

Compiling an early life human gut microbiome atlas and identification of key microbial drivers.

Autori: Tarracchini C, Longhi G, Gennaioli E, Muscò A, Rizzo SM, Viappiani A, Vitale SG, Mancabelli L, Lugli GA, Angioni S, Turrone F, van Sinderen D, Milani C, Ventura M

Rivista: NPJ biofilms and microbiomes

DOI: 10.1038/s41522-025-00868-7

PMID: 41350579

ABSTRACT

During the first year after birth, the infant gut microbiome undergoes a rapid and profound compositional and functional transformation, impelled by an intricate network of intrinsic and extrinsic factors. This process results in increased taxonomic and functional diversification, alongside greater interindividual variability. To better understand this early-life ecosystem, this study assessed the interindividual variability of the infant gut microbiome using a comprehensive infant gut microbiome database of 5288 fecal metagenomic data from healthy, full-term infants across various geographical locations. Our study identified six reference microbial communities, termed Early-Life Community State Types (ELi-CSTs), which not only capture specific compositional profiles and heterogeneity of the infant gut microbiome, but also record the extensive transformation experienced by this developing microbial community during the first year of human life. Indicative Species analysis and Random Forest modeling assisted the precise identification of unique, key taxonomic signatures that are critical to the structure of each ELi-CST, highlighting microbial taxa with pivotal roles in shaping the infant gut microbiota. To complement these findings, we established a bacterial biobank through dedicated cultivation efforts of the infant microbiota, comprising 182 genome-sequenced isolates corresponding to key taxa involved in early life gut microbiota assembly. This biobank provided the basis for co-cultivation experiments combined with transcriptome analyses, thereby enabling *in vitro* investigations into microbial cross-talk among key modulators, and yielding novel insights into the molecular interactions and cooperative dynamics behind early microbiome development.