

Gut microbiome alterations in alpha-synucleinopathies

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Background: Microbiome alterations have been found in Parkinson (PD) and Alzheimer's disease and might impact on brain vulnerability within the spectrum of Lewy body disorders. Aim of the study was to evaluate shared and divergent microbiome alterations in PD and dementia with Lewy bodies (DLB) compared to age-matched controls.

Method: Seventy-seven subjects including 28 PD, 21 DLB matched for age and disease duration and 24 age-matched controls entered the study. Each subject underwent an extensive clinical evaluation including motor, cognitive and dietary assessment and underwent stool and blood collection. Stool DNA was amplified using primers targeting the V3-V4 region of the bacterial 16S rRNA gene. Sequencing was performed according to the 16S-protocol on MiSeq (Illumina). Ecological measures as beta diversity, the similarity or difference in microbiota composition between individuals, as well as taxonomic abundance were computed with the free software package QIIME 2.

Result: Compared to HC, DLB and PD patients exhibited a shift in the abundance of the phylum Synergistetes (in DLB increased by 3.5 times than HC) and Actinobacteria (in PD increased by 1.5 times than HC). At genus level, DLB patients exhibited decreased abundance of *Clostridium sensu stricto 1*, *Fusicatenibacter*, *Lachnospiraceae ND3007 group*, *Rikenellaceae RC9 gut group* and *Ruminiclostridium 6* than HC as well as less *Fusicatenibacter* and *Lactobacillus* than PD (Linear discriminant analysis effect size (LEfSe), $P < 0.046$).

Conclusion: PD and DLB are accompanied by specific alterations in the abundance of specific gut microbes. Further analyses are needed in order to understand whether differences in gut microbiota composition between PD and DLB might explain different brain vulnerability and disease progression within the Lewy bodies spectrum.