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Schistosoma japonicum in Samar, the Philippines: infection in dogs and rats as a possible risk factor for human infection

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SUMMARY

The role that animals play in the transmission of *Schistosoma japonicum* to humans in the Philippines remains uncertain and prior studies have not included several species, adjustment for misclassification error and clustering, or used a cohort design. A cohort study of 2468 people providing stool samples at 12 months following praziquantel treatment in 50 villages of Western Samar, the Philippines, was conducted. Stool samples from dogs, cats, rats, and water buffaloes were collected at baseline (2003–2004) and follow-up (2005). Latent-class hierarchical Bayesian log-binomial models adjusting for misclassification errors in diagnostic tests were used. The village-level baseline and follow-up prevalences of cat, dog, and rat *S. japonicum* infection were associated with the 12-month cumulative incidence of human *S. japonicum* infection, with similar magnitude and precision of effect, but correlation between infection levels made it difficult to divide their respective effects. The cumulative incidence ratios associated with a 1% increase in the prevalence of infection in dogs at baseline and in rats at follow-up were 1·04 [95% Bayesian credible interval (BCI) 1·02–1·07] and 1·02 (95% BCI 1·01–1·04), respectively, when both species were entered in the model. Dogs appear to play a role in human schistosomiasis infection while rats could be used as schistosomiasis sentinels.

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DECLARATION OF INTEREST

None.

Keywords

Bayesian hierarchical model; cohort; misclassification error; *Schistosoma japonicum*; zoonosis

INTRODUCTION

Schistosomiasis, a chronic parasitic infection caused by trematode worms, is believed to be endemic in 76 countries and territories [1, 2]. *Schistosoma haematobium*, *S. japonicum*, and *S. mansoni* are estimated to account for 90% of the estimated 207 million schistosomiasis infections worldwide [1, 3]. *S. japonicum* occurs mainly in China, the Philippines, and parts of Indonesia, and, unlike other forms of schistosomes, *S. japonicum* can naturally infect humans and at least 46 other mammalian species [4, 5]. Schistosomiasis japonica symptoms include anaemia, chronic pain, and decreased nutritional status [6–8].

In the Philippines, it is believed that 12 million people are at risk for infection, with 2·5 million directly exposed to *S. japonicum* through water contact activities [3, 9]. In 2000, the Philippines' Department of Health adopted a mass drug administration (MDA) with praziquantel as their control strategy. However, implementing MDA has been challenging due to ubiquitous water contact, heterogeneous acceptance of MDA and the presence of other mammalian reservoirs [9–12]. All mammalian hosts contribute to transmission by shedding *S. japonicum* eggs into or near water bodies, thereby increasing the risk of infection in all hosts [5, 13]. In China, the results from a clustered randomized trial conducted in four pairs of villages suggest that biannual MDA of bovines with praziquantel improves the effectiveness of human annual MDA with praziquantel, thus supporting the hypothesis that bovines act as a reservoir, although the sample size was small (eight villages) [14]. However, bovines may not be the only animals playing a role in transmission. In Anhui Province, China, a 5-year intervention study evaluated the effectiveness of an integrated control strategy including the elimination of bovines from the study area, annual treatment of all residents aged 5–65 years that tested positive with *S. japonicum*, improvement of sanitation facilities, health education to limit water contact with snail-inhabited sites and changing agricultural methods to reduce contact with snail habitats [15]. Human infection decreased during the initial 3 years, but remained stable for the remaining 2 years, suggesting that other reservoirs contributed to the transmission [15], as was suggested from a cross-sectional study conducted in the hilly areas of Anhui Province [16].

In the Philippines, the role played by different mammalian hosts remains uncertain. In Western Samar, a cross-sectional association between the village-level intensity of cat and dog *S. japonicum* infection and the prevalence of human infection has been reported [17]. Genetic analyses using these samples showed a high frequency of parasite gene-flow across species, but particularly between dogs and humans [18]. However, a transmission dynamics model using the same data found humans to be the most important source of human infections, with rats possibly playing a role [19]. The previous studies conducted in Samar were cross-sectional and could not be used to assess causal relationships between non-human and human *S. japonicum* infections. In addition, the cross-sectional study by McGarvey *et al*. [17] used a cumulative-logit model for a relatively common outcome which

may result in the prevalence odds ratio estimates overestimating the prevalence proportion ratio estimates [20]. Such overestimation can lead to selecting control strategies based on the impression that some risk factors have a higher magnitude of effect, as suggested by an odds ratio, compared to the effect that would have been measured with a prevalence ratio. Finally, the lack of adjustment for misclassification error in animal infection could have biased the measures of association.

The purpose of this study is to estimate the magnitude of the effect of village-level prevalence of animal (dogs, cats, rats, water buffaloes) infection with *S. japonicum* on the 12-month cumulative incidence of infection with *S. japonicum* in humans in Western Samar Province, the Philippines.

MATERIALS AND METHODS

Study design

This cohort study was conducted in 50 villages of Western Samar Province, Eastern Visayas region, the Philippines. At baseline (August 2003–April 2004), participants were asked to provide three stool samples and answer a socio-demographic questionnaire to measure potential confounders. From 4 to 8 months after baseline, all villages were offered praziquantel MDA. All villages were visited 11–15 months after MDA (February–December 2005) and participants were asked to provide three stool samples. Stool samples from dogs, cats, rats, pigs, and water buffaloes were collected at baseline and follow-up.

Sampling strategy and study population

Seventy-five of 134 endemic villages met the eligibility criteria, namely safe and relatively easy access, at least 35 households, and not located on the seashore. Of these, 50 were sampled to represent the most ‘rain-fed’ (n = 25) and the most ‘man-made’ (n = 25) irrigation schemes [17, 21].

In each village, 35 eligible households were randomly selected. Each eligible household had at least five members with at least one working full time in a rain-fed farm in ‘rain-fed’ villages and at least 50% of the time in a man-made irrigated farm in ‘irrigated’ villages. In each household, at most six individuals including at least one full-time rice farmer were randomly selected and invited to participate.

MDA

From December 2003 to December 2004, all residents were offered two equal split doses praziquantel treatment (60 mg/kg) following community preparation activities. The village-level participation proportion in MDA varied from 16% to 81% [11]. Participants that tested positive for schistosomiasis were especially encouraged to receive treatment.

Follow-up stool collection in humans

Participants were asked to provide one stool sample per day for three consecutive days. Two slides were prepared from each stool sample 2–3 h after collection. Slides were placed in a

cooler at the end of each day and transferred to a refrigerator at the end of each week. The Kato-Katz technique was used to count the number of *S. japonicum* eggs/g stool [22].

Baseline and follow-up animal stool samples and analysis

At baseline and follow-up, the census of households that owned pigs, dogs and cats was used to randomly sample 35 animals of each species, one in each household, except in the first 10 villages where all animals were sampled. Rats were trapped in 30 cages placed at different locations that changed every day with the aim of trapping 35 rats in each village.

Pigs, water buffaloes and adult dogs had stool samples collected intra-rectally on two or three consecutive days. Cats, puppies and rats were placed in a cage and faeces collected for 2–3 consecutive days. The stool samples were analysed using the Danish Bilharziasis Laboratory (DBL) method [23].

Human and animal ethical review

The human participant research was approved by the institutional review board of Brown University and of the Research Institute for Tropical Medicine. The animal protocol was approved by the Brown University Institutional Animal Care and Use Committee, the Research Institute for Tropical Medicine's Animal Protection Committee, and the DBL Institute for Health Research and Development.

The authors assert that all procedures contributing to this work comply with the ethical standards of the relevant national and institutional committees on human experimentation and with the Helsinki Declaration of 1975, as revised in 2008. The authors assert that all procedures contributing to this work comply with the ethical standards of the relevant national and institutional guides on the care and use of laboratory animals.

Statistical analysis

Definition of the population at risk—Only participants answering the baseline questionnaire, receiving both doses of praziquantel and providing a stool sample at follow-up were considered at risk of infection. We assumed 100% efficacy of praziquantel for the treatment of schistosomiasis japonica, based on recent evidence from China reporting efficacies of over 99·8% [24, 25].

Adjustment for misclassification error in *S. japonicum* infection—Both the Kato-Katz and the DBL tests have imperfect diagnostic accuracies for *S. japonicum*, and no gold standards exist. In addition, the tests' sensitivities and specificities change with the number of stools examined [26–28]. Since we had 1–3 stool samples obtained on consecutive days for each animal and human participant, we used a Bayesian latent-class model adapted from Joseph *et al*. to adjust for the imperfect and changing sensitivities and specificities of the tests in all species [29]. The prior values (s.d.) for the sensitivity and specificity of the Kato-Katz test for human *S. japonicum* diagnosis were set at 54·1% (10·1%) and 94·7% (4·0%), respectively [17]. Prior values for the diagnosis of animal *S. japonicum* were taken from a pilot study conducted in the same area, with sensitivity and specificity values (s.d.) of 75·0% (3·9%) and 96·9% (0·8%) for dogs, 66·3% (7·5%) and 97·2% (0·9%) for cats, 76·8% (6·9%)

and 92·9% (2·6%) for rats, and 78·0% (15·0%) and 98·7% (1·0%) for water buffaloes, respectively [28]. Models with uniform priors between 0 and 1 for both sensitivity and specificity were also conducted for water buffaloes which showed very poor sensitivity values.

Description of the association between cat, dog and rat prevalence of infection—The village-level prevalence proportions of infection in animals at baseline, adjusted for misclassification error, were modelled in a Bayesian linear regression to estimate the regression coefficient.

Modelling the effect of animal infection on human 12-month cumulative incidence of infection—We used a hierarchical log-binomial model [30] with the latent variable for human cumulative incidence of infection as the outcome. The exposure of interest, the prevalence of infection at baseline or follow-up or their difference, adjusted for misclassification error, in dogs, cats, water buffaloes or rats, were modelled as fixed effects at the village level. Confounding variables included human age, sex, their interaction, and occupation as fixed effects at the individual level. The intercept was a random effect at the village level. A region effect was included at the village level, based on baseline results that these regions (Fig. 1) had an important impact on human prevalence [21]. The effect of MDA, irrigation status of the village, and number of days between the baseline and follow-up visits or between treatment and follow-up visit did not have an impact on the cumulative incidence of human infection and are not discussed further.

A number of models were fitted, exploring the effect of the difference between the baseline and follow-up prevalences of animal infection, or including the baseline prevalence of infection in several species simultaneously.

WinBugs software (version 1.4·3, MRC Biostatistics Unit, Cambridge, UK) was used to implement the Gibbs sampler algorithm. Even in routine regression models, whether frequentist or Bayesian, parameter constraints such as those required in the estimation of incidence ratios, require special numerical methods [30], and the computational challenges increase when there is hierarchy in the data. Bayesian modelling is naturally hierarchical and it can be done via Gibbs sampling as implemented in WinBugs. Posterior medians of random samples derived from marginal posterior densities were used as point estimates, reported with 95% Bayesian credible intervals (BCI). The regression coefficients were exponentiated to obtain cumulative incidence ratios (CIR). Each model was run with two chains with at least 20 000 iterations. The programs written in WinBugs are available upon request from the authors.

RESULTS

Of the 6918 individuals who agreed to participate in the study and completed a baseline questionnaire, 2394 (34·6%) did not provide a stool sample at follow-up, and 2056 (29·7%) did not receive praziquantel during MDA, resulting in 2468 (35·7%) participants ‘at-risk’ for this analysis. Table 1 compares the proportion of at-risk and not-at-risk participants according to age and gender, and the baseline parasitological examination results.

The proportion accepting praziquantel MDA was much higher in those with a positive schistosomiasis test at baseline [11]. This was expected since these individuals were particularly encouraged to receive treatment during the mass treatment period. However, having been infected with *S. japonicum* at baseline did not have an impact on the probability of providing a stool sample at follow-up for those people who did receive treatment (76% in those positive and negative at baseline). The proportion taking praziquantel was lower in people without a baseline stool sample (48%). Some of those individuals may have left the village at the time of the follow-up visit. The proportion of participants 'at risk' was lowest in women aged 16–40 years, since praziquantel was not offered to pregnant and lactating women. Men in that age group also showed lower participation, as did children aged <10 years since praziquantel was only offered to those aged ≥5 years.

Figure 1 depicts the 12-month cumulative incidence of human infection according to the three regions sampled. This map clearly shows that the cumulative incidence was highest in region B, followed by region A, and region C.

Dog, cat, and rat prevalence of infection at baseline (Table 2) and follow-up (Table 3) were all associated with the cumulative incidence of human infection in models including only one species.

When the baseline or follow-up dog and cat prevalence proportions were included in the same model, the width of the 95% BCI increased considerably for the effect of cat infection. This can be explained by the high correlation between dog and cat infections (Table 4) and the wide 95% BCI around the sensitivity estimate of the DBL for the diagnosis of cat infections (Table 5).

The models including the baseline or follow-up dog and rat prevalence proportions suggested that infection in both species is related to the cumulative incidence of human infection (Tables 2 and 3). The magnitudes of the association were reduced and the width of the 95% BCI increased in a model using the follow-up dog and rat prevalence proportions (Table 3) compared to a model using the baseline values. However, the magnitude of the effect remained quite strong and the 95% BCI stable in a model including baseline dog infection (CIR 1·03, 95% BCI 1·01–1·06) and follow-up rat infection (CIR 1·02, 95% BCI 1·01–1·03) prevalences (Table 6). The magnitude and the 95% BCI of the association between the difference in the prevalence of infection at baseline and follow-up in dogs, and rats were inconclusive, as were the CIR and 95% BCI for the effect of water buffalo infection at baseline (Table 2) and follow-up (Table 3). It is noteworthy that the sensitivity of the DBL to detect water buffalo infection was very poor (Table 5).

In addition to the association of animal infection prevalence, the region of residence influenced the 12-month cumulative incidence of infection, especially for people living in region B (Table 6). This association was independent from that of animal infection, as the inclusion of any village-level animal prevalence only minimally influenced the effect of region. Age was found to modify the impact of gender, and pupils or students were at lower risk of infection than those working on rice farms.

DISCUSSION

Our findings suggest that dog, rat and cat village-level *S. japonicum* infection prevalence proportions measured at baseline or follow-up were associated with the 12-month cumulative incidence of human infection after treatment with praziquantel in 50 villages of Samar. However, the poor precision of the estimated sensitivity of the test to detect cat infections combined with high correlation between the infection prevalence proportions between dogs and cats made it difficult to separate out these two associations.

This study confirms our prior cross-sectional and schistosome genotyping findings that *S. japonicum* infection in dogs is associated with *S. japonicum* infection in humans [17, 18]. The magnitude of the effect was similar in the cross-sectional model although it measured the odds ratio for the unadjusted unit increase in 1 egg/g in dog infection at the village level, which could have been an overestimate of the effect. The magnitude of the effect of dog infection on human infection is very similar in the current study, but more precise, as would be expected from a cumulative incidence measure [20], and indicates the increase in human risk per 1% increase in the adjusted prevalence of dog infection. We believe that estimate to be accurate and also easier to interpret for decision makers. The genotyping study found minimal genetic differences in schistosomes from human and dog samples thereby suggesting the possibility of high transmission between dogs and humans [18]. The cross-sectional data had found some associations between the village-level average number of dog and cat *S. japonicum* eggs/g (not adjusted for measurement error) with human infection [17]. Our findings support that of a longitudinal study conducted in marshland and hilly villages in China where a high transmission index in dogs in the absence of bovines was found [16]. However, our findings cannot determine if this association is due to dogs and humans sharing the same strains of *S. japonicum* and being exposed at the same sites or if dogs are the sources of human infection. Nevertheless, the cohort nature of our study and a more conclusive effect of baseline village-level prevalence of dog infection, instead of the less conclusive effect of follow-up prevalence or change in prevalence of dog infection, suggest that there may be a delay between the environmental contamination with dog faeces and the resulting infection in humans. First, biologically, there would need to be a delay of at least 2–3 months between a dog infection and the detection of human infection due to the complex life-cycle of schistosomiasis [31]. Second, our data from Samar show that the 12-month cumulative incidence of human schistosomiasis was almost as high as the prevalence estimates observed at baseline [17]. This is in contrast to the results of a transmission dynamics model using data from Bohol in the Philippines in the 1980s where the prevalence of infection 12 months following mass drug treatment with a coverage of 50% was about half of that estimated at baseline [13]. Hence, although we cannot be certain if the association between village-level prevalence of dog infection at baseline and human cumulative incidence of infection is due to dogs and humans sharing the same strains of *S. japonicum* and being exposed at the same sites or if dogs are the sources of human infection, our data and the literature tend to favour the latter hypothesis. The less conclusive association found with baseline village-level prevalence of infection in rats, but more conclusive association with the follow-up prevalence of infection, support our previous finding from a transmission dynamics model that rat infection may be weakly associated

with human infection [19]. It may suggest that rats are good indicators of the presence of the snail vectors, but may not share with humans the same strain of *S. japonicum*.

Our findings demonstrate that socio-demographic and geographical factors are risk factors for human *S. japonicum* infection. Age, gender, occupation, and region showed strong magnitude of effect on the 12-month cumulative incidence of infection. This supports the prior transmission dynamics model and the genetic analysis suggesting that the most important source of human infection with schistosomiasis remains the human host [18, 19]. The very strong effect of the region of residence will require more investigation to determine what environmental factors make some populations more at risk. The irrigation status of the village did not impact human infection.

Several strengths of this study are noteworthy. This is the first cohort study to report the cumulative incidence of human schistosomiasis in such a large number of villages and residents. The reported cumulative incidences are adjusted for misclassification error due to the poor accuracy of the Kato-Katz test and the fact that participants provided different numbers of faecal samples. It is unique in its estimation of the strength of the effect of village-level prevalences of infection in four mammalian species (cats, dogs, water buffaloes, rats) and the 12-month cumulative incidence of *S. japonicum* infection in humans, while adjusting for misclassification error in the diagnosis of infections in humans and other mammalian hosts, and taking the clustering of infection into account. This study used a log-binomial model to estimate CIRs, which are more appropriate measures of association than odds ratios for cohort studies and for outcomes that are common [20]. Therefore, we believe our estimated measures of association to have little bias.

This study has some limitations. First, treatment with praziquantel was assumed to be 100% effective based on previous studies [24, 25], so it is likely that those who did receive treatment, which was observed, were successfully treated. Second, relatively fewer women aged 17–40 years and individuals not providing a baseline stool sample were included in the ‘at risk’ population. Women in that age group were found to be less intensely infected than their male counterparts at baseline [21]. Moreover, MDA participation in those who had not provided a baseline stool sample was lower, most likely due to their absence from the village. Hence, the lower proportion of participants in these two populations will minimally bias our findings given their limited role in the transmission cycle of schistosomiasis, either by not working on the rice farm or being absent from the village. Third, recent studies of water buffalo *S. japonicum* infection in Leyte and Samar, using more sensitive molecular and coprological techniques [32, 33], showed much higher prevalence of infection in water buffaloes in results unadjusted for misclassification error. Our unadjusted results show a very low prevalence of infection in water buffaloes. However, our adjusted median prevalence results using unrestricted sensitivity and specificity prior values are consistent with previous findings [32, 33]. On the other hand, the very small number of animals found positive for *S. japonicum* limited our ability to obtain precise estimates. The studies in China which had suggested an association between infection in water buffaloes and humans had used the miracidia hatching technique [14, 16], which was found to be even less sensitive than the DBL method when compared to PCR [32]. Hence, if water buffaloes do play a role

in the transmission of infection to humans in Samar, it may be to a lesser extent than that reported in China.

CONCLUSIONS

Dogs, cats and rats were found to play a role in schistosomiasis transmission, with dogs and rats showing more consistent effects. Therefore, schistosomiasis elimination efforts should not exclude the possibility of targeting infection in dogs, and possibly cats, as well as in humans, as this approach could improve the effectiveness of MDA programmes in this area of the Philippines. Rats could be considered as a good sentinel to monitor infection levels in the environment. Further genetic and aetiological research is needed to understand the role of other animals in transmission to humans, as well as the environmental factors associated with the effect of the region of residence. Employing a One Health approach which would involve experts in environmental sciences, veterinary and human medicine may contribute to the elimination of schistosomiasis in human communities [34].

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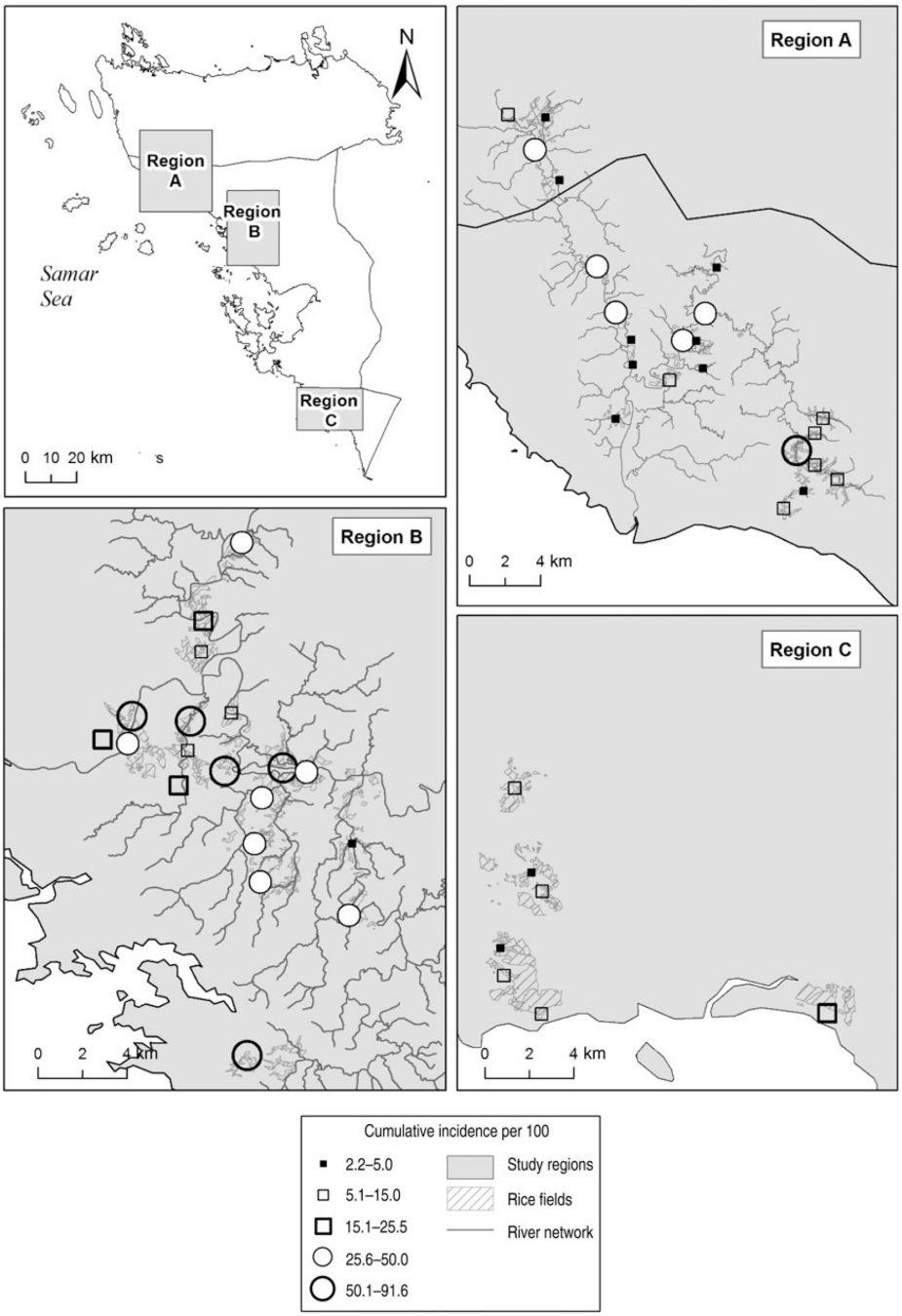

Fig. 1.

Twelve-month cumulative incidence (adjusted for age, sex, occupation and misclassification error) of human infection with *Schistosoma japonicum* in people having received praziquantel treatment in 50 villages of Samar province, the Philippines, 2005.

Table 1

Characteristics of the individuals who were included in the analysis ('at-risk' group) and the individuals who provided stool sample at baseline but were not included in the analysis ('not-at-risk' group) with the estimated ratio of participation for each characteristic*

Characteristic	At-risk group *n* (%)	Not-at-risk group *n* (%)	Proportion ratio (95% BCI)
N	2468 (35·7)	4450 (64·3)	
Males, age (years)			
<10	364 (33·9)	710 (66·1)	0·69 (0·62–0·78)
11–15	267 (44·3)	336 (55·7)	0·69 (0·62–0·78)
16–40	440 (32·7)	905 (67·3)	0·67 (0·60–0·75)
>40	328 (48·8)	344 (51·2)	Reference
Females, age (years)			
<10	359 (32·6)	742 (67·4)	0·66 (0·59–0·75)
11–15	178 (37·2)	301 (62·8)	0·76 (0·66–0·87)
16–40	237 (22·7)	805 (77·3)	0·46 (0·40–0·53)
>40	295 (49·1)	306 (50·9)	Reference
S. japonicum at baseline (based on results of the Kato-Katz test)			
Yes	537 (60·8)	347 (39·3)	1·64 (1·54–1·75)
No	1753 (37·0)	2987 (63·0)	Reference
Unknown	178 (13·8)	1116 (86·2)	0·37 (0·32–0·43)

BCI, Bayesian credible interval.

*One participant did not provide age and gender information.

Table 2

Adjusted* cumulative incidence ratio estimates of human infection with *Schistosoma japonicum* from a one unit increase (1%) in the baseline prevalence proportion of dog, cat, water buffalo and rat *S. japonicum* infection using a Bayesian hierarchical model adjusting for misclassification error

	Cumulative incidence ratio estimate (95% BCI)			
Animals species included in the model	**Dogs**	**Rats**	**Cats**	**Water buffaloes**
Dogs only	1·04 (1·02–1·07)			
Rats only		1·02 (1·00–1·04)		
Cats only			1·17 (1·01–1·39)	
Water buffaloes only				1·02 (0·98–1·05)
Dogs and rats	1·04 (1·02–1·07)	1·01 (1·00–1·03)		
Dogs and cats	1·05 (1·02–1·09)		0·95 (0·77–1·15)	
Dogs and water buffaloes	1·05 (1·02–1·07)			1·01 (0·98–1·04)

BCI, Bayesian credible interval.

*All models are adjusted for age, gender, occupation at the individual level and region at the village level and include village-level random-effect intercepts.

Table 3

Adjusted* cumulative incidence ratio estimates of human infection with *Schistosoma japonicum* from a one unit increase (1%) in the follow-up prevalence proportion of dog, cat, water buffalo and rat *S. japonicum* infection using a Bayesian hierarchical model adjusting for misclassification error

	Cumulative incidence ratio estimate (95% BCI)			
Animals species included in the model	**Dogs**	**Rats**	**Cats**	**Water buffaloes**
Dogs only	1·04 (1·02–1·06)			
Rats only		1·04 (1·02–1·06)		
Cats only			1·24 (1·01–1·46)	
Water buffaloes only				1·03 (0·96–1·06)
Dogs and rats	1·02 (1·00–1·05)	1·02 (1·00–1·05)		
Dogs and cats	1·03 (1·01–1·06)		1·16 (0·87–1·35)	
Dogs and water buffaloes	1·04 (1·02–1·06)			1·03 (0·97–1·05)

BCI, Bayesian credible interval.

*All models are adjusted for age, gender, occupation at the individual level and region at the village level and include village-level random-effect intercepts.

Table 4

Linear regression coefficient among animal infection at baseline

Animals	Baseline, coefficient (95% BCI)
Dogs and cats	3·73 (2·16 to 5·6)
Dogs and water buffaloes	0·05 (−0·63 to 0·60)
Dogs and rats	0·30 (0·01 to 0·61)
Cats and water buffaloes	−1·61 (−7·5 to 0·07)
Cats and rats	0·12 (−0·46 to 0·58)
Rats and water buffaloes	0·09 (−1·01 to 1·07)

BCI, Bayesian credible interval.

Table 5

Posterior sensitivity and specificity estimates the Danish Bilharziasis Laboratory test for the detection of animal infection using one stool sample

	Baseline (95% BCI)		Follow-up (95% BCI)	
	Sensitivity	**Specificity**	**Sensitivity**	**Specificity**
Dogs	66·7 (60·7–72·5)	98·3 (97·4–99·0)	74·6 (68·2–80·4)	98·4 (97·6–99·1)
Rats	54·9 (49·1–60·9)	98·4 (97·1–99·3)	64·9 (55·5–73·3)	99·1 (98·3–99·6)
Cats	42·5 (31·6–55·7)	99·5 (99·2–99·8)	51·5 (35·1–69·1)	99·1 (98·4–99·6)
Water buffaloes	5·1 (3·3–7·9)	99·9 (99·4–100·0)	3·3 (1·7–5·5)	99·6 (98·7–100·0)

BCI, Bayesian credible interval.

Table 6

Cumulative incidence ratio estimates of all variables included in the final Bayesian hierarchical log-binomial model of human infection with *Schistosoma japonicum*

Variable	Category	Reference	RR (95% BCI)
Dog prevalence of infection at baseline	Each percent increase in prevalence		1·03 (1·01–1·06)
Rat prevalence of infection at follow-up	Each percent increase in prevalence		1·02 (1·01–1·04)
Age effect, boys	10–15 yr	<10 yr	1·89 (1·21–3·00)
	16–40 yr		1·41 (1·01–2·05)
	>40 yr		0·74 (0·44–1·19)
Age effect, girls	10–15 yr	<10 yr	2·62 (1·35–5·65)
	16–40 yr		0·81 (0·31–1·59)
	>40 yr		0·67 (0·31–1·21)
Gender effect for age <10 yr	Male	Female	1·43 (0·92–2·30)
Gender effect for age 10–16 yr	Male		1·03 (0·53–1·87)
Gender effect for age 17–40 yr	Male		2·51 (1·39–6·16)
Gender effect for age >40 yr	Male		1·59 (0·87–3·51)
Rice farming	Some of the time	All the time	0·99 (0·51–1·67)
	Other type of farming		0·77 (0·10–2·03)
	No farming		0·69 (0·35–1·22)
	Pupil/student		0·54 (0·30–0·90)
Region effect	B	A	6·20 (2·47–18·20)
	C		2·58 (0·66–10·2)

RR, Risk ratio; BCI, Bayesian credible interval.