Title: Longitudinal Analysis of the Impacts of Urogenital Schistosomiasis on the Gut microbiota of Adolescents in Nigeria

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Abstract

The main causative species of urogenital schistosomiasis in sub–Saharan Africa is *Schistosoma haematobium*. The gut microbiome is important for many host physiological processes and helminths have the ability to colonise the same environment or have indirect systemic impacts on the gut, and these interactions may lead to microbial changes. We carried out a longitudinal study of the impacts of *S. haematobium* infection on the gut microbiome of adolescents (11-15 years) in northern Nigeria pre and post praziquantel treatment in order to establish the parasite as a cause of gut microbial changes or determine impact that praziquantel treatment may have. Using 16S sequencing a total of 267 DNA from faecal samples of infected versus uninfected adolescents were amplified following earth microbiome project protocols and sequenced on an Illumina Miseq. We observed that at baseline, the microbiomes of infected versus uninfected adolescents revealed a state of dysbiosis due to increased *Proteobacteria* and decreases in *Firmicutes* and *Cyanobacteria*. We assessed the diversity of the taxa using alpha diversity metrices and observed that using Shannon index we obtained significant differences when we compared infected samples at 3, 9 and 12 months to baseline uninfected controls (P= <0.0001, P=0.0342 and P=0.0003 respectively). Microbial community composition analysis revealed that there were only significant differences at 3, 9 and 12 months (P=0.001, P=0.001, P=0.001 and P=0.001, respectively). Across all time points we also observed significant differences in the differential abundance of the genera at baseline, while the genera at 3 and 6 months resembled the baseline genera changes, the changes at 9 and 12 months were more similar to each other with an increase in *Prevotella*. We also tested for the effects of the drug praziquantel on gut microbiome differences, and we demonstrated that the effects of the infection on the gut was more significant than the drug. Overall, our data suggests that *S. haematobium*, a non-gut resident parasite has indirect interactions with the gut. The bacterial taxa changes we have identified opens up the opportunity to investigate their role in human health, especially in urogenital schistosomiasis endemic communities.