

Variables influencing the distribution of freshwater mollusk intermediate hosts of *Schistosoma mansoni* in the Oicha Health Zone, North Kivu Province, Democratic Republic of the Congo

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ABSTRACT

Introduction

Schistosomiasis caused by *Schistosoma mansoni* remains a major neglected tropical disease in sub-Saharan Africa, where transmission depends on freshwater snail intermediate hosts.

Purpose

This study investigated environmental variables influencing the distribution and diversity of freshwater mollusk hosts in the Oicha Health Zone, Democratic Republic of the Congo.

Methods

A cross-sectional malacological survey was conducted across freshwater habitats. Mollusks were collected from 30 sites, with 21 sites included in statistical analyses due to species presence. Environmental variables were measured in situ. Community patterns were analyzed using non-metric multidimensional scaling (NMDS) with Bray-Curtis dissimilarity, and environmental associations were tested using permutation-based vector fitting (envfit). Multiple linear regression models were applied to assess predictors of species richness and Shannon diversity.

Results

Results showed five mollusk taxa belonging to two families (*Lymnaeidae*, *Planorbidae*). NMDS revealed clear structuring of communities along environmental gradients, particularly water velocity and vegetation cover. Regression analysis indicated that species richness decreased with increasing water velocity and altitude, while vegetation cover had a positive effect. Water chemistry variables influenced Shannon diversity, particularly conductivity and salinity.

Conclusion

These findings highlight hydrological conditions as the primary drivers of freshwater snail distribution and provide ecological insights for schistosomiasis control strategies in the region.

INTRODUCTION

Schistosomiasis (or snail fever) is a disease common among residents such as farmers, fisherfolk, and their families in communities where they are exposed to infected bodies of water, including irrigation systems, rice paddies, and swamps. It is estimated that 200 million people are infected and 500–600 million are at risk of infection (Végyvári et al., 2019).

The disease is caused by worms (blood flukes) of the genus *Schistosoma*, which live in the blood vessels of infected persons, particularly in the hepatic portal system. People acquire infection through exposure to water containing infected freshwater snails (Végyvári et al., 2019).

Cercariae released from snails can penetrate human skin during water contact. Once inside the body, the cercariae lose their tails and become schistosomula (immature parasites), which migrate through the bloodstream to the liver and intestinal blood vessels, where they mature and cause disease (Végyvári et al., 2019).

The pathogenic system of schistosomiasis relies on interactions between the parasite and its hosts: humans as definitive hosts, where sexual reproduction occurs, and mollusks as intermediate hosts, where asexual reproduction takes place in aquatic environments. The two main species infecting humans are *Schistosoma mansoni*, transmitted by snails of the genus *Biomphalaria*, and *Schistosoma haematobium*, transmitted by snails of the genus *Bulinus* (Appleton, 1978; De Vlas et al., 1992).

The geographic distribution of schistosome species depends on the ecology of their snail hosts. Natural streams, ponds, lakes, and artificial water bodies such as dams and irrigation canals are typical transmission sites (Brown, 1994; Charles et al., 2009).

The Democratic Republic of Congo (DRC), with its vast hydrographic network (Congo River, Great Lakes, rivers, and marshes), provides diverse aquatic habitats for mollusks. However, knowledge of ecological factors governing snail distribution remains limited, reducing the effectiveness of control strategies (Clennon et al., 2016). This is also the case in the Oicha region.

The Oicha region contains biodiversity of regional and international importance due to its proximity to Virunga

National Park. However, little attention has been given to mollusk biodiversity. Existing data mainly consist of historical taxonomic descriptions or general studies of Congo Basin mollusks (Graf et al., 2011). Recent studies indicate that many freshwater mollusk species in the region remain undescribed, and further sampling has been recommended (Schultheiß et al., 2017).

In addition, rapid urbanization is occurring in Oicha, while access to safe drinking water remains limited. Populations continue to use rivers, springs, and streams for domestic purposes, leading to permanent contact with aquatic environments harboring intermediate host mollusks, thereby increasing infection risk.

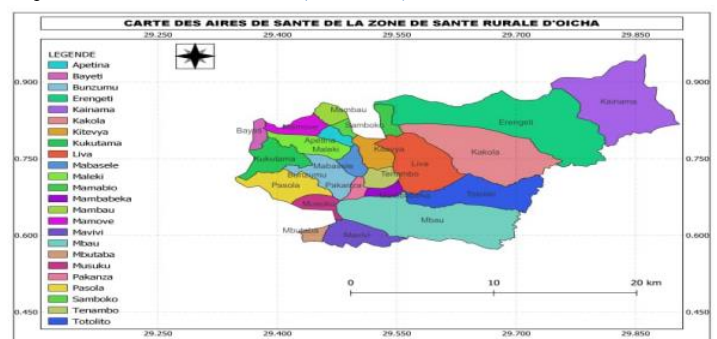
This study was therefore conducted to explore aquatic biotopes in the Oicha rural health zone in order to provide baseline quantitative data on intermediate host mollusk biodiversity and the environmental variables controlling their distribution. Mapping snail distribution may help identify high-risk areas and transmission periods, contributing to public health protection.

METHODS

Study Area

The study was conducted in the rural health zone of Oicha, Beni Territory, North Kivu Province, Democratic Republic of Congo. The area covers approximately 1,656 km², located at 77,696.989 m E and 780,671.652 m N, at an altitude of 1,050.9 m (± 1.5 m). It hosts an estimated population of 341,730 inhabitants distributed across 27 health areas (not health zones).

Figure 1:
Map of the Oicha rural health zone (WHO, 2020)



Data Collection

Because target snail species inhabit specific microhabitats (rocky substrates, detritus, artificial substrates, and low-velocity zones), sampling was conducted mainly by hand collection using gloves. A scoop net (20 cm diameter, 1 mm mesh) and dredge were also used for soft substrates and deeper water zones (Ndeo et al., 2018).

Collected mollusks were preserved in 80% ethanol and stored in the Hydrobiology and Aquaculture Laboratory of the Official University of Ruwenzori.

At each sampling site, water temperature (°C), pH, salinity, and conductivity were measured using a HACH LANGE HQ40d multiparameter device. Additional variables (depth, width, velocity, substrate type) were recorded using a standardized protocol. Geographic coordinates and photographs were taken using a Ricoh VG-4 GPS camera.

Laboratory Work

Mollusks were identified to species level using taxonomic keys from Pilsbry and Bequaert (1927), Mandahl-Barth (1988), Brown (1994), and Daget (1998), covering Congo and Nile Basin mollusk fauna. Individuals per taxon and species richness per site were recorded.

Statistical Analyses

Environmental effects on freshwater mollusk community composition and species richness were analyzed using multivariate ordination and regression approaches. All analyses were conducted in R (R Core Team, 2012).

Community composition analysis (NMDS)

Differences in mollusk community composition among sampling sites were explored using non-metric multidimensional scaling (NMDS). The analysis was performed on a site-by-species matrix constructed from presence/absence data of freshwater mollusk species recorded across 21 sampling sites where at least one mollusk species was detected.

Ecological dissimilarity among sites was calculated using the Bray–Curtis distance index, which is appropriate for community composition data based on binary (presence/absence) information. NMDS was used as an unconstrained ordination method to reduce multidimensional community data into a reduced number

of dimensions while preserving rank-order dissimilarities among sites.

The ordination was run using the *vegan* package in R (Oksanen et al., 2013), and model stability was assessed through multiple random starts to minimize stress values and ensure convergence on a stable solution.

Environmental variables were subsequently fitted onto the NMDS ordination space using the *envfit* function in the *vegan* package. This procedure estimates the strength and direction of correlation between environmental variables and the ordination configuration. Significance of environmental vectors was assessed using permutation tests ($n = 999$ permutations). Only statistically significant variables ($p < 0.05$) were interpreted in relation to community patterns.

It is important to note that NMDS is an exploratory technique and does not test causality; it is used here to visualize patterns of similarity among sampling sites and to identify environmental gradients associated with community structure.

Species richness and diversity modeling

The relationships between environmental variables and mollusk diversity were examined using multiple linear regression models. Two response variables were analyzed separately:

1. Species richness (number of species per site)
2. Shannon diversity index

Environmental predictors included:

- Water velocity (m/s)
- Vegetation cover (categorical/ordinal index)
- Altitude (m)
- pH
- Conductivity ($\mu\text{S}/\text{cm}$)
- Salinity (ppm)

Prior to analysis, all continuous predictors were examined for normality and collinearity. Where necessary, variables were standardized to improve model comparability and interpretability.

Model construction and selection

Initial full models were constructed using the `lm()` function in R. Due to the relatively small sample size ($n = 21$ sites), models were refined using a stepwise selection procedure based on Akaike Information Criterion (AIC) to reduce overfitting and improve model parsimony.

Stepwise selection was applied in both forward and backward directions. Final models retained only statistically supported predictors contributing to explained variance in the response variables.

Model performance was evaluated using:

- Coefficient of determination (R^2)
- Adjusted R^2
- Residual diagnostics to verify homoscedasticity and normality assumptions

Regression coefficients were interpreted as the direction and magnitude of association between environmental variables and mollusk diversity metrics. Statistical significance was assessed at $\alpha = 0.05$.

It is emphasized that regression models in this study describe statistical associations rather than causal relationships.

Dataset consistency statement

All multivariate (NMDS) and regression analyses were conducted on the subset of 21 sampling sites where freshwater mollusk presence was recorded. The remaining surveyed sites ($n = 9$) were excluded from community-level analyses due to absence of detectable mollusk populations.

Statistical robustness and limitations

Given the relatively small number of analytical sampling units ($n = 21$ sites), all statistical inferences were interpreted cautiously to avoid overgeneralization. Multivariate and regression analyses were designed primarily for exploratory and hypothesis-generating purposes rather than strict causal inference.

To reduce the risk of model overfitting, predictor selection in multiple linear regression models was guided by Akaike Information Criterion (AIC)-based stepwise procedures, which prioritize model parsimony by balancing explanatory power and complexity. In addition,

model diagnostics were examined to ensure that assumptions of linear regression, including normality of residuals, homoscedasticity, and absence of influential outliers, were not violated.

Because ecological field data are often subject to spatial heterogeneity, potential spatial autocorrelation among sampling sites cannot be entirely excluded. However, sampling was conducted across geographically separated freshwater habitats to minimize spatial clustering effects. Future studies incorporating explicit spatial modeling approaches and larger sample sizes would help further validate the observed relationships.

Non-metric multidimensional scaling (NMDS) was used strictly as an unconstrained ordination technique to visualize patterns in community composition, and environmental variables were evaluated using permutation-based vector fitting (`envfit`). This approach provides robust, non-parametric assessment of environmental associations without assuming linear relationships in the underlying community data.

Overall, the convergence of NMDS ordination patterns and regression model outputs suggests consistent ecological gradients influencing freshwater mollusk distribution, particularly hydrological structure and vegetation cover. However, these findings should be interpreted as correlative patterns describing ecological associations rather than deterministic causal mechanisms.

Ethical Approval

The study received approval from the Medical Ethics Committee of the University of Goma, Democratic Republic of Congo (Approval No. UNIGOM/CEM/010/2023, March 1, 2023). Authorization for the study was also obtained from local political and administrative authorities within the health zone. Populations living near the sampling sites were informed about the objectives, methods, and intended use of the collected data. Verbal consent was obtained for all interactions with local residents and for observations related to human activities. Mollusk sampling complied with local biodiversity conservation standards. All information obtained from residents was anonymized and used exclusively for scientific research purposes. The study adhered to the ethical principles governing

biomedical and environmental research, including respect for human, animal, and ecological life..

RESULTS

Species composition and distribution

A total of 1,174 freshwater mollusk specimens were collected during field surveys conducted across 30 freshwater sites in the Oicha Health Zone. However,

community composition analyses were restricted to 21 sites where at least one mollusk species was recorded.

These specimens belonged to five taxa identified at species or subspecies level, representing three genera, two families (*Lymnaeidae* and *Planorbidae*), one order (*Basommatophora*—noting that this classification is now considered outdated in modern gastropod taxonomy), and one class (*Gastropoda*) (Table 1).

Table 1:
Distribution of freshwater mollusk species across 21 surveyed sites in the Oicha region (out of 30 sampled sites)

Species	Site 1	Site 2	Site 3	Site 4	Site 5	Site 6	Site 7	Site 8	Site 9	Site 10	Site 11	Site 12	Site 13	Site 14	Site 15	Site 16	Site 17	Site 18	Site 19	Site 20	Site 21
<i>Lymnaea natalensis</i>	+	+	+	+	-	-	-	-	-	-	-	-	-	-	+	+	+	+	-	-	-
<i>Bulinus globosus</i>	+	+	+	+	-	-	-	-	-	-	+	+	+	+	-	-	-	-	-	-	-
<i>Bulinus cf. forskalii</i>	-	-	-	-	+	+	+	+	-	-	-	-	-	-	+	+	+	+	-	-	-
<i>Biomphalaria cf. pfeifferi</i>	+	+	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	+	+	+	+
<i>Biomphalaria sp.</i>	-	-	-	-	-	-	+	+	+	+	-	-	-	-	-	-	-	+	+	+	+

Legend: “+” = presence; “-” = absence **Note.** Thirty freshwater sites were initially surveyed in the Oicha Health Zone; however, only 21 sites yielded detectable snail populations and were included in the species distribution and multivariate analyses. Presence/absence data were used for all ordination and regression analyses.

The family *Planorbidae* exhibited the highest species richness, with four taxa recorded. Among all species, *Biomphalaria cf. pfeifferi* and *Biomphalaria sp.* showed the widest distribution, each occurring in up to nine sampling sites.

Among the recorded taxa, four species are known or suspected intermediate hosts of *Schistosoma* species. Only *Lymnaea natalensis* has not been consistently reported as an intermediate host of *Schistosoma mansoni* (Pitchford, 1977; Christensen et al., 1986; Rollinson & Southgate, 1987), although it has been associated with other trematode parasites in previous studies.

Community composition patterns (NMDS ordination)

Non-metric multidimensional scaling (NMDS) based on Bray–Curtis dissimilarity of presence/absence data revealed structured variation in freshwater mollusk community composition among the 21 analyzed sites.

The ordination showed that sampling sites clustered according to similarities in species composition, indicating non-random spatial structuring of mollusk assemblages across the study area.

Environmental vector fitting (envfit) indicated that:

- **Water velocity** was significantly correlated with the NMDS ordination space and showed the strongest relationship with community composition patterns.
- **Vegetation cover** was also significantly associated with the ordination structure.
- **Altitude** showed a weaker and non-dominant association with community variation.

These results indicate that mollusk assemblages vary along environmental gradients, particularly those related to hydrological conditions and habitat structure. However, NMDS results represent exploratory patterns of similarity and do not imply causality.

Species richness and diversity relationships

Multiple linear regression analyses conducted on the 21-site dataset indicated that environmental variables were associated with variation in species richness and diversity indices.

Species richness model

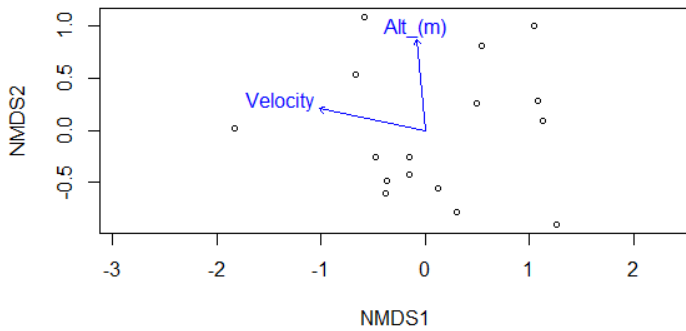
Species richness per site was significantly associated with:

- **Water velocity** (negative association)

- **Vegetation cover** (positive association)
- **Altitude** (weak and marginal association) - **Figure 2**

Figure.1:

Non-metric multidimensional scaling (NMDS) of sampling sites and families (in the same coordinate system) showing the variables that explain most of the variability in assemblage composition. The lengths of the arrows are proportional to the correlation between ordination and the variables



Sites characterized by lower flow velocity tended to support higher numbers of mollusk species, whereas higher flow conditions were associated with reduced richness.

Vegetation cover showed a positive relationship with species richness, indicating that structurally complex habitats tend to support more diverse mollusk assemblages.

Table 2:

Final multiple linear regression models explaining species richness and Shannon diversity in freshwater mollusk assemblages (n = 21 sites)

Model selection based on AIC stepwise procedure (forward-backward)

A. Species Richness Model

Predictor variable	Standardized effect (β direction)	Partial R ²	p-value	Ecological interpretation
Water velocity	Negative	0.126	0.009**	Higher flow reduces habitat suitability
Vegetation cover	Positive	0.062	0.001**	Structural habitat increases richness
Altitude	Negative (weak)	0.046	0.050 ·	Marginal effect on species distribution

Model statistics: R² = 0.188, Adjusted R² = 0.162, AIC-selected model retained 3 predictors

B. Shannon Diversity Index Model

Predictor variable	Standardized effect (β direction)	Partial R ²	p-value	Ecological interpretation
Conductivity	Positive	0.134	0.034*	Moderate solute levels associated with diversity shifts
pH	Positive/neutral	0.176	0.042*	Water chemistry influences community structure
Salinity (ppm)	Negative	0.144	0.043*	Increased salinity reduces diversity

Model statistics: R² = 0.280, Adjusted R² = 0.241, AIC-selected model retained 3 predictors

Table Notes:

1) Values represent results from **multiple linear regression models fitted using lm() in R** 2) Model selection was performed using **stepwise Akaike Information Criterion (AIC)** procedures in both forward and backward directions 3) **Partial R² values represent the individual contribution of each predictor within the final model** 4) Significance levels: **p < 0.01 = strong evidence (·)**, **p < 0.05 = moderate evidence (*)**, **p < 0.1 = marginal (·)****. All analyses were performed on **21 freshwater sites with recorded mollusk presence**

Shannon diversity index model

Shannon diversity was associated with water physicochemical properties, particularly:

- **Conductivity** (positive or variable association depending on site conditions)
- **pH**
- **Salinity (ppm)** (negative association)

These results suggest that water chemistry is related to variation in community diversity, although effects were generally weaker than those observed for hydrological variables.

Model performance and interpretation

Regression models explained a moderate proportion of variance in species richness and diversity indices (as indicated by R² values reported in **Table 2**). Model selection using stepwise AIC procedures retained a subset of environmental predictors that best explained variation in response variables while minimizing model complexity. Residual diagnostics indicated no major violations of normality or homoscedasticity assumptions.

It is important to emphasize that regression results reflect statistical associations between environmental variables and mollusk diversity patterns and do not demonstrate direct causal relationships.

Synthesis of multivariate patterns

Both NMDS ordination and regression analyses converged in identifying water velocity and vegetation

structure as the most consistent environmental correlates of freshwater mollusk community organization in the Oicha Health Zone.

Hydrological conditions appeared to play a dominant role in shaping species distribution patterns, while physicochemical variables contributed more modestly to variation in diversity indices.

Table 3:

Summary of species–environment associations for freshwater mollusks in the Oicha Health Zone (based on NMDS and regression outputs)

Species–environment relationships

Species	Water velocity	Vegetation cover	Altitude	pH	Conductivity	Salinity
<i>Biomphalaria cf. Pfeifferi</i>	↓ strong	↑ strong	↓ weak	↔	↔	↓ moderate
<i>Biomphalaria sp.</i>	↓ strong	↑ strong	↓ weak	↔	↔	↓ moderate
<i>Bulinus globosus</i>	↓ moderate	↑ moderate	↔	↔	↓ weak	↓ weak
<i>Bulinus cf. forskalii</i>	↓ moderate	↑ moderate	↔	↔	↓ weak	↓ weak
<i>Lymnaea natalensis</i>	↔ / weak ↓	↑ weak	↔	↑ weak	↔	↔

Legend: ↑ positive association | ↓ negative association | ↔ weak/no clear association

Species–environment relationships are synthesized from non-metric multidimensional scaling (NMDS) ordination fitted with environmental vectors (envfit) and supported by multiple linear regression models. Arrows indicate the direction of association between species occurrence and environmental gradients across the 21 analyzed sampling sites. Strength of association is based on the consistency of statistical signals across ordination and regression outputs.

DISCUSSION

The present study contributes new information on the distribution of freshwater mollusks in the Oicha region, where no previous records of these species existed. The occurrence of these taxa may reflect either insufficient historical sampling effort or a recent expansion of their geographic distribution. Given the increasing pressures of eutrophication, pollution, and anthropogenic disturbance on aquatic ecosystems (Aninakwah et al., 2025; Hailegebriel et al., 2022; Kyambadde, 2004), further investigations are needed to assess long-term changes in mollusk fauna within the region.

The NMDS analyses indicated that local environmental variables, particularly water velocity, strongly influence mollusk assemblage composition. Similar observations have been reported by Allan (2007) and Wroński et al. (2015), who demonstrated that hydrological characteristics

significantly affect freshwater species diversity. Brown (1994), Jan et al. (2013), and Kebede et al. (2020) further emphasized that both biotic factors, such as aquatic vegetation and food availability, and abiotic factors, including physical and chemical conditions, play essential roles in determining the ecology and distribution of freshwater snails.

The irregular distribution of snail populations observed in this study may be explained by variations in current velocity, wave action, desiccation risk, food availability, vegetation cover, and substrate suitability (Trentanovi et al., 2025; Voichiș et al., 2021). Human populations also tend to establish frequent contact with water bodies because of accessibility, domestic activities, and recreational uses. These interactions increase opportunities for transmission, particularly in areas where intermediate host snails thrive under moderate pollution conditions. Domestic waste materials, including plastic debris, may provide favorable surfaces for feeding, egg laying, and juvenile development.

Previous studies have shown that the destruction of aquatic vegetation can significantly reduce snail populations and consequently decrease the prevalence of trematode infections in grazing animals (Goll & Scott, 1978, 1979; Nyagura et al., 2022; Sun et al., 2020). These findings suggest that ecological management strategies

targeting hydrophytes and riparian vegetation may contribute to interrupting the transmission cycle of schistosomiasis. Furthermore, variations in river flow constitute a major determinant of snail aggregation patterns (Gazzinelli et al., 2012). The negative correlation observed between snail abundance and water velocity in this study is consistent with findings reported by Kariuki et al. (2004) and Woolhouse and Chandiwana (1990b).

Water velocity is recognized as a critical environmental variable influencing stream organisms and benthic community composition because of its effects on substrate structure, oxygen availability, nutrient turnover, and hydrophyte distribution. Species-specific preferences for flow conditions have been documented by several authors (Ahounty et al., 2024). Snails serving as intermediate hosts of *Schistosoma* generally prefer slow-flowing habitats, emphasizing the importance of hydrological conditions in disease transmission dynamics (Gazzinelli et al., 2010; Kloos et al., 2010).

The present study also demonstrated that physicochemical parameters significantly influence mollusk biodiversity. In agreement with Appleton (1978), temperature and current velocity appear to be major determinants of snail distribution and abundance in African freshwater ecosystems. Water chemistry may not necessarily determine species presence or absence under normal freshwater conditions, but it can strongly influence population dynamics (Levitz et al., 2013).

The significant relationships observed between biodiversity indices and pH, conductivity, and salinity further support the importance of water quality in shaping mollusk communities. Low pH conditions can increase the release of toxic heavy metals and impair calcium uptake, reproduction, and shell development in mollusks (McCullough, 1958). Similarly, elevated conductivity and salinity reflect higher concentrations of dissolved substances and may influence mollusk survival and reproduction. Consequently, the management of water physicochemical properties could represent an additional strategy for controlling populations of intermediate host mollusks of *Schistosoma mansoni* (Keiser et al., 2006; Steinmann et al., 2006).

CONCLUSION

This study conducted in the rural health zone of Oicha improves understanding of the distribution and density of intermediate host mollusks of *Schistosoma* and the environmental factors influencing their occurrence. The results demonstrated that mollusk distribution is closely associated with environmental variables such as pH, aquatic vegetation, substrate type, rainfall, and seasonality, all of which are further influenced by human activities.

These findings confirm that mollusk proliferation, and consequently the risk of intestinal schistosomiasis transmission, depends strongly on interactions between aquatic ecosystems and local human practices. Understanding these relationships facilitates the identification of high-risk areas and provides a scientific basis for developing targeted prevention and control strategies.

Ecological management of aquatic habitats, together with community awareness programs promoting safe water use, may represent effective approaches for reducing schistosomiasis transmission. Further comprehensive studies on freshwater mollusks in the Oicha region are recommended to better understand their distribution, population dynamics, habitat threats, and long-term ecological changes.

Study Limitations

- Rainfall and humidity measurements were not obtained from local meteorological stations or nearby weather monitoring systems.
- The study was limited to the Oicha rural health zone; therefore, the findings cannot be generalized to other health zones in North Kivu Province or the Democratic Republic of Congo, where ecological and climatic conditions may differ.
- Data collection was conducted over a 10-month period and may not have captured interannual variability or exceptional climatic events influencing mollusk distribution.
- Logistical and security constraints limited access to certain sampling sites, potentially reducing the representativeness of the sampling design.

Authors' Contribution: Bailanda Mumbere, P. designed the study and conducted field data collection. Wembo Ndeo, O. contributed to the

research methodology and data analyses. Paluku Sabuni, L. supervised the writing process. Muhindo Sahani, W. and Barhwamire Kabesha, T. contributed to manuscript review and editing.

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Ethical Approval: The study received approval from the Medical Ethics Committee of the University of Goma, Democratic Republic of Congo (Approval No. UNIGOM/CEM/010/2023, March 1, 2023).

Conflicts of Interest: None declared.

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