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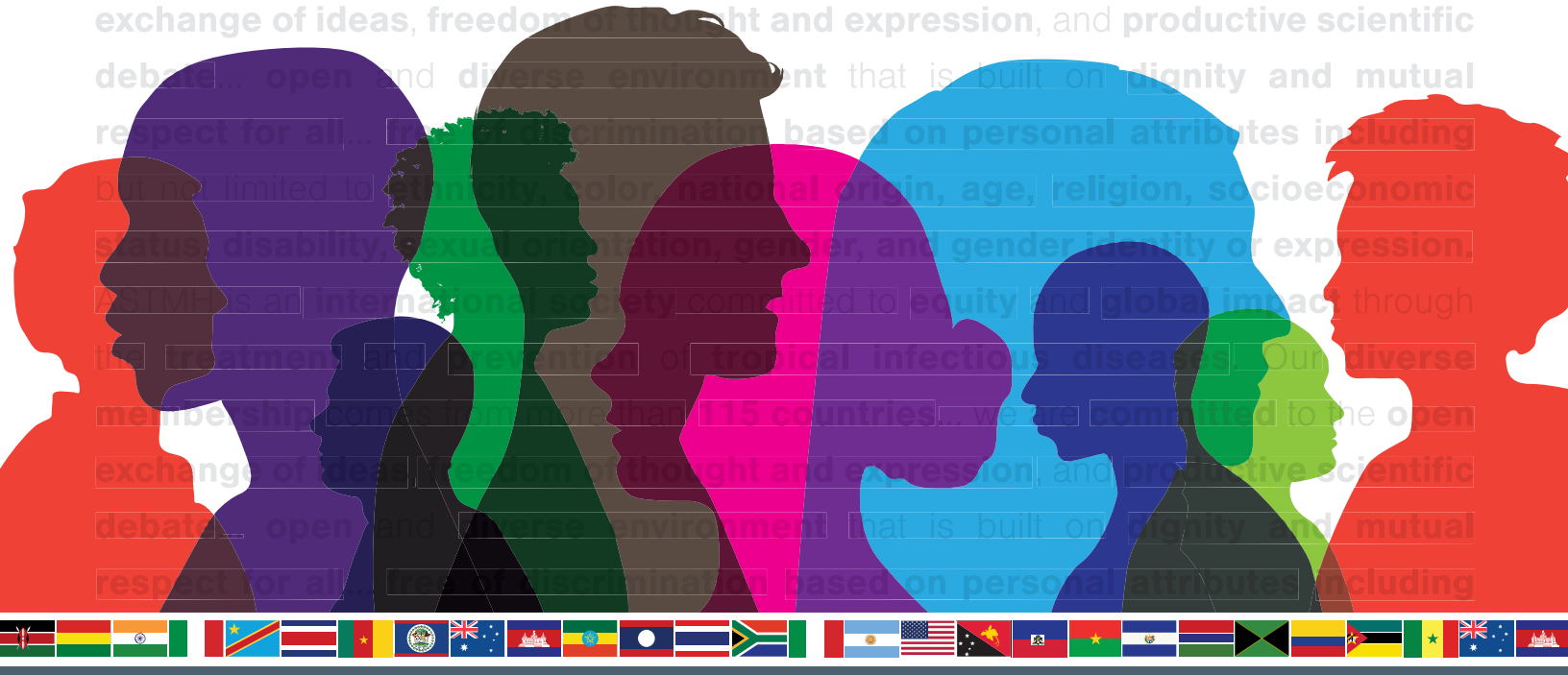
ABSTRACT BOOK



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seven sites in Kenya were analyzed. Twenty-three had previously been identified as positive for *E.* complex by microscopy. DNA was extracted using the QIAamp DNA Stool Mini Kit. Species detection was done using nested PCR with the resulting amplicons sequenced by Sanger method. Consensus sequences were compared to those on GenBank database and maximum likelihood phylogenies reconstructed using phyML 3.1. Out of the 46 samples, 22 (47.8%) were positive for *Entamoeba* species. Of these, 16 had initially been identified as microscopy positive for *Entamoeba* complex. Among the 22 PCR-positives *Entamoeba* complex species were identified as follows: 9 were *E. dispar* (40.9%), 2 were *E. moshkovskii* (9.1%), and 1 was *E. histolytica* (4.5%). Combinations of *Entamoeba* species detected were: 3 *E. histolytica* and *E. dispar* (13.6%), 2 *E. histolytica* and E. *moshkovskii* (9.1%), 4 *E. moshkovskii* and *E. dispar* (18.2%) and 1 *E. histolytica* and *E. dispar* and *E. moshkovskii*. Sequence analysis revealed 99% identity to *E. dispar* (SAW 760), *E. moshkovskii* (Laredo) and *E. histolytica* (HM-1: IMSS). Reconstruction of phylogenetic relationships revealed distinct species-specific clustering. It's possible that *E. moshkovskii* infections have been in circulation in Kenya for some time and are only now being reported. It is important to establish the molecular epidemiology of *E.* complex, so as to accurately treat amoebiasis in endemic areas like Kenya.

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PREVALENCE OF *BLASTOCYSTIS SP.* AND ASSOCIATED FACTORS TO INFECTION AND SYMPTOMATOLOGY IN PERIURBAN COMMUNITIES OF AREQUIPA, PERU

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Entero-parasitic infections are one of the most important causes of acute illnesses in humans. They are mainly present in poor areas with unhealthy environmental conditions. Periurban communities usually experience some of these conditions, including limited access to safe drinking water and inadequate disposal of human feces. Among entero-parasites, *Blastocystis sp.* is the most common protozoa in the human gut with wide distribution around the world. People infected with *Blastocystis sp.* do not show specific symptoms or are asymptomatic, making it difficult to assess its pathogenic potential and determine if and how much zoonotic transmission occurs. The aim of this study was to determinate the prevalence of *Blastocystis sp.* and the factors associated with infection, and symptomatology presentation in periurban communities from Arequipa city. We conducted epidemiological surveys and analyzed stool samples from 189 participants and 144 animals from participants' households using the concentration-spin method and direct stool exam by microscopy. We compared individual-level and household-level covariates between infected and uninfected participants and between symptomatic and asymptomatic cases. 49.2% of participants were infected with *Blastocystis sp.* Among infected, 61.3% had non-specific gastrointestinal symptomatology. We found an association between *Blastocystis sp.* infection and lack of access to safe drinking water (p=0.004) and inadequate disposal of human feces (p=0.03). Other variables such as age, sex, presence of animals or vectors at home, food consumption, and hygienic habits were not associated. Additionally, we found 34.4% of coinfections between *Blastocystis sp.* and other intestinal parasites. Only 8.3% of the animals were infected with *Blastocystis sp*. Our results suggest that *Blastocystis sp.* infection does not present a clear symptomatology and that the main factors associated with *Blastocystis sp.* infections ocurr at the household-level: water supply and the feces final disposition. The implications of these findings on the control and transmission of *Blastocystis sp.* are discussed.

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HEALTHY COMMUNITY STOOL SCREENINGS IN RURAL NICARAGUA REVEAL HIGH PREVALENCE OF PROTOZOAL INTESTINAL PARASITES AND POLYPARASITISM

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Individuals in tropical, rural regions of the world are at high risk for infectious diseases, including parasitic diseases. Protozoal and worm parasites are a public health challenge in low-income settings, where prevention, surveillance, detection, and access to treatment are stressed by limited infrastructure and resources. Identifying epidemiologic patterns within high-risk communities can inform vulnerable populations and serve as evidence to develop efficient treatment and prevention measures, such as water sanitation and filtration, education, and targeted surveillance. Stool and urine specimens were collected from individuals attending health fairs in 2 rural, agricultural communities in western Nicaragua. Stool was analyzed by microscopy. We generated descriptive statistics and report prevalence and characteristics with Chi-squared and ANOVA using Stata 15. We analyzed stool from 221 residents, ages 3 months to 89 years (median 21 years). *Endolimax nana* (67%), *Entamoeba coli* (44%), *Entamoeba histolytica* (33%), and *Giardia lamblia* (23%) were most common; *Necatur americanus* eggs were recovered from one 87-year old. One community had higher prevalence of *E. histolytica* (56%;p=0.004) and *E. coli* (51%;p=0.005) than the other. 28% harbored 3 or more species, but *G. lamblia* and *E. histolytica* were negatively correlated (p<0.05). Only 18 individuals (8%) were parasite-free. We document a high prevalence of parasites and polyparasitism, and we suggest widespread exposure or frequent transmission is likely occurring within these and neighboring communities. Although not all organisms identified are perceived as pathogenic, there is clearly a need for health education and interventions to reduce exposure to protozoal parasites in the community-at-large. Geographic differences we found may guide treatment campaigns, interventions to break transmission cycles, and health campaigns to prevent disease. These data can inform targeted public health efforts to reduce morbidity, mortality, and long-term health consequences of parasitic infections in high risk communities.

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INFLUENCE OF HOST NUTRIOME ON IMMUNOLOGICAL CONTROL OF PROTOZOAL INFECTIONS

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Immunologic control of parasitic infections arises from a combination of humoral and cellular mechanisms, both of which may be influenced by host nutritional status. Micronutrient depletion or over-repletion impairs the functioning of the immune system, potentially resulting in increased susceptibility to and poor immunologic control of protozoal infections. We aim to synthesize the knowledge surrounding the interplay between host micronutrient status and tissue-based protozoal infections. Specifically, we will map the literature of how nutrient deficiencies such as zinc, iron, and vitamin A impact immune response and defenses in infectious diseases such as malaria, Chagas disease, and leishmaniasis. Five electronic databases were searched including PubMed, Embase, Medline, Scopus, and LILACS with combinations of search terms such as Parasite* AND (Immunology OR Immunity OR Immune System OR Immune Function OR Immune Impairment OR Immune Response OR Immune Status) from database inception to March 13, 2019. A total of 30 872 articles were retrieved: 15 254 articles on PubMed, 8192 on Embase, 5909 on Medline,

1411 on Scopus, and 106 on LILACS. After eliminating duplicates using Mendeley software, a total of 21 821 articles remained for title screening. Titles, abstracts, and full-text articles will be systematically double screened by two reviewers with a tertiary arbitrator. The Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) will be implemented. Data extraction will be performed by two reviewers and the quality of the articles will be critically evaluated using the Grading of Recommendations Assessment, Development, and Evaluation (GRADE) approach. The data will be summarized to systematically map published literature that will illuminate a number of ways in which nutrient deficiencies or abnormal micronutrient status alter and impair immune function in persons with protozoal infections. This synthesized body of information will ultimately inform adjunctive therapeutic decisions in the context of protozoal infections, which has the potential to improve patient prognosis.

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THE ROLE OF PROTOZOAN PARASITES IN FEVERS OF UNKNOWN ORIGINS IN GHANA

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Fever is a major feature of many illnesses and remain one of the most challenging clinical evaluations for pediatric clinicians. In Ghana, parasitic diagnosis of fevers in children have focused on malaria but only half or less the number of such cases are observed to have malaria parasite. This study sought to determine other etiologies of FUO besides *Plasmodium* parasites and profiling cellular immune responses to parasitic infections in children. Children younger than 13 years who reported at the pediatric ward of the Cape Coast Teaching Hospital, Ghana with fever (a high temperature ≥ 38°) were enrolled in the study. Venous blood and stool samples were collected from 143 participants and transported to the Noguchi Memorial Institute for Medical Research for analysis. Differential diagnosis was performed for the presence or absence and further genotyping of *Plasmodium*, *Toxoplasma gondii*, *Babesia*, *Cryptosporidium*, *Giardia lamblia* and *Entamoeba* spp. using Polymerase Chain Reaction (PCR). Enzyme-linked immunosorbent assay was performed to obtain and compare the levels of cytokines with respect to infection status. *Plasmodium falciparum* was detected in 27.3% (39/143) of participants. Out of the 104 *P. falciparum* negative samples, 18 (16.7%) *G. lamblia*, 2 (1.9%) *E. histolytica*, 2 (1.9%) *Toxoplasma gondii* and 1 (0.9%) *Cryptosporidium* spp. were detected. Cytokine analysis revealed that, *Plasmodium* negative detected parasites had lower cytokine level than *Plasmodium* positive samples. Also, the level of cytokines established between *Plasmodium* positive infection and *Plasmodium* negative detected parasites were not significantly different (*P*-value > 0.05). Varying levels of parasites virulence can lead to modulating effect by either aggravating or alleviating immune responses.

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EPIDEMIOLOGY AND CLINICAL PRESENTATION OF *CRYPTOSPORIDIUM*-ASSOCIATED DIARRHEAL DISEASE IN CHILDREN UNDER FIVE FROM THREE COUNTRIES IN SUB-SAHARAN AFRICA

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Cryptosporidium causes significant diarrheal morbidity and mortality in children worldwide, including over 40,000 deaths in sub-Saharan Africa. We describe the epidemiology of *Cryptosporidium* in children <5 years of age from the Vaccine Impact on Diarrhea in Africa (VIDA) study in The Gambia, Mali and Kenya (2015-2018). VIDA enrolled healthcare-seeking cases with moderate-to-severe diarrhea (MSD, defined as diarrhea [≥3 loose stools/day] with dysentery or signs of dehydration, IV fluids or hospitalization). Diarrhea-free controls matched for gender, age, time, and community were enrolled at home. Each case and one control provided a stool sample at enrolment to be tested for a panel of enteropathogens, including *Cryptosporidium* species, by TaqMan Array Card quantitative PCR. Using conditional logistic regression, the association between *Cryptosporidium* and MSD status was assessed, adjusting for other pathogens and including interactions with age stratum and site. Episode-specific attributable fractions (AFes) were calculated for each case; cases with an AFe ≥ 0.5 were considered etiologic. Altogether, 4738 cases and 4738 matched controls were enrolled and analysed. *Cryptosporidium* was frequently detected among both groups (23.3% in cases v. 18.3% in controls) and common at all three sites (29.5% of MSD cases in The Gambia, 23.9% in Mali, 16.0% in Kenya). *Cryptosporidium* peaked annually in both The Gambia and Mali coinciding with the rainy season, but was prevalent year-round in Kenya. Among cases, *Cryptosporidium* detection was considered etiologic for 49.9% of detections. MSD cases with etiologic *Cryptosporidium* were younger than non-etiologic cases (median 13 v. 17 months), and 81.5% of etiologic cases were less than 24 months of age. *Cryptosporidium* cases had a longer duration of illness compared to watery diarrhea cases attributable to other causes (Median (IQR): 6 days (4-9) vs. 5 days (3-8), p<0.01) and had higher mean modified Vesikari severity scores (10.0 vs. 9.3, p<0.01). Our results suggest that *Cryptosporidium* infection is prevalent and pathogenic in the populations examined in VIDA.

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ENVIRONMENTAL EXPOSURES ARE A RISK FACTOR FOR *TOXOPLASMA GONDII* INFECTION IN AN URBAN SLUM IN SALVADOR, BRAZIL

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Toxoplasmosis, caused by the parasite *Toxoplasma gondii*, is one of the most common zoonotic diseases globally. Urban slum communities in tropical developing countries are especially vulnerable to the disease because of low socioeconomic status, increased exposure to contaminated environments, and the lack of sanitation infrastructure. Yet, our understanding of the transmission of the disease in these high-risk settings is very limited. Here, we performed a retrospective longitudinal study and an environmental survey of the pathogen in an urban slum in Salvador (Brazil). We enrolled a cohort of 728 young residents (aged 5-18) and followed them for 5 years. Serum samples were tested annually for *T. gondii* IgG antibodies with an enzyme immunoassay. We collected information on demographic and social status, household environment, and household related behaviors. We also measured the occurrence of *T. gondii* by qPCR in sewage from the precarious open sewer system. The overall prevalence of *T. gondii* antibodies was 49.0% (95% CI 44.3-51.5) with a cumulative incidence of 2.9% infections (95% CI 1.9-6.5) per 1,000 follow-up events. We used binomial regression multivariate analysis to evaluate risk factors for *T. gondii* antibodies and found that males were at greater risk than females (OR 1.9, 95% CI 1.4-2.6) and seroprevalence increased with age from 23.4% (95% CI 15.0-30.2) in the 4-6-year-old