THE ROLE OF THE GUT MICROBIOME AND DISEASE SEVERITY IN MALARIA

Authors: *Stije J. Leopold[1,2], Floor Hugenholtz[3,4], Annirudha Ghose[5], Katherine Plewes[1], Ashok Kumar Dutta[5], Willem de Vos[6], Nicholas J. White[1,2], W. Joost Wiersinga[3,4], Arjen M. Dondorp[1,2]*

Affiliations:
[1] Mahidol-Oxford Tropical Medicine Research Unit, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailan;[2] Centre for Tropical Medicine and Global Health, Nuffield Department of Medicine, University of Oxford, United Kingdom;[3] Department of Medicine, Division of Infectious Diseases, Academic Medical Center, University of Amsterdam, the Netherlands; [4]Center for Experimental and Molecular Medicine, Academic Medical Center, University of Amsterdam, the Netherlands; [5]Department of Internal Medicine, Chittagong Medical College Hospital, Chittagong, Bangladesh; [6]Department of Microbiology, University of Wageningen, the Netherlands

Introduction: Severe falciparum malaria remains an important cause of morbidity and mortality in malaria endemic countries. The role of the gut microbiome in the pathophysiology of malaria is ill defined. We here aimed to describe the composition of the gut microbiota in patients with severe malaria and its association with clinical outcome, parasite burden and metabolic acidosis.

Material and Methods: We conducted a prospective observational cohort study of adults with severe and uncomplicated malaria, and local healthy controls, in a tertiary referral hospital in Chittagong, Bangladesh. At baseline, microscopy, blood gas analysis and HRP2 measurements were carried out on blood samples. A stool sample was collected and analysed for 16S rRNA gene analysis for microbiota profiling with barcoded amplicons from V4 region of 16S rRNA genes.

Results and Discussion: Of 82 subjects enrolled, 28 had severe malaria and 20 had uncomplicated malaria caused by *Plasmodium falciparum*. Additionally, 34 healthy local controls were enrolled. Significant changes in the composition of the gut microbiota composition were observed between patients with malaria and healthy controls; mainly due to a reduction in observed species diversity among patients with malaria. Phylum level analysis identified low relative abundance of Firmicutes, and Tenericutes in severe malaria, while Proteobacteria were increased compared to healthy controls. This is the first analysis of the gut microbiome in patients with severe malaria and demonstrates its association with significant shifts in microbiota composition. Further analysis is ongoing to investigate the relation between the intestinal microbiome and markers of parasite burden, acidosis and coma. This may provide new insights into the role of the gut microbiota and disease pathogenesis in patients with malaria, which may aid in developing adjunctive therapies targeted at the gut the microbiome.

Position presenting author: second; e-mail: f.hugenholtz@amc.uva.nl
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