



## Commentary

## Hotspots and correlates of soil-transmitted helminth infections in a Venezuelan rural community: Which are the “wormy” houses?

Renzo Nino Incani<sup>a,\*</sup>, María Eugenia Grillet<sup>b</sup>, Lapo Mughini-Gras<sup>c,d</sup><sup>a</sup> Department de Parasitología, Faculty of Health Sciences, Universidad de Carabobo, Valencia, Venezuela<sup>b</sup> Laboratorio de Biología de Vectores y Parásitos, Instituto de Zoología y Ecología Tropical, Facultad de Ciencias, Universidad Central de Venezuela, Caracas, Venezuela<sup>c</sup> Center for Infectious Diseases Control, National Institute for Public Health and the Environment (RIVM), Bilthoven, the Netherlands<sup>d</sup> Faculty of Veterinary Medicine, Institute for Risk Assessment Sciences (IRAS), Utrecht University, Utrecht, the Netherlands

## ARTICLE INFO

## Article history:

Accepted 6 October 2020

Available online 1 December 2020

## Keywords:

Geospatial analysis  
 Geographical information system  
 Soil-transmitted helminthiasis  
*Ascaris lumbricoides*  
*Trichuris trichiura*  
 Hookworms  
*Strongyloides stercoralis*  
 Wormy houses  
 Hotspots

## SUMMARY

**Objectives:** To determine spatial clustering and risk factors for occurrence and intensity of infection for soil-transmitted helminthiasis (STH), namely *Ascaris lumbricoides*, *Trichuris trichiura*, *Strongyloides stercoralis* and hookworms in a Venezuelan rural community.

**Methods:** MIF-fixed faecal samples were individually collected for STH testing. The Getis–Ord statistic was used to determine significant STH clustering within 25/50/100 m radiuses around houses. Individual- and house-level factors associated with STH occurrence and intensity of infection were determined using generalized estimating equations.

**Results:** Significant clusters of “wormy” houses for one or multiple parasites were found at distances of 25–50 m around 13 houses. Risk factors differed between occurrence and intensity of infection. Overcrowding in the house increased occurrence of *S. stercoralis*, *T. trichiura* and hookworm infections, while poor housing conditions increased *A. lumbricoides* infection risk. Overcrowding, poor faecal disposal system, economic dependency and lack of basic services differentially influenced the STHs. The “wormy” houses were mainly those built with waste materials, under economic dependency and lacking indoor water supply.

**Conclusions:** STH distribution in a community is clustered, with significant hotspots of STH occurrence and intensity of infection and different associated risk factors. Targeting the “wormy” houses is expected to affect STH morbidity more efficiently.

© 2020 The British Infection Association. Published by Elsevier Ltd. All rights reserved.

## Introduction

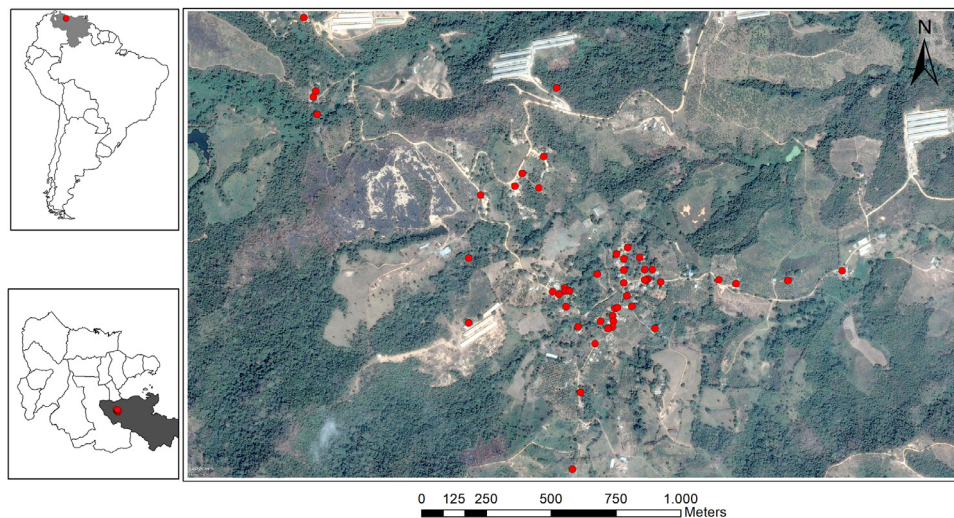
Soil-transmitted helminthiasis (STH) poses a heavy disease burden throughout the tropics and has been linked to malnutrition, anaemia, physical and mental growth and cognitive deficit in children.<sup>16,24,25,40,43</sup> Theoretical models have estimated 5.9 billion people to be at risk of infection and almost 3 billion people to be infected worldwide, with the three major STHs being caused by *Ascaris lumbricoides*, *Trichuris trichiura* and the two species of hookworms, *Ancylostoma duodenale* and *Necator americanus*,<sup>35,36</sup> although more recent estimates by WHO account for 1.5 billion people infected with STHs worldwide.<sup>45</sup> Geospatial analysis has been used extensively as a tool to assess geographical distribution and risk of infection for many infectious diseases (e.g. <sup>32,41</sup>). Predictive

risk maps for STH have been generated using Bayesian modeling in some cases, coupled with geographical information systems and remote sensing of climatic and environmental variables. Socioeconomic data were linked to these maps, with useful results at a local, national and even continental level in terms of predicting the distribution of the disease and resources to be allocated for mass drug administration (MDA).<sup>5,6,10,44,30,8,33,39,9,28,18,47,37,31</sup> However, the results varied considerably when the socioeconomic variables have been assessed in large-scale studies due to heterogeneity within or between communities.<sup>29</sup>

Using data from a well-studied rural community in northern Venezuela, we aimed to assess the intra-community spatial heterogeneity of STH infections and determine both individual- and dwelling-level risk factors for STH infection. By focusing on the dwelling as the analytical unit we assessed the occurrence and determinants of the so-called “wormy houses”, i.e. the hotspots of STH infection risk.

\* Corresponding author.

E-mail addresses: [rmincani@gmail.com](mailto:rmincani@gmail.com) (R.N. Incani), [maria.grillet@ciens.ucv.ve](mailto:maria.grillet@ciens.ucv.ve) (M.E. Grillet), [lapo.mughini.gras@rivm.nl](mailto:lapo.mughini.gras@rivm.nl) (L. Mughini-Gras).



**Fig. 1.** Maps of Venezuela in South America (upper left window), Carabobo State (lower left window) and the studied rural community (Caserio 25) in the north of the country (center image) showing the sampled houses (red symbols) and others relevant features of the landscape (Google Earth TMB image).

## Methods

### Study population and ethical clearance

Caserio El 25 is a rural community located in a hilly area in the northern part of Venezuela, with a mean altitude of 580 m a.s.l.,<sup>17</sup> 25 km southeast from the city of Valencia, Carabobo State (Fig. 1). The surrounding environment is characterized by tropical rainforest vegetation and the economy is based on commercial poultry breeding, agriculture and subsistence farming. The community is built around two main dirt roads extending for about 6 km. At the time of the study (March 2010), the community was composed by 470 inhabitants living in 85 houses, of which 224 from 55 houses participated in the study. Written informed consent was obtained from all adults, parents or official caretakers of children. The study adheres to local ethical criteria (Ethical Committee of the Carabobo State Health Authority, INSALUD), and was approved by the ethical committee of VU University, Amsterdam. At the end of the study, all participants were offered (free of charge) a single dose of Pirantel<sup>®</sup> as deworming agent.

### Coprology

Faecal samples were collected in pre-weighed tubes with Merthiolate-Iodine-Formaldehyde (MIF) fixative, and then reweighed after adding the faeces, to obtain the amount of faeces examined for each participant. After vortexing the tubes, 100  $\mu$ l of faecal suspensions were pipetted into microscopic slides, covered with 24  $\times$  50 mm coverslips, and sealed with melted paraffin to avoid desiccation. Two samples of faecal suspension per person were thoroughly examined at the microscope for parasite identification and parasite eggs were counted separately for each species, to obtain a final count of eggs per gram (EPG) or larvae per gram (LPG), the latter for *Strongyloides stercoralis*. When the difference between two counts was more than 20%, a third slide was included. For each house, the mean value of EPG per house (EPG/h) was calculated from the EPG values of each individual (infected and non-infected) living in the house.

### Epidemiological data

Demographic and socioeconomic data collected together with the faecal samples were: age, gender, socioeconomic level (Graffar

grading), educational level (none, incomplete or complete primary school), school absenteeism (for children 7–10 years-old: absent or present at school), overcrowding (3 or more people/bedroom), type of house (rural house constructed by the state with all sanitary services or dwelling made of waste material and soil floor), indoor water supply, faecal disposal system (WC, latrine, soil, or mixed WC and soil), number of unsatisfied basic services (lack or incomplete use of the following services: indoor water supply, WC, septic tank), and high economic dependency (>3 persons depending on one salary).

### Spatial analysis

We tested the hypothesis that an STH infection was equally likely to occur at any household within the community, regardless of the other households with infections. Consequently, the observed infection patterns would represent the normal variation in parasite incidence given the at-risk population distribution. For that, we used one local measure of spatial association, the local Getis–Ord statistic,  $G_i^*(d)$ , to analyze the infection events at household level.<sup>19</sup> Specifically, the statistic  $G_i^*(d)$  identified significant local clustering of highly positive values (i.e. hotspots) of STH infection surrounding a particular house within a radius (circular window) of specified distance  $d$  from that location. Specific infection cases were standardized as the total number of positive individuals for each STH species divided by the total number of individuals surveyed in that household. The distance  $d$  defined the neighborhood search for a particular house, with nearby locations being expected to have similar values. The value obtained was compared with the statistic's expected value to indicate if the degree of clustering of infection cases in the vicinity of a particular house was greater or less than expected by chance. We calculated  $G_i^*(d)$  at different scales by using various window sizes (100, 50, 25 and 10 m each). The final selected  $G_i^*(d)$  distance corresponded to the scale at which  $G_i^*(d)$  maximum value was found; i.e., the scale of the spatial dependence of the process under study.<sup>20</sup> The analyses of hotspots were carried out through the ArcGIS10 (ESRI Corporation, Redlands, CA) software which uses the  $z$ -score values as a measure of clustering or hotspot. The  $z$ -score is a statistical measure of the spread of values from their mean, expressed in standard deviation units, where the  $z$ -score of the mean value is zero and the standard deviation is one. The  $z$ -score values will be higher as much as clustering of infection cases occur in the study



area. In our case, those points or locations with +2 standard deviations from the mean are the hotspots. Risk maps at household level for each parasite species were drawn by using a satellite image of the study area from Google EarthTMB in order to show the specific “wormy houses” according to this analysis

### Risk factor analysis

Prevalence was calculated for each parasite species separately (*S. stercoralis*, *A. lumbricoides*, *T. trichiura* and hookworms) and combined, for the whole community under study as well as for children  $\leq 14$  years. Cluster-robust standard errors were used to account for clustering of participants living in the same households. The demographic and socioeconomic variables were assessed for association with infection with each parasite species using both univariate and multivariate GEE (generalized estimating equations) regression models with a logit link function and binomial error distribution. GEEs accounted for clustering of individuals living in the households using quasi-likelihood methods and cluster-correlated robust variance estimators.<sup>26</sup> Associations were expressed as odds ratios (OR) and corresponding 95% confidence intervals (95%CI). Afterwards, the EPG/LPG for each parasite species in the infected individuals were analyzed to identify factors associated with increased or decreased numbers of EPG/LPG using GEE regression models with a log link function and negative binomial error distribution. These models used the EPG/LPG as dependent variable providing Incidence Rate Ratios (IRR) and 95%CI. The same analysis was performed at the dwelling-level using the average EPG/LPG values per dwelling as dependent variable. The quasi-likelihood under the independence model information criterion (QIC) was used to guide the selection of the most parsimonious model and the best-fitting within-group working correlation structure in all GEE models.<sup>13</sup> The variables sex and age group ( $\leq 7$ , 8–13, 14–34,  $\geq 35$  years) were always retained in the models to adjust for potential confounding effects. Multivariate models were built including those variables with a  $p$ -value  $< 0.10$  at the univariate analyses and were reduced using a backward stepwise approach until all variables in the model had a  $p$ -value  $< 0.05$ . How-

**Table 1**

Percent prevalence (and respective 95% confidence interval) for each parasite infection and for any parasite infection by age of the participant in the studied community.

	$\leq 14$ years ( $n = 116$ )	$> 14$ years ( $n = 108$ )	$P$ -value
<i>Ascaris lumbricoides</i>	53.4 (38.5–67.8)	25.0 (16.1–36.7)	0.003
<i>Trichuris trichiura</i>	40.5 (26.7–55.9)	20.4 (12.3–31.8)	0.047
Hookworms	6.9 (2.4–18.5)	12.0 (4.3–29.2)	0.132
<i>Strongyloides stercoralis</i>	8.6 (2.9–22.8)	11.1 (5.8–20.1)	0.392
Any helminth infection	61.2 (45.2–75.1)	41.7 (29.5–54.9)	0.090

Number of individuals examined: 224 in 55 houses.

Coprolology was carried out using the MIF fixation method. Two slides per faecal sample were examined and eggs counted.

ever, when removing a variable caused a change in the association of the other covariates by  $> 10\%$ , then this variable was considered as potential confounder and was retained in the model regardless of significance. Biologically plausible interactions between covariates were also assessed. Statistical analysis was performed using STATA 13 (StataCorp, College Station, USA).

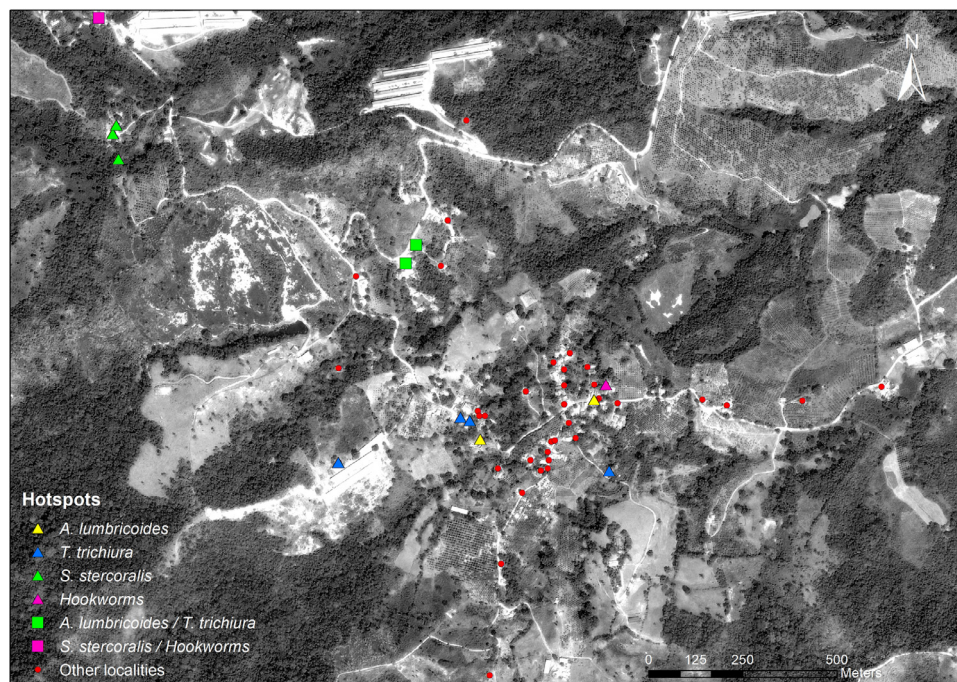
### Results

#### Prevalence of helminths

Overall, 39.7% (95%CI 29.1–51.5%) of the 224 participants were infected with *A. lumbricoides*, 30.8% (95%CI 20.9–42.9%) with *T. trichiura*, 9.4% (95%CI 4.1–20.1%) with hookworms, and 9.8% (95%CI 5.3–17.5%) with *S. stercoralis*. The prevalence of any STH infection was 51.8% (95%CI 39.2–64.1%), and although it was higher in children, it was not significantly different from the rest of the community. The prevalence of *A. lumbricoides* and *T. trichiura* was significantly higher in children of  $\leq 14$  years than the rest of the community (Table 1).

#### Spatial clustering

Local clustering maps of the mean infection density for each parasite species are shown in Fig. 2. Three significant clustering



**Fig. 2.** Significant clusters (hotspots) of worm infection per house (wormy houses) per parasite species according to the local Getis statistic ( $G_i^* [d]$ ,  $z$ -score  $> 2.58$ ,  $P < 0.01$ ) in the studied rural community in northern Venezuela.

**Table 2**

Intensity of infection and percent wormy houses for *Ascaris lumbricoides* and *Trichuris trichiura*, hookworms and *Strongyloides stercoralis* in the studied community.

Soil-transmitted helminth	N° of “wormy” houses	% “wormy” houses	N° of individuals infected in “wormy” houses	Σ EPG/LPG of infected individuals in “wormy” houses <sup>a</sup>	Σ EPG/LPG of all individuals infected <sup>c</sup>	% EPG/LPG of individuals in “wormy” houses <sup>d</sup>
<i>Ascaris lumbricoides</i>	4	7.7	14	209,083	515,442	40.6
<i>Trichuris trichiura</i>	4	7.7	14	12,193	27,256	44.7
Hookworms	3	5.8	13	12,417	13,032	95.3
<i>Strongyloides stercoralis</i>	2	3.8	4	351 <sup>b</sup>	1081 <sup>b</sup>	32.5 <sup>b</sup>

Number of individuals examined: 224 in 55 houses.

Coprolology was carried out using the MIF fixation method. Two slides per faecal sample were examined and eggs counted.

EPG = eggs per gram of faeces. LPG = larvae per gram of faeces.

<sup>a</sup> The mean number of EPG/LPG for each “wormy” house was added (Σ).

<sup>b</sup> Larvae of *S. stercoralis*.

<sup>c</sup> The mean number of EPG/LPG for each infected house of the sample of the community was added (Σ).

<sup>d</sup> Percent of Σ of mean EPG/LPG of wormy houses/Σmean EPG/LPG of all positive houses.

patterns of parasite infection levels were observed with the local Getis statistic ( $G_i^* [d]$ ,  $z$ -score  $> 2.58$ ,  $p < 0.01$ ) at distances from 25 to 50 m around 13 houses across the study area. Regarding *A. lumbricoides*, 3 hotspots were detected at 25 m in the north-central side of the community. A similar clustering pattern of high *T. trichiura* infection was observed at distances of 25 m around 3 houses in the south-central side of the community. Interestingly, there were co-occurrence of similar hot spots of *A. lumbricoides* and *T. trichiura* in two houses (helminth co-infections) localized in the central side of the community. Household density of *S. stercoralis* infection was also aggregated at 25 m just in two houses localized in the north and center of the community. By contrast, high levels of hookworm infection clustered around four houses at 50 m in the north side of the community.

The hotspots for prevalence were represented by two houses that concentrated 41% of infections with *A. lumbricoides*, four houses (45%) for *T. trichiura*, three houses (95%) for hookworms and two houses (32%) for *S. stercoralis* (maps not showed)

### Intensity of infection

The number of EPG/LPG for each parasite species in the infected individuals living in houses identified as hotspots in the spatial analysis, and those in all infected houses of the community, are reported in Table 2. Four “wormy” houses for ascariasis and tricuriasis each were identified, representing 7.7% of all infected houses and having a total of 14 individuals infected with each parasite species. Two houses were the same for both parasites. The number of EPG of these “wormy” houses accounted for 40.6% and 44.7% of the *A. lumbricoides* and *T. trichiura* EPGs, respectively, in the infected houses (Table 2). Three “wormy” houses (with 13 infected individuals therein) accounting for 5.8% of infected houses of the community were identified for hookworm infection; the number of EPG in these houses accounted for 95.3% of the total EPG in the community. No overlapping “wormy” houses for hookworms with *A. lumbricoides* or *T. trichiura* were found. For *S. stercoralis*, two “wormy” houses were identified with four individuals infected, accounting for 3.8% of all infected houses and 32.5% of the number of *S. stercoralis* LPG in the community. One “wormy” house for *S. stercoralis* infection coincided with one for hookworms, but none coincided with those for *A. lumbricoides* or *T. trichiura*. The frequencies of the intensity of infection for each parasite was also classified based on WHO’s classification of EPGs in Table 3. As expected, most infected individuals had low-medium parasite loads, with only a few highly infected with *A. lumbricoides* and *T. trichiura*. The low numbers of inhabitants infected with hookworms makes it difficult to ascertain if the 33% of individuals observed with heavy infection is not biased by sampling limitations.

**Table 3**

Frequencies of the intensity of infection based on WHO classification of eggs per gram of faeces for each parasite in the studied community.

	Light-intensity	Moderate-intensity	Heavy-intensity
<i>Ascaris lumbricoides</i>	33 (37%)	42 (47%)	14 (16%)
<i>Trichuris trichiura</i>	36 (52%)	31 (45%)	2 (3%)
Hookworms	13 (62%)	1 (5%)	7 (33%)

WHO = World Health Organization. EPG = eggs per gram. *A. lumbricoides*: light intensity 1–4999 EPG, moderate intensity 5000–49,999 EPG, heavy intensity > 50,000 EPG. *T. trichiura*: light intensity 1–999 EPG, moderate intensity 1000–9999 EPG, heavy intensity > 10,000 EPG. Hookworms: light intensity 1–1999 EPG, moderate intensity 2000–3999 EPG, heavy intensity > 4000 EPG.

### Risk factors

The results of the risk factor analyses associated with prevalence are summarized in Table 4. For *S. stercoralis*, *T. trichiura* and hookworms, only overcrowding in the household was associated with increased risk of infection, with people living in a house where there were  $\geq 3$  people sleeping in the same bedroom having an OR of 3.83 ( $p = 0.003$ ) for *S. stercoralis*, 3.47 ( $p = 0.015$ ) for *T. trichiura*, and of 21.05 ( $p = 0.001$ ) for hookworms as compared to people with  $\leq 2$  people sleeping in a bedroom. For *A. lumbricoides*, only the house type was significant, with people living in a house built with waste material being at increased risk (OR 3.19,  $p = 0.005$ ) for *A. lumbricoides* infection as compared to people living in regular houses. Regarding the factors significantly associated with EPGs (Table 5), those for *A. lumbricoides* were economic dependency and faecal disposal, i.e. individuals disposing their faeces in a latrine (IRR 4.87,  $p = 0.002$ ), outdoor/soil (IRR 4.80,  $p = 0.000$ ), or a combination of them (IRR 3.48,  $p = 0.002$ ) had higher *A. lumbricoides* EPGs than those using only a WC, and individuals with  $\geq 3$  people in the household depending on one salary (IRR 2.29,  $p = 0.025$ ) also had higher *A. lumbricoides* EPGs than those with  $\leq 2$  people depending on a salary. Moreover, when infected, people of 35 years of age or older eliminated significantly less EPGs than those < 7 years of age (IRR 0.42, 95%CI 0.19–0.88,  $p = 0.024$ ). Regarding *T. trichiura*, individuals lacking basic services eliminated more EPGs (IRR 3.33,  $p = 0.000$ ), as well as individuals of 8–13 years of age as compared to those  $\leq 7$  years (IRR 2.82, 95%CI 1.63–4.89,  $p = 0.000$ ). For hookworms, both overcrowding and faeces disposal were associated with EPGs; individuals living in a household with  $\geq 3$  people sleeping in the same bed eliminated more EPGs (IRR 24.92,  $p = 0.003$ ), and the same was true for people disposing their faeces outdoor instead of in a WC (IRR 9.76,  $p = 0.000$ ). No factor was significantly associated with increased or decreased LPG for *S. stercoralis*.

**Table 4**

Risk factors significantly associated with prevalence of infection with *Strongyloides stercoralis*, *Ascaris lumbricoides*, *Trichuris trichiura* or hookworms from the final multivariate generalized estimating equation regression models.

	<i>Strongyloides stercoralis</i> OR (95%CI)†	<i>Ascaris lumbricoides</i> OR (95%CI)†	<i>Trichuris trichiura</i> OR (95%CI)†	Hookworms OR (95%CI)†
<b>Overcrowding</b>				
≤2 people/bedroom	Reference		Reference	Reference
≥3 people/bedroom	3.83 (1.58–9.33)**		3.47 (1.27–9.43)*	21.05 (3.37–131.30)***
<b>House type</b>				
Regular		Reference		
Built with waste material		3.20 (1.43–7.16)**		

\* $p < 0.05$ , \*\*  $p < 0.01$ , \*\*\* $p < 0.001$ . OR = Odds Ratio. 95%CI = 95% Confidence Interval. †Estimates are corrected for sex, age group, and clustering of people at the household level.

**Table 5**

Factors significantly associated with intensity of infection (eggs/larvae per gram of faeces) for *Strongyloides stercoralis*, *Ascaris lumbricoides*, *Trichuris trichiura* or hookworms from the final multivariate generalized estimating equation regression models.

	<i>Strongyloides stercoralis</i> IIR (95%CI)†	<i>Ascaris lumbricoides</i> IIR (95%CI)†	<i>Trichuris trichiura</i> IIR (95%CI)†	Hookworms IIR (95%CI)†
<b>Faeces disposal</b>				
WC		Reference		Reference
Latrine		4.87 (1.71–13.86)**		2.14 (0.18–25.50)
Outdoor/soil		4.80 (2.69–8.57)***		9.76 (2.95–32.31)***
Combination		3.48 (1.59–7.63)**		2.02 (0.21–19.28)
<b>Economic dependency</b>				
≤2 people/salary		Reference		
≥3 people/salary		2.29 (1.11–4.72)*		
<b>Overcrowding</b>				
≤2 people/bedroom				Reference
≥3 people/bedroom				24.92 (2.95–210.54)**
<b>Lack basic services</b>				
No			Reference	
Yes			3.33 (2.05–5.41)***	

\* $p < 0.05$ , \*\*  $p < 0.01$ , \*\*\* $p < 0.001$ . IIR = Incidence Rate Ratio. 95%CI = 95% Confidence Interval. †Estimates are corrected for sex, age group, and clustering of people at the household level.

At the house level, significantly lower EPG values for *A. lumbricoides* and *T. trichiura* were observed in regular houses (IRR 0.15, 95%CI 0.06–0.38,  $p = 0.000$  and IRR 0.14, 95%CI 0.05–0.42,  $p = 0.000$ , respectively). Higher *A. lumbricoides* EPG values were found in houses with ≥3 people depending on one salary (IRR 5.16, 95%CI 1.24–21.37,  $p = 0.024$ ), while houses with indoor water supply had lower *T. trichiura* EPG values (IRR 0.12, 95%CI 0.03–0.52,  $p = 0.005$ ). No factors were significantly associated with EPG/LPG for the other parasites at the household levels.

## Discussion

We applied spatial analysis techniques to identify hotspots of STH activity, both in terms of occurrence and intensity of infection, in a well-studied rural community in Venezuela. Findings revealed that, overall, local clustering of parasite infection in a few “wormy” houses accounted for an important proportion of the total parasitic load in the community (~32–95%, according to parasite species). This suggests that even at such a small spatial scale, the risk of STH varies widely. Indeed, the parasite infection risk in our study area was highly focal, clustering within a radius of 25–50 m, suggesting that at the domestic level the necessary conditions for increased parasite transmission do exist. In addition, these results indicate that certain characteristics may be common to the epidemiology of single helminth species in the community, including household clustering and spatial heterogeneity, as observed in particular for *A. lumbricoides* and *T. trichiura*, with two common houses as hotspots. In addition, we confirm that these two helminths were more prevalent in school-aged children.

In Uganda, Brooker et al.<sup>5</sup> showed that temperature limits the distribution of *A. lumbricoides* and *T. trichiura*, but not hookworms, and that the latter are more related to rainfall. *A. lumbricoides* distribution in turn seems to be more dependent on smaller scale spatial factors, such as risk behaviors and socioeconomic proxies.

At larger scales, temperature is such a limiting factor that none or very low prevalence of *A. lumbricoides* and *T. trichiura* (as opposed to hookworms) was found in Sahelian countries like Chad<sup>4</sup> and Mali.<sup>15</sup> In our study, the high concentration (95%) of parasitic load of hookworms in three houses may be related to particular household characteristics, which identification might be limited by the relatively low sample size and prevalence, as the ecological conditions of the community are homogeneous. Previous studies have highlighted the relative importance of household-level socioeconomic factors linked to ecological conditions in the spatial distribution of STH infections. For instance, a study in Brazil found an association between environmental variables and poverty.<sup>39</sup> A cross-sectional survey carried out in Uganda showed that household variables influencing exposure play a greater role than host genetics in determining the distribution of hookworm infection intensity.<sup>34</sup> In Brazil, a longitudinal study evaluating hookworm post-treatment re-infection rates found that household-level socioeconomic variables, such as household construction characteristics, were more relevant than regional geographic variables (e.g., rurality, altitude, soil condition) for spatial parasite transmission,<sup>14</sup> whereas in Bangladesh, household-level risk factors accounted for more than half of the variability in household clustering of *Ascaris* infection.<sup>42</sup> Additionally, a study of STH in impoverished indigenous population of Panama found a high prevalence of spatial clusters for *Trichuris* and hookworms, but not for *A. lumbricoides*, and these clusters were associated with proxies like low household density and low household wealth indexes.<sup>23</sup>

The risk factor analysis showed common and differential individual- and house-level factors associated with occurrence and intensity of infection for each STH under study. Regarding prevalence, the variable overcrowding in the house was a common risk factor for *T. trichiura*, hookworms and *S. stercoralis*, but not for *A. lumbricoides*. For the latter, the type of house was a risk factor. However, when analyzing the intensity of infection among those



infected, a somewhat different picture emerged. Overcrowding remained a significant risk factor for intensity of hookworm infection, but not for the other STHs. Inappropriate faecal disposal appeared as a risk factor for intensity of hookworm and *A. lumbricoides* infections, economic dependency for *A. lumbricoides* infection and lack of basic services for *T. trichiura*. No factor was significantly associated with intensity of *S. stercoralis* infection due to limited frequency of infection and variability in larva excretion, although others<sup>11</sup> have reported household clustering for this parasite in Bangladesh, proposing close contact within household members and family genetic predisposition as potential risk factors. From such heterogeneous picture of significant risk factors, some elements were apparent. First, prevalence and intensity of infection are not necessarily related to one another and may be influenced differentially by some factors, such as household characteristics, individual/family behaviors or perhaps human or parasite genetics. In general, while the more indirect socioeconomic proxies appeared to influence prevalence, the intensity of infection seemed to be related to more direct risk factors like faecal disposal system and indoor water supply. It has long been demonstrated that prevalence and intensity of infection for *A. lumbricoides* have a non-linear relationship.<sup>21</sup> The use of the quantitative variable EPG/LPG defining the intensity of infection, as opposed to the dichotomous infected or non-infected status, has allowed for interesting insights into STH epidemiology to be identified. Counting of *A. lumbricoides* adult worms after chemotherapy (chemo-expulsion) has enabled to conclude that risk factors for *A. lumbricoides* infection are related to household-level socioeconomic factors like earthen floor, lack of adequate faecal disposal and lack of indoor water supply.<sup>42</sup> However, for intensity of *T. trichiura* infection, only the indirect proxy “lack of basic services” was significant despite having a similar environmental cycle and mode of acquisition as *A. lumbricoides*. If poverty and its proxies are a common risk factor for the acquisition of STHs, it appears that more detailed analyses are needed to detect specific risk factors for each STH, particularly if the “wormy” houses become the epidemiological units.

Interestingly, in Panama, reacquisition of parasitic load after treatment was positively associated with previous pre-treatment load and was higher in stunted children, suggesting individual susceptibility.<sup>23</sup> Household clustering of STHs might also be influenced by hitherto under-researched factors like genetic heterogeneity in parasite populations or host-related factors such as genetics and nutrition that could influence the immune response to specific STHs. At the individual level, it is relevant to quote that susceptibility to STHs may be associated with impaired immune function related to genetic regulation of B cell activation and the consequent secretion of immunoglobulins.<sup>46</sup> In addition, the impaired immune activities have been associated with nutrient deficiencies,<sup>22,38</sup> Hesham.<sup>1</sup> However, to date, information related to genes associated to susceptibility is limited and for the time being, the term “wormy” person may still have to be related to individual behaviors or perhaps immune status. Indeed, Walker et al.<sup>42</sup> suggested that individual susceptibility to different worm burdens may be small when the effect of household variables come into play, although this does not rule out a contribution of genetic predisposition. Parasite genetics may also play a role in aggregation at the house level. For example, Criscione et al.<sup>12</sup> found that adult *A. lumbricoides* obtained from Nepalese people clustered within the same households and that genetic similarities were found in worms of nearby houses.

We confirmed that infections with *A. lumbricoides* and *T. trichiura* are more prevalent in school-aged children and that hookworm and *S. stercoralis* infection, despite the low number of observations, seemed to have a different age distribution, either similar or somewhat more frequent in adult age groups.<sup>2,7</sup> The fact that there is no significant difference in the prevalence of all STH in-

fections between children and the rest of the community stresses the importance of reviewing WHO strategy of mass drug administration for children alone if the goal to control morbidity is to be changed into elimination of transmission.<sup>3,27</sup> The distribution of the intensity of infection also follows a typical pattern in the studied community: most hosts harbor lowly or moderately intense infections, while only a minority of hosts harbors the majority of the worm population.<sup>7</sup> Hence the term of “wormy persons” applied to the latter hosts, a term with ecological or immunological consequences that are not yet fully elucidated, as well as with consequences for the concept of “wormy houses” in terms of control by chemotherapy.

In conclusion, in addition to the hypothesized and observed interplay of geographical, household-, individual- and parasite-related factors in the transmission of STHs, the “wormy” houses or hotspots of parasite load represent a potential source of STHs in the community. Our findings point to the need for applying appropriate spatial scales and sampling strategies when planning a survey or control interventions (e.g. drug administration), which are especially relevant for neglected tropical diseases. The possibility of targeting those high-burden (“wormy”) houses and the risk factors associated with their “worminess” is an additional reason for conducting combined spatial and risk factor analyses in epidemiological studies like the present one. Indeed, the high concentration of STH burden in a few houses and the few significant correlates of STH suggest that control activities may be targeted and be expected to result in a high impact on STH morbidity.

#### Declaration of Competing Interest

The authors declare no competing financial interests.

#### Financial support

Financial support was received from the project LOCTI-Universidad de Carabobo N° 1.235 under the sponsorship of the enterprise Nascar Autopartes.

#### Acknowledgments

This work was part of two undergraduate medical students' projects under the supervision of RN Incani carried out by the then students Ivan Sequera, Luis Sequera, Ruth Salas, Luis Salas, Marisabel Salazar, Paola Santos and Carlos Sequera. Personnel involved in field and laboratory work: laboratory technicians Esmirna Colmenares and Milagro Armas from the Department of Parasitology, Faculty of Health Sciences, Universidad de Carabobo, Valencia, Venezuela.

#### References

- [1]. Al-Mekhlafi HM, Surin J, Atiya AS, Ariffin WA, Mahdy AKM, Abdullah HC. Pattern and predictors of soil-transmitted helminth reinfection among aboriginal schoolchildren in rural Peninsular Malaysia. *Acta Trop* 2008;**107**:200–4.
- [2]. Anderson RM, May RM. Helminth infections of humans: mathematical models, population dynamics, and control. *Adv Parasitol* 1985;**24**:1–101.
- [3]. Anderson RM, Turner HC, Truscott JE, Hollingsworth TD, Brooker S. Should the goal for the treatment of Soil Transmitted Helminth (STH) infections be changed from morbidity control in children to community wide transmission elimination? *PLoS Negl Trop Dis* 2015;**9**(8):e0003897.
- [4]. Brooker S, Beasley M, Ndinaromtan M, Madjiouroum EM, Baboguel M, Djenguinabe E, et al. Use of remote sensing and a geographical information system in a national helminth control programme in Chad. *Bull WHO* 2002;**80**:783–9.
- [5]. Brooker S, Kabatereine NB, Tukahebwa EM, Kasibwe F. Spatial analysis of the distribution of nematode infections in Uganda. *Epidemiol Infect* 2004;**132**:1065–71.
- [6]. Brooker S, Clements ACA, Bundy DAP. Global epidemiology, ecology and control of soil-transmitted helminth infections. *Adv Parasitol* 2006;**62**:221–61. doi:10.1016/S0065-308X(05)62007-6.
- [7]. Bundy DAP, Medley GF. Immuno-epidemiology of human geohelminthiasis: ecological and immunological determinants of worm burden. *Parasitology* 1992;**104**:S105–SS11.

- [8]. Chammartin F, Scholte RGC, Guimaraes LH, Tanner M, Utzinger J, Vounatsou P. Soil-transmitted helminth infection in South America: a systematic review and geostatistical meta-analysis. *Lancet Infect Dis* 2013;**13**:507–18.
- [9]. Chammartin F, Guimaraes LH, Scholte RGC, Bavia ME, Utzinger J, Vounatsou P. Spatio-temporal distribution of soil-transmitted helminth infections in Brazil. *Parasit Vectors* 2014;**7**:440. <http://www.parasitesandvectors.com/content/7/1/440>.
- [10]. Clements ACA, Brooker S, Nyandindi U, Fenwick A, Blair L. Bayesian spatial analysis of a national urinary schistosomiasis questionnaire to assist geographic targeting of schistosomiasis control in Tanzania, East Africa. *Int J Parasitol* 2008;**38**:401–15.
- [11]. Conway DJ, Hall A, Anwar KS, Rahman ML, Bundy DAP. Household aggregation of *Strongyloides stercoralis* infection in Bangladesh. *Trans R Soc Trop Med Hyg* 1995;**89**:258–61.
- [12]. Criscione CD, Anderson JD, Sudimack D, Subedi J, Upadhayay RP, Jha B, et al. Landscape genetics reveals focal transmission of a human macroparasite. *PLoS Negl Trop Dis* 2010;**4**:e665. doi:10.1371/journal.pntd.0000665.
- [13]. Cui J. QIC program and model selection in GEE analyses. *Stata J* 2007;**7**:209–20. doi.org/. doi:10.1177/1536867X0700700205.
- [14]. Cundill B, Alexander N, Bethony JM, Diemert D, Pullan RL, Brooker S. Rates and intensity of re-infection with human helminths after treatment and the influence of individual, household, and environmental factors in a Brazilian community. *Parasitology* 2011;**138**(11). doi:10.1017/S0031182011001132.
- [15]. De Clercq D, Sacko M, Behnke JM, Traore M, Vercruysse J. Schistosoma and geohelminth infections in Mali, West Africa. *Ann Soc Belge Med Trop* 1995;**75**:191–9.
- [16]. Drake LJ, Jukes MCH, Sternberg RJ, Bundy DAP. Geohelminth infections (Ascariasis, Trichuriasis and Hookworm): cognitive and developmental impacts. *Sem Ped Inf Dis* 2000;**11**:245–51.
- [17]. Esté ME, Esteller RM, Rondón de Esteller CA. *Diccionario toponímico del estado carabobo*. 2da Edición. Valencia, Venezuela: Universidad de Carabobo; 1996.
- [18]. Forrer A, Khieu V, Schär F, Vounatsou P, Chammartin F, Marti H, et al. *Strongyloides stercoralis* and hookworm co-infection: spatial distribution and determinants in Preah Vihear Province, Cambodia. *Parasit Vectors* 2018;**11**:33. doi:10.1186/s13071-017-2604-8.
- [19]. Getis A, Ord J. The analysis of spatial association by use of distance statistics. *Geogr Anal* 1992;**24**:189–206.
- [20]. Grillet ME, Martinez J, Barrera R. Focos calientes de transmisión de malaria: implicaciones para un control orientado y efectivo en Venezuela. *Bol Malarial Salud Amb* 2009;**49**:193–207.
- [21]. Guyatt HL, Bundy DAP, Medley GF, Grenfell BT. The relationship between the frequency distribution of *Ascaris lumbricoides* and the prevalence and intensity of infection in human communities. *Parasitology* 1990;**101**:139–43.
- [22]. Hagel I, Lynch NR, Di Prisco MC, Perez M, Sanchez JE, Pereyra BN, et al. Helminthic infection and anthropometric indicators in children from a tropical slum: ascariasis reinfection after anthelmintic treatment. *J Trop Pediatr* 1999;**45**:215–20.
- [23]. Halpenny CM, Paller C, Koski KG, Valdes VE, Scott ME. Regional, household and individual factors that influence soil transmitted helminth reinfection dynamics in preschool children from rural indigenous Panama. *PLoS Negl Trop Dis* 2013;**7**(2):e2070. doi:10.1371/journal.pntd.0002070.
- [24]. Hotez PJ, Brooker S, Bethony JM, Bottazzi ME, Loukas A, Xiao S. Hookworm infection. *N Engl J Med* 2004;**351**:799–807.
- [25]. Hotez PJ, Alvarado M, Basanez MG, Bolliger I, Bourne R, Boussinesq M, et al. The Global burden of disease study 2010: interpretation and implications for the neglected tropical diseases. *PLoS Negl Trop Dis* 2014;**8**(7):e2865. doi:10.1371/journal.pntd.0002865.
- [26]. James W, Hardin JMH. *Generalized estimating equations*. Boca Raton, FL: Chapman and Hall/CRC; 2012.
- [27]. Jourdan PM, Lambertson PHL, Fenwick A, Addiss DG. Soil-transmitted helminth infections. *The Lancet* 2018;**391**(10117):252–65. doi:10.1016/s0140-6736(17)31930-x.
- [28]. Karagiannis-Voules DA, Biedermann P, Ekpo UF, Garba A, Langer E, Mathieu E, et al. Spatial and temporal distribution of soil-transmitted helminth infection in sub-Saharan Africa: a systematic review and geostatistical meta-analysis. *Lancet Infect Dis* 2014. doi:10.1016/S1473-3099(14)71004-7.
- [29]. Karagiannis-Voules DA, Odermatt P, Biedermann P, Khieu V, Schar F, Muth S, et al. Geostatistical modelling of soil-transmitted helminth infections in Cambodia: do socioeconomic factors improve predictions? *Acta Trop* 2015;**141**:204–12. doi.org/. doi:10.1016/j.actatropica.2014.09.001.
- [30]. Lai YS, Zhou XN, Utzinger J, Vounatsou P. Bayesian geostatistical modelling of soil-transmitted helminths survey data in the People's Republic of China. *Parasit Vectors* 2013;**6**:359. doi:10.1186/1756-3305-6-359.
- [31]. Lai Y-S, Biedermann P, Shrestha A, Chammartin F, à Porta N, Montresor A, et al. Risk profiling of soil-transmitted helminth infection and estimated number of infected people in South Asia: a systematic review and Bayesian geostatistical Analysis. *PLoS Negl Trop Dis* 2019;**13**(8):e0007580 <https://doi.org/10.1371/journal.pntd.0007580>.
- [32]. Linard C, Tatem AJ. Large-scale spatial population databases in infectious disease research. *Int J Health Geog* 2012;**11**:7. doi:10.1186/1476-072X-11-.
- [33]. Montresor A, Gabrielli AF, Yajima A, Lethanh N, Biggs BA, Casey GJ, et al. Markov model to forecast the change in prevalence of soil-transmitted helminths during a control programme: a case study in Vietnam. *Trans R Soc Trop Med Hyg* 2013;**107**:313–18. doi:10.1093/trstmh/trt019.
- [34]. Pullan RL, Kabatereine NB, Quinnell RJ, Brooker S. Spatial and genetic epidemiology of hookworm in a rural community in Uganda. *PLoS Negl Trop Dis* 2010;**4**(6):e713. doi:10.1371/journal.pntd.0000713.
- [35]. Pullan RL, Brooker SJ. The global limits and population at risk of soil-transmitted helminth infections in 2010. *Parasit Vectors* 2012;**5**:81. doi:10.1186/1756-3305-5-81.
- [36]. Pullan RL, Smith JL, Jasrasaria R, Brooker SJ. Global numbers of infection and disease burden of soil transmitted helminth infections in 2010. *Parasit Vectors* 2014;**7**:37. doi:10.1186/1756-3305-7-37.
- [37]. Ruberanziza E, Owada K, Clark NJ, Umulisa I, Ortu G, Lancaster W, et al. Mapping soil-transmitted helminth parasite infection in Rwanda: estimating endemicity and identifying at-risk populations. *Trop Med Infect Dis* 2019;**4**:93. doi:10.3390/tropicalmed4020093.
- [38]. Saldiva SRM, Carvalho HB, Castilho VP, Struchiner CJ, Massad E. Malnutrition and susceptibility to enteroparasites: reinfection rates after mass chemotherapy. *Paediatr Perinat Epidemiol* 2002;**16**:166–71.
- [39]. Scholte RGC, Schur N, Bavia ME, Carvalho EM, Chammartin F, Utzinger J, et al. Spatial analysis and risk mapping of soil-transmitted helminth infections in Brazil, using Bayesian geostatistical models. *Geospat Health* 2013;**8**:97–110.
- [40]. Stephenson LS, Latham MC, Ottesen EA. Malnutrition and parasitic helminth infections. *Parasitology* 2000;**121**(Suppl):S23–38 PubMed: 11386688.
- [41]. Townsend PA. *Mapping disease transmission risk: enriching models using biogeography and ecology*. John Hopkins University Press; 2014. ISBN: 9781421414737.
- [42]. Walker M, Hall A, Basanez M-G. Individual predisposition, household clustering and risk factors for human infection with *Ascaris lumbricoides*: new epidemiological insights. *PLoS Negl Trop Dis* 2011;**5**(4):e1047. doi:10.1371/journal.pntd.0001047.
- [43]. WHO. Prevention and control of schistosomiasis and soil-transmitted helminthiasis: report of a World Health Organization expert committee. *WHO Tech Rep Ser* 2002;**912**:1–57.
- [44]. WHO. *Accelerating work to overcome the global impact of neglected tropical diseases*. Geneva: World Health Organization; 2012.
- [45]. WHO. *Integrating neglected tropical diseases into global health and development: fourth WHO report on neglected tropical diseases*. WHO; 2017. ISBN 978-92-4-156544-8.
- [46]. Williams-Blangero S, VandeBerg JL, Subedi J, Jha B, Correa-Oliveira R, Blangero J. Localization of multiple quantitative trait loci influencing susceptibility to infection with *Ascaris lumbricoides*. *J Infect Dis* 2008;**197**:66–71.
- [47]. Yaro CA, Kogi E, Luka SA. Spatial distribution and modelling of soil transmitted helminthes infection in Nigeria. *Res J Parasitol* 2018;**13**:19–35.