GLOBAL BRANCHES AND LOCAL STATES OF THE HUMAN GUT MICROBIOME DEFINE ASSOCIATIONS WITH ENVIRONMENTAL AND INTRINSIC FACTORS

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Danone Research & Innovation and the University of San Diego California, conducted one of the largest analyses of the composition of the human microbiome, examining approximately 35,000 fecal samples from diverse populations and locations.
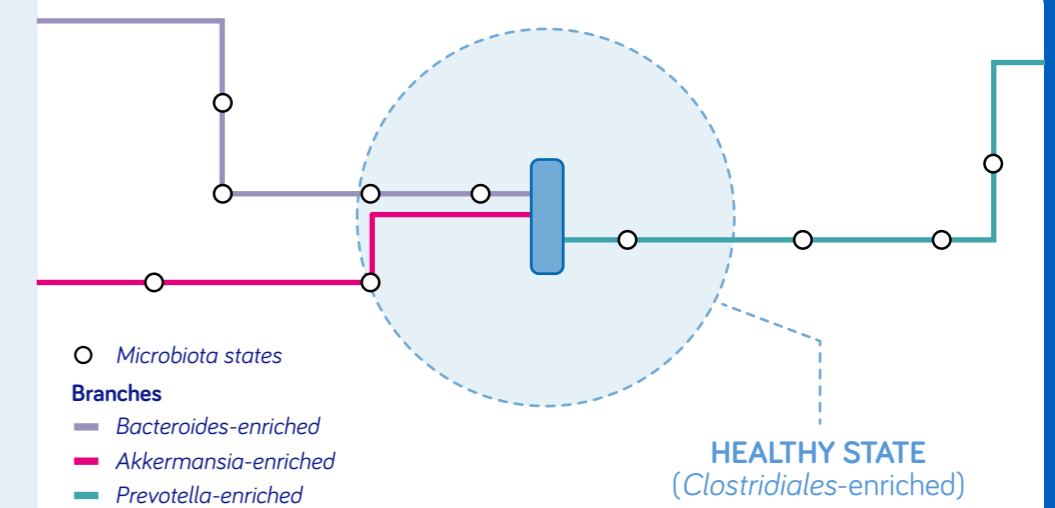
Researchers combined comprehensive public datasets and used advanced techniques to classify the microbiome into communities based on certain configurations of microorganisms.

The findings revealed finer microbial communities that are interconnected through more global groups called microbiome branches. These branches represent continuums of microbiome configurations that connect local ecological states.

THE FAECALIBACTERIUM/BACTEROIDES RATIO

The study found different branches in the adult human gut microbiome, stemming from a common root enriched in *Clostridiales*. Each of these branches tended to be enriched with certain types of bacteria: **Bacteroides, Prevotella, and Akkermansia.**

The researchers discovered that the ratio of **Faecalibacterium** to **Bacteroides** may be an important marker for the microbiome's dynamics, indicating potential relevance for maintaining a balanced and stable gut ecosystem.

○ Microbiota states

Branches
— Bacteroides-enriched
— Akkermansia-enriched
— Prevotella-enriched

HEALTHY STATE
(*Clostridiales*-enriched)

Key Findings:
- Distinct communities (ecological states) exist within the gut microbiome based on the diversity of specific microorganisms.
- These communities connect through global groups called microbiome branches.
- Microbiome branches form a continuum of configurations that link local ecological states.

Structuring human gut microbiome data locally and globally allowed for the observation of how transitions among states might occur and for the capture of health, diet, and lifestyle associations. Dietary factors, including plant diversity, snack frequency, vegetable consumption, and sugary food intake, notably influenced the gut microbiota, although host-related factors had a more significant impact.

CONCLUSION

Our findings highlight the intricate organization of the human gut microbiome. This knowledge can serve as a foundation for personalized nutrition and therapeutics, utilizing an individual's unique gut microbiome composition to deliver targeted interventions for optimal health.

References: Tap, J, Lejzerowicz, F., Cotillard, A. et al. Global branches and local states of the human gut microbiome define associations with environmental and intrinsic factors. Nat Commun 14, 3310 (2023). https://doi.org/10.1038/s41467-023-38558-7