

CHAPTER 4

Implementing a Geospatial Health Data Infrastructure for Control of Asian Schistosomiasis in the People's Republic of China and the Philippines

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Abstract

This review focuses on implementing a geospatial health infrastructure for control of schistosomiasis and other helminthic infections in Southeast Asia, with special focus on the People's Republic of China and the Philippines, using a model working group approach. Health workers have lagged in utilization of geospatial analysis and widely available, low-cost spatial data resources for epidemiological modelling and control programme management. The critical limitation on development of useful health applications to date has not been the availability of geospatial data and methods. Rather, the key barriers have been the speed of adoption of geospatial analysis tools by health scientists and the quality of geographic information system (GIS)-friendly medical databases. Regional GIS applications on Asian schistosomiasis are reviewed to illustrate recent geospatial health analysis applications. A model programme is presented for implementation of training programmes and establishment of regional working groups to facilitate development and use of geospatial health infrastructure resources by health workers in Southeast Asia.

4.1. INTRODUCTION

Global availability of geospatial health resource data and improved software analysis methodologies have enabled unprecedented, low-cost development of digital 'health maps' and transmission models for tropical diseases. With relatively modest investment in resources it is now possible for health workers in developing countries to depict where and when health problems may arise and how to better target control interventions (Malone, 2005). There has been steady progress in new research that indicates it is possible to develop useful geospatial models integrated with geographic information systems (GIS) for both epidemic and endemic diseases, including malaria (Hay et al., 2009; Thomson and Connor, 2001), Rift Valley Fever (Linthicum et al., 1987), schistosomiasis (Zhou et al., 2008a), soil-transmitted helminthiasis (Brooker et al., 2006) and leishmaniasis (Nieto et al., 2006). There has been a corresponding increase in interest by Ministries of Health in implementing a national geospatial health infrastructure as a routine part of operational programmes.

Health workers have lagged in utilization of geospatial analysis and widely available spatial data resources, much of which came at a cost of many millions of dollars by the United States, the European Union, the United Nations and other international agencies. This situation is changing with efforts by the United States Geological Survey (USGS) and international partners to develop a Global Spatial Data Infrastructure (www.GSDI.org) and Internet access to satellite imagery such as MODIS (Moderate Resolution Imaging Spectroradiometer), ASTER (Advanced Spaceborne Thermal Emission and Reflection Radiometer) and SRTM (Shuttle Radar Topography Mission) at minimal expense or nominal cost. For example, the increasing availability of Earth-observing satellite time-series data prompted by the needs of ecosystem scientists, the global climate change community, agriculturists and disaster management workers for remote sensing (RS) data and current climate data has provided public-access data resources needed for development of models of disease to generate dynamic, 'near real-time' map reports. The data needs for 'famine early warning' systems (Verdin et al., 2005) in East Africa are not fundamentally different from that needed for regional-scale disease predictions. The critical limitation on development of useful health applications to date has not been the availability of geospatial data and methods. Rather, the key barriers have been the speed of adoption of geospatial analysis tools by health scientists and the quality of GIS-friendly medical databases.

4.2. REGIONAL GEOSPATIAL HEALTH CAPABILITY

Establishing a geospatial health capability typically involves a three-step process—compilation of GIS layers of archival spatial data relevant to health applications, development of data layers on health surveillance systems and creation of control programme decision support systems (Brooker et al., 2006).

4.2.1. Minimum medical GIS databases

Public domain satellite imagery data (e.g. Landsat, MODIS and SRTM) and point, line or polygon feature (vector) data on the environment (e.g. climate, hydrology, ecological zone and soil), administrative/political boundaries (e.g. Africa Data Dissemination Service), infrastructure (e.g. roads and railroads) and populated places that will be useful for nearly any health GIS project may be archived as an open data resource and then supplemented with additional data depending on the application and the biology of the disease agent, for example, environmentally sensitive vector-borne agents versus agents spread by contact.

At a team residency sponsored by the Rockefeller Foundation in Bellagio and arranged in Italy on 10–14 April 2000, an organizational plan was conceived to create a global network of collaborating health workers and earth scientists dedicated to the development of computer-based models that can be used for improved control programmes for schistosomiasis and other snail-borne diseases of medical and veterinary importance (Malone et al., 2001). Agreement was reached on the use of compatible GIS formats, software, methods and data resources, including the creation of a ‘minimum medical database’ to enable seamless incorporation of results from each regional GIS project into a global spatial decision support systems model. Already compiled ‘off-the-shelf’ regional data is available upon request on CDROM or DVD or by download from organization websites, such as the Global Network for Geospatial Health (www.gnosisgis.org), the Environmental Systems Research Institute (www.esri.com) or national-local government sites.

One of the main outputs was the ‘Asia Minimum Medical GIS Database’ (MMDb) in collaboration with the Regional Network on Asian Schistosomiasis and Other Important Zoonotic Helminthes (RNAS+, www.rnas.org.cn), in which spatial data collected from public domain sources was compiled and standardized in decimal degree format, including (1) satellite images covering areas of Asia; (2) digital maps of Asia in vector files and (3) diseases databases and relevant models. Satellite images in the database include normalized difference vegetation index (NDVI) images from advanced very high resolution radiometer (AVHRR), land surface temperature (LST) images from AVHRR, GTOPO30 Digital Elevation Model (DEM) images from USGS and land use images from USGS. Digital vector files for GIS analysis collected include data on political boundaries (county, provinces and country), environmental features (drainage, land cover and soil type), population and climate. Data on diseases were mainly generated from survey or case reports. Relevant models on transmission of *Schistosoma japonicum* and models of *Oncomelania hupensis*, with selected higher resolution imagery (e.g. Landsat), were developed as case study examples, and relevant environmental factors related to schistosomiasis were mapped, to test and verify the usefulness of the database.

4.2.2. Health data

It is becoming routine practice to geolocate health infrastructure facilities (e.g. rural clinics, hospitals and service area) and survey/study sites in Asia and Africa in the field, and to map available surveillance data using handheld global positioning systems (GPS) units. Medical workers often have additional access to decades of excellent published field and laboratory studies, but much data in the early literature are imprecisely located by

geographic coordinates, and often must be looked up by name or other identifiers of study site in gazetteer databases such as the NIMA GEOnet Names Server (www.nima.mil) before it is useful in a GIS spatial decision support system for a given disease agent. More recently, virtual globe technologies, Google Earth™ and Google Maps™ in particular, have come into use for capturing point and polygon coordinates of health data records and for visualizing, exploring and disseminating health data (Stensgaard et al., 2009).

4.2.3. Decision support systems

Commercial and public domain spatial analysis software and spatial statistics packages, such as WinBUGS (London, UK) for Bayesian statistics (Raso et al., 2007), SaTScan™ (New York, NY) for time–space data analysis (Kulldorff et al., 2005), Neural Solutions (Gainesville, FL) for neural networks analysis (Kiang et al., 2006) and the Genetic Algorithm for Rule-set Prediction (GARP, <http://www.lifemapper.org/desktopgarp>; Nieto et al., 2006) are coming into wide use for development of disease risk prediction models (Box. 4.1). Using these programmes, it is possible to develop probability maps of disease risk using only limited case records and environmental databases so that researchers can define the spatial distribution of diseases by extrapolation to areas where quality health data does not yet exist; results are based on the ecological features found at points of known distribution and abundance.

Decision support systems must then be developed based on the biologic preferences and limits of tolerance of specific disease systems within a given environmental/ecological context. Environmental satellite imagery data and feature data resources are currently available for use in a GIS at spatial resolutions appropriate for studies ranging from continental/regional scale (e.g. 1 km², MODIS), agricultural field scale (e.g. 15–30 m², Landsat ETM+) or habitat scale analysis (e.g. 0.6–4 m², QuickBird).

A closer collaboration between groups such as RNAS+, the Global network for Geospatial Health and the Global Spatial Data Infrastructure Association (www.gisd.org) can play a central role in promoting the routine use of geospatial models in health decision-making processes (Zhou et al., 2002). A joint platform would not only serve the regional control programmes but also be instrumental in establishing geospatial health training programmes and trans-boundary working groups for regional health scientists, for example, groups interested in the neglected tropical diseases.

An increasing number of studies on Asian schistosomiasis and other zoonotic helminths are being developed and initiated with emphasis on GIS, RS and GPS applications and geospatial analysis approaches. A spatial database on multiparasitic infections, including geostatistics (spatial point pattern analysis and cluster analysis), has been proposed for Southeast Asia (Steinmann et al., 2007, 2010).

BOX 4.1

WinBUGS: The BUGS (Bayesian inference Using Gibbs Sampling) project is concerned with flexible software for the Bayesian analysis of complex statistical models using Markov chain Monte Carlo (MCMC) methods. The project began in 1989 in the MRC Biostatistics Unit and led initially to the 'Classic' BUGS programme, and then onto the WinBUGS software developed jointly with the Imperial College School of Medicine at St Mary's, London. Development now also includes the OpenBUGS project in the University of Helsinki, Finland (<http://www.mrc-bsu.cam.ac.uk/bugs/welcome.sh>).

SaTScanTM: It is a free software that analyses spatial, temporal and space-time data using the spatial, temporal or space-time scan statistics. It is designed for any of the following interrelated purposes: (1) Perform geographical surveillance of disease, to detect spatial or space-time disease clusters, and to see if they are statistically significant. (2) Test whether a disease is randomly distributed over space, over time or over space and time. (3) Evaluate the statistical significance of disease cluster alarms. (4) Perform repeated time-periodic disease surveillance for early detection of disease outbreaks. The software may also be used for similar problems in other fields such as archaeology, astronomy, botany, criminology, ecology, economics, engineering, forestry, genetics, geography, geology, history, neurology or zoology (<http://www.satscan.org/>).

Neural Solutions: Neural Solutions is a U.K. consultancy specializing in research, development and deployment of Artificial Intelligence and Electronic Commerce solutions, with a particular emphasis on Dynamic Pricing and the building of information-searching robots that trawl the Internet. Typical projects make use of one or more of the following techniques: neural networks, linear analysis, genetic algorithms, genetic programming, genetic optimization, pattern recognition, data fusion, data mining, web bots and autonomous agents. Web-based solutions deploy these solutions alongside content management-based software (cms) consisting of a scripting language and a database system. Either a general purpose cms is used (such as eZ publish or Drupal) or a bespoke solution is produced using typically css, php and mySql (<http://www.neuralsolutions.co.uk/>).

Genetic Algorithm for Rule-set Prediction (GARP): To predict the range of each of eleven chameleon species, GARP develops a random set of mathematical rules based on the environmental characteristics at a species occurrence point—rainfall, temperatures, elevation, etc. A rule might be "Where rainfall and temperature are high, this chameleon species will exist," or "Where elevation is higher than 900 m, this

species will not exist.” To GARP, each of those rules is a gene, which it combines in random ways to produce hundreds of possible models of where a species should and should not live (<http://earthobservatory.nasa.gov/Features/Chameleons/chameleons3.php>).

4.2.4. Applications of modelling

Recent studies have undertaken advanced modelling of schistosomiasis prevalence and incidence using random-effects modelling, spatio-temporal modelling, Bayesian modelling and transmission dynamic modelling (Yang et al., 2005a,b). A Bayesian approach employing *S. japonicum* prevalence data in the endemic counties of Jiangsu province between 1990 and 1998, proved useful to document the progress of control interventions and to better understand the relationship of climatic and environmental features and the frequency distribution of the disease (Yang et al., 2005a).

In a study aimed at overcoming the uncertainties of immunological diagnostics (an antibody-based ELISA (enzyme-linked immunosorbant assay)) and a parasitological test (Kato-Katz) (Doenhoff et al., 2004; Ross, et al., 2001; Wu, 2002) in the detection of *S. japonicum* infection, Wang et al. (2006) developed a Bayesian approach to estimate the community prevalences of *S. japonicum* infection in People's Republic of China (P.R. China). Bayesian hierarchical models incorporating random effects to reflect the nested data structure and uncertainty about test properties were employed to analyse the data. The outcome suggested that using data from ELISA alone or both ELISA and Kato-Katz tests resulted in similar prevalence estimates. The study confirmed the heterogeneity in the prevalence of *S. japonicum* infection as it was found that the estimated prevalence of *S. japonicum* infection in the sampled villages ranged from 0.02% to more than 50% (posterior median); the same variation of the prevalence estimates was observed among provinces (Wang et al., 2006). Results indicated that the disease remains a threat in some areas along the Yangtze River although great achievements have been made in the control programme of schistosomiasis in P.R. China.

Other investigations employing GIS and RS technology have focused on control strategy formulation after a long period of research in developing tools in the laboratory. For example, Chen et al. (2007) explored the application of spatial analysis to formulation of the strategy for schistosomiasis control in different environmental settings in P.R. China and found that the second-order ordinary Kriging approach of spatial analysis was an optimum method to predict human prevalence of *S. japonicum*

infection. A total of four strata of transmission areas were classified based on human prevalence to evaluate different candidate strategies to control transmission of schistosomiasis based on different environmental settings for each stratum in Dangtu County, P.R. China. The approach of predicting the spatial distribution of human prevalence of *S. japonicum* infection supported by spatial analysis was useful for formulation of strategies for schistosomiasis control in different environment settings at the county level.

Wu et al. (2007) performed correlation and regression analyses using data from the three national sampling surveys on schistosomiasis, carried out in 1989, 1995 and 2004, and established a geographical information system for use in spatial analyses to identify the high-risk areas of schistosomiasis in P.R. China. It was found that schistosomiasis is mainly distributed along the marshlands along the Yangtze River, and a positive correlation (Spearman correlation coefficient) that decreased over time was shown to exist between the infection prevalence in humans and in bovines. These results suggested that future schistosomiasis control efforts in P.R. China should more vigorously address the important role of bovines in the transmission of human schistosomiasis and the need to reduce environmental contamination of *S. japonicum* eggs by bovines. In 2009, Wang et al. described a comprehensive control strategy to control transmission of *S. japonicum* in P.R. China. The strategy includes elimination of environmental contamination of snail habitats by bovines as well as humans as central components of the comprehensive control strategy. These interventions have been adopted as a national strategy to control schistosomiasis in P.R. China.

The geospatial approaches to control of Asian schistosomiasis described earlier indicate that similar methods may ultimately be applied to research or control of other helminth zoonoses and that exploration of potential new applications of GIS and RS techniques is warranted. Use of quantitative GIS, WebGIS and emerging satellite information are new technologies that hold promise for enhanced infection risk mapping and disease prediction.

Additional GIS applications on Asian schistosomiasis in P.R. China and the Philippines are reviewed subsequently to illustrate the potential value of development and utilization of a regional geospatial health infrastructure by health workers in Southeast Asia.

4.3. GEOSPATIAL HEALTH APPLICATIONS IN P.R. CHINA

For the purposes of this review, geographic scales referenced are defined as: Micro (village), Meso (county or province) and/or Macro (national) level.

4.3.1. GIS applications at micro-level

Geospatial studies on schistosomiasis, have been carried out in P.R. China in different scales and with varying approaches but mainly focused on transmission. For example, the risk factors of transmission were explored from 2001 to 2004 in the Yangtze River valley employing infection data from human populations, cattle and the distribution of intermediate host snails. The vector layer of the distribution of fresh water bodies was extracted from a SPOT5 Satellite Pour l'Observation de la Terre (SPOT 5) image at a county level, and a spatial data set created by ArcGIS was established by SAS to analyse the spatial relationship among the variables studied (Chen et al., 2007). The results showed that 90% of all villages where the infection rate was above zero were located at a distance to water less than 1404 m. The rank regression model between the human infection rate (Y) and the snail infection rate (X_1), the cattle infection rate (X_2), the distance to water bodies (X_3) could be calculated from the equation: $Y = 42.19079 + 0.29026X_1 + 0.45365 X_2 - 0.47765X_3$. Among the three factors, the distance to water turned out to be the most important with regard to the human infection rate, followed by the cattle infection rate and the snail infection rate (in that order). Indeed, these three factors could explain 60.5% of the whole variation of the population prevalence.

4.3.2. GIS applications at meso-level

Other prominent GIS applications have been the prediction of infection risk due to ecological transformations, particularly those induced by floods and water resource developments, and the potential impact of climate change. For instance, to develop a regional climate-hydrology GIS model at the provincial level that can be used to predict short-term and long-term risk of schistosomiasis in the lower Yangtze River Basin, a model was established to predict the outbreak of the disease from environmental changes using historic terrestrial climate data and data from sensors on earth-observing satellites. The results indicated that in areas with an arbitrarily chosen risk index over 900, schistosomiasis can become established, since it is possible for the parasite to complete the development and reproduction stage in the snail intermediate host. In areas with a risk index over 1200, outbreaks of schistosomiasis were likely to occur. The forecast model and forecast map were evaluated by logistic regression analysis of Jiangsu province field prevalence data, which indicated a significant relationship to forecast predictions with an 88.9% correct classification rate (Zhou et al., 2001).

4.3.3. GIS applications at macro-level

In order to predict the intensity and scale of impact of global warming on the transmission of *schistosomiasis japonica* in P.R. China, a GIS database based on climate data from 193 climate stations in P.R. China from 1951 to 2000 was created to analyse the tendency of average daily temperature trends. The climate-transmission model was established for the entire country using spatio-temporal predictions to visualize the distribution of the *O. hupensis* snail host and the *S. japonicum* parasite, respectively. These maps showed the potential distribution of schistosomiasis in P.R. China in 2030 and 2050 and predicted that the expansion of schistosomiasis northward would be caused directly by global warming. Indeed, this type of study based on biological modelling (Fig. 4.1) shows very clearly the risk for dispersal northward of schistosomiasis, to facilitate decision-makers to locate areas for intensive surveillance. Under the scenario of all other contributing factors remaining unchanged, the models predict that a large proportion of the human population in these areas would be at risk (Zhou et al., 2008a). Thus, even a moderate temperature increase would contribute to adding tens of millions of people to those already at risk in the country.

4.3.4. Disease mapping and transmission modelling

Table 4.1 summarizes the different studies that applied GIS and RS technologies for infection risk mapping and transmission modelling of schistosomiasis in P.R. China. For each study, its aim, area, method and scale of application, and key environmental, demographic and/or epidemiological parameters are given. The majority of these studies focused on the meso (county or province) and/or macro (national) level.

4.3.5. Identification of risk areas

The frequency and transmission dynamics of *S. japonicum* is intimately linked with the distribution of *O. hupensis*, which in turn is a result of the distribution and abundance of suitable snail habitats that consist of an appropriate mix of vegetation and aquatic environments. Table 4.2 summarizes the studies published to date with an emphasis on identifying snail-infested areas through appropriate combinations of GIS and RS technologies. The majority of studies focused on the micro (village) or meso (county or province) scale.

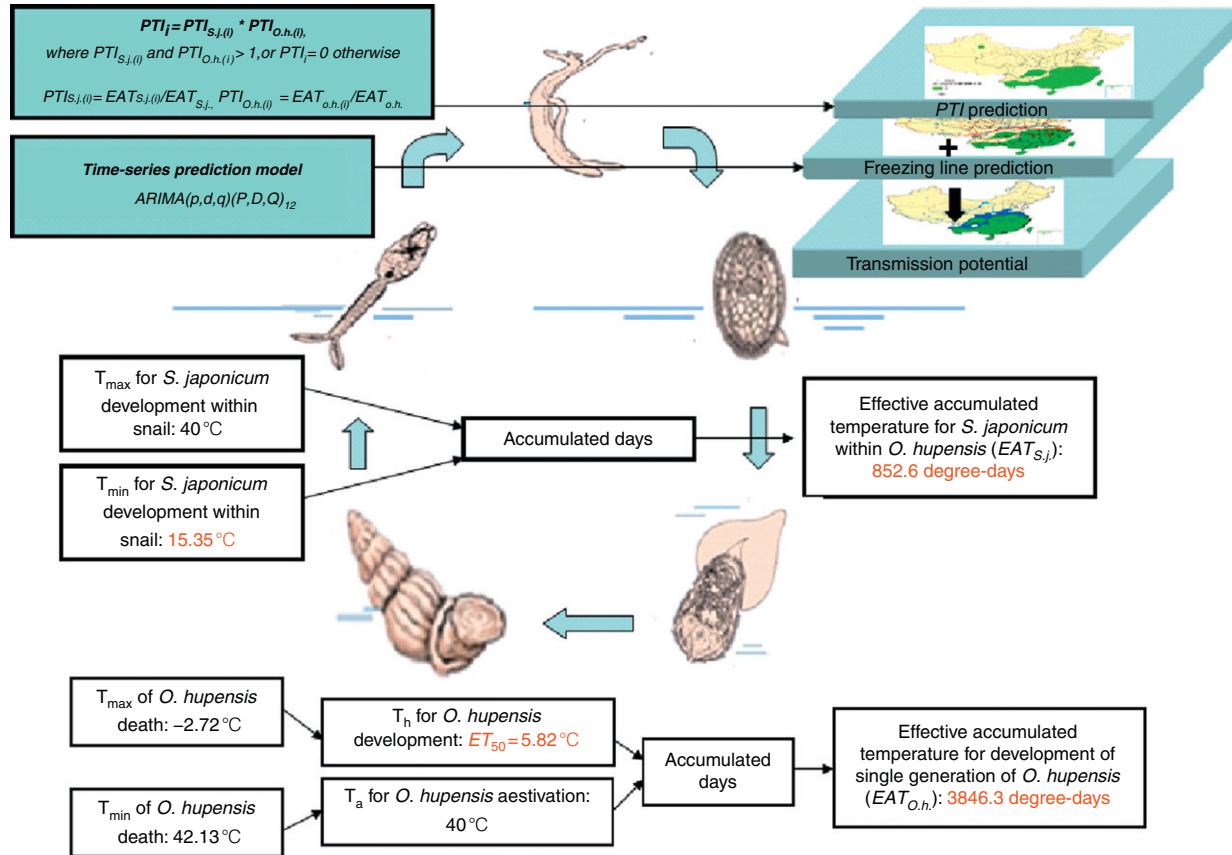


FIGURE 4.1 Biology-driven model to assess the effect of temperature on individual components of the transmission cycle of *Schistosoma japonicum*. From Zhou et al. (2008a), with permission.

TABLE 4.1 GIS and RS applications for schistosomiasis in P.R. China: disease mapping and transmission modelling

Reference (author, year)	Study aim	Area	Application		Data sources and parameters	
			Method	Scale	Environmental factors	Demographic and/or epidemiological factors
Maszle et al. (1998)	To assess hydrological models in transmission areas severely affected by schistosomiasis	Villages of Minhe and Hexing in Sichuan province	GIS modelling	Micro	Air, water and soil temperature, rainfall, irrigation networks and natural drainage systems	Disease incidence, residential location, water contact information and snail population densities, cercariae detection data
Zhou et al. (1998)	To predict the spatial transmission risk of schistosomiasis	Southern P.R. China	GIS modelling	Meso–macro	Temperature, rainfall, evaporation	–
Zhou et al. (1999a)	To identify ‘hotspots’ of high transmission intensity	Jiangsu province and adjacent areas	GIS modelling	Meso	NDVI, climate risk index, earth surface temperature and mean minimum temperature in January	Disease prevalence

Zhou et al. (2000)	To map the spatial distribution of schistosomiasis	P.R. China	GIS modelling	Macro	–	National sampling surveys in 1989 and 1995
MOH (2002)	To evaluate the impact of schistosomiasis control activities granted through the WBLP	Seven provinces in P.R. China	GIS mapping	Meso–macro	Wealth of environmental data accumulated during the implementation of the 10-year WBLP	Wealth of demographic and epidemiological data accumulated during the implementation of the 10-year WBLP
Liang et al. (2002)	To provide a framework for quantification of site-specific characterization of schistosomiasis transmission.	Chuanxing, Sichuan province	GIS modelling	Micro	Local environmental data	Residents' infection status and infection intensity, snail population densities
Yang et al. (2002)	To display and analyse time-series data	Anhui, Jiangsu and Jiangxi provinces	GIS mapping	Meso	–	Prevalence data of <i>S. japonicum</i> from 1980 to 1998
Chen et al. (2003)	To map schistosomiasis endemic areas	P.R. China	GIS mapping	Macro	–	Prevalence data of <i>S. japonicum</i> in 2002

(continued)

TABLE 4.1 (continued)

Reference (author, year)	Study aim	Area	Application		Data sources and parameters	
			Method	Scale	Environmental factors	Demographic and/or epidemiological factors
Yang et al. (2005a)	To examine spatio-temporal distribution of <i>S. japonicum</i> infection risk	Jiangsu province	GIS modelling	Meso	NDVI, land surface temperature	Annual prevalence data of <i>S. japonicum</i> from 1990 to 1998
Niu et al. (2005)	To develop schistosomiasis database and geographic distribution map	Zhongxiang city, Hubei province	GIS, RS	Micro	Correlated climate and hydrology data for the last 30 years	Epidemiological data of schistosomiasis for 30 years
Gong et al. (2006)	Using schistosomiasis as an example to simulate the spatio-temporal dynamics model of infectious diseases	Xichang, Sichuan province	RS, GIS spatial modelling	Micro	Elevation	–

Chen et al. (2007)	To explore the spatial transmission risk of schistosomiasis	Dangtu county, China	RS, GIS mapping	Micro	Different environmental settings	Human prevalence of schistosomiasis at the village level from 2001 to 2004
Steinmann et al. (2007)	To map and predict the seroprevalence of <i>S. japonicum</i>	Eryuan county, Yunnan province	RS, GIS modelling	Micro	Environmental factors, that is, location of village, altitude, slope, land surface temperature and NDVI	Local seroprevalence and demographic (i.e. age and sex), and socio-economic factors
Wu et al. (2007)	To understand the spatio-temporal relationship between the prevalence of human and bovine schistosomiasis	P.R. China	GIS modelling and mapping	Macro	–	National sampling surveys on schistosomiasis in 1989, 1995 and 2004
Zhang et al. (2008a)	To identify high-risk regions of schistosomiasis	Guichi, Anhui province	Disease mapping and spatial cluster analysis	Micro	–	Acute schistosomiasis cases from 2001 to 2006

(continued)

TABLE 4.1 (continued)

Reference (author, year)	Study aim	Area	Application		Data sources and parameters	
			Method	Scale	Environmental factors	Demographic and/or epidemiological factors
Raso et al. (2009)	To spatially model the effect of demographic, reservoir hosts and environmental factors on human <i>S. japonicum</i> infection prevalence	Dongting Lake area of Hunan province	Spatial modelling	Micro	Environmental factors, that is, NDVI, distance to the lake and endemic type of setting	Cross-sectional serological, coprological and demographic data from 2004 nationwide periodic epidemiologic survey. Age, sex and occupation of residents and the presence of infected buffaloes
Zhang et al. (2009a)	To identify high-risk regions of schistosomiasis	Guichi, Anhui province	Multiplicative and additive models with kernel density methods	Micro	–	Acute schistosomiasis cases among permanent residents of Guichi region between 2001 and 2006

Zhang et al. (2009b)	To locate active transmission sites (ATS) of schistosomiasis by combining the approaches of identifying high-risk regions for schistosomiasis and extracting snail habitats	Guichi, Anhui province	GIS modelling	Meso	Elevation, slope, distance, normalized difference water index (NDWI), NDVI, land surface temperature	Human behavioural factors
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TABLE 4.2 GIS and RS applications for schistosomiasis in P.R. China: identification of risk areas due to the presence of *O. hupensis*, the intermediate host snail of *S. japonicum*

Reference (author, year)	Study aim	Area	Application		
			Method	Scale	Data
Li et al. (1990)	To identify <i>O. hupensis</i> habitats	Xichang, Chengdu and three Gorges area	RS	Meso	MSS in 1976 and 1978, aerial images in 1982 and 1984
Chen and Hu (1991)	To identify risk areas due to the presence of <i>O. hupensis</i>	P.R. China	RS	Macro	Landsat MSS and NOAA
Tu and Wang (1995)	To identify <i>O. hupensis</i> habitats	Marshlands	RS	Meso	Landsat MSS in 1979 and TM in 1987
Zheng et al. (1998a)	To assess the effect of climatic factors on the ecology of <i>O. hupensis</i>	P.R. China	GIS	Macro	Snail data, climate data
Zheng et al. (1998b)	To determine the relationship between floods and snail distribution	Xinzi, Jiangxi province	GIS	Micro	Snail data, annual flooding records

Zhou et al. (1999b)	To determine the relationships between the distribution of <i>O. hupensis</i> and snail population genetics	P.R. China	GIS	Macro	Snail distribution and snail population genetics
Lin and Lin (2001)	To create land cover map of <i>O. hupensis</i> habitats in the marshland region	Chayegang, Jiangxi province	RS	Micro	Landsat TM
Guo et al. (2002)	To identify <i>O. hupensis</i> habitats	Poyang Lake, Jiangxi province	RS	Micro	Landsat TM images in 1998
Lin et al. (2002)	To assess the impact of the 1998 flood on the <i>O. hupensis</i> distribution in the marshland around the Poyang Lake	Poyang Lake, Jiangxi province	RS	Micro	Landsat TM images in 1998
Seto et al. (2002)	To assess the effect of soil chemistry on the distribution of <i>O. hupensis</i>	Sichuan province	RS	Meso	Landsat TM

(continued)

TABLE 4.2 (continued)

Reference (author, year)	Study aim	Area	Application		
			Method	Scale	Data
Wu et al. (2002)	To identify <i>O. hupensis</i> habitats	Poyang Lake, Jiangxi province	RS	Micro	Landsat TM image in 1999 and 2001
Zhang and Xu (2003)	To explore the vegetation landscapes in marshland snail habitats	Jiangning, Jiangsu province	RS	Micro	Landsat ETM+ image
Zhang (2003)	To analyse the relationship between NDVI and the distribution of <i>O. hupensis</i>	Jiangning, Jiangsu province	RS, GIS	Micro	Terra-MODIS
Guo et al. (2005)	To predict <i>O. hupensis</i> habitats	Poyang Lake, Jiangxi province	RS, GIS	Meso	Landsat TM image for dry and wet seasons
Zhang et al. (2005)	To predict <i>O. hupensis</i> habitats	Jiangning, Jiangsu province	RS, GIS	Meso	Landsat ETM+ image
Yang et al. (2008)	To predict <i>O. hupensis</i> habitats	Eryuan, Yunnan province	Landscape pattern analysis complemented with Bayesian spatial modelling	Micro	SPOT5

Zhang et al. (2008a)	To predict <i>O. hupensis</i> density	Guichi, Anhui province	Spatial statistical modelling	Micro	Elevation, air and soil temperature, type of vegetation, mean height of preponderant vegetation and soil humidity
Zhang et al. (2008b)	To predict <i>O. hupensis</i> distribution	Guichi, Anhui province	A new generalisation of negative binomial distribution model	Micro	Counts of <i>O. hupensis</i> early in the winter of 2005 and late in the spring of 2006
Zhou et al. (2008b)	To explore the spatial distribution of <i>O. hupensis</i>	Puge county in Tezi township	Spatial modelling	Micro	Ground information, that is, water, canals and farmlands
Yang et al. (2009)	To predict <i>O. hupensis</i> habitats	Eryuan, Yunnan province	RS, GIS modelling	Micro	SPOT5, environmental factors and landscape metrics

4.4. GEOSPATIAL HEALTH APPLICATIONS IN THE PHILIPPINES

4.4.1. GIS applications at micro-level

In a recent study to confirm two newly discovered endemic foci for schistosomiasis in the Philippines, [Leonardo et al. \(2009\)](#) used GIS to map snail sites to show their spatial distribution in the new endemic municipalities. The presence of snail colonies upstream poses the threat of possible spread of the snails downstream should there be overflows and accelerated water velocity from unusually heavy rains. Additional snail surveys are indicated to determine if the recent typhoons that flooded many parts of the Philippines, including the new endemic municipalities, dispersed snail colonies into new areas.

4.4.2. GIS applications at meso-level

[Leonardo et al. \(2005\)](#) used GIS to demonstrate significant correlations between schistosomiasis transmission pattern and environmental variables, providing the basis for development of models to predict disease prevalence in two municipalities. Proximity to snail breeding sites and irrigation networks and the highly agricultural nature of the barangays (villages) were identified as the major factors that define high prevalence areas for schistosomiasis, confirming that conditions that support snail host populations will in turn favour the presence of the disease ([Leonardo et al., 2005, 2007](#)).

4.4.3. GIS applications at macro-level

GIS maps on spatial distribution of schistosomiasis, soil-transmitted helminthes and heterophyidiasis were produced using data from the national survey of schistosomiasis in the Philippines conducted from 2005 to 2008 ([Leonardo et al., 2008a,b](#)). Additional GIS databases on schistosomiasis and other helminthic infections collected at the regional and provincial levels were supported by international funding agencies.

4.4.4. Identification of risk areas by modelling

A recent ecological study of *S. japonicum* was undertaken in 50 villages in the Province of Samar, the Philippines ([Carabin et al., 2005; Riley et al., 2005, 2008](#)). They assigned humans to three infection classes (none, light and heavy) and the animals into two classes (uninfected and infected), then built a model to track the transmission cycle from mammals to snails and back from snails to each category of mammalian host. Three

hypotheses were assumed in 50 villages to estimate transmission parameters: H_0 , transmission rates (snails to mammalian hosts and mammalian hosts to snails) are constant for all villages; H_1 , transmission rates from mammalian hosts to snails are site specific, varying by village; and H_2 , transmission rates from snails to mammalian hosts are site specific by village. Based on these comparisons, inferences were made subsequently with regard to relative roles of different hosts and transmission stages in the villages. Results showed that transmission from mammalian hosts to snails was site specific (H_1) and produced the best fit to human infection data. However, allowing the rate of transmission from snails to mammalian hosts to vary by village (H_2) resulted in a substantial improvement in explaining trends in human infection. Humans were found to be more susceptible to infection than any species of non-human host; by contrast, buffaloes and dogs played a marginal role in transmission, while rats were shown to be an important host for infections among animal hosts. The GIS modelling showed the spatial distribution of estimated site-specific values for $\beta_{SM}(j)$, where $\beta_{SM}(j)$ was the underlying rate of transmission from snails to mammals in the j th village, and that there was no excess mortality of heavily infected humans under H_2 . This is demonstrated in Fig. 4.2 in

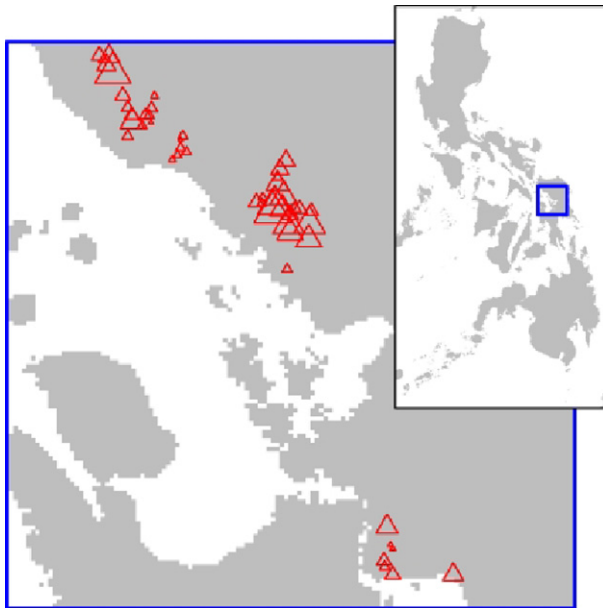


FIGURE 4.2 Spatial distribution of the underlying rate of transmission between snails and mammals. $\beta_{SM}(j)$ under the best fit hypothesis, H_2 (The linear size of the red triangles is proportional to the value of $\beta_{SM}(j)$). The outset chart shows the location of the study region in the Philippines. North is towards the top of the page in both charts). From Riley et al. (2008).

which three distinct geographical areas can be identified. There is obvious spatial clustering of the larger values of $\beta_{SM}(j)$ in the middle-latitude area of villages and similar spatial clustering of the smaller values of $\beta_{SM}(j)$ in the southern area. This result is consistent with estimates of average human prevalence using descriptive spatial models, and this finding led to the conclusion that the snail-to-mammal side of the *S. japonicum* life cycle affects the inter-village variability in human schistosome infection more than the mammal-to-snail side. Therefore, results indicate that the contribution of water buffaloes to human *S. japonicum* infection in the Philippines is not particularly important, which differed from the scenario in P.R. China in which water buffaloes are the major mammalian reservoir for *S. japonicum*. This research represents a useful contribution to elucidating the determinants of schistosomiasis transmission in an endemic area of the Philippines, and it illustrates the use of a mathematical model, complemented with statistical approaches, in exploring the roles of multiple mammalian hosts. The modelling approach can be a useful tool in exploring schistosomiasis transmission in other settings and may even apply to other macroparasites (Liang and Spear, 2008).

4.5. TRAINING PROGRAMMES

Implementation of a geospatial health infrastructure in Southeast Asia will be dependent on robust training programmes for health workers who will implement GIS capabilities in ministries of health, NGOs and other health organizations involved in research and geospatial health operational applications. Under the auspices of the Global Network for Geospatial Health's 'International School of Geospatial Health', a 'training node' has been established to offer standardized short courses at the National Institute for Parasitic Diseases, China CDC, in Shanghai (Zhou et al., 2005). Similar units at the Research Institute for Tropical Medicine (RITM) in the Philippines, the University of the Philippines and the Mekong Institute, Khon Kaen, Thailand are proposed to facilitate and 'internalize' routine adoption of geospatial health methodologies by regional health agencies. This will be done initially by offering 'train-the-trainer' courses. Course material from a manual adopted by the Global Network for Geospatial Health is taught by instructors selected from among a cadre of experienced geospatial health researchers who are certified to teach the course. Courses take a working group approach focused on application of geospatial health methodologies to individual diseases or health issues that affect multiple countries in each region. For example, each participant will be asked to bring data on a single disease entity, such as schistosomiasis, from home health units to apply course principles and compile a regional GIS reference database. A geospatial

database on schistosomiasis can thus be constructed by working groups, using a uniform GIS format, to create current 'health maps' on important diseases and enable step-wise development of an expanded MMDb health resource dataset for Southeast Asia.

Using this training model, trainees may be selected from currently funded international development projects and/or government health ministries in the region to take a 3–5 day intensive training course and begin work on a mentored project. Project work will continue over the next 3 months so that trainees can apply and implement course methods using health data from their home country. The working group can interact via bi-weekly virtual collaboration meetings via public domain conference software or organizational websites (e.g. www.rnas.org.cn; www.GnosisGIS.org), supported by course instructors. Results will be reported at scientific meetings and peer-reviewed publications. The aim is to enable real world learning by instructor-mentored application of GIS technology, development of project-based skills and trans-boundary collaboration.

4.6. CONCLUSIONS

This review revealed a growing number of geospatial health research studies, models and operational surveillance data sets on schistosomiasis and other helminthes that would be more valuable as a data resource if available in a standardized, seamless, open geographic format that can be shared by medical researchers and used by public health workers and administrators for decision support and operational health policy development.

GIS and RS applications are contributing to schistosomiasis control programme decisions by several avenues. Firstly, risk mapping supports decision-makers in planning prevention activities during the transmission season. In P.R. China, the highest risk areas are normally located where snail habitats and vast areas of animal pasture coincide in marshland and this can be detected by analysis of annual flooded areas by satellite imagery (Lin and Lin, 2001; Lin et al., 2002; Zhou et al., 2001), enabling local authorities to focus support of control programmes in those areas. In the mountain ecology of Yunnan province, Yang et al. (2009) reported that *O. hupensis* distribution and abundance was positively related by GIS to moisture regime. Secondly, geospatial analysis of specific risk factors, such as by identification of clusters, can guide the formulation of strategies to reduce the main transmission sources. Heightened concern for reducing environmental contamination by buffaloes in P.R. China, the major reservoir hosts of *S. japonicum* (Wu et al., 2007), was incorporated into the new national schistosomiasis control

strategy in lake and marshland regions of P.R. China based partly on GIS analysis tools (Wang et al., 2009), and classification and mapping of different ecological strata in Dangtu, P.R. China has enabled formulation of strategies for schistosomiasis control based on environmental features at the county level (Chen et al., 2007). Thirdly, geospatial correlation and modelling has been used to predict the future trends of disease transmission. The possible impacts of global climate change scenarios have been projected 50 years into the future, enabling monitoring activities in potential new areas of schistosomiasis transmission (Yang et al., 2006, 2010; Zhou et al., 2008a, 2010).

Further progress will be greatly dependent on practical training programmes for health workers who will implement GIS capabilities in ministries of health, NGOs and other health organizations, and it will depend on development of a comprehensive geospatial health data infrastructure resource. The 'Asia Minimum Medical GIS Database' resource, with Ministry of Health and RNAS+/GnosisGIS guidance and training, may serve as the nidus of a geospatial health data infrastructure resource for use in control programmes for schistosomiasis and other helminthes. Training nodes for geospatial health short courses and train-the-trainer programmes will promote broad-scale use of geospatial health tools and model development by disease-specific regional working groups.

It has been many years since Mao Zedong penned his famous poem 'Farewell God of Plague' and wisely set in motion a mass national campaign in 1956 to conquer schistosomiasis, knowing it was preventable and could be conquered. It is perhaps appropriate that a geospatial health data infrastructure has an early focus on schistosomiasis, which, once developed, can provide the context for similar methods and geospatial databases relating to 'place', environment and human behaviour of other zoonotic neglected tropical diseases in Southeast Asia.

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