Cerebrospinal fluid biomarkers in parkinsonian conditions: an update and future directions

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ABSTRACT
Parkinsonian diseases comprise a heterogeneous group of neurodegenerative disorders, which show significant clinical and pathological overlap. Accurate diagnosis still largely relies on clinical acumen; pathological diagnosis remains the gold standard. There is an urgent need for biomarkers to diagnose parkinsonian disorders, particularly in the early stages when diagnosis is most difficult. In this review, several of the most promising cerebrospinal fluid candidate markers will be discussed. Their strengths and limitations will be considered together with future developments in the field.

INTRODUCTION
Idiopathic Parkinson’s disease (iPD) is a progressive neurologological disorder initially described as a clinical entity by James Parkinson and then embellished by Charcot and other nineteenth-century physicians, including Trouseau, Gowers and Erb. It is a clinical construct, based upon the presence of bradykinesia accompanied by at least one other characteristic feature, such as resting tremor, rigidity and impaired postural reflexes.1 The signs and symptoms are usually asymmetrical at onset and, typically, there is a good response to levodopa treatment.

‘Parkinson-plus’ or ‘atypical parkinsonism’ are terms that refer to a heterogeneous group of neurodegenerative disorders that may masquerade particularly in the early stages of the disease as Parkinson’s disease (PD).2 The ‘plus’ or ‘atypical’ descriptor indicates the presence of additional characteristics not usually in patients with iPD, such as early autonomic disturbance and pyramidal signs exhibited by patients with multiple system atrophy (MSA), supranuclear gaze palsy and frontal/dysexecutive syndrome by those with progressive supranuclear palsy (PSP), dystonia and myoclonus in corticobasal degeneration (CBD) and early postural instability and falls by all of them. Another disease that could be classified as an atypical parkinsonian disorder is dementia with Lewy bodies (DLB), where dementia onset is before or within a year of onset of extrapyramidal features. The earlier onset of dementia differentiates DLB from Parkinson’s disease dementia (PDD).

Atypical parkinsonian disorders account for less than 10% of all parkinsonism and rarely respond with sustained improvement to levodopa. They usually follow a much more aggressive disease course than iPD and are characterised by atrophy to several different cortical and subcortical networks. Furthermore, atypical parkinsonism has been described in other conditions, such as Alzheimer’s disease (AD) and frontotemporal dementia (FTD).

PATHOLOGY
Protein misfolding and aggregation is seen with many neurodegenerative diseases. Based on pathological findings, parkinsonian syndromes are classified into α-synucleinopathies (PD, DLB and MSA) and primary tauopathies (PSP and CBD). For pathological lesions used in postmortem diagnosis of parkinsonism, see figure 1.

α-Synuclein (α-Syn) has been found to be the major constituent of the intracellular aggregates in Lewy bodies and Lewy neurites (pathological hallmark of PD and DLB) and in the glial cytoplasmic inclusions in MSA.1–4 The presence of abnormally aggregated tau proteins in the form of neurofibrillary tangles, for example, are diagnostic of PSP.5 Tau-positive intracellular inclusions are the neuropathological findings in CBD.6 Even though there are also neurofibrillary tangles in AD, Aβ plaques are closely tied to the primary disease process and thus AD is considered to be a secondary tauopathy. FTD can also have underlying tau pathology. There is often some overlap between synucleinopathies and tauopathies (for a review, see ref. 7).

Co-occurrence of tau and α-Syn pathology has been found in neurons and oligodendrocytes in AD, PD and DLB.8 α-Syn has complex and dynamic interactions with tau. Each of these two proteins has the tendency to seed the aggregation of the other.9 α-Syn induces aggregation and polymerisation of tau, which promotes formation of intracellular amloid-tau inclusions.10,11 Similar interactions have been described between α-Syn and Aβ pathology.11

GENETICS
Recent advances in genetics have shed light on the underlying pathophysiology because mutations in the gene for each misfolded protein can give rise to an inherited form of a relevant neurodegenerative condition. For example, rare hereditary forms of PD can be caused by mutations affecting the gene coding for α-Syn (SNCA); PARK1 (missense) and PARK4 (duplication, triplication).12 Furthermore, in both PD and to a lesser extent in MSA, population studies demonstrated an association between disease risk and distinct single-nucleotide polymorphisms in SNCA. DJ-1(PARK7) mutations can lead to rare forms of autosomal-recessive PD, pointing towards mitochondrial damage/oxidative stress pathways driven pathogenesis.13 Even though PD is not a ‘tauopathy’, population studies also showed variants in tau (MAPT) gene, particularly the H1 haplotype, as another risk factor for PD (for a review, see ref. 14). Several tauopathies are
associated with variants in MAPT, including CBD, FTD linked to chromosome 17 (FTDP-17T) and PSP. The fact that the MAPT/tau haplotype also shows an association with PD strongly suggests that the pathogenic cascades in the tauopathies may be related to those in the synucleinopathies.

**DIAGNOSTIC CHALLENGES**

Accurate diagnosis of parkinsonian disorders still relies heavily on clinical acumen, although imaging and ancillary investigations may be helpful in some situations. In one postmortem series, 24% of patients clinically diagnosed with idiopathic PD by a consultant neurologist during life were found to have an alternative diagnosis.

**CEREBROSPINAL FLUID BIOMARKERS**

A biomarker is “a characteristic that is objectively measured and evaluated as an indicator of normal biological processes, pathogenic processes or pharmacologic response to a therapeutic intervention.” An ‘ideal’ biomarker should be sensitive, reproducible, closely associated with the disease process, non-invasive and inexpensive.

Cerebrospinal fluid (CSF) has more physical contact with the brain than any other fluid and as such represents a potentially reliable biomarker source. Unlike plasma, CSF is not separated from the brain by the tightly regulated blood–brain barrier. Proteins/peptides that may be directly reflective of brain specific activities or disease pathology would most likely diffuse into the CSF. Furthermore, CSF can be tested serially, which makes possible the study of protein changes reflecting the evolving pathology throughout the clinical course of the disease. This is preferable to pathological studies, which only reveal the terminal changes of a disease process that has developed over decades.

**HISTORICAL BACKGROUND**

CSF has been widely investigated in parkinsonian disorders and is considered to offer the most promising insights into the
disease process. Historically, because of dopaminergic abnormalities in parkinsonism, the first compounds to be tested as potential markers were dopamine and other monoamines and their metabolites. In the 1960s and 1970s, reduced CSF monoamine concentrations (homovanillic acid and 5-hydroxyindoleacetic acid) were found in patients with parkinsonism and dementia. A study conducted at the National Hospital, Queen Square, London, assessed the effect of levodopa treatment in CSF homovanillic acid concentration of PD patients. Before levodopa treatment, homovanillic acid concentration was low in all patients, while after treatment it rose to a level that correlated significantly with the levodopa dose.

As these metabolic results were prone to be influenced by a multitude of other factors, the quest went further to investigate a priori defined compounds, such as α-Syn and tau. These were tested in patients and in healthy controls, looking for differences, patterns and associations. Even though several promising candidates exist, there is still no reliable biomarker.

METHODS
We reviewed the potential use of CSF proteins as biomarkers in parkinsonism, focusing on α-Syn, neuronal injury markers and Aβ42. In addition, we briefly reviewed the latest novel markers and the ‘omics’ approach. We performed a PubMed/Medline search and limited searches to studies reported in English and published after 2006, including antemortem, human, lumbar CSF; all studies included at least one parkinsonian cohort compared with healthy or neurological controls. We combined searches with ‘Parkinson’s disease’, ‘progressive supranuclear palsy’, ‘multiple system atrophy’, ‘corticobasal syndrome’ (CBD), ‘corticobasal degeneration’, ‘Parkinson’s disease dementia’, ‘dementia with Lewy bodies’, ‘Lewy body dementia’, ‘parkinsonism’, ‘synucleinopathies’, ‘tauopathies’, ‘neurodegenerative diseases’ with ‘CSF biomarkers’ and specific biomarkers (‘α-Syn’, ‘tau’, ‘phosphorylated tau’, ‘Aβ42’, ‘neurofilaments’, ‘neuronal injury markers’, ‘inflammatory’, ‘metabolic’ and ‘oxidative stress markers’). Further references were found manually from identified publications. For a review of the earlier literature, not captured using the time limit of our search criteria, see Eller and Williams.

CSF BIOMARKER CANDIDATES IN PARKINSONISM

**Aβ42**
Aβ42 is a 42 amino-acid long, aggregation-prone protein, derived from the proteolytic processing of amyloid precursor protein and is a major component of neuritic plaques in AD. Cognitive impairment and dementia are much more common in parkinsonism than in the general population and have a detrimental effect on quality of life and life expectancy. The link between Aβ42 and PD and dementia has been studied extensively (see Table 1).

In most studies, Aβ42 is significantly reduced in PD compared with controls and is associated with worse cognitive performance. However, other investigations showed no difference between PD and controls.

Compta et al collected CSF from 27 non-demented PD patients and followed them over time. Patients who converted to dementia within 18 months had a significantly lower baseline CSF Aβ42 than the patients who remained non-demented.

DLB patients have the lowest CSF levels of Aβ42 among the parkinsonian cohorts. One study found that almost half of DLB patients had a CSF biomarker profile consistent with AD, which agrees with the knowledge of Aβ pathology in this disease.

There is evidence that low Aβ42, a marker of Aβ plaque pathology, may predict cognitive decline in patients with PD, but other longitudinal studies with larger cohorts are necessary to clarify this further.

**α-Syn**
α-Syn is a 140 amino-acid long protein that localises to presynaptic terminals and is widespread in the brain, comprising 1% of cytosolic protein. In presynaptic terminals, α-Syn is present in close proximity to the synaptic vesicles. The precise...
function of \( \alpha \)-Syn is obscure, but it is speculated that its main role is in the control of neurotransmitter release.\(^{39} \) Although mostly considered an intracellular protein, \( \alpha \)-Syn is capable of transfer between cells leading to a speculation of a prion-like mechanism operating in PD pathology spread.\(^{40} \)

\( \alpha \)-Syn can be modified by truncation, acetylation, phosphorylation, oxidation, nitrosylation, glycation or glycosylation.\(^{41} \) Lewy bodies are formed mostly of post-translationally modified \( \alpha \)-Syn. \( \alpha \)-Syn deposition is key in the pathogenesis of synucleinopathies. In vitro, similar to AD, \( \alpha \)-Syn fibrillation involves \( \alpha \)-Syn oligomerisation followed by oligomer conversion into mature amyloid bodies.\(^{42} \)

**NEURONAL INJURY MARKERS**

**Tau**

Tau is important for the function of axonal microtubules and, as a result, plays an important role in the structural integrity of the neuron and axonal support. When hyperphosphorylated, it has reduced binding affinity for microtubules, causing their malfunction. At the same time, it adopts an abnormal conformation leading to aggregation and inclusion formation.\(^{64} \)

**Total and phosphorylated tau (t-tau and p-tau)**

In the past, there were inconclusive results when assessing tau levels in CSF of parkinsonian patients (see table 3). In PD, most studies found normal values,\(^{21} 24 25 26 27 29 30 \) but lower levels were also reported.\(^{22} 23 28 29 30 \) In atypical parkinsonism, high t-tau levels were found in DLB.\(^{25} 27 \) and low p-tau/t-tau ratio in MSA and PSP compared with PD.\(^{29} \) However, other investigations found no difference between parkinsonian syndromes.\(^{22} 26 30 \) In particular, no significant change has been seen in PSP.\(^{26} \) Age, not diagnosis, is thought to be the strongest factor affecting t-tau protein levels.\(^{64} \)

**Oligomeric and phosphorylated \( \alpha \)-Syn**

Tokuda et al evaluated soluble \( \alpha \)-Syn oligomers as potential early markers of PD and found that both the level of oligomeric \( \alpha \)-Syn and the oligomer/t-\( \alpha \)-Syn ratio were substantially higher in patients with PD (including those with mild and early-stage disease) compared with healthy controls and patients with non-neurodegenerative neurological conditions. CSF oligomer/t-\( \alpha \)-Syn ratio had a sensitivity of 89.3% and a specificity of 90.6% for PD.\(^{57} \) These findings were replicated in two further, independent studies.\(^{58} 59 \) Both oligomeric and phosphorylated oligomeric forms of \( \alpha \)-Syn were detected in postmortem ventricular CSF, which may be useful in distinguishing between PD, DLB and MSA.\(^{60} \) The results need to be replicated in larger groups of living patients.
not reproduced by another group, which did not find a reduced tau ratio in an independent cohort of PSP patients, suggesting that the 33/35 kDa bands seen are heavy and light IgG chains. Recent findings of other endogenous tau fragments in CSF suggest that specific assays for these fragments should be developed and evaluated in relation to different tauopathies.

**Neurofilament light chain protein (NF-L)**

Neurofilaments are major structural elements, whose main role is to maintain the axonal calibre and neuronal shape and size. They are, thus, critical for the morphological integrity of neurons and for the conduction of nerve impulses along axons. They are composed of three subunits of different molecular weights: light, medium and heavy chain.
Neurofilament heavy chain (NF-H) forms an important component of the cytoskeleton. Higher CSF levels of NF-H were found in PSP and MSA compared with PD, CBD and neurological controls.  

Neurofilament light chain forms the backbone of neurofilaments and can self-assemble. Increased levels in CSF reflect axonal degeneration of large myelinated axons. Recent studies showed consistent results in differentiating PD from atypical parkinsonian conditions but not in discriminating between atypical parkinsonian syndromes. Consecutive analyses of CSF showed no increase in NF-L levels with disease progression.

NF-L can be useful in the differential diagnosis of PD versus other neurodegenerative conditions as it is very sensitive in detecting more aggressive neuronal death than occurs in PD.

### Gliarial fibrillary acidic protein

Gliarial fibrillary acidic protein (GFAP) is a protein predominantly expressed in fibrous astrocytes. Disintegration of astroglial cells postacute brain injury can lead to high CSF GFAP levels. GFAP expressed in glial astrocytes. Disintegration of astroglial cells postacute brain injury can lead to high CSF GFAP levels.

### Table 3: CSF neuronal injury markers: tau, neurofilament light chain (NF-L) and glial fibrillary acidic protein (GFAP) in parkinsonian disorders

<table>
<thead>
<tr>
<th>Research groups</th>
<th>Participants</th>
<th>Analyte</th>
<th>Method</th>
<th>Main findings</th>
</tr>
</thead>
<tbody>
<tr>
<td>Kang et al 2014</td>
<td>PD n=39 (drug-naïve patients), HC n=63</td>
<td>t-tau, p-tau</td>
<td>Bead-based multi-analyte assay (Luminex)</td>
<td>Decrease in t-tau+p-tau in PD vs controls</td>
</tr>
<tr>
<td>Luk et al 2023</td>
<td>PDD n=11, PSN n=44, CBS n=22, AD n=11, controls n=34</td>
<td>t-tau, p-tau</td>
<td>Immuno-PCR (adapted from sandwich ELISA)</td>
<td>No difference in 3R-tau</td>
</tr>
<tr>
<td>Hall et al 2012</td>
<td>PD n=90, PDD n=33, DLB n=70, PSP n=45, CBD n=12, MSA n=48, AD n=48, controls n=107</td>
<td>t-tau, p-tau</td>
<td>Bead-based multi-analyte assay (Luminex)</td>
<td>No difference in 3R-tau</td>
</tr>
<tr>
<td>Bech et al 2012</td>
<td>PD n=22, PDD n=3, DLB n=11, MSA n=10, PDD n=20, CBD n=3</td>
<td>NF-L</td>
<td>ELISA</td>
<td>Increase in t-tau in AD vs DLB+PDD</td>
</tr>
<tr>
<td>Andersson et al 2016</td>
<td>DLB n=47, PDD n=17, AD n=150</td>
<td>t-tau, p-tau</td>
<td>ELISA</td>
<td>-Decrease in PD vs to controls</td>
</tr>
<tr>
<td>Shi et al 2018</td>
<td>Discovery cohort: PD n=126, MSA n=32, AD n=50, controls n=38</td>
<td>t-tau, p-tau</td>
<td>Bead-based multi-analyte assay (Luminex)</td>
<td>-Decrease in PD+MSA vs AD</td>
</tr>
<tr>
<td>Parnetti et al 2017</td>
<td>PD n=38, DLB n=32, AD n=48, FTD n=31, controls n=32</td>
<td>t-tau, p-tau</td>
<td>ELISA</td>
<td>Increase in AD&gt;FTD&gt;DLB vs PD and controls</td>
</tr>
<tr>
<td>Kuiperij et al 2019</td>
<td>NA</td>
<td>33/55 kDa tau forms</td>
<td>Immunoprecipitation assay and western blotting</td>
<td>Not able to detect tau form ratio</td>
</tr>
<tr>
<td>Borrioni et al 2020</td>
<td>PSP-RS n=20, PSP-P n=7, MSA-P n=11, MSA-C n=10, controls n=27</td>
<td>33/55 kDa tau forms</td>
<td>Immunoprecipitation assay and western blotting</td>
<td>Suggested that 33/55 kDa bands seen are heavy and light IgG chains</td>
</tr>
<tr>
<td>Constantinescu et al 2021</td>
<td>PD n=10, MSA n=21, PSP n=14, CBD n=11, HC n=59 (×2 consecutive samples)</td>
<td>NF-L</td>
<td>ELISA</td>
<td>No difference between parkinsonian groups</td>
</tr>
<tr>
<td>Montine et al 2022</td>
<td>PD n=41, PDD n=11, AD n=49, HC n=150</td>
<td>t-tau, p-tau</td>
<td>Bead-based multi-analyte assay (Luminex)</td>
<td>No difference between parkinsonian groups</td>
</tr>
<tr>
<td>Süssmuth et al 2023</td>
<td>PSP-RS n=20, PSP-P n=7, MSA-P n=11, MSA-C n=10, controls n=20</td>
<td>t-tau, p-tau</td>
<td>ELISA</td>
<td>p-tau: no difference between disease groups; p-tau/t-tau ratio lower in PSP and MSA vs PD</td>
</tr>
<tr>
<td>Alves et al 2024</td>
<td>PD n=109, AD n=20, HC n=36</td>
<td>t-tau, p-tau</td>
<td>ELISA</td>
<td>No difference between PD and controls</td>
</tr>
<tr>
<td>Ohrfelt et al 2025</td>
<td>PD n=15, DLB n=15, AD n=66, controls n=55</td>
<td>t-tau, p-tau</td>
<td>ELISA</td>
<td>No difference between parkinsonian groups</td>
</tr>
<tr>
<td>Compta et al 2026</td>
<td>PD n=20, PDD n=20, HC n=15</td>
<td>t-tau, p-tau</td>
<td>ELISA</td>
<td>t- and p-tau: increase in PDD vs PD and controls</td>
</tr>
<tr>
<td>Parnetti et al 2027</td>
<td>PD n=20, PDD n=8, DLB n=19, AD n=23, HC n=20</td>
<td>t-tau, p-tau</td>
<td>ELISA</td>
<td>p-tau: no difference between parkinsonian groups</td>
</tr>
<tr>
<td>Borrioni et al 2028</td>
<td>PSP-RS n=21, CBS n=20, FTD n=44, AD n=15, PD n=10, DLB n=15, controls n=27</td>
<td>33/55 kDa tau forms</td>
<td>Semiquantitative immunoprecipitation and western blotting</td>
<td>Tau forms significantly reduced in PSP vs other groups</td>
</tr>
<tr>
<td>Brettschneider et al 2029</td>
<td>PD n=22, MSA n=21, PSP n=21, CBD n=6, controls n=45</td>
<td>NF-H</td>
<td>ELISA</td>
<td>Increased in MSA and PSP vs PD, CBD and controls</td>
</tr>
</tbody>
</table>
similar GFAP levels in parkinsonian syndromes and healthy controls without significant change over time.\textsuperscript{71}

**OTHER CANDIDATE MARKERS**

**Oxidative stress markers**

DJ-1

DJ-1 is a multifunctional protein involved in many processes. It is thought to have a protective role in oxidative stress during neurodegeneration (table 4). As we have already discussed, it has been linked to autosomal-recessive PD. Results on DJ-1 as a CSF biomarker have been inconsistent so far. One study showed decreased levels in PD compared with controls with a sensitivity of 90\% and a specificity of 70\%.\textsuperscript{52} whereas another showed no difference among parkinsonian syndromes\textsuperscript{72} and the most recent one demonstrated significant increase in MSA compared with PD and controls.\textsuperscript{73} The diagnostic accuracy for discriminating MSA from PD was improved by combining DJ-1 levels with t-tau and p-tau levels.

**8-Hydroxydeoxyguanosine (8-OHdG)**

8-OHdG is a marker of oxidation and mitochondrial dysfunction in neurodegeneration and malignancy. CSF 8-OHdG levels were increased in non-demented PD patients compared with controls and there was a negative correlation with MMSE levels in PDD.\textsuperscript{74}

**Urate**

Urate is an endogenous and most potent antioxidant. Even though there is considerable evidence linking low serum levels of urate to PD,\textsuperscript{75,76} CSF studies have shown inconsistent results. Maetzler et al\textsuperscript{77} found increase levels in PD compared with DBL, but Constantinescu et al\textsuperscript{78} showed no difference among parkinsonian groups and healthy controls.

**Inflammatory markers**

**Fractalkine**

Fractalkine is an inflammatory cytokine that acts as a neurotrophic and antiapoptotic factor in the central nervous system. It was decreased in MSA and could alone differentiate between PD and MSA with a sensitivity of 99\% and a specificity of 95\%.\textsuperscript{72} In addition, the fractalkine/FH ratio was closely associated with disease severity and progression in PD. These results are in need of replication.

**Complement C3/factor H ratio**

The C3/factor H ratio in CSF was significantly decreased in MSA compared with PD, AD and healthy controls. Increased

### Table 4: CSF biomarkers for oxidative stress, inflammation and energy failure in parkinsonian disorders

<table>
<thead>
<tr>
<th>Research groups</th>
<th>Participants</th>
<th>Analyte</th>
<th>Method</th>
<th>Main findings</th>
</tr>
</thead>
<tbody>
<tr>
<td>Herbert et al\textsuperscript{73}</td>
<td>PD n=43, MSA n=23, controls n=30</td>
<td>DJ-1</td>
<td>ELISA</td>
<td>▶ Increase in MSA vs PD</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>▶ Significant difference in MSA vs PD, MSA vs controls and PD vs controls</td>
</tr>
<tr>
<td>Constantinescu et al\textsuperscript{79}</td>
<td>PD n=6, MSA n=13, PSP n=18, CBD n=6, HC n=18</td>
<td>Urate</td>
<td>Enzymatic method on a modular system</td>
<td>No difference</td>
</tr>
<tr>
<td>Wenstrom et al\textsuperscript{41}</td>
<td>PD n=38, PDD n=22, DLB n=33, AD n=46, HC n=52</td>
<td>Neurosin</td>
<td>ELISA</td>
<td>▶ Lowest levels in DBL, but no difference between synucleinopathies</td>
</tr>
<tr>
<td>Goldstein et al\textsuperscript{42}</td>
<td>PD n=34, MSA n=54, PAF n=20, HC n=38</td>
<td>Dihydroxyphenylacetic acid (DOPAC)</td>
<td>Batch alumina extraction followed by liquid chromatography with electrochemical detection</td>
<td>▶ When pooled, synucleinopathies decrease levels vs AD+HC</td>
</tr>
<tr>
<td>Salvesen et al\textsuperscript{72}</td>
<td>PD n=30, DLB n=17, MSA n=14, PSP n=19</td>
<td>DJ-1</td>
<td>ELISA</td>
<td>▶ Decrease in PD vs DBL</td>
</tr>
<tr>
<td>Maetzler et al\textsuperscript{77}</td>
<td>PD n=55, PDD n=20, DLB n=20, controls n=76</td>
<td>Uric acid</td>
<td>ADVIA analyser+photometric methods</td>
<td>Increase in PD vs DBL</td>
</tr>
<tr>
<td>Shi et al\textsuperscript{32}</td>
<td>Discovery cohort: PD n=126, MSA n=32, AD n=50, controls n=137</td>
<td>DJ-1</td>
<td>Bead-based multi-analyte assay (Luminex)</td>
<td>▶ DJ1: decrease in MSA+PD vs controls +AD</td>
</tr>
<tr>
<td></td>
<td>Validation cohort: PD n=83</td>
<td>Fractalkine</td>
<td></td>
<td>▶ Fractalkine: decrease in MSA vs PD, AD+controls</td>
</tr>
<tr>
<td>LeWitt et al\textsuperscript{81}</td>
<td>PD n=217 (samples collected ×2 occasions) HC n=26</td>
<td>Homovallinic acid/xanthine ratio</td>
<td>Gas chromatography-mass spectrometry</td>
<td>▶ Increased ratio in PD vs HC</td>
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<td></td>
<td></td>
<td></td>
<td></td>
<td>▶ Ratio increased further in PD specimens collected up to 2 years later</td>
</tr>
<tr>
<td>Wang et al\textsuperscript{79}</td>
<td>PD n=86, MSA n=20, AD n=38 HC n=91</td>
<td>Complement C3/factor H (FH)</td>
<td>Bead-based multi-analyte assay (Luminex)</td>
<td>▶ C3: decrease in MSA vs PD+HC; increase in AD vs all other groups</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>▶ FH: increase in AD vs PD+HC</td>
</tr>
<tr>
<td>Maetzler et al\textsuperscript{80}</td>
<td>PD n=38, PDD n=20, DLB n=21 m, controls n=23</td>
<td>Neprilysin</td>
<td>Fluorometric assay</td>
<td>Decrease in DBL+PDD vs PD+ controls</td>
</tr>
<tr>
<td>Hong et al\textsuperscript{82}</td>
<td>PD n=117, AD n=50, HC n=132</td>
<td>DJ-1</td>
<td>Bead-based multi-analyte assay (Luminex)</td>
<td>▶ Decreased levels in PD vs Controls and AD</td>
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<td></td>
<td></td>
<td></td>
<td></td>
<td>▶ No difference between AD+ controls</td>
</tr>
</tbody>
</table>

AD, Alzheimer’s disease; CBD, corticobasal degeneration; CSF, cerebrospinal fluid; DBL, dementia with Lewy bodies; HC, healthy controls; MSA, multiple system atrophy; PAF, pure autonomic failure; PD, Parkinson’s disease; PDD, Parkinson’s disease dementia; PSP, progressive supranuclear palsy.
levels of C3 or factor H, together with decreased levels of Aβ42, correlate positively with disease severity and progression in PD.79

Neurosin
Neurosin is a protein expressed in human brain tissue, and it is one of several enzymes suggested to cleave α-Syn. A study comparing neurosin levels in synucleinopathies showed lowest levels in DLB, but no difference among DLB, PDD and PD. However, when pooled together, synucleinopathies had significantly lower neurosin levels compared with AD and controls.47

Nepriysin
Nepriylisin is a membrane bound presynaptic protein involved in Aβ clearance. CSF levels were significantly decreased in DLB and PDD compared with PD and controls, and they correlated well with Aβ42 levels in all cohorts.80

Catecholamine metabolites
Homovanillic acid (HVA)/xanthine ratio
HVA is the major catabolite of dopamine and has been extensively studied in the past in relation to PD, as described above. Xanthine is the immediate precursor of urate. HVA/xanthine ratio was increased in PD compared with controls and correlated with diseased severity.81

Dihydroxyphenylacetic acid (DOPAC)
Depletion of dopamine (a catecholamine) in basal ganglia is a defining neurochemical characteristic in PD. DOPAC is a neuronal metabolite of catecholamines. It was found to be decreased in PD and MSA compared with healthy controls, but there was no difference between synucleinopathy groups.82

The above compounds may be promising candidate markers, but they need verification in further studies. CSF HVA has been extensively studied in relation to PD and treatment response but still has no definite place in the clinical routine.

Lysosomal dysfunction
Lysosomes are the cell’s waste disposal system, and their dysfunction is an early event in PD pathogenesis.83 Patients suffering from Gaucher disease, a rare, autosomal-recessive storage disorder caused by lysosomal enzyme β-glucocerebrosidase (GCase) deficiency, have an increased risk of parkinsonism,84 which appears to be driven by a direct effect of GCase deficiency and lysosomal dysfunction on α-Syn aggregation.85

Measuring GCase activity in the CSF could be a useful biomarker in PD. PD87 and DLB88 patients were found to have significantly reduced GCase activity compared with neurological controls. A recent study showed that the combination of GCase activity, oligomeric/total α-Syn ratio and age discriminates best PD from neurological controls.89 However, in a Dutch cohort of de novo PD patients and healthy controls, there was a trend towards a reduction in CSF GCase activity.90 The usefulness of GCase as a potential biomarker in parkinsonian conditions needs to be evaluated in future studies that include additional neurodegenerative groups to PD.

‘Omics’ approaches
The markers already discussed have been hypothesis driven based on pathophysiological studies, which have identified potentially deranged pathways in neurodegenerative diseases. The ‘omics’ techniques offer an unbiased approach of identifying biochemical pathways that are unexpectedly involved in neurodegeneration. Ultimately, the aim is to generate a list of candidate markers deserving further targeted studies.91 The ‘omics’ approach results in unbiased and systematic measurement of patterns of variations in genes (genomics), RNA (transcriptomics), proteins (proteomics) and small molecules (metabolomics). We have briefly discussed genomics and touched on metabolomics in previous sections, and we will now review proteomics in parkinsonian disorders.

Abdi et al92 used a multiplex quantitative proteomic platform to find 72 altered proteins in PD compared with healthy controls. Apolipoprotein H and ceruloplasmin seemed to differentiate PD from healthy controls and from non-PD patients (AD and DLB). Eight of the proposed proteins were validated using a multianalyte CSF profile and showed good PD discriminatory power compared with AD and healthy controls.93

Using surface-enhanced laser desorption/ionisation time-of-flight mass spectrometry (SELDI-TOF MS), Constantinescu et al94 found a CSF proteomic profile consisting of four proteins (ubiquitin, β2-microglobulin and two secretographin 1 fragments), which differentiated PD and healthy controls from atypical parkinsonian patients with an AUC of 0.8. Recently, Ishigami et al95 were able to differentiate PD from MSA, even at the early stages, using their proteomic pattern (ie, the combined set of many protein peaks), rather than a single peak. Multiple peaks differentiated MSA and PD from control groups, consistent with previous reports that a panel of potential biomarkers is essential to distinguish between disease states.96

Another recent study attempted to differentiate PD from PDD patients using proteomic technology. Six proteins were identified, but only serin-protease inhibitor Serpin A1 was verified using biochemical methods. Performing 2-D immunoblots, there was 100% specificity and 58% sensitivity for the test procedure.97 Testing CSF obtained from PD, PDD patients and non-demented controls using a gel-free proteomics mass spectrometry approach with iso-labelleed samples (T1RAQ) led to the identification of 16 differentially regulated proteins, which could be potentially diagnostic markers.98

While proteomics studies have produced a number of interesting candidate markers, these are still in need of replication and far from being established. It has also become clear that many of the protein expression changes seen so far represent changes that are common to several neurodegenerative diseases. Reliable detection of disease-specific changes most likely depends on the development of more advanced techniques that allow for deeper analyses of the CSF proteome.

Imaging markers
Even though imaging biomarkers are beyond the scope of this review, we would like to point out that combination of CSF and imaging markers can provide increased diagnostic accuracy compared with using either modality alone. For example, Borroni and colleagues used mid-sagittal midbrain-to-pons atrophy in addition to CSF tau fragments levels to increase the discriminative power in identifying PSP from other neurodegenerative conditions.66

DISCUSSION
The vast majority of the studies discussed are cross-sectional, retrospective and do not have pathological confirmation. The accuracy of the clinical diagnosis is uncertain, and the contribution of comorbidity to the clinical phenotype is unknown.

There is lack of standardisation both of preanalytical (sampling collection, handling and storage) and analytical (analysis execution/sample processing) factors. For example, CSF contamination by blood can alter study outcomes in α-Syn and DJ-1 assays. In addition, there is lack of assay standardisation;
different assays can give different absolute concentrations of the protein, making it almost impossible to use global reference limits and diagnostic cut-off points.

Furthermore, both disease groups and control groups are heterogeneous. The neurodegenerative groups differ in terms of age, disease duration and severity. The control groups include a very small proportion of healthy controls and are mostly non-neurodegenerative neurological patients. However, some studies include patients with possible neurodegenerative conditions, such as mild cognitive impairment or normal pressure hydrocephalus.

Finally, there is lack of combination of different biomarker modalities, such as imaging and CSF markers.

A very promising study is the Parkinson’s Progression Markers Initiative (PPMI), which aims to identify PD progression markers and to better define subsets of PD patients. It is a 5-year, multicentre, longitudinal study of drug-naive PD patients with early-stage disease, compared with healthy controls. Detailed motor and neuropsychological assessments, DaT-scan and CSF examinations are performed. There is strict standardisation of data acquisition, CSF collection and processing.

SUMMARY POINTS: CSF BIOMARKERS IN PARKINSONISM
► AP42 has a role in predicting cognitive decline in Parkinson’s disease (PD)
► t-α-Syn: most promising marker; differentiates synucleinopathies from other neurodegenerative diseases and controls but is not specific
► t-tau and p-tau: inconsistent data, can help differentiate PD from AD and can be useful in combination with other markers
► NF-L: useful in differentiating PD from atypical parkinsonian conditions
► 4R-tau: possible marker of disease progression in PSP
► DJ1: potential role in discriminating MSA from PD
► Oxidative stress/inflammatory/metabolic markers: promising initial results, requiring further validation

FUTURE DEVELOPMENTS FOR THE CSF FIELD IN PARKINSONISM
We think that several hypothesis-driven biomarkers are going to be investigated at the same time using multiplex platforms. The proteomics field is likely to expand and gain in analytical sensitivity, resulting in the identification of more candidate markers, some of which may be unexpected and give new clues on disease mechanisms. There needs to be large, prospective and longitudinal cohorts with serial CSF examinations and pathological confirmation in as many patients as possible. A very important issue to be resolved is the standardisation of protocols and improvement in quality controls in CSF analysis. Finally, like in AD, it will likely be important to combine several CSF markers with other modalities, like imaging.

Accurate diagnosis of parkinsonian conditions should occur as early as possible, before too much irreversible neuronal damage has accumulated. This is essential, especially with the emergence of potential disease-modifying drugs, which must be used to target the correct underlying pathology. There is promising progress in the development of an α-Syn imaging agent, using radio ligands that bind to α-Syn fibrils. This should enable the assessment of the distribution of brain α-Syn during life.

CONCLUSION
Parkinsonian conditions, like most neurodegenerative diseases, have complex and dynamic interaction of several underlying pathogenic mechanisms. A combination of biomarkers possibly from different modalities in large, longitudinal cohorts might be required for early diagnosis and accurate disease prognosis.

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