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Total number of authors:

12

Published in:

The Danish Microbiological Society Annual Congress 2023

Publication date:

2023

Document Version

Publisher's PDF, also known as Version of record

[Link back to DTU Orbit](#)

Citation (APA):

Yang, L., Shah, S., Kovačić, I., Russel, J., Mestre, M. R., Zachariasen, T., Krogfelt, K. A., Thorsen, J., Nesme, J., Stokholm, J., Sørensen, S. J., & Trivedi, U. (2023). Longitudinal characterization of escherichia coli in the infant gut microbiome. In *The Danish Microbiological Society Annual Congress 2023: Abstract book* (pp. 15-15). Article 10 The Danish Microbiological Society.

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ORAL SESSION 5

[10] LONGITUDINAL CHARACTERIZATION OF ESCHERICHIA COLI IN THE INFANT GUT MICROBIOME

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Introduction: The infant gut microbiome undergoes dynamic changes during the first year of life, with the initial colonization by facultative anaerobes like *Escherichia coli* giving way to strict anaerobes. Despite being a pioneer species of the human gut, information on the establishment and maintenance of *E. coli* at the strain-level in the infant gut and its effect on microbial maturation and community assembly remains poorly understood. This study aims to provide a comprehensive longitudinal characterization of *E. coli* in the infant gut microbiome, shedding light on its diversity, prevalence, and dynamics during the first year of life.

Methods: Approximately 700 *E. coli* isolates were collected from 172 infants in the COPSAC2010 cohort at 1-week, 1-month, and 1-year, and whole-genome sequenced. Additionally, we combined the metagenomes from the 1-month and 1-year infant gut to analyze the phylotype and clone complexes of *E. coli* present in all 662 children in the cohort.

Results: We clustered the isolates into different clades based on phylogenomic and analyzed their differences in respect to the number/type of genes related to antibiotic resistance, plasmids, prophages, anti-phage defense systems, surface adhesion proteins, and secreted proteins all likely to contribute to persistence. We found that the *E. coli* B2 phylotype was the most prevalent and persistent in infants, and the functional profiles potentially underlying this phylotype were elucidated. We also explore the competitive dynamics between *E. coli* and strict anaerobes present in early life. Furthermore, we plan to explore how these dynamics were influenced by the infant's exposure history.

Conclusion: Our findings indicate that *E. coli* plays a crucial role in the early development of the infant gut microbiome, with the *E. coli* B2 phylotype being a key player. The study underscores the importance of strain-level analysis in understanding the contributions of specific microbial populations to gut development. Additionally, it highlights the complex interactions between *E. coli* and other bacterial species during the first.