# Inflammation biomarker discovery in Parkinson's disease and multiple system atrophy

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*Background/Aim:* Parkinson's disease (PD) and atypical PD (aPD), such as Multiple System Atrophy (MSA) and Vascular Parkinsonism (VP) are neurodegenerative diseases primarily characterized by a movement disorder. Especially in the early phases of the disease, PD and aPD are difficult to discriminate from each other. Moreover, PD and aPD show different response to treatment and prognosis. Thus, reliable biomarkers capable to distinguish between the two conditions are needed. Because inflammation plays a role in neurodegeneration, biomarkers of inflammation in cerebrospinal fluid (CSF) may be useful to differentiate diagnosis and to establish prognosis.

*Methods:* Using O-link targeted protein analysis, based on the proximity extension assay, we analyzed 92 biomarkers of inflammation in CSF of 44 PD, 14 MSA, 9 VP, 7 PD/VP patients and 25 controls. Patients underwent UPDRS, ICARS, MMSE and Hoehn and Yahr (HY) score assessment at baseline and after 3-years follow-up. ANOVA with Games-Howel post-hoc test after a rank transformation with age as a covariant was performed to determine differences in the expression levels of proteins between groups. Spearman's correlation between proteins and disease progression was also performed.

*Results:* Fifty-three out of ninety-two proteins were detected in more than 30% of the samples. Three proteins distinguished PD from MSA. Seventeen proteins distinguished controls from PD and/or one or two types of aPD ($p < 0.05$). In PD, one protein correlated with disease progression (HY score) (rho = 0.413, $p < 0.007$, n=41).

*Conclusions:* Inflammatory proteins in CSF could be promising biomarkers to distinguish PD from MSA and controls from PD or aPD. Unexpectedly, CSF inflammatory proteins do not seem to be associated with disease progression. Validation studies using ELISA are in progress to confirm our findings.

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