



# Projecting the proliferation risk of *Oncomelania hupensis* in China driven by SSPs: A multi-scenario comparison and integrated modeling study

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## Abstract

Climate change has been known to cause variations in the geographically suitable areas for the schistosome-transmitting *Oncomelania hupensis* (*O. hupensis*). The spread of snails not only depends on the degree of warming but also on the socioeconomic development of the next few decades. Shared socioeconomic pathways (SSPs) published by CMIP6 consider carbon emission pathways as well as influences of distinct types of social development and land use on the regional climate, providing the possibility to accurately evaluate the impact of socioeconomic development and climate variation on the spread of *O. hupensis*. This study employed SSP126, SSP245, SSP370, and SSP585 and the correlative approach to explore the impacts of climate change and socioeconomic development on the potential diffusion areas for *O. hupensis* in China. The results exhibited strong evidence that *O. hupensis* will spread in the north of the middle and lower reaches of the Yangtze River and disappear from a small part of its current southern habitat, whereas in Sichuan and Yunnan, *O. hupensis* may spread slightly to the southeast. The projection also demonstrated that fossil fuel-driven development (SSP585) will be more conducive to the spread of *O. hupensis* breeding sites in the 2030s, whereas the continuous increase in snail breeding habitats under the regional rivalry path (SSP370) may lead to great challenges in snail control in the long term (2020–2080).

**Keywords:** *Oncomelania hupensis*; Shared socioeconomic pathways (SSPs); Climate change; China

## 1. Introduction

Schistosomiasis is a globally endemic and neglected tropical disease that infects about 250 million people, with 143,000 disability-adjusted life years every year (Anisuzzaman and Tsuji, 2020). Since the estimated schistosomiasis infection rate is based on the discovery of eggs and disease burden without considering growth retardation, cognitive impairment, and organ damage, the number of infections and the disease burden caused by schistosomiasis are seriously underestimated (King and Galvani, 2018). In China, schistosomiasis is caused by *Schistosoma japonicum*, which completes its life cycle through a single intermediate host,

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*Oncomelania hupensis* (*O. hupensis*), and more than 40 species of definitive hosts (bovines and other mammals) (McManus et al., 2018). The distribution of snails has a high correlation with the prevalence of schistosomiasis, and snail control is an effective measure to eliminate schistosomiasis at the stage of transmission interruption. Although molluscicides and environmental modification have been conducted to control snails, their growth area is still relatively large (maintained at 3.6 billion km<sup>2</sup>), with newly emerging and reemergent habitats continuing to appear (Yang et al., 2019; Gong et al., 2021). In particular, due to the rapid development of the Yangtze River economic belt and the completion of the South-to-North Water Diversion Project, the exchanges of personnel and materials between the north and the south have become more frequent, and the risk of *O. hupensis* spreading to non-epidemic areas has increased considerably via plants, ships, and flooding (Utzinger et al., 2011).

Climate change and socioeconomic development may lead to expansions in the geographical distributions of disease vectors, hosts, and pathogens, consequently increasing the potential harm due to vector-borne infectious diseases (Caminade et al., 2019). Numerous studies have demonstrated that snails move northward on a large scale based on old climate research and mechanistic models (Zhou et al., 2008; Yang et al., 2018). Previous predictions in the distribution of *O. hupensis* were mostly based on the representative concentration pathway published by the Coupled Model Intercomparison Project Phase 5 (CMIP5), which only considered the carbon emission (Yang et al., 2018; Zhu et al., 2017), indicating increased suitability and range expansion in the future with an eastward and northward shift in *O. hupensis*. The future risks of this disease under distinct socioeconomic development and the carbon emission scenarios remain miscomprehended. A new set of emission scenarios driven by shared socioeconomic pathways (SSPs) published by CMIP6 considers the impact of carbon emissions, distinct social developments, and other factors on regional climate, which facilitates evaluation of the impact of policies and development paths on disease vectors (Zhai et al., 2020).

Previous studies mainly focused on the consequences of greenhouse gas emissions and climate warming on snail diffusion and lacked the potential impact of human development patterns, development strategies, the synergy of climate change, and development paths on snail diffusion. In addition, previous studies paid disproportionately much attention to the influence of a certain climate scenario on the potential distribution of *O. hupensis* and were inadequate in comparative research on multi-scenario simulation. The shared socioeconomic paths provide more emission scenarios than RCPs and can provide more reasonable simulation results for regional climate prediction, mitigation, and adaptation research. To bridge these persistent gaps significant to informing public health, this research aims to study the temporal and spatial evolution characteristics of snail diffusion under the influence of climate change, social development, and joint action based on the four SSPs. The results will provide benefits in establishing a scientific basis for the subsequent monitoring and control of *O. hupensis* and a reference for evaluating policies and social development models for vector proliferation.

## 2. Data and methods

### 2.1. Study area and data collection

By incorporating a combination of systematic sampling and environmental sampling methods, a snail survey was conducted once a year in environments infested or possibly infested by snails. Snails were collected in the survey area along with latitude and longitude information and retrieved to the laboratory for dissection and microscope examination to identify the infection and mortal status (Xu et al., 2020). The monitoring activities were conducted by the county level center for disease control or schistosomiasis control institute, and the results were sent to the National Institute of Parasitic Diseases. The point incorporated here was obtained from the 2005–2019 data in the National Schistosomiasis Surveillance System that includes records of all *O. hupensis* found in all schistosomiasis-endemic areas for each survey site (Fig. 1). Infection of the intermediated snail host of *S. japonicum* is mainly distributed in seven southern Chinese provinces in close proximity to the Yangtze River.

Both prevailing (1970–2000) and future (2021–2040, 2041–2060, 2061–2080) climate data were downloaded from the World Climate database (<https://worldclim.org/>) at a spatial resolution of 5 km. The Beijing Climate Center Climate System Middle-Resolution Model version (BCC-CSM2-MR) that has a high capacity for simulating the temperature in China (Wu et al., 2019), was selected for the future climate data. Four SSPs were selected comprising SSP126, SSP245, SSP370, and SSP585 scenarios and bioclimatic data (Table 1) for three future periods of the 2030s (2021–2040), 2050s (2041–2060), and 2070s (2061–2080).

### 2.2. Model building and evaluation

The correlative methods employed environmental variables associated with the landscape to simulate the distribution of *O. hupensis* (Johnson et al., 2019). This geographical distribution is associated with biological interactions and diffusion effects. Therefore, the suitable habitat simulated for *O. hupensis* was relatively close to its actual niche. Furthermore, the correlative method is based on geographical events and large-scale environmental dimensions, avoiding the challenges caused by individual characteristics at the landscape level (Peterson et al., 2015).

We employed the BIOMOD2 package in R4.0.0 (R Development Core Team) to build a distinct set of correlative models using 10 model algorithms (Arenas-Castro et al., 2020; Thuiller et al., 2009; Thuiller, 2014), namely, surface range envelope (SRE), generalized linear model, generalized additive model (GAM), multivariate adaptive regression spline, generalized boosted model, classification tree analysis, flexible discriminant analysis, maximum entropy (MaxEnt), artificial neural network, and random forest (RF).

In order to reduce the uncertainty of a single model and improve the accuracy of the predictions obtained, we used two ensemble models to predict the changes in the distribution of

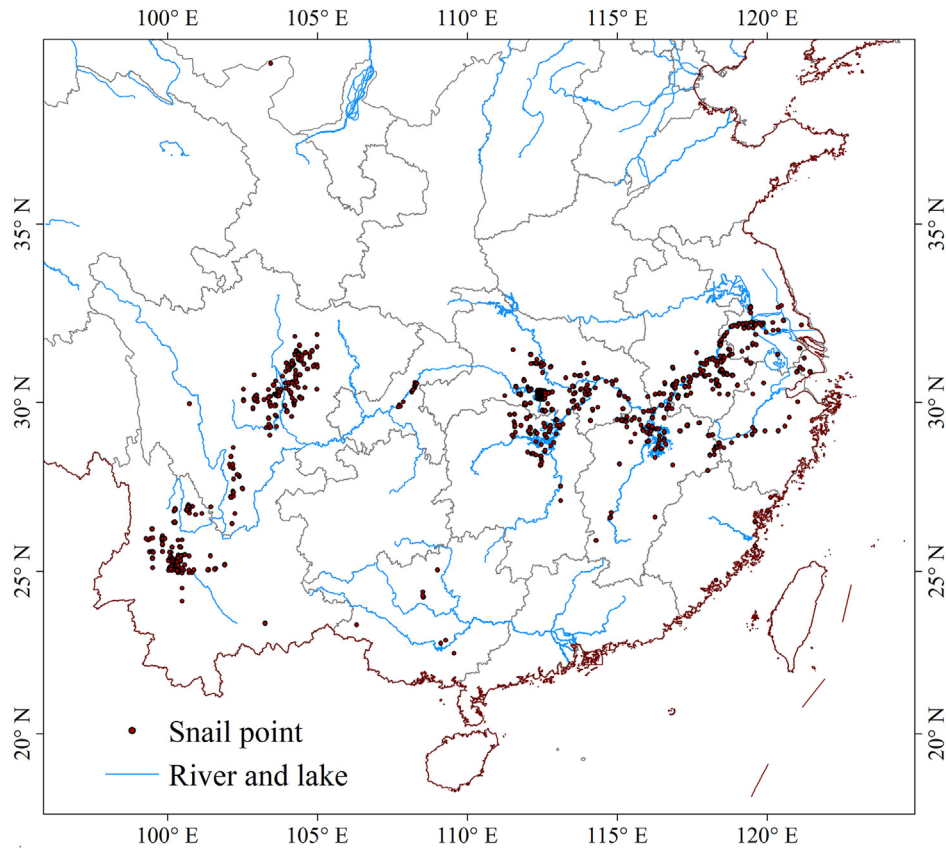


Fig. 1. Water distribution and locations of *O. hupensis* in the study area.

Table 1  
Abbreviations and descriptions of bioclimatic variables used.

Factor	Description	Unit
Bio1	Average annual temperature	°C
Bio2	Mean diurnal temperature range	°C
Bio3	Isothermality (bio2/bio7) ( $\times 100$ )	—
Bio4	Temperature seasonality (standard deviation $\times 100$ )	—
Bio5	Maximum temperature in the warmest month	°C
Bio6	Minimum temperature in the coldest month	°C
Bio7	Temperature annual range	°C
Bio8	Mean temperature in the wettest quarter	°C
Bio9	Mean temperature in the driest quarter	°C
Bio10	Mean temperature in the warmest quarter	°C
Bio11	Mean temperature in the coldest quarter	°C
Bio12	Annual precipitation	mm
Bio13	Precipitation in the warmest month	mm
Bio14	Precipitation in the driest month	mm
Bio15	Precipitation seasonality (coefficient of variation)	—
Bio16	Precipitation in the wettest quarter	mm
Bio17	Precipitation in the driest quarter	mm
Bio18	Precipitation in the warmest quarter	mm
Bio19	Precipitation in the coldest quarter	mm

suitable habitats for *O. hupensis* (Harrigan et al., 2014; Araújo and New, 2007). Committee averaging (CA) was used to convert the predicted probability of each model into a binomial distribution (with or without committee) before calculating the average value to test the consistency of the model. The weighted

mean (WM) of probabilities method was employed to evaluate the performance of each model by applying different weights to average the predicted probabilities.

Cross-validation evaluations were conducted for the models of the distribution data, where 75% of the data were used as training samples and 25% as test samples (Tan et al., 2020; Li et al., 2017). The true skill statistics (TSS), area under the curve (AUC), and Kappa statistics were utilized as indicators to evaluate each model (Harrigan et al., 2014). The AUC is not affected by the occurrence rates of distribution points and the judgment threshold. TSS indicates the ability of the predicted result to distinguish between ‘yes’ and ‘no’, where it does not depend on the incidence of the distribution points; however, it is affected by the threshold. The Kappa statistic describes the accuracy of the prediction relative to random occurrence, where it is affected by both the occurrence rate and threshold of distribution points.

### 2.3. Visual and statistical analyses of suitable habitat patterns

We employed the classification method described in the Fifth Assessment Report of the Intergovernmental Panel on Climate Change (IPCC, 2013), as follows: non-suitable habitat (0–0.33), low suitability habitat (0.33–0.66), moderate suitability habitat (0.66–0.90), and high suitability habitat (0.90–1.00). We compared the suitable habitats for *O.*

*hupensis* in future climate scenarios with the current suitable areas to obtain the changes in its geographical distribution: newly gained suitable habitats or potential future diffusion areas (gain), lost suitable habitats (lost), unchanged suitable habitats (presence), or no suitable habitats (absence). The current and future grid numbers for suitable habitats were evaluated to determine the changes in the distribution of *O. hupensis*.

### 3. Results

#### 3.1. Accuracy of projection by correlative niche models

As depicted in Table 2, RF (TSS = 0.970, AUC = 0.997, Kappa = 0.970) obtained the highest statistical accuracy and the most stable model each time, followed by GAM (TSS = 0.969, AUC = 0.996, Kappa = 0.962), however the performance of SRE was relatively poor (TSS = 0.595, AUC = 0.798, Kappa = 0.594). According to the model evaluation index (Table A1), except for SRE, the mean of TSS, AUC, and Kappa values for all model algorithms were greater than 0.70, 0.80, and 0.80, respectively, indicating the construction of successful models. The two ensemble (CA and WM) models performed better in comparison to the single models. In particular, the score for the WM ensemble model (TSS = 0.972, AUC = 0.999, Kappa = 0.972) was slightly higher than that for the CA ensemble model (TSS = 0.971, AUC = 0.998, Kappa = 0.972). Therefore, the subsequent simulations were obtained mainly based on the WM ensemble model.

#### 3.2. Assessment of environmental impact factors

The BIOMOD2 platform was employed to calculate the factor weights in each model before comprehensively multiplying the weights in the ensemble models to obtain the final weight of a single factor. The results demonstrated that among the 19 factors employed in the models, the top six factors of variable importance (bio6, bio7, bio1, bio12, bio11, and bio9) had the highest weights, with a cumulative weight of 71.2%,

thereby indicating that these six factors were most important for the distribution of habitats suitable for *O. hupensis* (Fig. 2). Among these six factors, five factors were related to temperature, and thus temperature was the main factor that affected the distribution of suitable habitats for *O. hupensis*. Furthermore, BIOMOD2 was used to integrate the response curves for environmental factors in single models to obtain comprehensive response curves for every single factor in the integrated model. The suitability response curves of the six factors with greater effects are shown in Fig. 3. The suitable range in bio6 was more than 0 °C, which reflects the low temperature tolerance threshold of *O. hupensis* (Fig. 3).

#### 3.3. Dynamic distribution of *O. hupensis* under SSPs

The WM prediction results demonstrated (Fig. 4) that the high suitability habitats for *O. hupensis* in the base period (2005–2019) are mainly distributed in the middle and lower reaches of the Yangtze River, central Sichuan province, and the northwestern part of Yunnan province, which is consistent with its current actual distribution. *O. hupensis* in lake areas and mountainous areas exhibit contrasting proliferation characteristics under SSPs, where *O. hupensis* will spread in the north of the middle and lower reaches of the Yangtze River

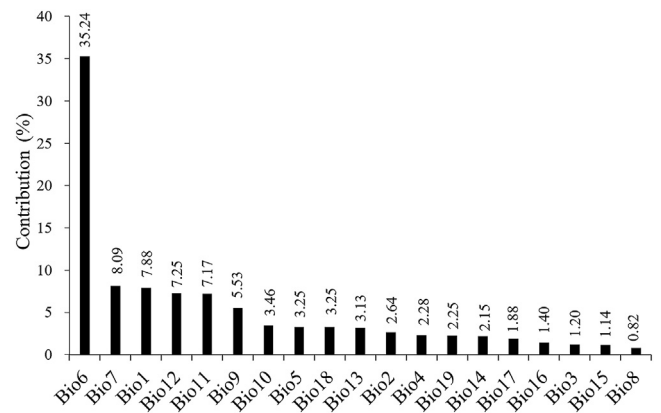


Fig. 2. Contribution of environmental factors in ensemble models.

Table 2  
Accuracy test results for different model algorithms.

Model	TSS			AUC			Kappa		
	Mean	SD	CV	Mean	SD	CV	Mean	SD	CV
Artificial neural network	0.867	0.040	0.046	0.964	0.014	0.015	0.867	0.040	0.046
Classification tree analysis	0.935	0.007	0.007	0.985	0.003	0.003	0.935	0.007	0.007
Flexible discriminant analysis	0.915	0.006	0.006	0.978	0.003	0.003	0.916	0.006	0.006
Generalized additive model	0.969	0.002	0.002	0.996	0.000	0.000	0.962	0.002	0.002
Generalized boosted model	0.928	0.004	0.005	0.992	0.001	0.001	0.928	0.004	0.005
Generalized linear model	0.841	0.041	0.049	0.924	0.027	0.029	0.841	0.041	0.049
Multivariate adaptive regression spline	0.911	0.013	0.014	0.984	0.003	0.003	0.911	0.013	0.014
Maximum entropy	0.734	0.028	0.038	0.877	0.016	0.018	0.733	0.028	0.038
Random forest	0.970	0.004	0.004	0.997	0.000	0.000	0.970	0.004	0.004
Surface range envelope	0.595	0.009	0.015	0.798	0.005	0.006	0.594	0.009	0.015

Note: TSS, true skill statistics; AUC, area under the receiver operating characteristic curve; SD, standard deviation; CV, coefficient of variation.

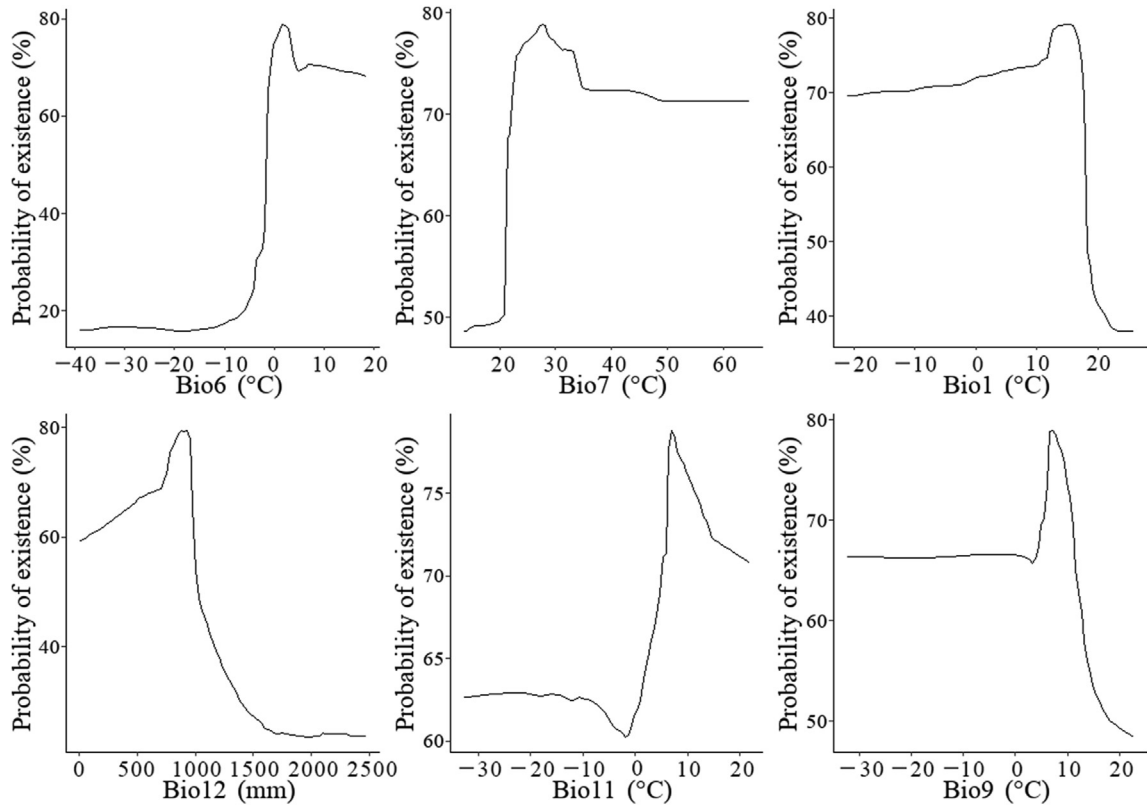


Fig. 3. Probabilistic relationships between dominant environmental factors and suitable habitat for *O. hupensis*.

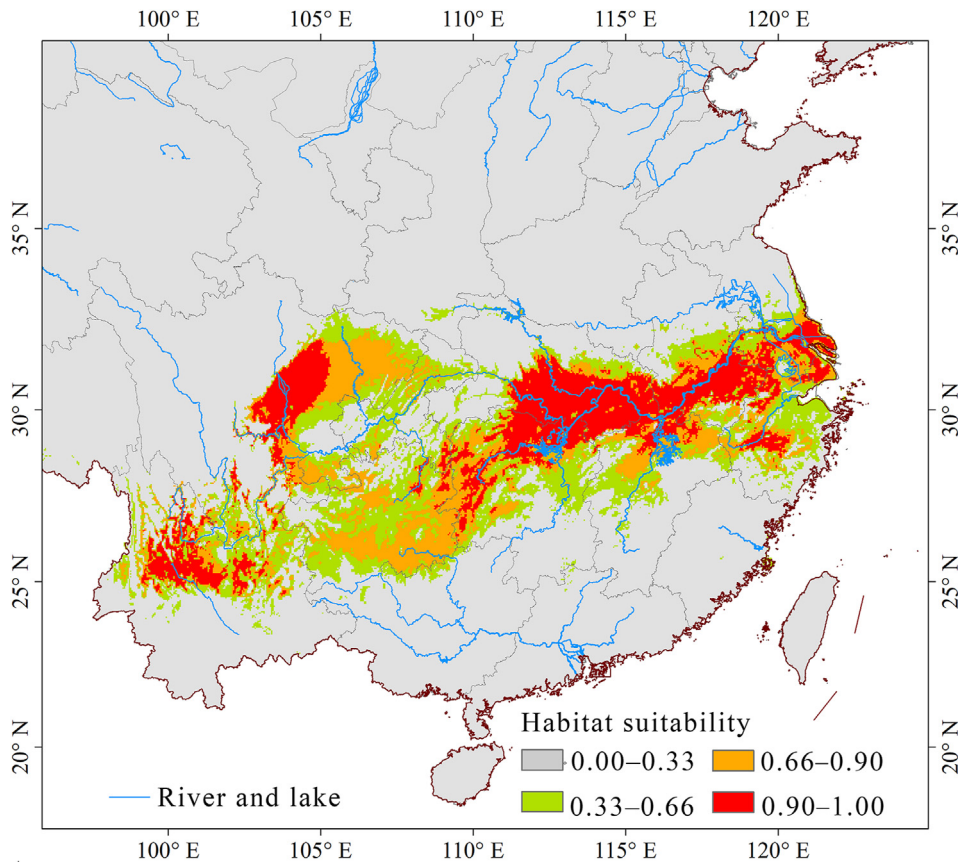


Fig. 4. Current (2005–2019) suitable habitats for *O. hupensis* based on the weighted mean of probabilities ensemble model.

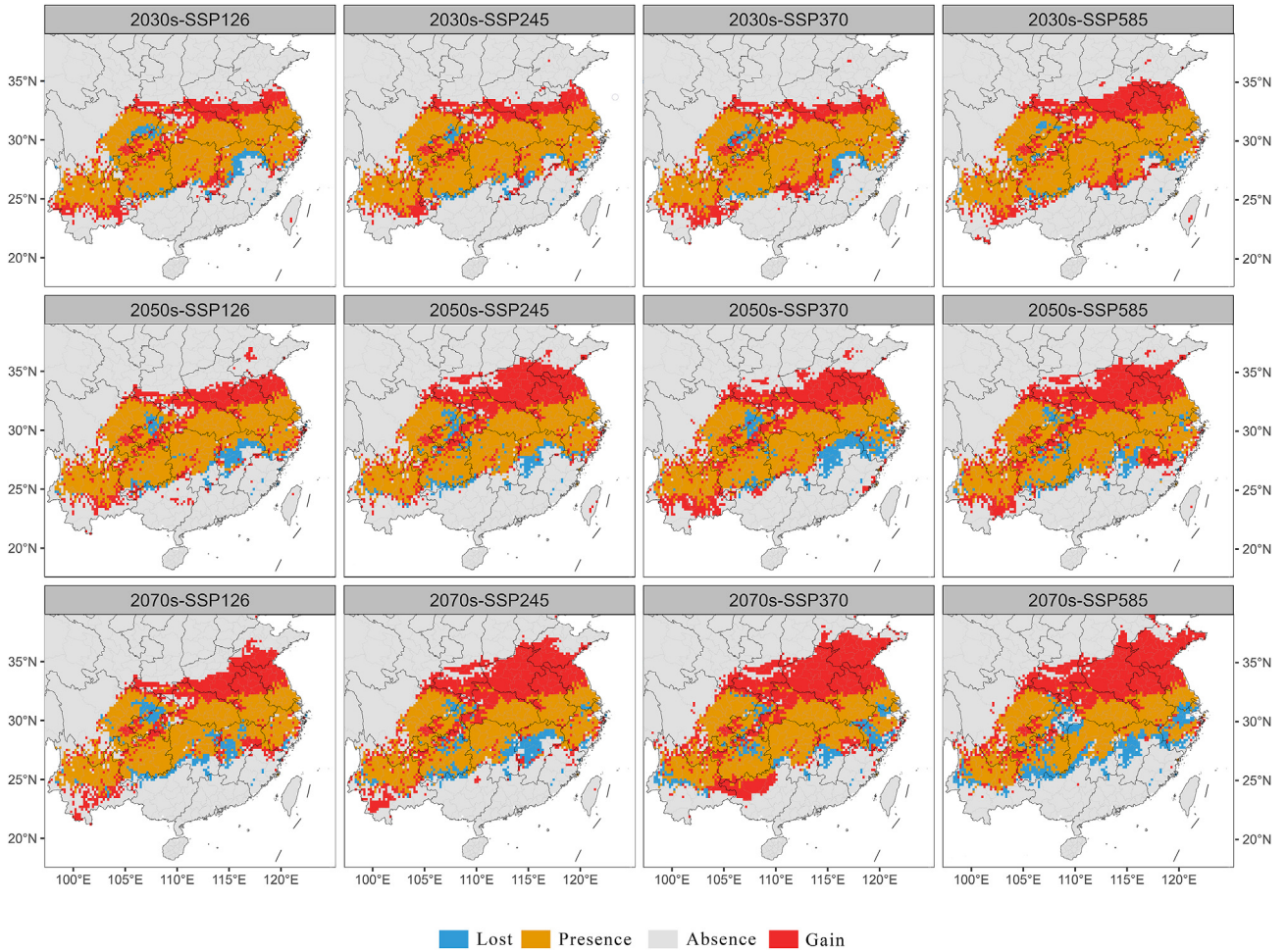


Fig. 5. Distribution of suitable habitats for *O. hupensis* under the four SSPs.

and disappear from a small part of its southern habitat, whereas *O. hupensis* may spread slightly to the southeast in Sichuan and Yunnan (Fig. 5). The suitable habitats determined under SSPs illustrated that the potential diffusion areas are mainly distributed in the northern part of Jiangsu and Anhui and the southern part of Shandong and Henan. By 2050, the suitable habitat is projected to cover the whole of Jiangsu, Anhui, and Hubei, as well as most of Sichuan, Yunnan, Chongqing, and Guizhou, eventually moving northward. By 2070, the suitable habitat will cover most areas of Henan and Shandong in the north.

As depicted in Fig. 6, the suitable habitat areas under SSP126, SSP245, SSP370, and SSP585 scenarios were found to increase by more than 20% in comparison to the base period (2005–2019). In particular, the growth of the suitable habitat areas was projected to be the most stable and moderate under SSP126, with a net increase of 20.4%–27.8%. The growth rates were determined as higher under SSP370 and SSP245 by 2070 with 62.8% and 54.7%, respectively. In different periods, climate scenarios have different effects on the suitable habitats for *O. hupensis*. SSP585, SSP245, and SSP370 were found to have the greatest impacts on the

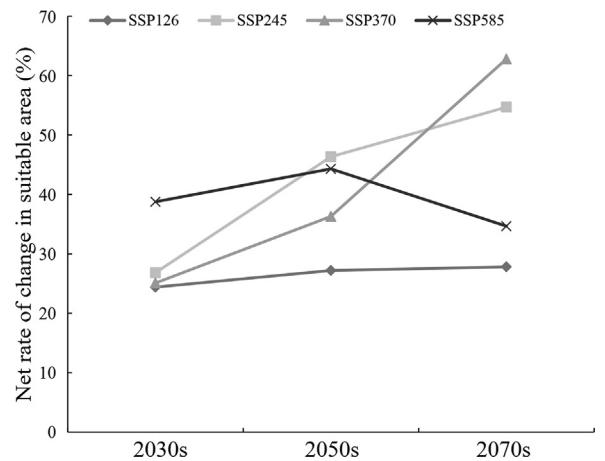


Fig. 6. Net rate of change in suitable habitats for *O. hupensis* under SSPs (net rate of change = (base area + gain area – loss area)/base area × 100%).

distribution of *O. hupensis* in the 2030s, 2050s, and 2070s, respectively. The effects of SSP245 and SSP370 on the possible increases in suitable habitats were predicted to be greater than those of SSP126 and SSP585.

#### 4. Discussion

This study reveals that the greater the challenge of climate mitigation and climate change adaptation, the greater the risk of snail proliferation. In comparison to changes in the proliferation range, greenhouse gas emissions have a positive impact on the distribution range of the possibly appropriate growing region for *O. hupensis*, as evidenced by the steady expansion of the suitable area over time and the shrinking of the risk-free area. The impact on the suitable areas under SSP126 was relatively moderate, whereas the suitable areas under SSP585 tended to rise initially and then diminish. SSP126 represents a green development road in which humans can control global warming within 2 °C, which explains that the spread of snails is at the bottom in the four scenarios (García-Peña and Rubio, 2021). SSP585 is a high-speed development road dominated by fossil fuels; strong economic growth and perfect infrastructure promote relatively low adaptation challenges to climate change (Wu et al., 2021). Therefore, snail proliferation follows a similar evolutionary pattern of ‘initially increasing, then swiftly decreasing.’ SSP245 has a certain dependence on fossil fuels, and the challenge of climate change mitigation is at a medium level. Therefore, the snail diffusion in this scenario is also medium. SSP370 is a rugged development path in which regional inequality continues to worsen, global issues such as the environment are not coordinated, and high climate change challenges exist (Theodoridis et al., 2021). Therefore, the diffusion of *O. hupensis* continues to increase and reach the highest in the 2070s in the four scenarios.

In contrast to the earlier CMIP5 evaluation (Yang and Bergquist, 2018; Zhu et al., 2017), we discovered that *O. hupensis* has distinct proliferation characteristics in lake and hilly environments. To be more specific, this study demonstrates that *O. hupensis* will spread in the north of the middle and lower reaches of the Yangtze River, and a little portion of its southern region will vanish, while *O. hupensis* may extend somewhat to the southeast in Sichuan and Yunnan. The disparity might be due to the fact that SSPs not only consider carbon emissions but also incorporate factors such as social development and land use. *O. hupensis* prefers a warm and humid environment with sufficient water, and its resistance to cold is limited (Niu et al., 2019). The Qinling–Huaihe line is the 0 °C isotherm in January, making it unsuitable for *O. hupensis* to reside close or north of the Huaihe River. However, under climate warming, the temperature will rise in the nearby areas, and it may become suitable for the growth of *O. hupensis*. In addition, climate change will lead to increases in temperature in South China as well as reduced precipitation, and the frequency of extreme high temperature events will increase significantly (Gao et al., 2019). These changes might explain why certain *O. hupensis*-friendly environments in South China have vanished.

This study illustrated that the climate compartment model represented by SRE was not effective at simulating the distribution of *O. hupensis*, whereas models such as RF and GAM obtained more accurate simulations. These results were in line with existing studies (Zhang et al., 2020; Xia et al.,

2019). Nevertheless, these better single models also have the problem of overfitting. The use of an ensemble model cannot solve the limitations of a specific model; however, it integrated the common results obtained by each model to improve the simulation accuracy for *O. hupensis* spread (Uusitalo et al., 2020; Assefa et al., 2020).

This study also is subjected to some limitations. The predicted geographic distribution may be wider than the actual range of *O. hupensis* because we did not consider the impact of human activities such as snail control (Stensgaard et al., 2013). Another limitation is niche conservatism (Wiens et al., 2010; Sales et al., 2017), where it is assumed that the adaptability of *O. hupensis* to the environment will not change with variations in the environment. Future research requires an emphasis on the factors affecting the fine-scale distribution of *O. hupensis* and an attempt to use a process-based simulation to further improve the simulation effect.

The Healthy China 2030 Program highlights that the vector control level is an important indicator of healthy cities and villages. Under the influence of environmental changes and social development, *O. hupensis* shows a trend of further spread, which adds uncertainty to eliminating schistosomiasis. The One Health approach should be applied to schistosomiasis control, where *O. hupensis*, the environment, and human and animal infections should be integrated into the monitoring and control system to eliminate the hidden danger of schistosomiasis (WHO, 2020; Deol et al., 2019; Zinsstag et al., 2018; Léger et al., 2020).

#### 5. Conclusion

This study exhibits strong evidence that *O. hupensis* will spread in the north of the middle and lower reaches of the Yangtze River and that a small part of its southern part will disappear, whereas *O. hupensis* may spread slightly to the southeast in Sichuan and Yunnan under four SSPs. In the near future (2020–2040), fossil fuel-driven development (SSP585) will be more conducive to the spread of *O. hupensis* breeding sites. The continuous proliferation of *O. hupensis* breeding habitats under the regional rivalry path (SSP370) will make its control challenging in the long term (2020–2080). While paying attention to the spread of snails caused by climate warming, we must not ignore the pressure of the spread of snails caused by environmental and climatic factors induced by vicious regional competition.

#### Declaration of competing interest

The authors declare no conflict of interest.

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## Appendix A. Supplementary data

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.accre.2022.02.004>.

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