

See discussions, stats, and author profiles for this publication at: <https://www.researchgate.net/publication/26766976>

Landscape Pattern Analysis and Bayesian Modeling for Predicting *Oncomelania hupensis* Distribution in Eryuan County, People's Republic of China

Article in *The American journal of tropical medicine and hygiene* · October 2009

DOI: 10.4269/ajtmh.2009.81.416 · Source: PubMed

CITATIONS

33

READS

103

8 authors, including:



Kun Yang

Chinese Center For Disease Control And Prevention

84 PUBLICATIONS 1,761 CITATIONS

[SEE PROFILE](#)



Xiao-Nong Zhou

Chinese Center For Disease Control And Prevention

742 PUBLICATIONS 14,718 CITATIONS

[SEE PROFILE](#)



Peter Steinmann

Swiss Tropical and Public Health Institute

224 PUBLICATIONS 7,629 CITATIONS

[SEE PROFILE](#)



Guojing Yang

Swiss Tropical and Public Health Institute

172 PUBLICATIONS 4,053 CITATIONS

[SEE PROFILE](#)

Some of the authors of this publication are also working on these related projects:



Towards the control of cestode zoonoses, cysticercosis and echinococcoses [View project](#)



Effects of a school-based health intervention programme in marginalized neighbourhoods of Port Elizabeth, South Africa: The KaziBantu project [View project](#)

Landscape Pattern Analysis and Bayesian Modeling for Predicting *Oncomelania hupensis* Distribution in Eryuan County, People's Republic of China

Kun Yang, Xiao-Nong Zhou,* Xiao-Hua Wu, Peter Steinmann, Xian-Hong Wang,
Guo-Jing Yang, Jürg Utzinger, and Hong-Jun Li

Jiangsu Institute of Parasitic Diseases, Wuxi, People's Republic of China; National Institute of Parasitic Diseases, Chinese Center for Disease Control and Prevention, Shanghai, People's Republic of China; Department of Public Health and Epidemiology, Swiss Tropical Institute, Basel, Switzerland; Eryuan Schistosomiasis Control Station, Eryuan, People's Republic of China

Abstract. Detailed knowledge of how local landscape patterns influence the distribution of *Oncomelania hupensis*, the intermediate host snail of *Schistosoma japonicum*, might facilitate more effective schistosomiasis control. We selected 12 villages in a mountainous area of Eryuan County, Yunnan Province, People's Republic of China, and developed Bayesian geostatistical models to explore heterogeneities of landscape composition in relation to distribution of *O. hupensis*. The best-fitting spatio-temporal model indicated that the snail density was significantly correlated with environmental factors. Specifically, snail density was positively correlated with wetness and inversely correlated with the normalized difference vegetation index and mollusciciding, and snail density decreased as landscape patterns became more uniform. However, the distribution of infected snails was not significantly correlated with any of the investigated environmental factors and landscape metrics. Our enhanced understanding of *O. hupensis* ecology is important for spatial targeting of schistosomiasis control interventions.

INTRODUCTION

Schistosomiasis is one of the most prevalent parasitic diseases in tropical and subtropical environments.¹ In the People's Republic of China, approximately 65 million persons residing along the middle and upper reaches of the Yangtze River are at risk of an infection with *Schistosoma japonicum*.^{2–4} The endemicity of *S. japonicum* is governed by the distribution of its intermediate host snail *Oncomelania hupensis*, and socioeconomic and behavioral determinants.³ Today, schistosomiasis mainly occurs in two distinct ecologic zones in China; the marshland and lakes region in the eastern and central parts of the country, and in hilly and mountainous regions in the provinces of Sichuan and Yunnan. In the latter area, snail habitats are mainly found along ditches, irrigation canals, and rivers. These snail habitats are often small and isolated from one another, and schistosomiasis transmission is highly focal.^{5–8} Data at a coarse spatial resolution therefore fail to capture local heterogeneity. Thus, such data do not enable investigating local risk factors in relation to small-scale ecologic and epidemiologic patterns.

Despite considerable progress made in the control of schistosomiasis in China,^{3,9} the disease has recently re-emerged in several counties in the mountainous area. Causes that might explain the re-emergence of schistosomiasis appear to be multifactorial and include environmental, socioeconomic, and health systems factors.^{5,10,11}

The development of new tools and improvement of existing approaches for the rapid and accurate identification of intermediate host snail habitats are critical to better target control measures using molluscicides and environmental management, as part of integrated, locally adapted control programs.^{9,12} A number of studies have shown that it is feasible to predict the regional distribution of *O. hupensis* using remote sensing (RS), geographic information system (GIS), and Bayesian geostatistical models for risk factor analysis and prediction.^{13–16} Most

studies currently rely on RS of low spatial resolution, confining their conclusions to the meso-scale and macro-scale, i.e., county, provincial, or national level. Only few studies focused on the micro-scale, i.e., individual snail habitats or village-level data.^{17,18}

The precision of spatial analyses is usually determined by the resolution of the underlying data (e.g., pixel size, time interval). High-resolution environmental data that can be readily obtained from new satellites facilitate the development of landscape ecology.¹⁹ Landscape pattern analysis is one of the most important tools of landscape ecology; it considers the environment as a mosaic of patches (landscape elements), edges (limits of areas) and corridors (connecting routes). Landscapes are regarded as the outcome of continuous interactions between their biotic and abiotic components. These landscape metrics are then used for analysis. A logical continuation of landscape ecology is landscape epidemiology, which involves identification of geographic areas where a particular disease is transmitted, and uses the landscape to identify the spatial and temporal distribution of disease risk. It is a holistic approach and investigates associations and interactions between elements of the physical and social environments, and provides a conceptual framework to study environmental determinants of disease transmission.^{20,21} Landscape pattern analysis and landscape epidemiology have been applied to various vector-borne diseases, and the effects of a number of environmental variables on the endemicity, activity, and longevity of pathogens, their vectors and intermediate hosts, and zoonotic reservoirs have been explored.^{16,20,22–24}

Previous applications of RS, GIS, and geostatistical modeling for the spatial study of schistosomiasis japonica often neglected discussing issues of sample size and spatio-temporal patterns because of statistical and computational problems. This finding is especially true for the study of *O. hupensis*. Snails, like other organisms, tend to cluster. Therefore, the contribution of spatial autocorrelation should be taken into account when predicting snail abundance. Recent progress in empirical Bayes and Bayesian hierarchical modeling provide new opportunities to overcome some of the challenges associated

*Address correspondence to Xiao-Nong Zhou, National Institute of Parasitic Diseases, Chinese Center for Disease Control and Prevention, Shanghai, People's Republic of China. E-mail: ipdzhounx@sh163.net

with the spatio-temporal patterning and focal occurrence of snails.^{25–27} Bayesian approaches have been used successfully to increase our understanding of the spatial distribution of tropical diseases and their vectors or intermediate hosts at various scales.^{27–32} For example, we have established an approach using spatial Bayesian and landscape pattern analysis for modeling *O. hupensis* distribution in mountainous regions.³³ However, in our previous work, we only included spatial but no temporal patterns.

The aims of this study were 1) to investigate the utility of landscape pattern analysis to enhance our ecologic understanding of village-scale or small scale heterogeneity of *O. hupensis*; 2) to study the relationship between village-scale variations in landscape composition and spatial variations in snail density; and 3) to identify risk factors that govern the density of *O. hupensis* in a mountainous area of western Yunnan province during over a five-year period (2000–2006). These aims were addressed by using GIS, high-resolution RS imagery, and Bayesian geospatial modeling, complemented with tools and indicators from landscape ecology.

MATERIALS AND METHODS

Study area. Historical data were used to identify natural villages around Cibi Lake in eastern Eryuan County, People's Republic of China, where *S. japonicum* prevalence is elevated. A total of 12 villages were selected. Eryuan County is located in northwestern Yunnan Province. Basic information about the county has recently been presented by Steinmann and others, who conducted a countywide survey of helminth infections, including *S. japonicum*.^{7,34} The study area is located between 26.15°N and 26.20°N and between 99.95° and 100.00°E at 1,700–1,900 m above sea level. The surface area is approximately 15 km² and the estimated population size in 2006 was 8,000 persons. The local climate and the available irrigation infrastructure, which includes rain-fed reservoirs and ditches, enable two crop cycles per year, mainly rice, corn, wheat, beans, garlic, eggplants, and tomatoes. Dairy cow farming is an important source of income (conducted by 80% of the families).

In Eryuan County, transmission of schistosomiasis occurs primarily during occupational activities (i.e., farming),³⁴ but domestic and recreational activities involving water contact at ditches also play a role. The recent local re-emergence of schistosomiasis has been attributed to different factors, including decreased funding for control; lack of coordination between the health, agriculture, and water resources sectors; increased cattle mobility through trading; and construction of additional irrigation infrastructures, which increase the potential for the spread of *S. japonicum* or the establishment of new *O. hupensis* habitats.^{10,11,35}

Data sources. Data on the distribution and ditch-level density of snails in the study area were obtained from annual reports of the local schistosomiasis control station available for 2000, 2001, 2004, 2005, and 2006. These reports include geo-referenced locations of individual ditches, which enabled us to establish a spatially and temporally-explicit snail density database. Each year, snail surveys had been carried out between March and April using a systematic sampling approach whereby the snail density was assessed every 10 m along the ditches. At each sampling location, the number of snails within a single sampling frame of 0.11 m² had been established. The

collected snails had been dissected and examined under a microscope for the presence of *S. japonicum* cercariae. The density of (infected) snails per sampling frame (0.11 m²) in individual ditches and across natural villages had been determined using the formula density of (infected) snails/0.11 m² = number of (infected) snails/number of sampling frames.

During the study period, local staff had investigated snail abundance in 554 ditches throughout the study area. Most of these ditches serve irrigation purposes. The ditches varied in length from 100 to 600 m, were 2–5 m wide, and their slopes ranged from 0° to 30° (Figure 1). Information on the year and exact location of snail control interventions using molluscicides were obtained from the available annual reports. Local mollusciciding typically involved the application of 50% niclosamide ethanolamine salt at a concentration of 2 grams/m². For subsequent data analysis, we considered mollusciciding as a dichotomous variable. The ditch characteristics (e.g., construction type, width, and depth) were recorded for individual ditch segments. Furthermore, the boundaries of each village were determined. All data were stored in a common database using FoxPro 6.0 software (Microsoft, Redmond, WA).

An area-wide ditch map was generated by tracing the ditch network on foot with a global positioning system (GPS) unit (Trimble GeoExplorer; Trimble Navigation Limited, Sunnyvale, CA). The GPS measurements were differentially corrected with data from a stationary base station (Trimble 4000 SSI), followed by an additional standard error-correction process. Mapped ditches were assigned unique codes, which subsequently were used to identify corresponding datasets in the snail density database. Each code identified a single ditch or distinctive segment thereof. This procedure enabled us to readily match recorded ditch locations with the observed ones. The spatially explicit data were displayed on a map and attribute data (i.e., snail density) were superimposed using ArcGIS version 9.0 software (Environmental Sciences Research Institute, Redlands, CA).

SPOT5 images covering the whole study area and acquired on March 16, 2006 were obtained from the China Remote Sensing Satellite Ground Station (Beijing, China). This imagery has a spatial resolution of 5 m in panchromatic mode and 10 m in colored mode. Three cloud-free Landsat-5 TM images of the study area with a spatial resolution of 30 m acquired in April 2000, April 2001, and April 2004 were obtained from the same source.

A standard supervised classification approach was used to determine the land-use types on the basis of the satellite images using Erdas Imagine version 8.6 software (ERDAS Inc., Atlanta, GA). The main classes were open water bodies, dry and paddy agricultural land, grassland, and residential areas.

The slope of each ditch within the study area was calculated on the basis of data obtained from a digital elevation model downloaded from the U.S. Geological Survey (www.usgs.gov) and using the spatial analyst module of ArcGIS version 9.0. The normalized difference vegetation index (NDVI) and wetness index were extracted from the images using Erdas. The NDVI and wetness data were standardized for each year using SPSS version 11.0 (SPSS Institute Inc., Chicago, IL). For each scene, the median NDVI and wetness within the perimeter of the study villages and along the ditches were calculated in ArcGIS version 9.0. The width of typical study ditches ranged between 2 m and 5 m. In view of the coarser spatial

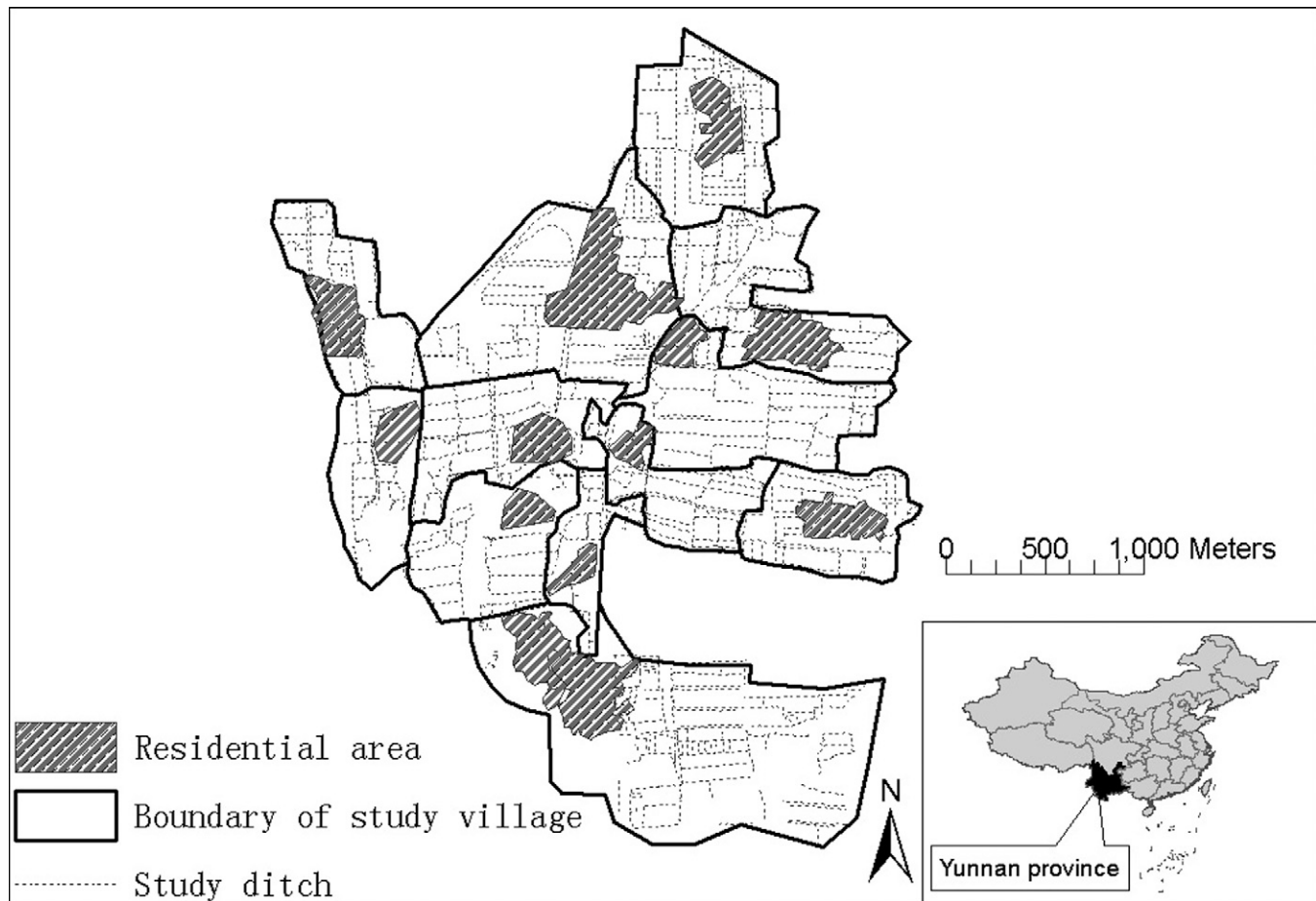


FIGURE 1. Location of study area and distribution of study ditches in Eryuan County, Yunnan Province, southwest People's Republic of China, 2006.

resolution of the available satellite images (approximately 30 m), for determining the ditch-specific values, buffer zones surrounding the ditches and equaling the resolution (pixel size) of the RS data were calculated and their mean NDVI and wetness were determined.

Landscape pattern analysis. Study village boundaries were overlaid on the map containing environmental data, and landscape metrics were determined for each natural village on the basis of the land-use image and the patches (elements) identified within the boundaries of individual villages using ArcView GIS and Patch Analyst version 2.1 (<http://flash.lakeheadu.ca/~rrempel/patch/>). Patch Analyst version 2.1 is an extension of ArcView GIS that facilitates the spatial analysis of landscape patches and the modeling of attributes associated with patches. The software recognizes more than 20 landscape metrics, which can be stratified into three indices: 1) individual patches (patch-level), 2) land cover types (class-level), and 3) the whole landscape (landscape-level). We selected landscape metrics that represented the whole landscape on the basis of their ecologic meaning. There are area/density metrics (e.g., mean patch size [MPS]), shape metrics (e.g., landscape shape index [LSI]), and diversity metrics (e.g., modified Simpson's diversity index [MSIDI]). Those used in our study are detailed in Appendix 1 (Appendix can be viewed at www.ajtmh.org).

Bayesian models. Bayesian statistical approaches were used to examine the spatio-temporal patterns of the snail distribution by using the area data in our study area at the unit of

the village. The relationship between ditch-level snail density and environmental, landscape metrics, and control-related covariates was also explored. Bayesian non-spatial, spatial and spatio-temporal Poisson models were fitted in WinBUGS (Medical Research Council Biostatistics Unit, Cambridge, United Kingdom). The deviance information criterion (DIC) was used to compare the goodness-of-fit of the models.³⁶ The model with the smallest DIC was considered the best fitting model. The parameters of the models were estimated using Markov chain Monte Carlo simulation.

We assumed that the observed snail counts O_{it} in ditch i and year t follow a Poisson distribution, that is, $O_{it} \sim \text{Poisson}(\mu_{it})$. We introduced the covariates, spatial and spatio-temporal effects on the log transformation of μ_{it} , i.e., $\log(\mu_{it})$, and developed three models for $\log(\mu_{it})$. In model 1, neither spatial nor temporal correlation was assumed, model 2 included village-specific and year-specific independent random effects, and model 3 was designed assuming spatial correlation evolving over time (space-time interaction). The models can be written as

$$\text{model 1: } \log(\mu_{it}) = \log(E_{it}) + \alpha + \sum_k \beta_k X_{itk};$$

$$\text{model 2: } \log(\mu_{it}) = \log(E_{it}) + \alpha + \sum_k \beta_k X_{itk} + u_j + v_t; \text{ and}$$

$$\text{model 3: } \log(\mu_{it}) = \log(E_{it}) + \alpha + \sum_k \beta_k X_{itk} + u_{jt}.$$

In each model, E_{it} represents the expected snail count in ditch i at time t , α is the intercept, β_k denotes the regression

coefficient, and X_{itk} is the environmental or landscape metrics covariate. In model 2, u_i and v_i represent village-specific and year-specific random effects, respectively; u_j is a random term that allows for spatially structured variation in the snail data, and v_i is a random term representing between-year variation. Spatial correlation was modeled using village-specific random effects, which were assumed to arise from a conditional autoregressive model, CAR (r), which implies that each u_j is conditional on the neighbor u_m , and follows a normal distribution with mean equal to the average of the neighboring u_m and variance equal to δ_j^2 scaled according to the number of the neighbors n_j of village j that is

$$u_j | u_{m,j \neq j} \sim N\left(r \sum_{m=1}^{n_j} u_m, \delta_j^2 / n_j\right),$$

where r quantifies the strength of spatial dependence. Temporal correlation was modeled by yearly random effects, under the assumption that they follow an auto-regressive process (1) with lag 1, assuming that temporal correlation ρ exists only with the preceding year.³⁷ In this model, spatial correlation between villages is independent of the year. In model 3, u_{jt} is the spatio-temporal random effect such that $u_{jt} \sim \text{CAR}(r_t)$ with the parameter r_t controlling the rate of decrease of spatial correlation with distance in year t .

Following a Bayesian model formulation, we adopted vague normal prior distributions for each regression coefficient β_k and intercept α , vague inverse gamma priors for variances, and a uniform prior ranging from -1 to $+1$ for spatial and temporal correlation. A two-chain Markov chain Monte Carlo simulation was used for parameter estimation. Model convergence was assessed by visual inspection of the time series plot of each parameter, and Gelman-Rubin statistics.³⁸ The inference of the parameters was based on a burn-in of 15,000 iterations of both chains after the 30,000th iteration.

Models were fitted using a randomly selected subset of the available data (training set) including 1,505 locations. The remaining data, consisting of 300 locations, were used for model validation (test set). In a first step, we compared the goodness-of-fit of the models according to DIC.³⁶ Next, we evaluated the predictive abilities of different models by calculating the relative error rate (in %) based on the posterior estimated value of the model and the observed value at each ditch as follows:

$$\text{relative error rate} = \frac{|\text{observed value} - \text{estimated value}|}{\text{observed value}} \times 100,$$

and stratified the relative error rates, e.g., 0–10% relative error. A better predictive ability was assumed if a model had a higher percentage of low relative error strata.

RESULTS

Snail habitats and density. The overall average density of snails and infected snails in our study area at the time of the surveys was 0.235 and 0.001 per 0.11 m², respectively. In 2006 and 2001, a maximum density of 22.25 snails and 0.27 infected snails per 0.11 m² was recorded.

Model selection. Table 1 shows the relative error rate of the posterior estimated value at the 300 model validation locations compared with the observed number of total and infected snails according to three different models used. The predictive ability of the models improved when spatial and/or temporal random effects were considered. However, the difference between the model considering the temporal evolution of spatial correlation and the model assuming independent spatial and temporal processes was not significant. The differences in relative error rates between the models were not uniform. These differences tended to be larger for small relative error rates when considering all snails. For infected snails, they were largest for very small and very high relative error rates.

Table 2 shows that according to DIC, the model considering spatial correlations evolving over time (DIC = 31,253.8) fitted the data better than the model assuming independent spatial and temporal random effects (DIC = 32,533.0). This finding could not be reproduced for infected snails where the DIC was 618.4 for the model with spatial correlation evolving over time and 599.2 for the model assuming independent spatial and temporal random effects (Table 3).

Factors influencing density of snails and infected snails. Tables 2 and 3 summarize the posterior estimates of the non-spatial and the two spatio-temporal models for the density of snails and infected snails, respectively. Snail density increased along with wetness and slope of the ditch, MPS, the area weighted mean patch fractal dimension (AWMPFD), and LSI. Conversely, snail density was negatively correlated with NDVI at the ditch, mean wetness of the study village, and MSIDI. The significant relationship between most covariates including recent mollusciciding, NDVI, wetness along the ditch and slope of the ditch, mean wetness at the level of the study village, and landscape metrics, i.e., largest patch index, LSI, MSIDI, and total snail density is similar in non-spatial and spatio-temporal models (Table 2).

We found a negative correlation between the density of infected snails and control measures, wetness around the ditch, and MPS. Positive correlations were found between density of infected snails and slope of the ditch and modified Simpson's evenness index (Table 3).

TABLE 1

Relative error rate of the posterior estimated value compared with the observed value of snail density and infected snail densities in 12 villages in Eryuan County, Yunnan Province, People's Republic of China, according to different models

Relative error rate, %	Snail density			Infected snail density		
	Non-spatial model	Spatio-temporal model 1*	Spatio-temporal model 2†	Non-spatial model	Spatio-temporal model 1*	Spatio-temporal model 2†
0	4.67	7.33	7.00	4.67	25.67	21.33
< 10	14.33	16.00	16.00	19.33	23.33	26.00
< 20	13.00	11.33	10.33	14.33	14.33	16.67
< 30	12.67	17.33	16.67	9.00	8.00	8.33
< 40	9.00	8.67	9.33	9.33	6.33	8.00
< 50	9.00	9.00	9.33	8.00	3.33	3.67
< 100	24.00	22.67	21.33	14.33	9.33	9.00
> 100	13.33	7.67	10.00	21.00	9.67	7.00

* Spatio-temporal model 1: independent spatial and temporal random effects assumed.

† Spatio-temporal model 2: spatial correlations evolving over time assumed.

TABLE 2

Posterior estimates of model parameters (median, 95% confidence interval [CI] or 95% Bayesian credible interval [BCI]) of non-spatial and spatio-temporal models of snail density in 12 villages of Eryuan County, Yunnan Province, People's Republic of China

Variable*	Spatio-temporal model					
	Non-spatial model		Model 1†		Model 2‡	
	Median	95% CI	Median	95% BCI	Median	95% BCI
Intercept	0.08	0.05, 0.12	0.77	0.26, 1.70	-0.11	-0.41, 0.44
Mollusciciding	-0.09	-0.13, -0.05	-0.13	-0.17, -0.08	-0.10	-0.15, -0.06
NDVI at ditch	-0.07	-0.10, -0.05	-0.07	-0.10, -0.05	-0.05	-0.07, -0.02
Wetness at ditch	0.08	0.05, 0.10	0.10	0.07, 0.12	0.06	0.03, 0.09
Slope of ditch	0.11	0.09, 0.12	0.04	0.02, 0.05	0.03	0.02, 0.04
MPS	0.36	0.26, 0.45	0.07	-0.07, 0.19	1.75	0.31, 2.59
PSSD	-0.70	-0.80, -0.60	-0.77	-0.96, -0.55	-1.90	-3.07, 0.33
AWMSI	-0.02	-0.07, 0.03	0.24	0.10, 0.37	0.15	-0.49, 0.80
AWMPFD	0.53	0.45, 0.60	0.22	-0.02, 0.44	0.96	0.29, 1.91
LPI	-0.26	-0.32, -0.19	-0.89	-1.04, -0.75	-0.64	-1.67, 0.36
LSI	0.81	0.76, 0.86	1.47	1.31, 1.70	0.56	0.07, 1.08
MSIDI	-2.23	-2.35, -2.11	-1.67	-1.89, -1.45	-2.47	-2.99, -1.51
MSEI	0.68	0.60, 0.76	0.59	0.46, 0.74	0.02	-0.40, 0.51
Proportion dry farm land	0.10	0.00, 0.20	1.16	0.93, 1.39	-0.71	-1.59, 0.78
Proportion paddy farm land	-0.55	-0.64, -0.46	-0.95	-1.13, -0.77	0.12	-1.24, 0.90
Proportion residential area	-0.13	-0.16, -0.11	0.12	0.06, 0.17	-0.14	-0.57, 0.59
NDVI at village level	0.00	-0.05, 0.05	1.05	0.90, 1.20	0.24	-0.27, 0.74
Wetness at village level	-0.62	-0.67, -0.56	-0.89	-0.99, -0.79	-1.18	-1.60, -0.53
Spatial correlation§			0.58	-0.65, 0.97		
2000					-0.90	-1.65, 0.75
2001					0.20	-1.38, 0.95
2004					-0.75	-1.61, 0.79
2005					-0.01	-1.43, 0.91
2006					-0.46	-1.56, 0.86
Spatial variation			1.94	1.34, 3.10		
2000					2.48	1.14, 4.80
2001					1.11	0.48, 2.44
2004					1.89	0.87, 3.87
2005					0.97	0.61, 1.63
2006					1.59	0.93, 2.98
Temporal correlation			0.42	-0.84, 0.96		
Temporal variation			1.84	1.06, 3.71		
DIC¶	35,576.5		32,533.0		31,253.8	

* NDVI = normalized difference vegetation index; MPS = mean patch size; PSSD = patch size standard deviation; AWMSI = area weighted mean shape index; AWMPFD = area weighted mean patch fractal dimension; LPI = largest patch index; LSI = landscape shape index; MSIDI = modified Simpson's diversity index; MSEI = modified Simpson's evenness index; DIC = deviance information criterion.

† Spatio-temporal model 1: independent spatial and temporal random effects assumed.

‡ Spatio-temporal model 2: spatial correlations evolving over time assumed.

§ Spatial correlation is a scalar parameter representing the rate of decrease of correlation with distance between points.

¶ Smaller DIC values indicate better model fit to the data.

Of note, the correlation between the proportion of the residential area and the density of infected snails is consistently and significantly positive in all models, which is different from the models considering the density of all snails. The regression coefficients of other covariates were not significant.

Spatio-temporal pattern of snail populations at village level.

Model 2 assumed that the spatial correlation between villages was stable over the entire study period. For snail density, estimates of spatial correlation r and temporal correlation ρ are 0.58 (95% Bayesian credible interval [BCI] = -0.65, 0.97) and 0.42 (95% BCI = -0.84, 0.96), respectively (see Table 2, spatio-temporal model, model 1). For density of infected snails, estimated spatial correlation r and temporal correlation ρ are -0.60 (95% BCI = -1.59, 0.82) and 0.27 (95% BCI = -0.94, 0.97), respectively (see Table 3, spatio-temporal model, model 1). Model 3 assumed village-specific temporal evolution of spatial correlation of the snail density, the parameters $r_1 - r_5$ present the spatial correlation of individual years. Their respective 95% BCIs all include zero, indicating no significant spatial and temporal correlation of snail density and infected snail density at the village level (Tables 2 and 3, spatio-temporal model, model 2).

DISCUSSION

Habitats of *O. hupensis* in mountainous areas of Sichuan and Yunnan provinces are usually small and often isolated from each other, resulting in distinct *S. japonicum* transmission foci rather than continuous disease-endemic areas.^{10,39-41} Examination of characteristics governing the observed patterns can best be achieved using statistical tools, which consider sampling variation and spatio-temporal correlation. We found that the performance of Bayesian spatio-temporal models, including the spatial and temporal neighbors in an autoregressive formulation, was superior to a non-spatial model. The habitats of the amphibious *O. hupensis* are subject to influences by different environmental factors. Our results indicate that the snail density is positively associated with wetness and negatively correlated with NDVI along ditches. This finding contradicts results from previous studies.⁴²⁻⁴⁴ One likely explanation is the small spatial scale of the study. The NDVI indicates how much vegetation is present at each location with higher values representing more intensive vegetation coverage. Values range between -1 and +1, with negative values corresponding to water bodies. At large scale, NDVI increases

TABLE 3

Posterior estimates of model parameters (median, 95% confidence interval [CI] or 95% Bayesian credible interval [BCI] of non-spatial and spatio-temporal models of infected snail density in 12 villages of Eryuan County, Yunnan Province, People's Republic of China

Variable*	Non-spatial model		Spatio-temporal model			
			Model 1†		Model 2‡	
	Median	95% CI	Median	95% BCI	Median	95% BCI
Intercept	0.19	−0.28, 0.61	−0.82	−2.17, 0.28	0.10	−0.51, 0.60
Mollusciciding	−0.90	−1.53, −0.31	−0.85	−1.50, −0.25	−0.86	−1.51, −0.25
NDVI at ditch	−0.02	−0.31, 0.30	−0.06	−0.35, 0.27	0.01	−0.28, 0.34
Wetness at ditch	−0.01	−0.35, 0.31	−0.01	−0.36, 0.32	−0.01	−0.35, 0.32
Slope of ditch	0.19	0.05, 0.29	0.14	0.01, 0.24	0.17	0.03, 0.27
MPS	−0.84	−1.95, 0.28	−1.10	−2.31, −0.01	−1.02	−2.11, 0.10
PSSD	0.70	−0.44, 1.81	1.20	0.07, 2.42	0.92	−0.24, 2.02
AWMSI	−0.42	−1.31, 0.46	−0.63	−1.53, 0.24	−0.47	−1.41, 0.39
AWMPFD	−0.09	−1.13, 0.91	0.13	−0.89, 1.16	−0.14	−1.15, 0.90
LPI	−0.22	−0.86, 0.43	−0.08	−0.75, 0.58	−0.17	−0.83, 0.48
LSI	0.44	−0.13, 1.06	0.47	−0.16, 1.13	0.39	−0.26, 1.07
MSIDI	−1.97	−3.46, −0.50	−1.85	−3.46, −0.34	−1.78	−3.33, −0.29
MSEI	1.22	0.28, 2.22	1.32	0.35, 2.33	1.17	0.22, 2.16
Proportion dry farm land	−1.24	−2.68, 0.20	−1.37	−2.93, 0.21	−1.35	−2.90, 0.30
Proportion paddy farm land	0.57	−0.64, 1.86	0.87	−0.36, 2.15	0.65	−0.67, 1.94
Proportion residential area	0.59	0.30, 0.87	0.55	0.25, 0.85	0.60	0.29, 0.91
NDVI at village level	0.23	−0.30, 0.82	0.09	−0.49, 0.72	0.15	−0.40, 0.75
Wetness at village level	0.19	−0.42, 0.80	0.29	−0.35, 0.96	0.24	−0.41, 0.88
Spatial correlation§			−0.60	−1.59, 0.82		
2000					0.77	−1.21, 0.99
2001					−0.43	−1.62, 0.92
2004					−0.40	−1.66, 0.93
2005					−0.73	−1.65, 0.88
2006					−0.40	−1.61, 0.92
Spatial variation			1.97	1.05, 3.77		
2000					3.28	1.09, 13.27
2001					0.20	0.06, 1.90
2004					0.14	0.05, 1.01
2005					0.45	0.06, 2.01
2006					0.24	0.06, 1.95
Temporal correlation			0.27	−0.94, 0.97		
Temporal variation			0.67	0.40, 1.39		
DIC¶	662.5		599.2		618.4	

* NDVI = normalized difference vegetation index; MPS = mean patch size; PSSD = patch size standard deviation; AWMSI = area weighted mean shape index; AWMPFD = area weighted mean patch fractal dimension; LPI = largest patch index; LSI = landscape shape index; MSIDI = modified Simpson's diversity index; MSEI = modified Simpson's evenness index; DIC = deviance information criterion.

† Spatio-temporal model 1: independent spatial and temporal random effects assumed.

‡ Spatio-temporal model 2: spatial correlations evolving over time assumed.

§ Spatial correlation is a scalar parameter representing the rate of decrease of correlation with distance between points.

¶ Smaller DIC values indicate better model fit to the data.

along with vegetation cover, possibly indicating more potential snail habitats, and snail density is the average from one county or large region rather than from individual snail habitats. At smaller scale, a low NDVI and high wetness values indicate the presence of water, and thus a higher probability of suitable snail habitats. The density of infected snails, however, showed no statistically significant association with NDVI and wetness. This finding indicates that different factors impact the distribution of *O. hupensis* and *S. japonicum*-infected snails. We speculate that socioeconomic factors, human and livestock population sizes, cattle farming techniques, and access to improved sanitation more strongly impact the density of infected snails than the total snail population because these factors are responsible for environmental contamination with *S. japonicum* eggs and maintenance of the parasite life cycle. Wild reservoir animals can also contribute to *S. japonicum* transmission, but they are not common in the study area.⁴⁵

Landscape pattern analysis can provide indications whether an area offers suitable habitats for *O. hupensis*. Repeated analyses and inference from comparable settings might also enable prediction of changes in the snail population resulting from ecologic transformation caused by human activities (e.g., water resources development and management^{1,46}) or deliberate tar-

geted interventions for snail control. The results of landscape pattern analyses also provide pointers for future landscape management activities with an aim to control *O. hupensis*. The snail density was inversely related to MSIDI. This finding could again be explained by specific habitat requirements of *O. hupensis*. An increased MSIDI indicates a more diverse landscape whereby the proportion of suitable snail habitats might decrease. The LSI increases as the patch types become more disaggregated.⁴⁷ Thus, edge lengths of individual patch types increase and provide more suitable snail habitats. The heterogeneity of a specific landscape impacts snail distribution. A high landscape complexity resulting from a dense network of corridors and linear elements is indicative of a higher probability for the presence of suitable snail habitats, which in turn promotes the survival and dispersal of snails. The association between the proportion of dry farmland, paddy fields, and residential areas and local snail density varied between non-spatial and spatio-temporal models, but their regression coefficients did not reach statistical significance even in the best-fitting model. Thus, identification of associations by conventional statistical methods might lead to erroneous conclusions if spatial autocorrelation is not taken into consideration. However, the proportion of residential areas was significantly

correlated with the density of infected snails. The proportion of areas occupied by residential areas might be a measure for the local land use patterns by humans and cattle, which in turn influences the extent of fecal contamination of the environment and the fraction of snails that are exposed to infection sources. Free-ranging cattle farming (for milk production) is believed to be the main source of fecal contamination in residential areas.

Our spatio-temporal analyses did not identify any significant spatial correlation r and temporal correlation ρ of the total snail population at the village level, again contradicting studies in the lake and marshland regions and in the waterway-networks environment.^{44,48} Three points are offered for discussion. First, the ecology of *O. hupensis* in mountainous areas shows distinct differences from the ecology in lake and marshland regions.⁴⁹ *O. hupensis* habitats are more isolated in mountainous regions compared with the lake and marshland zone. Second, the reference scale of the present study is smaller than that of most previous studies. Because spatial correlation might occur at small scales, i.e., within rather than between villages, the small scale in the current study was considered important but might not be small enough. The conversion of an *S. japonicum*-negative to a positive snail habitat is usually through a mobile source of infection, e.g., cattle that can bridge the gap between two otherwise isolated snail populations or the dispersal of fresh human and animal feces used as fertilizer (night soil). Third, a vigorous local re-launch of schistosomiasis control in 2004, in response to early signs of re-emergence,^{3,41} might have influenced the natural snail distribution, and thus disrupted the temporal correlation.⁴¹

The non-spatial and the best fitting spatio-temporal models showed a significant negative association between mollusciciding and *O. hupensis* density. Interestingly, the regression coefficient was higher for *S. japonicum*-infected snails than for the total snail density. This observation might indicate that mollusciciding exerts a stronger effect on the infected snail population than on the total snail density. If confirmed, this finding would indicate that by strengthening chemical snail control, it is possible to disproportionately decrease the risk of schistosomiasis japonica in humans, at least in certain environments.

It is also important to highlight the shortcomings of this study. First, we concentrated on landscape metrics and environmental variables, but did not take into account additional factors such as socioeconomic parameters and distribution of infection sources (humans, livestock), although these issues are likely to play a role in the local epidemiology of *S. japonicum*. Second, the scale of the study was the village, but we did not take into account additional factors influencing the distribution of snails within villages. Thus, spatial heterogeneity within villages was probably underestimated. Third, we concentrated on data from 2000–2006, with no data available for 2002 and 2003, thereby perhaps underestimating the true temporal correlation.

To our knowledge, this is the first study investigating the spatio-temporal pattern of *O. hupensis* densities in a mountainous area using landscape pattern analysis and Bayesian geostatistical models. Our results are encouraging and indicate that these approaches hold promise for studying snail distribution patterns in small-scale heterogeneous and complex environments typical for mountainous areas, but the scale of reference must be taken into account. Once established and validated, our approach might result in a new tool for the identification of high-risk areas of schistosomiasis japonica. Furthermore,

the methods presented here might also be adapted to the study of other vector-borne diseases that are characterized by focal distribution.

Received February 9, 2008. Accepted for publication March 10, 2009.

Note: The Appendix can be viewed online at www.ajtmh.org.

Acknowledgments: We thank the staff of the Eryuan Schistosomiasis Control Station and the Dali Institute for Schistosomiasis Control for kind collaborations and support in data collection.

Financial support: This work was supported by the National Natural Science Foundation of China (no. 30590373), the Research Foundation of the Health Department of Jiangsu Province (no. H200625), the Projects in the Science and Technology Pillar Program of Jiangsu Province (no. BS2007023), the Key Projects in the National Science and Technology Pillar Program during the Eleventh Five-Year Plan Period (2007BAC03A02), the UNDP/World Bank/World Health Organization Special Programme for Research and Training in Tropical Diseases (TDR nos. A30298 and A70530), and the National Project of Important Infectious Diseases (2008ZX10004-011). Peter Steinmann (project no. PBBSP3-123193) and Jürg Utzinger (project nos. PPOOB-102883 and PPOOB-119129) are supported by the Swiss National Science Foundation.

Authors' addresses: Kun Yang, Jiangsu Institute of Parasitic Diseases, Meiyuan117, Wuxi 214064, People's Republic of China and National Institute of Parasitic Diseases, Chinese Center for Disease Control and Prevention, 207 Rui Jin Er Road, Shanghai 200025, People's Republic of China, E-mail: jipyk76@hotmail.com. Xiao-Nong Zhou, Xiao-Hua Wu, and Xian-Hong Wang, National Institute of Parasitic Diseases, Chinese Center for Disease Control and Prevention, 207 Rui Jin Er Road, Shanghai 200025, People's Republic of China, E-mails: ipdzhouxn@sh163.net, wuxiaohua70@163.com, and rainwang111@163.com. Peter Steinmann, National Institute of Parasitic Diseases, Chinese Center for Disease Control and Prevention, 207 Rui Jin Er Road, Shanghai 200025, People's Republic of China and Department of Public Health and Epidemiology, Swiss Tropical Institute, PO Box, CH-4002 Basel, Switzerland, E-mail: peter.steinmann@unibas.ch. Guojing Yang, Jiangsu Institute of Parasitic Diseases, Meiyuan117, Wuxi 214064, People's Republic of China, E-mail: guojingyang@hotmail.com. Jürg Utzinger, Department of Public Health and Epidemiology, Swiss Tropical Institute, PO Box, CH-4002 Basel, Switzerland, E-mail: juerg.utzinger@unibas.ch. Hong-Jun Li, Eryuan Schistosomiasis Control Station, Xingyuan Road, Eryuan County 671200, People's Republic of China, E-mail: eylihongjun@sina.com.

Reprint requests: Xiao-Nong Zhou, National Institute of Parasitic Diseases, Chinese Center for Disease Control and Prevention, 207 Rui Jin Er Road, Shanghai 200025, People's Republic of China, E-mail: ipdzhouxn@sh163.net.

REFERENCES

- Steinmann P, Keiser J, Bos R, Tanner M, Utzinger J, 2006. Schistosomiasis and water resources development: systematic review, meta-analysis, and estimates of people at risk. *Lancet Infect Dis* 6: 411–425.
- Chen MG, Feng Z, 1999. Schistosomiasis control in China. *Parasitol Int* 48: 11–19.
- Utzinger J, Zhou XN, Chen MG, Bergquist R, 2005. Conquering schistosomiasis in China: the long march. *Acta Trop* 96: 69–96.
- Zhou XN, Guo JG, Wu XH, Jiang QW, Zheng J, Dang H, Wang XH, Xu J, Zhu HQ, Wu GL, Li YS, Xu XJ, Chen HG, Wang TP, Zhu YC, Qiu DC, Dong XQ, Zhao NQ, Xia G, Wang LY, Zhang SQ, Lin DD, Chen MG, Hao Y, 2007. Epidemiology of schistosomiasis in the People's Republic of China, 2004. *Emerg Infect Dis* 13: 1470–1476.
- Liang S, Seto EY, Remais JV, Zhong B, Yang C, Hubbard A, Davis GM, Gu X, Qiu D, Spear RC, 2007. Environmental effects on parasitic disease transmission exemplified by schistosomiasis in western China. *Proc Natl Acad Sci USA* 104: 7110–7115.
- Xu B, Gong P, Biging G, Liang S, Seto E, Spear R, 2004. Snail density prediction for schistosomiasis control using IKONOS and ASTER images. *Photogramm Eng Rem S* 70: 1285–1294.

7. Steinmann P, Zhou XN, Matthys B, Li YL, Li HJ, Chen SR, Yang Z, Fan W, Jia TW, Li LH, Vounatsou P, Utzinger J, 2007. Spatial risk profiling of *Schistosoma japonicum* in Eryuan County, Yunnan Province, China. *Geospatial Health* 2: 59–73.
8. Seto E, Xu B, Liang S, Gong P, Wu W, Davis G, Qiu D, Gu X, Spear R, 2002. The use of remote sensing for predictive modeling of schistosomiasis in China. *Photogramm Eng Rem S* 68: 167–174.
9. Wang LD, Chen HG, Guo JG, Zeng XJ, Hong XL, Xiong JJ, Wu XH, Wang XH, Wang LY, Xia G, Hao Y, Chin DP, Zhou XN, 2009. A strategy to control transmission of *Schistosoma japonicum* in China. *N Engl J Med* 360: 121–128.
10. Liang S, Yang C, Zhong B, Qiu D, 2006. Re-emerging schistosomiasis in hilly and mountainous areas of Sichuan, China. *Bull World Health Organ* 84: 139–144.
11. Wang RB, Wang TP, Wang LY, Guo JG, Yu Q, Xu J, Gao FH, Yin ZC, Zhou XN, 2004. Study on the re-emerging situation of schistosomiasis epidemics in areas already under control and interruption. *Chin J Epidemiol* 25: 564–567.
12. Wang L, Utzinger J, Zhou XN, 2008. Schistosomiasis control: experiences and lessons from China. *Lancet* 372: 1793–1795.
13. Gong P, Xu B, Liang S, 2006. Remote sensing and geographic information systems in the spatial temporal dynamics modeling of infectious diseases. *Sci China C Life Sci* 49: 573–582.
14. Zhou XN, Malone JB, Kristensen TK, Bergquist NR, 2001. Application of geographic information systems and remote sensing to schistosomiasis control in China. *Acta Trop* 79: 97–106.
15. Yang GJ, Vounatsou P, Zhou XN, Utzinger J, Tanner M, 2005. A review of geographic information system and remote sensing with applications to the epidemiology and control of schistosomiasis in China. *Acta Trop* 96: 117–129.
16. Brooker S, Hay SI, Bundy DAP, 2002. Tools from ecology: useful for evaluating infection risk models? *Trends Parasitol* 18: 70–74.
17. Yuan Y, Xu XJ, Dong HF, Jiang MS, Zhu HG, 2005. Transmission control of schistosomiasis japonica: implementation and evaluation of different snail control interventions. *Acta Trop* 96: 191–197.
18. Guo JG, Vounatsou P, Cao CL, Utzinger J, Zhu HQ, Anderegg D, Zhu R, He ZY, Li D, Hu F, Chen MG, Tanner M, 2005. A geographic information and remote sensing based model for prediction of *Oncomelania hupensis* habitats in the Poyang Lake area, China. *Acta Trop* 96: 213–222.
19. Gardner RH, Turner MG, O'Neill RV, 2001. *Landscape Ecology in Theory and Practice: Pattern and Process*. Bremen, Germany: Springer.
20. Kitron U, 1998. Landscape ecology and epidemiology of vector-borne diseases: tools for spatial analysis. *J Med Entomol* 35: 435–445.
21. Martens WJM, McMichael AJ, 2002. *Environmental Change, Climate and Health: Issues and Research Methods*. Cambridge, United Kingdom: Cambridge University Press.
22. Van Benthem BH, Vanwambeke SO, Khantikul N, Burghoorn-Maas C, Panart K, Oskam L, Lambin EF, Somboon P, 2005. Spatial patterns of and risk factors for seropositivity for dengue infection. *Am J Trop Med Hyg* 72: 201–208.
23. Linard C, Lamarque P, Heyman P, Ducoffre G, Luyasu V, Tersago K, Vanwambeke SO, Lambin EF, 2007. Determinants of the geographic distribution of *Puumala* virus and Lyme borreliosis infections in Belgium. *Int J Health Geogr* 6: 15.
24. Burel F, Baudry J, 2003. *Landscape Ecology: Concepts, Methods and Applications*. St. Albans, United Kingdom: Science Publishers.
25. Gelman AB, 2004. *Bayesian Data Analysis*. Boca Raton, FL: CRC Press.
26. Lawson AB, Rodeiro V, Carmen L, Browne WJ, 2003. *Disease Mapping with WinBUGS and MLwiN*. Chichester, United Kingdom: Wiley.
27. Gemperli A, Vounatsou P, Kleinschmidt I, Bagayoko M, Lengeler C, Smith T, 2004. Spatial patterns of infant mortality in Mali: the effect of malaria endemicity. *Am J Epidemiol* 159: 64–72.
28. Koukounari A, Sacko M, Keita AD, Gabrielli AF, Landouré A, Dembelé R, Clements AC, Whawell S, Donnelly CA, Fenwick A, Traoré M, Webster JP, 2006. Assessment of ultrasound morbidity indicators of schistosomiasis in the context of large-scale programs illustrated with experiences from Malian children. *Am J Trop Med Hyg* 75: 1042–1052.
29. Wang XH, Wu XH, Zhou XN, 2006. Bayesian estimation of community prevalences of *Schistosoma japonicum* infection in China. *Int J Parasitol* 36: 895–902.
30. Basáñez MG, Marshall C, Carabin H, Gyorkos T, Joseph L, 2004. Bayesian statistics for parasitologists. *Trends Parasitol* 20: 85–91.
31. Raso G, Vounatsou P, Gosoni L, Tanner M, N'Goran EK, Utzinger J, 2006. Risk factors and spatial patterns of hookworm infection among schoolchildren in a rural area of western Côte d'Ivoire. *Int J Parasitol* 36: 201–210.
32. Yang GJ, Vounatsou P, Zhou XN, Tanner M, Utzinger J, 2005. A Bayesian-based approach for spatio-temporal modeling of county level prevalence of *Schistosoma japonicum* infection in Jiangsu province, China. *Int J Parasitol* 35: 155–162.
33. Yang K, Wang XH, Yang GJ, Wu XH, Qi YL, Li HJ, Zhou XN, 2008. An integrated approach to identify distribution of *Oncomelania hupensis*, the intermediate host of *Schistosoma japonicum*, in a mountainous region in China. *Int J Parasitol* 38: 1007–1016.
34. Steinmann P, Zhou XN, Li YL, Li HJ, Chen SR, Yang Z, Fan W, Jia TW, Li LH, Vounatsou P, 2007. Helminth infections and risk factor analysis among residents in Eryuan County, Yunnan Province, China. *Acta Trop* 104: 38–51.
35. Li XB, 2006. Analysis for schistosomiasis status of Eryuan County from 2000 to 2004. *Parasit Infect Dis* 4: 148–149.
36. Spiegelhalter DJ, Best NG, Carlin BP, van der Linde A, 2002. Bayesian measures of model complexity and fit. *J R Stat Soc B* 64: 583–639.
37. Box GE, Jenkins GM, Reinsel GC, 1994. *Time Series Analysis: Forecasting and Control*. Third edition. San Francisco, CA: Prentice Hall.
38. Gelman A, Rubin DB, 1992. Inference from iterative simulations using multiple sequences. *Stat Sci* 7: 457–472.
39. Gurarie D, King CH, 2005. Heterogeneous model of schistosomiasis transmission and long-term control: the combined influence of spatial variation and age-dependent factors on optimal allocation of drug therapy. *Parasitology* 130: 49–65.
40. Jiang Z, Zheng QS, Wang XF, Guan LZ, Hua HZ, 1997. Analysis of social factors and human behavior attributed to family distribution of schistosomiasis japonica cases. *Southeast Asian J Trop Med Public Health* 28: 285–290.
41. Zhou XN, Wang LY, Chen MG, Wu XH, Jiang QW, Chen XY, Zheng J, Utzinger J, 2005. The public health significance and control of schistosomiasis in China: then and now. *Acta Trop* 96: 97–105.
42. Zhou XN, Li DD, Yang HM, Chen MG, Sun LP, Yang GJ, Hong QB, Malone JB, 2002. Use of Landsat TM satellite surveillance data to measure the impact of the 1998 flood on snail intermediate host dispersal in the lower Yangtze River Basin. *Acta Trop* 82: 199–205.
43. Kristensen TK, Malone JB, McCarroll JC, 2001. Use of satellite remote sensing and geographic information systems to model the distribution and abundance of snail intermediate hosts in Africa: a preliminary model for *Biomphalaria pfeifferi* in Ethiopia. *Acta Trop* 79: 73–78.
44. Zhang ZY, Xu DZ, Zhou XN, Zhou Y, Liu SJ, 2005. Remote sensing and spatial statistical analysis to predict the distribution of *Oncomelania hupensis* in the marshlands of China. *Acta Trop* 96: 205–212.
45. Li F, Xia DG, Ma CH, Jia XM, Zhang XZ, 1999. Reappearance of infected snails in positive snail spots in a mountainous region of Yunnan province. *J Appl Parasit Dis* 7: 61–64.
46. Li YS, Raso G, Zhao ZY, He YK, Ellis MK, McManus DP, 2007. Large water management projects and schistosomiasis control, Dongting Lake region, China. *Emerg Infect Dis* 13: 973–979.
47. Herzog F, 2001. Landscape metrics for assessment of landscape destruction and rehabilitation. *Environ Manage* 27: 91–107.
48. Yang GJ, Zhou XN, Wang TP, Li DD, Hong QB, Sun LP, 2002. Spatial autocorrelation analysis on schistosomiasis cases and *Oncomelania* snails in three provinces of the lower reach of Yangtze River. *Chin J Parasitol Parasit Dis* 20: 6–9.
49. Davis GM, Wilke T, Zhang Y, Xu XJ, Qiu CP, Spolsky C, Qiu DC, Li Y, Xia MY, Feng Z, 1999. Snail-Schistosoma, Paragonimus interactions in China: population ecology, genetic diversity, coevolution and emerging diseases. *Malacologia* 41: 355–377.