

Elucidating Metabolic Variations in Gut Microbiota During Health and Malnutrition Based on Genome Scale Metabolic Modeling

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Objectives

- We used genome scale metabolic modeling (GEMs) to evaluate metabolic variations in gut microbiota of healthy and malnourished children from Bangladesh, Malawi, and Sweden.

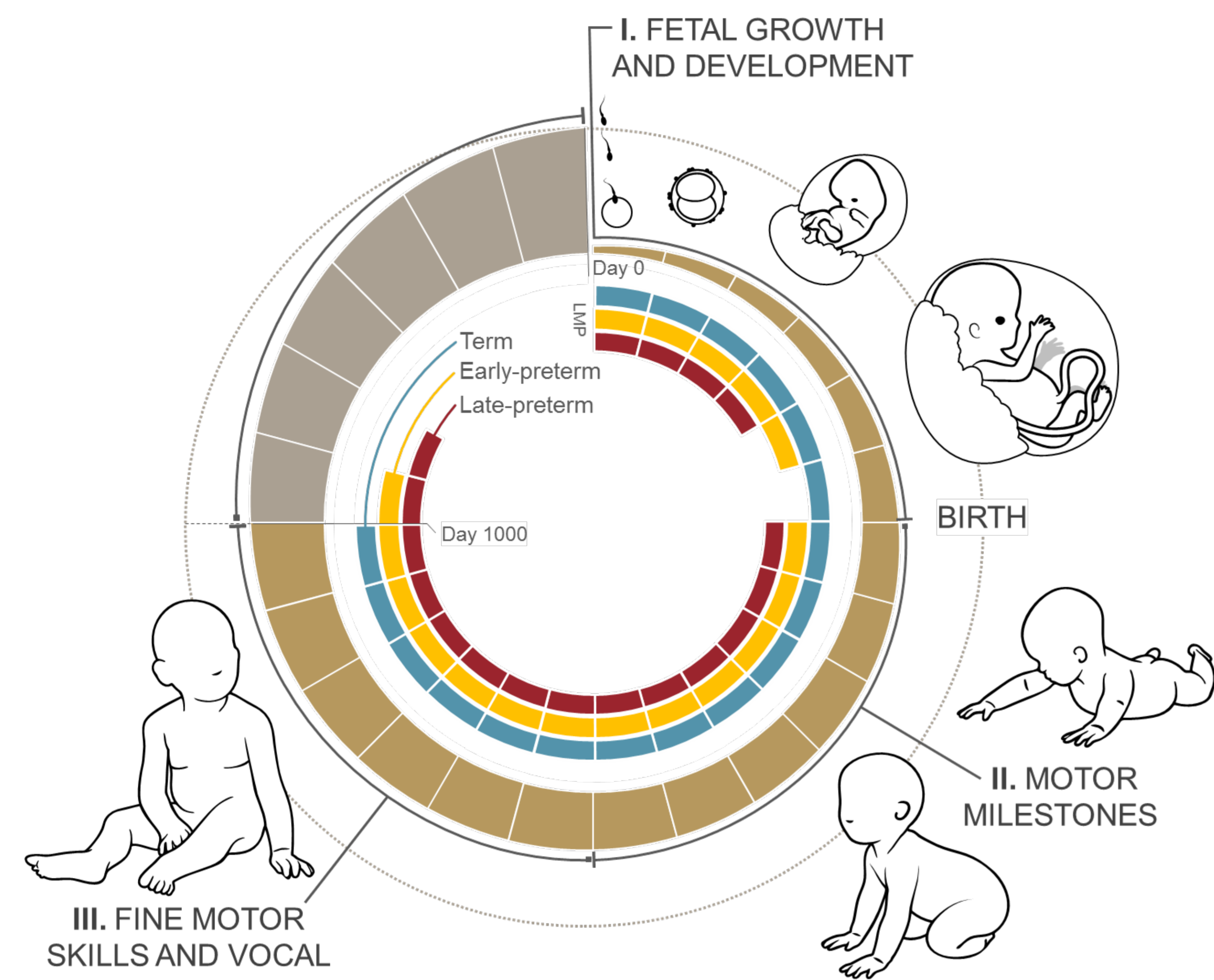


Fig. 1 Healthy Birth Growth and Development Lifecycle diagram.

Methods

- To quantify the contribution of gut microbiota to the metabolic differences between healthy and malnourished children, we reconstructed GEMs for 68 microbial species, representing the 20 most abundant species of gut microbiota in malnourished (Bangladeshi and Malawian) and healthy (Swedish, Bangladeshi, and Malawian) children.¹⁻³
- We inferred the metabolic signatures of the most abundant gut bacterial species to provide the basis for analysis of gut microbial communities by metabolic modeling.

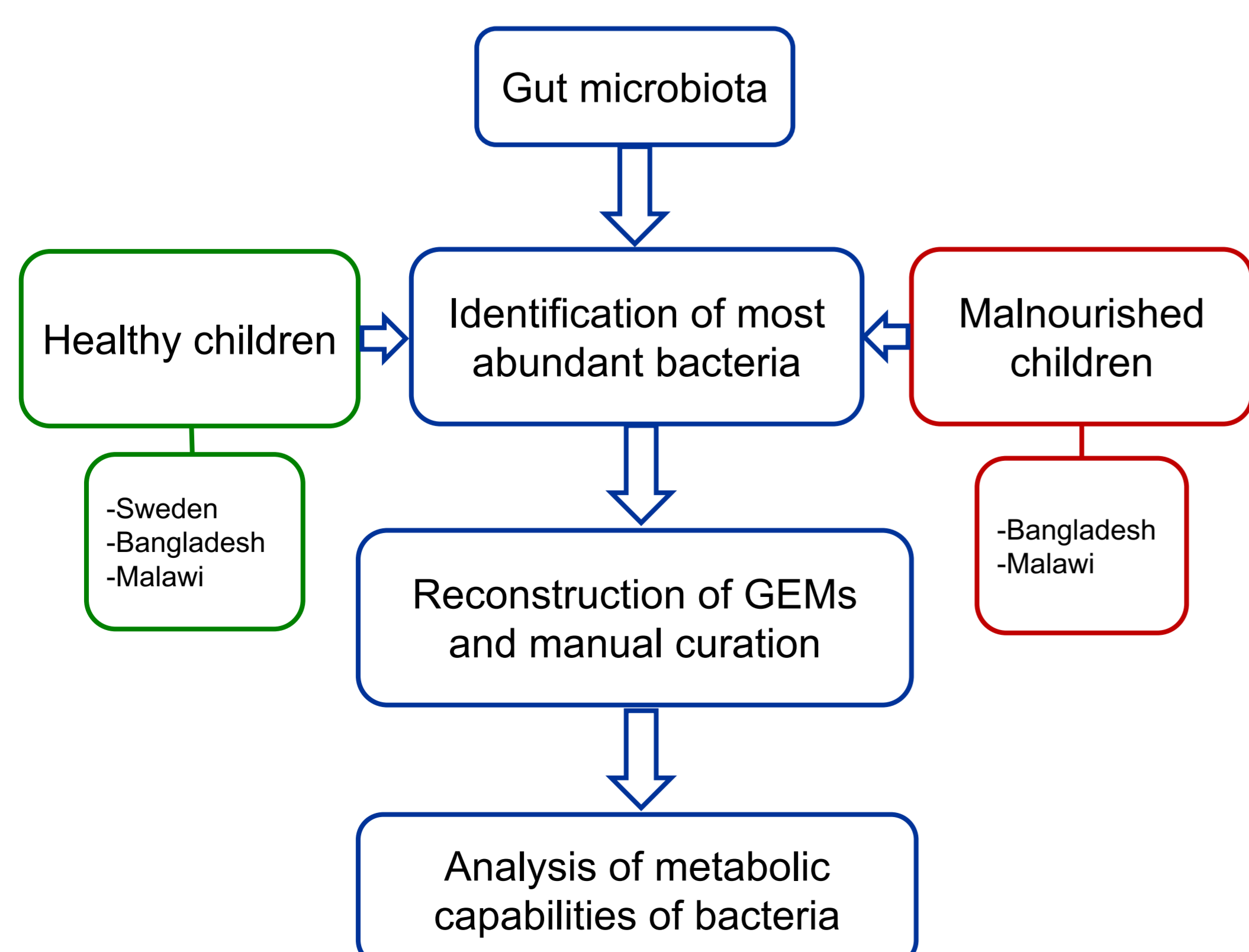


Fig. 2 Work flow diagram

Results

- Simulation of GEMs based on single species enabled us to quantify the production capabilities of gut bacteria toward synthesis of beneficial small molecules (short-chain fatty acids [SCFAs]; amino acids [AAs]).
- Variations in synthesis of small molecules were directly connected to changes in gut microbiota composition between healthy and malnourished children.
- Effects of food interventions on gut microbiota and host metabolism: there were transient effects of standard Ready-To-Use-Food (RTUF) treatment on gut microbiome.

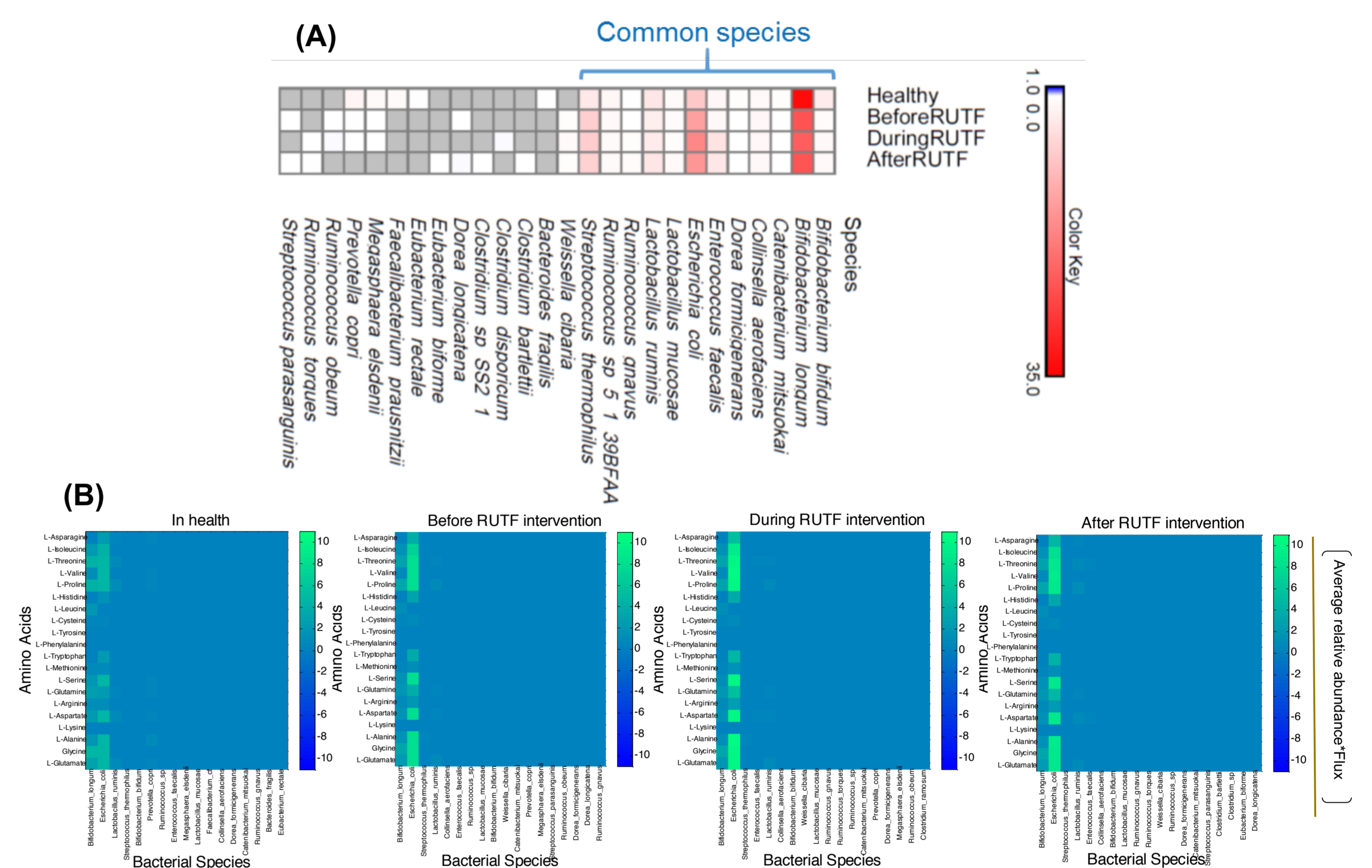


Fig. 3 Bangladeshi children. (A) Relative abundance of 20 most abundant bacteria. (B) Metabolic production capabilities (amino acids) of gut bacteria.

Conclusions

- Gut microbiota are less diverse in Bangladeshi and Malawian than Swedish children.
- There is a slight difference in production of SCFAs and AAs between healthy and malnourished Bangladeshi children.
- In Malawian children, there is no metabolic difference between healthy and malnourished children, possibly due to an effect of vitamins and/or minerals.
- Metabolic diversity is much lower in Malawian and Bangladeshi than Swedish children, possibly because of lack of microbiota diversity connected to malnutrition.

References

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