

DIVERSITY AND COMPOSITION OF GUT PROTIST IN YOUNG RURAL ZIMBABWEAN CHILDREN

AUTHORS

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AFFILIATIONS



BACKGROUND

- Human gut microbiome harbours diverse species of archaea, bacteria, fungi, protists and viruses.
- Previous gut microbiome studies have focused on bacteria, neglecting other microbial communities.
- Consequently, less is known about the diversity and abundance of the latter.
- Growing interest in investigating the diversity of microbiome in the healthy human population
- Little is known about the prevalence and factors that influence the abundance and diversity of gut protists in humans

AIM

To characterise the diversity and composition of protists in the gut of preschool-aged children (PSAC) in rural Zimbabwe relative to host age, sex, and schistosome infection status

METHOD

Study design, site and population:



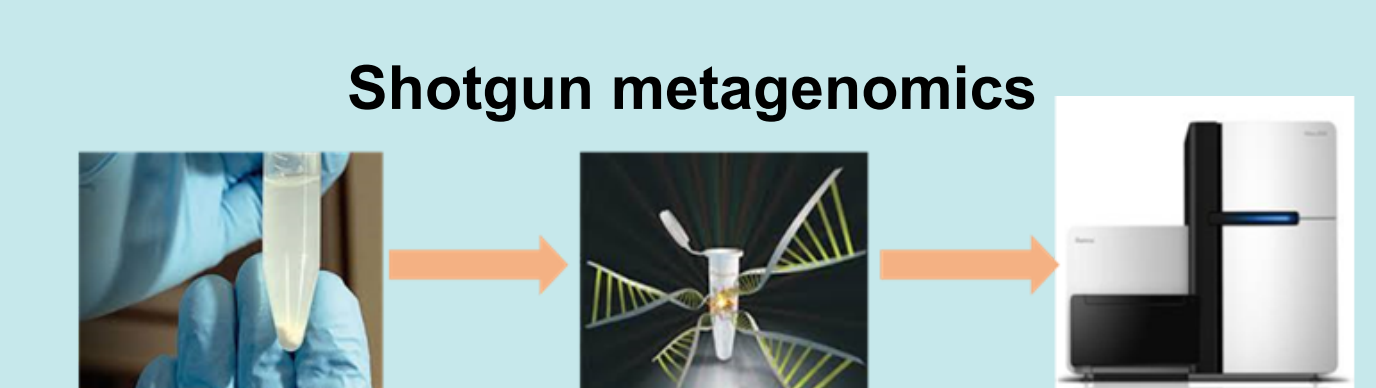
Pre-school-aged children (6mth-5years)

Sample collection and Parasitology:



Sample processing

Gut protist characterisation (NGS):



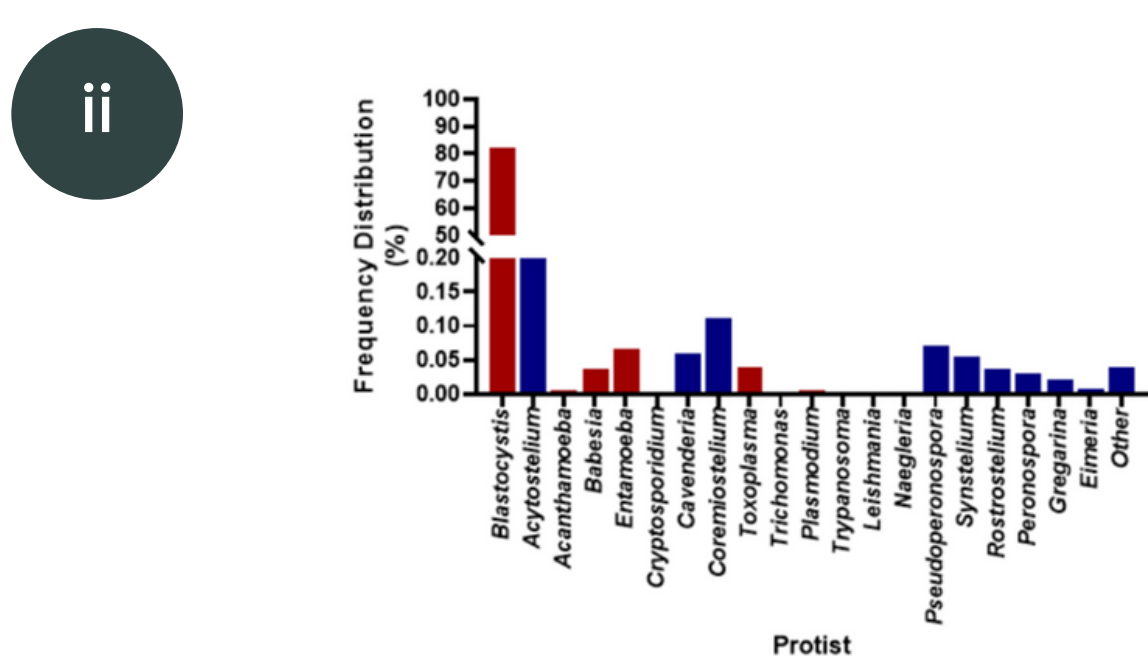
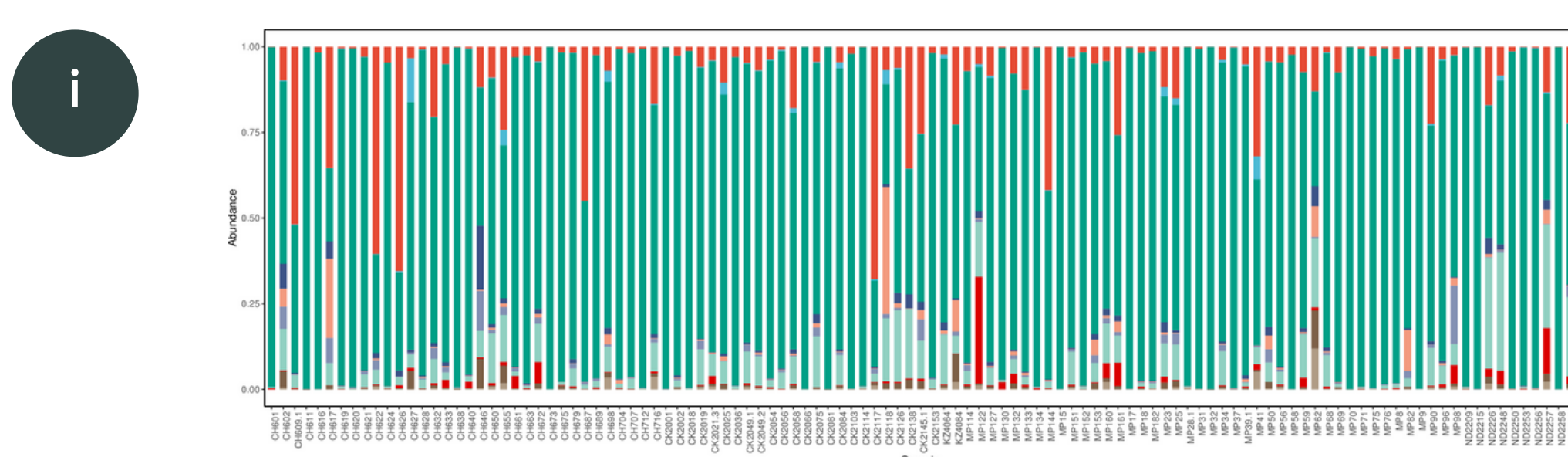
RESULTS

1. Demographic characteristics of study population:

Demographic categories	Frequency	Percentage (%; 95% CI)
Gender		
Female	56	49.6 (40.0 - 59.1)
Male	57	50.4 (40.8 - 60.0)
Age group (years)		
≤3	69	61.1 (51.4 - 70.1)
4	29	25.7 (17.9 - 34.7)
5	15	13.3 (7.6 - 21.0)
S. haematobium infection status		
Negative	95	84.1 (76.0 - 90.3)
Positive	18	15.9 (9.7 - 24.0)
Nutritional and growth factors		
Breastfed (months)		
<6	1	1.1 (0.03 - 6.0)
≥6	89	98.9 (94.0 - 100.0)
Solid food introduction (months)		
<6	32	31.4 (22.6 - 41.3)
≥6	70	68.6 (58.7 - 77.5)
Stunted (HAZ)		
Yes	16	14.7 (8.6 - 22.7)
No	93	85.3 (77.3 - 91.4)
Malnourished (WHZ)		
Yes	4	3.7 (1.0 - 9.3)
No	103	96.3 (90.7 - 99.0)
Malnourished (MUACZ)		
Yes	8	8.0 (3.5 - 15.2)
No	92	92.0 (84.8 - 96.5)
Underweight (WAZ)		
Yes	6	5.6 (2.1 - 11.7)
No	102	94.4 (88.3 - 97.9)
Total	113	100

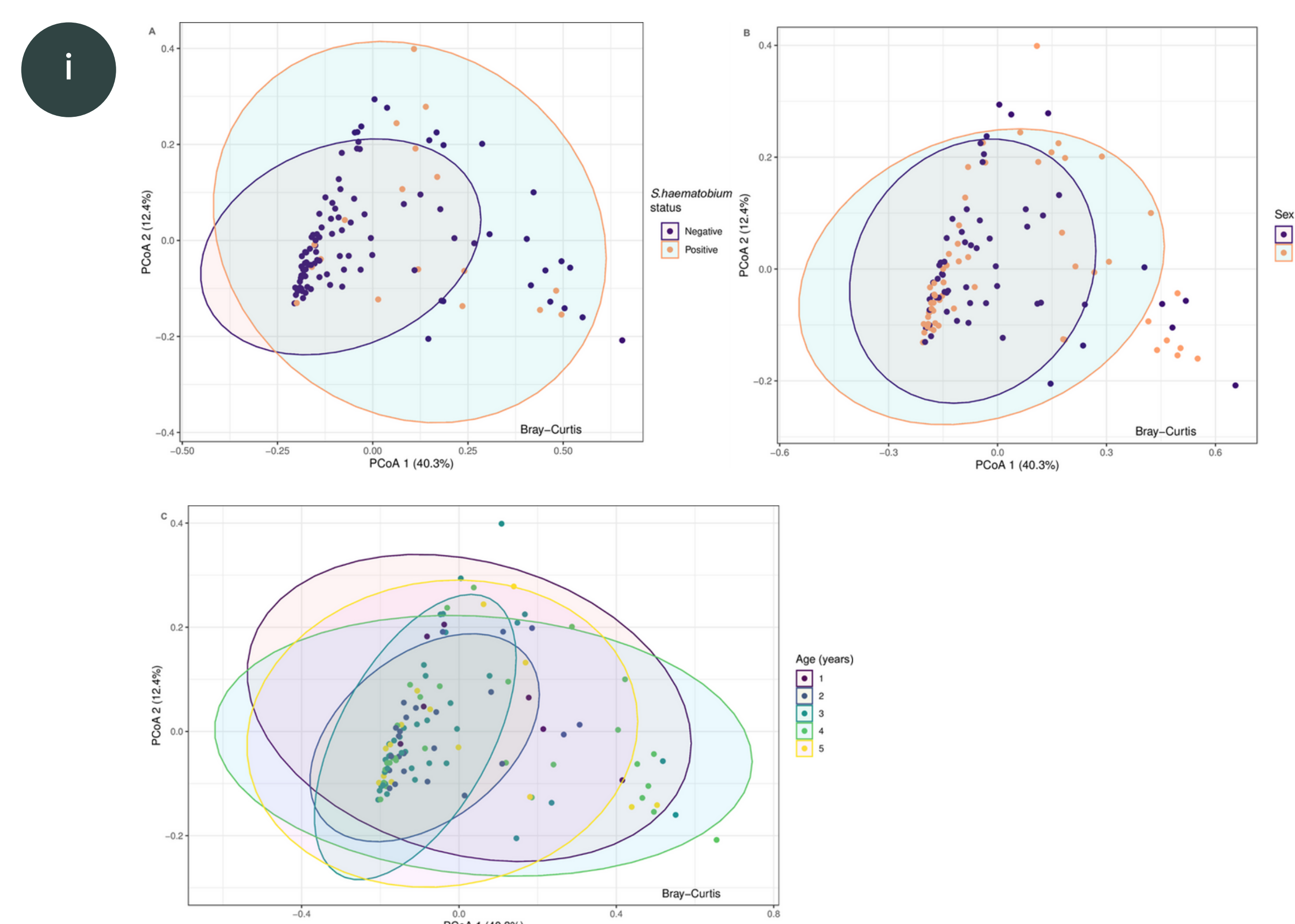
1. Classification of nutritional status was based on a cut off <-2 Z scores. WHA, weight-for height Z scores; HAZ, height-for-age Z scores; MUACZ, mid-upper arm circumference z score; WAZ, weight-for-age.

2. Characterisation of the intestinal protist microbiota :



2. Overall, 80 protist genera were detected in all 113 samples and were dominated by Blastocystis, representing 82% of the total protist (i). Prevalence of pathogenic protist was comparatively low with 12.1% and 3.4% of the participants' gut colonised by *E. histolytica* and *Cryptosporidium*, respectively (ii).

3. Variation in the protist and association with participant metadata



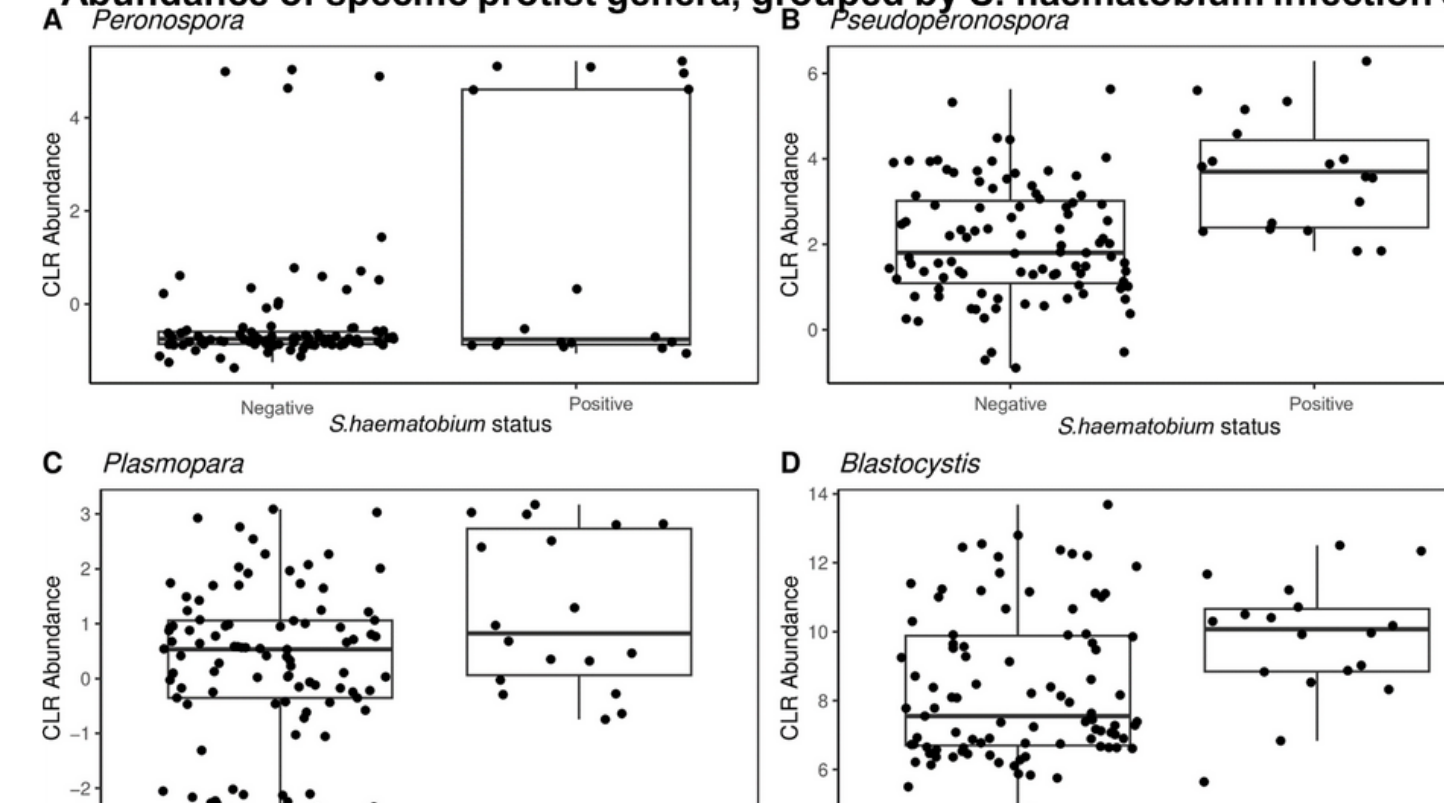
3 (i). Principal coordinate analysis (PCoA) plots for protists microbiota across samples, annotated by schistosome status (A), sex (B) and age (years) (C). PCoA explained 52.7% of the total variance between the samples.

Summary of sample metadata and association with gut protist microbiome

	n	P-value	SSExplain	SSTotal	FDR
Sex	113	0.184	60.465	5393.812	0.361
Age_years	113	0.089	73.629	5380.648	0.267
Malnourished_(WHZ)	107	0.440	47.550	5189.409	0.659
Malnourished_(MUACZ)	100	0.683	38.838	4829.721	0.769
Underweight_(WAZ)	108	0.201	62.146	5197.658	0.361
Stunted_(HAZ)	109	0.056	80.607	5212.288	0.252
S. haematobium status	113	0.001	203.737	5250.541	0.009
Months_breastfed	90	0.785	34.176	4211.254	0.785
Months_Solid_food	102	0.636	41.307	4941.892	0.769

Classification of nutritional status was based on a cut off <-2 Z scores. WHA, weight-for height Z scores; HAZ, height-for-age Z scores; WAZ, weight-for-age Z score; MUACZ, mid-upper arm circumference z score; p-value-unadjusted p-value; FDR- adjusted p-value (FDR-corrected).

Abundance of specific protist genera, grouped by S. haematobium infection status



3(ii). PERMANOVA analysis showed a significant effect of *S. haematobium* infection status. Analysis via ANCOM showed that the abundance of four specific protist genera was associated with *S. haematobium* infection.

SUMMARY

- Only *S. haematobium* infection status was associated with composition of specific taxa.
- Prevalence of pathogenic protist was relatively low
- Need for further research to investigate the interactions between pathogenic and non-pathogenic protists in individuals displaying clinical symptoms, in order to provide insights for the development of therapeutic interventions and nutraceuticals

ACKNOWLEDGMENTS

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