

Spatial prediction and analysis of Himalayan marmot plague natural epidemic foci in China based on HJ-1 satellite data

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Plague, caused by the gram-negative bacterium *Yersinia pestis*, is a serious and rapidly progressing illness in humans that can be fatal if not treated effectively. The Qinghai-Tibet Plateau is the largest area of natural Himalayan marmot (*Marmota himalayana*) plague foci in China and covers more than 630000 km². Akesai County in Gansu Province is a part of this natural focus of plague and was chosen as a study area. Our study used an ecological niche modeling (ENM) approach to predict the potential distribution of the Himalayan marmot. Environment and Disaster Monitor Satellite (HJ-1) data was used to investigate environment factors that affect plague host animal activity. Host animal point data from active surveillance was combined with environmental variables from the HJ-1 satellite and other databases, and the models of the potential distribution of Himalayan marmot were produced with the Genetic Algorithm for Rule-Set Production (GARP). The probability of marmot presence was divided into 0–5%, 5%–20%, 20%–40%, 40%–80%, and 80%–100% subgroups. Areas with 80%–100% probability exhibited the greatest potential for the presence of Himalayan marmot. According to the predicted potential distribution of Himalayan marmot in the study area, active surveillance of plague hosts and plague control and prevention could be more efficient.

Himalayan marmot, plague, spatial prediction, GARP, HJ-1 satellite

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Plague, caused by the gram-negative bacterium *Yersinia pestis*, is a serious infectious disease and anthroozoonosis that occurs in natural foci [1, 2]. In China, according to the “Infectious Diseases Prevention and Control law of PRC”, plague is classified as a class A infectious disease, indicating the serious nature of this contagion (http://news.xinhuanet.com/newscenter/2004-08/28/content_1909060.htm). Because of its high infectivity and fatality rate, plague has played an important role in human history. Three large-

scale pandemics have occurred since the 6th century causing millions of deaths, in addition to numerous smaller epidemics and sporadic cases [2, 3]. The second major pandemic (“the Black Death”) killed nearly one-third of Europe’s population and remains the standard by which the effects of AIDS, SARS, or other new diseases are measured. This pandemic started in Europe in the 14th century and recurred intermittently for more than 300 years, while the third pandemic started in China during the middle of the 19th century and spread throughout the world [2, 4].

The plague epidemic in China reached its peak between

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1900 and 1949, affecting more than 500 counties in 20 provinces and causing 1.15 million human cases and 1.02 million deaths [5]. Around 1955, plague was rapidly controlled, and only sporadic cases were reported in Qinghai Province until 1984 [5]. However, since the 1990s, multiple natural foci of plague are again becoming active in China, facilitating the spread of quiescent foci and recurring outbreaks of infection. Unfortunately, there are only about 1200 plague monitoring points in China, meaning there is a serious lack of resources for plague surveillance [6]. If antibiotic treatment is not initiated promptly, plague is fatal in 40%–70% of bubonic cases and nearly 100% of pneumonic cases [2]. Furthermore, outbreaks of plague in major political and economic cities may have catastrophic consequences [7]. In July 2009, a large-scale epidemic was avoided in Xinghai County in the Qinghai Province because of immediate government intervention (http://www.cnr.cn/gundong/200908/t20090809_505424867.html). It is therefore important to improve our understanding of plague in an effort to avoid or effectively manage this disease.

Although the mechanisms by which plague is maintained between epizootic cycles are not well understood, it is generally accepted that the disease cycles between enzootic infections and occasional epizootic outbreaks among susceptible hosts [2, 4, 8]. Plague transmission to humans may also occur through contact with wild rodents or infected pets, through exposure to infected tissue, or via respiratory exposure to infectious airborne droplets [3, 8]. Different natural plague foci often have specific hosts. Many species of rodents and other small mammals are susceptible to infection, yet are only occasionally infected and are not necessarily important reservoirs of infection. The Himalayan marmot is the main host animal in Qinghai-Tibet Plateau natural epidemic foci of plague in China [5, 6]. Therefore, continuous surveillance of rodent and vector populations is important even during periods when no human cases are reported (<http://www.who.int/toics/plague/en/>).

Several limitations exist with current plague monitoring points used to observe rodent hosts. Monitoring is laborious, uses extensive material resources and does not detect emerging epidemic sites. This current management is based on the Plague Prevention and Management Information System, which was developed by the Chinese Ministry of Health based on the China Information System for Disease Control and Prevention since 2005 [9]. The system was officially launched on September 1st, 2005, and produced the plague disease direct network report, which was able to constantly monitor the progress of plague and epidemic situations across the entire country. Further researching plague epidemic foci and predictive modeling of foci distribution patterns may greatly assist the control and prevention of plague.

Previous studies describing the development of the plague epidemic foci have focused on the use of spatial information technology in China [10, 11], especially the

technology of geographical information system (GIS), remote sensing (RS), and global positioning system (GPS), which are abbreviated as 3S. Moreover, attempts to use GPS for plague surveillance information collection and GIS analysis of natural foci of plague have offered promising results [12–16]. The ecological niche model (ENM) has also been used for predicting the geographic distribution and ecological habitats of plague [8, 17, 18].

Environmental factors play a role in the complex plague cycle, with many ecological habitat parameters available in research databases, such as WorldClim database. Environment and Disaster Monitor Satellite (HJ-1) data has also been used to obtain environment factors that affect the activity of the host animals of plague. If ecological factors affect the distribution of plague, and these factors can be identified, models can be developed to predict distributions of unknown plague foci [17]. In this study, Akesai County in Gansu Province, which is a natural epidemic focus of Himalayan marmot (*Marmota himalayana*) plague, was chosen as the study area. Based on HJ-1 satellite data, we developed models to predict the geographic distribution and spatial analysis of plague in Akesai County.

1 Study area

Recently, 12 natural plague foci distributed across 19 provinces were confirmed in China. The natural foci of Himalayan marmot plague across the Qinghai-Tibet Plateau are the largest area of natural infections in China and cover more than 630000 km², including Qinghai, Gansu, Tibet, Xinjiang and Sichuan provinces. Akesai Kazakh Autonomous County in Gansu Province was chosen as the study area and is at the junction of Gansu, Qinghai and Xinjiang provinces (Figure 1). The county area is 31000 km² and it is typical of Himalayan marmot plague natural foci.

2 Data and methods

2.1 Data

2.1.1 Himalayan marmot point data

The Himalayan marmot is the predominant plague host animal in Akesai County according to multiple investigations [5, 6]. Marmot point data were derived from plague surveillance data collected by Chinese Center for Disease Control and Prevention (CDC). Marmot samples were obtained by active surveillance of areas with a known history of plague-positive animals or human cases. Current Himalayan marmot data from active investigations between 2006 and July, 2009 included the place of origin and only a few had both accurate GPS position and area description. Therefore, all the marmot records were geo-located using GIS software for further use with history records, GPS position and area description. A total of 165 unique locations of marmot sam-

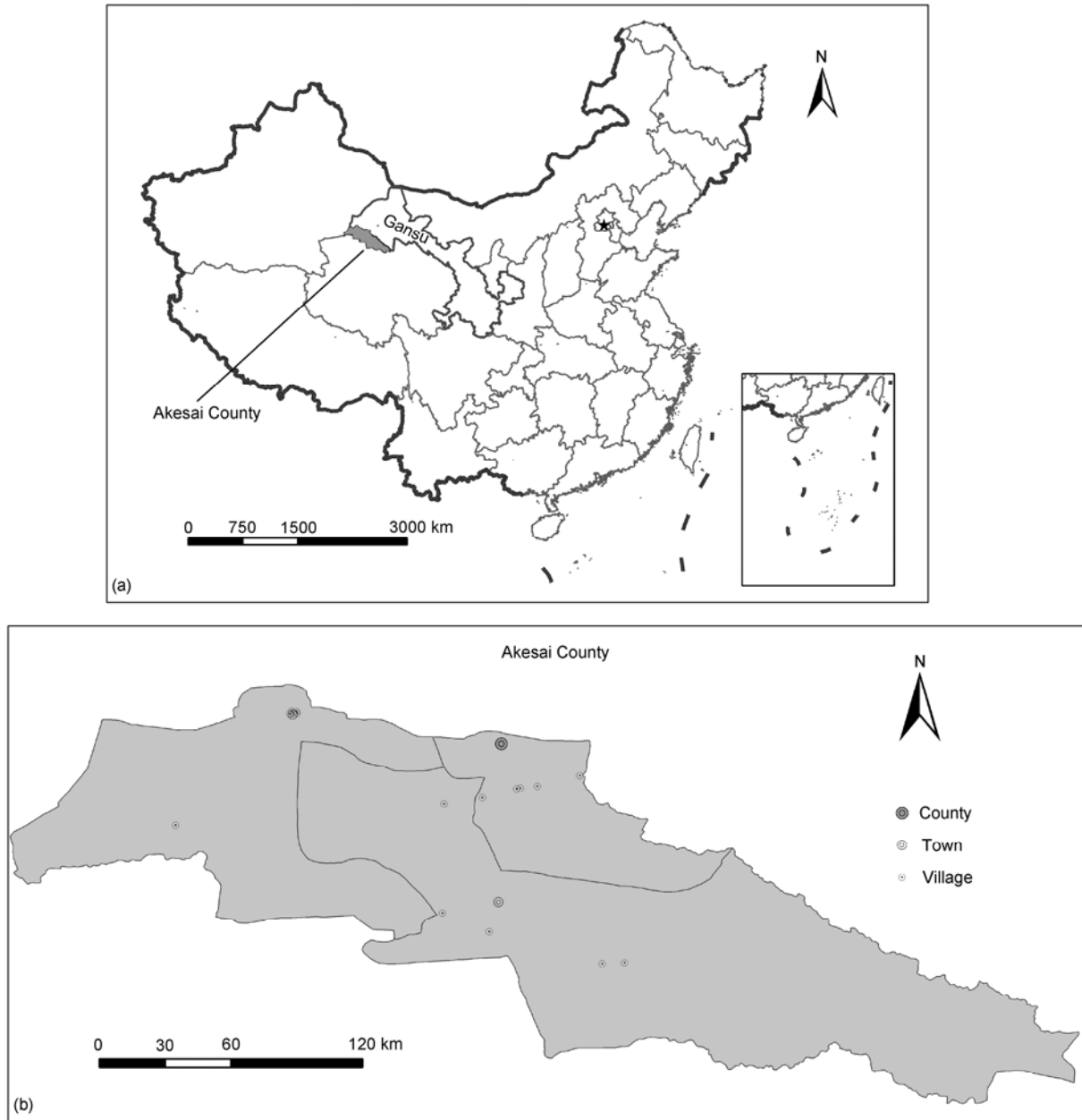


Figure 1 Study area location. (a) Location of Akesai County in China; (b) a simplified map showing the main towns and villages in the county.

ples were identified (Figure 2(a), (b)).

2.1.2 WorldClim data

WorldClim is a set of global climate layers (climate grids) with a spatial resolution of one square kilometer, which can be used for mapping and spatial modeling in GIS or other computer programs. Data are derived from monthly weather station measurements of altitude, temperature, and rainfall. These are biologically meaningful variables that capture annual ranges, seasonality, and other limiting factors useful for niche modeling [19]. The full set of 19 WorldClim bioclimatic variables in the Current WorldClim database averaged from 1950–2000 were downloaded (<http://www.worldclim.org>).

2.1.3 ASTER GDEM data

The Advanced Spaceborne Thermal Emission and Reflection Radiometer (ASTER) onboard the Terra spacecraft is a multispectral optical sensor that was launched on December 1999. The ASTER Global Digital Elevation Model (GDEM) was developed jointly by the Ministry of Economy, Trade, and Industry (METI) of Japan and the United States National Aeronautics and Space Administration (NASA). The accuracy of the GDEM data is within a 30 m spatial resolution.

2.1.4 HJ-1 data

Satellites of the Environment and Disaster Monitor Satellite constellation (HJ) were independently developed by China

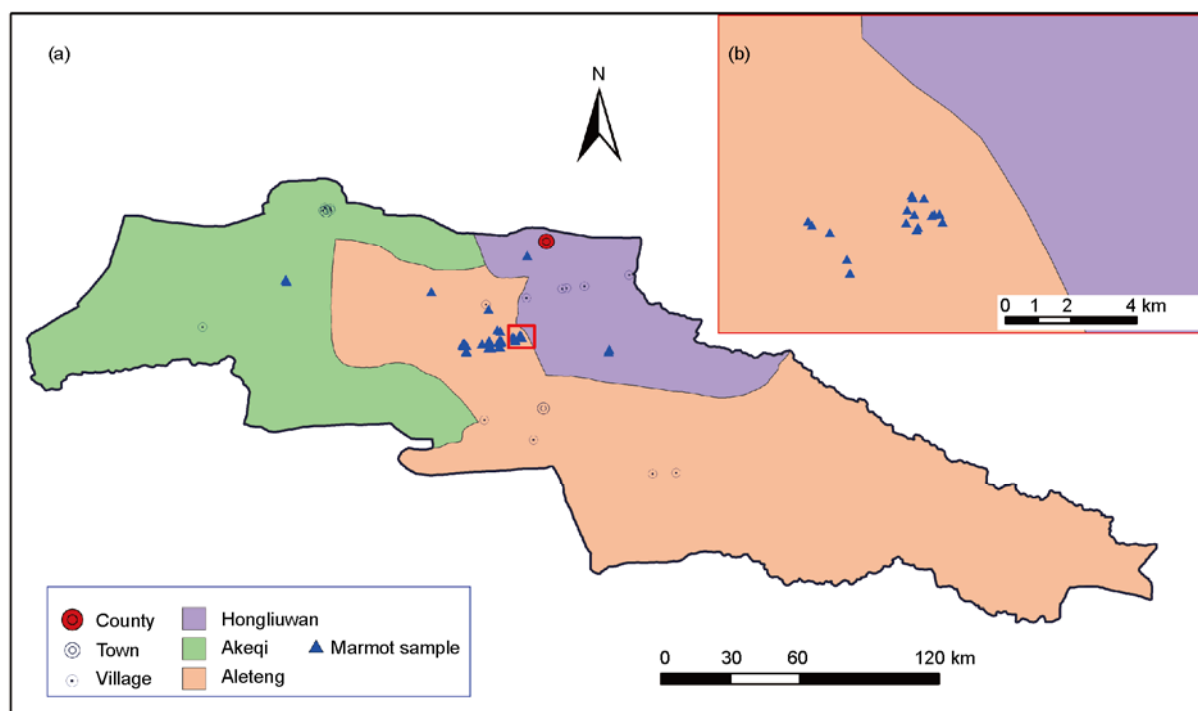


Figure 2 Himalayan marmot samples. (a) Geocoded data for marmot samples (165 unique locations); (b) an enlargement of the area indicated in red.

and launched in 2008. The revisit time of the satellite constellation is 2–4 days. Two CCD cameras in the HJ-1A and HJ-1B satellites were designed to have identical nadir symmetrical placement, split fields and parallel observations. Furthermore, HJ-1A carries a hyper-spectral imaging spectrometer and HJ-1B carries an infrared camera [20]. With high spatial resolutions, 30 m for the CCD camera and 150 m and 300 m for infrared camera, these satellites are the most useful for retrieving quantitative environmental parameters.

2.2 Environmental variables

Previous research predominantly focused on as many environmental variables as possible without selection [8, 17, 21]; however, we found that specific host animals of plague are often affected by particular environmental factors, such as temperature, precipitation, vegetation and soil [22–25]. We therefore selected suitable environmental parameters af-

fecting the Himalayan marmot on the basis of previous investigations (see Table 1). The summary indicated that geographical landscape elements (climate, soil and vegetation, and so on) determine the distribution of the main plague host animal.

In our study, environmental variables data sets for Himalayan marmots were obtained from three sources. (1) Climatic data layers in the form of six bioclimatic variables were chosen from the 19 variables of the WorldClim data set to avoid correlation error and summarized annual mean temperature, maximum temperature of the warmest month, minimum temperature of the coldest month, annual precipitation, and precipitation for the wettest and driest months. (2) Topographic data included elevation, slope, and aspect. The elevation of the research area was resampled to a spatial resolution of one square kilometer from the ASTER GDEM data. Both the slope and aspect variables were computed from the GDEM data of the research area with remote sensing software. (3) Vegetation and dryness index included

Table 1 Summary description of suitable environmental parameters of Himalayan marmot

Environmental layer	Description of suitable environmental parameters
Topography	Number of marmot holes is largest at an altitude between 3200–3500 m, followed by 3000–3200 m; when the altitude is more than 3500 m, hole numbers decline; the most appropriate gradient is between 5°–15°, with the number of holes reducing gradually as the slope increased.
Climate	Warm and sunny places are preferred for the establishment of marmot holes; the marmot starts hibernation from Sept. or Oct.; the plague epidemic did not change significantly in each quarter.
Vegetation	Number of marmot holes is the largest when grass height is between 10–15 cm; when the height is more than 15 cm, hole numbers decline; number of holes is the largest when vegetation coverage is more than 90%.

the Leaf Area Index (LAI), Global Vegetation Moisture Index (GVMI), and Temperature Vegetation Dryness Index (TVDI). All indices were calculated from CCD and IRS sensors data from the HJ-1 satellites. LAI indicated that the amount of foliage area per unit ground area was derived from small satellite of HJ-1B and the 3D canopy radiative transfer model was run as a forward model [26, 27]. GVMI was developed to retrieve vegetation water content [28], which is important for the host survival. TVDI showing the soil moisture using land surface temperature was derived from the brightness temperature dataset and NDVI dataset [29]. For modeling purposes, all environmental data layers were generalized to a pixel resolution of 1 km for analysis and projected with the same geographic coordinates.

2.3 Ecological niche modeling (GARP)

Ecological niche modeling (ENM), also termed species' distribution modeling, has gained increased attention in recent years. ENM has mostly been applied to predict the potential for the occurrence of plant and animal species, and is increasingly being used to identify and map the distribution of diseases [8], such as Chagas disease [30], avian influenza [31], and plague [17, 18]. The Genetic Algorithm for Rule-set Production (GARP) was used for ENM development and was originally developed by David Stockwell at the ERIN Unit of Environment in Australia and enhanced at the San Diego Supercomputer Center [32]. The GARP searches iteratively for non-random correlations between the presence and absence of species and environmental parameters using several different rules. Each rule implements a different method for building species prediction models. Currently, four rule types are implemented: atomic, logistic regression, bioclimatic envelope, and negated bioclimatic envelope rules [32].

2.4 Modeling with DesktopGarp

For GARP analyses, the available marmot occurrence data was subdivided as follows: 50% of occurrence points set aside for filtering among replicate models based on statistical error (extrinsic testing data), 25% used for developing rules (training data), and 25% used for model refinement within GARP (intrinsic testing data) [17]. All environmental variables were placed into the model system as environmental layers. The GARP program uses an iterative process for rules based on selection, evaluation, testing, and incorporation or rejection. A method is chosen at random from a set of 4 basic rule types, applied to the training data, and a rule is developed [30]. Predictive accuracy was then evaluated based on 1250 points resampled from the test data and 1250 points sampled randomly from the entire study region. A rule was incorporated into the model if it increased the predictive accuracy from one iteration to the next [18]. For our study, a rule was developed if the algorithm ran either

1000 iterations or until there was a convergence with a 0.01 difference in accuracy. Subsequently, this method was used to develop 1000 models, maps and ARC/INFO grid layers, choosing a different training and testing data set randomly each time.

The average omission of errors (basic omission error) for the 1000 models was calculated and compared with the individual omission errors for each model. Based on the omission and commission error statistics calculated from the extrinsic testing data, 100 models were selected to form the best model subset [33]. Each model in this subset was required to have less than the average omission error and at least 70% training and testing accuracy threshold. Finally, using the spatial analyst tools, the grid map for the 100 models in the best model subset were overlaid with equal weight value. The value of each grid in the final map was between 0–100, and then converted into a percentage to indicate the probability of marmot presence.

3 Results

The potential distribution of Himalayan marmot in Akesai County was modeled using marmot sample localities, environmental variables, and the GARP. The 1000 models and maps of Himalayan marmots in Akesai County were obtained as previously described. Each model had an omission and commission error, and the basic omission error for the 1000 models was 2.7707. Based on the comparison between each model omission error and the basic omission error, and with the training and testing accuracy of each model, the best model subset of 100 models was selected (for selected model parameters see Table 2). The final models selected were almost evenly distributed among the previously developed 1000 models. The chi-square test based on the independent external test data set showed that the 100 models were highly statistically significant ($P < 0.01$), which indicated the predictive ability of the selected model was far better than a random model [34].

ARC/INFO grid forms for the 100 models were imported into ArcGIS software, and overlaid with equal weight value using the "raster calculator" in the "spatial analyst" tools to generate the overall grid map that indicated the predicted distribution of Himalayan marmot in Akesai County. The resulting values in the final map were converted into percentages to indicate the probability of Himalayan marmot presence (Figure 3). The probability of marmot presence was divided into 5 classes, 0–5%, 5%–20%, 20%–40%, 40%–80%, and 80%–100%, indicating different probabilities for potential presence of Himalayan marmots.

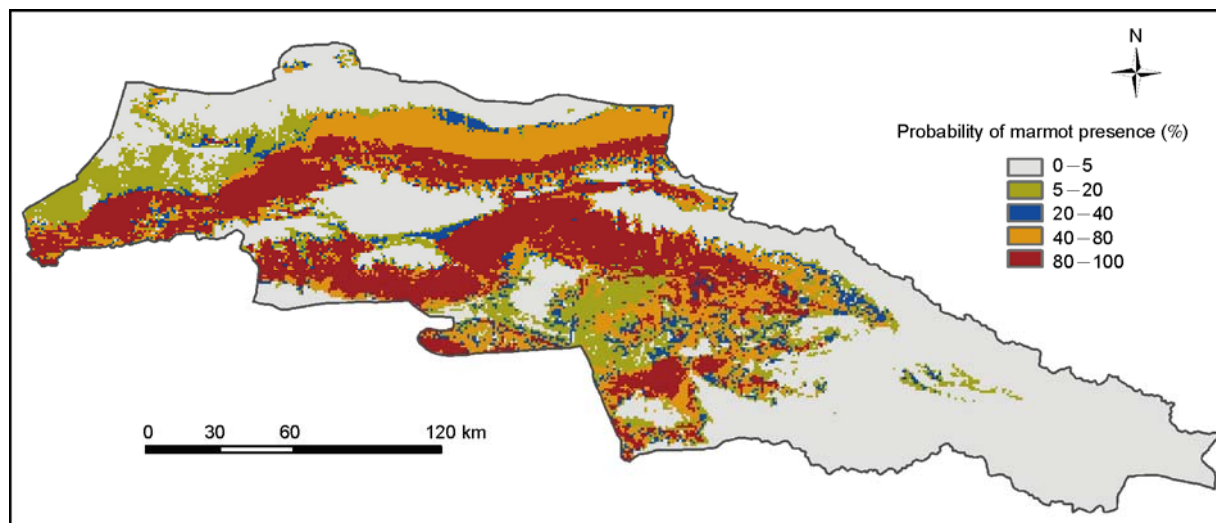
4 Discussion

Yersinia pestis is often persistent in historical natural epi-

Table 2 Parameter values for each model and the distribution percentage of the best 100 models^{a)}

Parameter	Value	Percentage	Parameter	Value	Percentage
Train Acc	0.7063–0.8	76%	Test Acc	0.7057–0.8	79%
	0.8018–0.85	24%		0.8032–0.85	21%
Pr:Pr/Ac:Pr	1250	100%	Pr:Pr/Ac:Pr	1126–1198	30%
				1200–1223	23%
				1250	47%
Pr:Ab/Ac:Pr	0	100%	Pr:Ab/Ac:Pr	0	100%
Pr:Pr/Ac:Ab	244–300	8%	Pr:Pr/Ac:Ab	253–297	8%
	303–397	39%		303–398	34%
	406–525	53%		401–522	58%
Pr:Ab/Ac:Ab	0	27%	Pr:Ab/Ac:Ab	0	27%
	65–97	29%		63–99	25%
	107–192	24%		101–194	26%
	204–239	7%		203–254	9%
	373	1%		371	1%
	513–758	11%		477–737	13%
ChiSq	120.65–199.45	78%	p	<0.001	100%
	204.47–290.18	22%			
Commission	20.97–29.81	27%	Omission (ext)	0	47%
	30.12–40.46	73%		1.22	33%
Omission (int)	0	100%		2.44	20%

a) The 'value' field shows the range of values for the 100 models and the 'percentage' field shows the percentage values for the 100 models. Train Acc: Accuracy calculated using the training data points. Test Acc: accuracy calculated using the data points for accuracy testing that have not been used for training of the model. Labels represent: Pr(edicted):Pr(esent)/Ac(tual record):Ab(sence). For a detailed description of every parameter see <http://www.nhm.ku.edu/desktopgarp/UsersManual.html> (Users Manual of DesktopGarp).

**Figure 3** Predicted distribution of Himalayan marmot in Akesai County using GARP.

demic foci and often infects marmots. This disease cycle is further facilitated by the high economic value of marmot leather and the continued habit of people to eat marmot meat or oil in some areas. Consequently, the plague outbreak in Wulan County during October 2004 in Qinghai Province resulted from a middle-aged man pelting and eating marmot meat infected with plague. Prediction and anal-

ysis of the potential distribution of marmot may therefore assist in the effective control and prevention of plague.

Currently, the limited plague monitoring capacity in China focuses on already established foci. Furthermore, many epidemics occurred in unknown foci, and thus these areas were not configured to monitor plague [35]. Active surveillance should therefore take advantage of the predic-

tive and analytical potential of data for all plague epidemics based on known host animals or plague-related environmental factors.

As an independently developed Chinese satellite, the HJ-1 satellite can potentially obtain variable environmental data across large regional areas. The satellite further revisits areas within 2–4 days and could efficiently monitor disasters and environmental changes. For these reasons, we used quantitative parameters for vegetation and dryness retrieved from the satellite for our research. Climatic data including annual mean temperature, maximum temperature of the warmest month, minimum temperature of the coldest month and others were chosen from the WorldClim database. Data were generated through interpolation of average monthly climate data from weather stations for the 1950–2000 period. However, due to the different time period between rodent points and these environmental variables, errors in data matching were potentially produced.

Using data obtained via active investigation of Himalayan marmots and related environmental variables, Akesai County in Gansu Province was selected as a study area using the GARP model system to generate an overall map indicating the predicted distribution of this species. Previous studies indicate that GARP is robust for sample sizes of 10 and greater [36]; therefore, we defined 165 independent marmot points and chose 100 models for the best model subset. Areas with 80%–100% probability had the highest potential for the presence of Himalayan marmot. Marmots were also often caught in these regions. Areas with 40%–80% probability also had the potential for marmot presence, while areas with a probability below 40% had a low potential presence of Himalayan marmot (Figure 4).

Plague surveillance is often dependent on field investigation and laboratory test results, with almost all of the plague rodent information being previously collected via monitored

observation and individual testing [35]. In Figure 4, yellow circles indicate the primary area where Himalayan marmots were monitored by active surveillance. As this was limited surveillance, a distinct difference was observed between the surveillance data and the predicted result. According to the prediction, a large area with suitable environment conditions for Himalayan marmot exists in Akesai County, which is typical of Himalayan marmot plague natural epidemic foci. Areas with the potential presence of marmot are therefore also at risk of a plague outbreak. Furthermore, the distance between the predicted distribution of Himalayan marmot and the main residential areas (shown as a red circle in Figure 4) indicated a risk of contact with marmots and increasing the probability of being infected with plague.

5 Conclusions

For our study, an ENM approach was used to ascertain the potential distribution of Himalayan marmot in Akesai County. Using GARP and marmot point data from active surveillance, environmental variables from HJ-1 satellite and other databases, models of the potential distribution of Himalayan marmot were produced. The best model subset of 100 models was selected according to the basic omission error, training and testing accuracy, and chi-square test. We also produced a predicted distribution of Himalayan marmot in Akesai County indicating presence probability.

Because plague foci maintenance is dependent on the rodent host and their associated fleas, the potential distribution of rodent host observed in our model is potentially closely associated with plague, especially in standard natural epidemic foci of plague. Inaccuracies between data collection times for satellite retrieved parameters and environmental parameters may have introduced some error into our

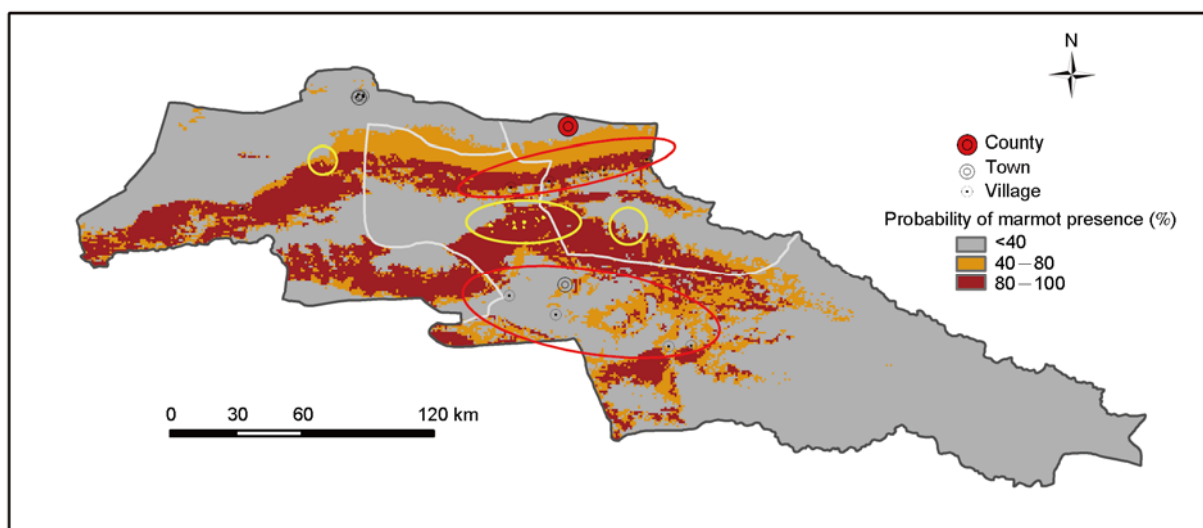


Figure 4 Field investigation points and the predicted distribution of Himalayan marmot in Akesai County. Yellow circles indicate the primary area that Himalayan marmot data was obtained by active surveillance, while red circles indicate the main residential areas.

model. Similarly, the climatic data used from the WorldClim database was for the 1950–2000 period and may have produced a minor yet important effect on rodent prediction. Therefore, it is necessary to further investigate the advantages of serial quantitative parameters for the dynamic surveillance of plague epidemic foci.

Although limitations exist within the data used to produce the potential distribution of the Himalayan marmot, our results may be beneficial for future studies focusing on rodent host. The methodology used by GARP to produce the predicted areas can also facilitate extensive surveys of the plague rodent host in the future by using more controlled, random sampling techniques. If spatial prediction and analysis of the main rodent hosts was for all natural epidemic foci of plague, the active surveillance of host species and plague control and prevention would be more efficient.

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