The infant microbiota hopscotches between community states toward maturation — longitudinal stool parameters and microbiota development in a cohort of European toddlers

Intze E et al. (2025) ISME Communications, Volume 5, Issue 1, ycaf016

Scanning the QR code will take you directly to the original study

Background and Aim

Development of the gut microbiome is critical during early life and is associated with infant health.

Trajectories of the infant faecal microbiota have been studied either at a small scale, during the first 20 months of life, or with limited metadata.

Here we investigated microbial profiles, predicted functional capacity and faecal parameters of 540 European infants on four occasions during the first three years of life (1,353 samples; NCT02221687). Faecal microbiota profiles from 216 young adults were included additionally and used as a reference for mature communities.

Material and Methods

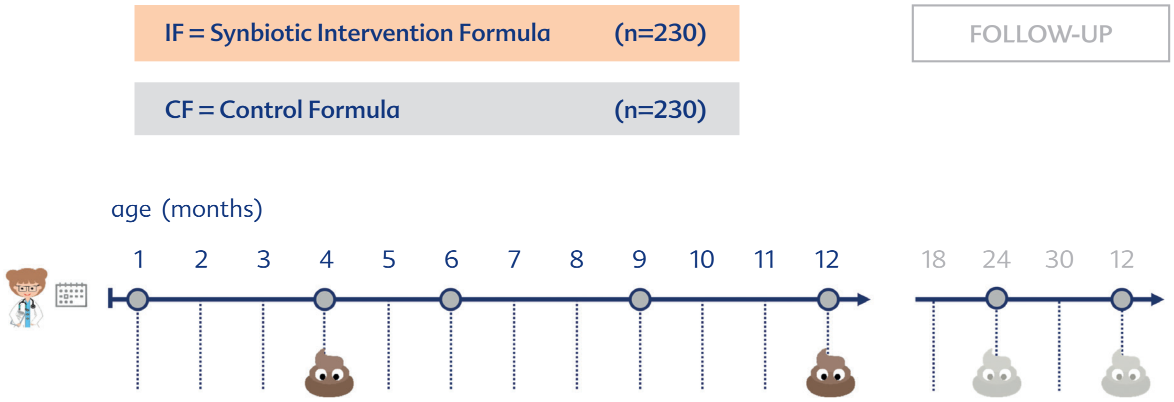
Infants were randomised to one of the two formula groups. The synbiotic formula contained *Limosilactobacillus (L.) fermentum* CECT 5716 ($\geq 2\text{x}10^8$ cfu/day) + Galactooligosaccharides (GOS). The trajectory of the infants' faecal microbiota (4, 12, 24, 36 months) was assessed by 16S rRNA sequencing. In addition to previous data[1], the effects of age, mode of birth and diet on community assembly and predicted functional capacity (PICRUST2) was determined.

Intervention Phase

HM = Human Milk group (n=79)

IF = Synbiotic Intervention Formula (n=230)

CF = Control Formula (n=230)



Results

At 36 months of age, microbiota profiles and predicted functional capacity converged to adult profiles. The influence of external factors on the microbiome changed over time.

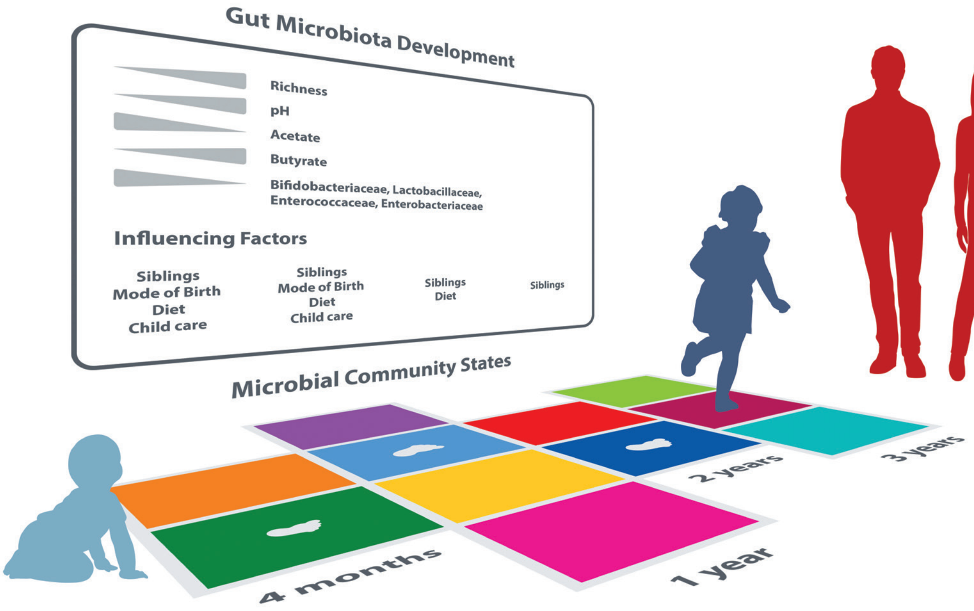
At 4 months, a significant difference between the interventions was observed with **the IF group showing a slightly reduced distance to the HM group** compared to CF. No differences were found after this time point. Distinct gut microbiota clusters were observed that differed at each stage of maturation and were not predictable but rather hopscotching between different states.

All diet groups displayed the same trajectory of maturation towards adult profiles. At 36 months of age, the profile of the CF group was significantly different from the HM group ($p = 0.01$), whilst **no significance was found between the IF and HM infants** ($p = 0.147$). Effects of mode of birth and diet within the clusters were seen at 4 months, with caesarean born infants receiving synbiotic formula showing a reduced distance to the HM groups.

Conclusion

This work provides new longitudinal data on the infant gut microbiome in relation to early diet and later microbial trajectory and infection incidence.

Graphical abstract



Reference:

1 Lagkouvardos et al. AJCN 2023; 117: 326–339

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