (PDD), atypical parkinsonian syndromes, a wide range of metabolic and infectious causes including HIV-associated dementia (HAD), and Creutzfeldt-Jakob disease (CJD). A dementia diagnosis is usually based on history of the illness, the pattern of cognitive deficits, with investigations including, *e.g.*, blood work used to rule out other possible causes, and imaging both to rule out alternative diagnoses and to provide positive evidence for a given diagnosis. Specific dementia diagnoses can be made using clinical criteria supplemented by biomarkers, but a definite diagnosis requires autopsy confirmation, based on the fact that each of the degenerative dementia-causing brain disorders is characterised by more or less distinct neuropathology. A striking feature is that most degenerative dementias show aggregates or inclusions of specific proteins in the brain extracellular matrix or within neurons or other cell types of the brain. There is however also a considerable degree of cerebral multimorbidity suggesting that pathologically deposited proteins may interact and are influenced by other factors, in particular cerebrovascular disease, to promote cognitive decline and other clinical symptoms (Jellinger and Attems, 2015).

Cerebrospinal fluid (CSF) may be used in two broad ways in the investigation of dementia. First, CSF cell count, CSF to serum albumin ratio (a blood-brain barrier test) and IgG- and IgM-indices may be used to exclude neuroinflammatory and neuroinfectious disorders. Second, molecular markers of different pathologies may be measured in the CSF. This is where this book chapter has its emphasis. Molecular CSF markers of the major dementia-causing CNS diseases are reviewed below both in regards to their use in clinical practice and in relation to current state of research.

CSF biomarkers for Alzheimer's disease

Key molecular pathways involved

Neuropathologically, AD is characterised by neuronal loss in specific brain regions, intraneuronal neurofibrillary tangles composed of aggregated and often hyperphosphorylated tau protein, and extracellular neuritic plaques – deposits of amyloid β peptide [$A\beta$], ending at amino acid 42 (Blennow et al., 2006). Additionally, synapse loss (Terry et al., 1991) and microglial activation (Ulrich and Holtzman, 2016) have been suggested as integral parts of typical AD pathology.

CSF A β 42

Initially, and following the identification of aggregation-prone $A\beta$ proteins ending at amino acids 40 and 42 in senile plaques (Masters et al., 1985), $A\beta$ production was thought to be an abnormal side-product of amyloid precursor protein (APP) metabolism invariably associated with AD. The natural secretion of $A\beta$ from untransfected primary cells therefore came as a surprise (Haass et al., 1992). Since then, it has been established that APP can enter at least three proteolytic clearance pathways: (i) amyloidogenic processing that primarily leads to production of $A\beta$ 42 and $A\beta$ 40 (but also some shorter, less aggregation-prone fragments) by successive β - and γ -secretase cleavage; (ii) non-amyloidogenic processing that leads to production of sAPP α and possibly also a C-terminal fragment called p3; and (iii) another non-amyloidogenic processing pathway involving concerted cleavages of APP by β - and α -secretase resulting in production of $A\beta$ 1-14/15/16 fragments at the expense of longer $A\beta$ fragments (Portelius et al., 2011).

The first enzyme-linked immunosorbent assay (ELISA) for CSF $A\beta$ 42 was published in 1995 (Motter et al., 1995). Using this technique, AD patients were shown to have reduced levels of CSF $A\beta$ 42, a finding which has since been replicated and verified in hundreds of papers (Olsson et al., 2016). This reduction is thought to reflect $A\beta$ 42 sequestration in senile plaques in the brain, as evidenced by both autopsy and *in vivo* imaging studies (Strozyk et al., 2003; Fagan et al., 2006; Forsberg et al., 2008; Seppala et al., 2012; Weston et al., 2015; Palmqvist et al., 2014). In 1999, the first paper showing a reduction in CSF $A\beta$ 42 in patients with mild cognitive impairment (MCI) who later developed AD dementia was published (Andreasen et al., 1999). Since then, numerous studies have verified that low CSF $A\beta$ 42 levels are highly predictive of future AD, both in MCI (Hansson et al., 2006; Shaw et al., 2009; Visser et al., 2009; Buchhave et al., 2012) and cognitively normal cohorts (Skoog et al., 2003; Fagan et al., 2009; Gustafson et al., 2007). Causal mutations aside, CSF $A\beta$ 42 remains the earliest

biomarker currently available in AD, and as a result CSF A β 42 is now incorporated into new criteria for the diagnosis of AD, including the pre-dementia stages (Dubois et al., 2014). Low CSF A β 42 concentrations in the absence of senile plaques have also been reported in neuroinflammatory conditions, *e.g.*, bacterial meningitis (Sjogren et al., 2001b), multiple sclerosis (Mattsson et al., 2009a), human immunodeficiency virus (HIV)-associated dementia (Gisslen et al., 2009) and Lyme neuroborreliosis (Mattsson et al., 2010), and are often accompanied by biomarker evidence of a general reduction in APP metabolites, *e.g.*, secreted forms of APP, which is not typical of AD (Rosen et al., 2013).

Besides A β 42, several other A β isoforms are present in CSF. The most abundant variant in CSF is A β 40, which is relatively unchanged in AD. The ratio of CSF A β 42 to A β 40 has been suggested to have stronger diagnostic accuracy for AD compared with CSF A β 42 alone (Schoonenboom et al., 2005; Wiltfang et al., 2007).

CSF T-tau

The first CSF total tau (T-tau) assay was published in 1993 (Vandermeeren et al., 1993). This was a sandwich ELISA in which a monoclonal antibody against the mid-domain of tau was combined with a polyclonal anti-tau antiserum. Two years later, the first assay based on three mid-region monoclonal antibodies, which recognises all tau isoforms irrespective of phosphorylation state, was published (Blennow et al., 1995). Using this assay, AD patients were shown to have clearly elevated T-tau levels (Vandermeeren et al., 1993; Blennow et al., 1995), a finding that has been replicated in hundreds of papers, using several different assays, in many different clinical contexts (Olsson et al., 2016). It has been shown that CSF T-tau levels correlate with imaging measures of hippocampal atrophy (Wang et al., 2012) and grey matter degeneration (Glodzik et al., 2012), findings in keeping with the known high expression of tau in thin unmyelinated axons of the cortex (Trojanowski et al., 1989). In response to acute brain injury, CSF T-tau levels are dynamic; they increase during the first few days following injury and stay elevated for a few weeks until they normalise (Hesse et al., 2001; Zetterberg et al., 2006). This has led to the view that elevated CSF T-tau levels reflect ongoing axonal degeneration, which in turn may indicate disease activity. Indeed, CSF T-tau predicts the rapidity of the clinical course in AD; the higher levels, the more rapid clinical disease progression (Wallin et al., 2010). Accordingly, in severe and rapid neurodegeneration,

e.g., as in CJD, CSF T-tau elevations orders of magnitude higher than in typical AD are seen (Sanchez-Juan et al., 2007; Skillback et al., 2014b).

Two recent discoveries have made the tau biomarker field more complex. These include: (i) the finding that tau secretion from cultured cells (Saman et al., 2012) and mouse neurons (Maia et al., 2013) may be stimulated by A β in the absence of neuronal death (Maia et al., 2013); and (ii) that most of the tau in CSF seems to be fragmented (Meredith et al., 2013). Tau secretion in the absence of neurodegeneration is not unexpected as it has been known for decades that tau is present in the CSF of healthy individuals (Blennow et al., 2010). Nonetheless this raises some important issues from a practical perspective as it confirms that tau elevation cannot simply be considered a surrogate marker of neurodegeneration. Moreover, the mechanism of tau elevation in AD may well be at least partially independent of neuronal death. The latter would be consistent with tau changes seen in other forms of brain injury and the observation of intraneuronal increase in tau expression following acute experimental brain injury in animals (Uryu et al., 2007).

The finding that most CSF tau seems to be in fragmented forms is consistent with well established evidence that endogenous tau fragments are found in tangles (Wischik et al., 1988). It may also explain why it has been important to have capture and detection antibodies located closely to each other in T-tau assays, and why combinations of distally located N- and C-terminal antibodies do not work (Meredith et al., 2013). The clinical significance of these fragments is not known and it remains challenging to accomplish a reliable quantification, including determination of reference samples.

CSF P-tau

The first CSF assay for phosphorylated tau (P-tau), the form of tau that is believed to show the closest association with neurofibrillary tangle load, was published in 1995 (Blennow et al., 1995). Since then, a variety of P-tau assays measuring different forms of phosphorylated tau proteins have been developed (Hampel et al., 2004). Broadly speaking, these assays correlate well with one another, and show similar findings in AD (Hampel et al., 2004). CSF P-tau levels correlate with neurofibrillary tangle pathology in AD (Buerger et al., 2006; Seppala et al., 2012), but a major outstanding research question is why other tauopathies, including some forms of FTD and progressive supranuclear palsy, do not show P-tau elevation, at least not as systematically as seen in AD. It is possible that these disorders show disease-specific tau

phosphorylation, or that tau is processed or truncated in a way that is not recognised by available assays. Another potential explanation for the apparent AD specificity of CSF P-tau is if the amount of pathology were simply greater in AD than in other tauopathies (although there is to the best of our knowledge no published data addressing this hypothesis).

Determining the relative specificity of P-tau elevation and AD has considerable advantages in differentiating different neurodegenerative diseases. For example, the ratio of T-tau to P-tau is a quite specific test for CJD (Riemenschneider et al., 2003; Skillback et al., 2014b). There are at present only three conditions in addition to AD in which elevated CSF P-tau levels have been reported: (i) term and pre-term newborns, possibly reflecting physiological tau phosphorylation in brain development (Mattsson et al., 2009b), (ii) herpes encephalitis (Grahn et al., 2013), and (iii) superficial CNS siderosis (Kondziella and Zetterberg, 2008; Ikeda et al., 2010). For obvious reasons, these conditions are not often considered as differential diagnoses for AD. Nevertheless, they may shed light on mechanisms behind CSF P-tau increase, as may emerging data on tau phosphorylation in hibernating squirrels (Williams et al., 2012) and hamsters (Hartig et al., 2007), as well as in anaesthesia (Whittington et al., 2013), pointing to physiological and pathological conditions in which tau phosphorylation occurs potentially as a consequence of reduced neuronal activity.

Diagnostic performance of combined CSF T-tau, P-tau and A β 42 tests

Multiple studies have investigated the diagnostic accuracy of combined CSF tests for T-tau, P-tau and A β 42 (Blennow et al., 2010). These studies collectively suggest that in cross-sectional studies aiming to distinguish AD from controls and in longitudinal studies aiming to determine which MCI patients who will develop AD a combined test outperforms each biomarker used alone (Blennow et al., 2010). Higher diagnostic performance is typically seen in single-centre studies (Johansson et al., 2011; Hansson et al., 2006), whereas large multi-centre studies tend to report slightly lower sensitivities and specificities (Mattsson et al., 2009c; Visser et al., 2009). The association of elevated T-tau and P-tau and reduced A β 42 with AD neuropathology has been validated in autopsy (Shaw et al., 2009) and brain biopsy (Seppala et al., 2012) studies. The influence of AD phenotype on CSF biomarkers has been less thoroughly explored in clinical variants of AD, including AD presenting with the logopenic variant of primary progressive aphasia (Bibl et al., 2011) or a corticobasal syndrome (Borroni et al., 2011).

Longitudinal changes in CSF AD biomarkers

Recent data show that it is possible to identify longitudinal changes in CSF A β 42, T-tau and P-tau in cognitively healthy controls followed over several years (Toledo et al., 2013; Mattsson et al., 2013b; Moghekar et al., 2013), although most studies (with exceptions (Toledo et al., 2013)) show that CSF AD biomarkers are essentially stable once patients have converted to AD (Zetterberg et al., 2007; Blennow et al., 2007; Mattsson et al., 2012a). This biomarker stability (at least during short term follow-up) may be useful in clinical trials to help identify effects of interventions on the intended biological target, such as altered A β homeostasis in response to an anti-A β treatment. One of the relatively few longitudinal studies of cognitively normal individuals, where repeated lumbar punctures were performed, suggests that A β 42 and tau changes occur in parallel and predict incident cognitive symptoms better than absolute baseline levels (Moghekar et al., 2013). CSF measurements may track trajectories of specific A β and APP metabolites (Mattsson et al., 2012b; Lannfelt et al., 2008; May et al., 2011; Portelius et al., 2010), as well as down-stream effects, such as reduced axonal degeneration in response to a disease-modifying drug (Gilman et al., 2005; Blennow et al., 2012).

CSF markers of synapse loss

Recently, several independent studies have shown that the CSF concentration of the dendritic protein neurogranin (Ng) is increased in AD (Thorsell et al., 2010; Kvartsberg et al., 2015a; Kvartsberg et al., 2015b; Hellwig et al., 2015; Kester et al., 2015), but not in other neurodegenerative disorders (Wellington et al., 2016), and that the marker predicts future cognitive decline, brain atrophy and reduction in glucose metabolism in prodromal disease stages (Portelius et al., 2015; Tarawneh et al., 2016). Currently, CSF Ng is the best established CSF biomarker for synapse loss in AD, although there are other promising markers, including SNAP-25, in development (Brinkmalm et al., 2014).

CSF markers of microglial activation

AD is tightly linked to activation of the inflammatory M1 phenotype of microglia, the resident macrophages of the brain. Chitotriosidase is an enzyme that is secreted by activated macrophages (Renkema et al., 1998) and its plasma levels are increased in patients with the lysosomal storage disorder Gaucher's disease (Hollak et al., 1994). Increased CSF chitotriosidase activity has been found in AD patients compared with non-demented controls

(Watabe-Rudolph et al., 2012; Mattsson et al., 2011b). A glycoprotein that has great homology with chitotriosidase but lacks its enzymatic activity is YKL-40 (Hakala et al., 1993). YKL-40 is expressed in both microglia and astrocytes and elevated levels have been reported in both prodromal AD and cerebrovascular disease (Craig-Schapiro et al., 2010; Olsson et al., 2013). Another microglial marker, the C-C chemokine receptor 2, is expressed on monocytes and one of its ligands, C-C chemokine ligand 2 (CCL2), that can be produced by microglia is important for the recruitment of monocytes in the CNS (Sokolova et al., 2009). Higher CSF CCL2 levels have been associated with a faster cognitive decline in MCI patients who developed AD (Westin et al., 2012). CCL2 levels in CSF were increased in AD patients compared with healthy controls (Correa et al., 2011; Galimberti et al., 2006b), as well as in the MCI stage of the disease (Galimberti et al., 2006a). However, one study failed to report any significant differences between AD patients and controls (Mattsson et al., 2011b). Another study found elevated CSF CCL2 levels in AD patients compared with controls, but there was an age-dependent increase in the biomarker level that may have affected the result (Blasko et al., 2006). Moreover, one study reported elevated levels of a soluble form of CD14 in the CSF from AD and PD patients compared with healthy controls (Yin et al., 2009). CD14 is a surface protein, mainly expressed by macrophages. As a cofactor for toll-like receptors, CD14 is essential for the recognition of pathogens by the innate immune system of the brain. Another microglial biomarker that has been detected in CSF of AD patients is neopterin, a degradation product deriving from the purine nucleotide guanosine triphosphate. However, no significant differences between AD and controls have been seen to date (Engelborghs et al., 1999). Finally, recent reports suggest that the CSF concentration of the secreted ectodomain of triggering receptor expressed on myeloid cells 2 (Trem2), a molecule that is selectively expressed by microglia in the CNS (Takahashi et al., 2005; Lue et al., 2015) and genetically linked to AD (Jonsson et al., 2013; Guerreiro et al., 2013), is increased in AD in a disease-specific manner and correlates with injury markers in the form of CSF T-tau and P-tau (Heslegrave et al., 2016; Piccio et al., 2016; Suarez-Calvet et al., 2016).

CSF biomarkers for Vascular Dementia

Key molecular pathways involved

Vascular dementia (VaD), sometimes more broadly referred to as vascular cognitive impairment (VCI), is a heterogeneous disease that is due to a variety of cerebrovascular

causes (Rosenberg et al., 2014). Pathological studies have shown that both large and small vessel damage occurs in VaD patients (Gold et al., 2007; Schneider et al., 2007). Large vessel disease leads to strokes with a step-wise course as a result of multiple infarctions that result in concomitant loss of intellect, but is a relatively rare cause of dementia. Much more common is small vessel disease which has several forms: it may either produce lacunes mainly in the basal ganglia without white matter damage or extensive changes in the white matter with or without lacunes. The term subcortical ischemic vascular disease is often used for both lacunar state and white matter disease, but there may be different pathophysiologies involved, particularly when there is cerebral hypoperfusion, which has a major impact on the vulnerable deep white matter (Rosenberg et al., 2014). Diagnosis of cerebrovascular disease has been revolutionised by the advent of neuroimaging, and MRI in particular. Cerebrovascular disease and chronic low-grade hypoxia seem to induce blood-brain barrier (BBB) impairment, extracellular matrix-remodelling and demyelination, which may be reflected in the CSF.

CSF markers of BBB impairment

The best-established fluid biomarker for BBB impairment is the CSF to serum albumin ratio. This marker has been most extensively studied and provides the strongest evidence of a disruption of the BBB in VaD (Wallin et al., 1990), although is not widely used in clinical practice.

CSF markers of tissue-remodelling

Elevated levels of matrix metalloproteinase 9 (MMP-9) in CSF have been shown in patients with VCI and mixed AD/VCI, but not in AD (Adair et al., 2004). Furthermore, tissue inhibitor of metalloproteinase-1 (TIMP-1), a regulator of the MMP system, has also been found to be elevated in CSF; the TIMP-1 CSF concentration has been shown to be correlated to the albumin ratio, possibly reflecting an overall regulation of different MMPs that might be involved in the BBB opening (Bjerke et al., 2011).

CSF markers of white matter injury

CSF markers of white matter injury include myelin basic protein, a protein component of myelin, sulfatide, a class of sulfolipids found in the myelin sheath, and neurofilament light (NFL), which is an axonal protein that is highly expressed in large calibre myelinated axons. All these markers are elevated in VaD and subcortical vascular impairment (Bjerke et al., 2009; Bjerke et al., 2011; Skillback et al., 2014a; Sjogren et al., 2001a; Tullberg et al., 2002;

Tullberg et al., 2000), but not in any disease-specific manner; similar changes are found in other CNS diseases that involve white matter, *e.g.*, multiple sclerosis (Haghighi et al., 2013; Burman et al., 2014).

Dementia with Lewy bodies

Key molecular pathways involved

α -Synuclein-containing, intra-neuronal Lewy bodies are the defining pathological hallmark of DLB, but most patients also have some degree of AD pathology, in particular amyloid plaques (Howlett et al., 2015). Their clinical impact is not known in detail, but there is some evidence from post-mortem studies that such AD changes (plaque and tangle pathology) lead to a more rapid cognitive decline in DLB (Kraybill et al., 2005).

CSF α -synuclein

α -Synuclein is the major component of intra-neuronal Lewy bodies, which are characteristic of Parkinson's disease (PD) and DLB (Mollenhauer et al., 2010). In PD and other synucleinopathies CSF α -synuclein levels are typically reduced (Hall et al., 2012; Mollenhauer et al., 2011), whilst in AD and CJD, the levels are elevated and correlate with T-tau, suggesting that in this context at least α -synuclein may also be a non-specific marker of neurodegeneration (Mollenhauer et al., 2011; Tateno et al., 2012; Wennstrom et al., 2013; Ohrfelt et al., 2009; Slaets et al., 2014). This has been reported not only in AD and CJD, but also in DLB, where there may be a competition between aggregation of α -synuclein into Lewy bodies and release of the protein from degenerating synapses, making the data hard to interpret (Kapaki et al., 2013). Importantly, α -synuclein is highly expressed in red blood cells, a reason why blood contamination during sample collection may further limit any diagnostic value (Barbour et al., 2008; Hong et al., 2010). Currently available assays for α -synuclein measure total amounts of the protein and not Lewy body-specific isoforms; sensitive and specific assays for the latter would resolve this issue.

CSF AD biomarkers in DLB

AD pathology is reflected in the CSF as increased concentrations of T-tau and P-tau and reduced concentration of A β 42 (Ahmed et al., 2014). High CSF T-tau and T-tau and low CSF

A β 42 concentrations are seen in 47% of DLB patients (Schoonenboom et al., 2012). This AD biomarker signature has also been demonstrated in PDD (Buongiorno et al., 2011), and low CSF A β 42 concentration has been found to predict future cognitive decline in PD (Siderowf et al., 2010). AD CSF biomarkers have been linked to earlier death in DLB (Brunnstrom et al., 2013), but their relationship with longitudinal cognitive decline in patients with DLB remains to be examined.

Frontotemporal dementia

Key molecular pathways involved

FTD is a clinically, genetically and pathologically heterogeneous neurodegenerative disorder that preferentially affects the frontal and anterior temporal lobes of the brain. FTD usually presents with behavioural disturbance (behavioural variant FTD, bvFTD) or language impairment (primary progressive aphasia, PPA) but there is also overlap with motor neurone disease (MND) and the atypical parkinsonian disorders, corticobasal syndrome (CBS) and progressive supranuclear palsy (PSP) (Warren et al., 2013). Pathologically, neuronal inclusions are usually found containing abnormal forms of one of two proteins, tau or TDP-43, although less commonly patients may have inclusions containing FUS protein. Around a third of cases are inherited in an autosomal dominant fashion, caused by mutations in progranulin (*GRN*), microtubule-associated protein tau (*MAPT*) or *C9orf72* (Rohrer et al., 2015), and in these cases the pathology can reliably be determined during life (TDP-43 in *GRN* and *C9orf72*, tau in *MAPT*). Whilst there is a fairly good correlation between clinical syndrome and underlying pathology in some sporadic cases, *e.g.*, semantic variant PPA (svPPA) and TDP-43, for the majority of bvFTD and nonfluent variant PPA (nfvPPA) cases there is poor phenotype/pathological correlation.

CSF NFL

Neurofilament biomarker candidates, *i.e.*, neurofilament light chain (NFL) and phosphorylated neurofilament heavy chain (pNFH), are important proteins of the axonal cytoskeleton. In FTD, CSF NFL has been shown to be higher compared with AD (de Jong et al., 2007; Landqvist Waldo et al., 2013; Sjogren et al., 2000); a result that was recently confirmed in a large retrospective analysis of data from the Swedish Dementia Registry (Skillback et al., 2014a).

CSF TDP-43

The presence of aggregates positive for the TAR DNA-binding protein of 43 kDa (TDP-43) accounts for about 50% of FTD patients and is found in FTD-MND, in most svPPA patients and only seldom in nvPPA or CBS. TDP-43 can be measured in CSF but, unfortunately, most of the protein appears to be blood-derived and its CSF concentration does not reflect neuropathology and is unaltered in FTD (Feneberg et al., 2014; Steinacker et al., 2008).

CSF progranulin

Progranulin concentration has been shown to be reduced in CSF and plasma in progranulin (*GRN*) mutation carriers but not in other FTD cases (Ghidoni et al., 2008). This was confirmed recently by several studies (Morenas-Rodriguez et al., 2016) and suggests progranulin determination as an alternative to genetic testing for the identification of *GRN* mutation carriers.

CSF AD biomarkers

BvFTD is the neurodegenerative disease with the smallest proportion of AD biomarker-positive cases (Skillback et al., 2015). Combining the classical AD biomarkers (CSF T-tau, P-tau and A β 42, all normal) with NFL (increased) results in diagnostic sensitivities of 75-86% and specificities of 94-100% for FTD as compared to AD and cognitively normal controls (de Jong et al., 2007).

Standardization efforts

The clinical utility of CSF tests for T-tau, P-tau and A β 42 is clear and their importance for selecting patients in pre-dementia stages of AD for clinical trials of disease-modifying drug candidates is undisputed (Lleo et al., 2015). However, most of the commercially available assays for these biomarkers are still research-grade, and there is a lack of common calibrators or certified reference measurement systems that can be used for standardisation (Mattsson et al., 2012c). This leads to a risk of bias in the biomarker measurements across different assay platforms. A recognisable consequence of this is that optimal CSF A β 42 cut-points for differentiating AD patients from control individuals vary from 192 ng/L (Shaw et al., 2009) to around 550 ng/L (Hansson et al., 2006; Duits et al., 2014) or even higher (Palmqvist et al., 2014), depending on the assay format and reference standard for diagnosis used. The

development of certified reference methods and materials for CSF T-tau, P-tau and A β 42, led by the International Federation of Clinical Chemistry and Laboratory Medicine (IFCC) Working Group on CSF Proteins, will at least partly solve this issue. This work has come the furthest for CSF A β 42 for which two mass spectrometry-based reference methods have been published and formally certified by the Joint Committee for Traceability in Laboratory Medicine (JCTLM; database identification numbers C11RMP9 and C12RMP1, respectively) (Korecka et al., 2014; Leinenbach et al., 2014). A CSF-based reference material for CSF A β 42 is currently under evaluation (Bjerke et al., 2015).

Another issue is random variation in the biomarker measurements, even when the same assay is used. This can be seen in multi-centre comparisons of measurements, including the Alzheimer's Association QC Program for CSF Biomarkers (Mattsson et al., 2011a; Mattsson et al., 2013a). This program includes around 90 participants around the globe and shows that the inter-laboratory coefficients of variation (CVs) for commercially available tau and A β assays are between 20-30%, whereas intra-laboratory studies show that CVs of <10% should be feasible. Recent advancements in the development of fully automated assays have resulted in inter-laboratory CVs of 1-4% in the Alzheimer's Association QC Programme, thus showing promise for the future (Bittner et al., 2015).

Important pre-analytical sources of variation for the most variable AD biomarker, A β 42, are storage tube type (polypropylene tubes are recommended but different brands seem to show different analyte adsorption (Perret-Liaudet et al., 2012)); sample aliquot volume (Toombs et al., 2013); the number of tube transfers of the collected CSF (Toombs et al., 2014); and blood contamination (Bjerke et al., 2010). Analytical sources of variation include the composition of the diluent buffer – low concentrations of detergent increase the measured A β 42 concentration, which has to be standardised (Bjerke et al., 2010). Several additional factors may be important in an assay-specific manner and close adherence to kit inserts is recommended, as is participation in the Alzheimer's Association QC programme and other inter-laboratory comparison programmes to ensure that proper laboratory procedures are in place.

CSF biomarker-supported diagnostic criteria

Patients with AD are routinely diagnosed by clinical criteria, commonly the international classification of diseases (ICD10) or NINCDS-ADRDA criteria (McKhann et al., 1984). However, the “gold standard” diagnostic method for AD is to perform an autopsy to find neuropathological AD changes (neuronal loss along with plaque and tangle pathology) at a sufficient degree to confer a diagnosis (Mirra et al., 1991). The recently published updated diagnostic criteria from the International Working Group (IWG-2) for New Research Criteria for the Diagnosis of AD propose that AD can be diagnosed when the specific clinical phenotype of episodic memory impairment is present together with low levels of CSF A β 42 and high levels of either T-tau or P-tau (Dubois et al., 2014). Additionally, these new criteria also recognise “atypical” AD, the latter comprising posterior (visual or biparietal), logopenic (language) and frontal (behavioural) clinical variants, if there is also biomarker evidence of AD pathology (Dubois et al., 2014). Biomarker-supported criteria have also been proposed by the US National Institute on Aging (NIA) allowing for a diagnosis of preclinical AD, MCI due to AD and dementia due to Alzheimer’s disease. For VaD, DLB and FTD, no biomarkers accurate enough to be included in clinical criteria have been presented as of to date.

Concluding remarks

Three CSF biomarkers reflecting the core pathological features of AD are in common use: T-tau (broadly, but not entirely reflecting neurodegeneration), P-tau (reflecting tau hyperphosphorylation and tangle formation) and A β 42 (which inversely correlates with plaque pathology). According to revised clinical criteria, these markers may help diagnose AD more accurately and open up the possibility of detecting pre-dementia stages of the disease (Dubois et al., 2014). At present, their most obvious utility is in clinical trials of novel disease-modifying treatments against AD. In the future, they may help selecting the right treatment for individual patients by making it possible to assess which molecular pathology that is most likely to cause the patient’s symptoms at different stages of the disease. In addition, there is considerable promise that CSF biomarkers will be able to provide *in vivo* measurement of a range of additional pathophysiological processes in AD, including microglial activation and synapse loss. In regards to other neurodegenerative disorders, CSF NFL is a promising marker to detect degeneration of large calibre axons in VaD and FTD. Specific CSF markers for TDP-43, Lewy bodies and other protein inclusions (e.g., FUS and dipeptide repeats) are urgently needed.

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