

Wednesday July 24, 2013

MICROBIOME COLONIZATION AND ASSEMBLY

Human Microbiome Science:
Vision for the future

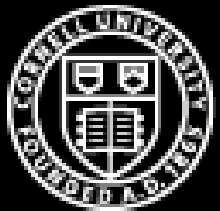
Ruth E. Ley

Department of Microbiology

Department of Molecular Biology and Genetics

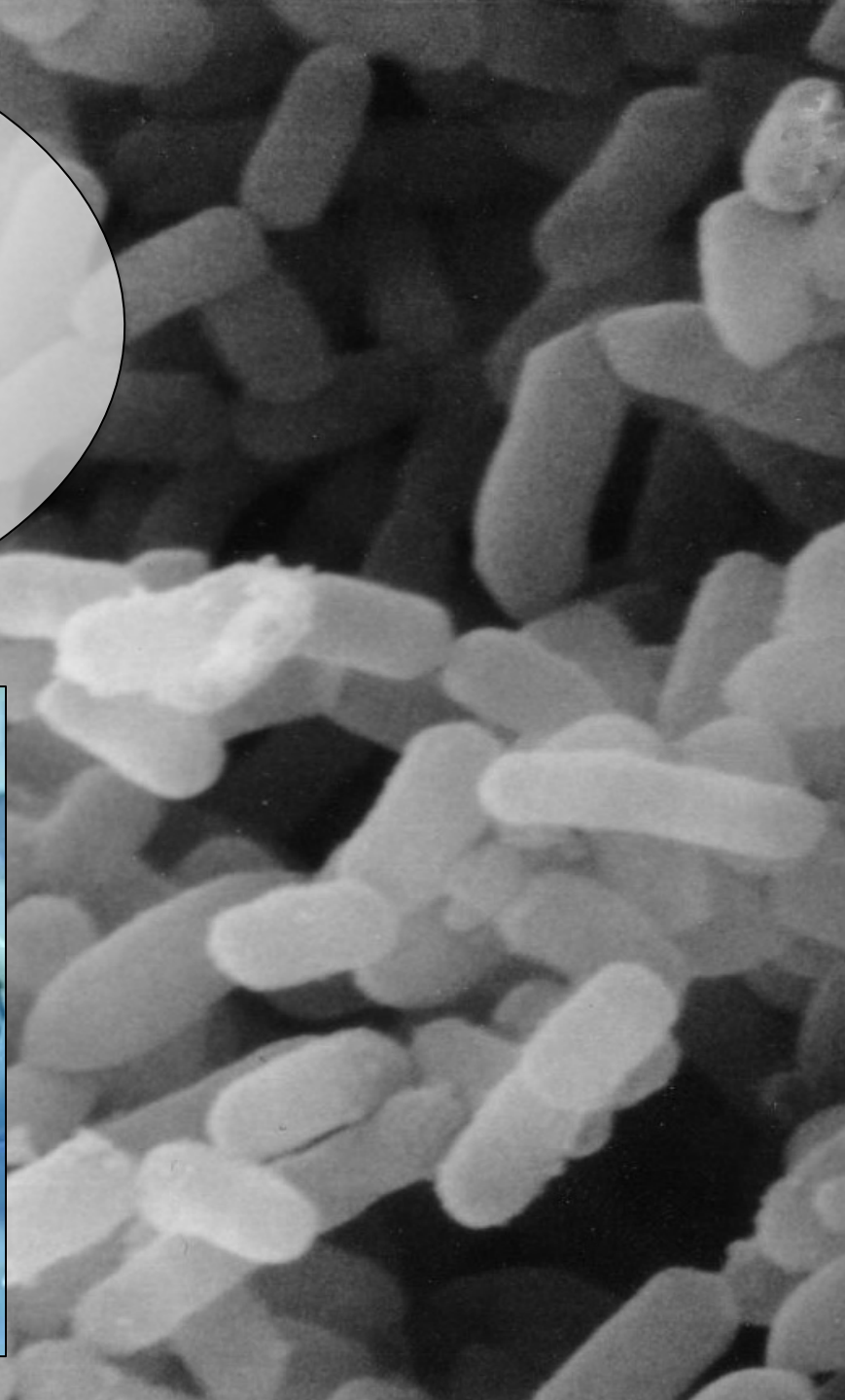
Cornell Center for Comparative and Population Genomics

Cornell University, Ithaca NY 14853, USA

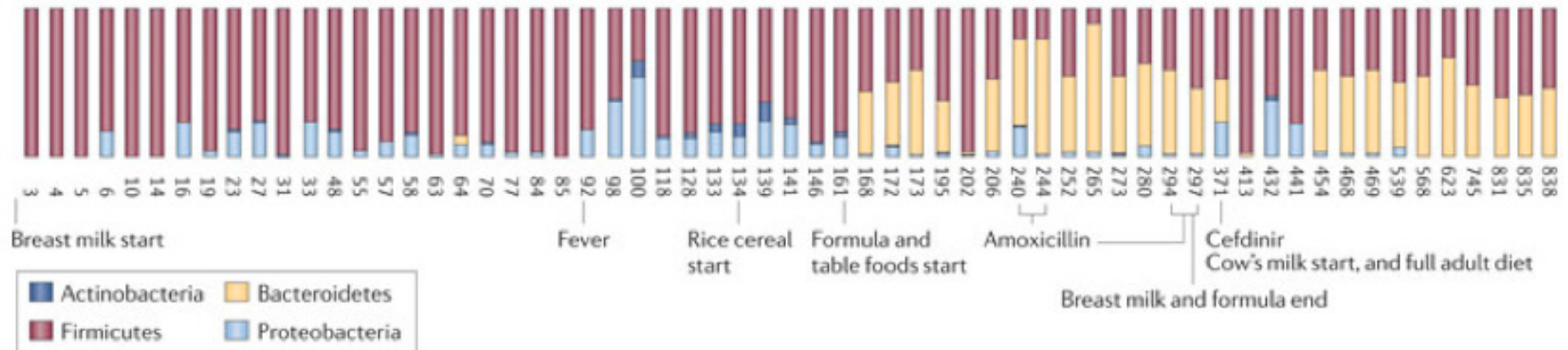
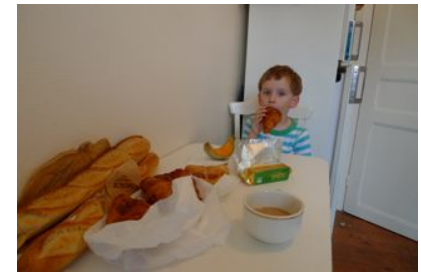


Cornell University

I need
microbes!!!!



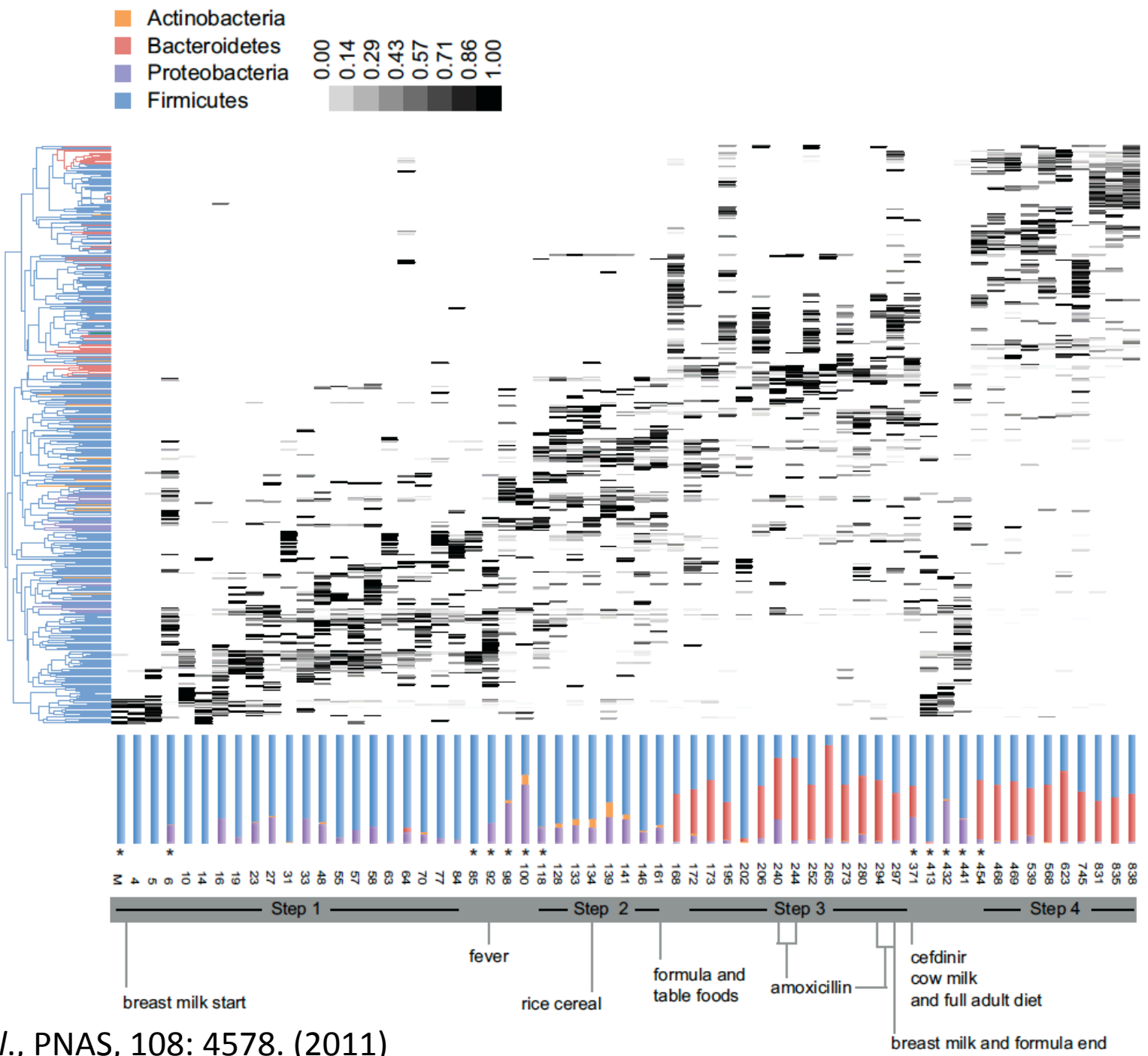
Life events such as diet changes, antibiotics and fever influence microbiome structure



Case study of 1 individual followed for 2.5 years

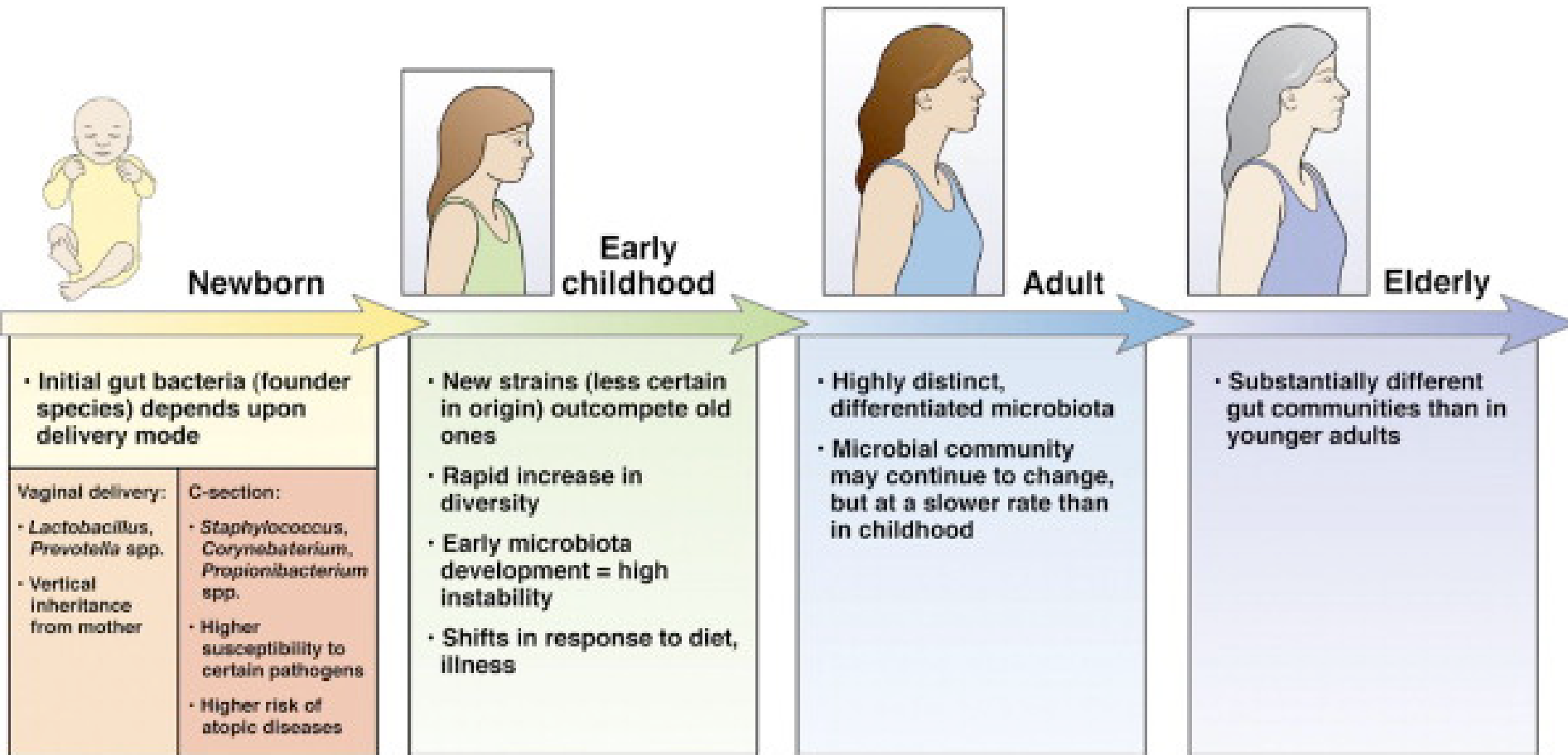
Spor, Koren and Ley. Nature Reviews Microbiology 9: 279. (2011)

Koenig *et al.*, PNAS, 108: 4578. (2011)



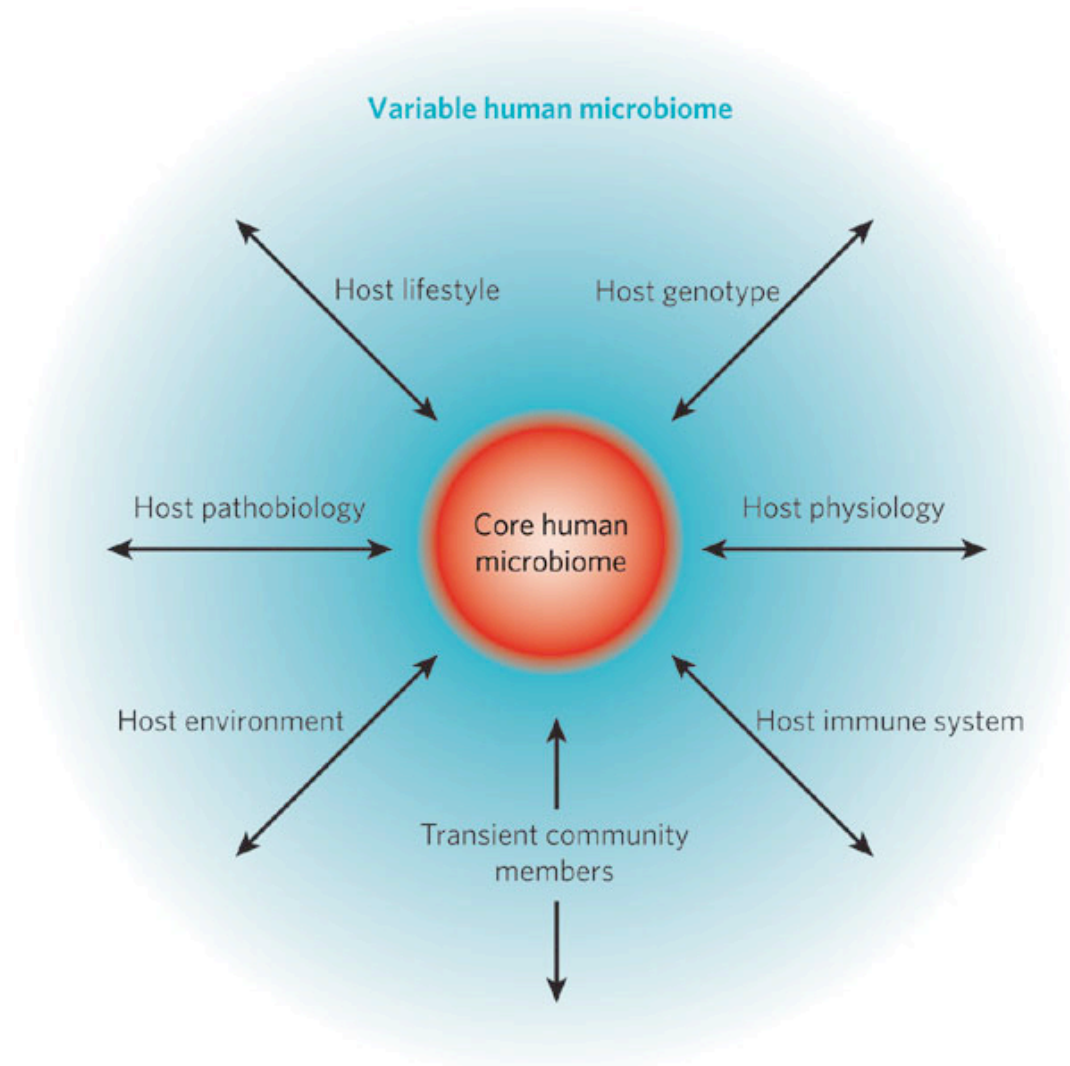
Koenig *et al.*, PNAS, 108: 4578. (2011)

Do early colonizers impact microbiome later in life?

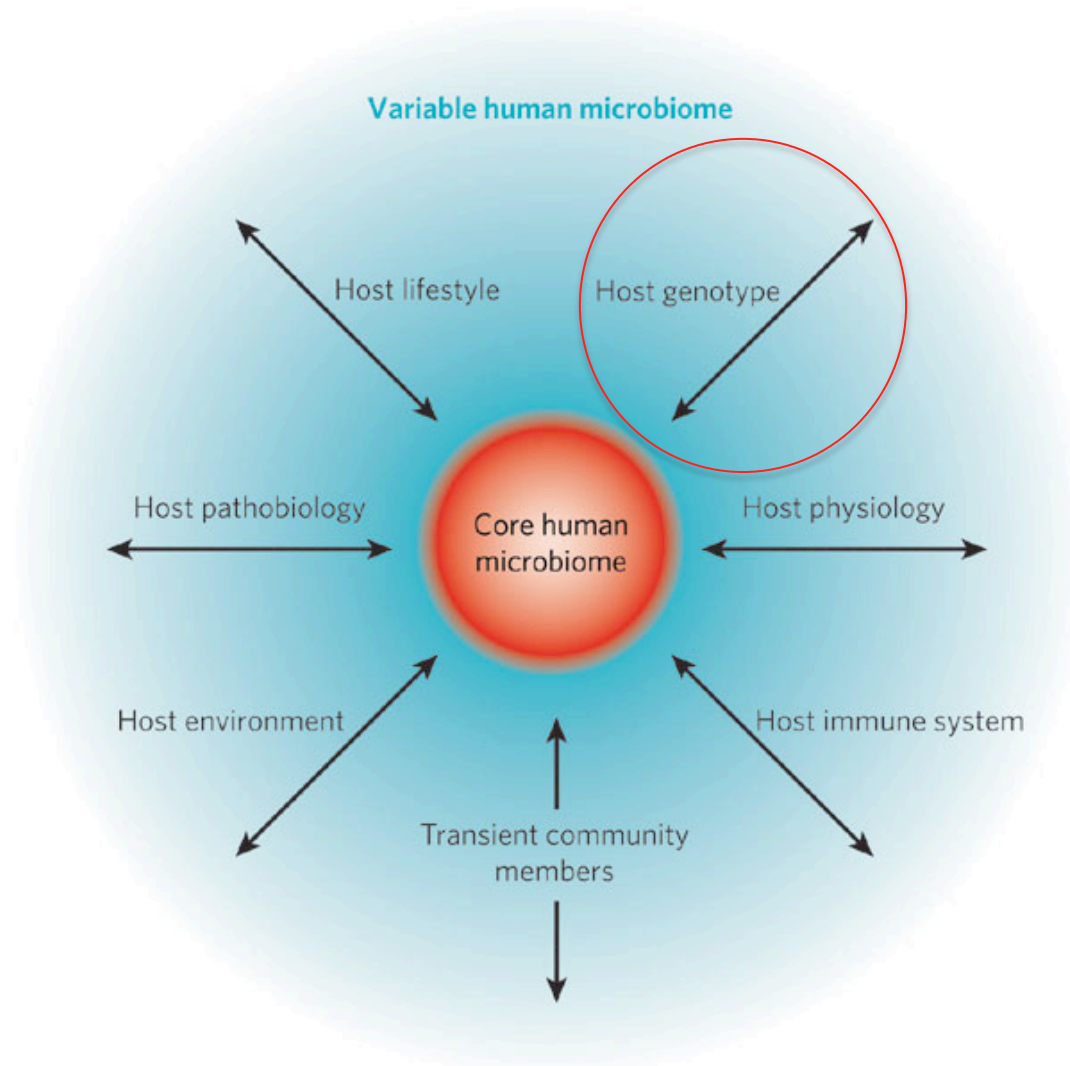


Dominguez-Bello, M. G., M. J. Blaser, R. E. Ley and R. Knight. Development of the infant gut microbiota: insights from high-throughput sequencing. *Gastroenterology* 140: 1713-1719. (2011)

What does impact microbiome later in life?



What does impact microbiome later in life?



A need for genetic studies in humans:

- QTL mapping studies in mice have revealed associations with loci
 - Loci can be quite big
- Studies with candidate genes in humans
 - e.g., NOD2 (Li *et al.*, PloS One, 2012)
 - You know what you are looking for
- No published genome-wide association studies in humans

Monozygotic versus dizygotic twins

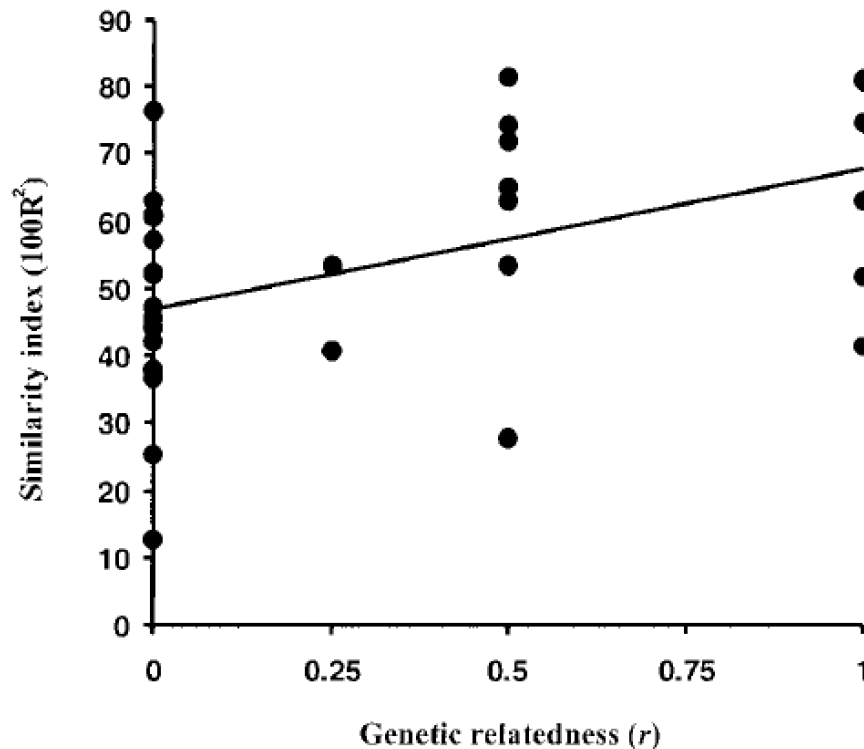


Human Mirror, NYC Subway

The Host Genotype Affects the Bacterial Community in the Human Gastrointestinal Tract

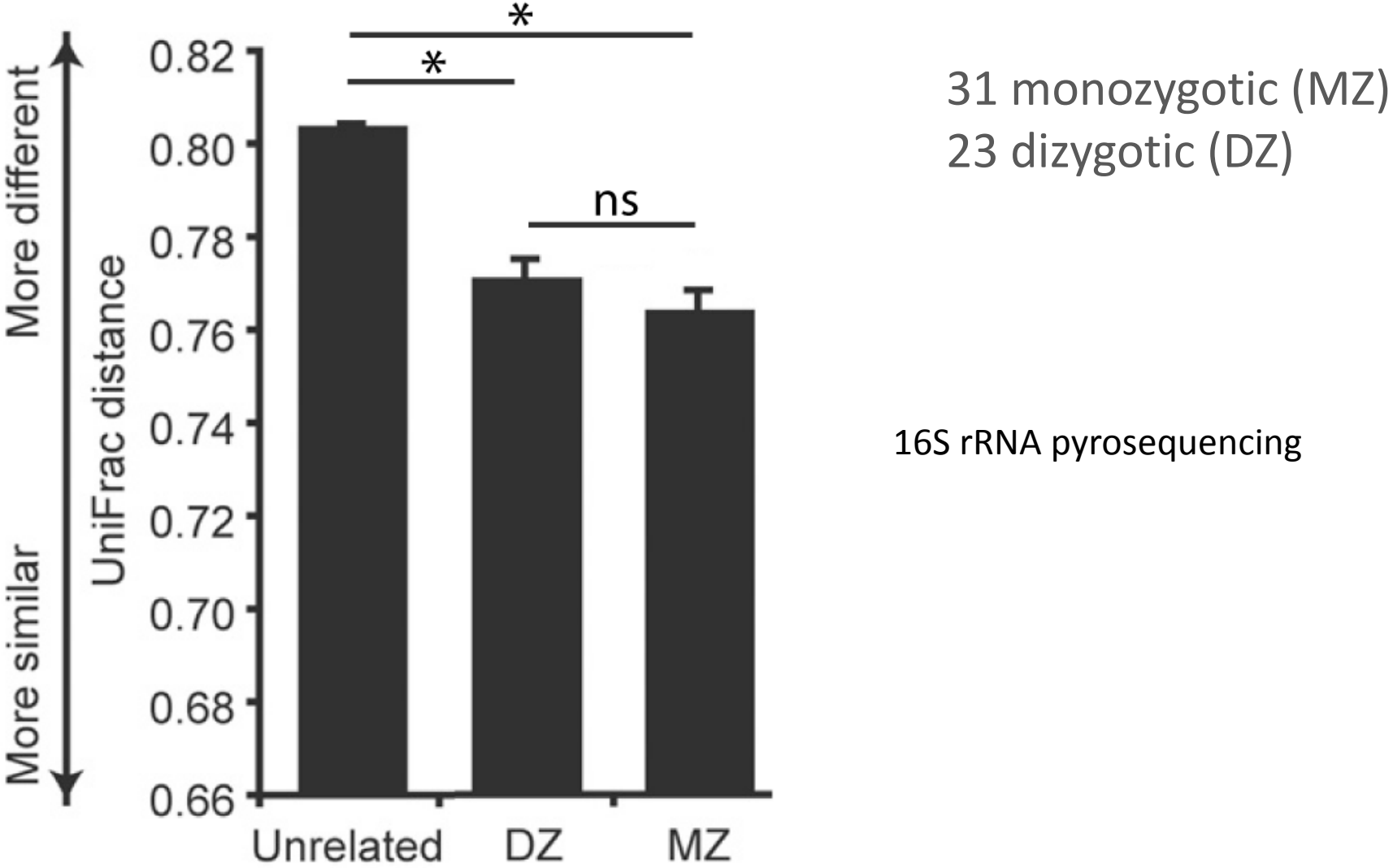
Erwin G. Zoetendal^{1,2}, Antoon D. L. Akkermans¹, Wilma M. Akkermans-van Vliet¹, J. Arjan G. M. de Visser¹ and Willem M. de Vos^{1,2}

From the ¹Laboratory of Microbiology, Wageningen University, Hesselink van Suchtelenweg 4, 6703 CT, Wageningen, ²Wageningen Center for Food Sciences, PO Box 557, 6700 AL, Wageningen, The Netherlands



DGGE patterns

Within MZ = within DZ bacterial diversity



Genotyped MZ and DZ twins



Twin Registry (TwinsUK)

- 2,300 twins genotyped with Illumina 300 HapChip
- 3,500 twins genotyped with the Illumina 600 HapChip

- ~1,000 Fecal samples collected to date

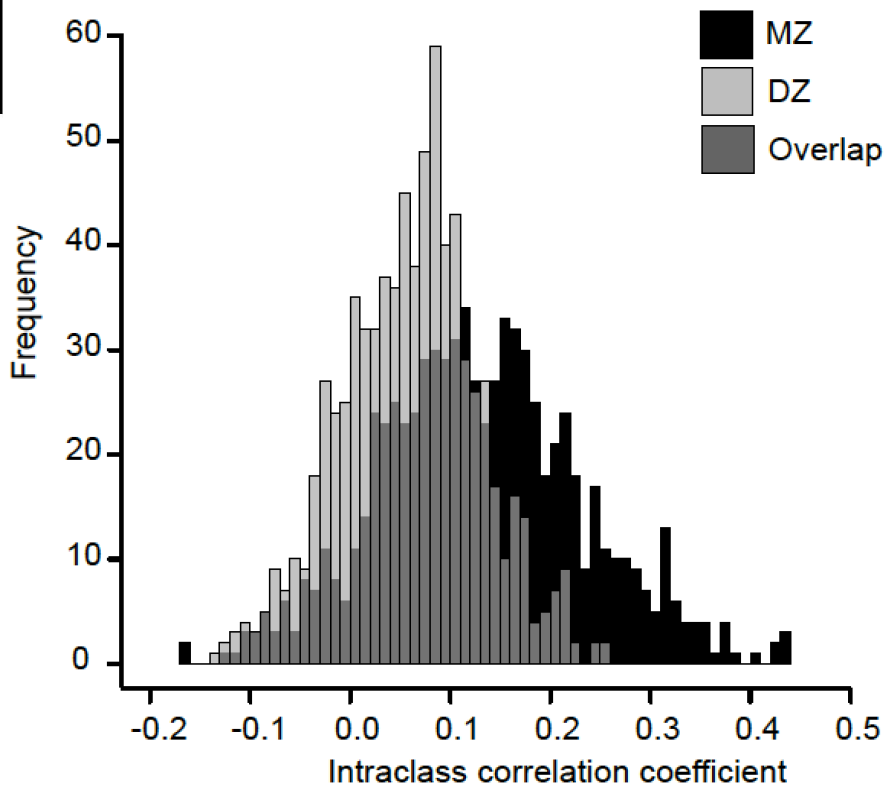
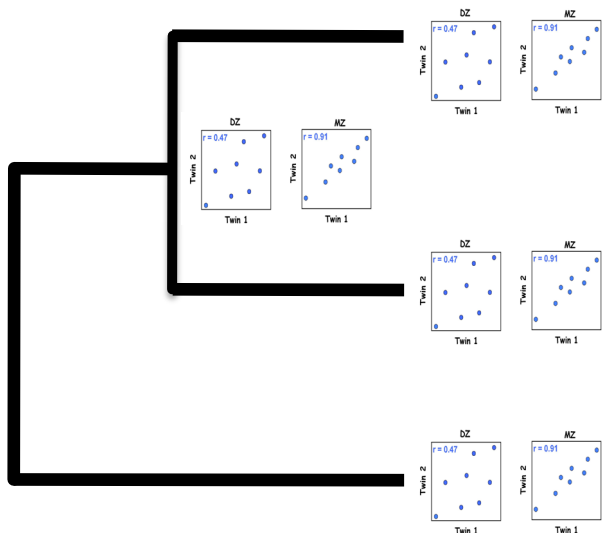
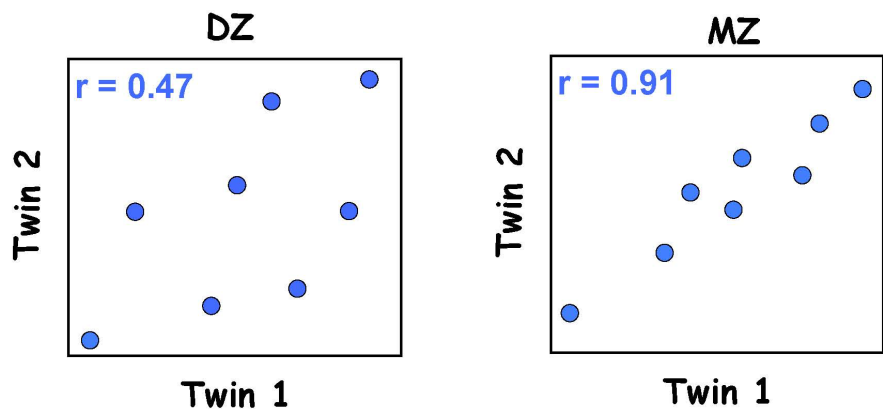
- 249 DZ pairs
- 157 MZ pairs
- 163 unrelated
- 36 repeat samples
- 32 to 87 (average 64) years old
- Mostly Female

Collaborators:

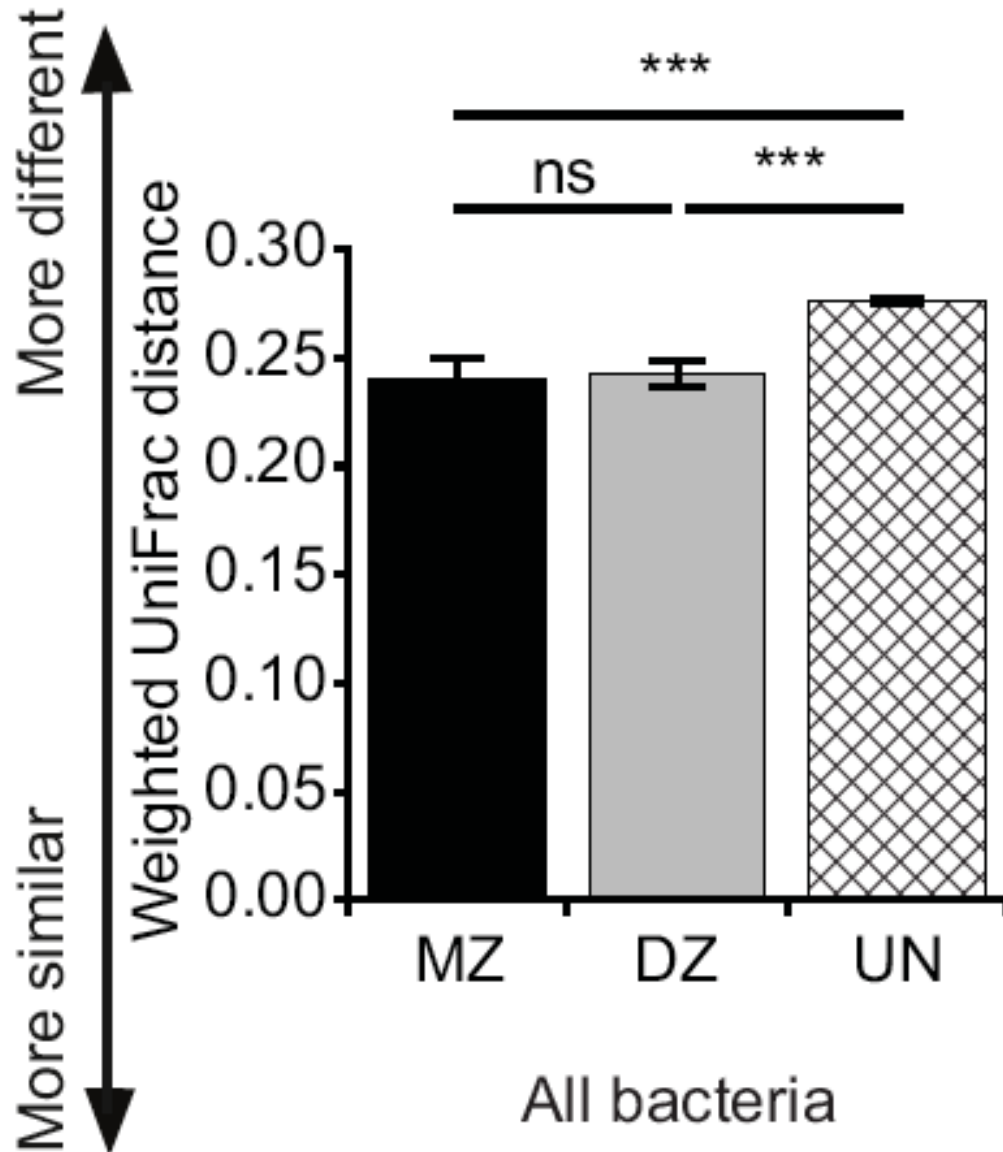
Andy Clark (Cornell)
Tim Spector, Jordana Bell
(KCL)

16S rRNA diversity with MiSeq

MZ twins have stronger correlations than DZ twins



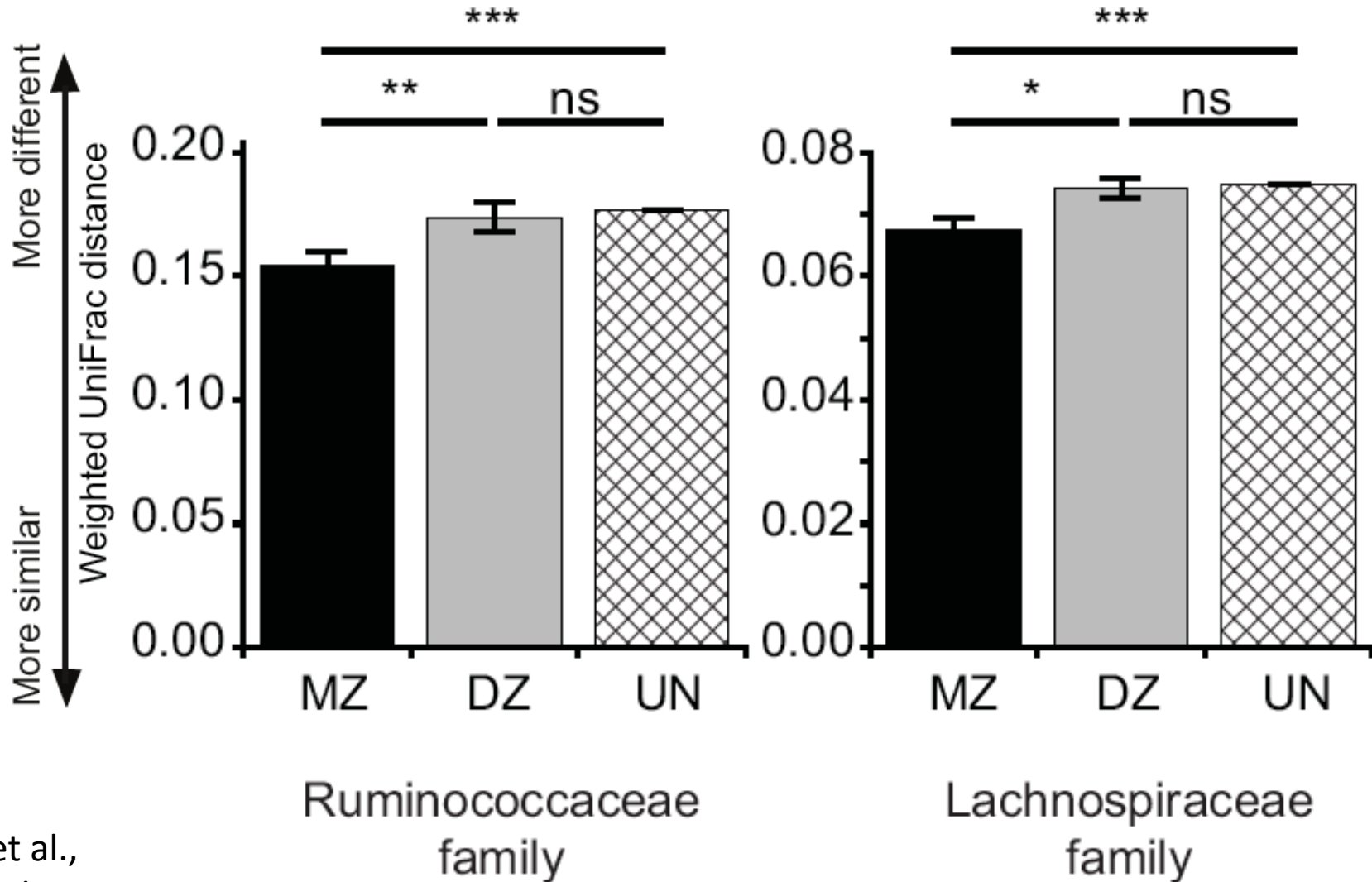
MZ = DZ for total diversity



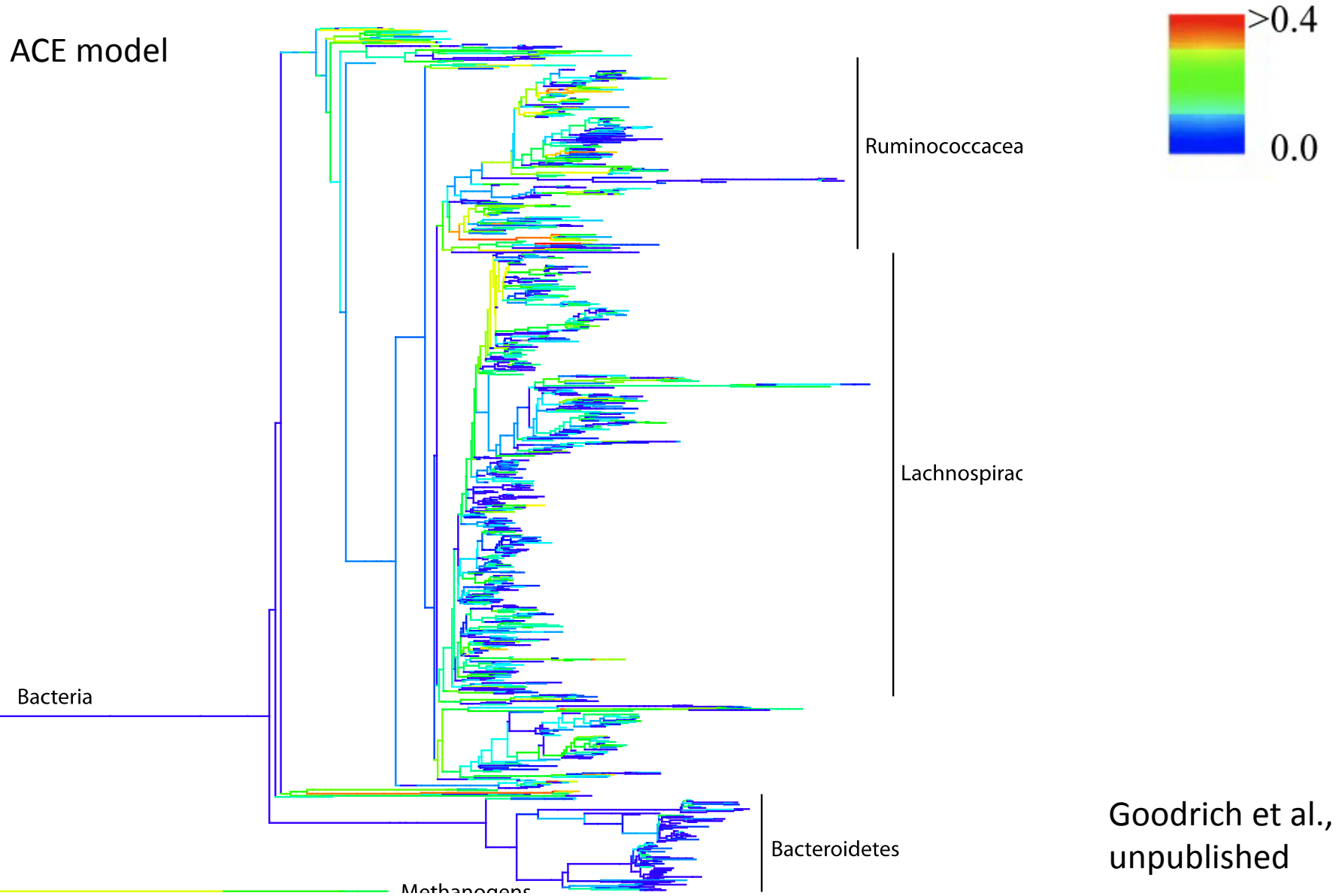
All bacteria

Goodrich et al.,
unpublished

MZ < DZ for specific families of Firmicutes



Heritable branches within the bacterial tree

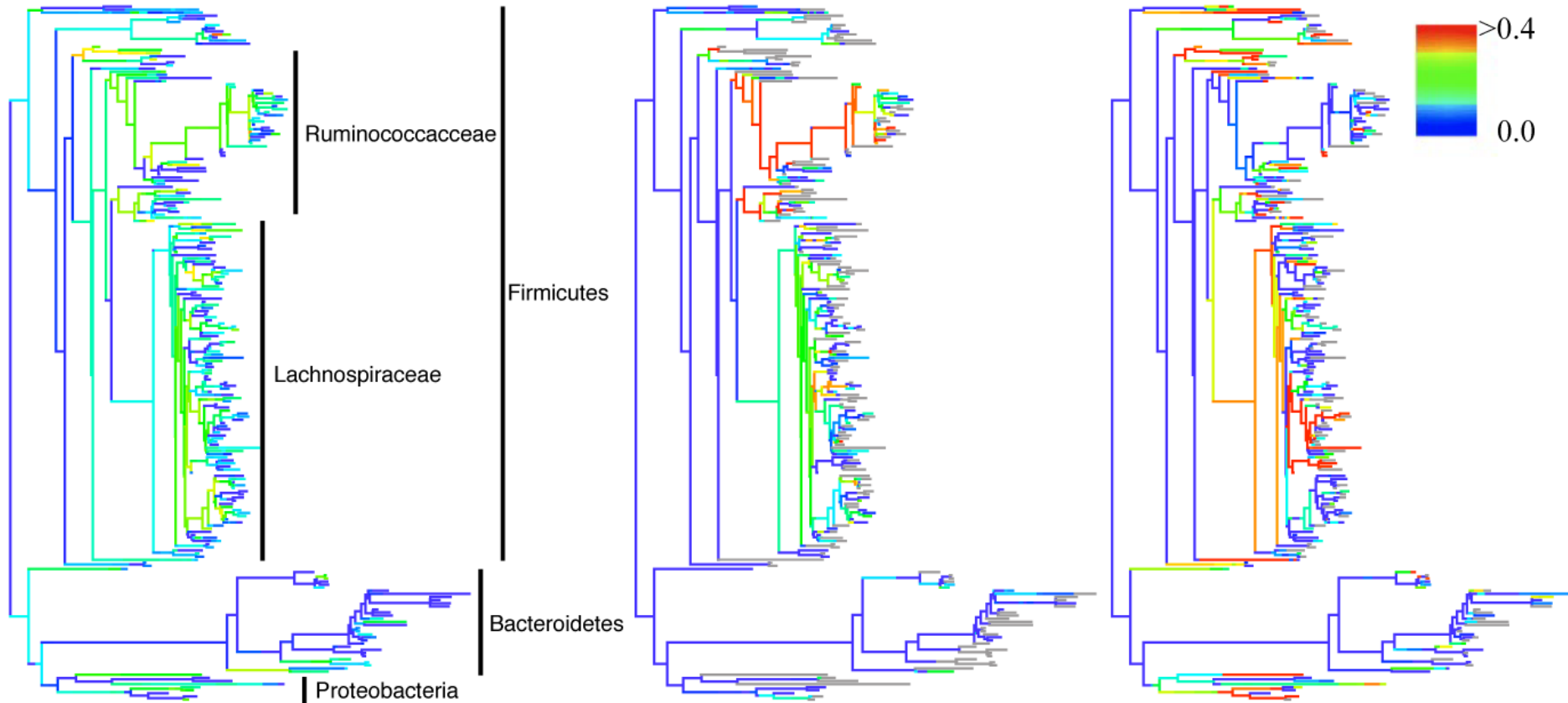


Similar pattern of heritability across studies

This study
UK Twins 32-87 yrs

Turnbaugh 2009
US Twins 21-32 yrs

Yatsunenکو 2012
US Twins 13-17 yrs

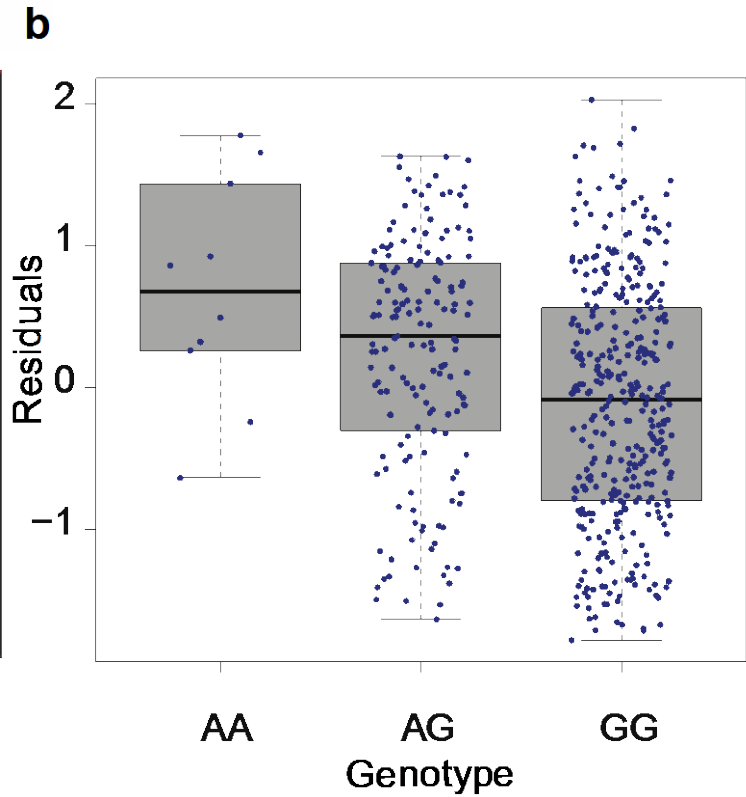
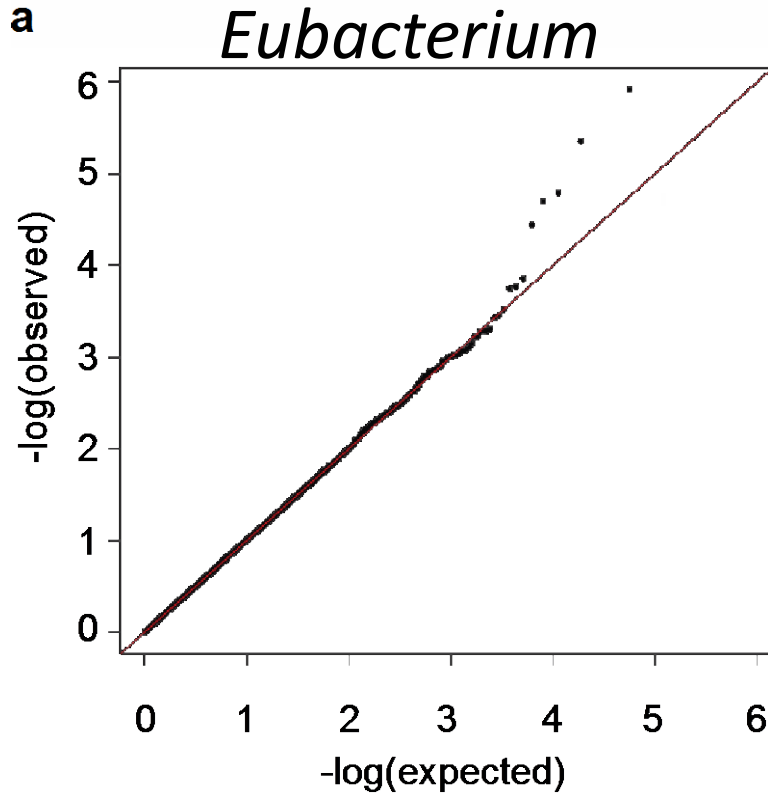


Example of early result

GWAS

SNP rs1016883 on chromosome 2

In gene for phospholipase C-like 1 (*PLCL1*)



G = Risk allele for Crohn's

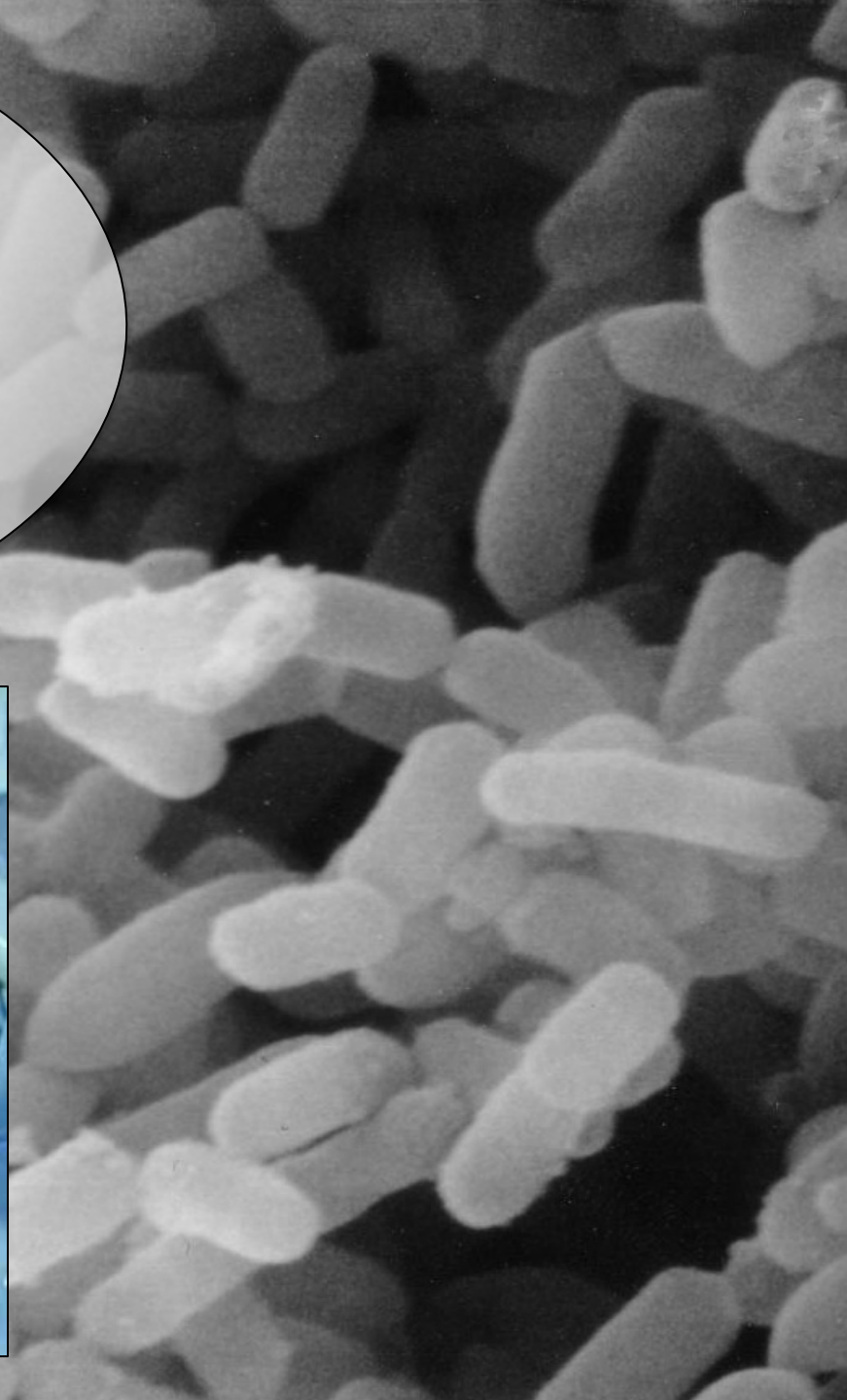
PLCL1 had a role in insulin-induced GABA (A) receptor expression

Goodrich et al.,
unpublished

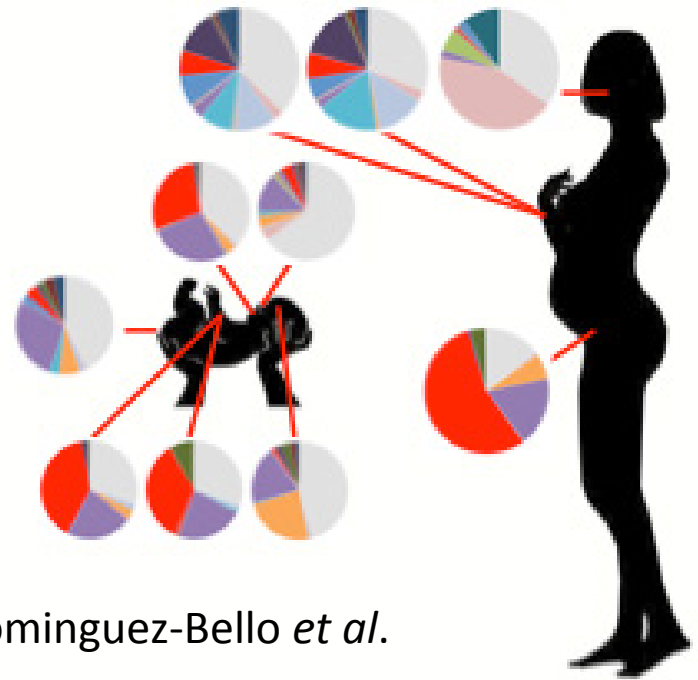
Gaps

- How does the host genotype determine the microbiome?
- How does the microbiome interact with the host genotype to determine risk susceptibilities to diseases?
- How much more variation (in any host trait) can be explained with a microbiota component in addition to, or in combination with genotype?

I want my own
personalized
microbes!!!!



I got Mummy's microbes???



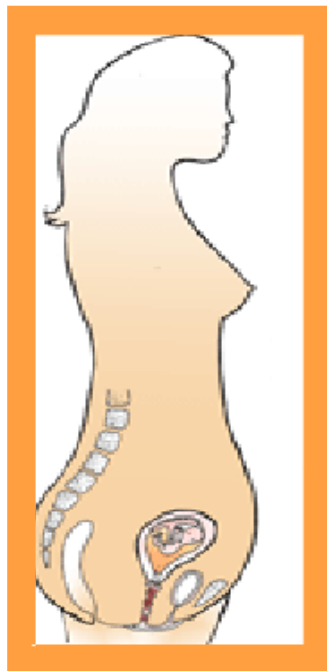
Dominguez-Bello *et al.*



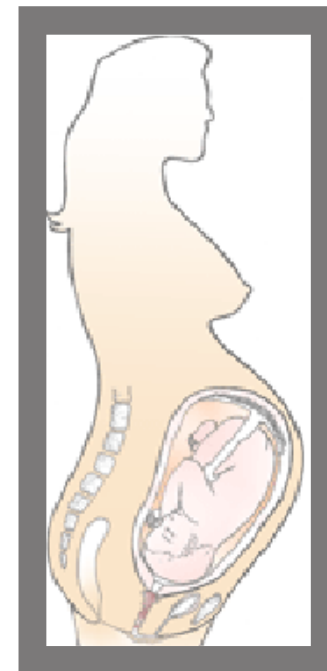
Microbiome in pregnancy

First trimester

Third trimester



T1



T3



Fat Mass



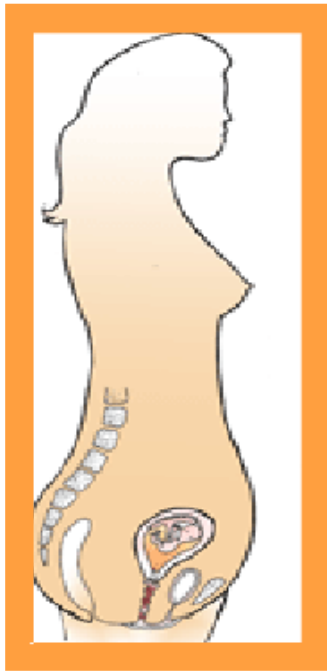
Blood glucose



Insulin sensitivity

Normal pregnancy

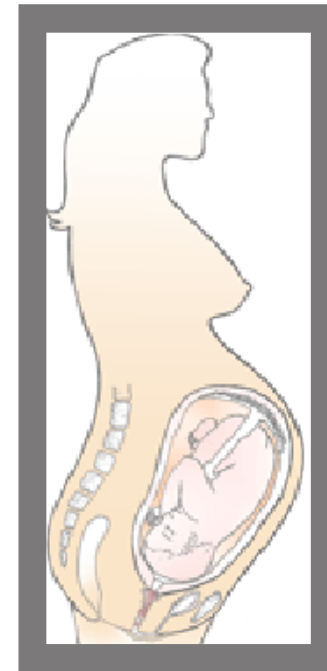
First trimester



T1



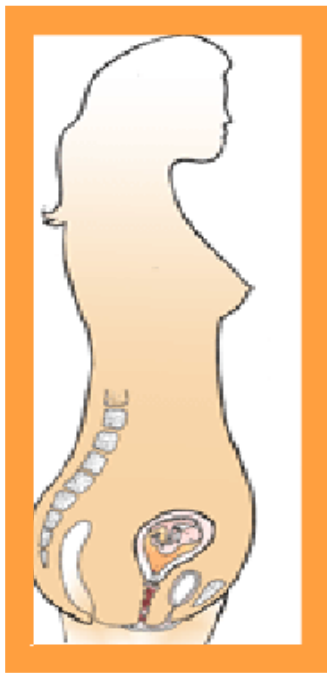
Third trimester



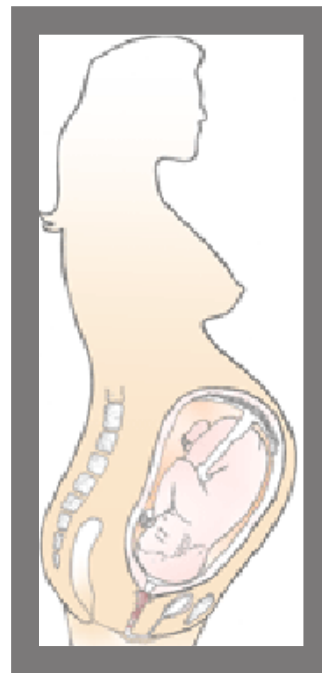
T3

91 women from Finland

First trimester Third trimester



T1

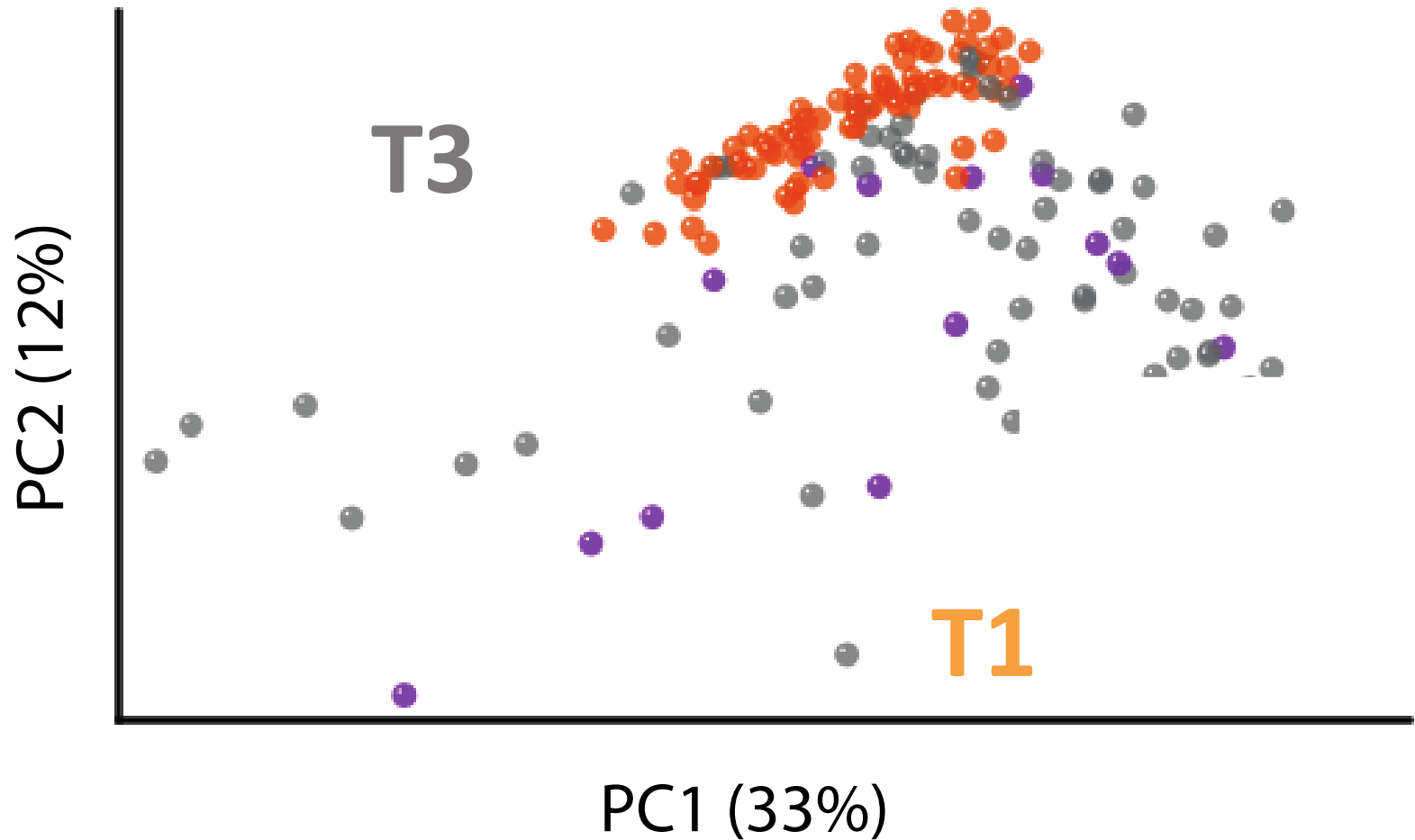


T3

Stool samples
Diet data
Clinical Data
Stool from babies

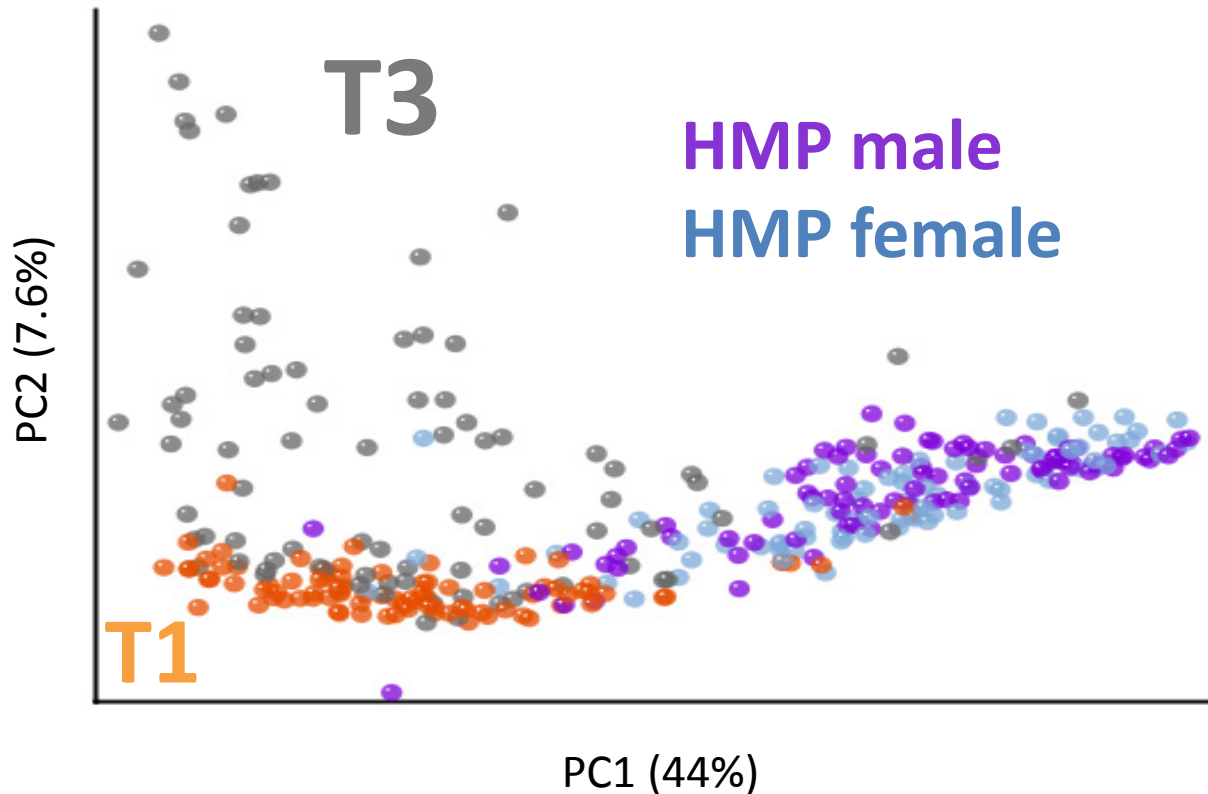
Erika Isolauri
Seppo Salminen

Between-individual diversity expands

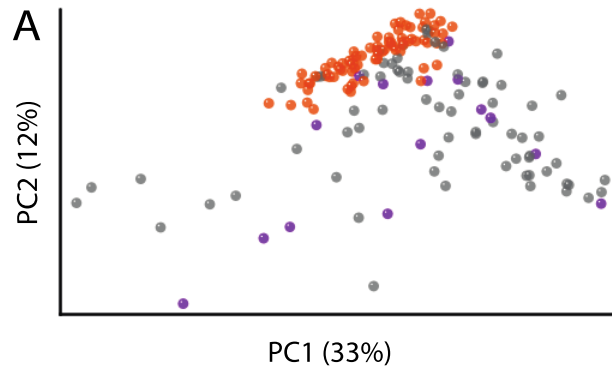


Which is normal? T1 or T3?

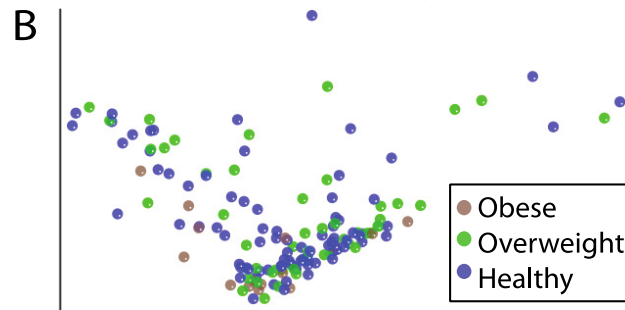
T1 diversity similar to “Normal” from Human Microbiome Project



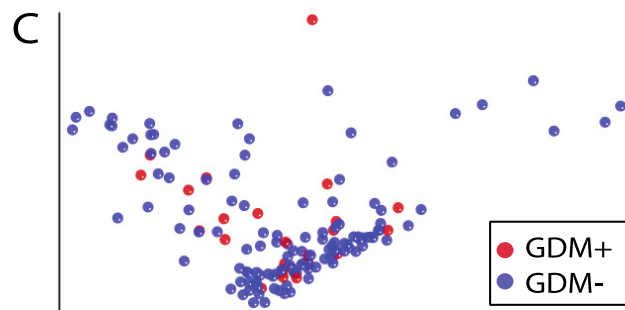
What does the pattern associate with?



No association with:

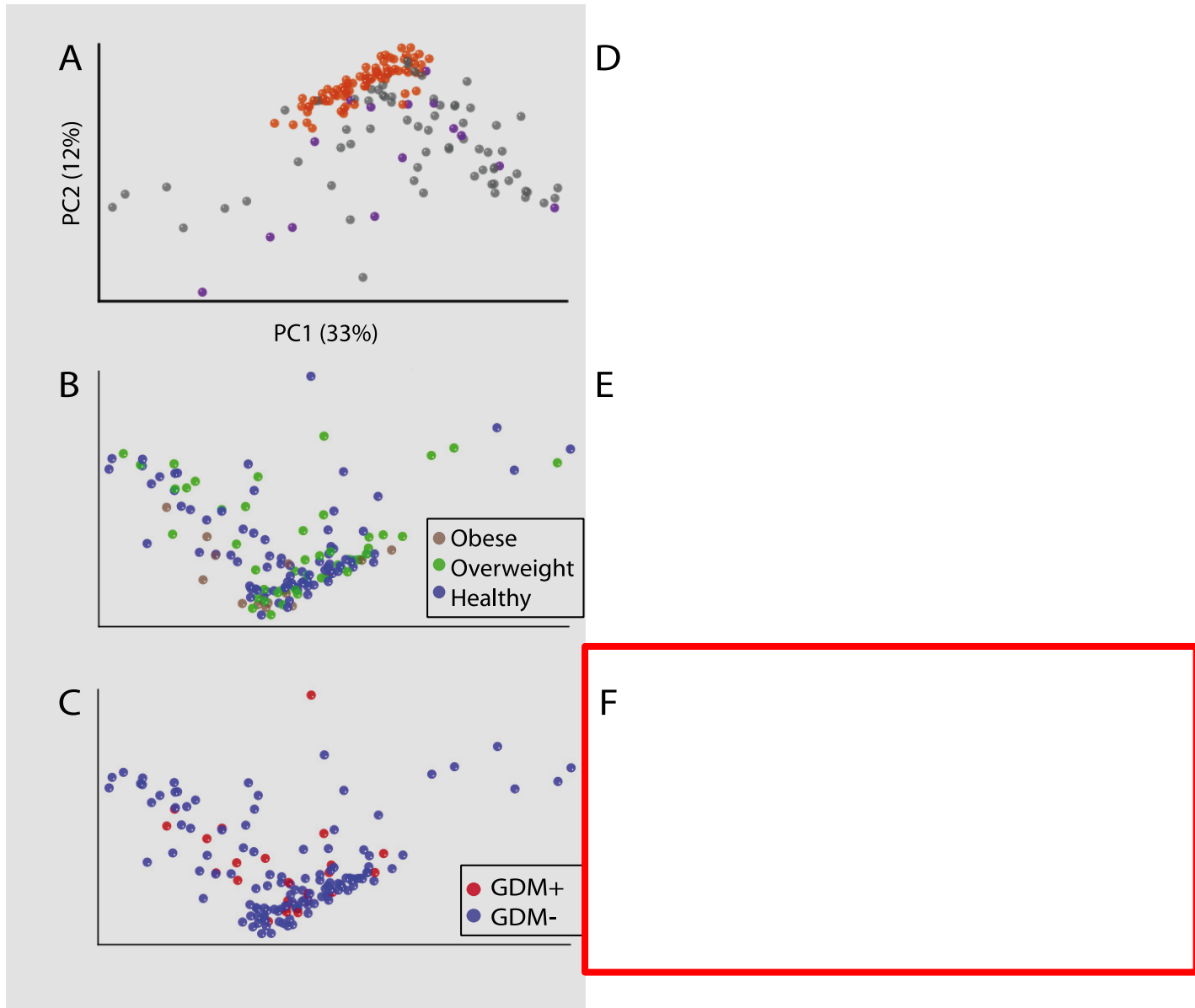


Pre-pregnancy obesity
and overweight



Gestational diabetes status

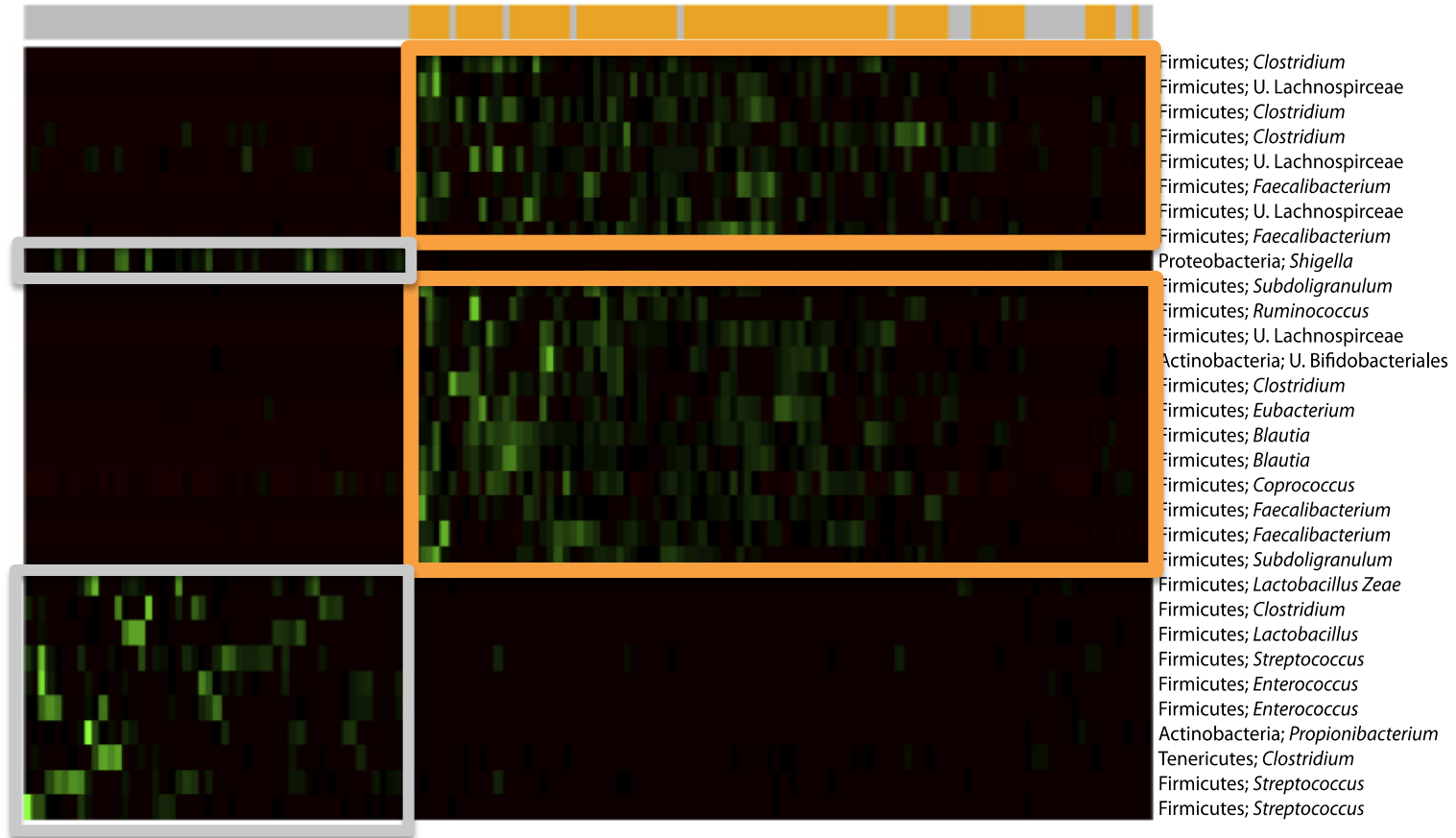
Gradients of abundances of taxa



Shift in abundant bacterial genera

T3

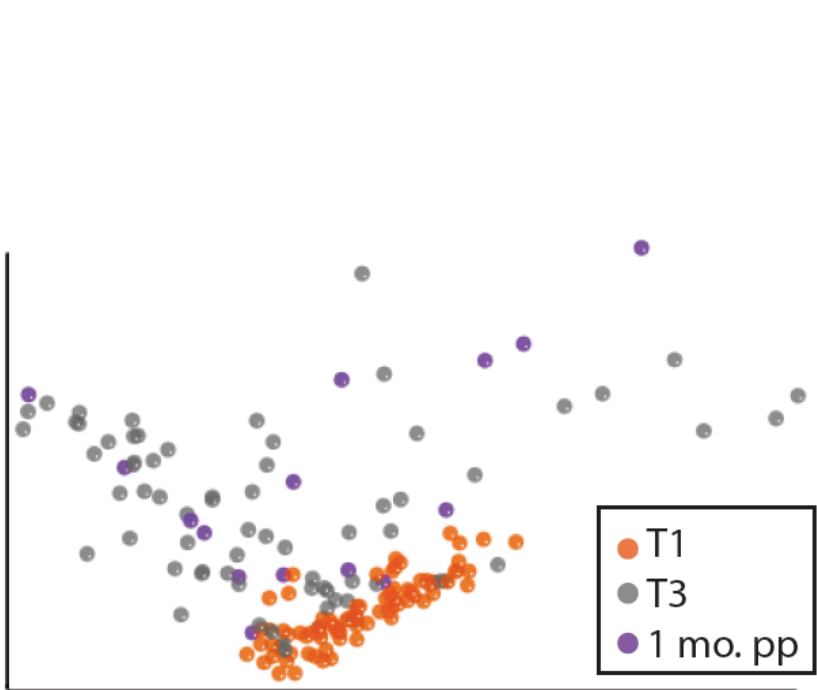
T1



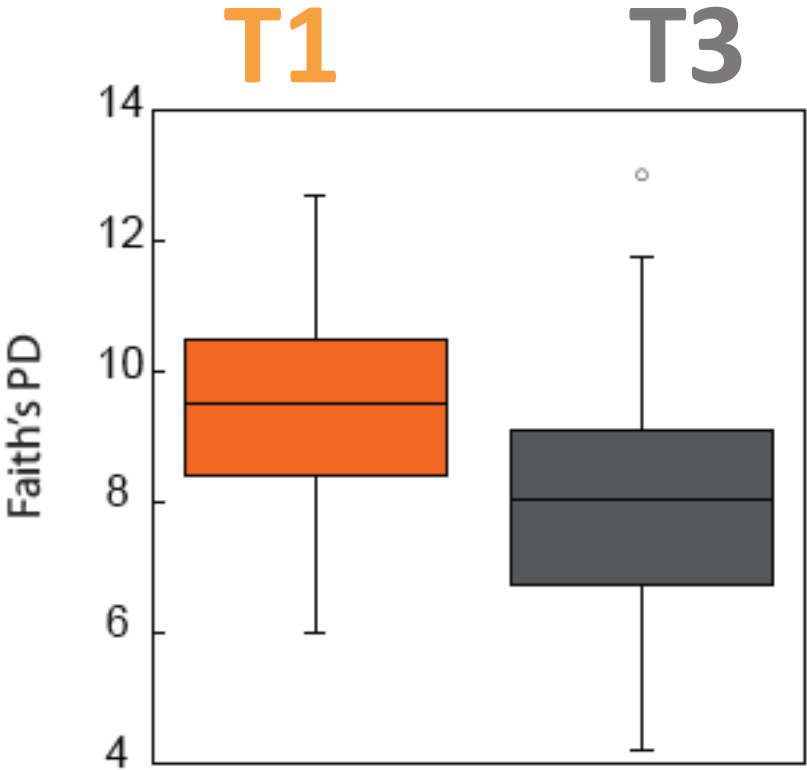
T1: More SCFA producers

T3: More opportunistic pathogens

Each microbiota is depleted in its own way

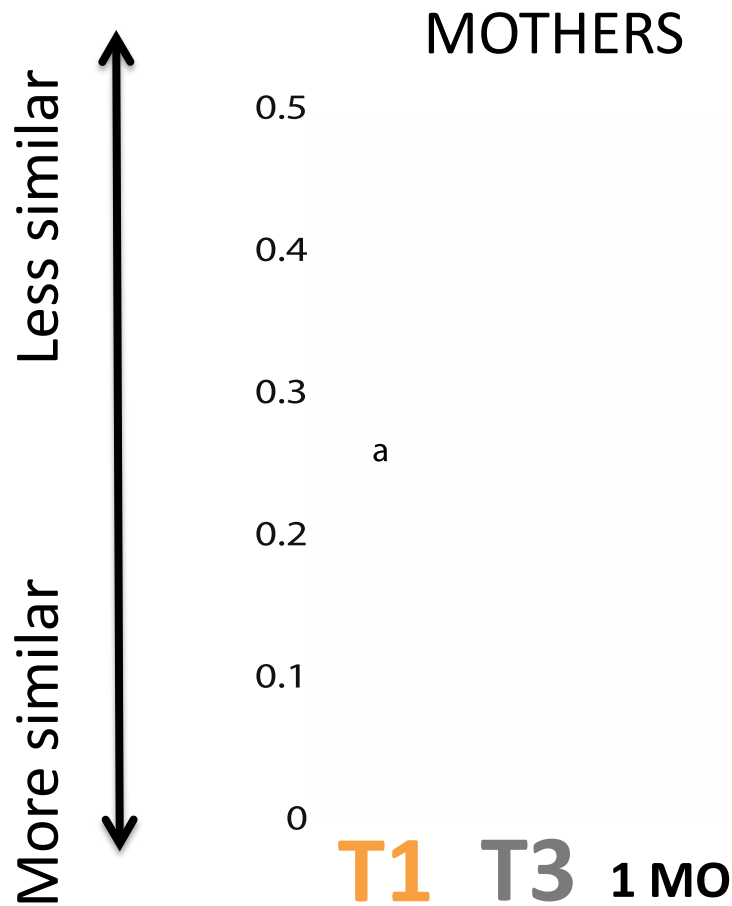


Between individuals
T3: High

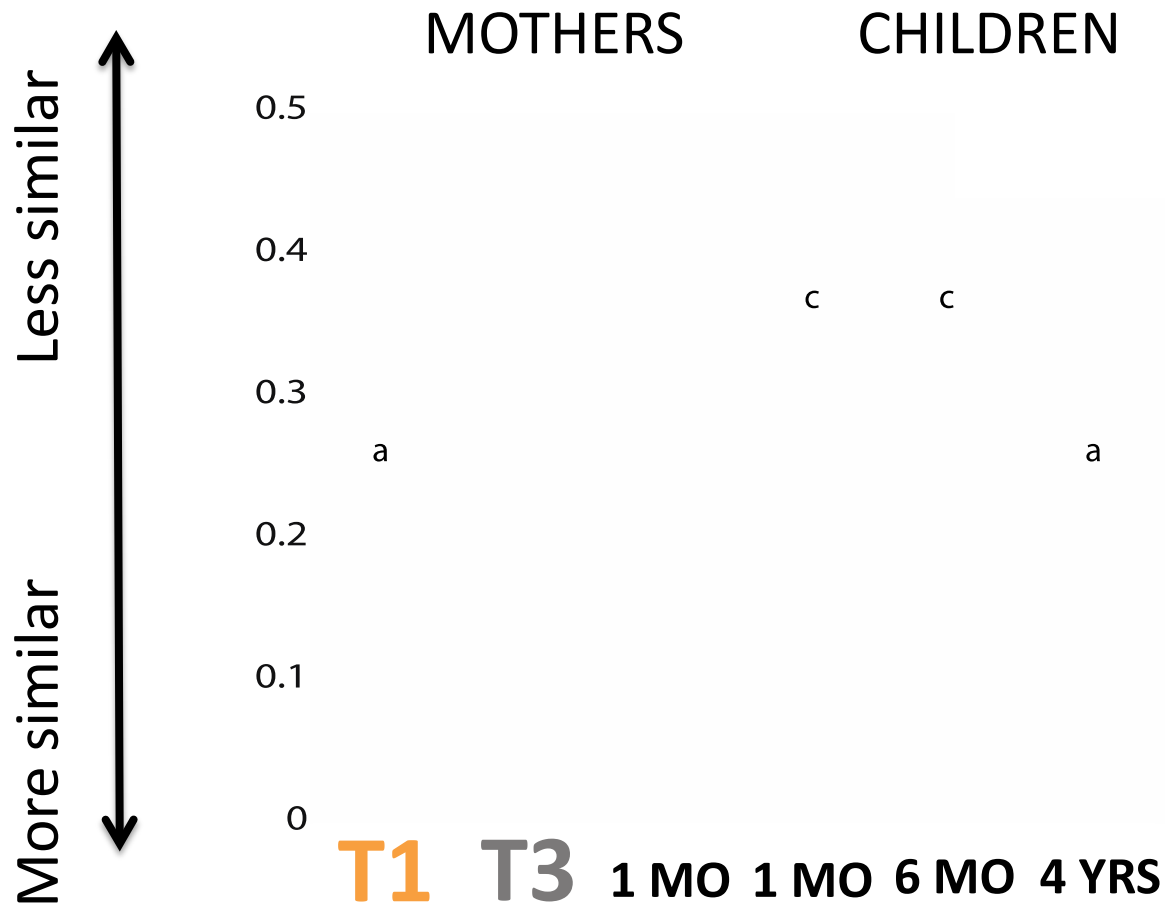


Within individuals
T3: Low

High between-individual diversity persists 1 month post-partum...

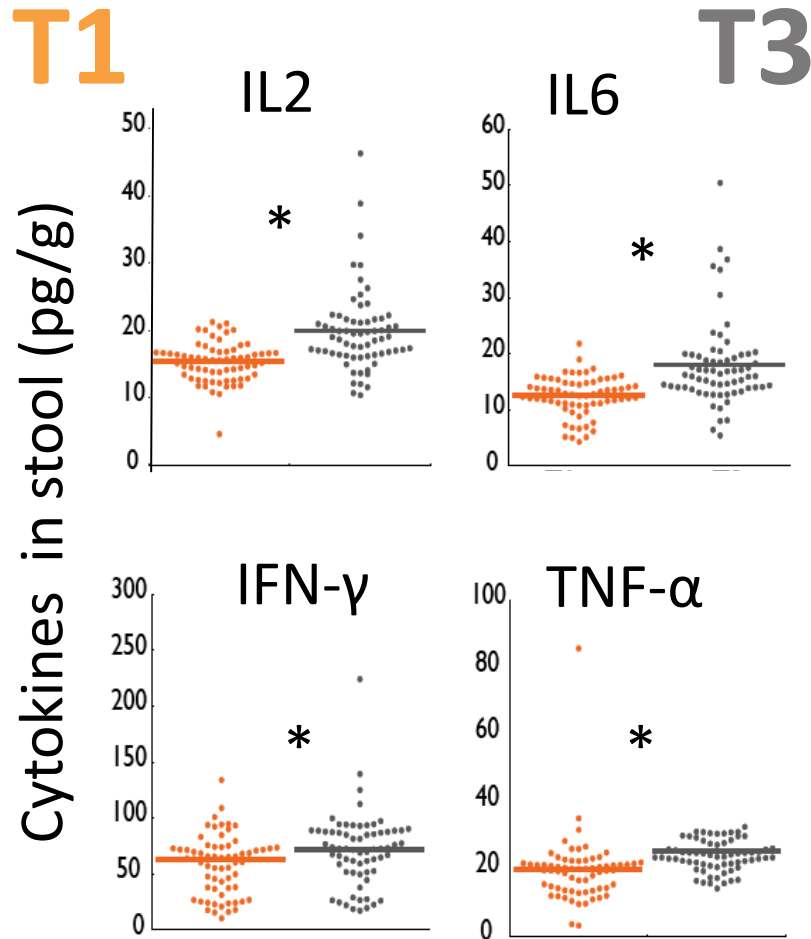


....and in the babies



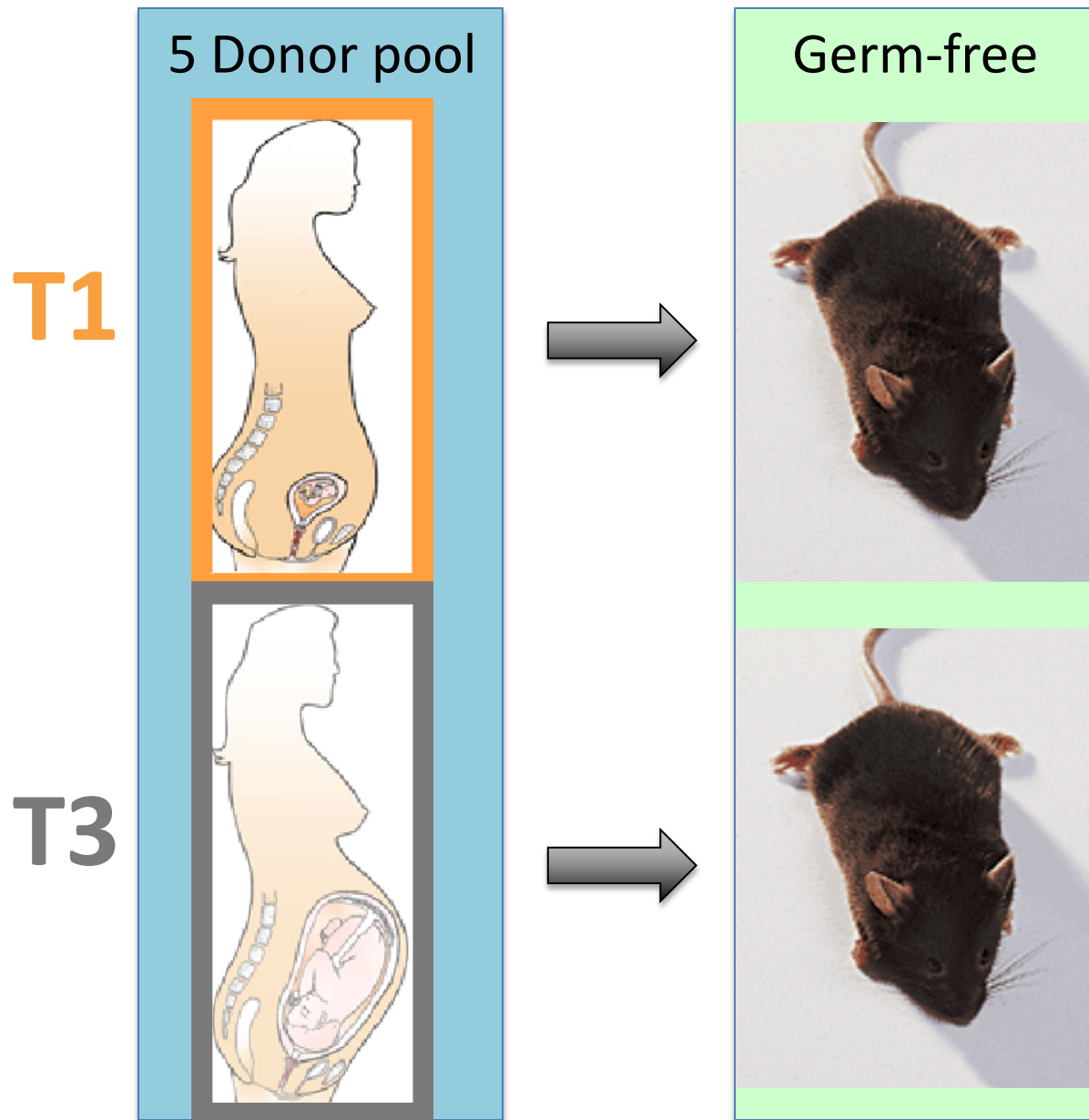
Baby gut microbiotas not more similar to own mother than unrelated mothers
BUT similarities greatest for 4yrs- own mother T1 (p=0.003)

Greater inflammation in T3 stool

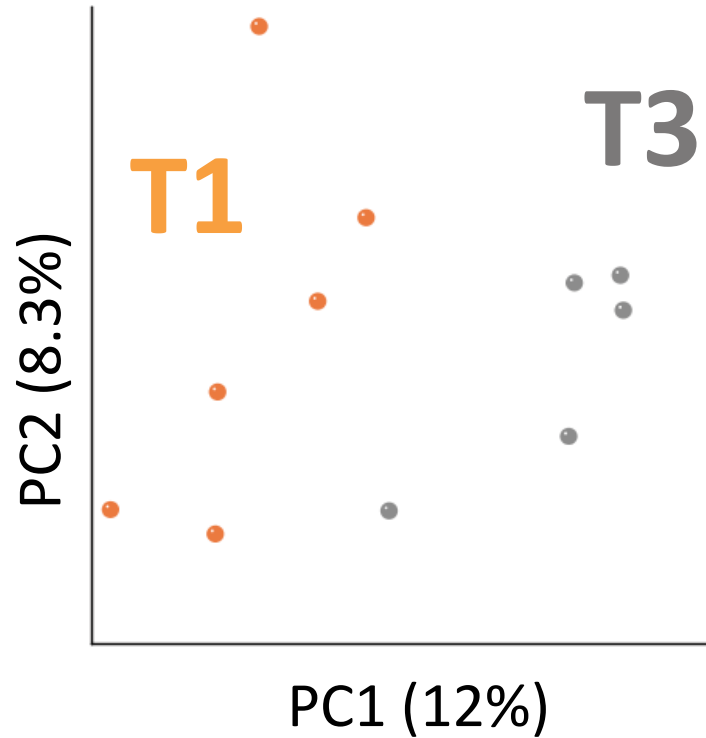


Elevated levels of inflammatory cytokines in T3 stool

Pregnant microbiome transfer to GF mice

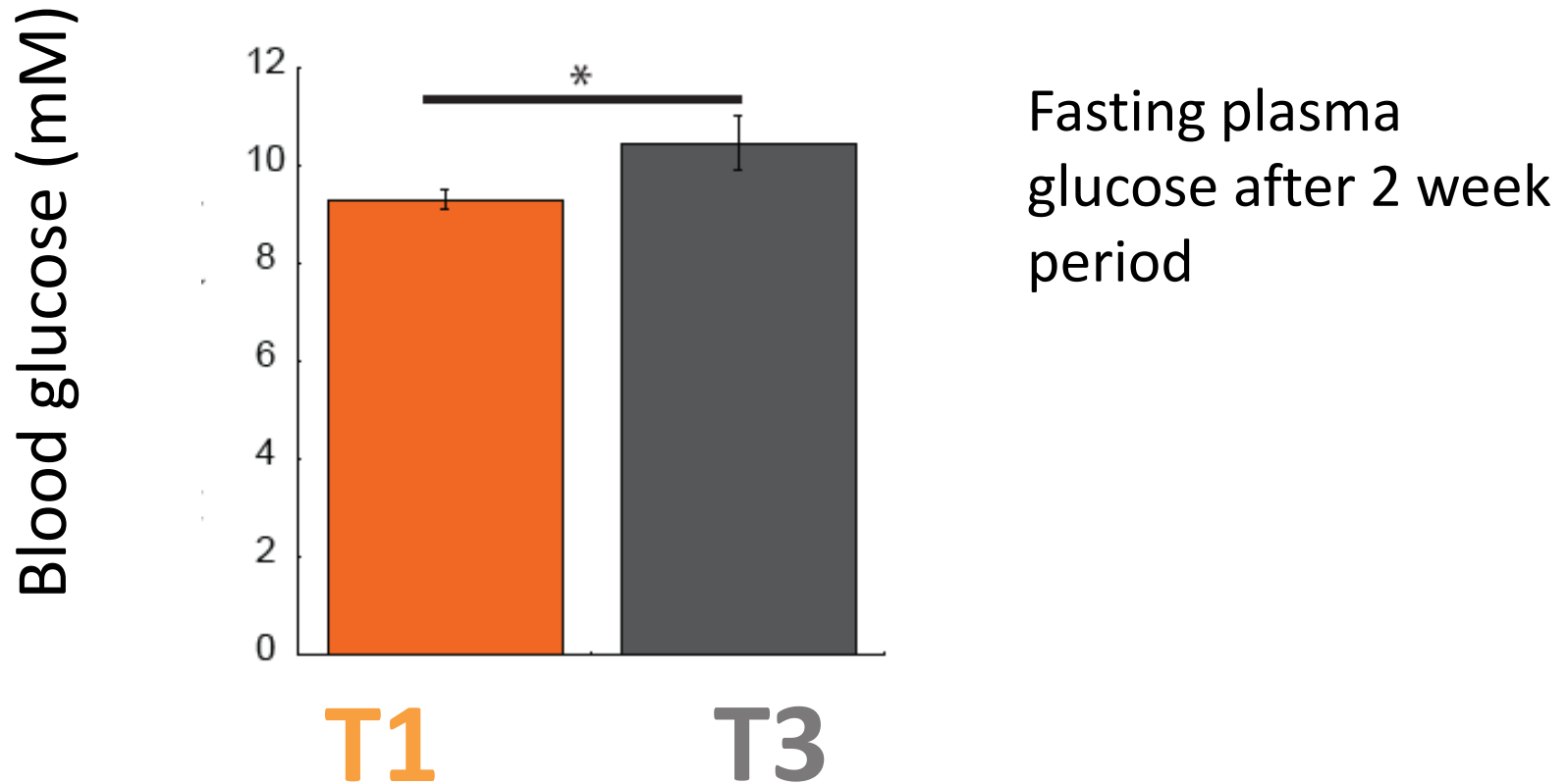


Recipient mice of T3: greater inflammation

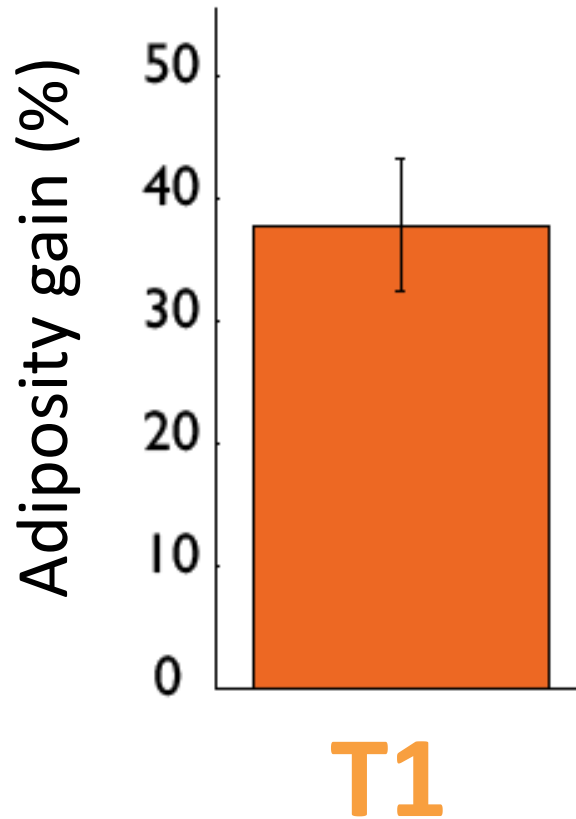


Differences in microbiota between T1 and T3 are maintained for 2 weeks

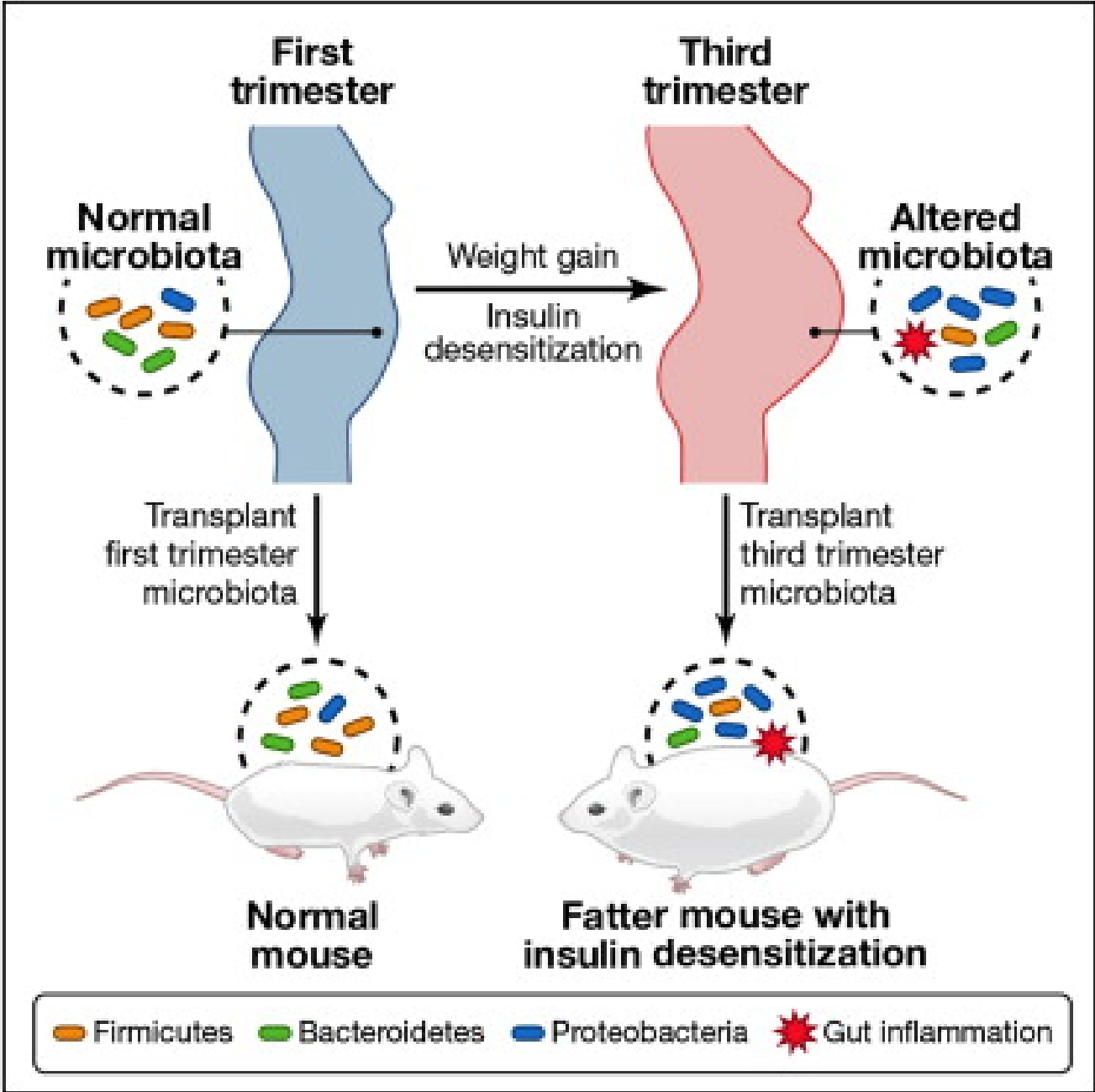
T3 microbiota induce higher blood glucose levels



T3 microbiota make a fatter mouse



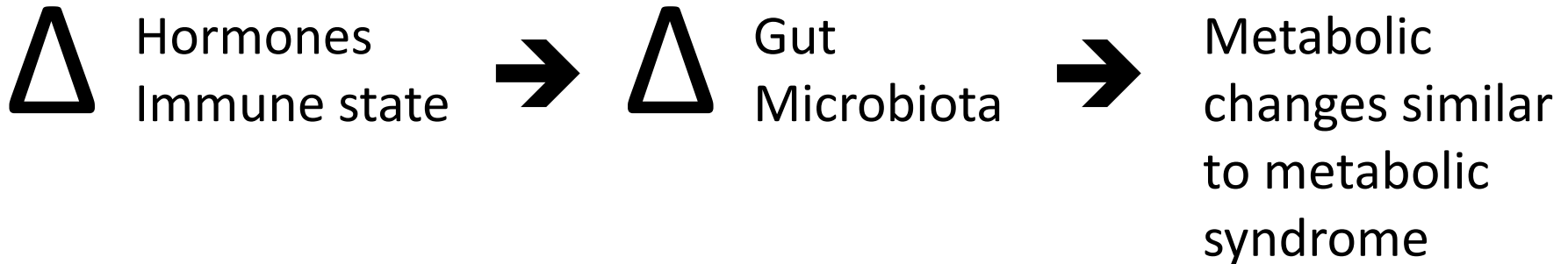
Greater adiposity gain
in T3 recipients after 2
weeks



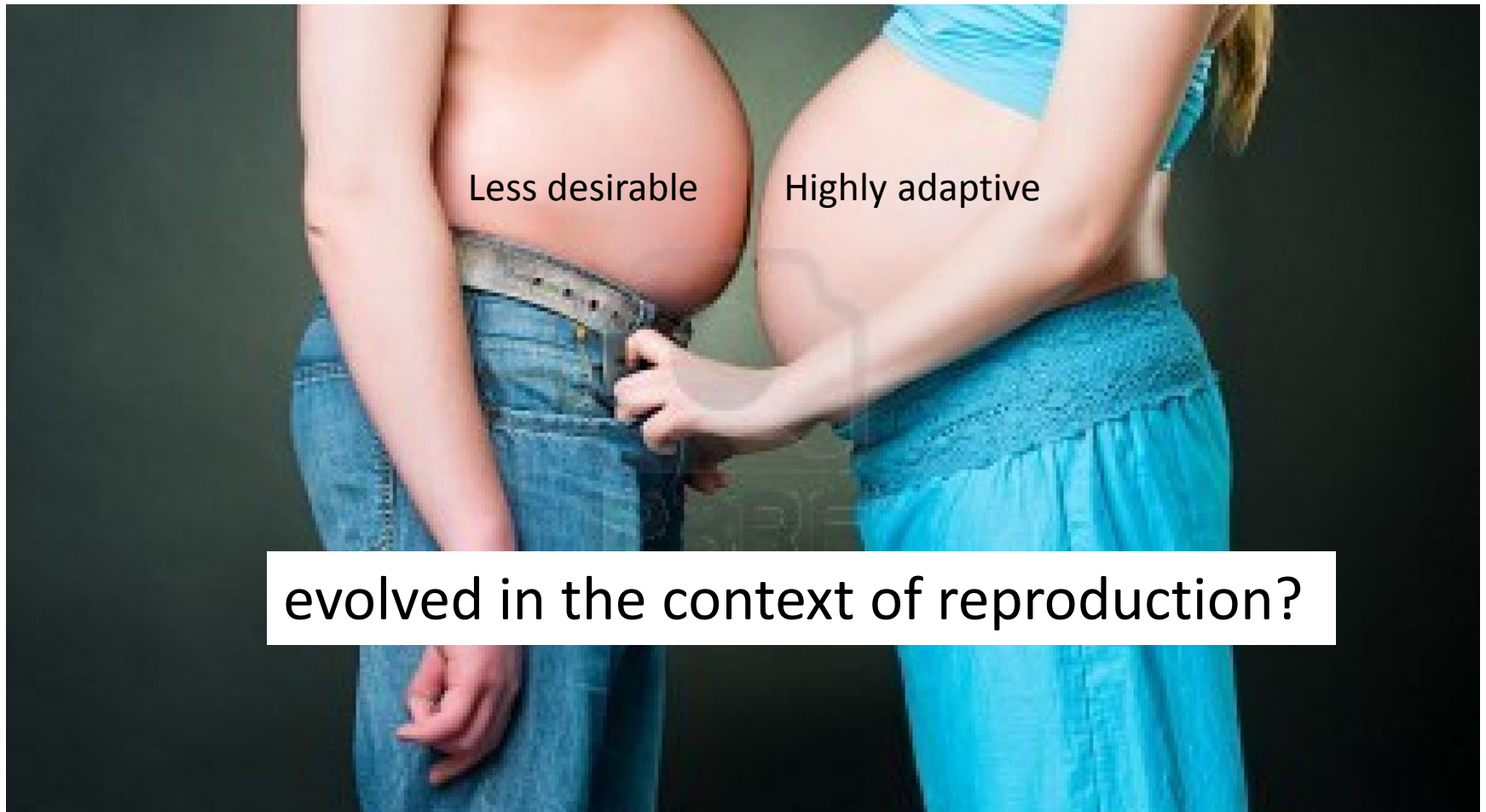
Healthy pregnancy

Metabolic changes include reduced insulin sensitivity, low-grade inflammation

- Highly adaptive in the context of pregnancy
- Are the gut microbes a link in the chain?



Gut microbes impact host metabolism



evolved in the context of reproduction?

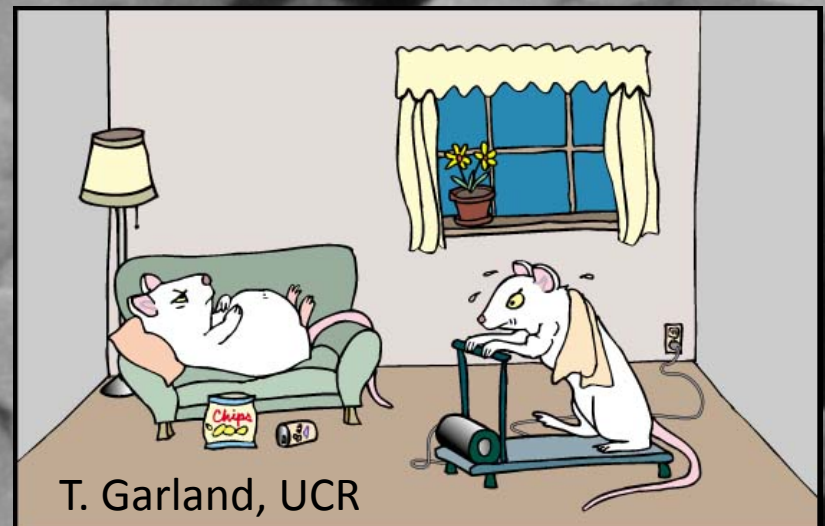
What is the extent of microbial effect on host phenotype?

What is known:

Some aspects of metabolism, immunity, behavior

What is not known:

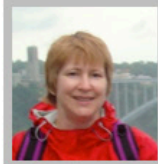
Fertility, longevity, activity, physiology, etc...



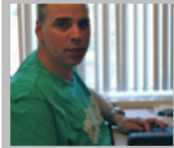
T. Garland, UCR



Ruth E. Ley, Ph.D.
Assistant Professor
re222 at cornell.edu
Profile in Science:
Gut_Reactions.pdf



Beth Bell, D.V.M., Ph.D.
Research Support
Specialist
meb1 at cornell.edu
Animal Research
Specialist and Laboratory
Supervisor



Omry Koren, Ph.D.
Post Doc
ok46 at cornell.edu
Human Microbiome
Project: gut
microbiota and
pregnancy



Sara Di Rienzi, Ph.D.
Post Doc
sdrrienzi at cornell.edu
Microbiota and metabolism



Angela Poole, Ph.D.
Post Doc
ap234 at cornell.edu
Host: gene copy number
variation and the
microbiome



Anders Janzon, Ph.D.
Post Doc
aj53 at cornell.edu
Antibody coating of gut
microbiota



Sha Li, Ph.D.
Post Doc
sl979 at cornell.edu
Gut microbial ecology &
immunity



Ludovic Glotieux
Post Doc, with Maureen
Hanson
lg349 at cornell.edu
Gut microbiome in Chronic
Fatigue Syndrome



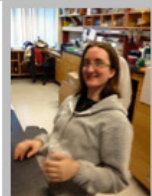
Zhao Jin
PhD Student (Micro)
zj29 at cornell.edu
Rhizosphere functional
genomics



Julia Goodrich
PhD student (Gen & Dev)
jg559 at cornell.edu
GWAS of the gut
microbiome



Wei Zhang, Ph.D.
Visiting Scholar
wz67 at cornell.edu



Jessica Sutter
Research
Technician
js644 at cornell.edu

Selected Collaborators:

USA: Dirk Gevers (Broad Institute)
Andrew Gewirtz, Matam Vijay-Kumar
(Georgia State University), Rob Knight
(CU Boulder, HHMI), Curtis
Huttenhower (Harvard), Lora Hooper
(UT Southwestern, HHMI)

Europe: Tim Spector, Jordana Bell,
Michelle Beaumont (King's College
London), Fredrik Backhed
(Gothenburg University)
Erika Isolauri, Seppo Salminen
(Turku University)

Cornell: Andy Clark, Ran Blekhman,
Alon Keinan, Qi Sun, Robert Bukowski,
Ed Buckler, Jeff Werner, Lars Angenent

THANK YOU:



THE HARTWELL FOUNDATION

BENEFITTING CHILDREN BY
INSPIRING INNOVATION
AND ACHIEVEMENT

