Gut microbiota wellbeing index predicts overall health in a cohort of 1000 infants

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Presenter: Wan-Hsuan,Ju **Date/Time:** 2025/12/4, 15:10 -16:00

Commentator: Dr. Hsiu-Ch, Cheng **Location:** Room 601, Med College Building

Background: The human gut microbiota is essential for immune, metabolic, and physiological development in early life. Yet longitudinal cohorts with dense microbiota sampling and parallel health assessments remain limited. Consequently, it is unclear whether infants follow a single healthy microbial developmental trajectory or whether multiple trajectories may lead to divergent or similar health outcomes.

Objective: To characterize early-life gut microbiota developmental trajectories in a large infant cohort, identify key microbial drivers of healthy maturation, and develop a microbiota wellbeing index that predicts long-term health outcomes.

Results: Clustering and trajectory modelling revealed five distinct developmental patterns of the infant gut microbiota. Across trajectories, Bifidobacterium and Bacteroides consistently emerged as keystone taxa guiding healthy maturation.Building on these microbial signatures, the authors developed a microbiota wellbeing index (MWI) that incorporated taxa positively or negatively associated with health. Bifidobacterium and Bacteroides contributed most strongly to healthy development, whereas taxa such as Klebsiella and Veillonella were linked to dysbiosis. Infants following dysbiotic trajectories exhibited higher risks of allergies, infections, and abnormal growth through age five. MWI values measured early in life successfully predicted later health outcomes, demonstrating strong discriminatory power for allergy- and growth-related conditions.

Conclusion: Early-life gut microbiota follows predictable developmental trajectories shaped by initial colonization and early exposures. A microbiota wellbeing index derived from these patterns provides a powerful tool for predicting long-term health in children.