Exploring the genomic traits of infant-associated microbiota members from a Zimbabwean cohort

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Abstract

Introduction

Our understanding of particular gut microbiota members such as Bifidobacterium and Enterococcus in low-middle-income countries remains very limited, particularly early life strain-level beneficial traits. This study addresses this gap by exploring a collection of bacterial strains isolated from the gut of Zimbabwean infants; comparing their genomic characteristics with strains isolated from infants across North America, Europe, and other regions of Africa.

Materials and method

From 110 infant stool samples collected in Harare, Zimbabwe, 20 randomly selected samples were used to isolate dominant early-life gut microbiota members Bifidobacterium and Enterococcus. Isolated strains were subjected to whole genome sequencing and bioinformatics analysis including functional annotation of carbohydrates, human milk oligosaccharide (HMO) and protein degradation genes and clusters, and the presence of antibiotic resistance genes (ARGs).

Results

The study observed some location-based clustering within the main five identified taxonomic groups. Furthermore, there were varying and overall species-specific numbers of genes belonging to different GH families encoded within the analysed dataset. Additionally, distinct strain- and species-specific variances were identified in the potential of Bifidobacterium for metabolizing HMOs. Analysis of putative protease activity indicated a consistent presence of gamma-glutamyl hydrolases in Bifidobacterium, while Enterococcus genomes exhibited a high abundance of aspartyl peptidases. Both genera harboured resistance genes against multiple classes of antimicrobial drugs, with Enterococcus genomes containing a higher number of ARGs compared to Bifidobacterium, on average.

Conclusion

This study identified promising probiotic strains within Zimbabwean isolates, offering the potential for early-life diet and microbial therapies. However, the presence of antibiotic resistance genes in infant-associated microbes raises concerns for infection risk and next-stage probiotic development. Further investigation in larger cohorts, particularly in regions with limited existing data on antibiotic and probiotic use, is crucial to validate these initial insights.

Impact statement

This research represents the first investigation of its kind in the Zimbabwean context, focusing on potential probiotic strains within the early-life gut microbiota. By identifying local probiotic strains, this research can contribute to the development of probiotic interventions that are tailored to the Zimbabwean population, which can help address local health challenges and promote better health outcomes for infants. Another essential aspect of the study is the investigation of antimicrobial resistance genes present in Zimbabwean bacterial strains. Antimicrobial resistance is a significant global health concern, and understanding the prevalence and distribution of resistance genes in different regions can help inform public health policies and interventions.