P53 – **Metagenomic analysis of gut microbiota in patients with Parkinson's disease**

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Recent studies suggest an involvement of gut microbiota in the communication between gut and brain. An altered microbiota composition has been associated with the pathogenesis of several diseases, including neurodegenerative disease. Parkinson's disease (PD) is a neurodegenerative disorder caused by aggregation and accumulation of misfolded α-synuclein (α-syn) protein in neuronal cells in both enteric and central nervous system. Gastrointestinal symptoms, such as constipation and colonic inflammation, are reported in over 80% of PD patients and often precede the motor symptoms.

The objective of this study is to evaluate the relationship between gut microbiota and PD, to correct the effects of confounders, and identify taxa and functional pathways that could be involved in the pathogenesis of PD.

The microbial composition of 79 PD cases and 71 healthy controls (HC) was determined by 16S rRNA gene sequencing of DNA extracted from stool samples. Information about 31 potentially confounding variables, such as medications, diet and lifestyle habits were collected.

A statistical model was developed to analyse the differences in microbiota and taxa composition of PD versus HC without the influence of potential confounders and predictors.

A functional prediction was performed to identify metabolic pathways potentially involved in the pathogenesis of PD.

Age, sex and loss of weight in the last year were identified as potential confounders.

PD-status, age, BMI, eat cereals, eat yogurt and physical activity were identified as predictors.

Among patients, treatment with catechol-O-methyltransferase-inhibitors (iCOMT) was found to affect microbiota composition. We found significantly altered abundances of the *Enterobacteriaceae*, *Lactobacillaceae*, *Verrucomicrobiaceae Lachnospiraceae* and *Erysipelotrichaceae* families. Functional predictions revealed changes in numerous pathways, including synthesis of lipopolysaccharide, biosynthesis and metabolism of amino acids, and metabolism of fatty acids and butyrate.

PD is associated with an altered gut microbiota composition. We report altered abundance of several taxa and identify functional pathways potentially involved in PD pathogenesis. Also, we demonstrate an effect of PD medication iCOMT on the microbiome. These findings provide an interesting starting point to develop new hypotheses and experimental models to investigate the cause and effect of microbiota composition in PD.

References

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