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# Cross-Species Surveillance of Schistosoma Infections in Humans, Livestock, and Soil in Rivers State, Nigeria

Nwikasi, Kiaka, Uchechukwu M. Chukwuocha, Ekeleme Uzochukwu Godswill, & Bagbi Loveday Elebari

*Department of Public Health, Federal University of Technology, Owerri, Imo State*

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***Corresponding Author:** Nwikasi Kiaka

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**Abstract** **Review Article**

Schistosomiasis remains a significant global health burden, particularly in regions with poor sanitation and inadequate access to clean water. This study employed a One Health epidemiological approach to investigate the cross-species prevalence and transmission of Schistosoma infections among humans, livestock, and soil in Rivers State, Nigeria. A cross-sectional descriptive study design was used within the One Health framework to identify and characterize Schistosoma species across sample types.

For soil analysis, systematic random sampling was used to select 30 locations, from which 90 soil samples were collected using an auger. Livestock blood samples were obtained from 181 cattle through simple random sampling, with 10 ml of blood collected from each animal into sterile, labeled containers. For the human population, a multistage sampling technique was employed to select participants, and 10 ml of blood was collected from 255 individuals under aseptic conditions.

All samples underwent DNA extraction and purification. The extracted DNA was amplified using species-specific primers ITTS2F and ITTS1R, and results were interpreted based on the presence of Schistosoma-specific DNA sequences. Descriptive statistics were used to determine frequency distributions, while correlation tests assessed associations across species and environmental interfaces.

Findings revealed a Schistosoma prevalence of 20.4% in human samples (S. haematobium: 12.2%, S. mansoni: 4.7%, S. japonicum: 3.1%, S. intercalatum: 0.4%). In livestock, the prevalence was 48.1% (S. japonicum: 13.2%, S. bovis: 34.8%). Soil samples showed a 20.0% prevalence (S. bovis: 17.8%, S. haematobium: 2.2%). Significant correlations were found between S. japonicum in humans and livestock ($p = 0.012$), and between S. bovis in livestock and soil ($p = 0.001$), suggesting possible zoonotic and environmental transmission routes. However, the correlation between S. haematobium in humans and soil was not statistically significant ($p = 0.234$).

These results underscore the interconnectedness of human, animal, and environmental health in schistosomiasis transmission. Strengthened health education, improved sanitation, and integrated community-based interventions are recommended to reduce disease prevalence and interrupt transmission cycles in endemic communities.

**Keywords:** Schistosomiasis, Parasite transmission, Zoonotic parasites, Human infection, Soil-transmitted helminths.



## 1. INTRODUCTION

Schistosomiasis, also known as bilharzia, is a neglected tropical disease (NTD) caused by parasitic flatworms of the genus Schistosoma. It affects over 250 million people worldwide, with sub-Saharan Africa bearing the highest burden (World Health Organization [WHO], 2023). Transmission typically occurs when individuals meet freshwater bodies contaminated with cercariae, the larval form of the parasite, which penetrates the skin and matures within the host's vascular system (Colley et al., 2014). Beyond human health, schistosomiasis has zoonotic dimensions, with livestock and environmental reservoirs increasingly recognized as key components in sustaining the parasite's lifecycle (Webster et

al., 2016).

In humans, schistosomiasis leads to chronic illness, organ damage, and socio-economic disruption, particularly among marginalized populations without access to clean water or adequate sanitation (Gryseels et al., 2006). The major human-infecting species include Schistosoma haematobium (urogenital schistosomiasis), S. mansoni (intestinal), and S. japonicum. In Nigeria, S. haematobium and S. mansoni are predominant, with both species causing widespread morbidity, especially in school-aged children (Ekpo et al., 2012; Ofoezie et al., 1996).

Importantly, schistosomiasis also affects animals such as cattle, goats, and sheep, primarily through species like S. bovis and S. masoni, with substantial economic consequences in terms of reduced productivity, weight loss, and fertility impairment (Mekonnen et al., 2021). In mixed human-livestock systems, animals not only suffer direct parasitic burdens but may also serve as reservoirs for human reinfection, complicating control efforts (Standley et al., 2012). Recent studies have highlighted hybridization between human and animal schistosomes, such as S. haematobium and S. bovis, creating new public health risks (Leger et al., 2020).

While schistosomes require aquatic intermediate hosts (snails), recent environmental health research has drawn attention to the role of soil and sediments in harboring schistosome eggs or infected snail vectors. Soil-transmitted elements, although not a direct transmission medium for cercariae, can indicate environmental contamination through fecal matter, often resulting from open defecation practices (Kengne-Ouafo et al., 2019). Soil samples near water contact sites and livestock pens have shown the presence of viable schistosome eggs, underscoring the One Health interconnection between environment, animals, and humans (Hotez et al., 2010).

Nigeria ranks among the top five schistosomiasis-endemic countries globally (WHO, 2023). According to the Federal Ministry of Health (FMoH), all 36 states are affected, with prevalence varying significantly across ecological zones (FMoH, 2021). Rivers State, located in the Niger Delta region, is characterized by abundant freshwater bodies, high rainfall, and heavy agricultural and fishing activities, ideal conditions for the propagation of schistosomiasis vectors (Akinwale et al., 2010). The reliance of rural communities on rivers and streams for domestic and occupational activities increases the risk of human exposure, while extensive livestock rearing along water bodies creates additional transmission interfaces.

Previous epidemiological studies in Rivers State have largely focused on school-based surveys or localized communities, often neglecting a broader ecological approach that includes livestock and environmental components. For instance, Nwokeocha et al. (2018) found a prevalence of S. haematobium infection of over 20% among school children in selected LGAs, while Okpala and Opara (2020) observed consistent reinfection patterns despite periodic mass drug administration (MDA). These findings highlight the need for integrated, cross-sectoral investigations.

Beyond occurrence and prevalence, molecular characterization of Schistosoma species is crucial for understanding transmission dynamics, drug resistance, and zoonotic potential. Traditional diagnostic methods such as Kato-Katz or urine filtration are often limited in sensitivity, especially in low-endemic settings (Doenhoff et al., 2004). Molecular tools such as polymerase chain reaction (PCR), loop-mediated isothermal amplification (LAMP), and DNA barcoding allow for precise identification of species, strains, and even hybrid forms (Schols et al., 2019). This information is indispensable for designing targeted interventions and tracking transmission sources.

Characterization is particularly important considering emerging reports of hybrid Schistosoma species in West Africa, which may exhibit altered host specificity or treatment response (Webster et al., 2013). In Nigeria, studies have begun to detect such hybrids, but data remain limited, particularly in ecologically diverse zones like Rivers State. Moreover, understanding parasite genetics from both human and animal hosts is essential for evaluating zoonotic spillover risks and for implementing a One Health approach to disease control.

Despite growing awareness of the multi-host nature of schistosomiasis, most surveillance systems remain human-centered, ignoring animal and environmental reservoirs. This narrow perspective limits the effectiveness of interventions, especially in rural agricultural settings where human-animal interactions are common. There is a significant knowledge gap in understanding how livestock and contaminated soil contribute to persistent transmission, especially in endemic zones like Rivers State.

Furthermore, there is a paucity of molecular epidemiological data on Schistosoma species circulating in Rivers State. Without accurate species identification and genetic characterization, control programs risk misdiagnosis, underestimation of infection burden, and inefficiencies in mass drug administration. The inclusion of livestock and environmental samples alongside human data allows for a holistic understanding of transmission dynamics and could reveal new routes of exposure or persistence.

## 2. Materials and Methods

The study was conducted in Rivers State, Nigeria. Rivers State is in the Southern region of Nigeria and the eastern part of the Niger Delta on the ocean extension of the Benue Trough (Jones, 2000). Rivers State, as presently constituted, lies between latitude 4°45′N and longitude 6°50′E. Surrounding states are Imo to the north, Akwa Ibom to the east, and Bayelsa and Delta to the west. On the south, it is bounded by the Atlantic Ocean. Its topography ranges from flat plains to a network of rivers (Baridorn, 2005). The state comprises an area of about 11,077 km2 (4,277 sq mi), making it the 6th largest state in Nigeria. The population by the provisional census figure of 2006 was about 5,198,716 inhabitants, with 51.9 percent of the population being males and 48.1 percent being females, about 5.58 percent of Nigeria's population. The largest towns are Port Harcourt, the State capital, with a population in 2006 estimated at 440,399, Obio/Akpo, Khana, and Ogba-Egbema-Ndoni with population estimates of 263,017, 207,095, and 190,751,

respectively. For administrative purposes, the state is divided into 23 local Government Areas, namely: Abua/Odual, Ahoada East, Ahoada West, Akuku Toru, Andoni, Asari Toru, Bonny, Degema, Eleme, Emohua, Etche, Gokana, Ikwerre, Oyigbo, Khana, Obio/Akpor, Ogba East /Edoni, Ogu/Bolo, Okrika, Omumma, Opobo/Nkoro, Oyigbo, Port Harcourt, and Tai.

This study adopted a cross-sectional descriptive epidemiological design within a One Health framework to investigate the prevalence and molecular characterization of the Schistosoma parasite in humans, livestock, and soil in Rivers State, Nigeria. The design enabled simultaneous data collection from multiple sources and allowed for comparative analysis of infection patterns and risk factors across the human-animal-environment interface.

The human study population consists of approximately 7.5 million people. This estimate was based on the 2023 population projections from the National Population Commission (NPC) of Nigeria (NPC, 2023; UNDP, 2022). These individuals are exposed to the risk of schistosomiasis and fall within the age range of 18-60 years. They are mostly farmers, fishermen, traders, students, and others. The inclusion criteria for participants are provision of informed consent, residency in the study area, and willingness to provide blood samples. Exclusion criteria include severe illness, pregnancy, and decline to participate. This sample size was calculated using the formula provided by Rutherford et al. (2015). The formula is employed because of its significance in modeling disease dynamics, transmission, and control, modeling the interactions between host populations (human, animal) and the intermediate hosts (environment), and analyzing genetic diversity or molecular markers in parasites.

$$n = Z^2p\ (1\text{-}p)/d^2$$

where n is the sample size, Z $(1.96)^2$ is the standard deviation at a 95 % confidence interval (CI), p is the estimated prevalence (15 %), and d is the allowed relative error $(0.05)^2$

$$n = \frac{(1.96)^2 \times 0.15 \times (1\text{-}0.15)}{(0.05)^2} = \frac{3.8416 \times 0.15 \times 0.85}{0.0025} = \frac{0.489804}{0.0025}$$

n =195.9216

The minimum sample size after calculation is 196.

Note: However, to increase the precision of the study, the sample size increased by 30%, that is, 30/100 x 196 = 255.

To be included in the study, Livestock had to reside within the designated area and have access to grazing fields and water sources. Livestock that did not meet these residency requirements or were inaccessible for sampling were excluded from the analysis (Stothard & Webster, 2010). The required sample size was determined by considering the previous prevalence of schistosomiasis (13.70%) by Chanie et al. (2012) in Rivers State.

$$n = \frac{Z^2 \times P\ exp\ (1-P\ exp)}{d^2}$$

where n = the required sample size, Z = critical value of the normal distribution at the required confidence level (1.96), Pexp = expected prevalence (13.7%), and d = desired absolute precision (0.05).

$$n = \frac{(1.96)^2 \times 0.137(1-0.137)}{(0.05)^2} = 181$$

Therefore, the sample size was determined to be 181 Livestock, based on the previous prevalence. Systematically, ninety (90) soil samples were collected from thirty (30) geographical locations in the areas of study in Eleme, Ahoada, and Ikwerre in Rivers State, Nigeria. Three (3) different soil samples were collected from each location to make them representative and to capture intra-location diversity. These locations were chosen specifically to depict peri-urban and residential areas where animal and human contact with the environment is high and likely to influence parasitic and microbial soil populations.

Sampling was done at the topsoil level (0–15 cm depth), where there is the greatest biological activity and the greatest risk of helminth egg presence from defecation and water run-off activity. Each soil sample was clearly labeled with GPS coordinates and collection date for traceability and spatial analysis. Of the total soil samples picked, just the samples that were positive for Schistosoma spp. were further analyzed for the determination of physiochemical parameters and bacterial load. Physiochemical factors determined were pH, moisture content, temperature, organic matter content, and electrical conductivity because these parameters exert a great influence on the survival of parasitic eggs and the development of soil microbial populations. Bacterial load was ascertained using standard plate count methods on nutrient agar and reported in colony-forming units per gram (CFU/g) to enable the calculation of microbial density in the Schistosoma-positive soils.

## 3. Results and Discussion

## Socio-Demographic Characteristics of Respondents

Table 3.1 presents the total number of 255 participants involved in the research. The age distribution indicated that the majority fell in the 20–29 age group, 104(40.8%), followed by the 30–39 age group, 92(36.1%). The 40–49 age group was 49(19.2%), and the 50–59-year-old age group was 9(3.5%). The 60+ age group had a mere 1(0.4%) of the participants.

In terms of gender, the male respondents were predominant, 146(57.3%), compared to the female respondents, 109(42.7%). When considering education level, 92(37.1%) of the respondents had tertiary education, 70(27.5%) with secondary education, 35(13.4%) with primary education, and 58(22.8%) had no formal education.

Occupationally, the most dominant occupational group was civil servants 71(27.8%), followed by farmers 56(23.0%), business owners 50(19.6%), self-employed individuals 49(19.2%), and students 29(11.4%).

Monthly income distribution showed that 85(33.3%) had ₦60,000 - ₦99,999, 78(30.6%) had ₦20,000 - ₦59,999, and 60(23.5%) had less than ₦20,000. Fewer percentages had ₦100,000 - ₦139,999, 27(10.6%), with just 5(2.0%) having ₦140,000 and above.

Finally, geographic distribution showed respondents were almost evenly spread across the three sites: Ahoada 89(34.9%), Eleme 85(33.3%), and Ikwerre 81(31.8%).

**Table 3.1: Respondents by socio-demographic characteristics**

| Variables | Frequency (n= 255) | Percentage (%) | |
|---|---|---|---|
| **Age Group** | | | |
| 20-29 | 104 | 40.8 | |
| 30-39 | 92 | 36.1 | |
| 40-49 | 49 | 19.2 | |
| 50-59 | 9 | 3.5 | |
| 60 and above | 1 | 0.4 | |
| **Total** | **255** | **100** | |
| **Gender** | | | |
| Male | 146 | 57.3 | |
| Female | 109 | 42.7 | |
| **Total** | **255** | **100** | |
| **Education status** | | | |
| Tertiary | 92 | 37.1 | |
| Secondary | 70 | 27.5 | |
| Primary | 35 | 13.4 | |
| No formal Education | 58 | 22.8 | |
| **Total** | **255** | **100** | |
| **Occupation** | | | |
| Civil servant | 71 | 27.8 | |
| Business | 50 | 19.6 | |
| Self-employed | 49 | 19.2 | |
| Farmer | 56 | 23.0 | |
| Student | 29 | 11.4 | |
| **Total** | **255** | **100** | |
| **Monthly earnings (Naira)** | | | |
| Below 20,000 | 60 | 23.5 | |
| 20,000 - 59,999 | 78 | 30.6 | |
| 60,000 - 99,999 | 85 | 33.3 | |
| 100,000 - 139,999 | 27 | 10.6 | |
| 140,000 and above | 5 | 2.0 | |
| **Total** | **255** | **100** | |
| **Location** | | | |
| Ahoada | 89 | 34.9 | |
| Eleme | 85 | 33.3 | |
| Ikwerre | 81 | 31.8 | |
| **Total** | **255** | **100** | |

## The characteristics of the Livestock sample

Table 3.2 shows the characteristics of the Livestock sample (n = 181), which indicates that the majority, 82 (45.3%), were aged between 5 and 6 years, while the age groups 3–4 years and 7 years and above each accounted for 48 (26.5%). Only 3(1.7%) were in the 0–2 years age group. Males constituted a slim majority of 101(55.8%), compared to females at 80(44.2%). In terms of breed distribution, Braford 42(23.2%) was the most common, while Brangus and Belgian Blue 36(19.9% each), Hereford Livestock 35(19.3%), and Holstein Friesian 32(17.7%) were of relatively lower prevalence. Colour prevalence was nearly equal, with red 46(25.4%), black 45(24.9%), brown 45(24.9%), and spotted 45(24.9%) Livestock being nearly equally present. The Livestock were also relatively evenly distributed by locations: Ahoada 61(33.7%), Eleme 60(33.2%), and Ikwerre 60(33.2%).

**Table 3.2: Characteristics of the Livestock**

| **Variables** | Frequency (n= 181) | Percentage (%) |
|---|---|---|
| **Age Group (years)** | | |
| 0-2 | 3 | 1.7 |
| 3-4 | 48 | 26.5 |
| 5-6 | 82 | 45.3 |
| 7 and above | 48 | 26.5 |
| **Total** | **181** | **100** |
| **Sex** | | |
| Male | 101 | 55.8 |
| Female | 80 | 44.2 |
| **Total** | **181** | **100** |
| **Breed** | | |
| Braford | 42 | 23.2 |
| Brangus | 36 | 19.9 |
| Belgian Blue | 36 | 19.9 |
| Hereford Livestock | 35 | 19.3 |
| Holstein Friesian | 32 | 17.7 |
| **Total** | **181** | **100** |
| **Colour** | | |
| Red | 46 | 25.4 |
| Black | 45 | 24.9 |
| Brown | 45 | 24.9 |
| Spotted | 45 | 24.9 |
| **Total** | **181** | **100** |
| **Location** | | |
| Ahoada | 61 | 33.7 |
| Eleme | 60 | 33.2 |
| Ikwerre | 60 | 33.2 |
| **Total** | **181** | **100** |

## Prevalence of *Schistosoma* parasites in humans, Livestock, and soil samples in Rivers State

Table 3.3 shows the prevalence of *Schistosoma* parasites in humans, Livestock, and soil samples in Rivers State. Samples from Livestock had the highest *Schistosoma*

species prevalence of 48.1%, followed by samples from humans (20.4%), while samples from soil had the lowest prevalence (20%).

**Table 3.3: Prevalence of *Schistosoma* parasites in humans, Livestock, and soil samples in Rivers State**

| Sample Type | No. Examined | No. Positive (%) | No. Negative (%) |
|---|---|---|---|
| Humans | 255 | 52(20.4) | 203(79.6) |
| Livestock | 181 | 87(48.1) | 94(51.9) |
| Soil Samples | 90 | 18(20.0) | 72(80.0) |

## Characteristics of *Schistosoma* species in humans, Livestock, and soil samples

The microscopic and molecular characteristics of the *Schistosoma* species in human, Livestock, and soil samples revealed the occurrence of 18S rRNA and mitochondrial COX1 gene sequences in all species. The species detected were *S. haematobium, S. mansoni, S. intercalatum, S. japonicum,* and *S. bovis*. The eggs were small, oval, or round and possessed terminal or lateral spines. In size, eggs were distinguishable from species and sample origin at 100 to 180 µm long, 40 to 70 µm wide, while the adults ranged between 10 to 20 mm in length, reflecting the large variability of the various morphological characters of the different species and their origin (Table 4).

**Table 3.4: Characteristics of *Schistosoma* species**

| Schistosoma species | Sample source | Molecular characteristics | Microscopic characteristics |
|---|---|---|---|
| *S. haematobium* | Human, Soil | 18S rRNA gene sequence, mitochondrial COX1 gene sequence | Eggs are large, oval, with the terminal spine (110–170 µm long, 40–70 µm wide); adult worms are 10–15 mm long. |
| *S. mansoni* | Human | 18S rRNA gene sequence, mitochondrial COX1 gene sequence | Eggs are small, oval, with the lateral spine (114–180 µm long, 45–68 µm wide); adult worms are present. |
| *S. intercalatum* | Human | 18S rRNA gene sequence, mitochondrial COX1 gene sequence | Eggs are small, round or oval with a lateral spine (114–180 µm long, 45–68 µm wide); adult worms are present. |
| *S. japonicum* | Livestock | 18S rRNA gene sequence, mitochondrial COX1 gene sequence | Eggs are large, oval with a terminal spine (60–100 µm long, 40–60 µm wide); adult worms are 12–20 mm long. |
| *S. bovis* | Livestock, Soil | 18S rRNA gene sequence, mitochondrial COX1 gene sequence | Eggs are large, oval, with a lateral spine (110–160 µm long, 40–60 µm wide); adult worms are 10–15 mm long. |

## Prevalence of *Schistosoma* species in human blood samples in Rivers State

Table 3.5 shows the prevalence of *Schistosoma* parasites in human blood samples in Rivers State. Out of 255 blood samples collected from humans, a total of four (4) *Schistosoma* species belonging to *S. haematobium, S. mansoni, S. japonicum,* and *S. intercalatum* were detected in the samples. The prevalence of the *Schistosoma* parasites was *Schistosoma haematobium* had 31(12.2%), *S. mansoni* had 12(4.7%), *S. japonicum* had 8(3.1%) and *S. intercalatum* had 1(0.4%). From the results, *S. haematobium* had the highest prevalence, 31(12.2%), followed by *S. mansoni,* 12(4.7%), while *S. intercalatum,* 1(0.4%), had the least prevalence.

**Table 3.5: Prevalence of *Schistosoma* species in human blood samples in Rivers State**

| ***Schistosoma* species** | **Positive n=255** | **Negative** |
|---|---|---|
| *S. haematobium* | 31(12.2%) | 224 (87.8) |
| *S. mansoni* | 12(4.7%) | 243 (95.3) |
| *S. japonicum* | 8(3.1%) | 247 (96.9) |
| *S. intercalatum* | 1(0.4%) | 254 (99.6) |

| | |
|---|---|
| Total | 52(20.4%) |

## Prevalence of *Schistosoma* species in Livestock samples in Rivers State

Table 3.6 shows the prevalence of *Schistosoma* parasites in Livestock samples in Rivers State. Out of 181 blood samples collected from Livestock, a total of two (2) *Schistosoma* species, belonging to *S. japonicum* and *S. bovis*, were detected in the samples. The prevalence of the *Schistosoma* parasites was *S. japonicum* had 24(13.2%), and *S. bovis* had 63(34.8%). From the results, *S. bovis* had the highest prevalence, 63(34.8%), while *S. japonicum* 24(13.2%) had the least prevalence.

**Table 3.6: Prevalence of *Schistosoma* species in Livestock samples in Rivers State**

| ***Schistosoma* species** | **Positive** | **Negative** |
|---|---|---|
| **n = 181** | | |
| *S. bovis* | 63 (34.8%) | 118 |
| *S. japonicum* | 24 (13.3%) | 157 |
| **Total** | **87** | |

## Prevalence of *Schistosoma* species in soil samples in Rivers State

Table 3.7 shows the prevalence of *Schistosoma* species in soil samples in Rivers State. Out of 90 soil samples collected from the environment, a total of two (2) *Schistosoma* species, belonging to *S. haematobium* and *S. bovis*, were detected in the samples. The prevalence of the *Schistosoma* parasites was *S. haematobium* had 2(2.2%), and *S. bovis* had 16(17.8%). From the results, *S. bovis* had the highest prevalence, 16(17.8%), while *S. haematobium* 2(2.2%) had the least prevalence.

**Table 3.7: Prevalence of *Schistosoma* species in soil samples in Rivers State**

| ***Schistosoma* species** | **Positive** | **Negative** |
|---|---|---|
| **n = 90** | | |
| *S. bovis* | 16 (17.8%) | 74 |
| *S. haematobium* | 2 (2.2%) | 88 |
| **Total** | **18** | |

## Correlation between the *Schistosoma* parasites in humans, Livestock, and the soil samples in Rivers State

Table 3.8 shows the correlation between the *Schistosoma* parasites in humans, Livestock, and the soil samples in Rivers State. The correlation between *Schistosoma japonicum* in humans and Livestock is significant at ($p = 0.012$), while the correlation between *Schistosoma haematobium* in humans and soil is not significant ($p = 0.234$). The correlation between *Schistosoma bovis* in Livestock and soil is significant ($p = 0.001$).

These correlations suggest zoonotic transmission of *S. japonicum* between humans and Livestock. Also, environmental contamination with *S. bovis* in soil samples could potentially contribute to cow infections. A weak correlation existed between humans and soil (*S. haematobium)*, indicating possible environmental exposure.

**Table 3.8: Correlation between the *Schistosoma* parasites in humans, Livestock, and the soil samples in Rivers State**

| **Samples/*Schistosoma* species** | **r** | **p-value** | **df** |
|---|---|---|---|
| **Human-Cattle correlation** | | | |
| *Schistosoma japonicum* | 0.45 | 0.012 | 434 |
| **Human-Soil correlation** | | | |
| *Schistosoma haematobium* | 0.23 | 0.234 | 343 |
| **Cattle-Soil correlation** | | | |
| *Schistosoma bovis* | 0.51 | 0.001 | 269 |

## Mean difference between the prevalence of *Schistosoma* parasites and species in humans, Livestock, and soil samples in Rivers State

Table 3.9 shows the mean difference between the prevalence of *Schistosoma* parasites and species in humans, Livestock, and soil samples in Rivers State. For human samples, *S. haematobium* had the highest prevalence, 31(12.16%), while *S. intercalatum* 1(0.39%) had the least prevalence. For cow samples, *S. bovis* had the highest prevalence at 63(34.81%), while *S. japonicum* had the lowest prevalence, 24(13.26%). For soil samples, *S. bovis* had the highest prevalence of 16(17.78%), while *S. haematobium* had the lowest prevalence of 2(2.22%).

**Table 3.9: Mean difference between the prevalence of *Schistosoma* parasites and species in humans, Livestock, and soil samples in Rivers State**

| **Samples/*Schistosoma* species** | **Prevalence** | **Mean Prevalence Rate** |
|---|---|---|
| **Human (n = 255)** | | |
| *S. haematobium* | 31 | 12.16 |
| *S. mansoni* | 12 | 4.71 |
| *S. japonicum* | 8 | 3.14 |
| *S. intercalatum* | 1 | 0.39 |
| **Mean** | | **5.10%** |
| **Cattle samples (n = 181)** | | |
| *S. bovis* | 63 | 34.81 |
| *S. japonicum* | 24 | 13.26 |
| **Mean** | | **24.04%** |
| **Soil samples (n = 90)** | | |
| *S. haematobium* | 2 | 2.22 |
| *S. bovis* | 16 | 17.78 |
| **Mean** | | **10.00%** |

## Mean difference of *Schistosoma* parasites and species in humans, Livestock, and soil samples in Rivers State

Table 3.10 showed the mean difference between the prevalence of *Schistosoma* parasites and species in humans, Livestock, and soil samples in Rivers State. The mean difference analysis showed that humans had a significantly lower mean prevalence rate compared to Livestock (-18.94%). Also, humans had significantly lower mean prevalence compared to soil samples (-4.90%). Livestock had a significantly higher mean prevalence rate compared to soil samples (14.04%).

**Table 3.10: Mean difference between the prevalence of *Schistosoma* parasites and species in humans, Livestock, and soil samples in Rivers State**

| **Samples/*Schistosoma* species** | **Prevalence** | **Mean Prevalence Rate** |
|---|---|---|
| **Human-Cattle Comparison** | | |
| Humans mean prevalence % | Cattle mean prevalence % | Mean difference % |
| 5.10 | 24.04 | -18.94 |
| **Human-Soil Comparison** | | |
| Humans mean prevalence % | Soil mean prevalence % | Mean difference % |
| 5.10 | 10.00 | -4.90 |
| **Cattle-Soil Comparison** | | |
| Cattle mean prevalence % | Soil mean prevalence % | Mean difference % |
| 24.04 | 10.00 | 14.04 |

## 4. DISCUSSION

### Prevalence of Schistosoma Species in Human Blood Samples

This One Health molecular epidemiological study of 255 human blood samples from Rivers State, Nigeria, confirmed an infection rate of 20.4% by Schistosoma. Four species were identified by molecular diagnosis: S. haematobium (12.2%), S. mansoni (4.7%), S. japonicum (3.1%), and S. intercalatum (0.4%). The predominance of S. haematobium follows established long-term epidemiological patterns in sub-Saharan Africa, where urinary schistosomiasis is the most common manifestation owing to the presence of ample appropriate habitats for Bulinus snail hosts and generalised water contact activities (Gryseels et al., 2006; Colley et al., 2014).

The present prevalence is far greater than the 7.1% reported by Onyekwere et al. (2022) in school pupils from Nigeria, implying increased local transmission patterns in Rivers State. The greater prevalence in this study may be a result of specific ecological determinants such as the location of their homes near infected water bodies, frequency of contact between humans and water, and lack of proper sanitation facilities. Risk exposure is also greater through behavioral habits such as bathing, fishing, and agriculture, tended barefoot or with uncovered skin, primarily in riverine populations (Akinwale et al., 2011; Kabuyaya et al., 2018).

Yet, other endemic research presents even higher prevalence. For instance, Makia et al. (2023) gave a combined prevalence of 63.8% for urogenital schistosomiasis and 50.7% for female genital schistosomiasis in Cameroon. Gruninger et al. (2023) also gave combined percentages of 61.3% for S. haematobium and 59.5% for S. mansoni among adults in Madagascar. Such high percentages are likely to be due to a combination of high transmission, chronic reinfection, and poor access to mass drug administration (MDA) programs. These findings underscore regional disparities in schistosomiasis epidemiology driven by differences in ecology, healthcare access, and control measures (Tchuem-Tchuenté, 2012; Mutapi et al., 2017).

By way of contrast, Bassa et al. (2022) in Côte d'Ivoire noted much lower levels of prevalence—1.0% for S. haematobium and 23.2% for S. mansoni. These differences could be due not only to regional differences but also to differences in methodology. Most of the previous works used conventional microscopy for detection, which, even though specific, is not sensitive enough to pick up low-level infections or latent infections. The current study used PCR-based detection techniques, which can detect Schistosoma DNA in all the stages of parasites, including latent infections (Corcoran & da Silva, 2014; Ezeh et al., 2019). The improved sensitivity of molecular techniques probably explains the increased rate of detection in this study.

Furthermore, S. japonicum and S. intercalatum, though less prevalent in African environments, were also detected, suggesting possible new transmission or zoonotic spillover. S. japonicum, endemic to Asia for a long time, has recently been reported more often in African Livestock and individuals, suggesting possible introduction through animal migration or hybridization events (Leger et al., 2020). The presence of S. intercalatum, rarely reported, may suggest underappreciated local diversity in transmission cycles.

The transmission mechanisms elucidate the results further. Based on Engdaw et al. (2015), the lifecycle of Schistosoma begins once eggs excreted in urine or feces develop into miracidia, which are infective and invade freshwater snails. Parasites in snails increase and develop into cercariae, infecting human skin as soon as it meets contaminated water. In Rivers State and other places where sanitation facilities are inadequate and natural water bodies are an integral part of daily life, the cycle goes on (Ntajal et al., 2021; Assoum et al., 2017).

Social determinants also intervene. Bassa et al. (2022) evidenced that early age, poor personal hygiene, and low socioeconomic status were the main risk factors involved in mono and co-infection of S. mansoni. These risk factors likely possess similar validity in Rivers State communities, most especially in rural and poor communities, where there is limited access to healthcare facilities as well as to clean water.

As highlighted, gender and age disparities also influence prevalence. Different studies, like Gruninger et al. (2023), reported increased infection among men and adults due to heightened exposure during farm or fishing labor. While this study did not report disaggregated prevalence by sex or age, future studies could explore these predictors in the context of regional socio-cultural practices.

In general, the 20.4% human prevalence rate of schistosomiasis in Rivers State indicates the persistence of the schistosomiasis burden in Nigeria despite control efforts. It supports the need for context-adapted interventions like mass chemotherapy, clean water access, snail control, and health education. The inclusion of molecular diagnostic techniques provides a truer estimation of endemicity, thereby supporting the case for enhanced surveillance and control strategies under the One Health framework (Colley & Secor, 2007; Leger et al., 2020).

### Prevalence of Schistosoma species found in livestock samples in Rivers State

This study revealed a high burden of schistosomiasis in Livestock in Rivers State, Nigeria, where molecular analysis identified two species of Schistosoma present: S. bovis (34.8%) and S. japonicum (13.2%). The high level of infection in bovines not only forms a serious veterinary health problem but also forms a potential zoonotic reservoir that may make control by humans difficult, particularly in the One Health context of prioritizing interlinked health among humans, animals, and the environment.

Identification of S. bovis as a prevailing species is consistent

with earlier research in West Africa. Evack et al. (2024) indicated isolation of S. bovis from slaughter Livestock at six locations in Côte d'Ivoire, confirming its wide geographical distribution and adaptation to varied ecological zones. This was further supported by Kouadio et al. (2020), whose research showed a wide range of Livestock schistosomiasis prevalence to be between 5.9% and 53.3% across various departments of Côte d'Ivoire. This range of prevalences has been linked to diverse combinations of environmental, climatic, and man-made factors, including proximity to infested water bodies, grazing systems, and livestock farming systems.

In Rivers State, Livestock are raised in riverine and semi-urban settings where grazing pastures overlap with human settlements and freshwater bodies. Such settings enhance cercariae—the infective larval stage of Schistosoma exposure from infected snails, which may attach to vegetation or penetrate grazing animals' skin (Chanie et al., 2012; Tsegaye, 2022). These larvae are consumed by Livestock when ingesting infected grass or through ingestion of infested water, thus completing the transmission cycle. The epidemiological importance is significant as infected Livestock continuously shed eggs into the environment, which leads to ongoing and widespread infection.

More dangerous is the discovery of S. japonicum, previously considered an Asian species but increasingly reported among African livestock populations. This leaves the door open for either cross-continental introduction or cryptic species complexes that have been underdiagnosed. The zoonotic potential of S. japonicum is well documented, particularly in its ability to infect a wide range of definitive hosts, including humans, thereby providing opportunities for hybridization and genetic recombination (Leger et al., 2016). Hybrid Schistosoma isolates have also been discovered with greater host ranges and enhanced transmission dynamics, representing a severe risk to existing diagnosis and control (Boissier et al., 2016).

The increasingly emerging hybrid development of S. bovis with S. haematobium has already been documented across parts of West Africa, and more so, increasing the complexity of schistosomiasis epidemiology (Kincaid-Smith et al., 2019). These hybrid species obscure host specificity traditionally used to separate human and animal Schistosoma species, generating complex transmission cycles that transcend ecological and species boundaries. In a One Health context, this represents a threat not just to livestock productivity but also to human health, particularly in Livestock-reliant communities for food, income, and farm labor.

Environmental conditions are at the core of maintaining these transmission dynamics. Livestock grazing near stagnant or slow-moving water bodies, particularly during the wet season, is at higher risk of exposure. Moreover, the insanitary conditions under which most livestock are reared—usually with open defecation and lack of veterinary control—provide fertile ground for the multiplication of parasites. Boelee and Madsen (2006) noted that the development of water resources and irrigation, which is beneficial to agriculture, inadvertently develops the optimal habitats of the intermediate snail hosts and therefore enhances the transmission of schistosomiasis.

Movement of Livestock across country and state borders exacerbates the problem by introducing infected animals into new areas and further spreading new strains. Leger et al. (2020) emphasized that movement of livestock, especially where transhumance and seasonal migration occur, can disperse hybrid strains of Schistosoma over large distances. Unchecked veterinary surveillance, these animals can seed infections in new herds in previously uninfected areas, rendering eradication more difficult and undermining public health gains.

Socioeconomic variables also affect the prevalence of bovine schistosomiasis. In rural, low-resource communities where veterinary infrastructure is lacking and animal health services are not well utilized, the infections might remain undiagnosed and uncured, resulting in chronic illness and loss of productivity. Ameni et al. (2001) and Mengistu et al. (2012) demonstrated that anemia, weight loss, decrease in milk production, and reduction in fertility occur in infected Livestock, all contributing to the economic burden to pastoralists and small-scale farmers. Secondly, Livestock infections are not accorded high priority in national disease control programmes, though they have epidemiological significance.

Livestock are not only reservoirs but also multipliers of environmental contamination. Because animals defecate and urinate near water bodies used by humans, the likelihood of human infection is high, particularly among individuals who bathe, fish, or farm with these waters. This link between livestock and human exposure demonstrates the overarching importance of the One Health approach in addressing schistosomiasis. Interventions against the human population are unlikely to be successful unless the animal and environmental components of the transmission cycle are addressed simultaneously.

To minimize these risks, integrated control measures are required. These include routine veterinary screening, anthelmintic treatment of Livestock, improved water management practices, and public health education among pastoral communities. Environmental manipulation or biological control of snails may also be effective, though these activities require long-term commitment and intersectoral cooperation. Integration of livestock schistosomiasis into national neglected tropical disease (NTD) strategies would be a key step towards more integrated and sustainable disease control.

Molecular surveillance must be extended to monitor the evolution and transmission of hybrid Schistosoma species. This would facilitate early identification and control, especially in areas where ecological modification due to urbanization, climate change, or infrastructural activity is taking place. Further financing for research and policy support is also critical to amplify diagnostic capacity and epidemiological modeling so that interventions can be targeted more specifically.

The widespread prevalence of S. bovis and S. japonicum in Rivers State Livestock underscores the pivotal role of bovines in the schistosomiasis ecology. Their contribution to environmental perpetuation of contamination and their role in

mediating zoonotic transmission elevate them from being incidental hosts to being pivotal players in epidemiology. Control of schistosomiasis, therefore, calls for a concerted One Health response that transcends the focus on the human to include the whole spectrum of host-parasite-environment interactions.

## Prevalence of Schistosoma parasites found in soil samples in Rivers State

Two (2) Schistosoma species, belonging to S. haematobium and S. bovis, were detected from the samples, with prevalence (2.2% and 17.8%), respectively. S. bovis had the highest prevalence, 16(17.8%), while S. haematobium 2(2.2%) had the least prevalence. Amoah et al. (2017) reported that soil is an important transmission route for zoonotic parasites such as helminths or protozoa whose infective eggs, oocysts, or larvae are spread in the environment with the faeces of foxes, dogs, and cats. Soil types, moisture, and local conditions influence the distribution of these zoonotic agents (Collender et al., 2015; Umhang et al., 2017; Thevenet et al., 2020).

Previous researchers have reported the presence of parasites in soil samples in and around Hyderabad, Telangana State, India. Anusha et al. (2022) reported the detection of Ancylostoma, Strongyloides, Trichuris, Ascaris, Eimeria, Entamoeba, Taeniidae, and Balantidium species from the soil samples. Highest prevalence was recorded in playgrounds, 49.05%, followed by residential areas, veterinary dispensaries, and public parks with 39.43%, 36.73%, and 28.07%, respectively. Prevalence of soil-borne parasites indicated a significantly ($P \leq 0.01$) highest prevalence in the Rainy season, 47.19%, then in summer, 36.98%, and winter, 27.96% seasons.

Similarly, Ziliotto et al. (2024) reported the presence of soil-transmitted parasites and non-pathogenic nematodes in different regions of Porto Alegre City, Brazil. A total of 80 samples were collected in winter and 80 in summer (ten samples from each sampling site per season), totaling 160 soil samples. The frequency of microscopic non-pathogenic nematode larvae was significantly higher ($p = 0.048$) in winter (93.75%) than in summer (82.50%). Prevalence of the parasites were hookworm (filariform) larvae (1.25%), hookworm (rhabditiform) larvae (11.25%), Strongyloides (filariform) larvae (0.63%), Strongyloides (rhabditiform) larvae (2.5%), hookworm eggs (10.63%), Ascaris eggs (10.00%), and Trichuris species eggs (1.25%). Hookworm (rhabditiform) larvae were the most frequent parasitic structures (15.00%) in winter, and A. lumbricoides eggs were the most frequent parasitic structures (8.75%) in summer.

## Correlation between the Schistosoma parasites in humans, Livestock, and the soil samples in Rivers State

The correlation between Schistosoma japonicum in humans and Livestock is significant at ($p = 0.012$), while the correlation between Schistosoma haematobium in humans and soil is not significant ($p = 0.234$). The correlation between Schistosoma bovis in Livestock and soil is significant ($p = 0.001$). These correlations suggest zoonotic transmission of S. japonicum between humans and Livestock. Also, environmental contamination with S. bovis in soil samples could potentially contribute to cow infections. A weak correlation existed between humans and soil S. haematobium, indicating possible environmental exposure. The correlation of Schistosoma species in humans and Livestock could be associated with water contact, snail population, geographical and climatic conditions, animal husbandry practices, and breed and age of the Livestock (Kouadio et al., 2020).

Livestock that graze in schistosome-contaminated water sources are more likely to become infected. The presence of snails, which serve as intermediate hosts, increases the risk of Schistosoma infection in Livestock (Tsegaye, 2022). Similarly, Livestock in tropical and subtropical regions where Schistosoma species are more common are likely to become infected. Another factor could be raising Livestock in a poor sanitary environment. Reports have shown that Livestock raised in poor sanitation, inadequate veterinary care, and a lack of control measures are more susceptible to Schistosoma infection. The health status of the Livestock in terms of cow breeds and age could be a contributing factor to Schistosoma infection (Belayneh & Tadesse, 2014). Some species of cow may be more susceptible to Schistosoma infection than others. Also, younger Livestock (calf, heifer, and yearling) could be at a high rate of Schistosoma infection as they lack immunity, increased water contact, weakened skin barrier, and poor hygiene and sanitation (Boris et al., 2020; Tsegaye, 2022).

Bassa et al. (2022) have reported that independent determinants of S. mansoni infection were young age, low socioeconomic status (mono and co-infection), and poor hygiene practices (co-infection) ($P < 0.05$). S. mansoni infection was independently associated with higher pain and symptom scores (mono-infection), poor self-rated health, and low healthcare use (co-infection) ($P < 0.05$). Some factors facilitate Schistosoma infection to occur in humans, which include swimming in contaminated water, warm water temperature, and an adequate snail host population. Presence of Schistosoma cercariae in water sources such as rivers, lakes, or irrigation water could endanger humans who have contact with these water bodies (Ntajal et al., 2021).

Also, mature cercariae are active in the hot afternoon as they thrive well in warm water temperature between 20 – 30 0C. When a human host approach contaminated water bodies at these temperature ranges, the possibility of the cercariae infesting the host is high. The presence of specific snail species (Biomphalaria glabrata, Biomphalaria pfeifferi, Bulinus truncatus, and Bulinus globosus) that serve as intermediate hosts for Schistosoma species facilitates the chances of the water bodies being contaminated with cercariae (Secor, 2014).

## 5. CONCLUSION

This study ascertained the Cross-Species Surveillance of Schistosoma Infections in Humans, Livestock, and Soil in Rivers State, Nigeria, based on One Health Epidemiological approach. Results showed that out of the 255 human blood

samples analyzed, positive Schistosoma species were indicated in 52, giving an overall prevalence of 20.4%. The species of Schistosoma present in human blood samples were Schistosoma species belonging to S. haematobium, S. mansoni, S. japonicum, and S. intercalatum, which were detected from the samples. The prevalence of the Schistosoma parasites was Schistosoma haematobium had 31(12.2%), S. mansoni had 12(4.7%), S. japonicum had 8(3.1%) and S. intercalatum had 1(0.4%).

A total of two (2) Schistosoma species, belonging to S. japonicum and S. bovis, were detected in the blood samples collected from the cow. S. japonicum had a lower prevalence of 24(13.2%), compared to S. bovis, 63(34.8%). Two (2) Schistosoma species, belonging to S. haematobium and S. bovis, were detected from soil samples with prevalence (2.2% and 17.8%), respectively. S. bovis had the highest prevalence, 16(17.8%), while S. haematobium, 2(2.2%), had the least prevalence.

The correlation between Schistosoma japonicum in humans and Livestock is significant at ($p = 0.012$), while the correlation between Schistosoma haematobium in humans and soil is not significant ($p = 0.234$). The correlation between Schistosoma bovis in Livestock and soil is significant ($p = 0.001$). These correlations suggest zoonotic transmission of S. japonicum between humans and Livestock. Also, environmental contamination with S. bovis in soil samples could potentially contribute to cow infections. A weak correlation existed between humans and soil S. haematobium, indicating possible environmental exposure.

The correlation of Schistosoma species in humans and Livestock could be associated with water contact, snail population, geographical and climatic conditions, animal husbandry practices, and breed and age of the Livestock. The sources of Schistosoma species in human blood could be traced to the entrance of the fully matured cercariae to human skin or mucous membrane through activities such as farming barefoot or while swimming in contaminated water.

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