

Gut Microbiota Profile in Stunted Children in Labuapi Health Center, Lombok: A Pilot Study

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BACKGROUND AND OBJECTIVES:

Stunting remains a major public health problem among children in Indonesia. Nutritional intake during growth is influenced by multiple factors, including the composition of the gut microbiota. The relationship between a child's nutrient intake and gut microbiota is bidirectional: diet shapes the gut microbial community, and gut microbes, in turn, influence nutrient metabolism and absorption. Imbalance of gut microbiota (dysbiosis) can disrupt intestinal homeostasis and impair digestive and absorptive functions, which may consequently affect overall child growth. This pilot study aimed to analyze the metagenomic profile of gut microbiota in stunted children.

CONCLUSION

In sample 1, Bacteroidota dominated (>50%) the gut microbiota, while approximately 35% of sequences were classified as Unknown, indicating incomplete taxonomic classification. This may reflect either database limitations or high microbial diversity, suggesting the need for improved reference databases or alternative classification methods such as long-read metagenomics. A similar pattern was observed in sample 2. In sample 3, Unknown taxa outnumbered all other species, while the rest were primarily dominated by Bacteroidota. Antibiotic resistance analysis revealed a strong potential resistance to chloramphenicol, macrolides, lincosamides, and streptogramin B, partial resistance to β -lactam antibiotics, and likely resistance to sulfamethoxazole and tetracycline classes.

METHODS

A metagenomic study was conducted on fecal samples from three stunted children aged 24–59 months attending the Labuapi Primary Health Center, Lombok. Approximately 5–10 grams of feces were collected in sterile containers and processed using the Mebep Stool DNA Minikit (DNK2301), which included stages of sample input, cell lysis, protein and inhibitor precipitation, DNA binding, washing, and elution. Library preparation was performed using the Native Barcoding Kit (Oxford Nanopore Technologies) compatible with the PromethION P2 Solo platform, followed by sequencing to generate long reads for each flow cell. Bioinformatic analyses were subsequently performed.

RESULT

The gut microbiota profile of stunted children at the Labuapi Health Center, Lombok, was dominated by Bacteroidota, a common component of normal gut flora. However, a significant proportion of unclassified bacterial sequences suggests the presence of novel or poorly characterized taxa, warranting further investigation using long-read metagenomic approaches. Additionally, a high potential for multi-class antibiotic resistance was observed among the detected microbial communities.

Keywords: stunting¹, dysbiosis², gut microbiota³, metagenomics⁴

REFERENCE

