ABSTRACT

The association between submicroscopic *Plasmodium* infections and gut microbiota among children in Ahanta West, Ghana.

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Asymptomatic and submicroscopic *Plasmodium* infections pose challenges to malaria control due to their silent contribution to transmission. The gut microbiome is increasingly recognized for its role in modulating host susceptibility to infectious diseases, yet its relationship with malaria remains underexplored in endemic populations. This study aimed to investigate the role of gut microbiota in asymptomatic *Plasmodium* infections among school-aged children in Ahanta West, Ghana. A cross-sectional exploratory study was conducted to screen school-aged children for *Plasmodium* infections and stool samples were collected for 16S rRNA gene V4 sequencing. *Plasmodium* infection status and species were determined using malaria microscopy, Rapid Diagnostic Tests, and Realtime-PCR. Alpha and beta diversity metrics, differential abundance analysis, and redundancy analysis (RDA) were used to explore the association between asymptomatic *Plasmodium* infection and gut microbiota. There were 113 participants with an average age of 12.1±2.3 years and with disproportionately more females, 70 (61.9%). The prevalence of submicroscopic *Plasmodium* infection was 53.1% with *Plasmodium malariae* significantly associated ($p < 0.001$). Alpha and beta diversity metrics did not show significant differences within and between both infection and *Plasmodium* spp. groups, respectively. However, there was generally reduced abundance in the infection groups compared to the uninfected. *Plasmodium* spp. causing infection was identified to significantly influence gut microbiota ($p = 0.024$) in the RDA. Differential abundance analysis showed enrichment of pro-inflammatory gut bacteria such as *Treponema* spp. and *Rikenellaceae* and depleted beneficial and anti-inflammatory gut bacteria such as *Coprococcus eutactus* and *Rhodospirillales*. This study shows evidence of subtle gut microbiota dysbiosis in asymptomatic *Plasmodium* infection with potential core microbial enrichment. This suggests the role of gut microbiota in susceptibility to *Plasmodium* infection and the potential for microbiota mediated strategies in malaria control.

Keywords: *Plasmodium*, gut microbiota, submicroscopic infection, dysbiosis