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Short Communication

Geographical Spatial Distribution of a Tropical Freshwater Snail, *Oncomelania hupensis* and Influencing Factors on its Distribution

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ZT and YG provided the idea and collected the data. ZT and HZ analyzed the data. LL and WC designed the study. HZ contributed in manuscript writing.

Key words
***Oncomelania hupensis*, Spatial durbin model, Moran's I, local Moran's I value**

ABSTRACT

This study describes the spatial and temporal distribution characteristics of *Oncomelania hupensis* a tropical freshwater snail in mainland China from 2011 to 2020. It assesses the impact of factors, including newfound snail distribution area, eliminated snail area, and population in the snail region. Data on *O. hupensis* distribution was downloaded from the internet, and both section data and panel data were constructed. We used a spatial matrix to investigate the spatial aggregation and autocorrelation of the *O. hupensis* distribution area. Moran's I and local Moran's I values were applied as the two indices. The spatial durbin model (SDM) with a time fixed effect was employed to explore the correlation between the natural distribution area and the other factors. LM test was used to distinguish the best-fit model. LR and Hausman tests were conducted as robust tests, and an effect test was also performed. The distribution area of *O. hupensis* decreased from 2011 to 2020 and showed spatial aggregation and autocorrelation. The SDM revealed that eliminating snail areas had a positive main effect and a positive spill-out effect on the actual distribution of *O. hupensis*. The decomposition of the effect showed that the elimination area had a positive total effect on the actual distribution through positive direct and indirect methods. The snail elimination program effectively decreased the actual distribution of *O. hupensis*, which might also be an efficient way to prevent and control the disease transmitted by *O. hupensis*, Schistosomiasis.

Schistosomiasis is the second most serious parasitic disease in the world, following closely behind malaria (Barnett, 2018). According to the World Health Organization (WHO), the disease is prevalence in 78 tropical and sub-tropical countries worldwide, leading to 230 million people affecting and 700 million at risk.

In China, Schistosomiasis affects tens to thousand people (Li *et al.*, 2020; Zhou, 2023). The helminth *Schistosoma japonicum* is the causative agent of schistosomiasis. This disease has been prevalent in the Yangtze River valley for thousands of years (Chen *et al.*, 2022). The life cycle of the parasite is complex. Adult worms colonize the vessels of final hosts, including mice, buffalo, and humans that come into contact with infested water. Adult worms produce ten to a thousand eggs daily, and fertilized eggs hatch into miracidia in freshwater. The miracidia invade the intermediate host, the freshwater snail *Oncomelania hupensis*, where they asexually reproduce into cercariae. Cercariae are the infectious stage of *S. japonicum* for the final host. In China, the unique intermediate host of *S. japonicum* is *O. hupensis*, which is mainly distributed in the Yangtze River valley. Currently, there is no clinical vaccine for schistosomiasis (McManus *et al.*, 2020; Molehin, 2020); therefore, the prevention and control of the disease mainly rely on eliminating its transmitter (Gordon *et al.*, 2022). Importantly, the actual distribution area of *O. hupensis* impacts the prevalence of schistosomiasis (Li *et al.*, 2023). In this study, we focused on the spatial and temporal distribution characteristics of *O. hupensis* in China, with particular emphasis on the influence of factors such as new-found distribution area, eliminated area, and population in *O. hupensis* distribution locations.

Materials and Methods

The data used in this study were accessed through

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internet databases (Anonymous, 2020). The data on *O. hupensis* distribution included the actual distribution area, newfound distribution, eliminated distribution, and human population in the snail location. These data were obtained from the Chinese Health Yearbook and the Annual Report on Schistosomiasis Control in China. We focused our study on Anhui, Hubei, Hunan, Jiangsu, Jiangxi, Sichuan, and Yunnan from 2011 to 2020.

A spatial matrix of 01 was used in this study, where 0 represents no bordering with each other, and 1 refers to bordering with each other. The spatial aggregation and autocorrelation were analyzed on section data of *O. hupensis* real distribution by the 01 spatial matrix. The impact of factors on *O. hupensis* accurate distribution was obtained on the panel data using the same spatial matrix. Spatial aggregation was measured by global Moran's I. Evaluation indices for spatial autocorrelation were local Moran's I values. The models used in this study included the spatial durbin model (SDM), spatial error model (SEM), and spatial lag model (SLM). The LM, robust, and effect tests determined the best-fit model. The LM test determined the best-fit model among the three models. If the best-fit model was SDM, the robust test was used to determine if the SDM would return to SEM or SLM. The effect test was used to ensure the model was random or fixed effect, time, individual, or both.

Data downloaded online was edited in Excel (Microsoft Office 2016). GraphPad Prism 10 generated the overall trends for the actual distribution area, newfound area, and eliminated area of *O. hupensis*. ArcGIS generated the map of the average distribution. Figures were also edited using GraphPad Prism 10. Stata was used to analyze spatial and temporal distribution characteristics.

Results

Figure 1 shows distribution, newfound and eliminated areas of overall distribution of *O. hupensis* in mainland China. The distribution area of its snails decreased continuously while eliminated area of *O. hupensis* declined continuously and slowly in the mainland China during 2011-2020. The rise and fall of Newfound area is shown Figure 1B.

At the provincial level, the largest distribution area was, followed by in Figure 1A, C. The average distribution area of HN among 2011-2020 was 174 268 m^2.

Table I shows the distribution area exhibited spatial aggregation from 2011 to 2020 (Moran's I value > 0, p-value < 0.05). The highest spatial aggregation occurred in 2011, and the lowest was in 2016. Local Moran's I indicated that there were 2 clusters of distribution: A high-high cluster in the first quartile and a low-low cluster in the third quartile. The high-high cluster included Hunan, Jiangxi, and Hubei. Local Moran's I changed minimally, but the overall spatial autocorrelation was essentially similar. The high-high cluster remained consistent in each year (Fig. 2).

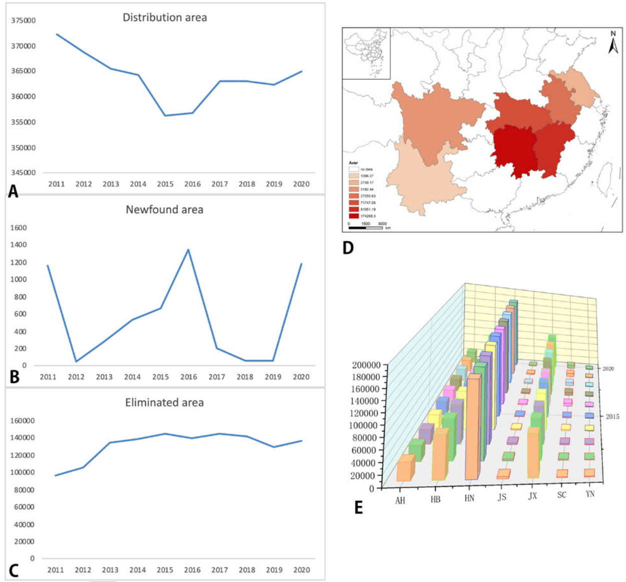

Fig. 1. Overall distribution trends of *O. hupensis* in china
Notes: A) distribution area of *O. hupensis*, B) new found area of *O. hupensis*, C) eliminated area of *O. hupensis*, D) annual average geographic distribution of *O. hupensis* in Yangtze valley and E) real distribution area at the national level

Table I. Spatial aggregation of real distribution of *O. hupensis* during 2011-2020.

	Moran's I	z value	p value
2011	0.474	2.034	0.021
2012	0.475	2.032	0.021
2013	0.468	2.027	0.021
2014	0.464	2.021	0.022
2015	0.437	1.998	0.023
2016	0.435	1.985	0.024
2017	0.446	1.977	0.024
2018	0.444	1.974	0.024
2019	0.442	1.969	0.024
2020	0.458	1.984	0.024

Table II. LM test result.

Spatial error		Statistic	p value
	Moran's I	6.07	0.000
	Lagrange multiplier	31.743	0.000
	Robust lagrange multiplier	1.792	0.181
Spatial lag			
	Lagrange multiplier	30.122	0.000
	Robust lagrange multiplier	0.172	0.679

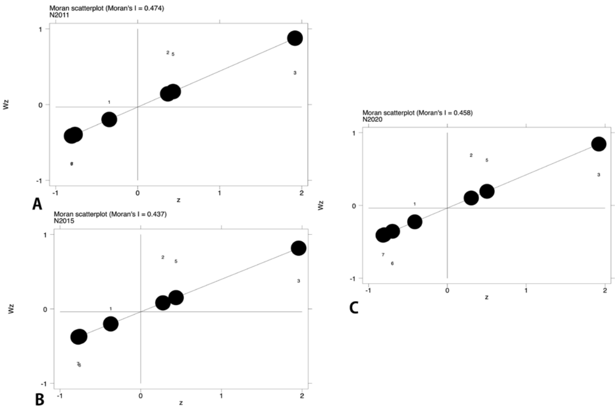

Fig. 2. Local Moran's I value for real distribution of O.hupensis. A) local Moran's I value in 2011, B) local Moran's I value in 2015 and C) local Moran's I value in 2020.

Table III. Results of robust and effect test.

		x2 value	p value
Robust test	SLM vs.SDM	71.98	<0.05
	SEM vs.SDM	78.84	<0.05
Hausman test		35.02	<0.05
Effect test	Lr-test both vs. ind	6.91	0.73
	Lr-test both vs. time	379.55	0.00

The LM test result indicated a statistically significant difference between SEM and SLM; therefore, we chose SDM for this study (Table II). Table III shows robust test results indicating that SDM could not be simplified to SLM or SEM. The Hausman test result demonstrated that the fixed model fit better than the random model. The LR effect test further indicated that the time-fixed effect should be used. Thus, the time-fixed effect of SDM was utilized for this study. The coefficient value in the main effect indicated that the area of eliminated *O. hupensis* location and the population in the snail area had positive effects on the distribution of *O. hupensis*, both with statistically significant differences. Spatial autoregression showed spatial conduction and was measured by the Wx value. The area of eliminated *O. hupensis* location and population in the snail area exhibited spatial spillover effects on the distribution of *O. hupensis*; the snail elimination area had a positive spatial spillover effect, while the population showed a negative spatial spillover effect (Table IV).

Analyzing the direct, indirect, and total effects of spatial lag explanatory variables revealed that the elimination area had a total effect on the actual distribution area of *O. hupensis*. The decomposition of the total effect showed that the elimination area had both direct and indirect effects on the distribution area of *O. hupensis*, both statistically significant. The population in the snail area had only a statistically significant direct effect (Table V).

Table IV. Result of SDM.

	Coefficient	p value	95% conf. interval
Main effect			
x_1	-2.44	0.89	-33.51~28.63
x_2	1.86	<0.05	1.03~2.69
x_3	105.36	<0.05	65.65~145.07
Wx effect			
x_1	22.5	0.266	-17.18~62.19
x_2	11.59	<0.05	9.33~13.83
x_3	-78.28	<0.05	-119.43~-37.13

x1: newfound area with *O. hupensis* distribution; x2: area eliminated with *O.hupensis*; x3: population in area with *O. hupensis*

Table V. Effect decomposition of the influencing factors on *O. hupensis* distribution.

	Coefficient	p value
LR_Direct		
x_1	2.02	0.92
x_2	4.16	<0.05
x_3	98.3	<0.05
LR_Indirect		
x_1	26.63	0.32
x_2	15.08	<0.05
x_3	-58.52	0.03
LR_Total		
x_1	28.65	0.49
x_2	19.23	<0.05
x_3	39.77	0.36

Discussion

In this study, we utilized Moran's I value and local Moran's I value to determine the spatial aggregation and autocorrelation of *O. hupensis* distribution area in Anhui, Hubei, Hunan, Jiangsu, Jiangxi, Sichuan, and Yunnan during 2001-2020. Results indicated that the distribution of *O. hupensis* exhibited spatial aggregation, with high-high clusters observed in Hunan, Jiangxi, and Hubei, which are also the largest endemic regions of Schistosomiasis in China. Jiangxi and Hunan boast the first and second largest freshwater lakes in China (Alene *et al.*, 2022; Jiang *et al.*, 2023), respectively, while Hubei is renowned for its numerous lakes, providing ample habitat for freshwater snails (Chen *et al.*, 2018; Zhu *et al.*, 2022). Consequently, these three provinces demonstrated the most extensive distribution of *O. hupensis*.

Previous research has also highlighted these provinces as the most severe endemic regions of Schistosomiasis. Therefore, rigorous prevention and control programs are imperative in these provinces.

Snail elimination has been an essential tool for Schistosomiasis prevention and control for many decades. Here, we found that the elimination area critically influenced the actual distribution of *O. hupensis*, with a positive main effect, positive spill-out effect, and a positive total effect. The population in endemic regions also showed a positive main effect and negative spill-out effects on the actual distribution of *O. hupensis*. However, the newfound snail distribution area showed no correlation with the real distribution of *O. hupensis*. Theoretically, the snail elimination area and population size in these regions should be negatively correlated with the actual distribution, while the newfound snail distribution should positively correlate with the actual distribution of *O. hupensis*. However, the theory contradicted the field reality while may be because schistosomiasis has been effectively controlled and prevented in China over the past decades, primarily through snail elimination, chemotherapy of patients, and positive animals (Cao *et al*., 2020; Yang *et al*., 2016). The elimination area has expanded over time, but enlarging it has become increasingly challenging in recent years. Concurrently, the rise and decline of newfound snail areas indicate the difficulty in identifying new habitat areas for *O. hupensis*. Furthermore, this study was conducted at the provincial level, and the correlation between accurate snail distribution and newfound snail areas, elimination areas, and local populations might be closer to the theoretical expectations at the county or village level. Therefore, a more detailed survey at lower administrative levels is warranted.

Thirdly, various other factors may also impact the distribution of *O. hupensis* snails, including floods, land use changes such as returning farmland to grassland, and local water conservancy projects (Wang *et al*., 2022; Xu *et al*., 2023). While significant progress has been made in the past decades, studies suggest that there is still a long way to go in eliminating Schistosomiasis in China. Moreover, recent factors have complicated the distribution of *O. hupensis*, indicating the need to discover and include more factors in future studies. Nonetheless, snail elimination remains an effective strategy for disease control and prevention, especially in provinces like Hunan, Jiangxi, and Hubei.

In summary, while Schistosomiasis is likely to be eliminated in China in the near future, the distribution area of *O. hupensis* is currently confined to some historical natural habitats. Spatial aggregation and autocorrelation may persist for a long time, underscoring the importance of continuing efforts to eliminate snails as a strategy for preventing and controlling Schistosomiasis.

Statement of conflict of interest

The authors have declared no conflict of interest.

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