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Bifidobacterium Deficit in U.S. Infants: Translating Microbiome Science into Probiotic Solutions

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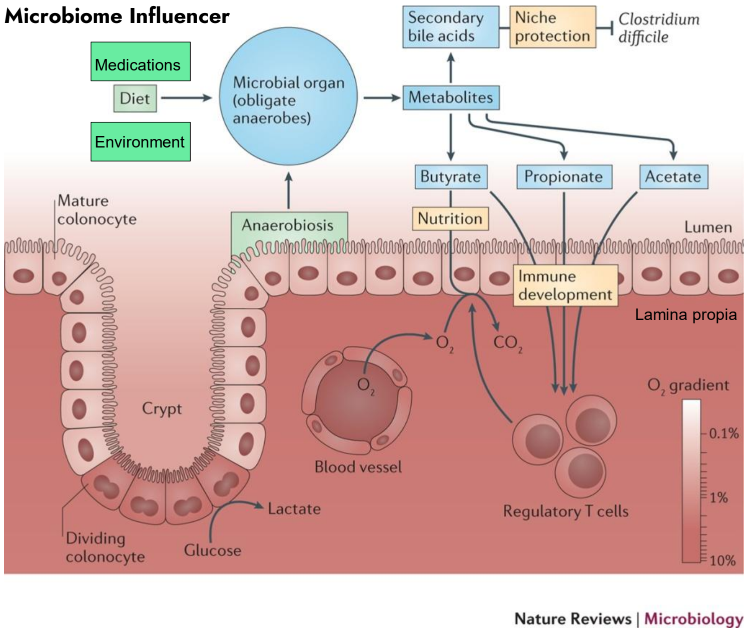
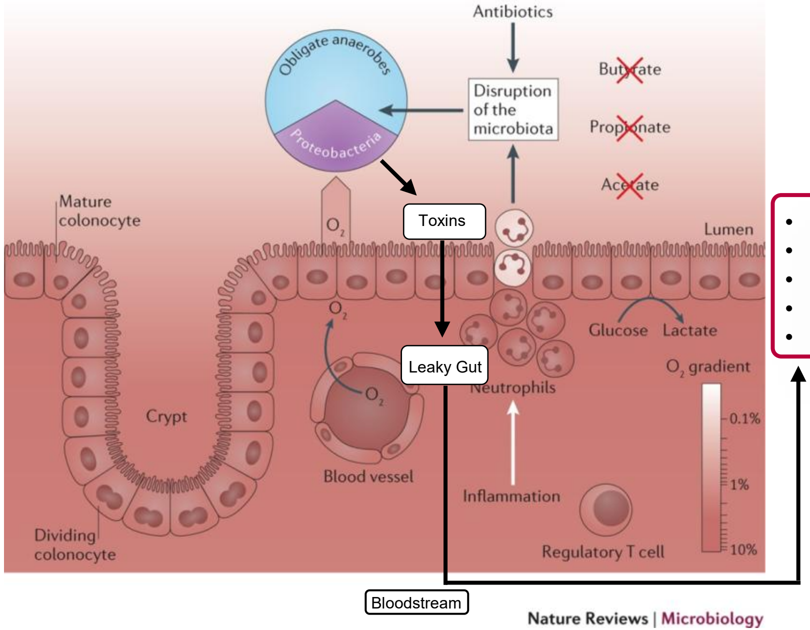
Gut dysbiosis is associated with many noncommunicable diseases (NCDs)



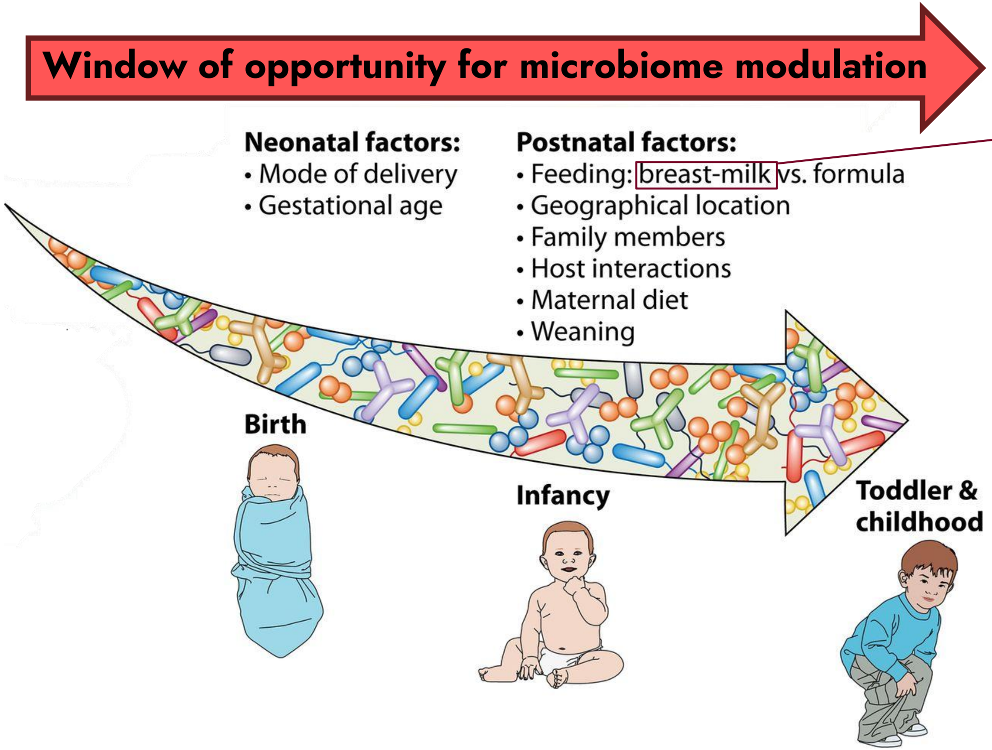
Healthy



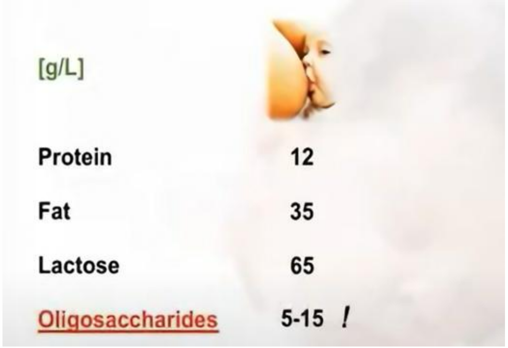
- Asthma
- Obesity
- Arthritis
- Diabetes
- Cancer

Dysbiosis

Factors influencing the microbiome

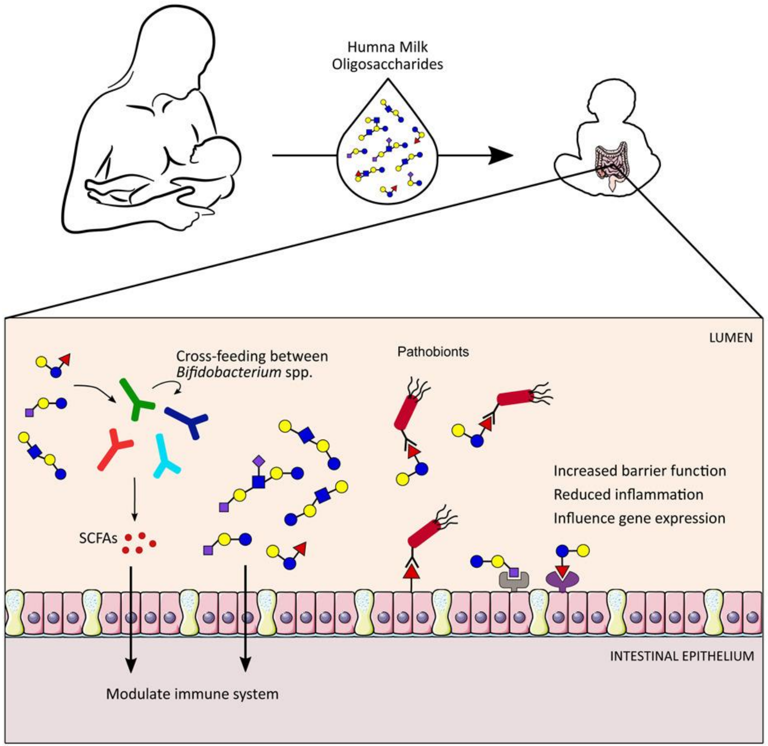


Macromolecules in human milk



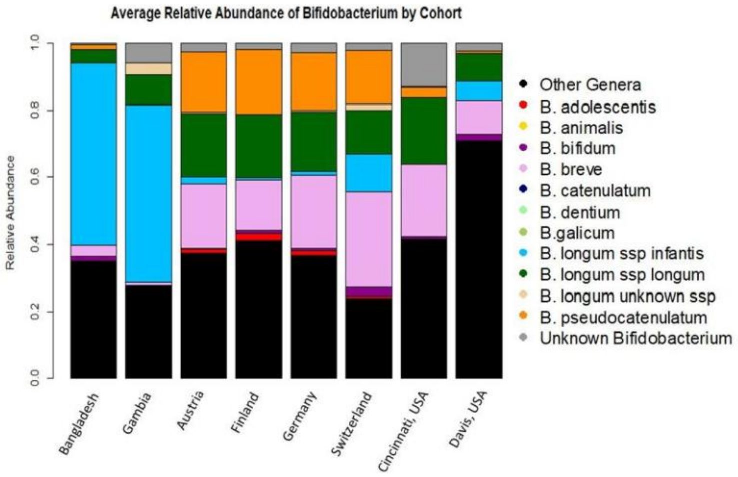
Dr. Lars Bode. University of California San Diego

Human milk oligosaccharides (HMOs) in Infants' health



Masi and Stewart. iScience. 2022

Bifidobacterium infantis disappearing in Western populations



Taft et al. Nutrients. 2022

Article | Open access | Published: 24 June 2025

Bifidobacterium deficit in United States infants drives prevalent gut dysbiosis

John B. Jarman, Pedro J. Torres, Sean Stromberg, Hirokazu Sato, Caroline Stack, Angelica Ladrillono, Shannon Pace, Natalia Livier Jimenez, Robert J. Haselbeck, Richard Insel, Stephen Van Dien & Stephanie J. Culler

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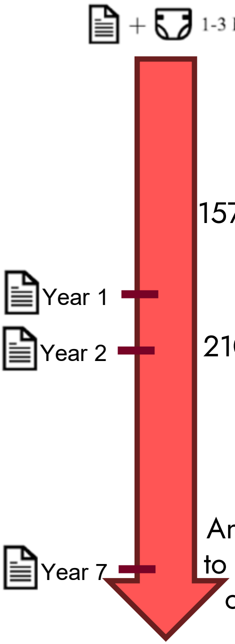
My Baby Biome was designed to deliver novel biomarkers specifically for infant probiotic development



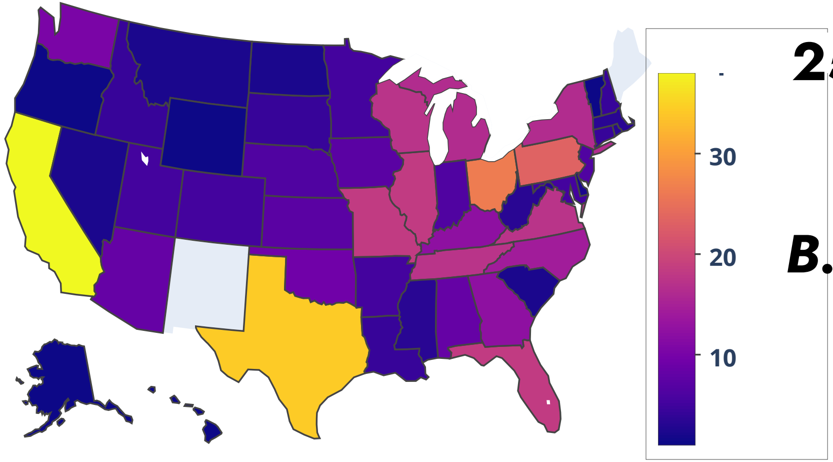
412 samples sequenced with metadata

157 samples evaluated with Metabolomics

210 provided longitudinal metadata

Annual lifestyle questionnaire to evaluate atopy, obesity and other health developments

Largest US study to map the infant microbiome

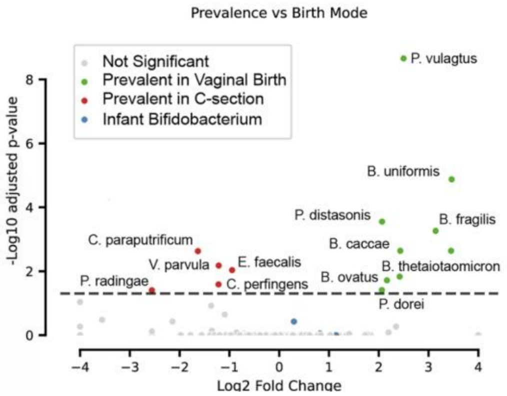


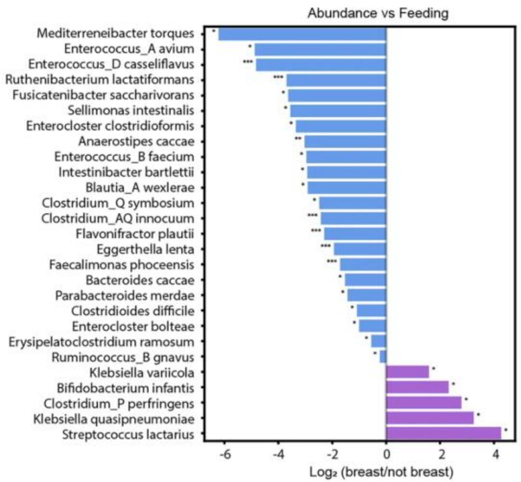
25% of infants lack *Bifidobacterium*

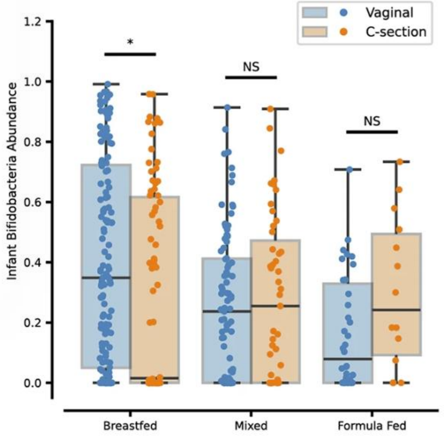
***B. infantis* observed in only 8% of samples**

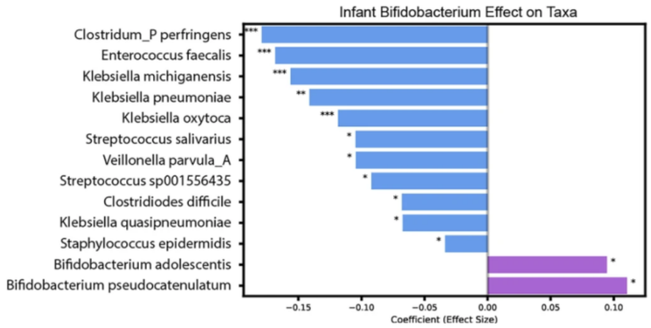
Colonization of *Bifidobacterium* species in the infant gut influenced by priority and niche effects

- **Birth mode impacts prevalence**
- **Feeding mode impacts abundance**: breastfeeding increases *Bifidobacterium* and other HMO consumers including potential pathogens
- **Bifidobacterium acquisition not tied to birth mode**: suggest environmental sources
- *C. perfringens* increases most when infant lacks Infant *Bifidobacterium*



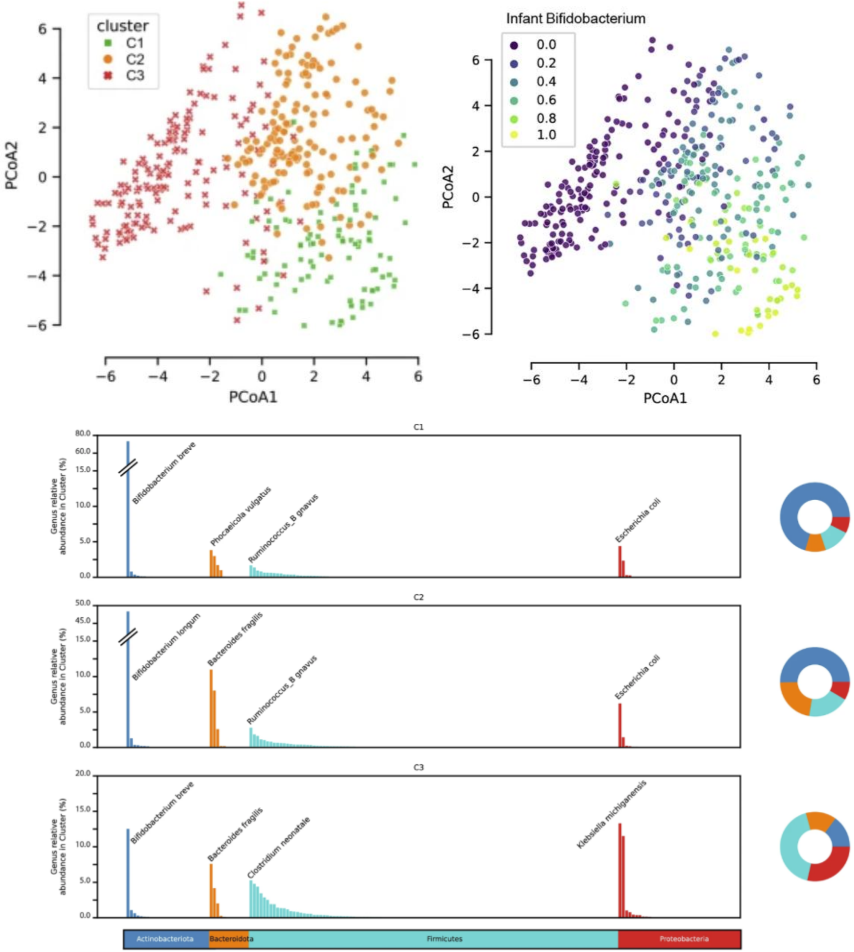






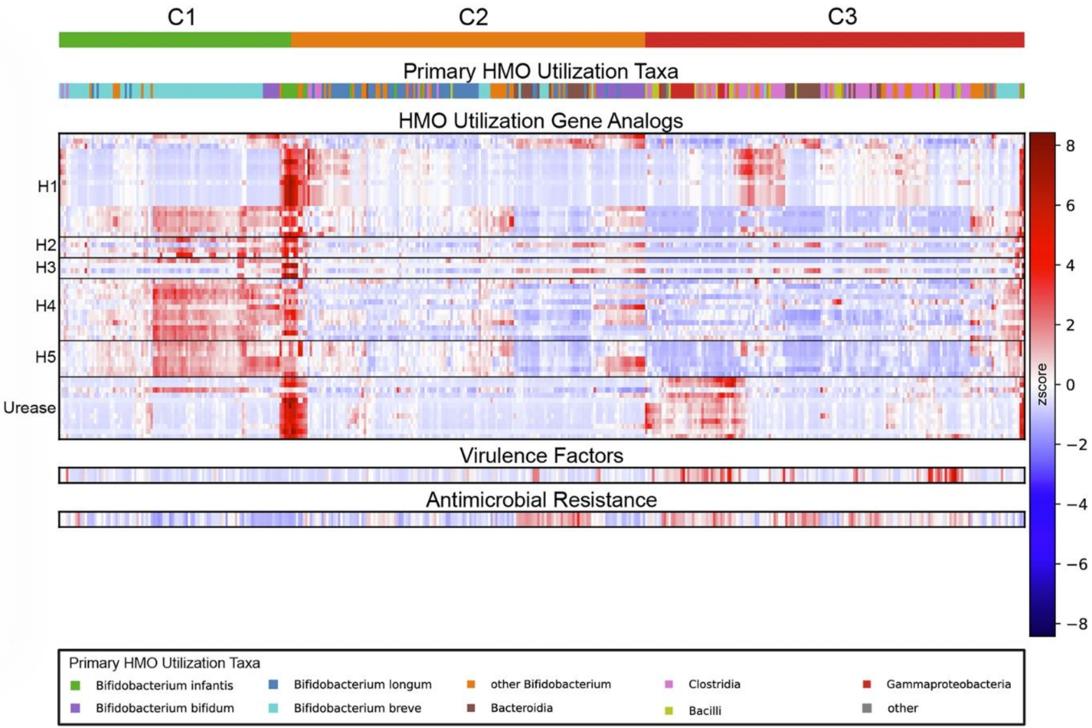
My Baby Biome reveals three infant enterotypes driven by *Bifidobacterium* species

- **C1 (24%)**: Healthy, *Bifidobacterium*-rich (*B. breve*), breast fed dominant
- **C2 (37%)**: Unhealthy, enriched *B. longum* and *Bacteroidota*, vaginal birth dominant, adult like microbiome
- **C3 (39%)**: Unhealthy, enriched in *Firmicutes/Proteobacteria*, opportunistic pathogens, C-section dominant



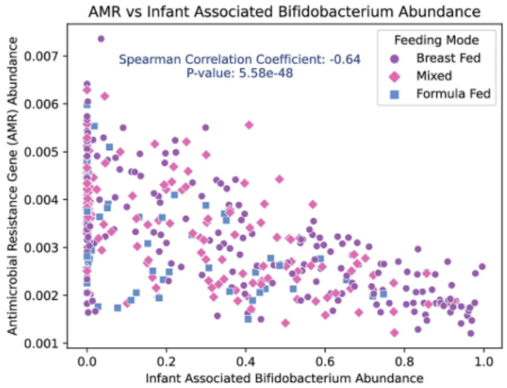
HMO utilization, antibiotic resistance and virulence factor patterns differ across enterotypes

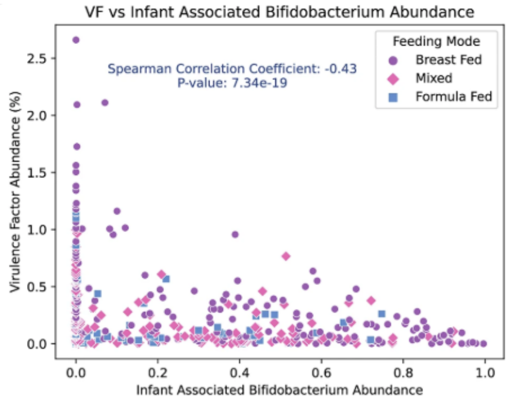
- **C1**: *B. breve* top and broad HMO user
- **C2**: *B. longum* top but reduced HMO clusters (H4,H5)
- **C3:** *Clostridia* top HMO consumer, limited functional breadth, high Urease abundance
- **Dysbiosis indicators:** AMR and virulence factor (VF) genes highest in C3, intermediate in C2, lowest in C1



Loss of Infant *Bifidobacterium* associated with increased antibiotic resistance and virulence factors

Suggest a protective association of infant *Bifidobacterium*, highlighting its potential importance in shaping a healthier microbiome

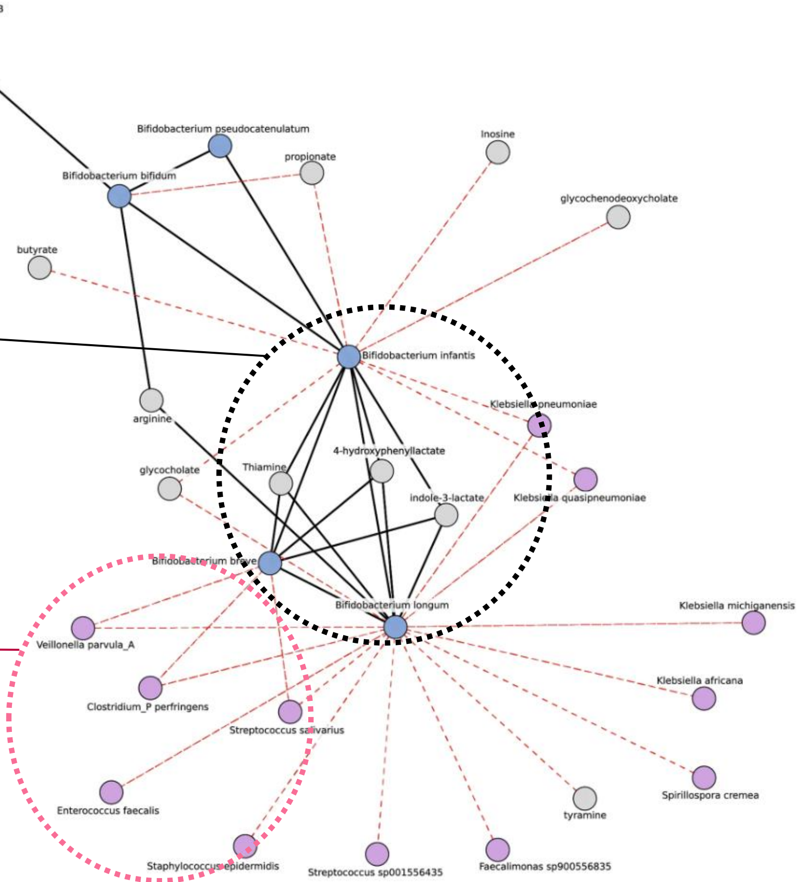




Network analysis reveals microbiota-metabolite patterns of health in infant microbiomes

Complementary roles of *B. breve, B. longum* and *B. infantis* **promote immune regulation via metabolism**

B. breve and *B. longum* **suppress potential pathogens like C. perfringens**



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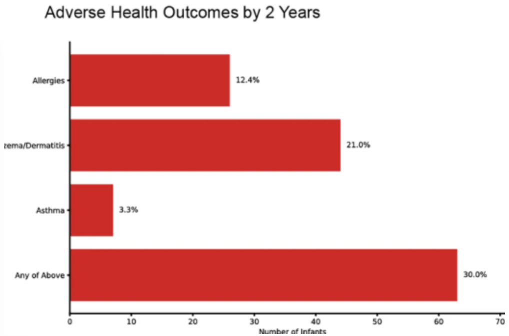
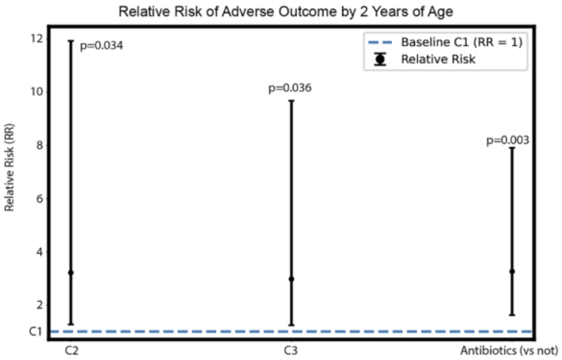
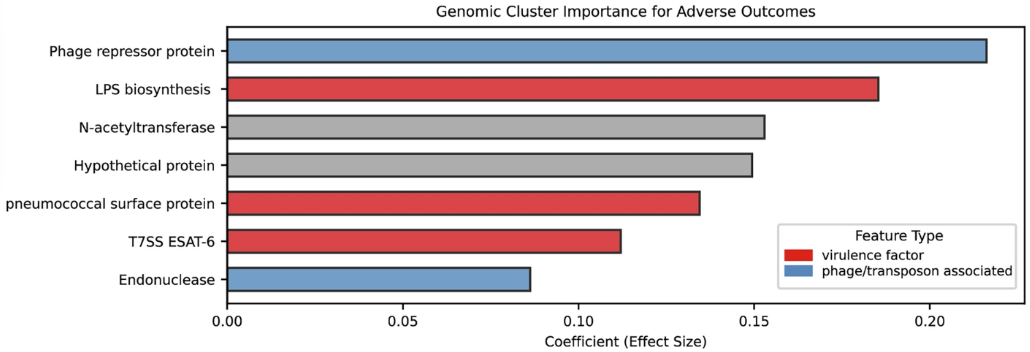
Infant microbiome features predict 2-year health outcomes

- **Cohort**: 210 surveys at age 2, 54% antibiotic use, 30% adverse outcomes
- **Microbiome clusters and risk:** Relative to C1, C2 (3.2× risk) and C3 (3.0× risk) were significantly associated with higher adverse outcomes, similar in magnitude to early antibiotic exposure (3.3× risk)
- **Functional features linked to adverse outcomes:** multiple phage/transposon-associated and virulence factor genes.







Conclusion

- **Large U.S. infant cohort**: Identified three distinct enterotypes — *Bifidobacterium*-dominated, high *Bacteroidota*, and *Proteobacteria/Firmicutes*-dominated.

- **Loss of cornerstone microbes**: ~25% of infants lacked detectable *Bifidobacterium*; *B. infantis* absent in 92%, replaced by mucin-utilizers or potentially pathogenic taxa (e.g., C. perfringens).

- **Functional consequences**: Loss of *Bifidobacterium* → disrupted HMO utilization, increased AMR and virulence factor genes, and shifts in the metabolome.

- **Clinical implications**: By age 2, 30% of infants had allergies, eczema, or asthma; clusters C2/C3 (76% of cohort) carried higher risk. B. breve abundance associated with strong protective effect.

- Future directions: Longitudinal monitoring to 7 years will clarify long-term health impacts; early interventions targeting microbiome restoration may offer preventive potential against NCDs.

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Thank You!

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