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Analysing risk factors of co-occurrence of schistosomiasis haematobium and hookworm using bivariate regression models: Case study of Chikwawa, Malawi

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ABSTRACT

Schistosomiasis and soil-transmitted helminth (STH) infections constitute a major public health problem in many parts of sub-Saharan Africa. In areas where prevalence of geo-helminths and schistosomes is high, co-infection with multiple parasite species is common, resulting in disproportionately elevated burden compared with single infections. Determining risk factors of co-infection intensity is important for better design of targeted interventions. In this paper, we examined risk factors of hookworm and *S. haematobium* co-infection intensity, in Chikwawa district, southern Malawi in 2005, using bivariate count models. Results show that hookworm and *S. haematobium* infections were much localised with small proportion of individuals harbouring more parasites especially among school-aged children. The risk of co-intensity with both hookworm and *S. haematobium* was high for all ages, although this diminished with increasing age, increased with fishing (hookworm: coefficient. = 12.29; 95% CI = 11.50–13.09; *S. haematobium*: 0.040; 95% CI = 0.0037, 3.832). Both infections were abundant in those with primary education (hookworm: coef. = 0.072; 95% CI = 0.056, 0.401 and *S. haematobium*: coef. = 0.286; 95% CI = 0.034, 0.538). However, much lower risk was observed for those who were farmers (hookworm: coef. = −0.349, 95% CI = −0.547,−0.150; *S. haematobium*: coef. −0.239, 95% CI = −0.406, −0.072). In conclusion, our findings suggest that efforts to control helminths infection should be co-integrated and health promotion campaigns should be aimed at school-going children and adults who are in constant contact with water.

1. Introduction

Hookworm and schistosomiasis are some the of helminth infections that are prevalent in most tropical and sub-Saharan countries. However, of the two infections, hookworm is more prevalent than schistosomiasis. Estimates indicate that 1.2 billion people worldwide are infected by hookworm (WHO, 1996) and the infection is widely distributed throughout tropical and subtropical areas with prevalence in some communities as high as 90% (Hotez et al., 2003). With regards to Schistosomiasis, an estimated 207 million people worldwide are infected and that 85% of all cases are now in sub-Saharan Africa (Mbabazi et al., 2011). Overall,

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helminth infections affect between 20% and 30% of the general population with prevalence as high as 60–80% in endemic areas (Pan American Health Organization (PAHO), 1997).

Polyparasitism is common in regions where different parasites co-exist (Pan American Health Organization (PAHO), 1997; WHO, 2002; Bethony et al., 2006; Raso, 2004; Utzinger and Keiser, 2004; Pullan and Brooker, 2008), and predominantly in rural areas or where there is poor sanitation found in sub-Saharan Africa, Southeast Asia and tropical regions of the Americas (Pan American Health Organization (PAHO), 1997; WHO, 2002; Bethony et al., 2006). The large overlap in the geographic distribution of geo-helminths implies that co-infection is a norm than an exception (Raso, 2004). Globally, several million children could be concurrently infected with multiple helminth species even at low intensity (Utzinger and Keiser, 2004). Polyparasitism is most prevalent in school-aged children, while adults remain at considerable risk of harbouring multiple helminth species, although at reduced intensity, and are often neglected in the helminthological literature (Pullan and Brooker, 2008). The multiple infections due to helminths are believed to persist throughout the life course, resulting in reduced physical capacity for work (Gilgen et al., 2001). Moreover, co-infection exacerbates common illnesses such as anaemia in infected population. New research provides evidence that the risk of anaemia is amplified in children simultaneously infected with hookworm and *Schistosoma* or hookworm and *Trichuris*, when compared to the sum of risks for children with singular infections (Hotez et al., 2003).

Although co-infections may simply arise by chance; shared risk factors have been a major contribution (Utzinger and Keiser, 2004; Pullan and Brooker, 2008; Gilgen et al., 2001; Mwangi et al., 2006). Fewer studies, however, have examined such (Bethony et al., 2006; Raso, 2004; Utzinger and Keiser, 2004; Pullan and Brooker, 2008; Gilgen et al., 2001; Mwangi et al., 2006). Interest in understanding polyparasitisms or multiple helminths infections has been rekindled with the goal for integrated resource deployment, but also that if risk factors are shared, prevention efforts will be much easier than if separate (Utzinger and Keiser, 2004; Pullan and Brooker, 2008; Gilgen et al., 2001; Mwangi et al., 2006; Centre for Food Security and Public Health, 2005).

Several methods have been employed in the modelling of helminths co-infection. However, most scholars have used univariate models, see for example (Lwambo et al., 1992). Recently, Magalhães et al. (Magalhães et al., 2011) reported use of multinomial geostatistical regression models in predicting *S. haematobium*-hookworm co-infections. Further applications of multinomial spatial models can be found in (Raso et al., 2006; Brooker and Clements, 2009), who used these models for predicting the risk of co-infection with multiple helminth infections. The multinomial approach involves stratifying egg counts, leading to a loss of information whereas the Poisson or the negative binomial approach make full use of infection intensity data on a continuous scale as measured by number of eggs found in both slides per individual. A similar multi-categorical approach is reported in Botelho et al. (Botelho et al., 2008), who used proportional odds models to investigate the relationship between hookworm and *Ascaris lumbricoides* infection. In another study, Sturrock et al. (Sturrock et al., 2013) used bivariate logistic regression for joint spatial analysis of questionnaire and parasitological data in order to predict the prevalence of *S. haematobium* infection for schools with missing questionnaire data. Schur et al. (Schur et al., 2011), again using the multinomial construct, employed a Bayesian geostatistical shared component models (which allows for covariates, disease-specific and shared spatial and non-spatial random effects) to model the geographical distribution and burden of co-infection risk from single-disease surveys in Côte d'Ivoire.

According to our knowledge, little, if any, literature exist that considered co-infection that employs the use of bivariate count models, despite several applications elsewhere (Karlis, 2003; Karlis and Ntzoufras, 2005; Gurmu and Elder, 2011; Efron and Bradley, 1986; Zou et al., 2011; Lao et al., 2011; Jung and Winklemann, 1993; Bermudez and Karlis, 2011). This study, therefore, used bivariate count models to model co-infection of hookworm and *S. haematobium*, to better understand the epidemiology of the two and their co-intensity and account for outcome dependency.

2. Materials and methods

2.1. Dataset

The dataset used was collected in 2005 from a cluster randomised study conducted in Chikwawa district in the lower Shire Valley, southern Malawi (Fig. 1). Full details of the study are found elsewhere (Ngwira, 2005). In brief, the study was designed as follows. Subjects aged 1 year and above were drawn from each selected household to participate in the study, after informed consent was obtained. All consenting participants were given a full body clinical examination for chronic manifestation of human helminth. In addition, each participant was requested to provide a fresh stool and urine sample transported in cooler boxes and examined in the laboratory at Montfort hospital, Nchalo, Chikwawa. Stool samples were examined by a single thick smear technique using *Kato-Katz* template then examined under a light microscope to observe parasite eggs. Ova for each parasite observed were counted and expressed as eggs per gram of stool (EPG). Urine samples were centrifuged at 300 rpm for 5 min and sediments were then examined under a light microscope to detect number of parasite eggs. Helminth infection intensity is measured by counting microscopic eggs that host excretes through urine and faecal. The Malawi College of Medicine Research Ethics Committee (COMREC) and the Ethics Committee of London School of Hygiene and Tropical Medicine (LSHTM) approved the study.

2.2. Statistical methods

Various statistical models have been developed to model helminths infection. The egg counts, obtained from a human urine sample, are a measure of infection intensity and can be modelled as a count variable. Given certain individuals will harbour two or more parasite infections, bivariate models are developed to jointly model co-infection. Four types of models were