Distinct inflammatory profile in brains with multiple system atrophy

A. P Kiely[1], C.E. Murray[1], Y.T Asi[1], Z. Ahmed[1], T. Lashley[1], T. Revesz[1], J.L Holton[1]

1. *Queen Square Brain Bank, Department of Molecular Neuroscience, UCL Institute of Neurology, London, UK*

Aims:

Multiple system atrophy (MSA) is an adult onset neurodegenerative disease characterised by aggregation of α-synuclein in oligodendrocytes to form glial cytoplasmic inclusions (GCIs). We have observed both pro- and anti-inflammatory microglia in MSA and control brain. We aim to obtain a detailed view of the complex inflammatory environment of MSA and control brain using NanoString technology and cytokine array analysis.

Methods:

Control and MSA cases (N=6) were selected from the Queen Square Brain Bank where tissue is stored for research under ethically approved protocols and is stored under a license from the Human Tissue Authority. Tissue was isolated from the frontal cortex, homogenised and total RNA was then isolated. NanoString nCounter technology was used to analyse the levels of mRNA from genes associated with inflammation. Data analysis was performed using NanoString nSolver software. Proteome profiler Human Cytokine Array (R&D systems) was used to assay for cytokine levels in sample homogenate. Analysis was performed using Image J Protein Array analyser.

Results:

Thirteen inflammation associated genes of a panel of 286 genes were found through NanoString analysis to have significantly altered levels in MSA frontal cortex compared to control. Furthermore, four pro-inflammatory cytokines were observed to be significantly altered in MSA compared to control by cytokine array analysis.

Conclusions:

Our work confirms that neuroinflammation is a feature of MSA and may be important in disease pathogenesis. These findings improve our understanding of this rare disease and may point to potential treatment strategies for MSA.