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Channing Microbiome Seminar

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The gut microbiome and Parkinson's disease

Prior studies on the gut microbiome in Parkinson's disease (PD) have yielded conflicting results, and few studies have focused on prodromal (premotor) PD or used shotgun metagenomic profiling to assess microbial functional potential. We conducted a nested case-control study within 2 large epidemiological cohorts to examine the role of the gut microbiome in PD. We profiled the fecal metagenomes of 420 participants in the Nurses' Health Study and the Health Professionals Follow-up Study with recent onset PD (N=75), with features of prodromal PD (N=101), controls with constipation (N=113), and healthy controls (N=131) to identify microbial taxonomic and functional features associated with PD and features suggestive of prodromal PD. Omnibus and feature-wise analyses identified bacterial species and pathways associated with prodromal and recently onset PD. We observed depletion of several strict anaerobes associated with reduced inflammation among participants with PD or features of prodromal PD. A microbiome-based classifier had moderate accuracy (area under the curve [AUC]=0.76 for species and 0.74 for pathways) to discriminate between recently onset PD cases and controls. These taxonomic shifts corresponded with functional shifts indicative of carbohydrate source preference. Similar, but less marked, changes were observed in participants with features of prodromal PD, in both microbial features and functions. PD and features of prodromal PD were associated with similar changes in the gut microbiome. These findings suggest that changes in the microbiome could represent novel biomarkers for the earliest phases of PD.

Hosted by Yang-Yu Liu