

Modulation of the human gut microbiota by short chain Fructo-oligosaccharides

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Humans: More Microbes Than Human Cells?

SUPRA-ORGANISMS: CONGLOMERATES OF MAMMALIAN AND MICROBIAL CELLS

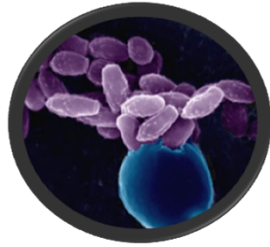
SITE OF LARGEST COLLECTION



Archaea



Bacteria



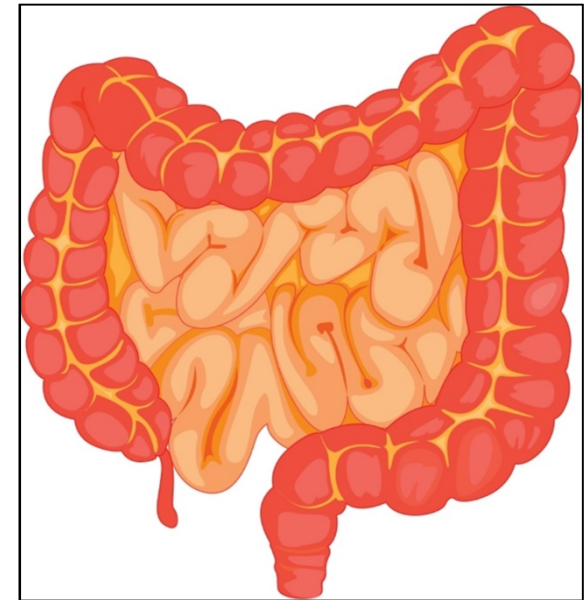
Fungi



Protozoans

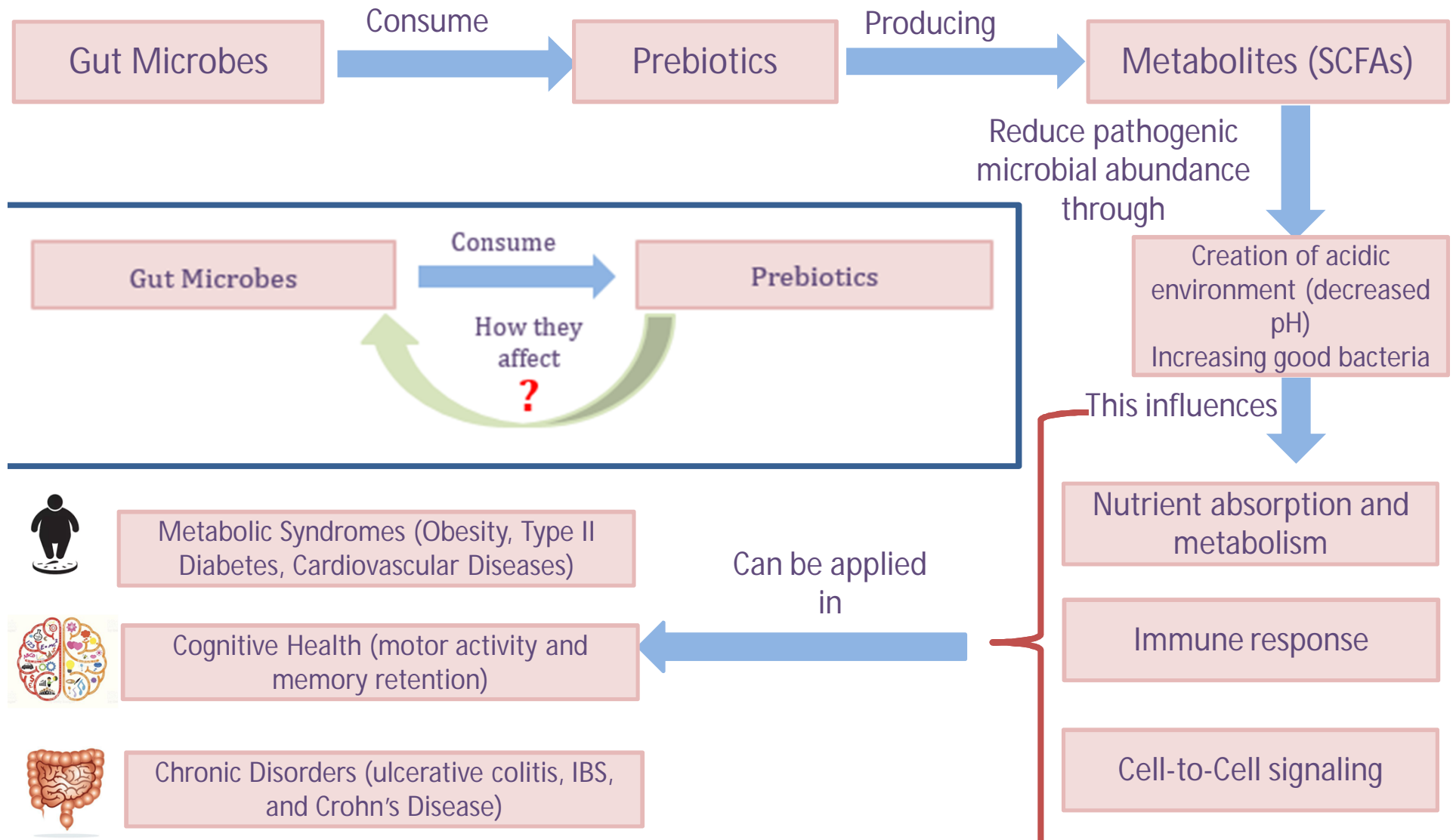
MICROBIAL ROOTS

- ✓ 100 trillion bacterial cells
- ✓ 100X more bacterial cells than host cells
- ✓ 1000X more bacterial genes than host genes

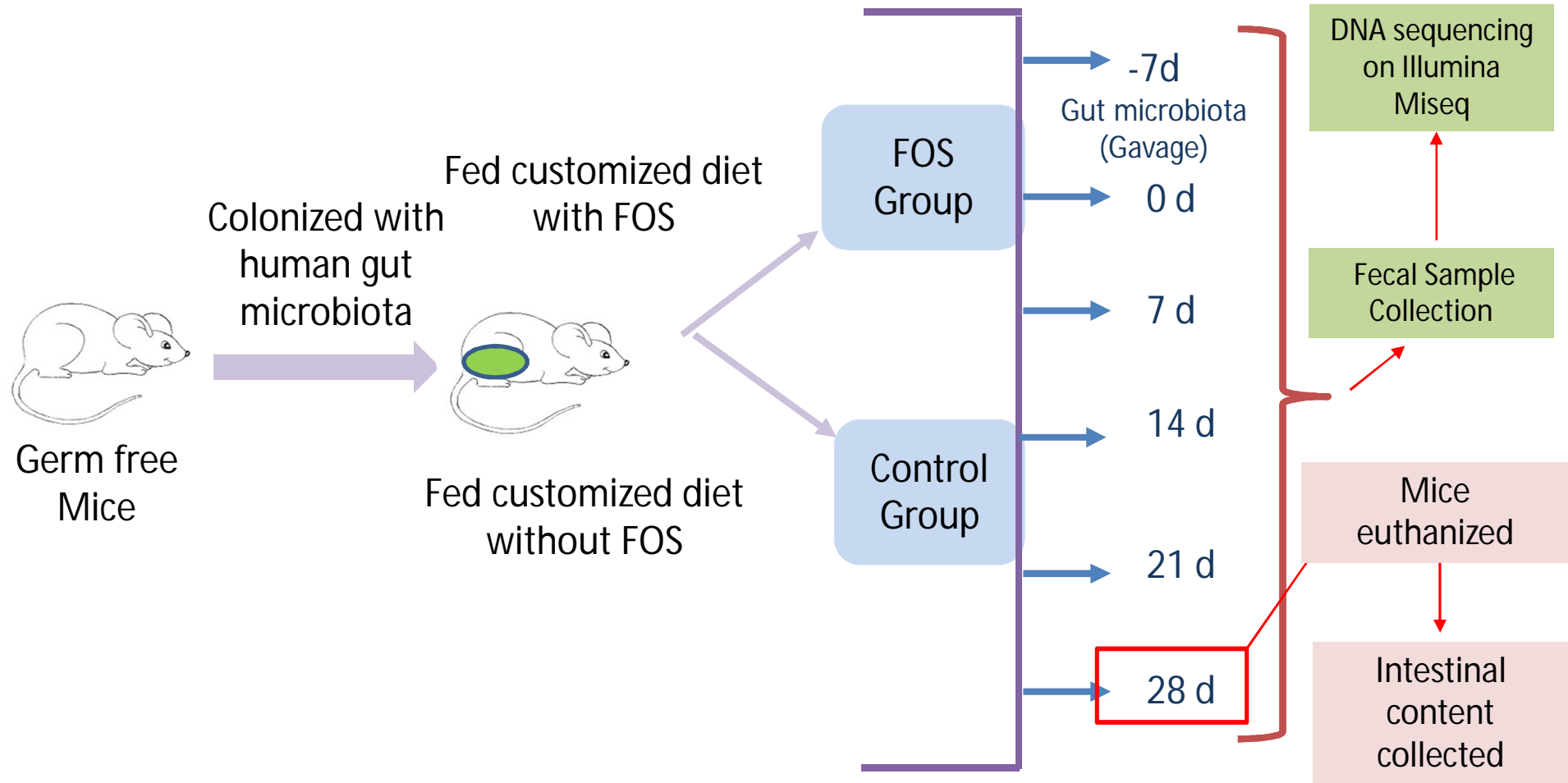


THE INTESTINE
(~100 trillion organisms)

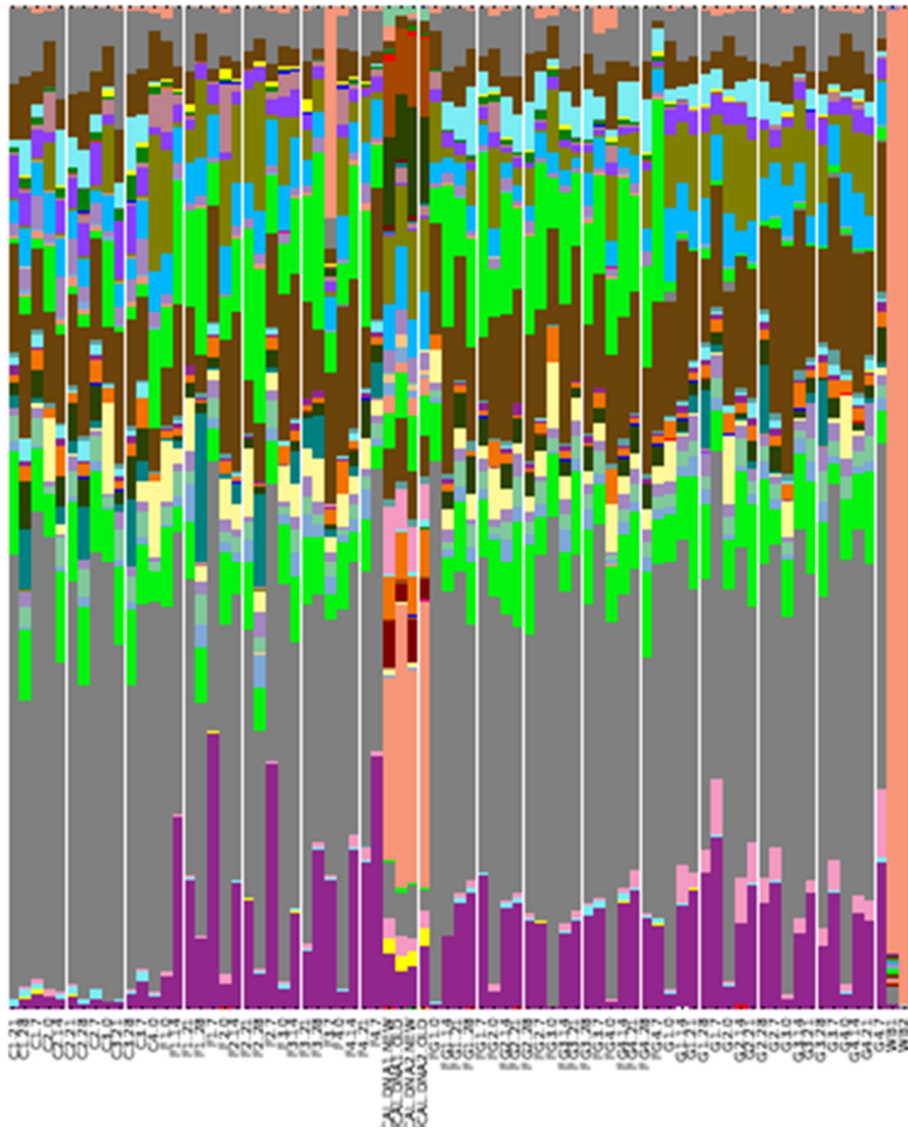
Prebiotics: Beneficial Modulation of the Gut Microbiome



TATA-Yale Collaborative Study: Design



FOS Supplementation response

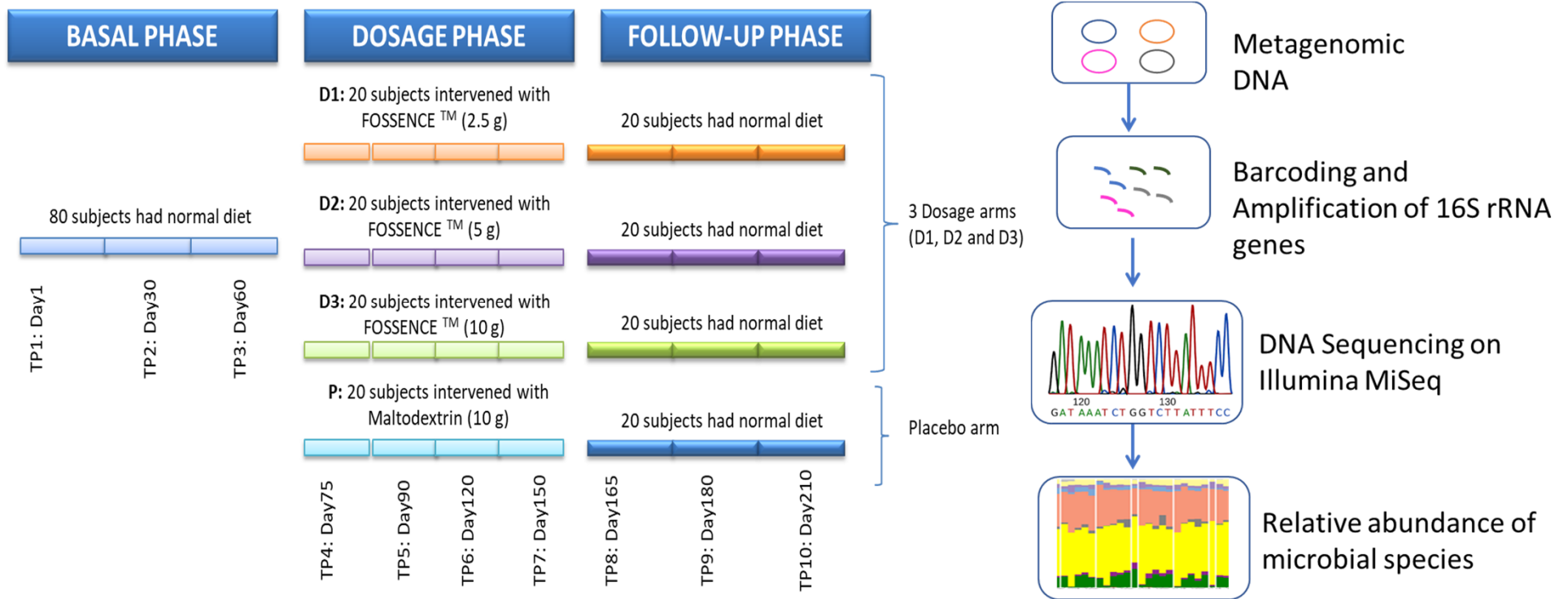


Snapshot of microbial relative abundance

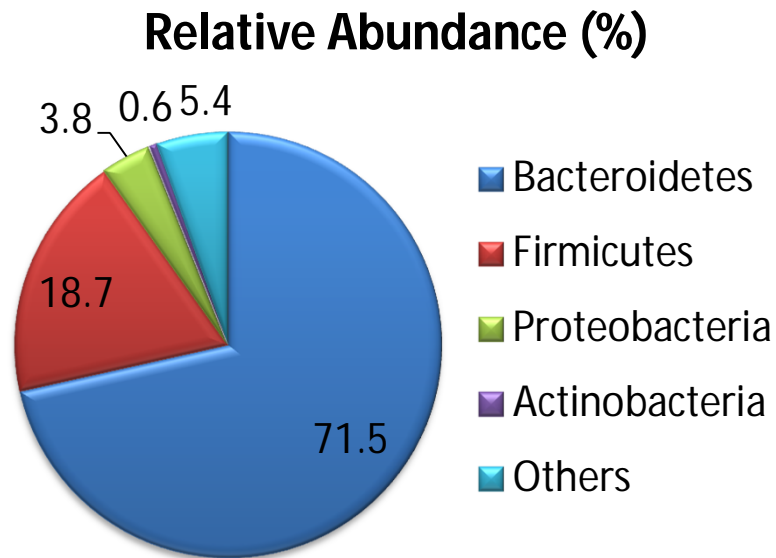
Summary

- ❖ FOS promoted the growth of *Bifidobacterium* , *Faecalibacterium prausnitzii*, *Blautia* and bacteria belonging to *Lachnospiraceae* family
- ❖ Bio-geographical and Spatial arrangement of gut bacteria play a role in determining the impact of prebiotics
- ❖ Utilization of FOS by good gut bacteria results in reduction of *Sutterella*, a pathogenic bacteria
- ❖ Consumption of FOS enhanced production of SCFAs

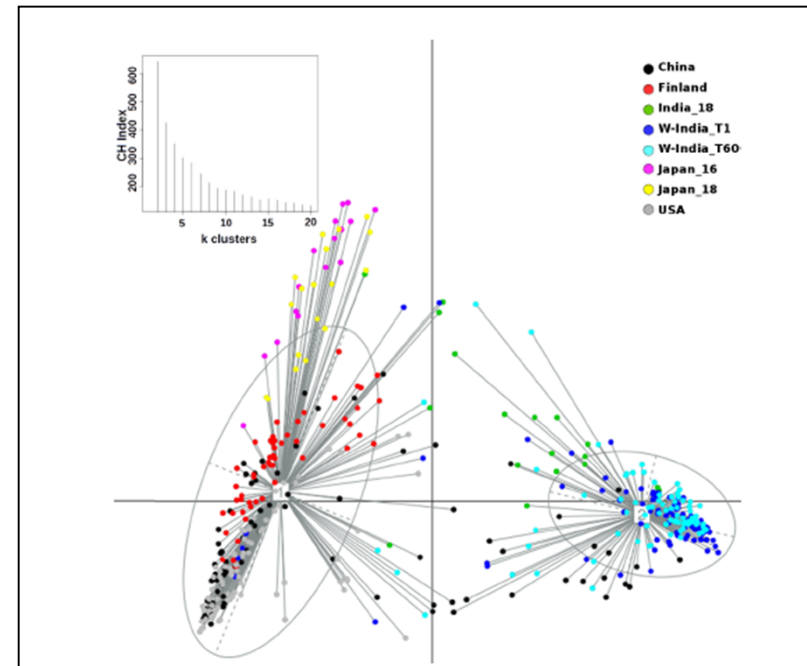
Impact of Fructo-oligosaccharides (FOS) on human gut microbiota: A clinical trial



Analysis of basal phase sample revealed uniqueness



- ❖ 95% of sequences were found to belong to microbes belonging to the four phyla
- ❖ Remaining 5% belonged to 16 other phyla
- ❖ More than 80% of sequences were assigned to 5 genera - *Prevotella*, *Faecalibacterium*, *Alloprevotella*, *Roseburia*, and *Bacteroides*



- ❖ Two distinct clusters were obtained
- ❖ Cluster 1 was further divided into 2 subclusters
- ❖ subcluster 1a (core taxa): *Bacteroides*, *Faecalibacterium*, and *Roseburia*
- ❖ Subcluster 1b (core taxa): *Bacteroides*, *Faecalibacterium*, *Bifidobacterium*, *Blautia*, *Dorea*, *Lachnospiraceaincertaedis*, and *Streptococcus*
- ❖ Cluster 2 (core taxa): *Prevotella* and *Faecalibacterium*

Summary

- ❖ *Prevotella*, *Faecalibacterium* were predominantly present in the Western Indian subjects
- ❖ FOS consumption increased the relative abundance of OTUs belonging to *Bifidobacterium* and *Lactobacillus*.
- ❖ FOS at higher dosage appear to promote the selective proliferation of OTUs belonging to *Lactobacillus*.
- ❖ A significant change was also observed in certain butyrate-producing microbes
- ❖ Positive impact of FOS on butyrate-producing bacteria reinforces the role of prebiotics in conferring beneficial functions to the host.

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Collaboration



Thank you