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013

PROGRESSION OF CLINICAL FEATURES IN LEWY BODY DEMENTIA CAN BE DETECTED OVER SIX MONTHS

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10.1136/bmjno-2021-ANZAN.13

Objective This study aimed to quantify the trajectory and magnitude of change of the key clinical features and corresponding symptom domains of Dementia with Lewy bodies (DLB) and Parkinson's disease dementia (PDD) including global cognition, parkinsonism, recurrent visual hallucinations, cognitive fluctuations and sleep disturbance.

Methods 116 patients with Lewy body dementia (DLB=72, PDD=44) underwent assessment at baseline, 3 and 6 months as part of a prospective multi-centre randomized control trial. Linear mixed models were constructed for core outcome measures using the Mini-Mental State Examination (MMSE), motor section of the Unified Parkinson's disease rating scale (UPDRS-III), Dementia Cognitive Fluctuations Scale (DCFS) and the Neuropsychiatric Inventory (NPI).

Results Within the timeframe of our study (6 months) we were able to identify a significant cognitive decline of 1.3 points on the MMSE ($P=0.002$) and significant worsening of motor parkinsonism with an increase in UPDRS-III score of 3.2 points ($P=0.018$). Fluctuation severity also increased using the DCFS with a 6 month change in score of 1.3 points ($P=0.001$). Uniquely, a signal for increased severity of sleep symptoms of 1.2 points (NPI-sleep) was also detectable ($P=0.04$). Significant changes in neuropsychiatric symptoms were not detected. There was no difference in rates of change of scores between DLB and PDD.

Conclusion Clinically significant rates of change in core clinical features can be detected and quantified in Lewy body dementia over a relatively short period (6 months) using common clinical instruments, and thus may be useful as clinical endpoints for therapeutic trials of disease modifying and symptomatic agents.

014

VISUALISING THE TOPOGRAPHIC PATTERN OF TAU DEPOSITION IN PATIENTS WITH PROGRESSIVE SUPRANUCLEAR PALSY USING PI2620-PET

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10.1136/bmjno-2021-ANZAN.14

Objectives The accumulation of tau in the basal ganglia and later cerebellum and frontal cortex is a key pathogenic

mechanism in Progressive Supranuclear Palsy (PSP). The ability to detect tau in the living brain has the potential to revolutionise the diagnosis of PSP and other tauopathies, and to monitor the effectiveness of therapeutic interventions targeting tau-based mechanisms. This study investigates the use of a new tau-specific PET radiotracer, PI-2620, as a tool for visualising tau in the living brain.

Methods Ten patients with PSP (age 62-75 years, 6 male) underwent a 60 minute dynamic PET scan with PI2620 (185MBq). The dynamic PET data was processed in to a single parametric image of binding potential (BP) using the simplified reference tissue model and the corpus callosum as the reference region.

Results Visual inspection of the images showed clear uptake in the basal ganglia nuclei. BP was highest in pallidum (1.99), putamen (1.67), thalamus (1.63), substantia nigra (1.62), cerebellum (1.6) and caudate (1.55), compared to 1.2-1.5 across the cortical regions. Higher BP in the basal ganglia nuclei were associated with higher scores on the PSPRS (putamen, $r=0.77$, $p=0.01$).

Conclusion PI2620-PET shows promising potential as a technique for specifically imaging and quantitating the topographic pattern of tau distribution in patients with PSP. Further studies are needed to evaluate its use as a diagnostic and treatment monitoring tool for PSP and other tauopathies.

015

GUT MICROBIOTA AND NUTRITIONAL PROFILES OF PARKINSON'S DISEASE PATIENTS

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10.1136/bmjno-2021-ANZAN.15

Objectives Imbalances in the composition of the gut microbiome (GM) from Parkinson's disease (PD) patients have been reported previously. Collectively, the limited literature indicates a reduction in short-chain fatty-acid-producing bacteria that negatively influence colonic permeability and inflammation. We investigated GM composition in association with various clinical features and nutritional data in a large cross-sectional Australian PD cohort, to determine whether short-chain fatty-acid-producing bacteria representation in the GM was altered in association with clinical or nutritional differences between PD patients and controls.

Methods Clinical outcome measures derived from PD-validated questionnaires and stool samples were collected from 103 PD patients and 81 spousal healthy controls (HCs). GM composition, determined from 16S amplicon sequencing of the V3-V4 region of stool bacterial DNA, was compared between groups and with clinical outcome measures.

Results We identified significant compositional differences in the GM profiles of PD patients compared to HCs, across order, family and genus taxonomic levels. Multiple taxa were associated with a variety of clinical PD characteristics. Predictive models using GM profiles were developed to identify PD and were improved by incorporating nutritional data.