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Gut microbiome of helminth-infected indigenous Malaysians is context dependent

Mian Zi Tee^{1†}, Yi Xian Er^{2†}, Alice V. Easton³, Nan Jiun Yap², Li Li Lee⁴, Joseph Devlin³, Ze Chen³, Kee Seong Ng⁵, Poorani Subramanian⁶, Angelina Angelova⁶, Oyebola Oyesola⁷, Shushan Sargsian^{3,8}, Romano Ngu², Daniel P. Beiting⁹, Christopher Chiong Meng Boey¹⁰, Kek Heng Chua¹, Ken Cadwell^{3,8,11}, Yvonne Ai Lian Lim^{2*}, P'ng Loke^{7*} and Soo Ching Lee^{7*}

Abstract

Background: While microbiomes in industrialized societies are well characterized, indigenous populations with traditional lifestyles have microbiomes that are more akin to those of ancient humans. However, metagenomic data in these populations remains scarce, and the association with soil-transmitted helminth infection status is unclear. Here, we sequenced 650 metagenomes of indigenous Malaysians from five villages with different prevalence of helminth infections.

Results: Individuals from villages with higher prevalences of helminth infections have more unmapped reads and greater microbial diversity. Microbial community diversity and composition were most strongly associated with different villages and the effects of helminth infection status on the microbiome varies by village. Longitudinal changes in the microbiome in response to albendazole anthelmintic treatment were observed in both helminth infected and uninfected individuals. Inference of bacterial population replication rates from origin of replication analysis identified specific replicating taxa associated with helminth infection.

Conclusions: Our results indicate that helminth effects on the microbiota were highly dependent on context, and effects of albendazole on the microbiota can be confounding for the interpretation of deworming studies. Furthermore, a substantial quantity of the microbiome remains unannotated, and this large dataset from an indigenous population associated with helminth infections is a valuable resource for future studies.

Keywords: Helminth, Microbiome, Metagenomic sequencing, Indigenous population, Albendazole

Introduction

Industrialization is associated with reduced diversity of the microbiome in the human population [1], which could influence a range of physiological processes including nutrition, metabolism, immunity, neurochemistry, and drug metabolism [2]. Traditional indigenous populations have substantially greater microbial diversity than individuals living in industrialized societies. Nonetheless, our current knowledge of the human gut microbiome [3] is overrepresented by data available from industrialized countries and does not fully address the undersampling of indigenous populations.

[†]Mian Zi Tee and Yi Xian Er contributed equally to this work.

*Correspondence: limailian@um.edu.my; png.loke@nih.gov; sooching.lee@nih.gov

² Department of Parasitology, Faculty of Medicine, Universiti Malaya, Kuala Lumpur, Malaysia

⁷ Type 2 Immunity Section, Laboratory of Parasitic Diseases, National Institute of Allergy and Infectious Diseases, National Institute of Health, Bethesda, MD, USA

Full list of author information is available at the end of the article

