

METHOD TO CHARACTERIZE GUT MICROBIOME

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Technology Description

Researchers at Washington University in St. Louis have developed a method to stratify gut microbiota dysbiosis and monitor treatments to correct it. In order to efficiently treat microbiota imbalance, it would first be beneficial to understand the healthy organization and interaction of the human gut microbiome. However, characterizing the interactions and organization of the microbiome is incredibly challenging as there are numerous different microbial species (and strain variation within the species) and interactions involved in a healthy microbiome. Other methods have been developed to describe the microbial community organization but the methods are not optimal. To overcome the limitations, the inventors have developed this method of modeling microbiota diversity using principle component analysis (PCA). This method may be used to characterize healthy microbiomes, stratify diseased from healthy microbiota and monitor the efficacy of therapeutic interventions. This technology provides a much-needed method to characterize the gut microbiome.

Stage of Research

The method has been used to characterize the microbiota organization of a Bangladeshi birth cohort sampled from 1 to 60 months of age.

Publications

Raman AS, Gehrig JL, Venkatesh S, Chang HW, Hibberd MC, Subramanian S, Kang G, Bessong PO, Lima AAM, Kosek MN, Petri WA Jr, Rodionov DA, Arzamasov AA, Leyn SA, Osterman AL, Huq S, Mostafa I, Islam M, Mahfuz M, Haque R, Ahmed T, Barratt MJ, Gordon JI. [A sparse covarying unit that describes healthy and impaired human gut microbiota development](#). Science. 2019 Jul 12;365(6449). pii: eaau4735. doi: 10.1126/science.aau4735.

Applications

- Tool for:
 - Development of nutritional supplements
 - Characterizing a gut microbiome
 - Stratifying diseased from healthy microbiome
 - Monitoring therapeutic efficacy in ameliorating an unhealthy microbiome

Advantages

- Provides a method to understand gut microbiome organization and interaction

- Accounts for both abundance and composition of microbiome members
- Generalizable to any states of dysbiosis wherein changes in the microbiota are seen in correlation with disease phenotype

Patents

- Provisional patent application has been filed.

Related Web Links

- [Dr. Gordon profile](#)