

Fungal microbiome

Gwen Falony

BVMDM symposium

19th of November 2015



KU LEUVEN

How human are you?

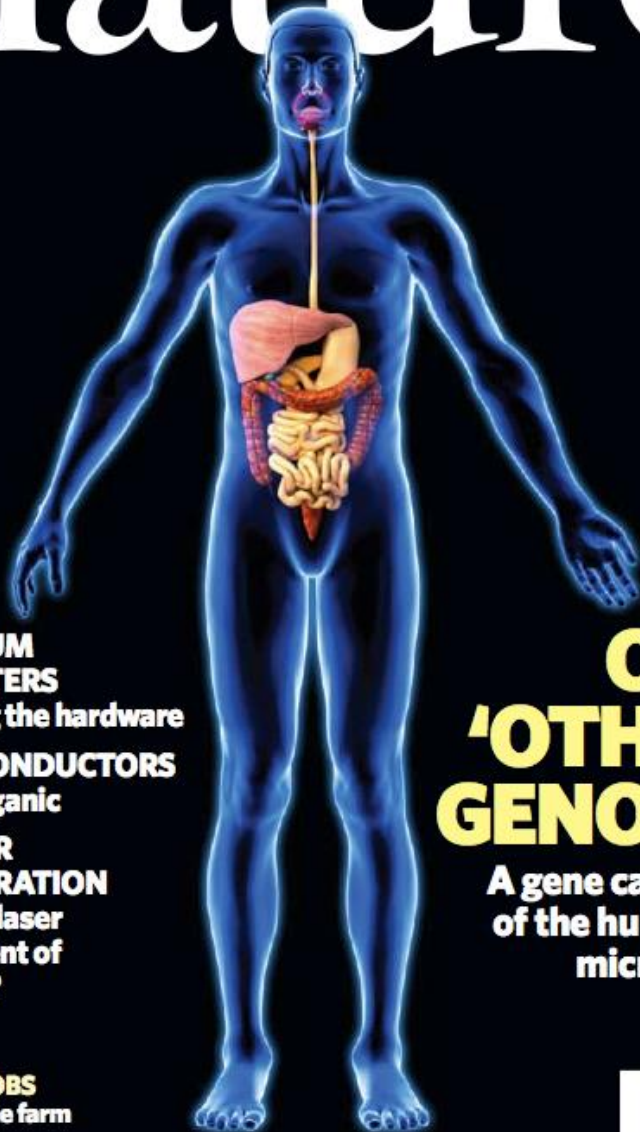


- There are **100.000 times more bacteria on your body than there are humans on earth.**
- You have **10 times more bacterial cells than human ones.**
- You have **100 times more bacterial genes than human ones.**

3 March 2010 | www.nature.com/nature | £10

THE INTERNATIONAL WEEKLY JOURNAL OF SCIENCE

nature



**QUANTUM
COMPUTERS**
Choosing the hardware
SUPERCONDUCTORS
Going organic
**NUCLEAR
PROLIFERATION**
A ban on laser
enrichment of
uranium?

NATUREJOBS
Down on the farm

**OUR
'OTHER'
GENOME**
A gene catalogue
of the human gut
microbiome



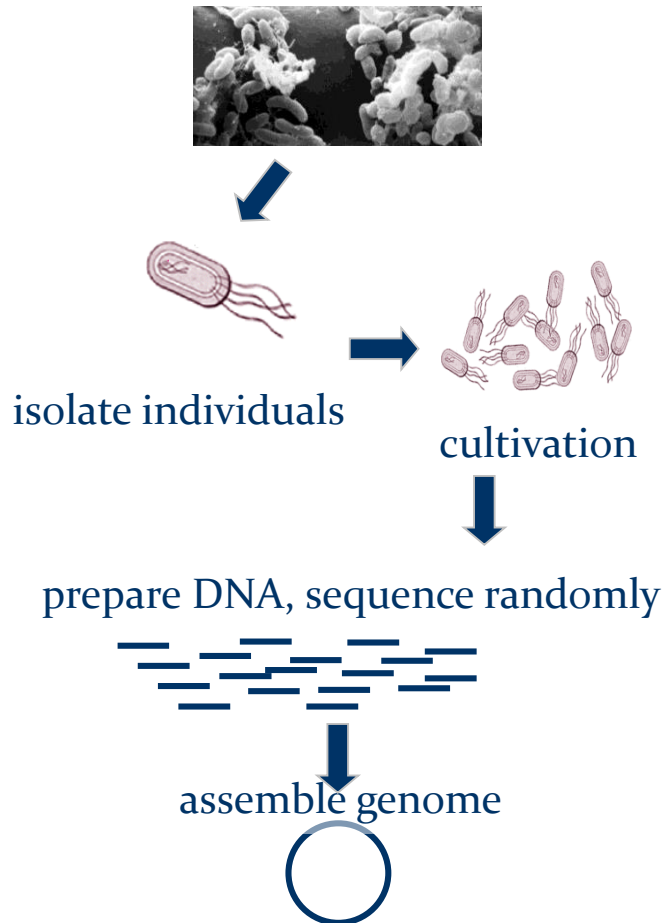
The human gut microbiota

- expands our digestive capacity,
- produces essential nutrients
- increases colonization resistance against pathogenic intruders
- assists in the detoxification of xenobiotics

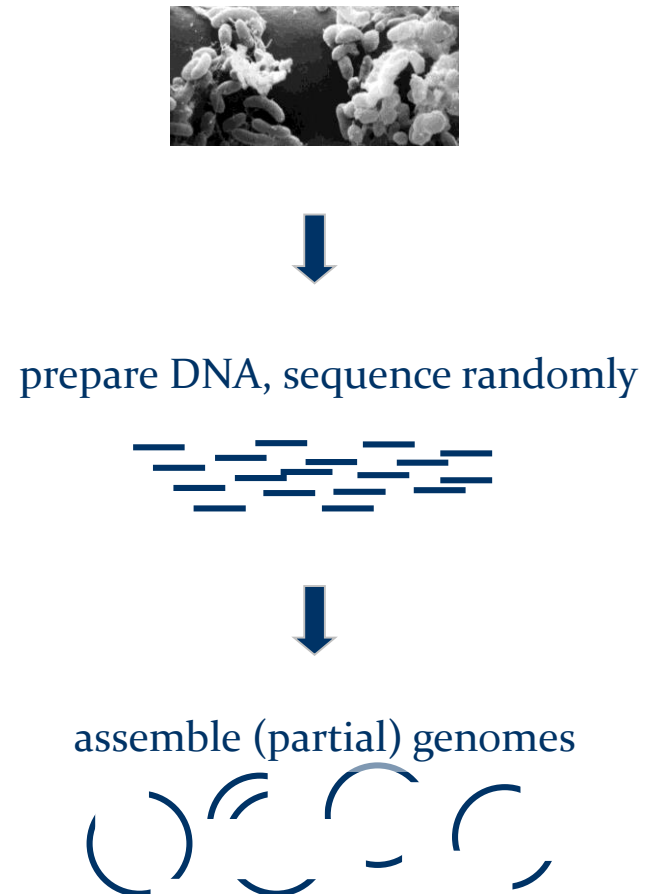


Metagenomics – Access to the uncultivable fraction of microbial life

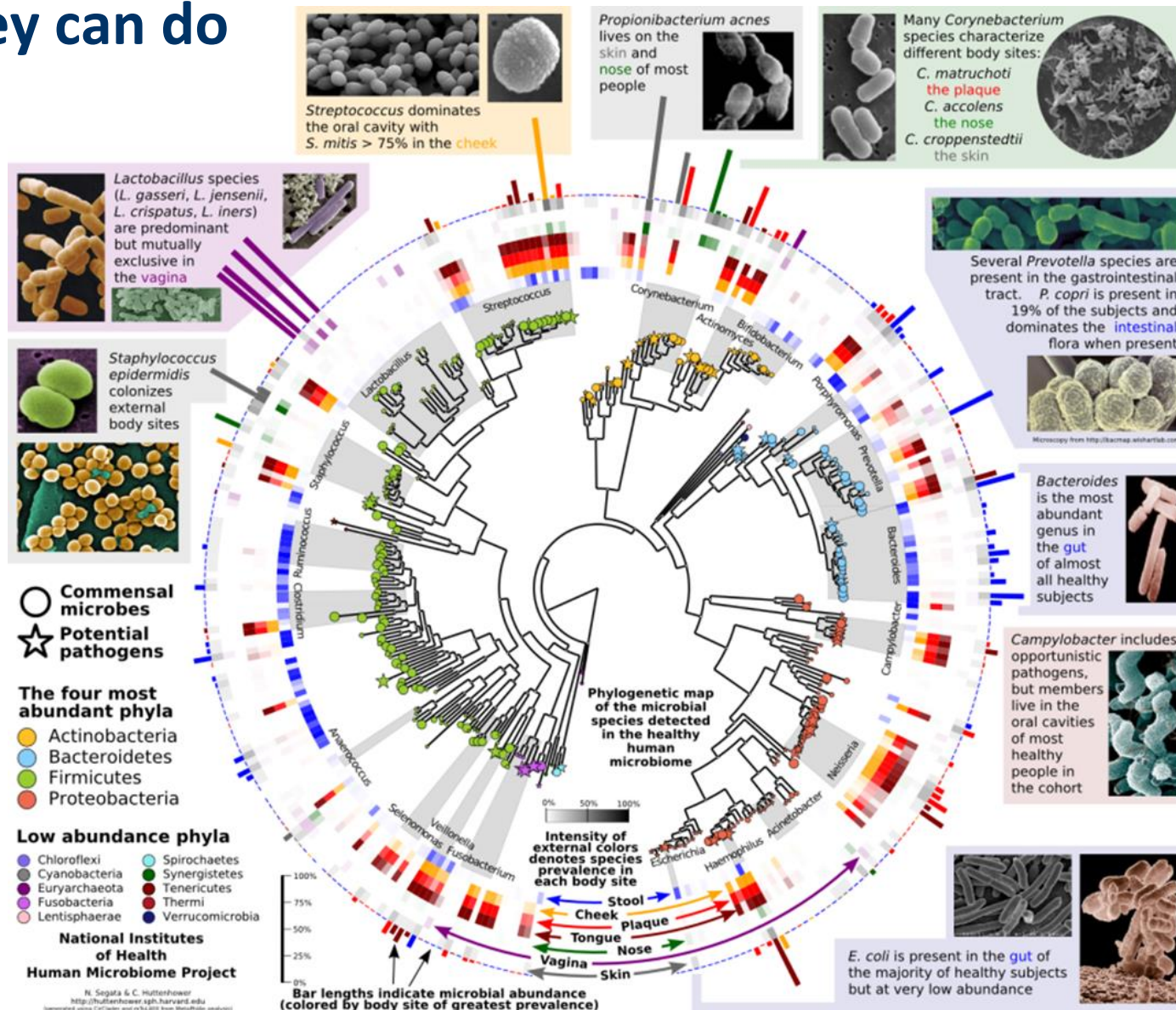
Traditional Microbial Genomics



Environmental Genomics



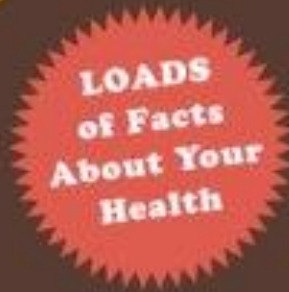
Metagenomics teach you **who** lives where and **what** they can do



What's Your Poo Telling You?

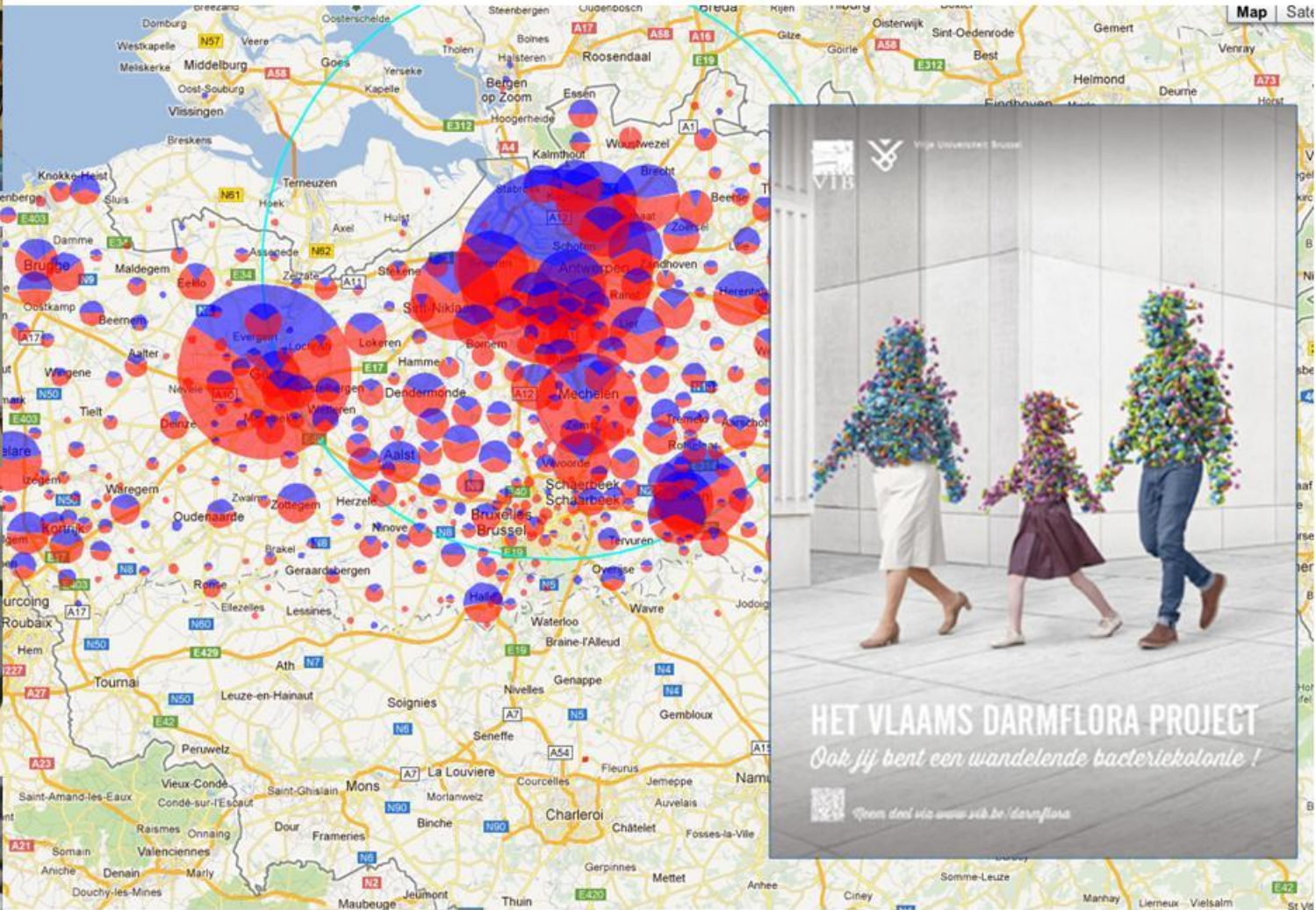
**Josh Richman and
Anish Sheth, M.D.**

**Illustrations by
Peter Arkle**



**Towards health
monitoring
through gut
microbiota
screening**

Flemish Gut Flora Project



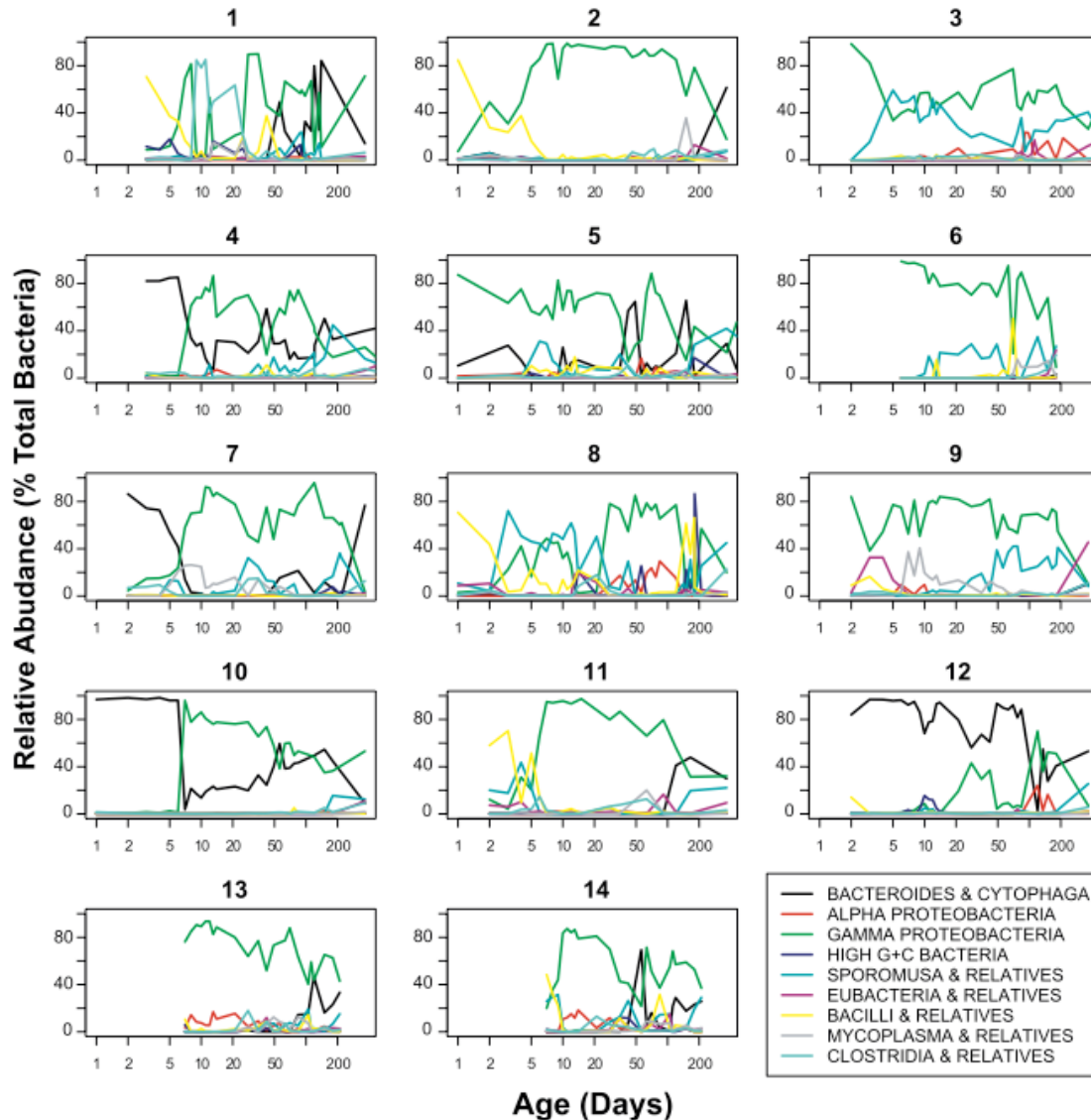
www.facebook.com/VlaamsDarmfloraProject
www.vib.be/nl/mens-en-gezondheid/darmflora-project



The flora is 'seeded' at birth

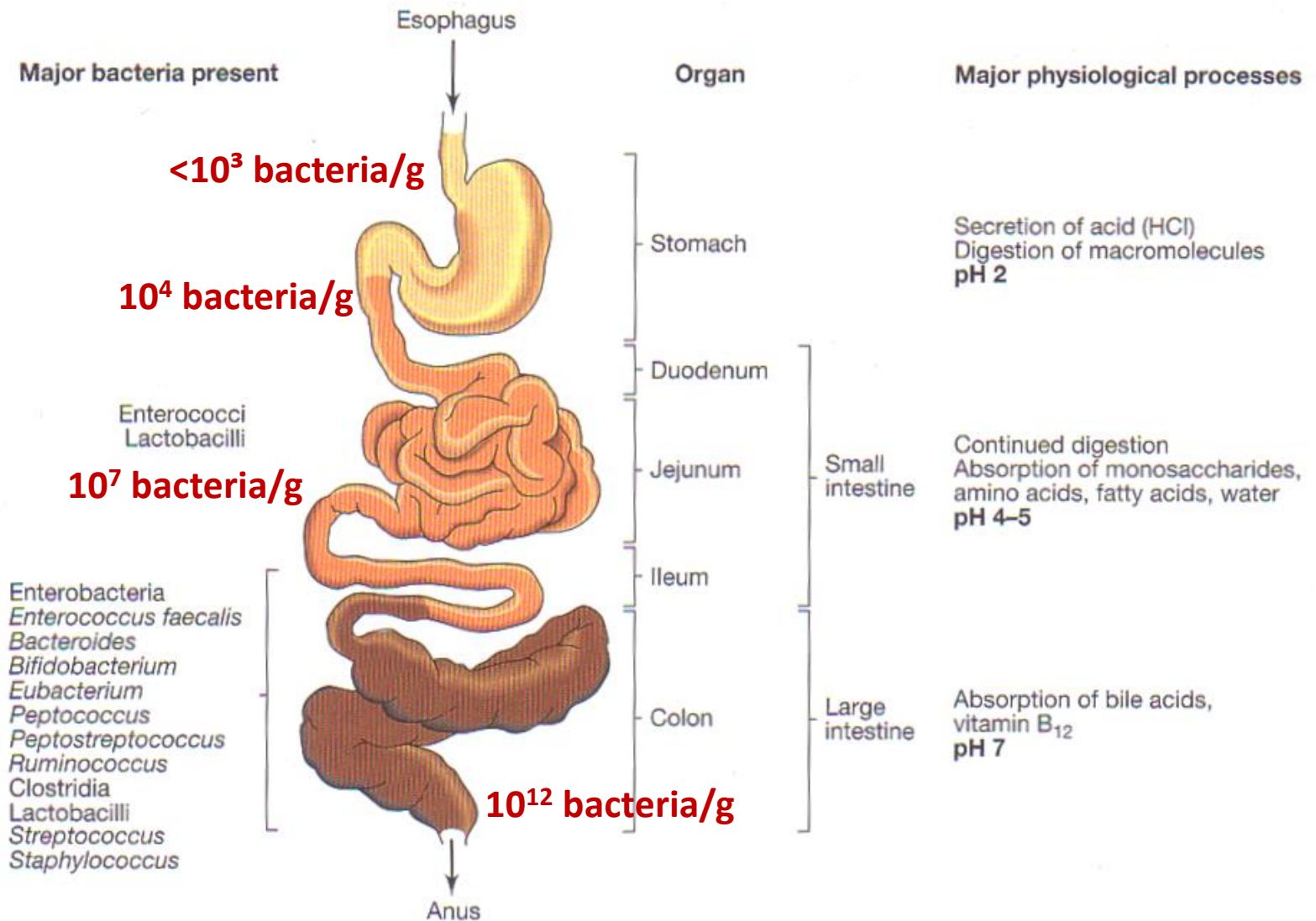


Inoculation at birth: unstable microbiota development of until weaning

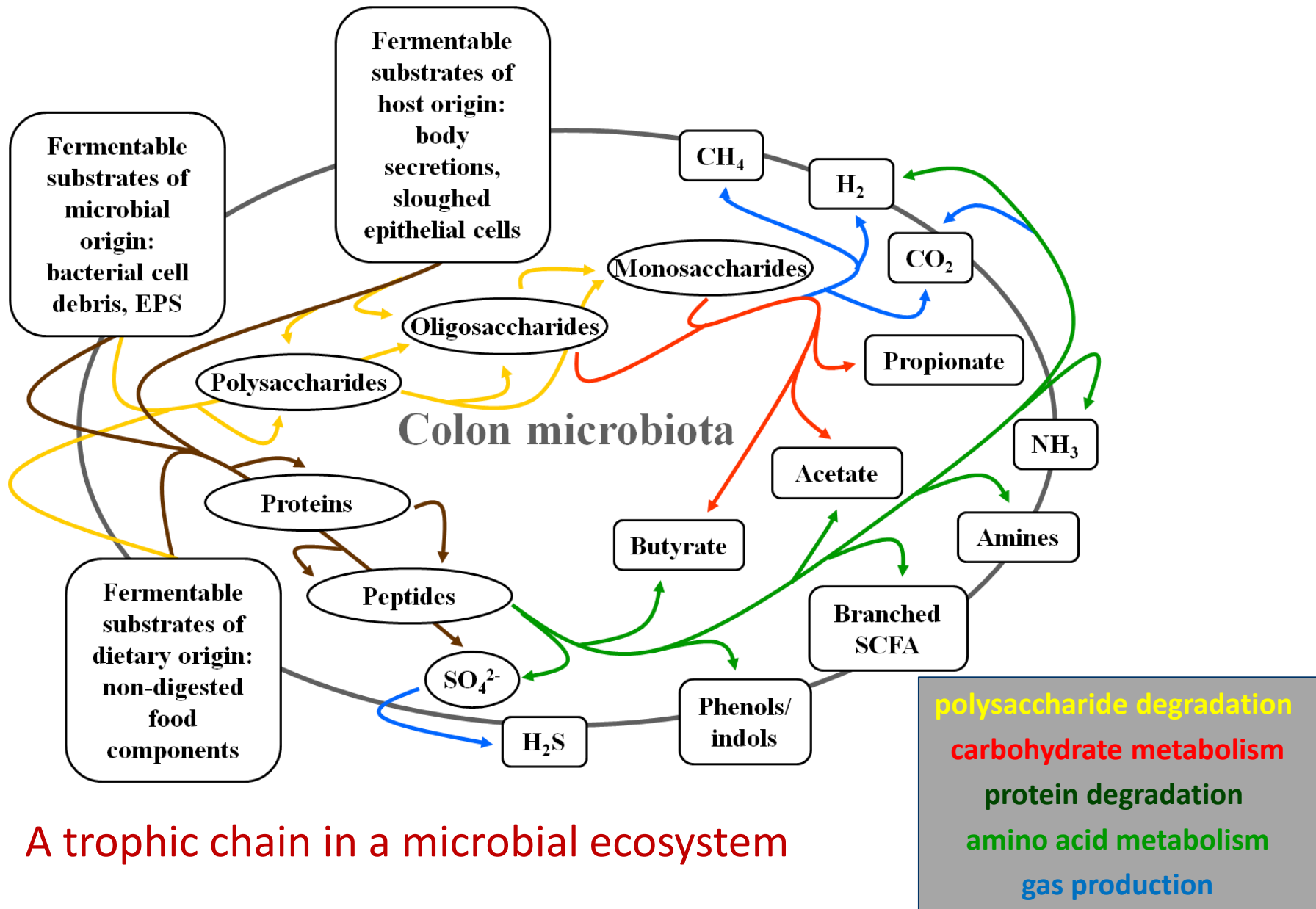


Infant guts

Gut microbiota distribution

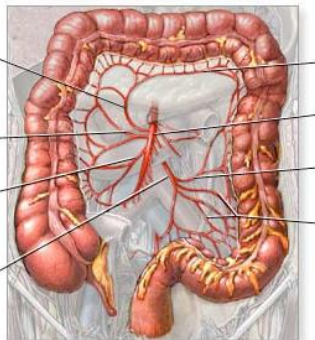


Colon microbiota fermentation processes

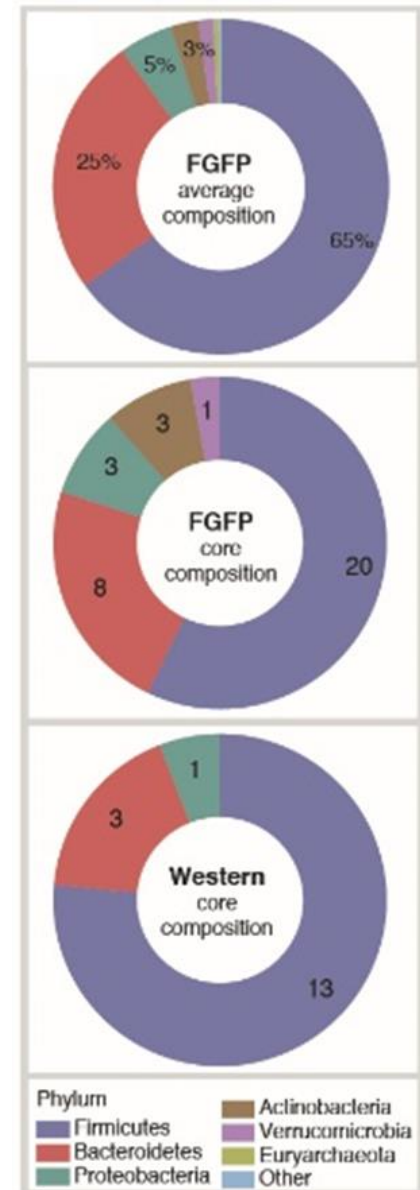
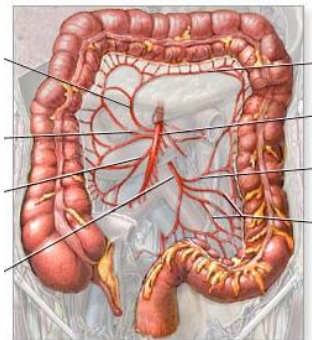


Substantial overlap in gut microbiota between individuals

- 1/3rd of species present in almost all individuals
- 1500 species in total
- 160 species/individual



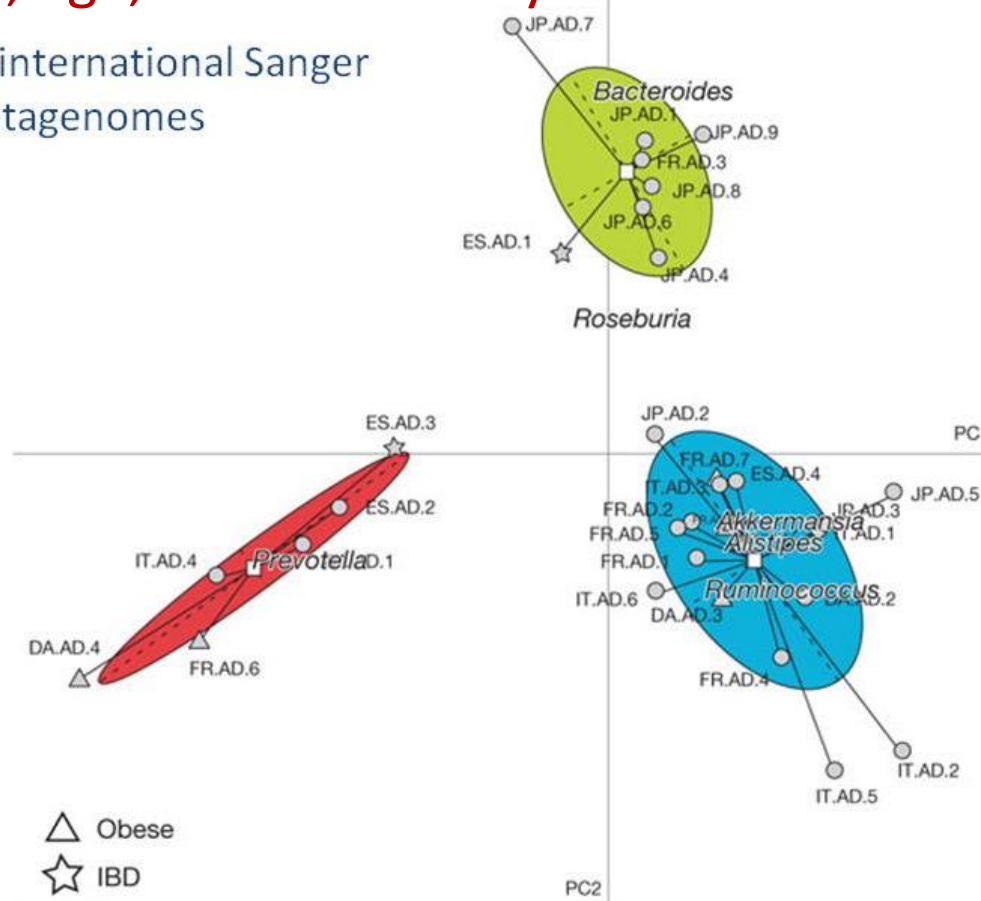
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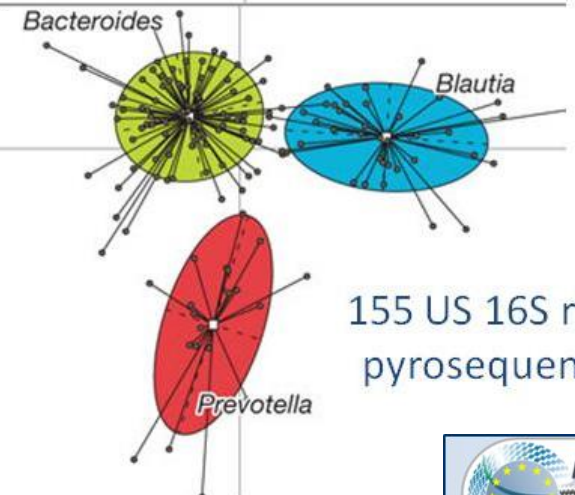
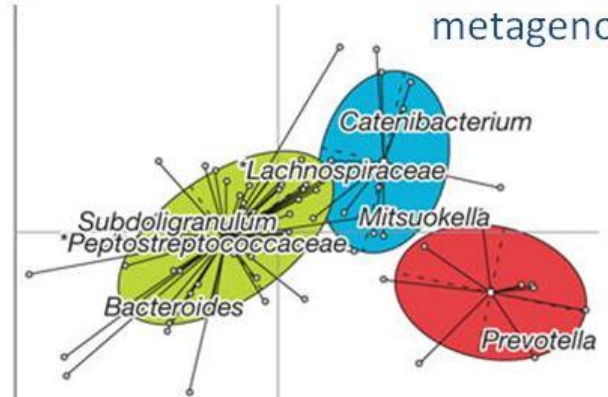
Enterotypes - microbiota configurations in gut microbiome space

Microbiota constellations independent from gender, age, and nationality

33 international Sanger metagenomes



85 Illumina Danish metagenomes



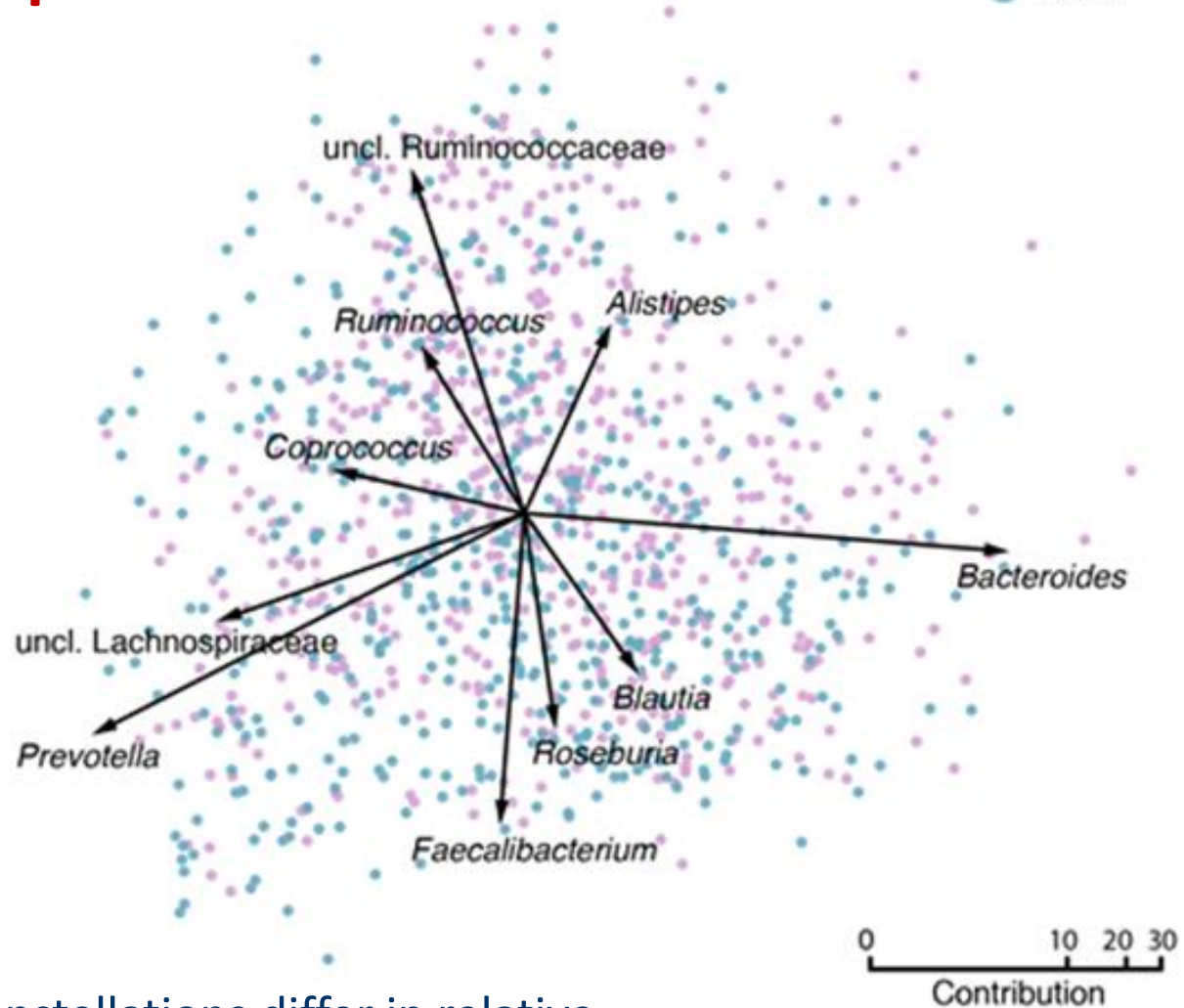
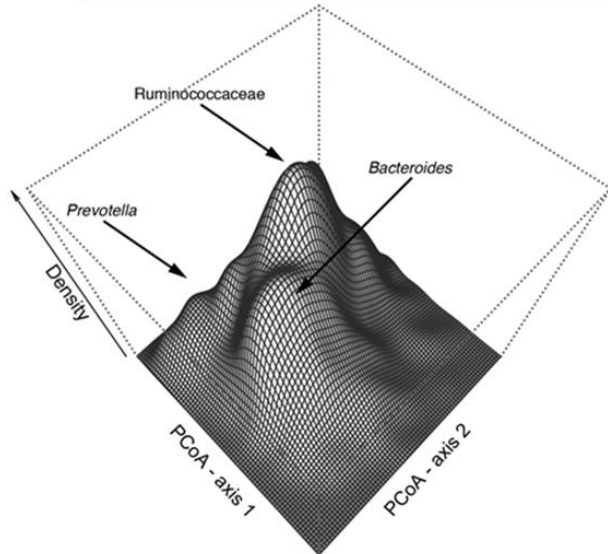
155 US 16S rDNA pyrosequencing



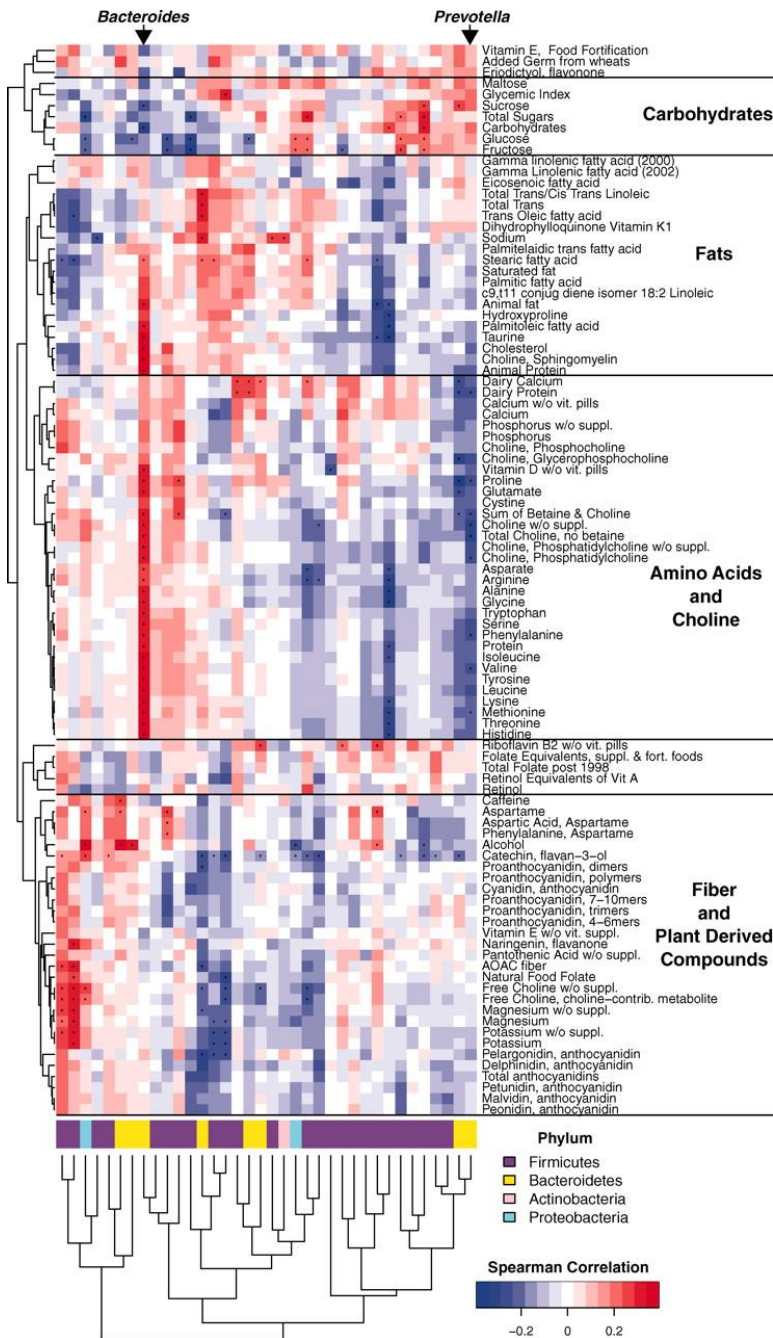


Enterotype configurations in the Flemish population

Female
Male



Prevalent microbiome constellations differ in relative abundances of enterotype identifiers

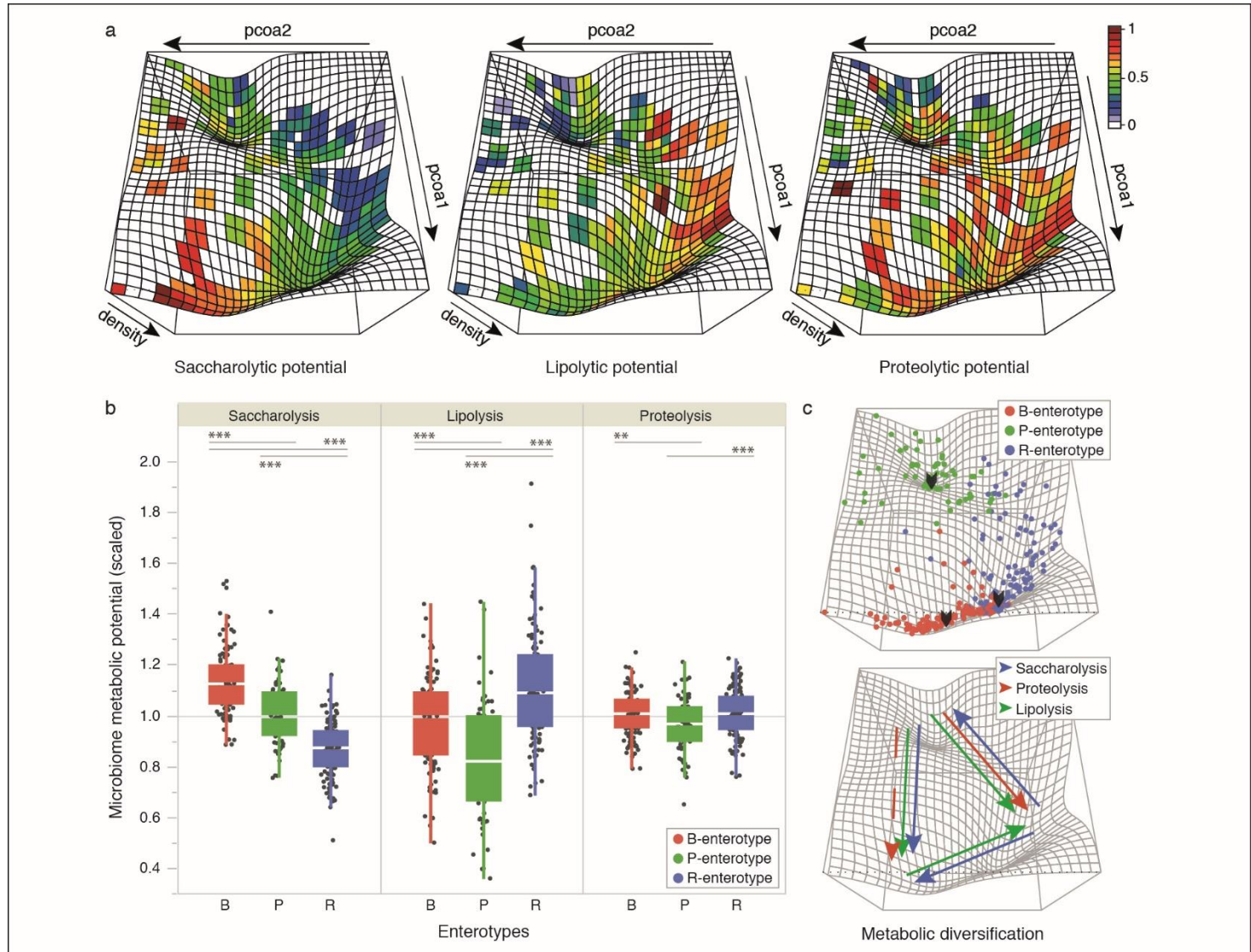


Long term dietary patterns might determine enterotype

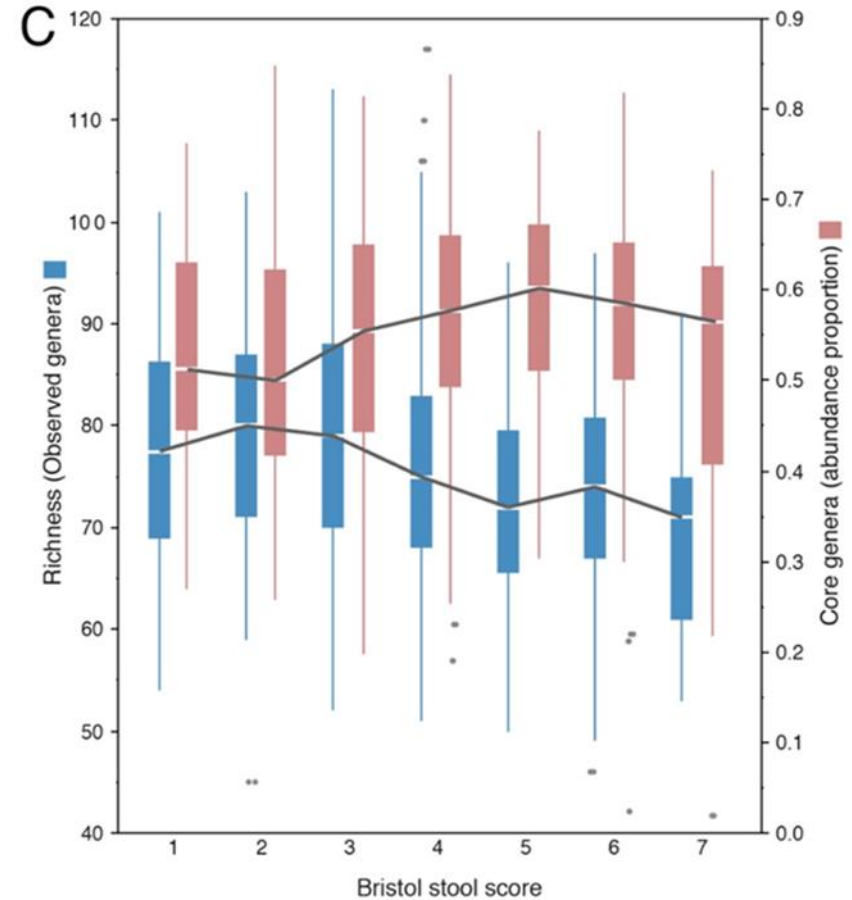
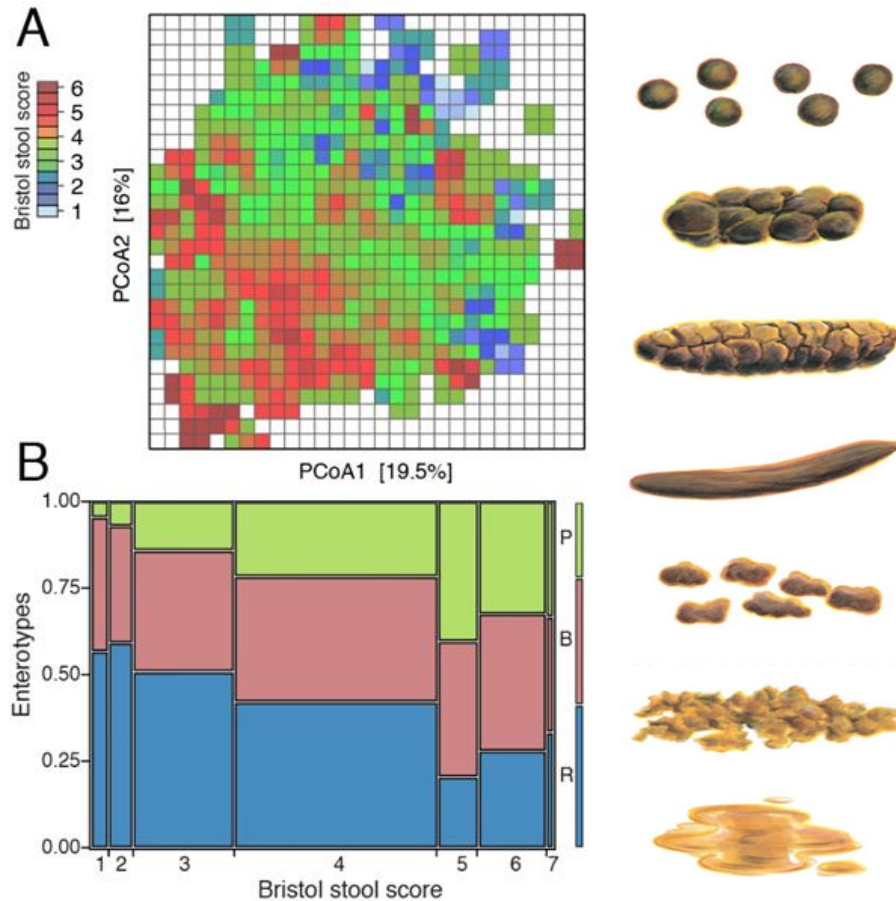
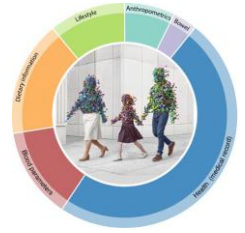


No effect shown by short term interventions

Enterotype stratification is linked to microbial substrate preference



Stool consistency is associated with microbiota richness and enterotypes

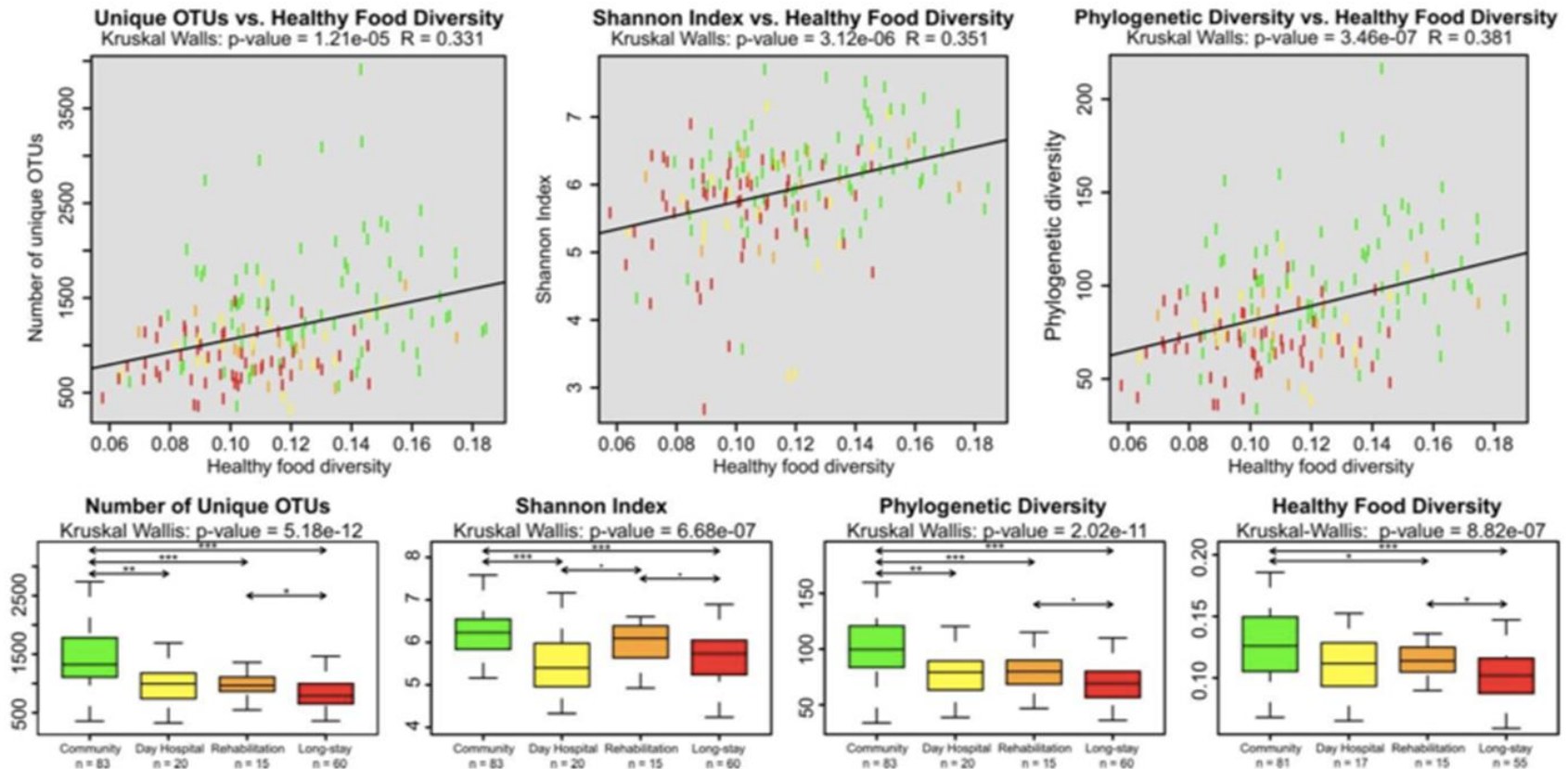


Vandeputte *et al.*, Gut 2015

diet – stool consistency – microbiome composition



Recurring theme: a 'healthy' microbiota is a diverse microbiota



Claesson *et al.*, Nature 2012

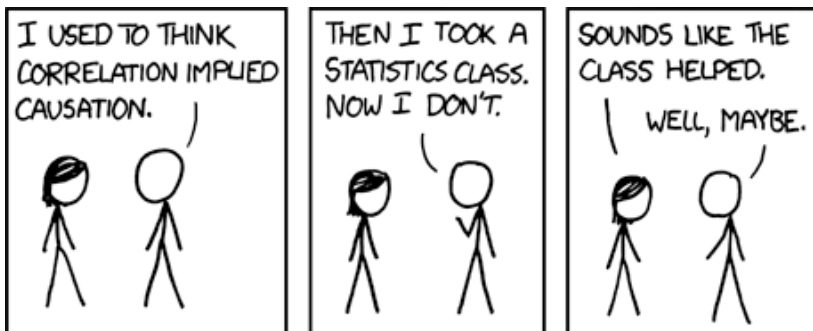
Microbiota diversity thought to reflect colon ecosystem stability and resilience

More and more diseases linked to disturbed gut microbiota





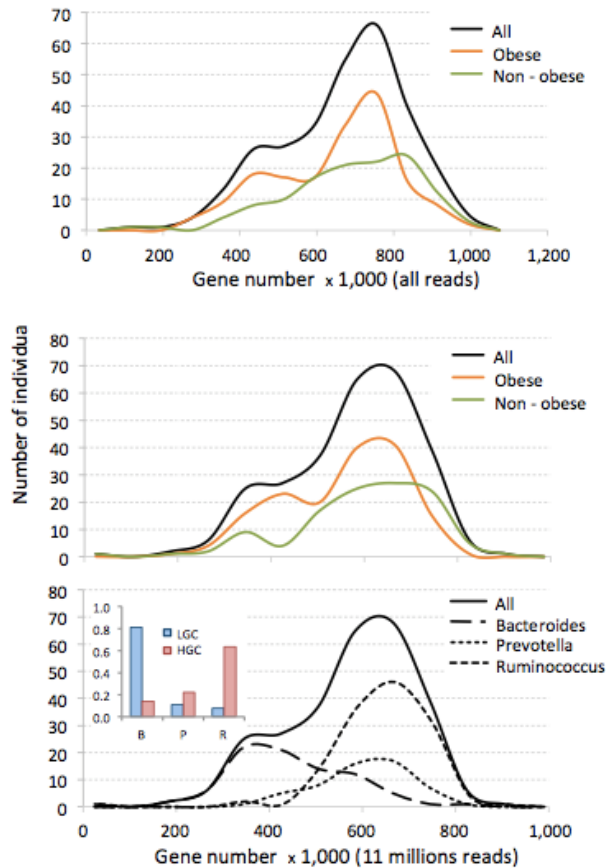
Association \neq Causality



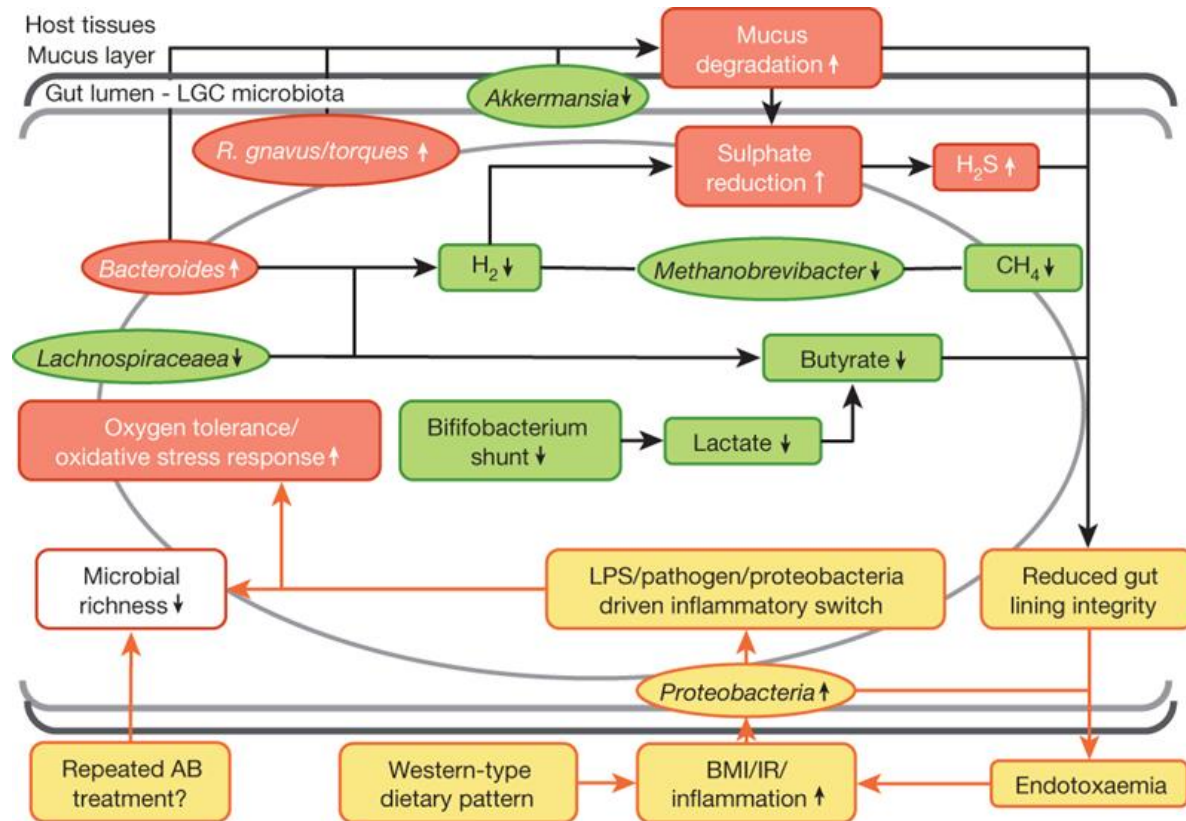
**Confounder
analyses are
required**



Obesity is associated with microbiota dysbiosis



292 individuals



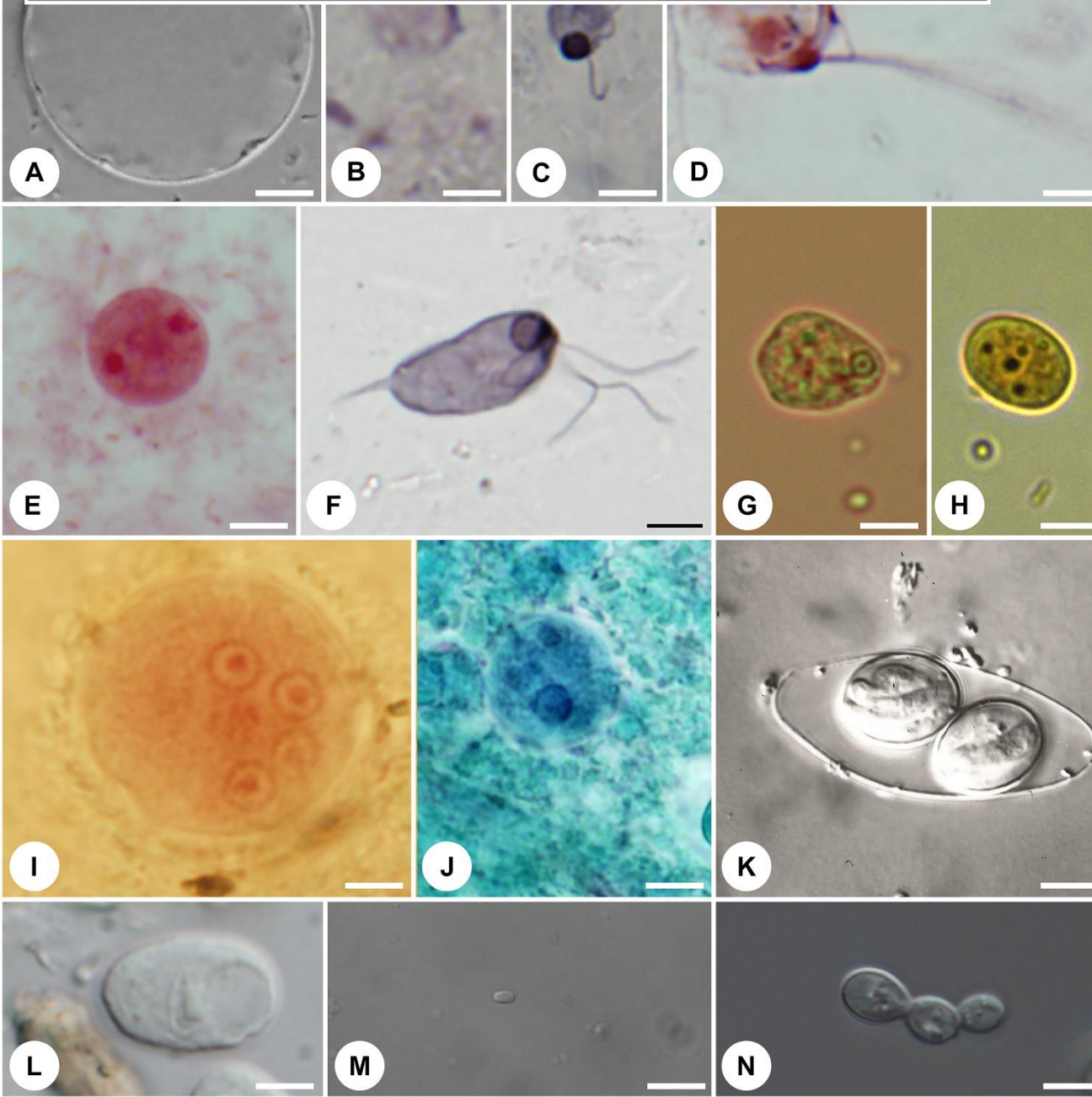
Microbiota modulation as therapy - **Fecal Microbiota Transplantation**



Vrieze *et al.*, Gastroenterology 2012

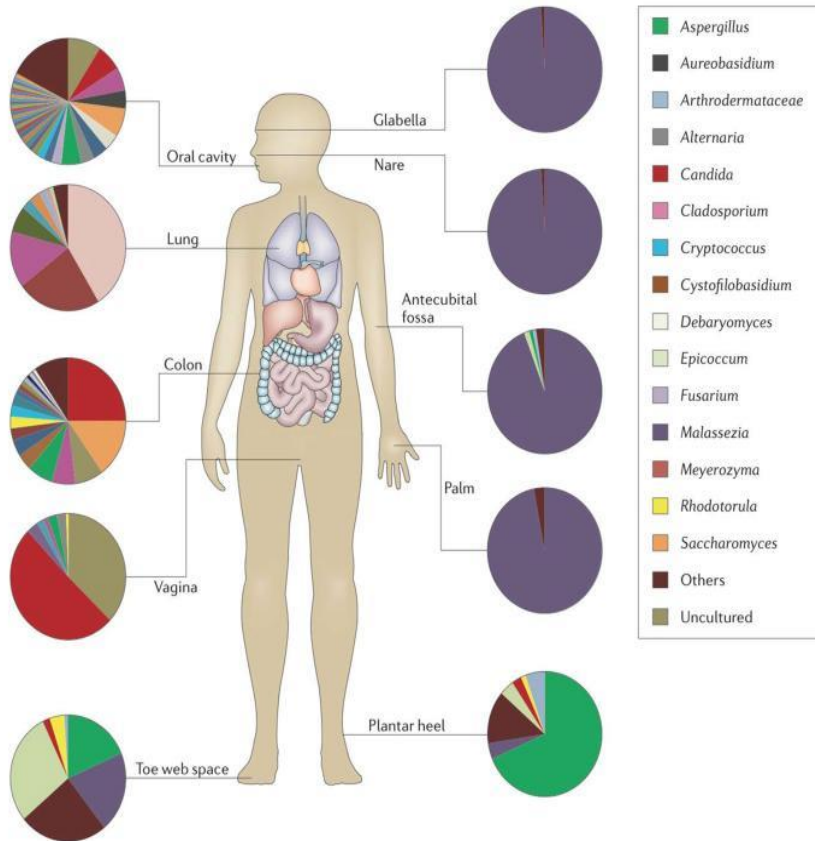
Transfer of intestinal microbiota from lean donors increases Insulin Sensitivity in individuals with Metabolic Syndrome

Gut microbiota: more than bacteria



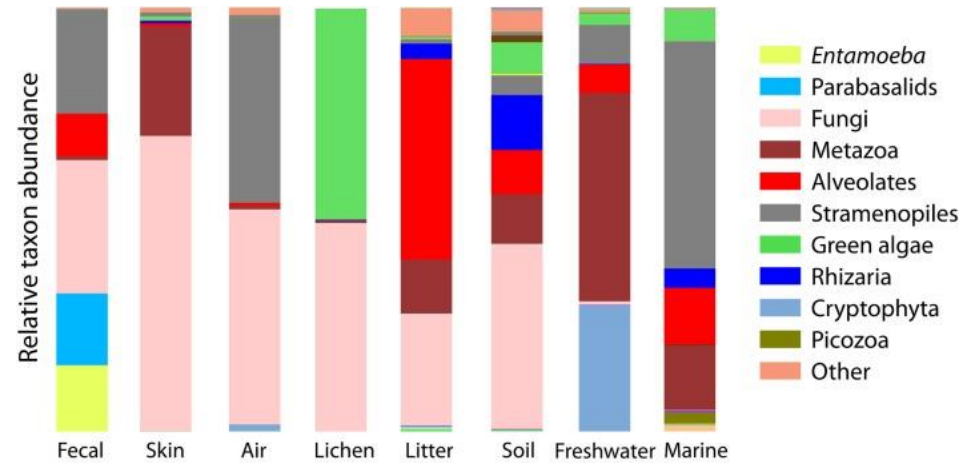
- (A) stramenopile *Blastocystis hominis*
- (B) diplomonadid *Enteromonas hominis*
- (C) retortamonadid *Retortamonas intestinalis*
- (D) trichomonadid *Pentratrichomonas hominis*
- (E) tritrichomonadid *Dientamoeba fragilis*
- (F) retortamonadid *Chilomastix mesnili*
- (G) amoebozoan *Entamoeba hartmani*
- (H) amoebozoan *Endolimax nana*
- (I) amoebozoan *Entamoeba coli*
- (J) amoebozoan *Entamoeba dispar*
- (K) coccidian *Isospora belli*
- (L) amoebozoan *Iodamoeba buetschli*
- (M) microsporidian *Encephalitozoon cuniculi*
- (N) ascomycete *Candida albicans*

The human mycobiota



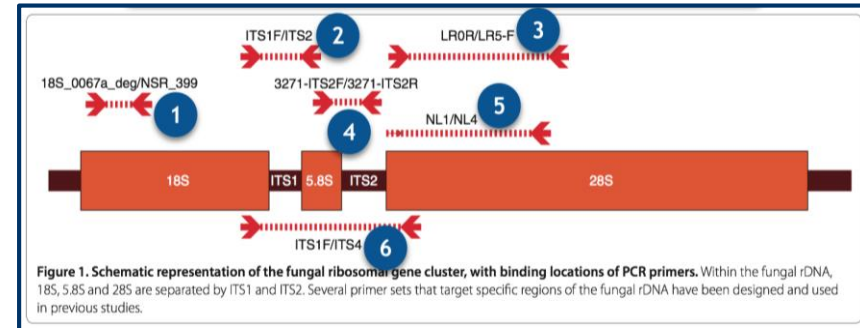
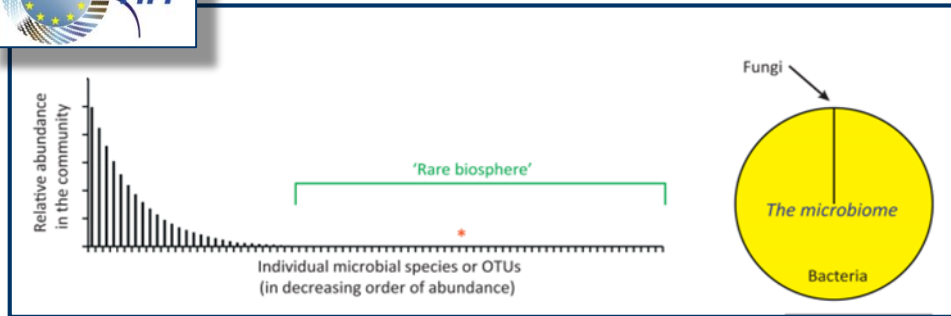
Underhill *et al.*, Nature Reviews Immunology 2014

Parfrey *et al.*, Frontiers in Microbiology 2014

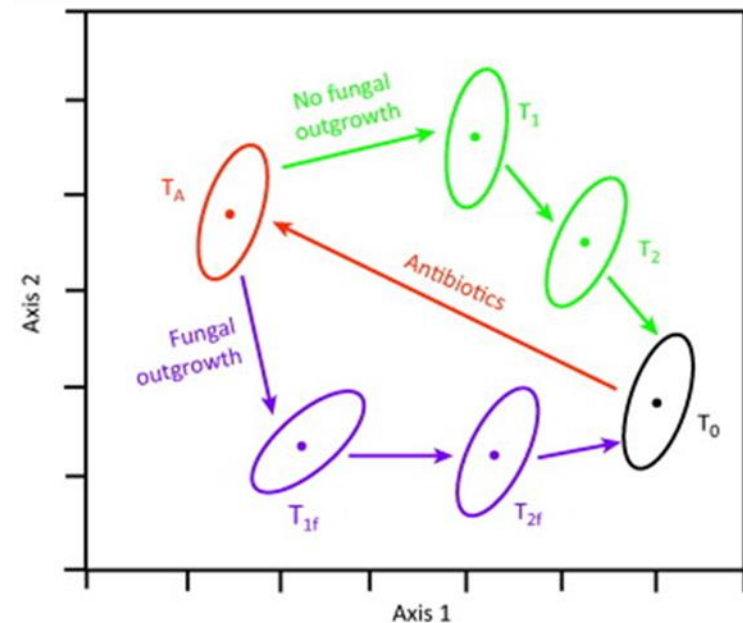
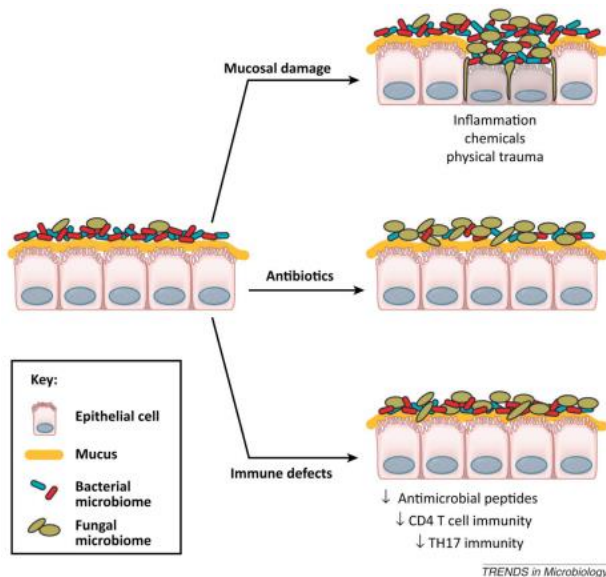


The rare biosphere

Less abundant (<0.1%), but more diverse, component of the microbiome



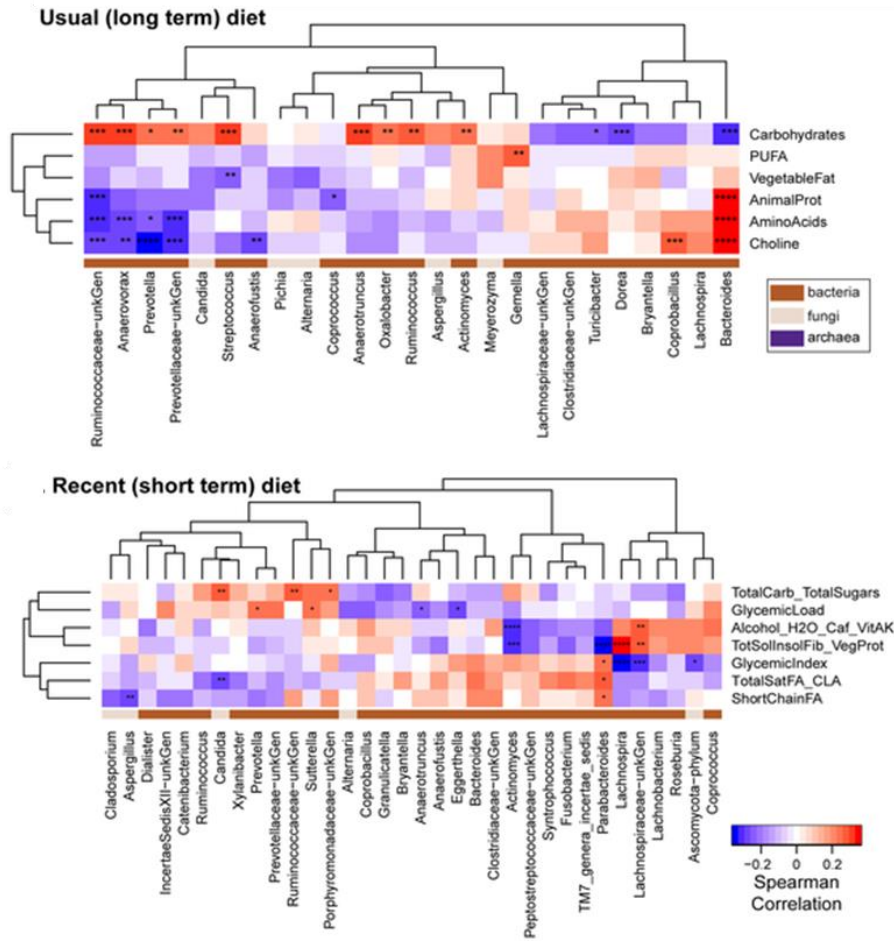
Amplicon-based markers for mycobiome studies: Nuclear ribosomal internal transcribed spacer (ITS) region



Correlations with diet and bacterial residents

98 healthy volunteers, US

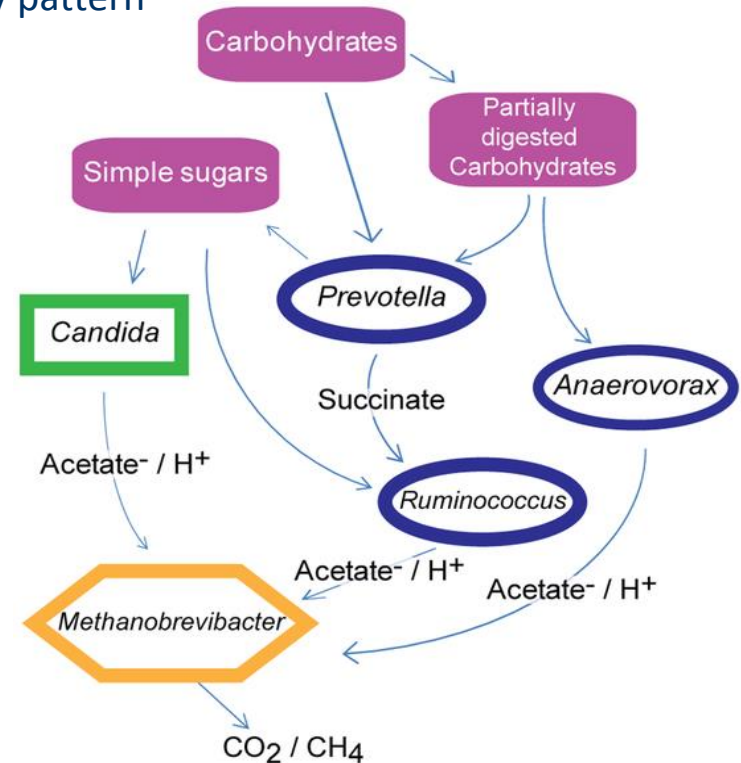
Saccharomyces present in 89% of fecal samples, *Candida* in 57%



Candida: positive correlation with carbohydrates and negative with total saturated fatty acids consumption

Aspergillus: negative correlation with SCFA consumption

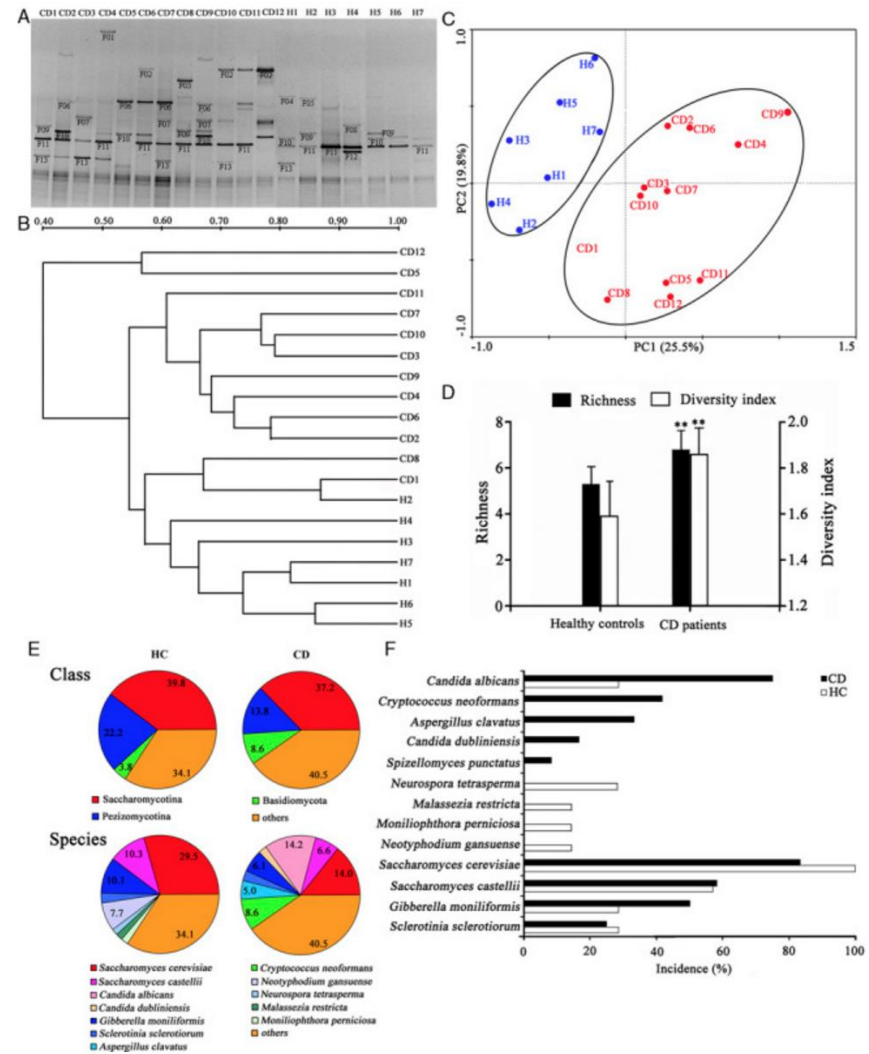
Saccharomyces: not associated to defined dietary pattern



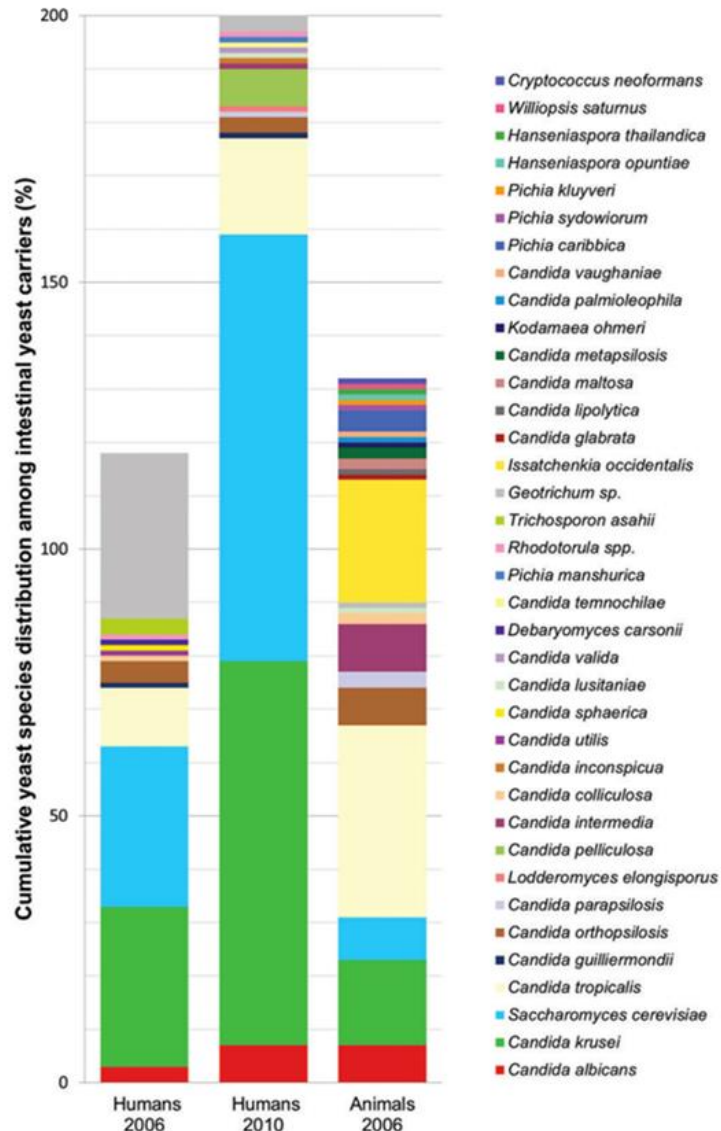
Mycobiome research focusses on disease

19 Crohn's disease patients versus 7 healthy controls

- Perturbation of fungal fecal community in CD – fungal dysbiosis?
 - Increased diversity
 - Increase prevalence of *Candida albicans*
 - Fungal diversity correlates with CRP levels and CD activity index



Candida albicans is not always the preferential yeast colonizing the human intestine



Wayampi people, an indigenous tribe from French Guiana
151 individuals, fecal samples collected in 2006 and 2010

Rectal swabs of 213 wild and domestic animals

Culture/isolation/identification approach

- *Candida krusei* and *Saccharomyces cerevisiae* identified as most abundant gut fungal species
- Carriage of foodborne origin, associated with a common environmental source, such as plants or water
- Specific risk factors associated with *Candida albicans* carriage are gender (female) and living in a crowded household

Thanks for your attention

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