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Prevalence and Molecular Characterization of *Schistosoma haematobium* among Secondary School Students in Challawa, Kano State, Nigeria

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ABSTRACT
Urogenital schistosomiasis caused by *Schistosoma haematobium* remains a major public health concern in Nigeria, particularly among school-aged children with frequent exposure to contaminated water. This study assessed the prevalence, risk factors, and molecular identity of *S. haematobium* among public and private secondary school students in Challawa, Kano State. Urine samples from 370 students were examined microscopically for *S. haematobium* eggs. Sociodemographic, behavioral, environmental, and clinical data were collected using a semi-structured questionnaire. Associations between infection and risk factors were analyzed using chi-square tests and odds ratios. The overall prevalence was 39.46%, indicating active transmission. Infection was significantly higher in public schools (42.07%) than private schools (30.00%) ($P < 0.01$). Males had higher prevalence (45.00%) than females (31.33%) (OR = 2.21; 95% CI: 1.85–2.63). The highest burden occurred among ages 11–20 years (40.5%). Key risk factors included swimming, bathing in natural water bodies, water fetching, proximity to water sources, and poor sanitation ($P < 0.01$), while clinical morbidity indicators were haematuria, dysuria and frequent urination ($p < 0.01$) Molecular analysis using nuclear *ITS2* rDNA and mitochondrial *cox1* markers confirmed all isolates as *S. haematobium*. Sequences showed high similarity (98-100%) with GenBank references, while phylogenetic analysis revealed close clustering with minimal divergence, indicating low genetic variation. In conclusion, urogenital schistosomiasis remains endemic in Challawa, driven by behavioral and environmental exposures, with evidence of genetically homogeneous parasite populations. Molecular analysis confirmed the occurrence of pure *S. haematobium* isolates in the study population.

Keywords: Urogenital Schistosomiasis, *Schistosoma haematobium*, Prevalence, Molecular Characterisation, Risk Factors

INTRODUCTION

Schistosomiasis is an acute and chronic parasitic disease caused by blood flukes (trematode worms) of the genus *Schistosoma*. It is a major health problem with significant socioeconomic impact in areas where control efforts and sanitation are inadequate and the majority of the populations are impoverished (Sady *et al.*, 2013). Urogenital schistosomiasis, classified as a Neglected Tropical Disease (NTD) by the WHO (2021) is among the most prevalent human parasitic infections. The disease ranks second beneath malaria in the list of parasitic diseases in terms of morbidity and mortality (Alemu *et al*., 2018; Mohammed *et al*., 2018). It is widespread in the tropics and subtropics, existing in many developing countries in Africa, Asia, South America and several Caribbean islands.

At least six *Schistosoma* species are known to infect humans. These are; *Schistosoma haematobium, S. intercalatum, S. japonicum, S. mansoni, S. guineensis* and *S. mekongi* (Alemu *et al*., 2018; Mohammed *et al*., 2018). While *S. haematobium* causes urogenital morbidities, *S. mansoni, S. intercalatum, S. japonicum, S. guineensis* and *S. mekongi* cause intestinal schistosomiasis. However, only two *Schistosoma* species cause human schistosomiasis in Nigeria, *S. mansoni* and *S. haematobium*. Transmission occurs when an infected person passes urine or faeces into water bodies. The eggs passed into the water hatch into miracidia which are released from the eggs and swim to locate specific freshwater snail intermediate hosts. They develop in the snail into sporocysts which in turn develop into the infective stage of the parasite called cercariae. Humans acquire the infection during contact with cercariae-infested freshwater bodies (Oyeyemi *et al*., 2020). The highest burden of the disease is seen in children, especially in the ages between 10-15 years (Lawiye *et al*., 2020). Children harbouring these infections usually remain asymptomatic and may show complications such as lesions of the bladder as adult worms and eggs migrate through the body. Even though infection due to *S. haematobium* is rarely fatal, disability morbidities such as anaemia and impaired cognitive development have been observed in school-aged children (Lawiye *et al*., 2020), as well as squamous cell carcinoma of the bladder which arises from the intricate interplay of molecular pathways and cellular processes, including persistent inflammation, deoxyribonucleic acid damage, altered signaling pathways, and epigenetic dysregulation (Altwairgi 2024). In Nigeria, schistosomiasis is a disease of considerable and growing importance, mainly affecting rural areas and vulnerable age groups. School children are the major victims of this disease (ESPEN, 2024). *S. haematobium*, a major pathogen of urogenital schistosomiasis has been reported to be affecting an estimated 30 million people in Nigeria (Odeniran *et al*., 2020). The disease is endemic across all 36 states in the country (FMOH, 2020). The first case was documented in the country around 1881 in the old Borno Empire, which is comprised of regions

that form the present Borno State in North-Eastern Nigeria and has since been shown to be widespread across the country, although prevalence varies by district (Balogun *et al*., 2022). Urogenital schistosomiasis remains highly prevalent in Nigeria despite efforts to control it. Mass Drug Administration (MDA) using praziquantel (PZQ) has been the main disease control strategy. However, reinfections have been reported especially as people revert to water contact activities even after being treated successfully with PZQ (Monde *et al*., 2015).

Most epidemiological assessments on the burden of urogenital schistosomiasis have relied on microscopy, providing a cheap way for the detection of schistosome eggs in urine in many endemic countries (Kosinski *et al*., 2011; Aryeetey *et al*., 2013). In Nigeria for example, most prevalence studies conducted have been based on urine microscopy (Eze *et al*., 2019). Diagnosis is based on the detection of parasite eggs in the urine and differentiating the parasite based on egg morphology. However, this method is associated with low sensitivity and is also highly unspecific because it cannot characterize the parasites into species and sub-species (Leger and Webster, 2017; Mendy *et al*., 2020). Molecular based tools such as the use of nuclear and mitochondrial genes have proved to be efficient tools for the detection and identification of *Schistosoma* (Mendy *et al*., 2020).

Molecular techniques based on the nuclear *internal transcribed spacer 2* (*ITS2*) region can be used to type strains which also allows for the detection of hybrids between animal and human schistosomes (Kosinski *et al*., 2011). Additionally, other studies have employed DNA sequence-based identification techniques by targeting the species-specific genes encoding for the mitochondrial *cytochrome c oxidase subunit 1* (mit.*cox1*) to identify schistosome species (Sady *et al*., 2015; Webster *et al*., 2018). The *cox1* gene is found universally within mitochondrial genomes and is recognized as a useful DNA barcoding region to infer species identification and explore haplotype diversity (Trobajo *et al*., 2010; Viricel and Rosel, 2011). Most studies conducted in Kano State rely only on microscopy, which underestimate true infection rates and do not provide information on parasite genetic diversity or transmission patterns. The current study, therefore, set out to investigate the prevalence of urogenital schistosomiasis among secondary school students in Challawa, Kumbotso Local Government Area (L.G.A.) of Kano State using microscopy, and to characterize the *S. haematobium* strain detected on microscopy using molecular techniques based on the nuclear *ITS2* gene and mit.*cox1* gene. This knowledge will provide insights for understanding the evolution and epidemiology of urogenital schistosomiasis in Kano State to inform policy decision for effective transmission control.

MATERIALS AND METHODS

Study Site and Design

Challawa, one of the locations in Kumbotso L.G.A lies between latitude 11°54'N and 11°30'N and longitude 8°25'E and 8°21'E. It is characterized by the Challawa River, a major water source and a tributary of Kano River, which is itself a tributary of the Hadejia River, and is located southwest of Kano city. The study was conducted in selected public secondary schools and a private secondary school in Challawa, Kumbotso L.G.A of Kano State. The site was chosen based on the proximity of the study population to Challawa River, and a dearth of reports on *S. haematobium* infection in the study area.

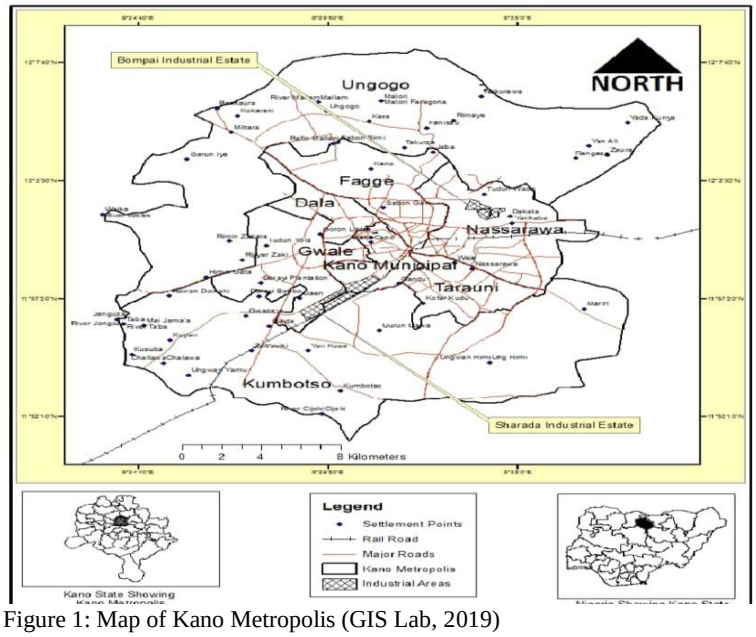

Figure 1: Map of Kano Metropolis (GIS Lab, 2019)

Sample Size

The sample size used for this study was calculated using Fischer equation (Naing *et al*., 2006) as follows;

$$n = \frac{Z^2 P(1-P)}{e^2}$$

where

n = sample size

Z = level of confidence = 1.96 at 95%

P = prevalence obtained from previous similar research 61.25% (Gambo *et al*., 2021)

e = margin of error = 5%

$$n = \frac{(1.96)^2 \times 0.6125\ (1 - 0.6125)}{0.05^2}$$

$$n = \frac{3.8416 \times 0.23734375}{0.0025}$$

$$n = \frac{091177975}{0.0025}$$

n = 364.7119
n ≈ 365
Therefore, the minimum calculated sample size is approximately 365. Whereas, the sample size used in this research was 370.

Ethical Approval and Informed Consent
Ethical clearance for the conduct of this study was obtained from Kano State Ministry of Health (NHREC/17/03/2018), and permission obtained from Kano State Secondary Schools Management Board, Kano State Universal Basic Education Board and Kano State Private and Voluntary Institution Board. Written informed consent signed or thumb-printed was obtained from parents and guardians of the study participants.

Questionnaire Administration
A semi-structucted questionnaire was administered to each student to obtain information on transmission risk factors including age, gender, grade, knowledge about schistosomiasis, health and hygiene practices, involvement in water contact activities such as swimming, bathing, playing, washing and fetching water, and experience regarding clinical features such as haematuria (bloody urine), dysuria (painful or difficult urination), and frequent urination.
Prior to administration, the semi-structured questionnaire was subjected to face and content validation by experts in Parasitology and public health to ensure its relevance and clarity. Thereafter, it was pretested among a small group of secondary school students from a school outside the study area but with similar characteristics to the study population. Feedback obtained from the pretest was used to revise the questionnaire before the main data collection.

Urine Sample Collection and Preservation
A total of 370 urine samples were collected from the study participants. Two hundred and ninety (290) urine samples were obtained from the public secondary schools, namely; Government Secondary School (GSS) Kayi, Panshekara (n=34), Government College (GC) Zawachiki (n=40), Government Secondary School (GSS) Panshekara (n=36), Government Girls Secondary School (GGSS) Challawa (n=40), Government Girls Arabic Secondary School (GGASS) Panshekara (n=40), Government Junior Secondary School (GJSS) Co-exist Panshekara (n=100), while eighty (80) urine samples were obtained from the private secondary school, namely; Nasara Academy Labi, Panshekara (n=80).
All the students from whom urine samples were obtained were randomly selected, and aged between 10 and 21 years. About 15ml urine sample was collected from each student in clean sample bottle between 10am and 2pm (period when the highest concentration of *S. haematobium* eggs are shed in urine) and stored in a cooler box containing ice blocks. The samples were taken to the laboratory for microscopic examination.

Urine Microscopy
Urine samples were examined for the presence of *S. haematobium* eggs using sedimentation method of Cheesbrough (1998). Each urine sample was mixed thoroughly with a glass rod and 10ml transferred into centrifuge tube and centrifuged at 2000rpm for 5 minutes at room temperature. The supernatant was discarded and the sediment obtained using a pasture pipette and 2 drops of the sediment were placed on a microscopic glass slide. A drop of Lugol's iodine was added onto the sediment and covered with a coverslip. The slides were then examined using a light microscope at 10× and 40× objective lenses for the presence of *S. haematobium* eggs. The eggs were identified by the presence of a conspicuous terminal spine.

Selection of Isolates for Molecular Characterization
Four *S. haematobium* positive isolates were purposively selected from the positive samples identified during the study. The selection was designed to provide a balanced molecular snapshot of the parasite circulating within the study population. The four isolates comprised samples from both public and private secondary schools and from both male and female participants. This ensured that the molecular characterization was not limited to a single school type or sex and allowed the selected isolates to capture variations across the major population groups included in the study. Therefore, the molecular findings were interpreted as representative of the selected isolates and indicative of the genetic characteristics of *S. haematobium* circulating in the study area, rather than as an exhaustive measure of population-wide genetic diversity.

DNA Extraction
DNA was extracted directly from parasite eggs in urine samples using a commercial genomic DNA extraction kit, Quick Genomic DNA Extraction Kit (GDSBio, China) according to the manufacturer's instructions. Proteins and other cellular debris were removed and the extracted DNA was eluted in Tris-Borate-EDTA (TBE) buffer.
The following protocol was used for DNA extraction:

i. 1 ml of urine sample was added to a 1.5 ml microcentrifuge tube and centrifuged for 5 mins at 13,000 rpm to pellet the cells. The supernatant was discarded.
ii. 500 µl of Digestion Buffer was added and mixed thoroughly by brief vortexing, then incubated at 55°C for 30 mins. It was centrifuged at 5,000 rpm for 10 min and the supernatant removed.
iii. 300 µl of Binding Buffer was added and mixed thoroughly by brief vortexing.
iv. 200 µl of absolute ethanol was added to the lysate and mixed thoroughly by brief vortexing.
v. The mixture from step 4 was pipetted into the spin column placed in a 2ml collection tube, and centrifuged at 12,000 rpm for 1 min and the flow-through was discarded.
vi. 500 µl of Wash Buffer (PS) was added, centrifuged for 1 min at 12,000 rpm and flow-through discarded.
vii. 500 µl of Wash Buffer (PE) was added, centrifuged for 1 min at 12,000 rpm and flow-through discarded.
viii. Step 7 was repeated.
ix. Centrifuging was done for 3 min at 12,000 rpm to dry the column membrane. The flow-through and collection tube were discarded.
x. The spin column was placed in a clean 1.5ml microcentrifuge tube and 60µl Elution Buffer (AE) was added directly into the column membrane, which was then incubated at room temperature for 2 min. Prior to use, the Elution Buffer was pre-warmed to 63°C.
xi. After incubation, it was centrifuged for 1 min at 12,000 rpm. The tube contained the pure DNA elute.
xii. The DNA was stored at -20°C for downstream molecular analyses.

DNA Amplification
Amplification of *S. haematobium* genomic DNA (gDNA) in urine samples was done using PCR. This method was used to

detect and amplify the parasite DNA, aiding in the diagnosis of schistosomiasis (Van Bergen *et al*., 2024)

The extracted DNA was amplified using primers namely *ITS1*-Forward (F): TCCGTAGGTGAACCTGCG and *ITS2*-Reverse (R): GACGCTTCTCCAGACTACAAT targeting the *ITS2* region of *S. haematobium* according to a previously described PCR protocol (Webster *et al*., 2012). Amplification of *S. haematobium* gDNA was also done using mitochondrial *cox1* primers namely Shb-F: TTTTTTGGTCATCCTGAGGTGTAT and Sh-R: TGATAATCAATGACCCTGCAATAA targeting the mitochondrial *cox1* gene (Elzain *et al*., 2025).

The PCR reaction volume for each of the primers was 20 µl and comprised of 10µl of PCR master mix, 1µl of forward primer, 1 µl of reverse primer, 5 µl of DNA template, and 3 µl of nuclease-free water. The following PCR conditions were used for *ITS2*: pre-denaturation at 94°C for 5min, denaturation at 94°C for 30s, annealing at 56°C for 30s, extension at 72°C for 30s, and final extension at 72°C for 5min. The amplicon band size was 600 base pairs (bp). The number of cycles was 35.

The following PCR conditions were used for mitochondrial *cox1*: pre-denaturation at 94°C for 5min, denaturation at 94°C for 30s, annealing at 55°C for 30s, extension at 72°C for 50s, and final extension at 72°C for 5min. The amplicon band size was 700bp. The number of cycles was 35.

Characterization of PCR Products

Characterization of PCR products was done by 1.5% agarose gel electrophoresis. In brief, 1.5g of agarose powder was measured and poured in 100ml of 1× TBE, then heated in a microwave for about 3min to dissolve the agarose powder. The resulting solution was allowed to cool and 4 µl of ethidium bromide added. The solution was poured in a gel casting tray, the comb placed and the solution allowed to cool and solidify for about 30min which was then placed in an electrophoresis tank. Exactly 20 µl of PCR product was pipetted, already mixed with DNA loading dye, and then dispensed into the gel lanes. One hundred (100) bp DNA ladder as size standard and negative control were also loaded. The gel was subjected to an electric field at 120V for 40min and visualized on a UV trans-illuminator for band detection (Esiere *et al*., 2022).

DNA Sequencing

The amplified PCR products were purified and sequenced using Sanger sequencing, to determine the nucleotide sequences of the target regions. The obtained nucleotide sequences were subsequently analyzed.

Data Analyses

Epidemiological Data Analysis

Data were entered, cleaned and validated in a Microsoft Excel spreadsheet (MS Office Excel 2021). Urogenital schistosomiasis test results (positive or negative) were the dependent variables. The data were then exported to SPSS software version 30. A univariate analysis was conducted for descriptive results such as frequencies and proportions. An analysis of association for potential risk factors with urogenital schistosomiasis positivity was conducted using Pearson chi-square in a bivariate analysis. Thereafter, a multivariate linear regression model was fitted, which included variables that retained significance (P<0.05) at a univariate linear regression analysis. For the multivariate analysis, a stepwise regression method and forward algorithm were used, then independent variables with P-value less than 0.05 were considered significant risk factors of schistosomiasis.

Molecular Analysis

The obtained nucleotide sequences were subjected to a BLAST (Basic Local Alignment Search Tool) analysis on the NCBI website (https://blast.ncbi.nlm.nih.gov/Blast.cgi) to confirm the species of *Schistosoma* obtained. This was then followed by assembling and editing of raw sequences using the ATGC plug-in Genetype. ATGC plug-in Genetype is a bioinformatics software used for DNA sequence editing, alignment, and genotype determination. The software analyzes nucleotide sequences by comparing them with reference sequences to identify sequence variations, including single nucleotide polymorphisms, insertions and deletions (Kumar *et al*., 2018). Reference sequences were downloaded from GenBank and together with the obtained sequences, a multiple sequence alignment was constructed using ClustalW (Thompson *et al*., 1994). The resultant FASTA file of the multiple sequence alignments was then converted to a MEGA file format and then utilized to construct a Neighbour-joining phylogenetic tree based on the Kimura 2-parameter method and 1000 bootstrap replicates as a measure of the confidence interval in MEGA version 11. All the generated sequences in this study have been submitted to GenBank, with accession numbers PZ809573 - PZ809576.

RESULTS AND DISCUSSION

Sociodemographic Characteristics of Study Participants

The results in Table 1 present sociodemographic characteristics of the study participants. A total of 370 participants were enrolled in the study. The majority were recruited from public schools (290/370, 78.4%), while 80 (21.6%) attended private schools. In terms of sex distribution, males constituted a higher proportion of the study population (220/370, 59.5%) compared to females (150/370, 40.5%). Age distribution showed a marked predominance of adolescents, with most participants aged 11–20 years (328/370, 88.6%). Only small proportions were aged ≤10 years (22/370, 5.9%) and ≥21 years (20/370, 5.4%).

Table 1: Sociodemographic Characteristics of Study Participants in Reservoir-Adjacent Communities in Kano State (n = 370)

Variable	Category	Frequency	Percentage (%)
School type	Public school	290	78.4
	Private School	80	21.6
Sex	Male	220	59.5
	Female	150	40.5
Age group	≤ 10 years	22	5.9
	11-20 years	328	88.6
	≥ 21 years	20	5.4

Prevalence of Infection by Sociodemographic Characteristics

The results in Table 2 present the prevalence of *S. haematobium* infection in the study population. The overall prevalence of urogenital schistosomiasis in Challawa was 39.46% (146/370). Participants attending public schools had higher prevalence of infection (42.07%) compared to those in private schools (30.00%). There was statistically significant difference in the prevalence of *S. haematobium* infection between school types ($\chi^2 = 39.4$; 95% CI: 0.59-0.70; $p < 0.01$). Infection prevalence was significantly higher among males (45.00%) than females (31.33%). Males had significantly increased odds of infection (OR = 2.21; 95% CI: 1.85-2.63), and this association was statistically significant ($\chi^2 = 154.5$; $p < 0.01$). The highest prevalence was observed among participants aged 11–20 years (40.55%), followed by those aged ≤10 years (36.46%), while the lowest prevalence occurred among individuals aged ≥21 years (25.00%). This association was significant ($\chi^2 = 48.8$; $p < 0.01$).

Table 2: Prevalence and Bivariate Analysis of Urogenital Schistosomiasis Among Study Participants (n = 370)

Variable	Category	No. Examined	No. Positive	Prevalence (%)	OR	95% CI	χ^2	*p*-value
School Type	Private school	80	24	30.00	1.00 (Ref)*	—	39.4	<0.01
	Public school	290	122	42.07	0.65	0.59-0.70		
	Total	370	146	39.46				
Sex	Female	150	47	31.33	1.00 (Ref)	—	154.5	<0.01
	Male	220	99	45.00	2.21	1.85–2.63		
	Total	370	146	39.46				
Age Group (years)	≥ 21	20	5	25.00	1.00 (Ref)	—	48.8	<0.01
	≤ 10	22	8	36.46	0.53	0.48-0.60		
	11–20	328	133	40.55	1.52	0.76-3.03		
	Total	370	146	39.46				

Key: %= Percentage; OR= Odds Ratio; CI= Confidence Interval; χ^2= Chi-Square; *p*-value= 0.05; *Lowest-Risk Category was Used as the Reference Group (Ref)

Risk Factors for Schistosoma haematobium Infection

The results in Table 3 present reported behavioural and environmental risk factors for *S. haematobium* infection in the study populations. Several behavioural and environmental factors were significantly associated with *S. haematobium* infections among the study participants. Participants who engaged in water contact activities had markedly higher odds of infection. Swimming showed the strongest association, with 110 of 119 individuals infected, corresponding to significantly increased odds (OR = 72.9; 95% CI: 33.9-157.0; $\chi^2 = 202.8$, $p < 0.01$). Similarly, bathing in open water sources (OR = 42.2; 95% CI: 19.3-92.0; $\chi^2 = 147.5$, $p < 0.01$) and water fetching (OR = 23.2; 95% CI: 13.2-40.7; $\chi^2 = 148.5$, $p < 0.01$) were strongly associated with infection. Lack of knowledge about the disease was significantly associated with higher infection odds (OR = 4.99; 95% CI: 3.2-7.9; $\chi^2 = 49.3$, $p < 0.01$). Participants with a prior history of infection were also more likely to be infected than those without prior infection (OR = 1.97; 95% CI: 1.3-3.1; $\chi^2 = 8.1$, $p < 0.01$). However, prior treatment was not significantly associated with infection (OR = 1.03; 95% CI: 0.7-1.6; $\chi^2 = 0.00$, $p = 0.98$). Proximity to water bodies was a strong predictor of infection. Individuals living within 5 km of a water source had significantly higher odds of infection compared to those living farther away (OR = 8.88; 95% CI: 5.4-14.5; $\chi^2 = 84.0$, $p < 0.01$). Participants with poor sanitation had significantly higher odds of infection compared to those with good sanitation (OR = 16.7; 95% CI: 9.8-28.3; $\chi^2 = 127.9$, $p < 0.01$).

Table 3: Behavioural and Environmental Risk Factors Associated with *Schistosoma haematobium* Infection

Variable	Category	Positive	Negative	OR	95% CI	χ^2	*p*-value
Swimming	No	36	215	1.00 (Ref)*	—	202.8	<0.01
	Yes	110	9	72.9	33.9-157.0		
Bathing	No	57	216	1.00 (Ref)	—	147.5	<0.01
	Yes	89	8	42.2	19.3-92.0		
Water fetching	No	40	201	1.00 (Ref)	—	148.5	<0.01
	Yes	106	23	23.2	13.2-40.7		
Distance to water	Far (>5 km)	31	158	1.00 (Ref)	—	84.0	<0.01
	Near (<5 km)	115	66	8.88	5.4-14.5		
Sanitation	Good	42	195	1.00 (Ref)	—	127.9	<0.01
	Poor	104	29	16.7	9.8-28.3		
Knowledge	Yes	60	174	1.00 (Ref)	—	49.3	<0.01
	No	86	50	4.99	3.2-7.9		
Prior infection	No	89	169	1.00 (Ref)	—	8.1	<0.01
	Yes	57	55	1.97	1.3-3.1		
Prior treatment	No	102	158	1.00 (Ref)	—	0.00	0.98
	Yes	44	66	1.03	0.7-1.6		

Key**:** F= Frequency; n= Number of Respondents; NP= Number Positive; NN= Number Negative; OR= Odds Ratio; CI= Confidence Interval; %= Percentage; χ^2= Chi-Square; *p*-v= Probability Value.*Lowest-Risk Category was Used as the Reference Group (Ref)

Clinical Indicators of Schistosoma haematobium Infection

The results in Table 4 present clinical morbidity indicators of *S. haematobium* infection among the study participants. Clinical symptoms were significantly associated with infection. Haematuria (OR = 6.66; χ^2 = 131.5, p < 0.01), dysuria (OR = 45.4; 95% CI: 17.5-117.9; χ^2 = 108.7, p < 0.01), and frequent urination (OR = 6.84; 95% CI: 2.5-18.7; χ^2 = 18.9, p < 0.01) were all strongly linked to infection status.

Table 4: Clinical Morbidity Indicators Associated with Urogenital Schistosomiasis Among Study Participants

Clinical indicator	Positive (n =146)	Negative (n =224)	% among positives	χ^2	*p*-value
Haematuria	66	20	45.2	131.5	<0.01
Dysuria	54	24	37.0	108.7	<0.01
Frequent urination	20	59	13.7	18.9	<0.01
None	6	121	4.1	—	—

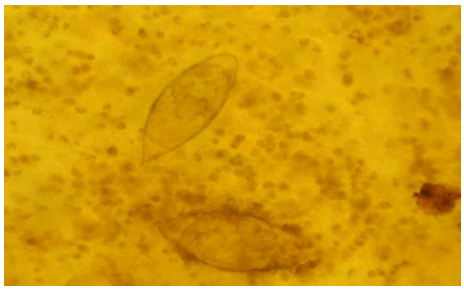

Figure 2: *Schistosoma haematobium* Eggs Isolated from Study Participant

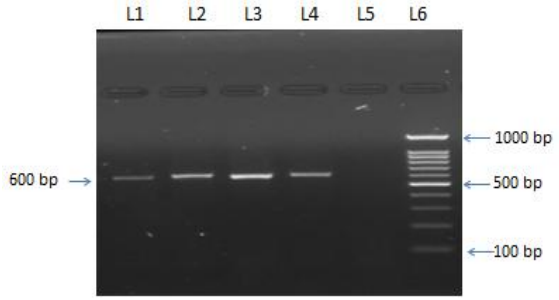

Figure 3: Agarose Gel Electrophoresis of *Schistosoma haematobium* Nuclear *ITS2* Gene. Lane 1-4: Samples 1-4; Lane 5: Negative Control; Lane 6:100bp DNA Ladder

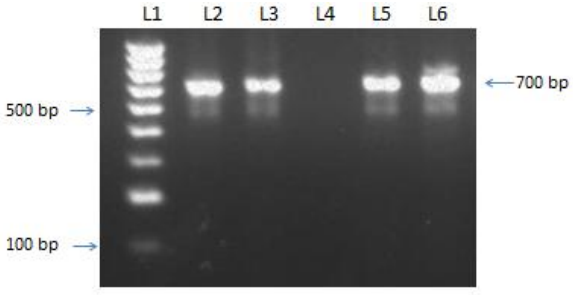

Figure 4: Agarose Gel Electrophoresis of *Schistosoma haematobium* Mitochondrial *cox1* gene. Lane 1, 100 bp DNA Ladder; Lane 2 and 3, Sample 1 and 2; Lane 4, Negative Control; Lane 5 and 6, Sample 3 and 4

Phylogenetic Analysis of *Schistosoma haematobium* Isolates

Neighbour-joining phylogenetic analysis based on *ITS2* rDNA sequences revealed that all study isolates clustered within the *Schistosoma haematobium* clade, confirming species identity. The Kano isolates (CHW01–CHW04) showed close genetic relatedness (98-100%) to reference sequences obtained from GenBank, forming well-supported clusters with previously reported *S. haematobium* isolates.

Two of the study isolates (CHW01 and CHW04) clustered tightly with reference strains (e.g., DDA76, BDU26, and DDA35), indicating high sequence similarity and low genetic divergence. In contrast, CHW02 and CHW03 formed a slightly distinct sub-cluster, suggesting minor genetic variation within the local population. *Fasciola hepatica*, used as outgroup was clearly separated from all *S. haematobium* sequences, confirming correct tree rooting and the robustness of the phylogenetic reconstruction. Finally, the phylogenetic findings suggest limited intra-population genetic variations among the isolates obtained from the study area.

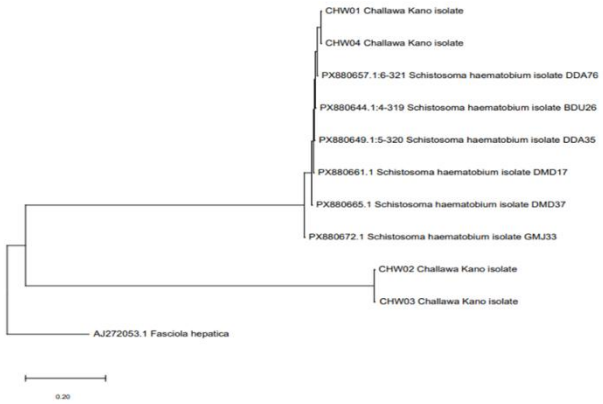

Figure 5: Neighbour-Joining Phylogenetic Tree Based on *ITS2* rDNA Sequences Showing the Relationship Between *Schistosoma haematobium* Isolates and Reference Sequences Retrieved from GenBank. *Fasciola hepatica* was Included as Outgroup to Root the Tree

Discussion

This study demonstrates that urogenital schistosomiasis remains highly endemic among secondary school students in Challawa, Kano State, with an overall prevalence of 39.46%. The higher infection prevalence observed in public schools (42.07%) compared to private schools (30.00%) highlights underlying socioeconomic and environmental disparities that sustain transmission. These findings are consistent with regional reports identifying school-aged children as a high-risk group due to frequent and intense contact with infested water sources (Dawaki *et al*., 2016; Abdulkadir *et al*., 2017; Orpin *et al*., 2017).

Although lower than the 70% prevalence reported in a community-based study in Kano (Umar *et al*., 2016), the current findings highlight a substantial burden among school children, indicating gaps in ongoing control efforts. Persistent transmission may be driven by reinfection following praziquantel (PZQ) treatment, particularly in settings with continued exposure to infested water bodies (N'goran e*t al*., 2001; Saathoff *et al*., 2004). This supports previous evidence that single-dose mass drug administration (MDA) is insufficient without sustained monitoring and repeated treatment (Kabuyaye *et al*., 2017).

Consistent with prior studies, infection prevalence was higher in males, likely reflecting greater involvement in water-related activities such as swimming and livestock watering (Abdullahi *et al*., 2011; Umar *et al*., 2016; Naphtali and Ngwamah, 2019; Joof *et al*., 2021). However, contrasting findings from other regions suggest that gender differences are context-dependent and influenced by sociocultural roles (Hajissa *et al*., 2018; Angora *et al*., 2019; Okoye *et al*., 2024). The highest prevalence observed among individuals aged 11–20 years further emphasizes the vulnerability of highly active age groups with frequent water exposure (Tembo *et al*., 2022; Dahal *et al.*, 2023; WHO, 2023; Obademi *et al*., 2024). Notably, infections detected in younger children (≤10 years) suggest early exposure, possibly through household water-related activities, reinforcing the need to include younger age groups in control programs (Betson *et al*., 2013; Tembo *et al*., 2022).

Behavioural and environmental risk factors, including swimming, bathing, water fetching, poor sanitation, and proximity to water bodies—were significantly associated with infection, reinforcing their central role in *S. haematobium* transmission.

The current study observed that the appearance of urine on macroscopy or physical observation has a positive linear association with urogenital schistosomiasis, similar to another study conducted in Kano State, Nigeria, that reported that visible blood in urine (macrohaematuria) and microhaematuria were associated with the presence of *S. haematobium* in urine (Umar *et al*., 2016). Similarly, another study conducted in Enugu State, Nigeria, found a positive correlation between macrohaematuria and the presence of *S. haematobium* eggs in urine (Ogbonna *et al*., 2012). The findings of these studies corroborate findings in the present study in which the appearance of urine on macroscopy was positively associated with urogenital schistosomiasis. The strong association between haematuria and infection supports its continued utility as a rapid, low-cost proxy indicator in endemic settings, although it should be complemented with parasitological or molecular diagnostics for improved accuracy.

Molecular characterization confirmed all isolates as *Schistosoma haematobium*, with high sequence similarity (98-100%) to reference strains. The observed low genetic diversity and tight phylogenetic clustering suggest a relatively homogeneous parasite population, indicative of stable, localized transmission. The absence of distinct sub-structuring implies that infections likely originated from a common transmission focus, consistent with shared water contact sources identified in the epidemiological analysis. Such genetic homogeneity has been reported in other endemic settings and may reflect limited parasite introduction from external populations (Huyse *et al*., 2009; Webster *et al*., 2013). While this stability may simplify control efforts, it also highlights the persistence of entrenched transmission cycles.

CONCLUSIONS

Urogenital schistosomiasis remains a significant public health concern in Challawa, with evidence of sustained transmission among school-aged children. Infection is strongly associated with water contact behaviors, environmental exposure, and sanitation conditions, with variations observed across gender, age and school type. Molecular findings confirm the presence of *S. haematobium* with low genetic diversity, suggesting stable, localized transmission. These findings underscore the need for intensified regular and comprehensive PZQ distribution among school-aged children, school-based awareness campaigns, provision of safe drinking water and improved sanitation infrastructure, and implementation of snail control strategies. Additionally, continued molecular surveillance using molecular markers such as nuclear *Internal Transcribed Spacer* regions and mitochondrial genes (*cox1*) through targeted PCR amplification, DNA sequencing, comparative sequence and phylogenetic analysis, is essential to monitor parasite population dynamics and inform targeted intervention strategies.

REFERENCES

Abdullahi, M. K , Bassey, S. E., Oyeyi, T. I. (2011). The epidemiology of *Schistosoma haematobium* infection in 44 local government areas of Kano State, Nigeria. *Nigerian Journal of Parasitology 32*(1): 19-24.

Abdulkadir, A., Ahmed, M., Abubakar, B. M., Suleiman, I. E., Yusuf, I., Imam, I. M., Sule, A. A., Tela, U. M., Dogo, H. M., Yakasai, A. M., & Musa, B. M. (2017). Prevalence of urinary schistosomiasis in Nigeria, 1994-2015: Systematic review and meta-analysis. *African Journal of Urology 23*, 228-239.

Alemu, M., Zigta, E. and Derbie, A. (2018). Under diagnosis of intestinal schistosomiasis in a referral hospital, North Ethiopia. *BMC Res Notes.* Apr; *11*: 245. Doi: https://doi.org/10.1186/s/3104-018-3355-0.

Altwairgi, A. (2024). Chronic Infection with *Schistosoma Haematobium* Leads to the Development of Squamous Cell Carcinoma of the Bladder. *Georgian Medical News.* Dec; (357): 99-103.

Angora, E. K., Bossier, J., Menan, H., Ray, O., Tuo, K., Toure, A. O., Coulibaly, J. T., Mēitē, A., Raso, G., N'goran, E. K., *et al*. (2019). Prevalence and risk factors for schistosomiasis among school children in two settings of Côte d'Ivoire. *Trop. Med. Infect. Dis. 4*, 110.

Aryeetey, Y. A., Essien-Baidoo, S., Larbi, I. A., Ahmed, K., Amoah, A.S., Obeng, B.B., van Lieshout, L., Yazdanbakhsh, M., Boakye, O. A., Verweij, J.J. (2013). Molecular diagnosis of *Schistosoma* infections in urine samples of school children in Ghana. *Am. J. Trop. Med. Hyg. 88*, 1028 – 1031.

Atalabi, T. E., Adoh, S. D., & Eze, K. M. (2018). The current epidemiological status of urogenital schistosomiasis among primary school pupils in Katsina State, Nigeria: An imperative for a scale up of water and sanitation initiative and mass administration of medicines with praziquantel. *PLoS Negl. Trop. Dis., 12*, e0006636.

Balogun, J. B., Adewale, B., Balogun, S. U. Lawan, A., Haladu, I.S., Dogara, M.M., Aminu. A.U., Caffrey, C.R., De Koning, H.P., Watanabe, Y., Balogu, E.O. (2022) Prevalence and Associated Risk Factors of Urinary schistosomiasis Among Primary School Pupils in the Jidawa and Zobiya Communities of Jigawa State, Nigeria – *Annals of Global Health. 88*(1): 71, 1-4. Doi: https://doi.org/10.5334/aogh.3704

Betson, M., Sousa-Figueiredo, J. C., Kabatereine, N. B., & Stothard, J. R. (2013). New Insights into the Molecular Epidemiology and Population Genetics of *Schistosoma mansoni* in Ugandan Pre-school Children and Mothers. *PLoS Negl. Trop. Dis. 7*, e2561.

Cheesbrough, M. (1998). District Laboratory Practice in Tropical Countries Part 1. *Cambridge University Press*. 236 – 239.

Cisse, M., Sangaree, I., Djibougou, A. D., Tahitia, M. C., Gnissi, S., Bassinga, J. K., Kinda, S., Diallo, A. H. (2021). Prevalence and risk factors of *Schistosoma mansoni* infection among preschool-aged children from Panamasso village, Burkina Faso. *Parasite Vectors, 14*, 185.

Dahal, S. A., Jabba, J. R., Ezekiel, T., Salu, G., Naubol, C. M., Longwap, S. A., & Jatau, D. E. 2023). Prevalence of Urinary Schistosomiasis Among Primary School Pupils in Jos, North Central Nigeria. *International Journal of Pathogen Research 12*(6), 11-18.

Dawaki, S., Al-mekhlafi, H. M., Ithoi, I., Ibrahim, J., Abdusalam, A. M., Ahmad, A., Sady, H., Atroosh, W. M., Al-Areeq, M.A., Elyana, F.N., Nasr, N.A., Shrin, J. (2016). Prevalence and Risk Factors of schistosomiasis Among Hausa Communities in Kano State, Nigeria. *Rev Inst Med Trop Sao Paulo – Jul 11*:58: 54. Doi: https://doi.org/10.1590/51678–994620/658054.

Elzain, I. A., Idris, A. B., Karim, A. A., *et al*. (2025). Analysis of DNA *cox1* bar coding revealed novel haplotype in *Schistosoma haematobium* isolated from Western Sudan. *Sci Rep 15*, 2062. Doi: https://doi.org/10.1038/s41598-025-85986.0.

Esiere, R. K., Ibeneme, E. O., Effanga, E. O., *et al*. (2022). Detecting *Schistosoma haematobium* infection by microscopy and polymerase chain reaction (PCR) in school children in three senatorial districts of Crossriver State, Nigeria. *J parasit Dis 46*, 272-279. Doi: https://doi.org/10.1007/s12639-021-01446-2.

ESPEN. ESPEN/Expanded Special Project for Elimination of Neglected Tropical Diseases. Available online: https://espen.afro.who.int (accessed on 19 May 2024).

Eze, C.O., Onyekwelu, K.C., Akinwale, O.P., Shan, L., Wei, H. (2019). Urinary schistosomiasis in Nigeria: a 50 year review of prevalence, distribution and disease burden. *Parasite 26*, 19.

Federal Ministry of Health (FMOH), Neglected Tropical Diseases Master Plan 2015 – 2020. https://espen.afro.who.int/system/files/content/resources/N. GIS Lab, Bayero University Kano, 2019).

Hajissa, K., Muhajir, A. E., Eshang, H. A., Alfadel, A., Nahied, E., Dahab, R., Ali, S. M., Mohammed, M., Gaafar, M., & Mohamed, Z. (2018). Prevalence of schistosomiasis

and associated risk factors among school children in Um-Asher Area, Khartoum, Sudan. *BMC Res. Notes, 11*, 779.

Huyse, T., Webster, B. L., Geldof, S., Stothard, J. R., Diaw, O. T., Polman, K., & Rollinson, D. (2009). Bidirectional introgressive hybridization between schistosome species. *PLoS Pathogens, 5*(9), e1000571.

Joof, E., Sanyang, A. M., Camara, Y., Sey, A. P., Baldeh, I., Jah, S. L., Ceesay, S. J., Sambon, S. M., Sanyang, S., Wade, C. M., *et al*. (2021). Prevalence and risk factors of schistosomiasis among primary school children in four selected regions of the Gambia. *PLoS Negl. Trop. Dis. 15*, e0009380.

Kabuyaye, M., Chimbari, M. J., Manyangadze, T., & Mukaratirwa, S. (2017). Efficiency of praziquantel on *Schistosoma haematobium* and reinfection rates among school-going children in the Ndumo area of Umkhanyakude district, Kwa Zulu-Nata, South Africa. *Infect. Dis.Poverter, 6*, 83.

Kosinski, K. C., Bosompem, K. M.,Stadecker, M. J., Wagner, A. D., Plummer, J., Durant, J. L., & Gute, D. M. (2011). Diagnostic accuracy of urine filtration and dipstick tests for *schistoomia haematobium* infection in a highlyinfected population of Ghanaian school children. *Acta Trop. 118*, 123 – 127.

Kounab, L. C., Ouegue-Liabagui, S. L., Atiga, C. N., Mbani Mega Ntigui, C. N., Imboumy-Limoukou, R. K., Biteghe, B. I., Essone, J. C., Ontoua, S. S., Moukodoum, D. N., Okouga, A. P., & Lekana-Douki, J. B. (2025). Molecular Detection of Urogenital Schistosomiasis in Community Level in Semi-rural Area in South-East Gabon. *Diagnostics, 15*(9), 1052. Doi: https://doi.org/10.3390/diagnostics15091052.

Kumar, G., Li, M., Knyaz, C. & Tamura, K. (2018). Mega X: Molecular Evolutionary Genetics Analysis Across Computing Platforms. *Molecular Biology and Evolution, 35*(6), 1547-1549.

Leger, E., and Webster, J.P. (2017). Hybridizations Within the Genus *Schistosoma*: Implications for epidemiology and control. *Parasitology, 144*, 65- 80.

Lawiye, J., Vandi, P.V. Godly, C., Midala, A., Watirahel, P., & Enamola, W. (2020). Prevalence and Risk Factors of *Schistosoma haematobium* infections among primary school children in Igbokuta village, Ikorodu North Local Government, Lagos State. *IOSR J. Nurs. Health Sci. 2* , 62 – 68.

Mendy, A., Kargbo, A., Ibrahim, Y.K.E., Entonu, M.E., & Gbem, T.T. (2020). Molecular Epidemiology of schistosomiasis in Central River Region of the Gambia. *Afr. J. Biotechnol. 19*, 508 – 519.

Mohammed, I.O., Kinung'hi, S., Mwinzi, P.N.M., Onkanga, I.O., Andioge, K., & Muchir, G. (2018). Diet and hygiene Practices Influence Morbidity in School children living in schistosomiasis endemic areas along Lake Victoria in Kenya and Tanzania – A Cross-sectional study. *PLoS Negl Trop Dis. March; 12*(3). Doi: https://doi.org/10.1371/journal.pntd.0006373.

Monde, C., Syampungani, S., & Van den Brink, P. J. (2015). Exploring the potential of host-environment relationships in the control of schistosomiasis in Africa. *Afr. J. Aquat. Sci, 40*, 47-55.

Naphtali, R. S., and.Ngwamah, J. S. (2019). Prevalence and Intensity of Urinary Schistosomiasis among Residence: A Case Study in River Benue, Adamawa State, Northeastern Nigeria. *Asian Journal of Research in Zoology 2*(2): 1-10. Doi: https://doi.org/10.9734/AJRIZ/2019/v21230065.

Ndassi, V. D., Anchang-Kimbi, J. K., Sumbele, I. U. N., Wepuje, G. B., & Kimbi, H. K. (2019). Prevalence and risk factors associated with *S. haematobium* egg excretion during the dry season, six months following mass distribution of praziquantel in 2017 in the Bafia Health Area, South West Region Cameroon: A Cross-Sectional Study. *J. Parasitol. Res. 2019*, 4397263.

N'goran, E. K., Utzinger, J., N'guessan, A. N., Müller, I., Zamblé, K., Lohouriguon, K. L., Traoré, M., Sosthène, B. A., Lengeler, C., & Tanner, M. (2001). Reinfection with *Schistosoma haematobium* following school-based chemotherapy with praziquantel in four highly endemic villages in Côte d'Ivoire. *Trop. Med. Int. Health, 6*, 817-825.

Obademi, S. J., Aliyu, S. M., Suleiman, B. A., Musa, I. A., Adeyemi, F. A., Joseph, I. G., & Balogun, O. E. (2024). Molecular detection of *Schistosoma haematobium* infection among school children in Sabon-Gari Local Government Area, Kaduna State, Nigeria. *African Journal of Biotechnology 23*(11), 318-326. Doi: https://doi.org/10.5897/AJB2024.17695.

Odeniran, P. O., Omolabi, K. F., Ademola, I. O. (2020). Epidemiological Dynamics and Associated Risk Factors of *S. haematobium* in Humans and it's Snail Vectors in Nigeria: A Meta-analysis (1983-2018). *Pathogen Global Health. March; 114*(2): 76-90. Doi: https://doi.org/10.1080/20477724.2020.1728164

Ogbonna, C. C., Dori, G. U., Nweze, E. I., Muoneke, G., Nwankwo, I. E., & Akputa, N. (2012). Comparative Analysis of Urinary schistosomiasis among primary school children and rural farmers in Obollo-Eke, Enugu State, Nigeria: Implications for control. *Asian Pac. J. Trop. Med. 5*, 796-802.

Okoye, E. P., Ekwunife, C. A., Onyido, A. E., Obijiofor, E. C., Nzekwu, C. I., Nnatuanya, I. O., Okeke, U. M., & Ude, E. A. (2024). Prevalence of Urogenital Schistosomiasis Among School-Age Children in Riverine Area of Anambra West L.G.A, Anambra State, Nigeria. *South Asian Journal of Parasitology 7*(2): 98-109.

Orpin, J. B., Bem, A. A., Usman, A. (2017). Prevalence of urinary schistosomiasis in selected secondary school students of Faskari L. G. A, Katsina State. *FUDMA Journal of Sciences 1*(1): 7-11.

Oyeyemi, O.T., Jeremias, W., Grenfell, R. F. Q. (2020). Schistosomiasis in Nigeria: Gleaning from the past to improve current efforts towards control. *"One Health." 14* (7): 160-170.

Rollinson, D., Webster, B. L., Knopp, S., Allan, F., Person, B., & Stothard, J. R. (2013). Genetic diversity of schistosomes

and implications for control. *Transactions of the Royal Society of Tropical Medicine and Hygiene*, *107*(7), 389-398.

Saathoff, E., Olsen, A., Magnussen, P., Becker, W., & Appleton, C. C. (2004). Patterns of *Schistosoma haematobium* Infection, Impact of Praziquantel Treatment and Reinfection After Treatment in a Cohort of School Children from Rural KwaZulu-Natal, South Africa. *BMC Infect. Dis. 4*, 40.

Sady, H., Al-Mekhlafi, H. M., Lim, Y. A., Mahmud, R., & Surin, J. (2013). Prevalence and associated factors of Schistosomiasis among children in Yemen: Implications for an effective control program. *PLoS Negl Trop Dis. 7*(8): e 2377.

Sady, H., Al-Mekhlafi, H. M., Ngui, R., Atroosh, W. M., Al-Delaimy, A. K., Nasr, N. A., Dawaki, S., Abdulsalam, A. M., Ithoi, I., Lim, Y. A., Chua, K. H., Surin, J. (2015). Detection of *Schistosoma mansoni* and *Schistosoma haematobium* by Real-time PCR with high resolution melting analysis. *Int. J. Mol. Sci. 16*, 16085-16103. Doi: https://doi.org/10.3390/ijms160716085

Tembo, R., Muleye. W., Ibrahim, Y.K.E., Entonu, M.E., Bamba, K.S., Zulu, M., Mwamba, F., Saad, S.A., Kamwela, M., Mukubesa, A. N., Monde, N., Kallu, S.A., Mbewe, N., & Phiri, A.M. (2022). Prevalence and Molecular Identification of *Schistosoma haematobium* Among Children in Lusaka and Sigvonga Districts, Zambia. *Trop Med Infect Dis. Sep 10; 7*(9): 239. Doi: 10.3390/tropical med 7090239.

Thompson, J. D., Haggins, D. G., & Gibson, T. J. (1994). Clustal W: Improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. *Nucleic Acids Res. 22*, 4673-4680.

Trobajo, R., *et al*. (2010). The use of partial *cox1*, rbcL and LSU rDNA sequences for phylogenetic and species identification within the *Nitzschia palea* species complex (Bacillariophyceae). *Eur. J. Phycol. 45*, 413-425.

Umar, M. A., Umar, A. U., Idris, H. U., Abdullahi, Y., & Sabiu, M. A. (2016). "*Schistosoma Haematobium* Infections: Prevalence and Morbidity Indicators in Communities Around Wasai Dam, Minjibir, Kano State, Northern Nigeria". *International Journal of TROPICAL DISEASE & Health 17*(2): 1-8. Doi: https://doi.org/10.9734/IJTDH/2016/23448

Umar, S., Shinkafi, S. H., Hudu, S. A., Neela, V., Suresh, K., Nordin, S. A., & Malina, O. (2017). Prevalence and molecular characterization of *Schistosoma haematobium* among primary school children in Kebbi State, Nigeria. *Ann Parasitol. 63*(2): 133-139. Doi: https://doi.org/10.17420/ap6302.7.

van der Werf, M. J., de Vlas, S. J., Brooker, S., Looman, C. W., Nagelkerke, N. J., Habbema, J. D., & Engels, D. (2003). Quantification of Clinical Morbidity Associated with Schistosome Infection in sub-Saharan Africa. *Acta Trop. May; 86* (2-3): 125-39. Doi: https://di.org/10.1016/s0001-706×(03)00029-9.

van Bergen, K. j. M., Brienen, E. A., Randrianasalo, B. S., Ramarokoto, C. E., Leutscher, P., Kjetland, E. F., van Diepen, A., Dekker, F., Saggiomo, V., Velders, A. H., & van Lieshout, L (2024). Next step towards point-of-care molecular diagnosis of female genital schistosomiasis (FGS): evaluation of an instrument-free LAMP procedure. *Front. Parasitol. 3*:1297310. Doi: https://doi.org/10.3389/fpara.2024-1297310

Viricel, A., and Rosel, P. E. (2011). Evaluating the utility of *cox1* for *Cetacean* species identification. Mar. *Mammal Sci. 28*, 37-62.

Webster, B. L., Emery, A. M., Webster, J. P., Gouvras, A., Garba, A., Diaw, O., Seye, M. M., Tchuente, L. A., Simoonga, C., Mwanga, J., *et al*. (2012). Genetic Diversity Within *Schistosoma haematobium*: DNA Barcoding Reveals Two Distinct Groups. *PLoS Negl. Trop. Dis. 6*, e1882.

Webster, B. L., Diaw, O. T., Seye, M. M., Webster, J. P., & Rollinson, D. (2013). Introgressive hybridization of schistosomes in Senegal. *PLoS Neglected Tropical Diseases, 7*(2), e2113.

Webster, B. L., *et al*. (2018) Occurrence of *Schistosoma bovis* on Pembla Island, Zanzibar: implications for urogenital schistosomiasis transmission monitoring. *Parasitol. 145*, 172-1731.

World Health Organization (2021). Urogenital Schistosomiasis, a Neglected Tropical Disease.
World Health Organization. (2023). Schistosomiasis fact sheet. WHO.