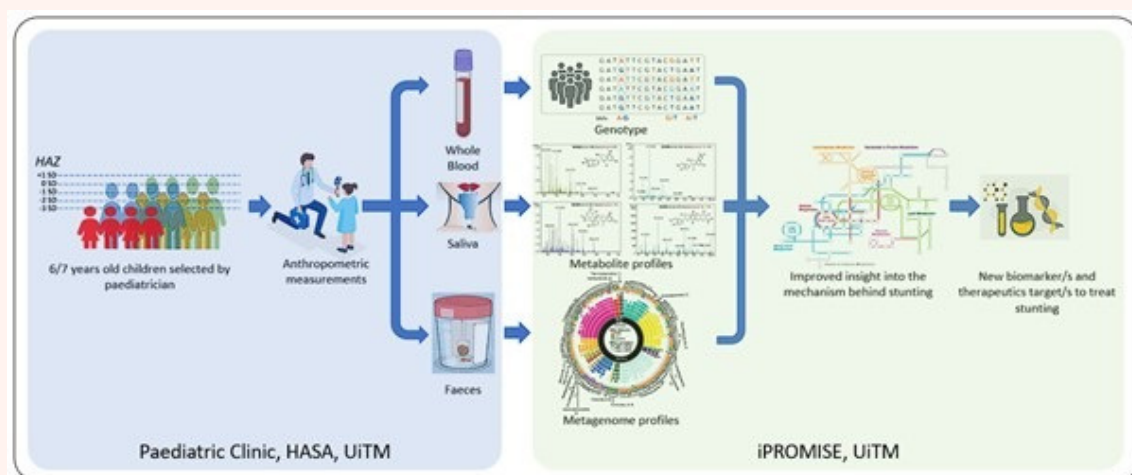


# Unraveling the Mechanisms of Stunting in Malaysian Children: A Metagenomics and Metabolomics Approach

By: Dr. Mohd Nur Fakhruzzaman bin Noorizhab

Stunting, a significant public health concern, affects one in every five children in Malaysia [1]. This prevalence is higher than in some conflict-ridden and underdeveloped countries, such as Palestine and certain African nations [1]. Despite Malaysia's relative prosperity, which ensures better access to nutrition and healthcare, the rates of stunting are alarmingly high [1]. Stunting is characterised by impaired growth and development resulting from chronic malnutrition, and it poses severe health risks, including increased mortality and morbidity [2]. Children who are stunted are more likely to experience long-term cognitive and motor skill deficits, leading to poorer educational outcomes and reduced economic productivity in adulthood [3]. Additionally, stunted children are at a higher risk of developing obesity and related health issues as adults [4,5]. This condition perpetuates a cycle of poor health across generations, as stunted girls often grow into stunted women, who may then give birth to another generation of stunted children. The urgency to address stunting in Malaysia is underscored by the need to understand the specific mechanisms behind it, particularly the roles played by gut microbiota and metabolic processes.

This study aims to fill the current knowledge gap by using advanced metagenomics and metabolomics approaches to investigate the underlying mechanisms of stunting in Malaysian children. The research is guided by three primary hypotheses: that stunting causes alterations in the gut microbiota profiles of children, affects the distribution of functional clusters in the gut microbiota, and results in significant differences in the metabolic profiles of normal and stunted children. To address these hypotheses, the study will focus on answering several key questions: How do the gut microbiome profiles of normal and stunted children differ? Which functional groups in the gut microbiome are affected by stunting? What metabolic changes are associated with stunting in children?



### Appendix A: Study Design Diagram

The research methodology involves using metagenome sequencing to analyse the taxonomy and functional gene clusters in the gut microbiota of stunted children. This technique will provide a comprehensive view of the gut microbiome's composition and its functional capabilities, offering insights into how stunting affects gut health and functionality. The study will also employ metabolomics, a relatively new platform that profiles differential metabolite expressions. Metabolomics will help identify the metabolic pathways disrupted by stunting, shedding light on the specific metabolic challenges faced by stunted children. By profiling these differential metabolites, the study aims to understand how these metabolic disruptions contribute to the delayed and poorer psycho-cognitive performance observed in stunted children.

This research is also highly relevant to government policy, particularly in the context of Malaysia's healthcare sector, which is a key component of the National Key Economic Areas (NKEA). The government aims to grow the healthcare sector to drive Malaysia towards high-income status and global competitiveness. Addressing stunting is essential for achieving these goals, as a healthy population is fundamental to economic growth. High stunting rates among children can impede the country's progress, as stunted children are less likely to reach their full educational and economic potential. By providing a deeper understanding of stunting, this study contributes to the broader goals of improving public health and economic productivity. The insights gained from this research will enable the implementation of precision medicine approaches to prevent and treat stunting, fostering a healthier and more productive future generation in Malaysia.

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