



Research Article

Spatial Distribution and Ecological Niche Modelling of *Schistosoma Haematobium* Bilharz and *Schistosoma Mansoni* Sambo: Assessment of Risk Maps for Schistosomiasis Spread in Benin (West Africa)

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A B S T R A C T

Introduction: Schistosomiasis is an infection caused by a parasite that remains silent for a long period of time and induces severe complications. *Schistosoma haematobium* and *Schistosoma mansoni* are the incriminating agents with freshwater gastropod molluscs as the disease vectors. However, it is useful to have an idea of the potential vector populations in order to model their spatial distributions and ecological niches to anticipate and avoid the disease spread in risk areas.

Methods: In order to map the potential for schistosomiasis transmission in the present and future, pathogen and vector occurrence data were collected from the Global Biodiversity Information Facility (GBIF) website, literature and fieldwork in high disease endemicity areas. Also, occurrences were processed and environmental data were downloaded to model the spatial distribution and ecological niche of the disease using various algorithms (Maxent, BRT, and GLM).

Results: A total of four disease vectors (*Bulinus globosus*, *Bulinus truncatus*, *Bulinus forskalii*, and *Biomphalaria pfeifferi*) were considered in our study. As per the different models used, almost all of Benin is exposed to the disease at present, except the Alibori department which has low-risk areas. The future projection indicates that the northern and central departments of the country are likely to present much more favourable conditions for the disease.

Conclusion: Our results call for rigorous monitoring and surveillance in the departments of Alibori, Atacora, Borgou, and Danga to limit the potential expansion of schistosomiasis in Benin.

Keywords: Schistosomiasis, Mollusc Vectors, Spatial Distribution, Modelling, Benin



Introduction

Schistosomiasis, which constitutes a significant public health problem, is a parasitic disease showing an epidemiological characteristic of prevalence in tropical regions.^{1,2} It is a chronic endemic disease with a slow progression, high mortality and severe or even fatal complications, often leading to serious physical, social and economic disabilities.³⁻⁵ Its spread is a complex phenomenon involving a large number of entities (host, vector, pathogen, environment, geography, climate, vegetation, rainfall, etc.) interacting on several spatial and temporal scales. By prevalence, schistosomiasis ranks first among water-borne diseases and only second to malaria in public health importance in tropical and subtropical regions.^{6,7} Populations at risk include children, pregnant women, fishermen, farmers who use irrigation technology, and livestock keepers.^{8,9}

There are five species of schistosomes that parasitise humans.¹⁰⁻¹² However, only three of them are found in Africa, namely *Schistosoma haematobium* Sambo, *Schistosoma intercalatum* Fisher, and *Schistosoma mansoni* Bilharz. In Benin, two species of schistosomes have been identified: *S. haematobium* (widely distributed) and *S. mansoni* (that can reach a prevalence of 74%).¹³

They are transmitted to humans by freshwater gastropod molluscs of the genus *Biomphalaria* of the family *Planorbidae* and of the genus *Bulinus* of the family *Bulinidae*. According to statistics from the "Programme National de Lutte contre les Maladies Transmissibles",^{14,15} schistosomiasis is endemic

in almost all of Benin and affects 76 municipalities out of the 77 in the country.

The fight against schistosomiasis, like that of most vector-borne diseases, is based on prevention through vector control and the medical management of those who are already ill. However, in order to better prevent schistosomiasis, it is useful to have an idea of the potential vector populations in order to model their spatial distributions and ecological niches to anticipate and avoid the disease spread in risk areas.

The research questions that guided our investigations were as follows:

- What are the potential populations of vectors involved in schistosomiasis transmission in the study area and what are their characteristics?
- What is the risk map for schistosomiasis spread (analysed using spatial distribution and ecological niche modelling of potential vectors)?

Material and Methods

Study Area

Study municipalities were chosen based on endemicity with a focus on high endemicity areas, with a prevalence greater than 50%.¹⁴ Thus, a total of eight municipalities were selected for the study (Figure 1), namely: Aguégué, Sô-Ava, Dangbo, Tchaourou, Ouaké, Copargo, N'Dali, and Bembéréké. This study was conducted from August 2021 to September 2022.

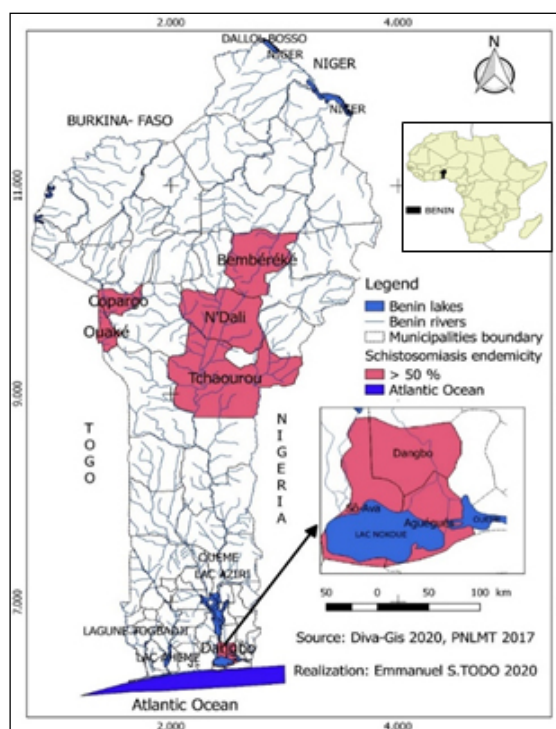


Figure 1.A Map showing the River System and Study Area^{15,16}

Review of the Occurrence Data of Potential Vectors and Pathogens of Schistosomiasis

The occurrence data of the *schistosomiasis pathogens* (*Schistosoma haematobium* and *Schistosoma mansoni*) and their respective vectors (*Bulinus africanus*, *Bulinus truncatus*, *Bulinus globosus*, *Bulinus forskalii* and *Biomphalaria pfeifferi*) were obtained from quite heterogeneous sources. They were downloaded from the Global Biodiversity Information Facility (GBIF) website via the link <http://www.gbif.org>. Additional occurrence data were collected from the literature^{8,13–15,17,18} and from fieldwork. In the field, the epidemiological surveillance services' databases, data available in the registers of curative care and the District Health Information System 2 (DHIS2) database of the statistical services were consulted in the zonal hospitals of each municipality of the study area.

Spatial Distribution and Ecological Niche Modelling of Schistosomiasis

The spatial distribution modelling process involved collecting occurrence data and downloading environmental data (predictors). Once these data had been analysed and processed, they were imported into RStudio for the modelling step using the Species Distribution Models (SDM) module. Predictors were first tested for collinearity using the *Vifstep* function. After excluding collinear variables, predictors with linear correlation were selected to run the models (GLM, MaxEnt and BRT). The *predict* function was used to predict the spatial distribution of species, and the results were mapped using the QGIS 3.24.2 software. Species distribution projection was also modelled according to greenhouse gas emission scenarios RCP 4.5 and RCP 8.5.

Regarding occurrence data, a database was obtained in an Excel file by merging the occurrence data from fieldwork, literature, and the Global Biodiversity Information Facility (GBIF) website. All data sets were grouped in an Excel database and processed. The raw data are available on the GBIF website at <https://www.gbif.org/dataset/d34deb78-9f33-461c-a3a9-8aa7f02496e9>. The present Bioclimate data were downloaded from the WorldClim database, version 2 via the link <https://www.worldclim.org/data/worldclim21.html>¹⁹ while future climate projections were obtained from AfriClim 3.0 (<http://webfiles.york.ac.uk/KITE/AfriClim>) at 2.5 arc minutes resolution.²⁰ AfriClim database was chosen for the future projections because it presents Africa-specific climate data and fits well with the ecological realities of the continent.²⁰ Many regression-type models are sensitive to collinearity for it may cause instability in parameter estimation and biases in inference statistics.^{21,22} For this, we selected 15 bioclimatic variables (bio1–bio7 and bio10–bio17) on WorldClim to perform the collinearity test with the module “SP Thin” in R software.²³ This allowed

to retain four bioclimatic variables: bio1 (average annual temperature) with a 4.2% contribution, bio3 (isothermality) with a 66% contribution, bio13 (precipitation of the wettest month) with a 12.3% contribution and bio14 (precipitation of the driest month) with a 17.5% contribution. These variables were selected from WorldClim for the present prediction¹⁸ and from AfriClim for future projections (by 2055) under two greenhouse gas emission scenarios: RCP 4.5 (optimistic) and RCP 8.5 (pessimistic).²⁰

The algorithms were executed in R software;²⁰ more precisely in the SDM package. The SDM method was chosen due to its ability to predict species occurrence based on environmental characteristics.^{24–26} The algorithms used include generalised linear models (GLM),²⁷ maximum entropy modelling (MaxEnt),^{28,29} and boosted regression trees (BRT).³⁰ GLMs are an extension of “simple” linear regression models, which predict the variable response as a function of several predictor variables. They find the equation that best predicts the species occurrences for the values of the environmental variables. The model has three important components: the distribution probability of the response variable, the Linear Predictor (LP), and the link function.²⁷ MaxEnt is a stand-alone Java application for geographical distribution modelling of species; an algorithm that predicts a greater proportion of species occurrence and is more useful for exploration purposes aimed at discovering new species ranges. The unique feature of this algorithm is its ability to work with both continuous and categorical data.²⁹ BRT models are a combination of two techniques: decision tree algorithms and boosting methods.²⁵ This statistical method is particularly suited to explore ecological variables and optimise prediction performance.³⁰ Fitting multiple trees in BRT overcomes the biggest drawback of single-tree models: their relatively poor predictive performance. Moreover, it is flexible and easy to read.²⁵ BRTs take into account collinearity between variables.

To fit the models, these three algorithms were used with 10 replications; 10,000 background points were randomly generated and cross-validation was used as the replication method. Then to evaluate the model's performance using the *get_evaluations* function, we focused on True Skill Statistic (TSS), Receiving Operator Curves (ROC), and Area Under the Curve (AUC). The values of AUC were interpreted as follows:^{31,32} $0.50 \leq AUC \leq 0.70$: the model has low accuracy; $0.70 \leq AUC \leq 0.90$: the model has moderate accuracy; $AUC > 0.90$: the model has high accuracy. The standard deviation was calculated in order to assess the variability of AUC and TSS values around their means. The results of distributions generated by the models were mapped using the QGIS 3.24.2 software.

Results

Point of Occurrence Data of Potential Vectors and Pathogens of Schistosomiasis

The numbers of occurrence data for schistosomiasis pathogens and their respective vectors downloaded from the GBIF website were 54 occurrences of vectors and 23 occurrences of disease pathogens. Also in the field, 180 occurrences of vectors and 452 occurrences of disease pathogens were observed. Similarly in the literature, 77 occurrences of vectors and 1106 occurrences of disease pathogens were reported. After data cleaning, 979 occurrences were obtained for modelling through different algorithms (Figure 2). Together, these data indicate a strong presence of schistosomiasis in southern and central

Benin. This is due to the strong presence of stagnant waterways favourable for vector development and the social behaviour of populations.

Spatial Distribution and Ecological Niche Modelling with Different Algorithms

Through the different model parameters used in Table 1, the model results were overall acceptable. Indeed, the AUC of the different models used were Maxent (0.77) with a $4.8 \cdot 10^{-2}$ standard deviation, GLM (0.71) with a $6.10 \cdot 10^{-2}$ standard deviation, and BRT (0.77) with a $4.2 \cdot 10^{-2}$ standard deviation. It should also be noted that the future projections of all models through scenario 4.5 (pessimistic future) present almost the same output as scenario 8.5 (optimistic future) by 2055.

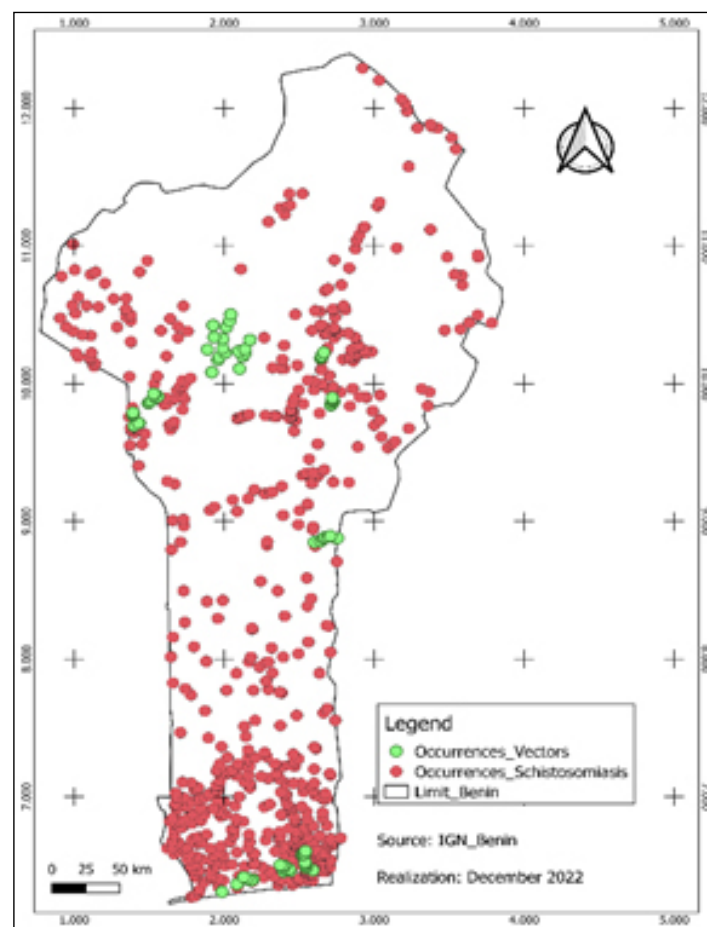


Figure 2. Schistosomiasis and Vectors Occurrence Data Set

Table 1. Parameters of Different Models Used

Methods	AUC	Standard Deviation of AUC	COR	TSS	Standard Deviation of TSS	Deviance
Maxent	0.77	$4.8 \cdot 10^{-2}$	0.43	0.44	$6.8 \cdot 10^{-2}$	1.22
GLM	0.71	$6.10 \cdot 10^{-2}$	0.33	0.37	$9.7 \cdot 10^{-2}$	1.11
BRT	0.77	$4.2 \cdot 10^{-2}$	0.42	0.45	$8.4 \cdot 10^{-2}$	1.08

AUC: Area Under the Curve, COR: Correlation, TSS: True Skill Statistic, Maxent: Maximum Entropy Modelling, GLM: Generalised Linear Models, BRT: Boosted Regression Trees

Results of the MaxEnt Model

The model indicated a moderate disease intensity in the department of Alibori and high intensity in some parts of other departments at present (Figure 3a). It predicted a high intensity of the disease presence in most parts of the Atacora department, in the whole department of Alibori, and in the northern parts of the Borgou department in the future. Overall, the future prediction of the MaxEnt model indicated a very high disease intensity in the northern parts and a very low intensity in the southern parts of Benin by 2055 (Figures 3b and 3c).

Results of the BRT Model

The model indicated a low intensity of the disease in the department of Alibori and high intensity in some parts of Atacora, Borgou, Donga, Collines, Zou, Plateau, Kouffo, Mono, Ouémé, Atlantique, and Littoral departments at present (Figure 4a). Its future projections showed a high intensity of the disease in most parts of the Atacora department, in the whole department of Alibori and in the northern parts of the Borgou department. Overall, the future prediction of the BRT model indicated a very high disease intensity in the northern parts and a low intensity in the southern parts of Benin by 2055 (Figures 4b and 4c).

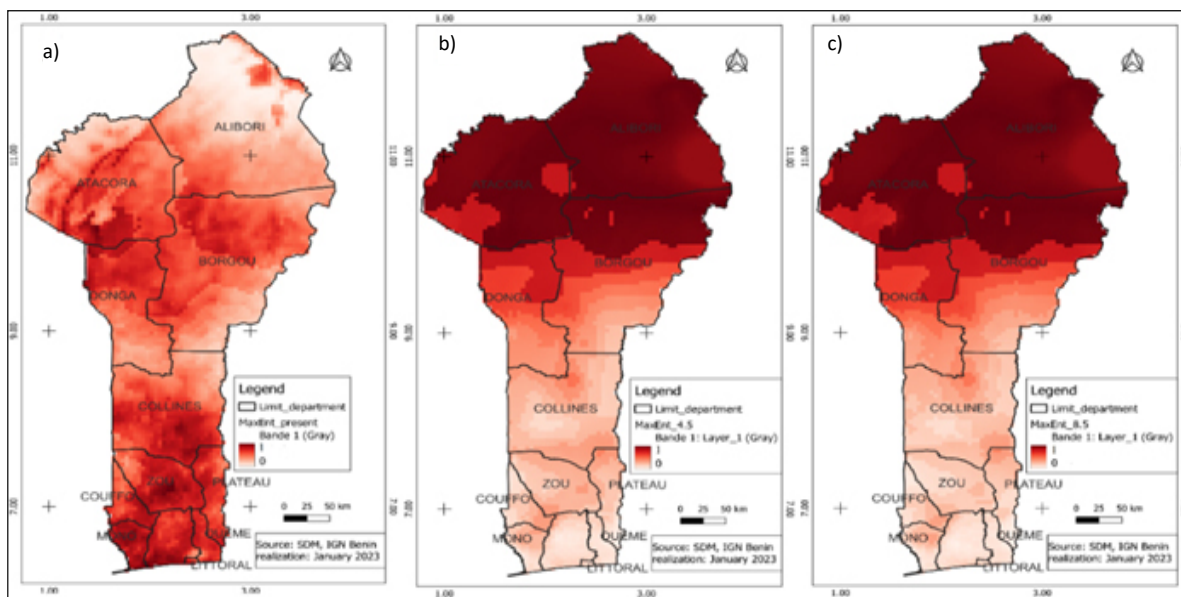


Figure 3. Spatial Distribution of Schistosomiasis in Benin through MaxEnt at Present and in Future

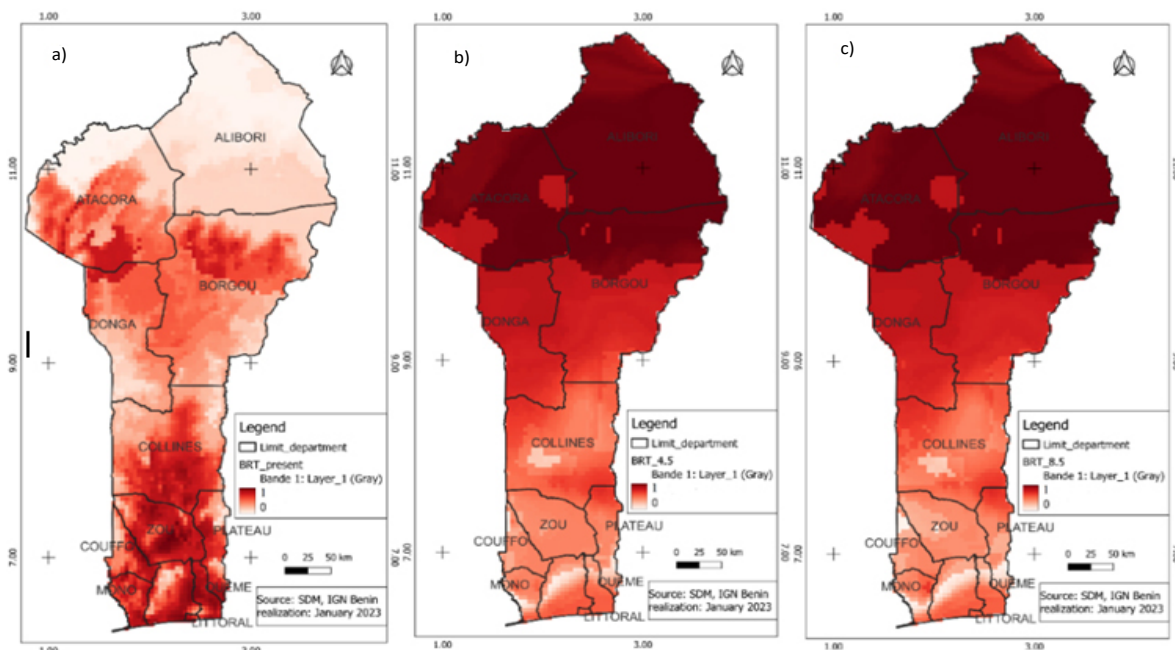


Figure 4. Spatial Distribution of Schistosomiasis in Benin through BRT at Present and in Future

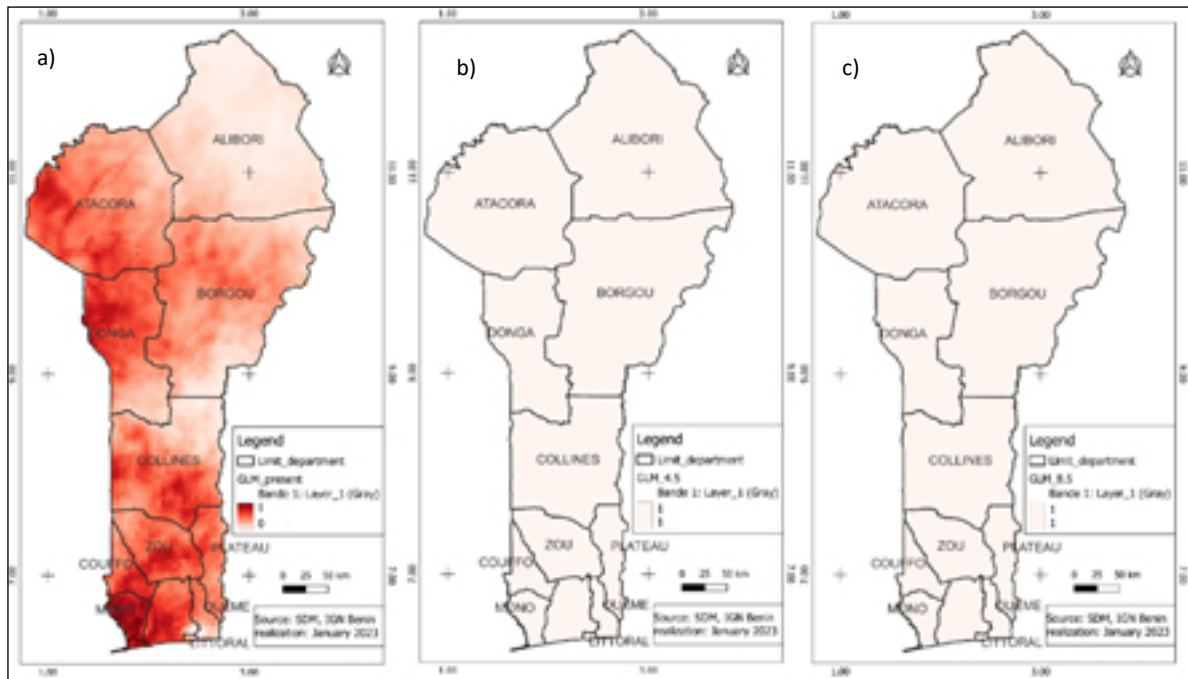


Figure 5. Spatial Distribution of Schistosomiasis in Benin through GLM at Present and in Future

Results of the GLM Model

The model indicated a low intensity of disease in the department of Alibori and a high intensity in some parts of Atacora, Donga, Collines, Zou, Plateau, Kouffo, Mono, Ouémé, Atlantique, and Littoral departments in Benin (Figure 5a). It predicted a very low intensity of schistosomiasis throughout Benin in the future. This reveals a lack of model accuracy in predicting the presence of disease (Figures 5b and 5c).

Discussion

Environmental Variables Governing the Spatial Distribution of Schistosomiasis Pathogens

From the bio-ecology of schistosomiasis pathogens, bio1, bio3, bio13, and bio14 are the variables retained in the models after selection.³³ These variables take into account temperature and precipitation. The temperature could reflect the transmission mechanism of the pathogen and precipitation could be more important than other factors in limiting the mollusc vector distribution.³⁴ Indeed, temperature affects the abundance of mollusc vectors^{35,36} and the development of the parasite within molluscs is highly dependent on temperature: a temperature below 25 °C would inhibit the asexual multiplication phase while too high temperatures would deparasite mollusc vectors and increase their mortality.¹¹ The work of Fan et al.³⁴ also selected the variables in this study with the exception of isothermality. The selection of isothermality (bio3 = bio2/bio7) in Gaudreau et al. and Hijmans et al.^{37,38} could be due to the non-selection of bio2 and bio7 variables in this study.

Algorithms Performance Used in View of the Biology and Ecology of Pathogens

The results showed that schistosomiasis is present in almost all departments of Benin at present; more precisely in the south and centre according to the distribution of species occurrence data. The Maxent and BRT models identified the northern regions of Benin as possible high-risk areas and the southern regions as possible low-risk areas in the future. On the other hand, the GLM model had a lack of accuracy in predicting the disease presence. The AUCs (Table 1) belonged to the interval of $0.70 \leq \text{AUC} \leq 0.90$ and indicated that the models had moderate accuracies.³⁹ The TSS of the BRT model was the highest (0.45) with a standard deviation of $8.4 \cdot 10^{-2}$; while the TSS of Maxent was 0.44 with a standard deviation of $6.8 \cdot 10^{-2}$; and that of GLM was 0.37 with a standard deviation of $9.7 \cdot 10^{-2}$ (Table 1). Overall, the lowest AUC and TSS were noted in GLM, indicating that the GLM model did not perform well in predicting schistosomiasis. It should be noted that the predictive ability of the Maxent and BRT algorithms was much better than that of the GLM algorithm. This result is in line with previous studies^{33,40,41} where MaxEnt and BRT were among the best-performing models.

Strengths

- It is the first study on spatial modelling of schistosomiasis in Benin.
- It has used five algorithms in order to identify better prediction models.
- It has used the occurrence data from two entities (schistosomes and their vectors).

- It is a study on the current status of schistosomiasis in Benin and a projection into the future.

Limitations

- It has used only climatic variables in the modelling section.
- Schistosomiasis simulation would allow for a better understanding of the transmission mechanism at the local level.
- A malacological survey would provide much more precision on vector location and identification.

Conclusion

We mapped the potential transmission of schistosomiasis by predicting potential distributions at present and in future using ecological niche modelling approaches. According to the different models used, it can be seen that all of Benin is exposed to the disease at present. In the future, the northern and central departments of the country are likely to present much more favourable conditions for the disease. Schistosomiasis transmission may occur in lake areas and unsanitised areas where the population has difficulty accessing drinking water. However, our results call for rigorous monitoring and surveillance in the departments of Alibori, Atacora, Borgou, and Danga to limit the potential expansion of schistosomiasis in Benin.

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Conflict of Interest: None

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