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Environmental Determinants Influencing the Diversity of Snail Intermediate Hosts of Schistosomes in Burkina Faso

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Abstract

The diversity of snail intermediate hosts of schistosomes and infection rates are influenced by environmental determinants. Knowledge of these local environmental determinants is an important basic step in epidemiology for the control of schistosomiasis. In this study, we investigate the local environmental determinants of the diversity of snail intermediate hosts of schistosomes in 24 sites in the Sudano-Sahelian and Sudanian zones of Burkina Faso based on accessibility and epidemiological data. The study was conducted every two months between November 2020 and September 2021. Samples were collected at each sampling point using flexible forceps and an Eckman grab by two surveyors on all available supports for 15 minutes. The collected samples were preserved in 75% ethanol and then transported to the laboratory for identification and enumeration. The BRT-optimised model was used to model species abundance as a function of local variables. A total of 14,587 snails belonging to seven families and 21 species were collected. Five intermediate host species of human schistosomes, namely *Bulinus truncatus*, *Bulinus forskalii*, *Bulinus globosus*, *Bulinus senegalensis* and *Biomphalaria pfeifferi*, were collected with relative abundances ranging from 7% for *B. globosus* to 42% for *B. truncatus*. The occurrence of *B. truncatus* was positively correlated with conductivity, pH, and latitude and negatively correlated with altitude. The occurrence of *B. forskalii* was positively correlated with vegetation, while the occurrence of *Bi. pfeifferi* and *B. senegalensis* was positively correlated with temperature and altitude but negatively correlated with ammonium and total iron. The optimised BRT model explained 43.36%, 77.047%, 73.906%, 48.169%, and 23.23% of the variation in abundance of *B. senegalensis*, *B. truncatus*, *B. globosus*, *B. forskalii*, and *Bi. pfeifferi*, respectively. The nature of the water regime (24.9%) and the vegetation cover (18.6%) were relatively more important in explaining the abundance of *B. globosus*. The most important parameters to explain the abundance of *B. senegalensis*, *B. truncatus*, *B. forskalii*, and *Bi. pfeifferi* were all physicochemical parameters.

Keywords

Snail Intermediate Hosts of Schistosomes, Abiotic Parameters, Diversity, BRT Model, Burkina Faso

1. Introduction

Parasitic diseases transmitted by snails pose serious risks to human and animal health and cause major socio-economic problems in many tropical and subtropical countries [1]. Among these parasitic diseases, schistosomiasis is a severe neglected tropical disease caused by trematodes and transmitted by freshwater snails [2] [3]. More than 200 million people worldwide are infected [4] [5], with 200,000 deaths each year [6] due to hidden pathologies such as renal and liver failure [5]. Although the global burden of schistosomiasis has decreased over the last few decades, it remains a cause for concern in certain regions of Africa [7]. More than 80% of people affected by this disease live in Sub-Saharan Africa [6] [8] [9]. This alarming situation is maintained and aggravated by hydro-agricultural development, the construction of small dams, and the multiplication of irrigation canals [10] [11]. These environmental modifications and poor drainage systems are factors that increase the distribution and density of snail intermediate hosts, while the lack of health education on the choice of water bodies for recreational purposes is a major factor that predisposes people to the risk of infection [12]. Furthermore, water environmental factors can strongly influence host physiological status [13], demography [14], and distribution, and modulate host-parasite encounter patterns, hence transmission dynamics and probability of infection [15]. For example, natural environmental variables such as temperature, salinity, and pH have important effects on species survival rates and developmental stages [16] [17]. In this study, we investigate the effect of physicochemical and climatic parameters on the distribution and density of snail intermediate hosts of human schistosomes in the Volta Basin.

2. Methods

2.1 Study Area

The study was carried out in the central and western parts of the Volta basin (**Figure 1**). These two regions have two alternating seasons, one rainy (3 to 5 months) and the other dry (7 to 9 months) [18], and three climatic zones that can be distinguished on the basis of annual rainfall and temperature regime. The Centre region, located in the Sudano-Sahelian zone, is characterised by an average annual temperature of 29.6˚C. Rainfall is relatively low, ranging from 600 mm to 900 mm. Previous work had indicated the presence of all the potential intermediate host species in this region [19]. Notwithstanding this, the results were encouraging in epidemiological terms [20] [21]. The Hauts-Bassins region is largely located in the Sudanian zone. The extreme north of the region is located in the Sudano-Sahelian zone. The region has an average annual temperature of 27.2˚C. Rainfall ranges from 800 mm to 1200 mm. The relief is made up of plateaux, plains, a few hills, and valleys. The region is home to the two oldest hydro-developments, the Banzon plain and the Kou Valley [22]. Prevalences are still high in this region at 25% according to [21]. According to [23], the Hauts-Bassins region is known to be an endemic area for *Schistosoma mansoni*, which has replaced *S. haematobium*. These observations were consolidated by the work of [24], who found a prevalence of 8.7% out of 480 pupils examined.

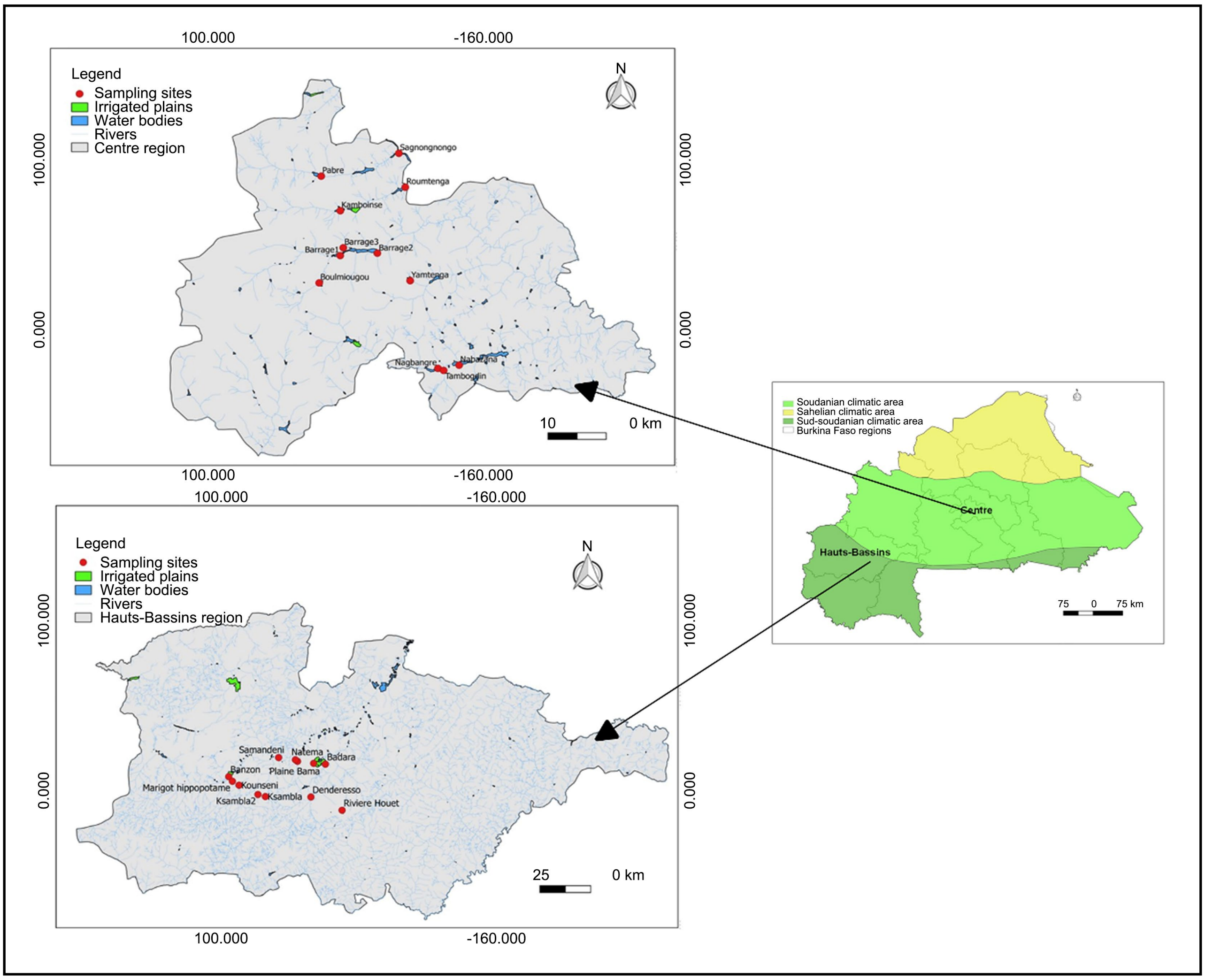

Figure 1. Map of the study area. (The author created the figure with the coordinates of the sampling points using QGIS 3.40.1. The shapefiles for the regions were taken from the 2012 BNDT data from the Burkina Geographic Institute.)

2.2. Measurement of Physicochemical Parameters

Five physicochemical parameters of the water were measured *in situ* using a HI

9829 multi-parameter. These were water temperature, electrical conductivity, salinity, pH, and dissolved oxygen. The nature of the bottom and the vegetation cover were also assessed visually. The habitat type, level of human activity, bottom composition, vegetation cover, and water regime at each measurement point were assessed subjectively based on standardized criteria. Habitat type was classified as follows: 1 for river, 2 for stream, and 3 for irrigated plains. Human activity was categorized by intensity: 1 for low, 2 for moderate, and 3 for high activity levels. The nature of the bottom was assessed using the following scale: 1 for mud, 2 for gravel, 3 for a mixture of gravel and mud, 4 for a mixture of gravel and rocks, and 5 for irrigation canals. Vegetation cover was recorded as 1 for low, 2 for medium, and 3 for high. The water regime was classified as 1 for non-permanent, 2 for intermediate, and 3 for permanent flow conditions.

At each site, water samples were taken as described in [25] and analyzed in the laboratory using an ORION AQUAMATE 8000 spectrophotometer. The parameters measured were nitrate, ammonium, total iron, and alkalinity.

2.3. Snails Collected and Identification

At each sampling point on the site, two surveyors collected snails by direct examination of all the micro-habitats available in the water using flexible forceps for 15 minutes. For finer sediments, snails were collected by dredging with an Eckman grab. The snails collected were placed in plastic pillboxes and labeled by site, microhabitat, and collection period. The snails were taken back to the laboratory for identification and enumeration. Identification was carried out in the laboratory by examining the shell and confirmed using the identification guides of [26] [27], and [28].

2.4. Data Analysis

2.4.1. Effects of Local Environmental Parameters on Snails Distribution

Redundancy analysis (RDA) was used to determine the influence of local environmental variables on the distribution of snail intermediate host using the vegan rda function. Not all environmental variables follow a normal distribution, so a logarithmic transformation log1p() was performed to reduce skewness and improve the power of the statistical tests. As the data were all in different units, we standardized them using vegan's decostand() function. A Hellinger transformation was applied to the snail abundance data to preserve the Euclidean distance between sites, reduce the influence of very abundant species, and preserve information about rare species [29]. A progressive selection of explanatory variables was carried out using the ordiR2step() function in the vegan package in order to identify significant independent variables and obtain a better RDA model. The statistical significance of the overall model was tested using anova.cca().

2.4.2. Individual Contribution of Environmental Variables to Snails Abundance Using the Boosted Regression Trees (BRT) Model

The relationship between local biotic and abiotic parameters and the abundance of schistosome intermediate host snails was assessed using the Boosted Regression Trees or BRT method [30] [31]. BRT models are machine learning algorithms built from the combination of the advantages of two algorithms [30]-[32]: models fitted from decision trees [33] and the bagging algorithm for calculating the global prediction from the combination of decision tree results [34]. BRTs have several advantages because: 1) BRT models can handle large databases with predictors having different characteristics, 2) they adapt to complex non-linear response curves, 3) they efficiently handle data with missing values, 4) they are insensitive to tooling, 5) BRTs also have better predictive performance, and 6) predictor independence is not a requirement as interactions are automatically modelled by the hierarchical structure of the tree [35]. Furthermore, BRTs are robust against the presence of uninformative predictors, as these predictors are discarded when selecting the best split [32]. All these advantages make the BRT model useful for ecologists to explore relationships between predictor variables and species abundance dynamics [35]-[37].

In addition, BRTs are robust against the presence of uninformative predictor variables because these predictors are discarded during the selection of the best split [32]. BRT models were built using the gbm.step() function of the dismo v1.3.3 package [38]. To find the optimal parameters based on the recommended rules for ecological modelling, we regulated the BRT model by jointly optimising the learning rate (lr), which determines the contribution of each tree to the growing model, the tree complexity (tc), which controls the actual level of interaction in the BRT, and the bag fraction (bf) to specify the proportion of data to be selected at each step (stochasticity control) [30]. Cross-validation was used to fit and evaluate the model [30]. It specifies the number of times to randomly divide the data in order to fit and validate the model [39]. A lower value for deviance and standard error for cross-validation [37]. We fitted 20 models based on the combination of these different parameters: tc: 1, 2, 3, 4, 5; lr: 0.01, 0.05, 0.005, 0.001; and bf: 0.5 or 0.75. Among the fitted models, we found that the best model had an lr of 0.001, a tc of 4, and a bf of 0.75, with small cross-validation gaps as well. For each species, the optimal number of trees (nt) was chosen by internal cross-validation to avoid overfitting due to overdispersion. We then fitted all other models using these same optimal parameters. All BRT models were fitted using the Poisson error distribution [39], which is appropriate for count data [40]. The selected variables are those that explain at least 40% of the variability in species abundance [31] [36] [41]. We assessed the fit of the BRT model to the data by calculating the percentage of deviance explained: 1-(residual deviance/total deviance) [42].

3. Results

3.1 Specific Richness

A total of 14,587 freshwater snails belonging to 7 families and 21 species were collected. Of the specimens collected, 8535 specimens were intermediate hosts of human schistosomes (*i.e.*, 58.51% of the snails). These were *B. truncatus*, *B. forskalii*, *B. globosus*, *B. senegalensis* and *Bi. pfeifferi*. *B. truncatus* (3618 specimens) and *B. forskalii* (2123 specimens) were the most abundant species, while *B. globosus* and *B. senegalensis* were the least abundant (**Figure 2**).

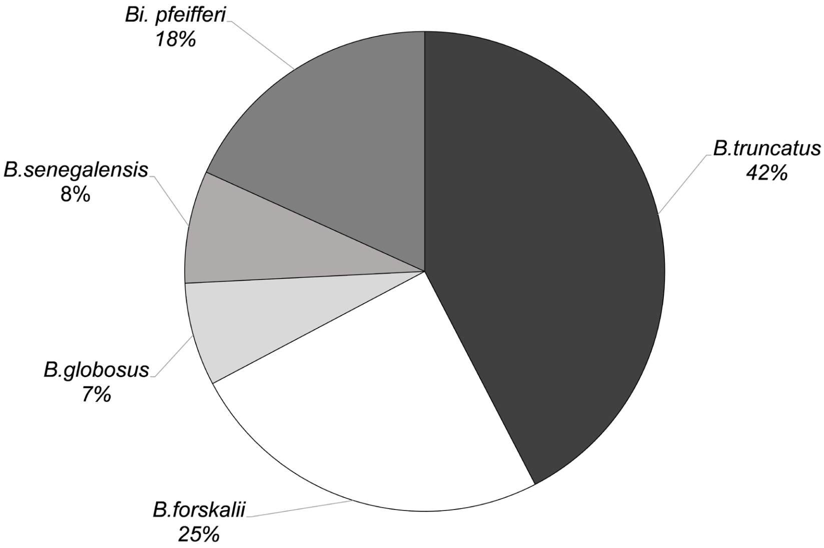

Figure 2. Relative abundance of intermediate host species.

Species such as *B. forskalii*, *B. senegalensis*, and *B. truncatus* are more abundant in reservoirs and irrigated plains but rare in rivers (**Table 1**). The Kruskal-Wallis test shows that the difference in abundance is significant between habitat types (p = 0.00072). For *B. senegalensis*, the difference in abundance was also significant between habitat types (p = 0.019). For *B. forskalii*, the difference was significant between rivers and irrigated plains (p = 0.038), rivers and reservoirs (p = 0.023), and reservoirs and irrigated plains (p = 0.038). Although *Bi. pfeifferi* was more abundant in reservoirs and irrigated plains, the Kruskal-Wallis test showed that the difference in abundance was not significant between habitat types (p = 0.069). As for *B. globosus*, it is more abundant in reservoirs but rare in irrigated plains and rivers (p = 0.0075).

Table 1. Species abundance by habitat type.

Habitats	*B. forskalii*	*B. globosus*	*Bi. pffeiferi*	*B. senegalensis*	*B. truncatus*
Irrigated plaines	1313	03	427	498	342
Reservoirs	745	574	1080	110	3067
Rivers	65	16	47	39	209
p-value	0.0032	0.0075	0.069	0.019	0.00077

3.2. Influence of Environmental Factors on the Distribution of Snails

The RDA results show that environmental variables explain 62.32% of the variation in the presence-absence of snail species. The ANOVA permutation test used to test the overall significance of the RDA shows that the overall model is significant (p = 0.003) and that the first axis is also significant (**Table 2**).

Table 2. Eigenvalues and proportions of values expressed by the RDA axes.

Importance of components	RDA1	RDA2	RDA3	RDA4	RDA5
Eigenvalues	0.1708	0.0814	0.02540	0.01133	0.001343
Explained proportions	0.5884	0.2804	0.08751	0.03904	0.004627
p-value	0.004**	0.317	0.975	1.000	1.000
Cumulative proportions	0.5884	0.8688	0.95634	0.99537	1.000000

** = Very significant.

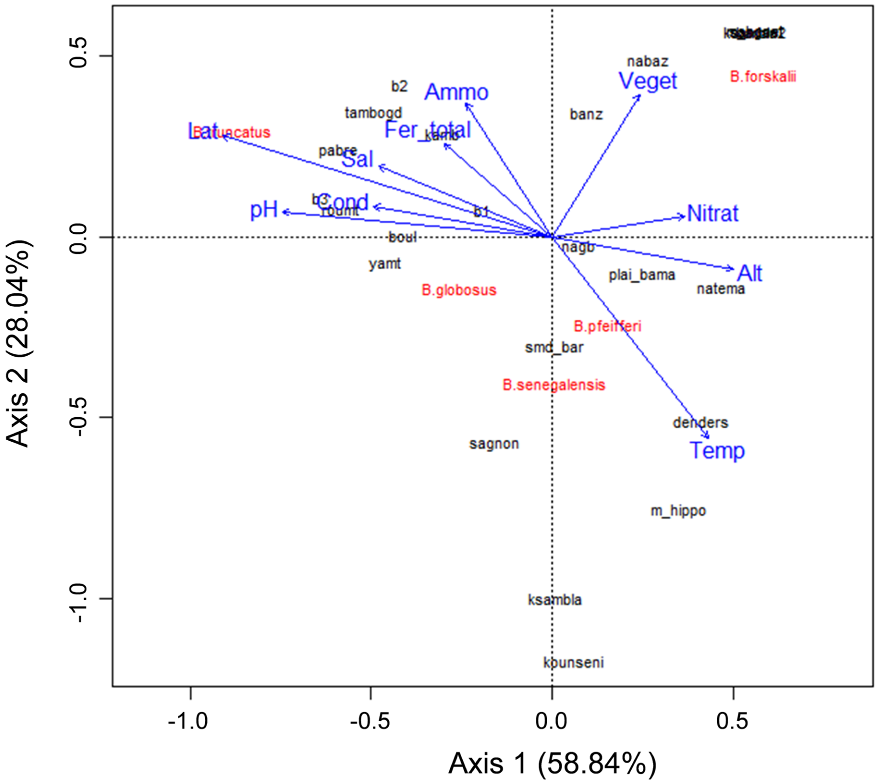

Figure 3. Ordering of the 24 sites according to species and environmental parameters. Legend: b1 = reservoir N˚1; b2 = reservoir N˚2; b3 = reservoir N˚3; boul = Boulmiougou; yamt = Yamtenga; roumt = Roumtenga; sagnon = Sagnongnongo; nagb = Nagbangré; tambogd = Tambogdin; nabaz = Nabazana; kamb = Kamboinsin; pabre = Pabré; banz = Banzon; m_hippo = hippopotamus backwater; kounseni = Kounséni; ksanbla2 = Karangasso sambla2; ksmbla = Karangasso sambla; denders = Denderresso; smd_bar = Samandéni reservoir; natema = Natéma; sangoul = Sangoulema; plai_bama = Bama plain; badar = Badara; m_houet = Houet backwater; Alt = Altitude; Cond = Electrical conductivity; Nitrat = Nitrates; Lat = Latitude; Veget = Vegetation; Sal = Salinity; Ammo = Ammonium; Temp = Temperature; B. globosus = *B. globosus*; B. pfeifferi = *Bi. pfeifferi*; B. truncatus = *B. truncatus*; B. senegalensis = *B. senegalensis*; B. forskalii = *B. forskalii*; B. truncatus = *B. truncatus.*

The RDA results show that the presence of *B. truncatus* is positively correlated with conductivity, pH, and latitude, but negatively correlated with altitude. The presence of *B. forskalii* is more positively correlated with vegetation. As for *Bi. pfeifferi* and *B. senegalensis*, their presence is positively correlated with temperature and altitude but negatively correlated with ammonium and total iron (**Figure 3**).

3.3. Modeling Snail Intermediate Hosts of Schistosome Abundance Using Environmental Parameters

The optimized BRT model explained 43.359%, 77.047%, 73.906%, 48.169%, and 23.23% of the spatiotemporal variation in abundance of *B. senegalensis*, *B. truncatus*, *B. globosus*, *B. forskali*, and *Bi. pfeifferi*, respectively (**Table 3**).

Table 3. Optimal explanatory performance of the fitted BRT model.

Species	Optimal setting			Explicative performance			
	Tc	Lr	bf	CV deviance SE	% explained deviance	% mean correlation (training data correlation)	nt
B. senegalensis	4	0.001	0.75	6.824 ± 1.576	43.36	66	2350
B. truncatus	4	0.001	0.75	21.191 ± 3.792	77.047	89.6	7000
B. globosus	4	0.001	0.75	5.618 ± 2.591	73.906	80.7	2850
B.forskalii	4	0.001	0.75	13.743 ± 1.637	48.169	67.7	3050
Bi. pfeifferi	4	0.001	0.75	17.501 ± 2.892	23.23	47.7	1100

With the exception of *B. globosus*, the main factors influencing the abundance of snail intermediate hosts of schistosomes were the physicochemical parameters of the water. Furthermore, the fitted functions reveal a non-linear and sometimes complex relationship between the explanatory variables and snail abundance. The abundance of *B. senegalensis* and *B. truncatus* was more influenced by conductivity and/or salinity and alkalinity. These associated factors contributed respectively to 58.4% and 78.2% of the predictive power of the optimized model for *B. truncatus* and *B. senegalensis* (**Figure 4** and **Figure 5**). The abundance of *Bi. pfeifferi* was mainly influenced by electrical conductivity (27.7%), pH (16.6%), water temperature (12.1%), and habitat type (9.2%). These variables contributed 65.6% of the model's predictive power (**Figure 6**). For *B. globosus*, the main factors influencing abundance are permanence (24.9%), vegetation cover (18.6%), alkalinity (12.6%), and salinity (9.3%). These cumulative explanatory variables contribute 65.4% of the predictive power of the optimized model (**Figure 7**). The species was abundant in water bodies with intermediate regimes. The abundance of *B. forskalii* was mainly influenced by total iron (26.8%), temperature (20.9%), and pH (8.7%). These variables contributed 56.4% of the model's predictive power (**Figure 8**).

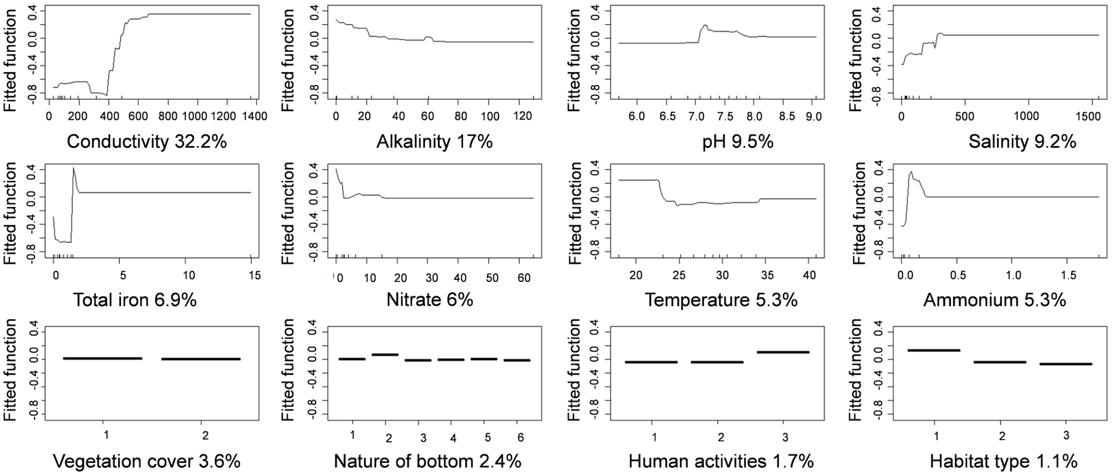

Figure 4. Fitted functions and relative importance for environmental explanatory variables by the BRT model relating to the abundance of *Bulinus truncatus*.

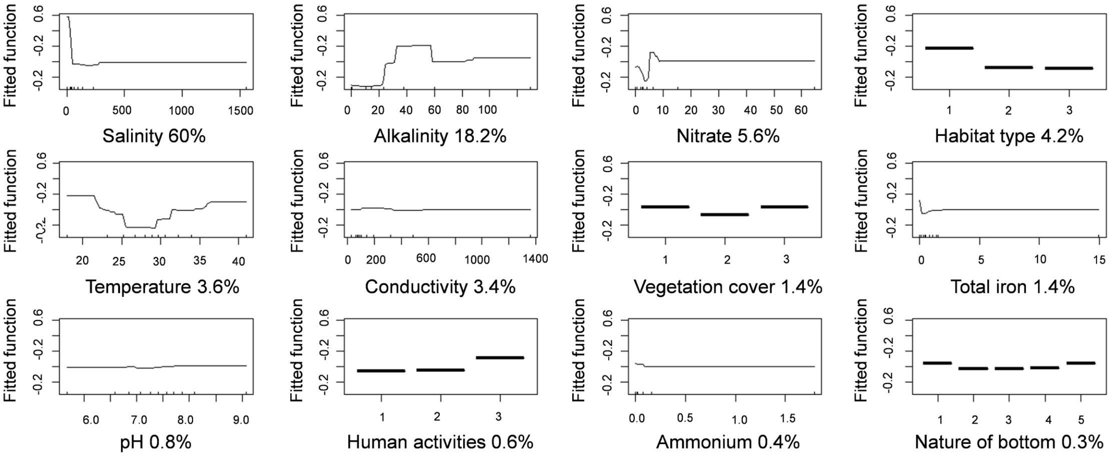

Figure 5. Fitted functions and relative importance for environmental explanatory variables by the BRT model relating to the abundance of *Bulinus senegalensis*.

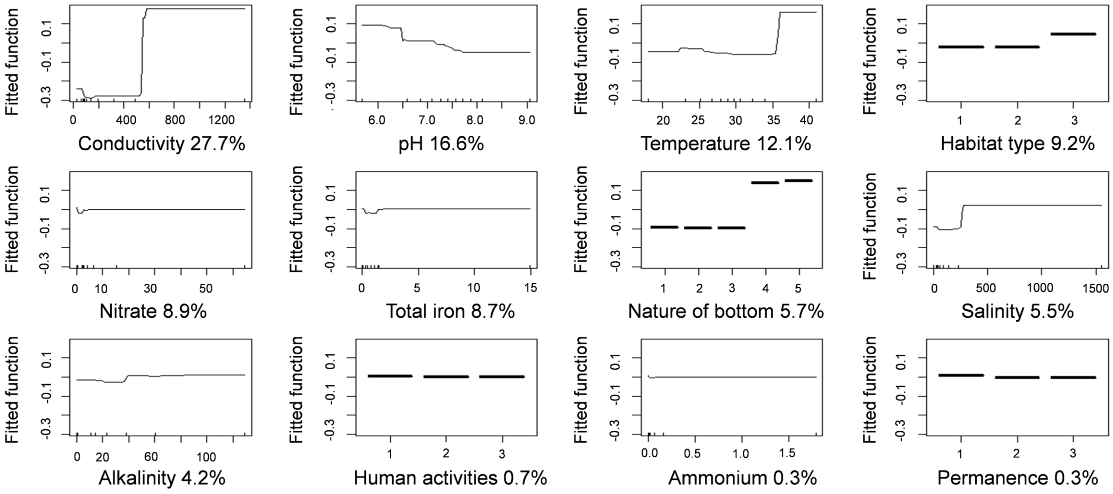

Figure 6. Fitted functions and relative importance for environmental explanatory variables by the BRT model relating to the abundance of *Biomphalaria pfeifferi*.

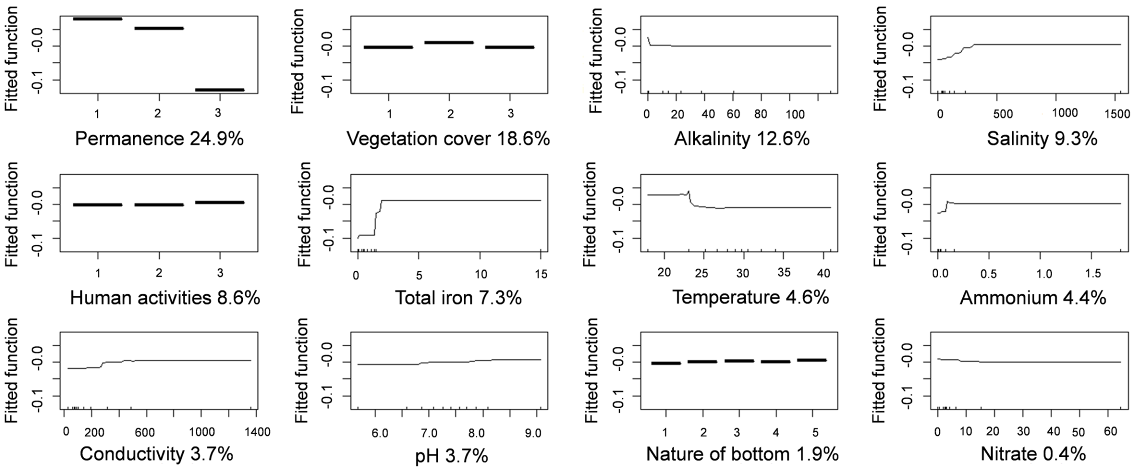

Figure 7. Fitted functions and relative importance for environmental explanatory variables by the BRT model relating to the abundance of *Bulinus globosus.*

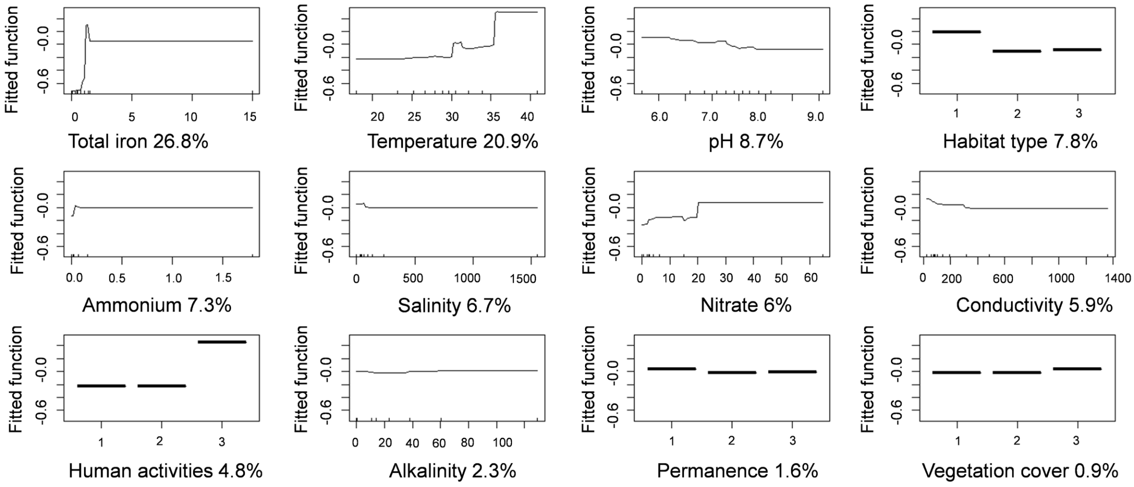

Figure 8. Fitted functions and relative importance for environmental explanatory variables by the BRT model relating to abundance of *Bulinus forskalii.*

4. Discussion

4.1. Diversity and Spatial Distribution of Snail Intermediate Hosts of Schistosomes

This study revealed the presence of five species of snail intermediate hosts of human schistosomes in the Centre and Hauts-Bassins regions. With the exception of *B. truncatus*, which was absent from the Hauts-Bassins region, the presence of all the other species in these regions had already been reported since 1994 [19]. The dispersal methods of *B. truncatus* require further study. Nevertheless, their geographical distribution pattern can be deduced by analogy with other snail species and from the limited observations that have been made. The sudden appearance of these snails in isolated basins in the Gezira region of Sudan, up to thirty kilometres from the nearest river or irrigation canal [43], has led to the deduction that they must have been carried on the feet of aquatic birds or buried under the skin of aquatic animals. *B. truncatus* could also have been transported to this region by the action of run-off or floodwaters on vegetation or floating debris. It remains to be seen to what extent the country's other rivers play a role in the spread of *B. truncatus*. *Bulinus forskalii*, which is ubiquitous in Africa, is the species most frequently encountered at the various sites surveyed. The high frequency of occurrence of this species could be explained by the natural behavioural adaptation mode, which is different for each species. *B. pfeifferi* is a calm-water snail that feeds on the surface and can easily be carried to the dam [44], finding a resting place when the water current is greatly reduced, whereas *B. globosus* can cling to or settle on the bottom of the water and then rise to the surface [45]. In general, habitat type, vegetation cover, and human disturbance were the most important variables determining the occurrence and abundance of snail intermediate hosts. Our results are in agreement with those of Utzinger and Tanner (2000) [44], who found that the abundance and distribution of freshwater snails were governed by both biotic and environmental factors. Our results indicate that the preferred sites for snails in terms of occurrence and abundance were habitats disturbed by waste dumps, agriculture, and other human activities (in this case, urban marshes and dam lakes characteristic of Burkina's hydrographic network). This will lead to an increase in the concentration of detritus and eventually the proliferation of algae and aquatic plants, the basis of the diet and attachment support of Planorbid and Prosobranch snails [46]-[48]. This high occurrence could also be attributed to the low abundance and diversity of other invertebrates and fish in highly disturbed habitats, which can suppress snail populations through predation and competition. Indeed, predators reduce snail abundance directly through predation and avoidance of oviposition or indirectly through competition for food resources [49].

4.2. Environmental Factors Influencing the Occurrence and Abundance of Snail Intermediate Hosts of Schistosomes

The main local factors influencing the occurrence of snail populations were salinity, nitrates, pH, temperature, latitude, and vegetation. This can be explained by the fact that factors such as temperature are very important for the survival and reproduction of snail intermediate hosts of schistosomes [50]. Recent studies on the effects of temperature change on the growth, fecundity, and survival of intermediate hosts of schistosomiasis indicate that increasing temperature can modify the distribution, reproduction, growth, and survival of snail intermediate hosts of schistosomes [51] [52]. Snail intermediate hosts of schistosomes are poikilothermic. Their body temperature changes according to that of the surrounding environment [52] [53]. Snail intermediate host appears to be tolerant of salinity, conductivity, and pH. According to Camara *et al.* (2012), the distribution of snail species was associated with high conductivity and pH values and low dissolved oxygen values. This is the case for *B. truncatus* and *Bi. pfeifferi*, which were abundantly encountered in habitats with high electrical conductivity during this study. High conductivity values are generally associated with organic pollution and decreasing water quantity [54] [55].

In addition to water physicochemistry, the optimised BRT model showed that snail abundance could be influenced by water body regime, vegetation cover, and habitat type. This was the case for *B. globosus*, whose high abundance was positively correlated with water bodies with intermittent regimes and high vegetation cover. *B. globosus* has already been reported in previous studies as a species that prefers biotopes with high vegetation cover [10]. In the *Bi. pfeifferi* species, high abundances of the species were positively correlated with developed plains. Irrigated plains provide a suitable environment for the development of snail intermediate hosts of schistosomes. The development of irrigated plains in Burkina Faso has contributed significantly to the development of snail intermediate hosts of schistosomes and to the explosion of the two forms of schistosomiasis (urinary and intestinal schistosomiasis) [10] [11] [56]. In this study, season was not included as a covariate, which is a limitation. These observations show that the occurrence and abundance of snail intermediate hosts of schistosomes cannot be associated with a single factor but rather are the result of more complex interactions of several habitat factors [57]. Integrated schistosomiasis control combines efforts to fight against morbidity and control intermediate host snails. Identifying these predictors is an important step that can guide the factors to target in implementing strategies to control the abundance of intermediate host snails of human schistosomes in aquatic ecosystems of Burkina Faso.

5. Conclusion

This study shows that 5 species of snail intermediate hosts of schistosomes have been identified in the western and central parts of Burkina Faso. These were *Bulinus trunatus*, *Bulinus forskalii*, *Bulinus globosus*, *Bulinus senegalensis*, *and Biomphalaria pfeifferi*. Reservoirs and developed plains harboured the highest abundances of snail intermediate hosts. Their occurrence was influenced by physicochemical and geographical parameters. The outputs of the BRT model were robust in explaining the abundance of snail intermediate hosts using biotic and abiotic factors. Physicochemical parameters such as pH, conductivity, water temperature, and alkalinity were more suitable for the abundance of *B. trunatus*, *B. forskalii*, *B. senegalensis*, and *Bi. pfeifferi*, while intermittent water flow and vegetation cover were the parameters that favoured the abundance of *B. globosus*. This study provides clues as to the predictors of abundance of snail intermediate hosts of schistosomes.

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Data Availability Statement

The data that support the findings of this study are available from the corresponding author (Salam Sankara) upon reasonable request.

Authors' Contributions

Noellie Winkom Kpoda and Idrissa Ouédraogo designed the study. Noellie Winkom Kpoda and Salam Sankara developed the methodology, coordinated, and supervised the research. Noellie Winkom Kpoda, Salam Sankara, and Noellie Débora Balima collected the data. Salam Sankara, Idrissa Ouédraogo, Noellie Débora Balima, Awa Gneme, and Noellie Winkom Kpoda analysed and interpreted the data. Salam Sankara wrote the first draft of the manuscript. Noellie Winkom Kpoda supervised the research. All authors reviewed and approved the final manuscript.

Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this paper.

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