

Implementation of prediction modeling to assess oral and gut microbial signatures associated with brain or body-first Parkinson's disease - a Fox Insight data study.

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Parkinson's disease (PD) is an age-related neurodegenerative syndrome. The progressive nature of PD has been suggested to correlate not only with continued loss of dopaminergic innervation in the striatum but also with the spread of α -synuclein aggregates throughout the brain and in the periphery (Braak hypothesis). More recently, studies have shown that Parkinson's can occur from separate etiologies — the gastrointestinal (GI) system and the olfactory bulb (OB). As such, there are now believed to be two Parkinson's subtypes — body-first and brain-first, respectively. Given that environmental factors are considered to increase the risk of Parkinson's and the microbiome is strongly amenable to change from various environmental triggers, microbial signatures can present helpful biomarkers in diagnosis, progression, and uncover underlying disease mechanisms. However, microbial signatures have not yet been examined in relationship to the etiological differences between body-first and brain-first PD. In order to approach this question, we analyzed human microbiome and questionnaire data made available from Fox Insight (Michael J. Fox Foundation) to determine whether bacterial signatures from stool and saliva samples can predict body-first or brain-first Parkinson's. After filtering the data, we found the 31 participants could be grouped into one of the two groups. Our results show that there are three gut bacteria and three saliva bacteria which show strong predictive strength in distinguishing body-first from brain-first individuals. From stool samples, these bacteria are *Phocaeicola dorei*, *Phocaeicola vulgatus*, and *Ruminococcus bicirculans*. From saliva samples, these bacteria are *Neissera subflava*, *Haemophilus influenzae*, and *Rothia SGB49305*. Importantly, *P. dorei* and *R. bicirculans* are more abundant in those with brain-first PD, while *P. vulgatus* is more abundant in body-first individuals. From saliva samples, we see that *N. subflava* and *H. influenzae* are more abundant in individuals with brain-first PD, while *R. SGB49305* is more abundant in body-first PD. In the future, we hope to model how altering these microbiomes with 'exercise-probiotics' (bacterial hits we uncovered in a parallel project exploring the effects of exercise on the PD microbiome) may impact Parkinson's symptoms.