



Person-to-person transmission of the gut microbiome

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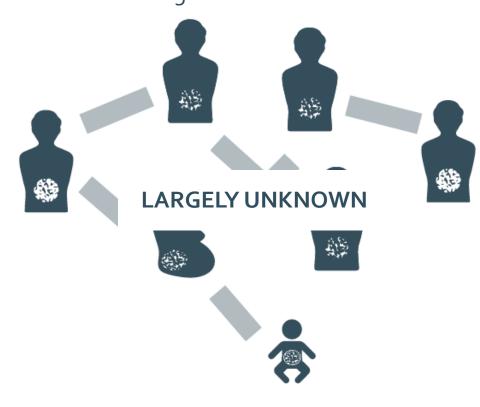


Transmission of the human microbiome

- Known role of the human microbiome in maintaining host health
- Some knowledge on what factors modulate microbiome composition



 How do we acquire such health- and diseaseassociated microorganisms?



How are they **transmitted** and **spread** in populations?

Importance of understanding microbiome transmission

• Fundamental question for microbiome research

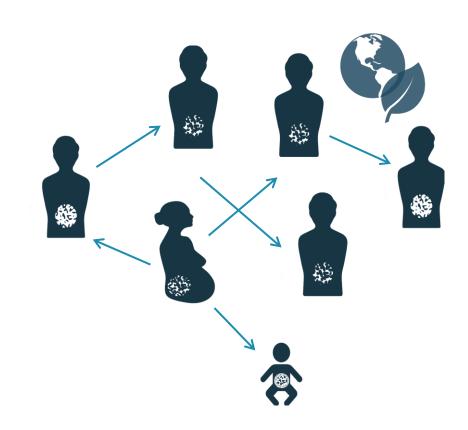
HYPOTHESIS

Science

Are noncommunicable diseases communicable?

Numerous noncommunicable diseases could have a transmissible microbial component By B. B Finlay^{1,2} and CIFAR Humans

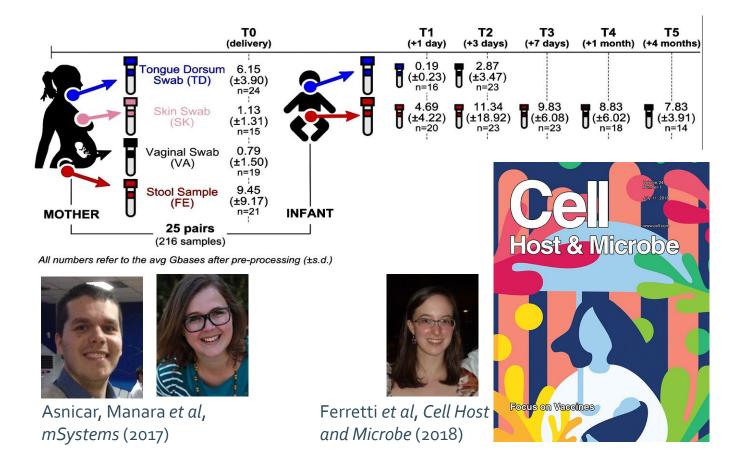
- Potential to alter transmission of health- and disease-associated microorganisms
- Improved microbiota modulations:
 - Timing: early life vs adulthood
 - Composition: specific strains

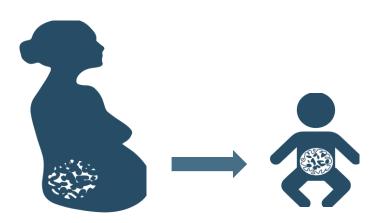


What do we know so far?

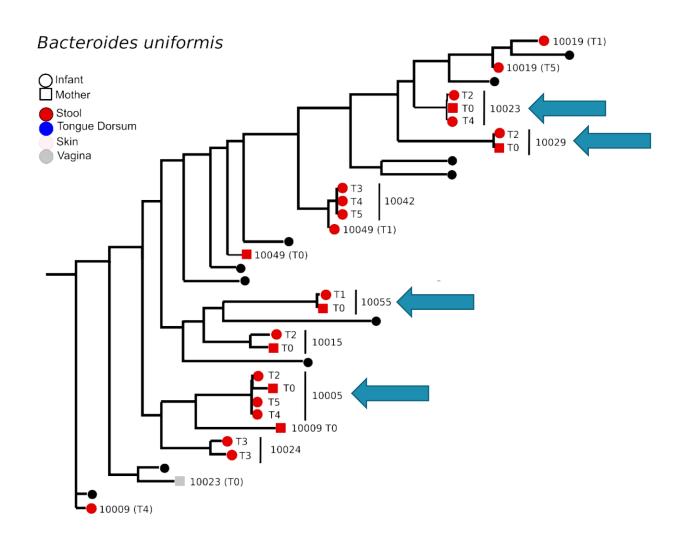
Vertical transmission

• First gut colonizers: maternal microorganisms, followed by microbial succession





Strain-resolved metagenomics

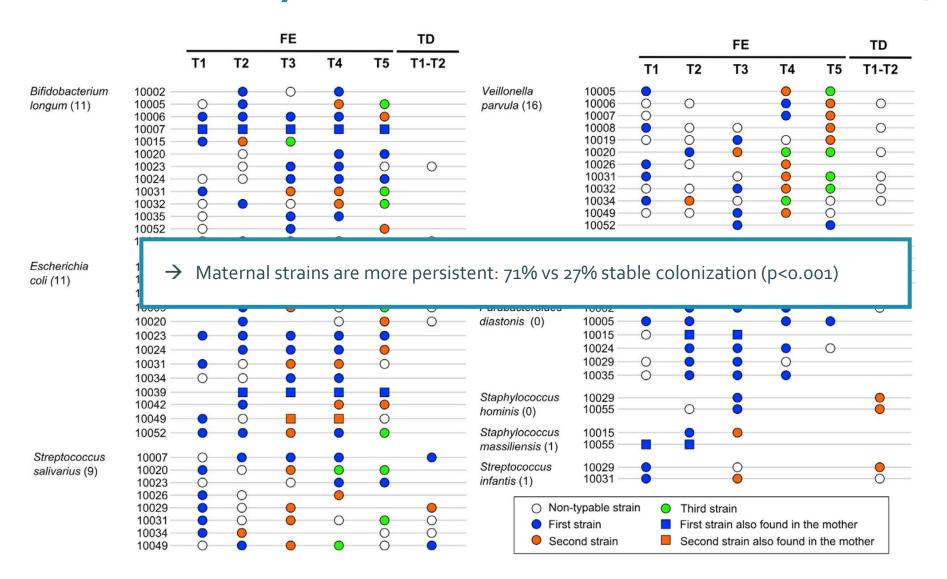


→ Advances in metagenomics:

Strain resolution in

shotgun metagenomic sequencing to identify potential transmission events

Maternally-transmitted strains are more persistent



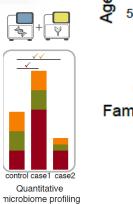
→ But maternal transmission is unlikely to account for all diversity found in adults

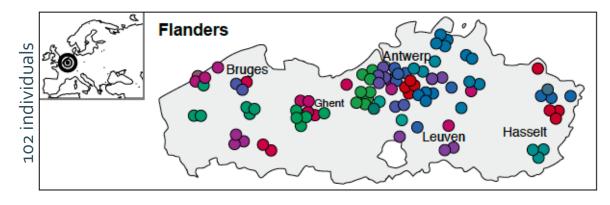
Does transmission also occur across multiple familial generations?

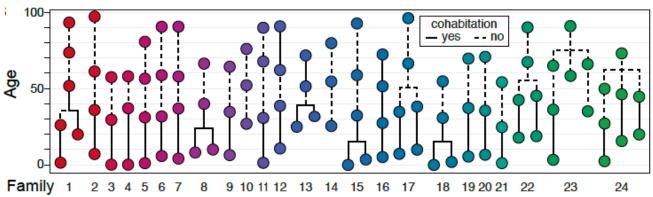
A multigenerational family cohort



- 24 families
- [3:5] generations of women
- [o:98] years old



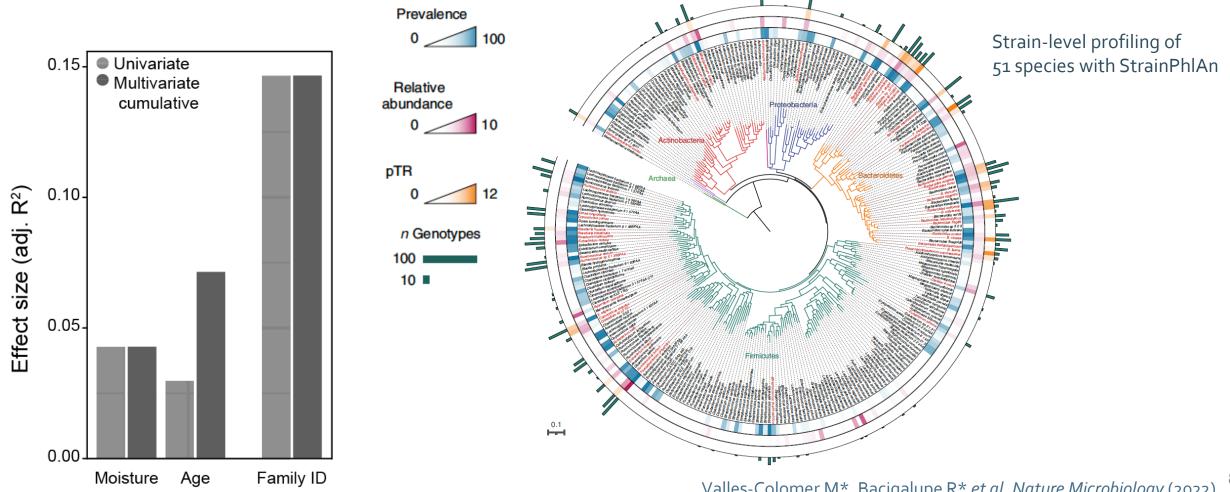




Shotgun sequencing + flow cytometry (QMP) Vandeputte et al, Nature (2017) Vieira-Silva et al, Nature Microbiology (2019)

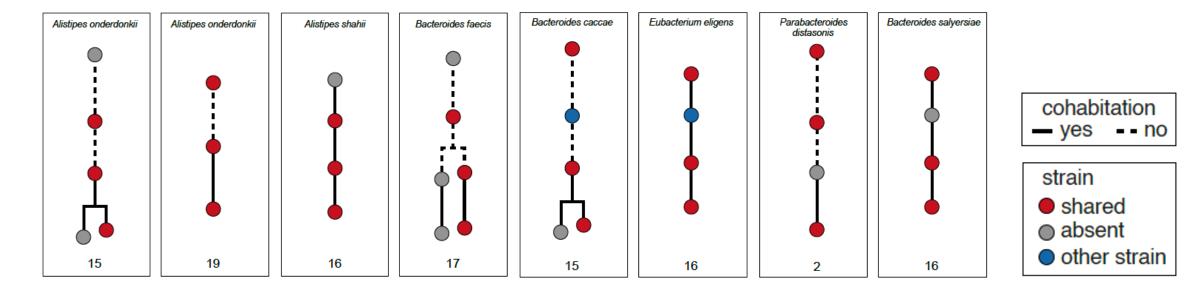
Does transmission also occur across multiple familial generations?

Strain-level profiling



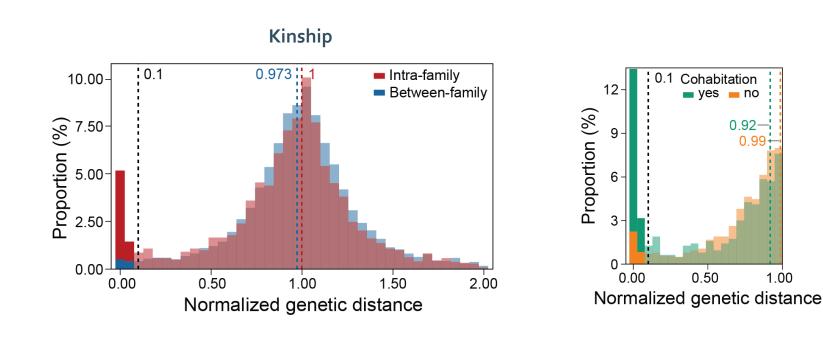
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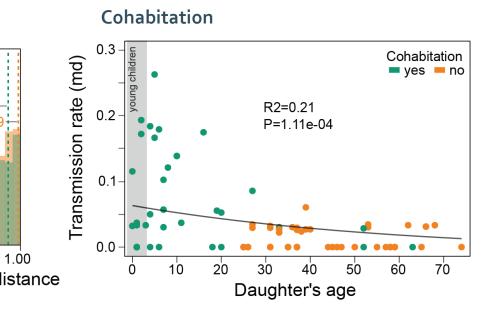
Not frequently, but it does!



Does transmission also occur across multiple familial generations?

But... is that vertical or horizontal transmission?





→ Both?

A large-scale study of microbiome transmission

StrainPhlAn 4 (Blanco-Miguez et al (2022), bioRxiv)



646 SGBs (365 uSGBs) **477,141** strains



55% of profiled species are so-far uncultured

Longitudinal sets

1,676 samples [0]

495 individuals [0]

5 datasets [0]

4 countries [0]

Mother-offspring pairs

3,598 samples [619]

711 pairs [261]

18 datasets [8]

14 countries [3]

Households

1,123 samples [432]

211 households [70]

7 datasets [3]

8 countries [1]

Adult twins

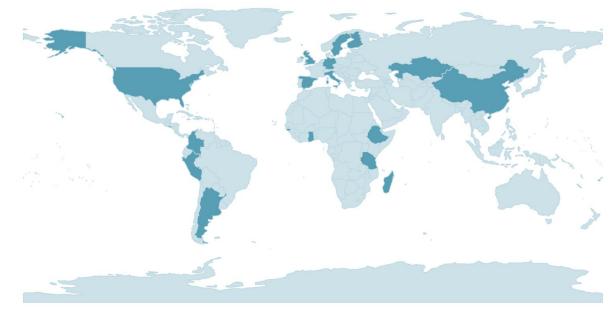
1,734 samples [0]

712 pairs [0]

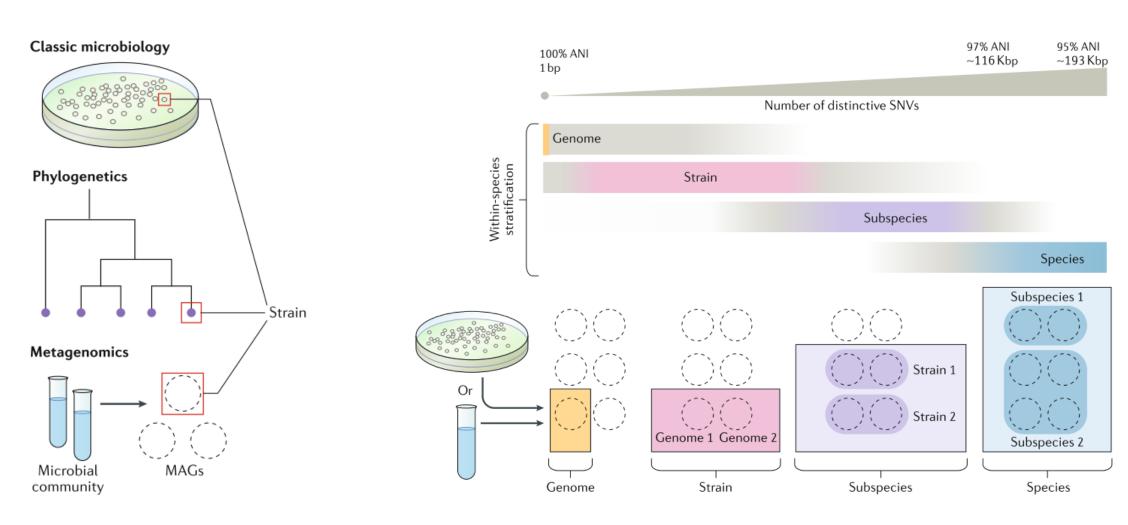
3 datasets [0]

1 country [0]

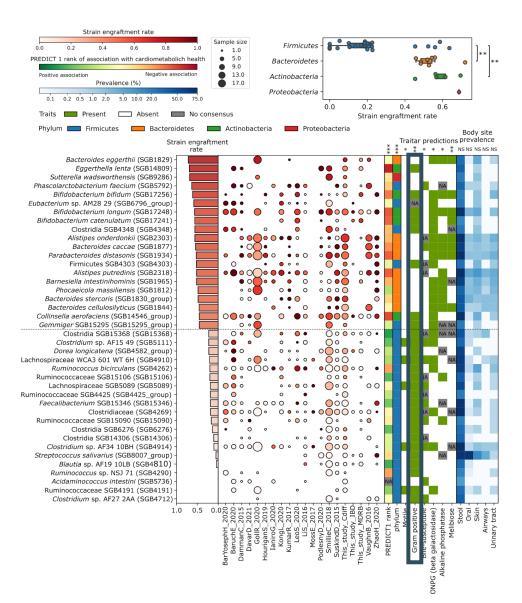
9,715 samples [2,880 novel] 31 datasets 20 countries



Using strains to infer transmission events



... and also strain engraftment upon FMT



- 1,255 metagenomic samples
- 203 FMT procedures (donor, recipient-pre, recipient-post)
- Any disease/condition

- → Strain engraftment linked to FMT success
- → Combined administration route for best performance
- → Antibiotic pre-treatment
- → Bacterial phenotypic characteristics
- → Predictable (ML)

Take home messages

- Evidence of extensive **vertical** but also **horizontal** transmission of the microbiome
- Sharing an **environment** plays a key role (cohabitation)
- Microbiome transmission is not left to chance:
 - Dispersal specialists (with certain phenotypical properties) are transmitted more frequently

Thank you!

The Laboratory of Computational Metagenomics



http://segatalab.cibio.unitn.it

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DI TRENTO E ROVERETO



