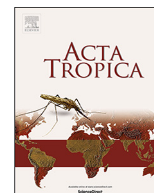
Acta Tropica 203 (2020) 105289

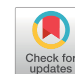
Contents lists available at ScienceDirect

Acta Tropica

journal homepage: www.elsevier.com/locate/actatropica



Malacological survey to identify transmission sites for intestinal schistosomiasis on Ijinga Island, Mwanza, north-western Tanzania



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ARTICLE INFO

Keywords:
Biomphalaria
Malacology
Intestinal schistosomiasis
Real-time PCR
Ijinga Island
North-western Tanzania

ABSTRACT

The role of malacological surveys to identify potential transmission sites for schistosomiasis control in this era of mass drug administration have received little attention. In that context, the present study was conducted to determine the abundance, identity and disease transmission potential of intermediate host snails for intestinal schistosomiasis on Ijinga Island, north-western Tanzania.

A cross-sectional malacological study was conducted between February and March 2016 on Ijinga Island, Lake Victoria, north-western Tanzania. Snails were collected at points where humans are in frequent contact with water using a standardized scooping technique and have been identified using shell morphological features. The *Schistosoma* infection status of the collected snails was determined by using real-time Polymerase Chain Reaction (real-time PCR). A total number of 4,888 snails were putatively identified as *Biomphalaria* species. A random sample of 788 snails underwent molecular analyses for *Schistosoma* infection. Overall, 279 (35.4%) of *Biomphalaria* species were identified to be infected with parasites of the lateral spined *S. mansoni* group.

The findings confirm that *Biomphalaria s*pecies collected in areas with high human water contacts are infected with *Schistosoma* and that there is a likeliness of local risk for schistosomiasis transmission at most water contact points around Ijinga Island.

1. Background

Schistosomiasis remains one of the serious public health problems in sub-Saharan Africa (SSA); almost 93% of the 290 million infected people worldwide live in this region (Hotez and Kamath, 2009; Steinmann et al., 2006). The disease is a public health concern, particularly in rural communities with limited access to safe water and adequate sanitation (Stothard et al., 2017; Colley et al., 2014). In the tropics, the two prevailing types of human schistosomiasis are: intestinal schistosomiasis caused by *Schistosoma mansoni,* and urogenital schistosomiasis caused by *S. haematobium* (World Health Organization 2013; Inobaya et al., 2014). Tanzania is one of those countries with the highest number of cases of human schistosomiasis (Hotez and Kamath, 2009; Olsen et al., 2015). According to recent estimates, the overall country prevalence of schistosomiasis is placed at 51.5% (Rollinson et al., 2013; Mazigo et al., 2012). Almost 50% of the population is either infected or lives in areas with very high transmission rates of schistosomiasis (Steinmann et al., 2006; Rollinson et al., 2013).

The causative agents of schistosomiasis are blood dwelling trematodes belonging to the genus *Schistosoma* (Gryseels et al., 2006). Schistosomes have a complex life cycle that include freshwater snails as intermediate hosts and mammalians as definitive hosts (Gryseels et al., 2006). The geographical distribution of schistosomiasis depends on the occurrence of these intermediate host snails (Magendantz, 1972; Gouvras et al., 2017; Angelo et al., 2014; Lwambo, 1988) as well as climatic factors (Gouvras et al., 2017; Sturrock, 1966). In the north-western region of Tanzania, along the Lake Victoria basin, the main intermediate host snail of *S. mansoni* belongs to the genus *Biomphalaria* and includes *Biomphalaria choanomphala, B. pfeifferi, B. sudanica* and *B. angulosa* (Mazigo et al., 2012; Magendantz, 1972; Gouvras et al., 2017). *Biomphalaria choanomphala* is mainly found in the lake waters whereas *B. sudanica* is predominantly found in shallow vegetation along the banks of the lake and in the marshes close to the lake (Magendantz, 1972; Gouvras et al., 2017; Angelo et al., 2014).

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https://doi.org/10.1016/j.actatropica.2019.105289
Received 12 April 2019; Received in revised form 28 November 2019; Accepted 3 December 2019
Available online 16 December 2019
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Biomphalaria pfeifferi is principally found in seasonal and swamp water bodies in inland areas (Mazigo et al., 2012; Magendantz, 1972; Mccullough, 1972; Malek, 1981).

Following the discovery of the drug praziquantel in the late 1970s, the control of schistosomiasis shifted to mass drug administration (MDA) strategies in endemic communities (WHO). MDA campaigns are effective in reducing morbidity associated with schistosomes by decreasing worm burden and the intensity of infection (WHO). Several rounds of annual MDA have been conducted in SSA, nevertheless the prevalence of the disease still remains very high in many areas (Hotez and Kamath, 2009; Hotez, 2009). Although praziquantel is the backbone of control programs, it is not suitable as a sole component to limit the transmission in high prevalence regions (King et al., 2015; Evan Secor, 2014). In transmission and maintenance of schistosomiasis, the intermediate host snail plays a central role (Bakuza et al., 2017). Through extensive malacological surveys, it is possible to identify and locate hotspot areas for transmission before and after MDA and use the knowledge to guide and implement focused control measures and monitor the effect of MDA in human populations (Angelo et al., 2014; Cnops et al., 2013; Opisa et al., 2011; Kazibwe et al., 2006).

Despite the availability of this knowledge, very few studies have used molecular techniques to identify and map potential areas for transmission of schistosomiasis using intermediate host snails (Bakuza et al., 2017; Abath et al., 2006; Melo et al., 2006). Most of these studies have used cercariae shedding technique to assess snail infection status (Opisa et al., 2011; Odongo-Aginya et al., 2008). However, the snail shedding technique has its own limitations in detecting the parasite in situations such as low parasite burden, prepatent infections, aborted development of sporocysts as well as death of the snail after collection and prior to light exposure. This results in underestimation of the true prevalence of infection in the intermediate host snail (Abath et al., 2006; King et al., 2006). In order to overcome these limitations, molecular techniques which detect *Schistosoma* DNA in intermediate host snails using conventional Polymerase Chain Reaction (PCR) methods have been developed and are capable of identifying patent and prepatent infections (Angelo et al., 2014; Bakuza et al., 2017; Melo et al., 2006; Steinauer et al., 2008; Lu et al., 2016).

In this context, the main objective of the present study was to identify snail intermediate hosts involved in transmission, use of DNA based molecular techniques to determine *S. mansoni* infection in collected snails and to map transmission hotspots in relation to physical and biotic factors and human water contact behavior on Ijinga Island, north-western Tanzania.

2. Materials and methods

2.1. Study area

The study was conducted on Ijinga Island at Lake Victoria, located in Magu District, north-western Tanzania. Ijinga Island and the Magu District are located between 2°10′ and 2°50′ south of the equator and 33° to 34° east. The area is characterized by tropical climate with two rainy seasons (a short rainy season from October to December and a long rainy season between March and May). The average annual rainfall is 1200 mm and the average annual temperature is 26.5 °C. According to a population census (house-to-house) conducted in December 2016, the island has 1850 permanent inhabitants and their majority is involved in subsistence farming, fishing and livestock keeping. The island has five sub-villages, namely Kashishi, Mwamalangale, Ngambaji, Ilago and Igadi. Lake Victoria serves as the main source of water for domestic and recreational use as well as for irrigation purposes. . Intestinal schistosomiasis is highly endemic on the island and the ecology supports the transmission of intestinal schistosomiasis. The island was selected for this study because the disease is highly prevalent in adults and children. Control of schistosomiasis in Tanzania focuses mainly on mass drug administration of schoolchildren with the drug Praziquantel. Adult individuals and children under-five are not involved in treatment programs (Mazigo et al., 2012).

2.2. Site selection, snail collection and identification of hotspots

Snail sampling sites were selected along the shorelines where people had direct water contact as a result of routine activities such as collecting water, bathing or occupational work like farming and fishing. The type of activities taking place at the water collection points were recorded following direct observations and interviewing residents of Ijinga Island. The following activities were recorded: 1. washing/bathing, 2. washing dishes, 3. collecting water, 4. swimming/playing, 5. rice cultivation, 6. defecation, 7. washing clothes, 8. washing bicycles, 9. fording, 10. fishing, 11. farming. All 16 selected sites were mapped via handheld GPS. Snail sampling was done between February and March 2016 before the usual beginning of the long rainy season. Handheld scoops were used for the collection of snails (Gouvras et al., 2017). Two experienced technicians carried out scooping for 15 to 30 min. The scoop was pushed through the vegetation, the snails were picked out of the scoop using a pair of forceps and stored in labeled containers. Collected snails were morphologically identified using the "Key to the identification of East and Central African freshwater snails of medical and veterinary importance" (Mandahl-Barth, 1962). Snails with features suggestive of *Biomphalaria* species were preserved in absolute ethanol and transported to the Medical Mission Institute in Wuerzburg, Germany, for real-time PCR analyses. Although it is still important to perform cercarial shedding during snail screening of African schistosomiasis, which can be performed directly in the country - this method was not used in our study due to the known limitations (Abath et al., 2006; King et al., 2006). After collection of snails, a baseline survey was conducted among 930 community members (children and adults, 50% of the entire population) to determine the prevalence of *S. mansoni* infection. An overall prevalence of 68.9% was recorded using the Kato–Katz method (for microscopic detection of *S. mansoni* eggs in stool). In the age group of 6 to15 years, the prevalence of *S. mansoni* was 86.1% (Mueller et al., 2019). Swahili translated consent and assent (for children aged 8 to16 years) were used to obtained participants' permission to participate in the study. Parental written informed consent was requested for all the children aged 3 to16 years who participated in the study. Participants with positive results in the microscopic examination or POC−CCA test cassette for *S. mansoni* were treated with PZQ using the WHO recommended clinical dosage (40 mg/kg body weight).

2.3. Environmental and physico-chemical characteristics

At all snail collection points, environmental data were recorded using a portable multimeter device (PCE-PHD 1) (PCE Germany GmbH, Meschede, Germany) and the following were recorded: temperature (°C), pH, conductivity (mS/cm) and dissolved oxygen (mg/L). Different habitat characteristics such as the type of soil of the lake bottom, vegetation and presence of domestic animals were also recorded.

2.4. DNA extraction of collected snails

From each collection site, 50 randomly selected snails were used for DNA extraction. After the snails were removed from their shells, each snail was washed three times with phosphate-buffered saline (PBS) and placed in a 2 ml microcentrifuge tube with 500 µl PBS. For DNA extraction, the Qiagen QIAamp® cador® Pathogen Mini Kit (Qiagen, Hilden, Germany) was used according to the protocol described by the manufacturer (including the pretreatment protocol for rapid partial disruption of tissue).

The extracted DNA was eluted in 150 µl Buffer AVE and a 2.5 µl aliquot was used for each real-time PCR reaction.

2.5. Amplification by real-time PCR

Real-time PCR primers and probe designed to target *S. mansoni* were used to detect infections within the snail. The assay is based on a 121-bp tandem repeat sequence of *S. mansoni* strain SM 1–7 (GenBank accession number M61098) described by Hamburger et al., (1991). Primer sequences were: Sm FW 5′-CCG ACC AAC CGT TCT ATG A-3′; Sm RV 5′CAC GC TCT CGC AAA TAA TCT AAA-3′; Sm probe 5′-[FAM] TCG TTG TAT CTC CGA AAC CAC TGG ACG [(BHQ1]) – 3′ (Espírito-Santo et al., 2014). The primers and probe were synthesized by Eurofins Genomics, Ebersberg, Germany.

The 25 µl reaction mix contained 2.5 µl snail DNA, 1x QuantiFast Pathogen Master Mix (QuantiFast® Pathogen PCR + IC Kit, Qiagen, Hilden, Germany), 400 nM of each Sm Primer and 200 nM of Sm probe. The program consisted of an initial step of 5 min at 95 °C followed by 40 cycles of 15 s at 95 °C and 30 s at 60 °C. The reaction was run on the StepOne real-time PCR system (Applied Biosystems). DNA detection was expressed by cycle threshold (Ct)-values. In every run, the non-template control (water sample) was negative (Ct = 0), the positive control (DNA of laboratory-infected *Biomphalaria* snails with *S. mansoni* (kindly provided by the working group of Professor Grevelding, Justus–Liebig-University Giessen, Germany)) was positive and the exogenous Qiagen Internal Control (added to all snail extracts) to test successful amplification and to exclude the presence of PCR inhibitors was positive (Ct < 33) (The QuantiFast Pathogen PCR + IC Kit provides a ready-to-use Internal Control for universal use). A test was considered positive when the threshold was attained within 38 PCR cycles (Ct < 38) (Fuss et al., 2018) (a log 10 dilution series of purified DNA from 100 *S. mansoni* eggs was amplified to assess the limits of detection of the PCR assay). An amplification plot is shown in Fig. 1. Because it is known that *S. mansoni* and its sister species *S. rodhaini* can infect *Biomphalaria* snails and cross reactions may occur when using SM 1–7 as PCR target, 20% of PCR amplicons positively tested for *S. mansoni* were subjected to DNA sequencing in both directions (forward and reverse primer) (Microsynth Seqlab, Goettingen, Germany). The results were aligned using the Global Alignment Tool (NCBI-BLAST) (https://blast.ncbi.nlm.nih.gov/Blast.cgi) and the alignment blasted using WormBase (https://parasite.wormbase.org/index.html) (Howe et al., 2017; Howe et al., 2016).

2.6. Data analysis

All collected data were entered into spreadsheets (Microsoft Excel

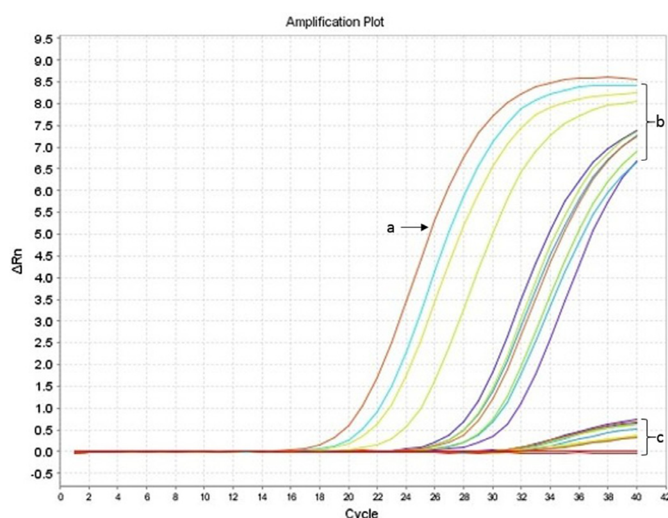

Fig. 1. Amplification plots for the real-time PCR targeting the 121-bp tandem repeat sequence of *S. mansoni* strain SM 1–7. Amplification plots of *S. mansoni* positive control (a), test samples (b) and internal positive control (c).

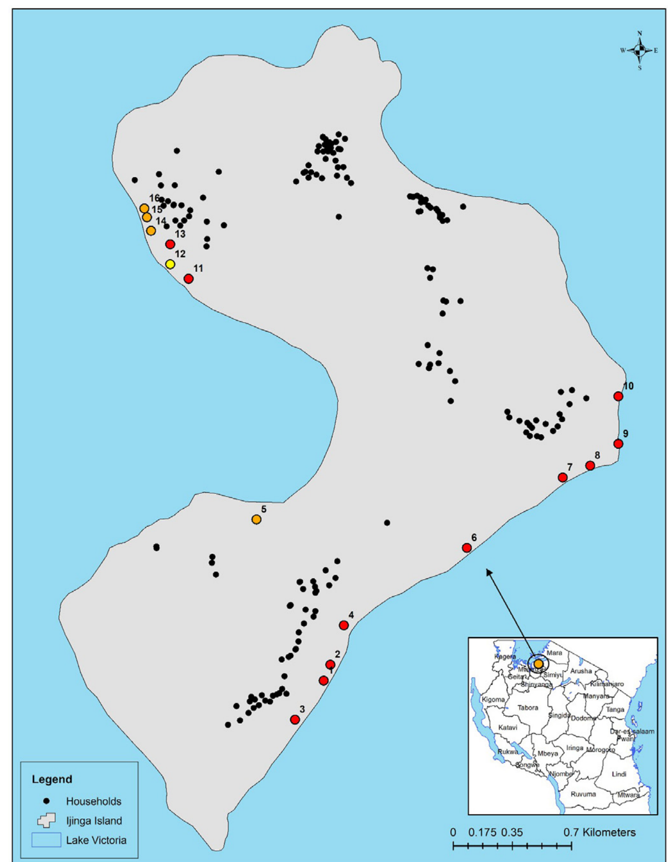

Fig. 2. Snail collection points on Ijinga Island**.** The colors of the dots represent the abundance of *Biomphalaria* snails at that location: high (> 30 snails/15 min = red), moderate (10–30 snails/15 min = orange), and low (< 10 snails/15 min = yellow) (Standley et al., 2012). Map generated with ExpertGPS software (TopoGrafix, Massachusetts, USA). (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

2013) and all snail collection points (GPS codes) were entered into ExpertGPS software (TopoGrafix, Massachusetts, USA) for creation of maps. All statistical analyses were carried out using IBM SPSS™ Statistical package version 24 (SPSS Inc., Chicago, USA). Tests for normality and homogeneity of variance showed that the data were not normally distributed. Therefore, Spearman correlations (rs) were used to determine associations between snail abundance, snail infectivity, environmental/physico-chemical variables, vegetation and activities. A *P*-value of < 0.05 was considered to be statistically significant.

3. Results

3.1. Snail abundance and species distribution

A total of 16 sites where people had direct water contact were visited along the Lake Victoria shoreline around Ijinga Island. A total of 4888 freshwater snails were collected and putatively identified as *B. sudanica* based on morphological features (Mandahl-Barth, 1962). To compare the data, the number of snails collected per 15 min at a constant collection rate was calculated. Fig. 2 shows the snail collection points on Ijinga Island. Overall, 11 points were classified as high abundant (> 30 snails), four sites had moderate abundance (10 - 30 snails), and one had low abundance (< 10 snails) (Standley et al., 2012). *Biomphalaria sudanica* was observed in all 16 collection sites.

Table 1
Number of *Biomphalaria* snails collected in each collection point, examined by real-time PCR and infected with *Schistosoma*.

Collection site	Number of *Biomphalaria* snails	Number of *Biomphalaria* tested	Number (%) of *Biomphalaria* infected with *Schistosoma*
1	340	50	15 (30)
2	126	50	15 (30)
3	571	50	46 (92)
4	509	50	9 (18)
5	96	50	47 (94)
6	441	50	16 (32)
7	568	50	17 (34)
8	705	50	2 (4)
9	702	50	11 (22)
10	127	50	0 (0)
11	196	50	9 (18)
12	42	38	37 (97.4)
13	175	50	10 (20)
14	82	50	38 (76)
15	100	50	7 (14)
16	108	50	0 (0)
Total	**4888**	**788**	**279 (35.4)**

Table 2
Water physicochemical parameters at the different collection sites.

Collection site	Temperature in °C	pH	Salinity in%	Conductivity in mS	Dissolved Oxygen in mg/L
1	26.8	6.74	0.01	0.107	6.8
2	30.4	7.08	0.01	0.153	1.6
3	30	6.91	0.02	0.416	4.9
4	31.5	9.78	0.01	0.224	4.5
5	29.4	7.1	0.01	0.275	13.1
6	30	6.89	0.01	0.175	1.4
7	27	6.61	0.03	0.575	8.5
8	27.1	7.01	0.03	0.581	8.5
9	27.5	6.84	0.03	0.613	8.7
10	27.2	6.84	0.03	0.634	8.1
11	30.6	7.5	0.02	0.325	8
12	26.1	6.88	0.02	0.483	6.8
13	28.1	7.05	0.03	0.556	7.1
14	28.3	7.85	0.02	0.304	8
15	27.6	6.77	0.03	0.633	7.7
16	28.1	6.68	0.03	0.572	7.8
Mean ± SD	**28.5 (± 1.6)**	**7.16 (± 0-.77)**	**0.021 (± 0.0-089)**	**0.41 (± 0.19)**	**6.97 (± 2.83)**

3.2. *Schistosoma mansoni* infection status of the collected snails

Out of the 788 examined snails, 35.4% (279/788) were positive for *Schistosoma* by real-time PCR. Overall, 14 collection sites had snails that tested positive. At three collection points (No. 3, 5 and 12), over 90% of the snails tested were positive. At four sites, the prevalence of infected snails was below 20% (No. 4, 8, 11 and 15). No infected snails were detected by real-time PCR in two collection points (10 and 16). Fifty-five (55) of the 279 (19.7%) positive real-time PCR amplicons were tested by sequencing. All sequences showed the highest similarity to *S. mansoni* (BioProject PRJEA36577 (Berriman et al., 2009; Protasio et al., 2012)). The e-values ranged between $4.0E^{-14}$ and $3.4E^{-112}$.

Table 1 shows the number of infected snails at the different collection sites.

3.3. Environmental factors

In all habitats, the common vegetation observed were grasses, macrophytes weeds, water hyacinths and rushes. *Biomphalaria sudanica* were found in all types of vegetation coverage, but were most significantly attached to grass (rs = 0.621, P = 0.010, n = 16). The mean water temperature was 28.5 °C ± 1.6 °C (range = 26.1 °C to 31.5 °C). The pH levels of water varied greatly between sites, with a mean pH of 7.16 ± 0.77 (range = 6.61–9.78). The mean water conductivity was 0.41 mS ± 0.19 (range = 0.107–0.634 mS). The mean salinity was 0.021% ± 0.0089 (range = 0.01–0.03) and the mean dissolved oxygen content was 6.97 mg/l ± 2.83 (range = 1.4–13.1 mg/l). However, we did not observe a significant correlation between water temperature (P = 0.8), water pH (P = 0.6), water conductivity (P = 0.9) and dissolved oxygen (P = 0.8) and the snail abundance. In contrast, we could show a significant correlation between the number of infected *Biomphalaria* snails and salinity (rs = 0.504, P = 0.047, n = 16). Table 2 shows the water physicochemical parameters at the different collection sites.

3.4. Human activities at the snail collection points

In-depth interviews with residents of Ijinga were conducted by two experienced research assistants to establish the behaviors surrounding the potential exposures to cercaria-contaminated water. In addition, observations were made on practices around the water points. At collection point 1, only one activity was named (washing dishes). All other collection points were used for personal hygiene, washing clothes and washing dishes, collecting water, swimming/playing and fishing. Contamination of the lakeshore with human faces was observed in most of the snail sampling sites. At the time of the study, the only source of water for domestic and recreational use was the Lake Victoria. Thus, all inhabitants of the island had intensive lake water contact.

4. Discussion

The findings demonstrate that the Lake Victoria shorelines along Ijinga Island are a suitable habitat for *Biomphalaria* species and this indicates that the genus is an important intermediate host of *S. mansoni* in this area. Most of the collection sites showed a high abundance of snails as well as a moderate to high number of infections with parasites of the lateral spined *S. mansoni* group (*S. mansoni* and *S. rodhaini)*. It is very suggestive that these frequently visited areas by human population are potential transmission hotspots for intestinal schistosomiasis. Our findings corroborate the findings of previous studies which demonstrated that *Biomphalaria* snails were widely distributed along the shoreline of Lake Victoria in a variety of habitats (Mazigo et al., 2012; Angelo et al., 2014; Standley et al., 2012, 2010). Angelo et al. also demonstrated high abundance of *B. sudanica* in collection points along and within the Lake Victoria basin in north-western Tanzania (Angelo et al., 2014).

Environmental factors that influence snail distribution and abundance vary considerably from site to site, even within a short distance. In the present study, the environmental factors examined in snail sampling sites included vegetation cover, which was a major determinant factor for the abundance of *B. sudanica*. Similar studies have observed the relationship between vegetation cover and abundance of *B. sudanica* along the Lake Victoria shoreline (Angelo et al., 2014; Ofulla et al., 2010). *Biomphalaria sudanica* is usually found in fringing vegetation, such as water hyacinths or in temporary marshes set back from the main lake (Standley et al., 2012, 2011). Ofulla et al., (2010) demonstrated that the distribution of schistosomiasis snail hosts was more associated with water hyacinths than grass. In contrast our present study showed a significant association of *B. sudanica* with grasses. However, we did not observe any association between water temperature and snail abundance, which was similar to previous findings (Kariuki et al., 2004; Rowel et al., 2015). This may be due to the narrow range of temperature in our study area. Contrasting findings have been reported from Uganda, Kenya and Tanzania, indicating that the water temperature correlated significantly with snail abundance

(Angelo et al., 2014; Opisa et al., 2011; Kazibwe et al., 2006). Our findings and those of other authors noted the lack of association between snail abundance and water pH (Opisa et al., 2011). Contrasting findings have been demonstrated by Standley et al. which showed that the distribution of *B. sudanica* was significantly negatively associated with pH, indicating that snails were rather found in habitats with lower, more acidic, pH values (Standley et al., 2012).

The use of PCR based methods which detect the DNA of schistosomes in the intermediate snail hosts have shown to be more sensitive in identifying hotspot areas for transmission of schistosomiasis than the conventional methods (Abath et al., 2006; Odongo-Aginya et al., 2008). Bakuza et al., (2017) used PCR to detect *S. mansoni* infections in intermediate host snails and were also able to detect a very high number of infected snails (47%). For further analysis, Bakuza et al. performed sequence analyses, which confirmed that most infections were caused by *S. mansoni*, but also other trematodes could be detected by sequencing. These results underline the importance of confirming species identification by sequencing rather than relying solely on PCR-based diagnostics or cercarial shedding, as the relationships between snails and trematodes may be more diverse than previously known (Bakuza et al., 2017). It should be considered that PCR detects early prepatent (non-shedding) and patent (shedding) infections (Farghaly et al., 2016). By detecting prepatent infections, assumptions can be made about the transmission from humans to snails. Even if, according to the inhabitants, most water points are not used for defecation purposes, we suggested that in the study area, PCR positivity rates were primarily related to the level of contamination with schistosome ova. In the past, it has been shown that both *S. mansoni* and the sister species *S. rodhaini* are capable of infecting the same species of *Biomphalaria* snails (Norton et al., 2008). Cross reactions can occur by using SM 1–7 as PCR target. Therefore, randomly selected real-time PCR amplicons were sequenced in this study. All tested samples showed the highest similarity with *S. mansoni*. In addition, Steinauer et al. showed in their study in western Kenya in the Lake Victoria Basin, that snails infected with *S. mansoni* are eight times more common and more widespread than *S. rodhaini* (Steinauer et al., 2008). Presumably, this is due to the different distribution and longevity of the definitive hosts. Humans have generally larger, less subdivided, and more widespread populations and live longer than rodents. Therefore, humans serve as a more stable reservoir. This is also reflected in genetic diversity, as *S. rodhaini* showed little variation compared to *S. mansoni* (Steinauer et al., 2008). An existing PCR, targeting the *S. mansoni* ND5 gene, enables the differentiation of *S. mansoni* from other relevant schistosome species at a high sensitivity (>0.1 fg *S. mansoni* DNA). This assay also distinguishes *S. mansoni* and *S. rodhaini* by amplicon size (Lu et al., 2016) and so this assay could help further support the analysis of this data to distinguish between *S. mansoni* and *S. rodhaini* infections within the snails from Ijinga Island.

The compatibility of *B. sudanica* and *B. pfeifferi* with *S. mansoni* was investigated in several studies and contradictory results were shown. Adriko *at al.* (Adriko et al., 2013) found no significant differences in the compatibility between *B. sudanica* and *B. pfeifferi*. The results of *Lu* et al. (Lu et al., 2016) indicated a higher compatibility with *S. mansoni* for *B. pfeifferi* than *B. sudanica*. Since *B. sudanica* is the major snail host for *S. mansoni* in most places on the Kenyan shore of the lake, compatibility for transmission seems sufficient (Lu et al., 2016). In future developments it will be necessary to use species-specific targets as this will significantly improve the monitoring of the transmission. It is likely that animal pathogenic schistosomes will remain at a high level as human infection decreases, so it is of paramount importance to identify precisely what the snail is infected with.

Since in our study the detection of schistosomal DNA in the intermediate snail host was performed by real-time PCR and no distinction could be made between pre-patent and patent infections, it was not possible to make statements about the direct risk of infection by cerariae in water.

This study was not conducted without limitations: the snails collected were only identified using morphological features. Molecular tools have recently shown that the taxonomy of the *Biomphalaria* species should be revised. *Biomphalaria sudanica* and *B. choanomphala* morphotypes suggest that the *Biomphalaria* from Lake Victoria should be considered one of the most highly diverse species, both in molecular and morphological terms (Standley et al., 2011). However, experiments showed that both variants of *Biomphalaria* are capable of transmitting *S. mansoni*. The use of real-time PCR in the present study allowed to identify a large number of *Schistosoma* infected snails and to determine areas of intense transmission. However, despite the fact that this method is useful in assessing snail infectivity and also in monitoring the effects of mass drug administration in schistosomiasis endemic areas, the technique is comparably expensive and cannot be used directly in field settings for routine assessment of *Schistosoma* infection in snails. In addition, further testing is required to rule out cross-reactions with other trematodes. The PCR marker was designed a long time ago before the diversity of trematodes that may be present in the intermediate host snails was known.

5. Conclusion

The findings show a high abundance of *Biomphalaria* snail along the shorelines of Ijinga Island and a high percentage of snails were presumably infected with *S. mansoni*, indicating that the snail is a responsible intermediate host in the area. Furthermore, the findings indicate that the majority of human water contact sites could be potential areas for *S. mansoni* transmission. Given the nature of the island and the Lake Victoria environment, it may not be possible to implement molluscicides for the control of snails. Thus, repeated mass drug administration using praziquantel to human population accompanied by public health education focusing on water, sanitation and hygiene may help in reducing transmission and re-infection in such rural setting.

Funding

This study was funded by the Georg Ludwig Rexroth Foundation (http://www.rexroth-stiftung.de) and the German Academic Exchange Service (Deutscher Akademischer Austauschdienst (DAAD)) (https://www.daad.de/de/). The funders did not play any part in study design, data collection and analyses, decision to publish, or preparation of the manuscript.

Availability of data and materials

The datasets supporting the conclusions of this article are included within the article. The raw data can be obtained from the corresponding author upon reasonable request.

Ethical consideration

This study was conducted as part of a proof of concept study on sustainable control of schistosomiasis and soil-transmitted helminths through an integrated community-based approach on Ijinga Island, north-western Tanzania. The project was reviewed and specifically approved by the National Institute for Medical Research in Dar es Salaam, Tanzania (NIMR/HQ/R.8a/Vol. IX/2679) and by the Catholic University of Health and Allied Sciences (CUHAS), Ethics Review Board, Mwanza, Tanzania (Research Clearance Certificate No CREC/156/2016).

Consent for publication

Not applicable.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Acknowledgment

We gratefully acknowledge the participation of the technicians of the National Institute for Medical Research, Mwanza, who were involved in snail collection, snail identification and collecting the information and data necessary for this study. We would also like to thank the population of Ijinga Island for their cooperation.

Supplementary materials

Supplementary material associated with this article can be found, in the online version, at doi:10.1016/j.actatropica.2019.105289.

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