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Geographical Information Systems in Determination of Cutaneous Leishmaniasis Spatial Risk Level Based on Distribution of Vector Species in Imamoglu Province, Adana

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Abstract

The Imamoglu district located in the southeast of Adana province in Turkey is an endemic focus of cutaneous leishmaniasis (CL) owing to dominancy of *Phlebotomus tobbi*, which is a probable vector of *Leishmania infantum*. About 11.26% of CL cases reported each year are from Imamoglu, Adana, and between 2008 and 2015, 223 cases of CL were reported. *Leishmania infantum*, which may be transmitted by *P. tobbi*, *Phlebotomus neglectus/syriacus*, and *Phlebotomus perfiliewi*, is referred as leishmaniasis factor in Adana. Thus, the aim of this study was to map the risk areas for each sand fly species using remote sensing images based on environmental factors and geographical characteristics. Two field works in two consecutive years (2013 and 2014) were conducted and six sand fly species were caught, four of which were identified as probable vector species. Field work results were compared with environmental data obtained from satellite images by univariate and binary logistic regression in PASW. ARCMAP 10.2 software was used for geographical adjustments, creating a database and estimating a risk model by using previous risk value formulas. The results showed that the distribution of three probable leishmaniasis vectors (*P. tobbi*, *P. neglectus/syriacus*, and *P. perfiliewi*) was associated with normalized difference vegetation index (NDVI), digital elevation model (DEM), night-time land surface temperature (LSTNIGHT), and emissivity (EMIS31) values, which were related to the local authorities, who take these findings into account when deciding on high risk areas for CL.

Key words: sand fly, leishmaniasis, cutaneous, risk model, geographical information system

Leishmaniasis is a worldwide vector-borne disease affecting 98 countries located in the intertropical zones of America and Africa, temperate regions of South America, Southern Europe, and Asia. Leishmaniasis is a disease complex caused by protozoan members of the genus *Leishmania*, parasites transmitted by the bite of phlebotomine sand flies (Desjeux 2005). Although cutaneous leishmaniasis (CL) caused by *Leishmania infantum* and *Leishmania tropica* is endemic in southeastern and eastern Mediterranean regions of Turkey, it may also tend to spread to other regions of Turkey because of the suitable environmental conditions (Ok et al. 2002, Olgen et al. 2012). More than 800 sand fly species have been described to date throughout the world. Of >800 species, only 30 species are known as proven vector of leishmaniasis (Kato et al. 2005, World Health Organization [WHO] 2010). In Turkey, there are 29 sand fly species belonging to five subgenera, and 18 of them have been identified as probable or proven vector of leishmaniasis (Houin et al. 1971, Özcel and Daldal 1997, Yaman and Ozbel 2004, Svobodova et al. 2009, WHO 2010, Erisoz Kasap et al. 2015, Kavur et al. 2015).

This study was carried out in the Imamoglu district, where 223 CL cases were reported between 2008 and 2015 (Ministry of Health [MoH] statistics 2015). In the previous field works conducted in this area marked as an endemic area of cutaneous leishmaniasis disease, *Phlebotomus tobbi* was reported as the dominant species (Svobodova et al. 2009, Kavur et al. 2015).

The geographic information system (GIS) is a computer-based tool which is efficient in determining spatial information for research and in vector-borne diseases. It is also efficient in establishing the geographical distributions of sand fly based on environmental factors of altitude, climate, emissivity, and vegetation. In this study, we identified environmental factors that appear to predict the presence or absence of sand fly species and disease risk (Momeni and Saradjian 2007, Kahime et al. 2016, Ebrahimi et al. 2016). Geographic information systems equipped with new technologies

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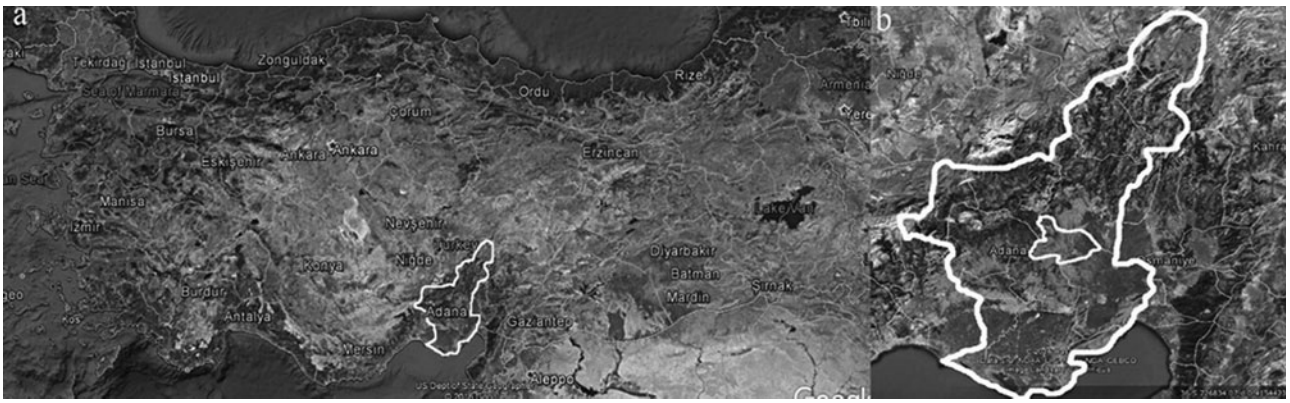


Fig. 1. Maps of Turkey. (**a**) Adana province; (**b**) Imamoglu district.

enable researchers to generate risk maps including the relationships between vector-borne diseases, environmental factors, and vector arthropods.

Materials and Methods

Study Area

The study area, with an area of 424 km^2, was located in the southeastern mountain range of Taurus, and it is 50 km away from the Adana province (altitude—78 m, latitude—37° 15′33.94″ N, longitude—35° 39′41.34″ E; Fig. 1). The average temperature of Imamoglu province between 1950 and 2014 was 20.8 °C (maximum 21.7°C; minimum 0.9 °C). The annual mean rainfall between 1950 and 2014 was 389 mm (Turkish State Meteorological Service [TSMS] 2015). The field works were carried out twice—between 24 August 2013 and 04 September 2013, and between 28 June 2014 and 8 July 2014.

Sand Fly Collections and Identification

In total, 100 CDC light traps which caught 650 sand fly specimens were set up during field works in the 2013 and 2014 summer season (Fig. 2). In each area, during the collection period, traps were set up under or close to the animal (goat, cattle, sheep, or poultry) sheds, which are usually made of brick, mud, wood, or stone. Specimen identification was verified based on the morphology of male genitalia and female spermatheca and pharynges using the several keys (Theodor 1958, Lewis 1982, Killick-Kendrick 1990).

Environmental Data and Analyses

Data for this study were collected from two groups: The environmental data corresponding to the coordinates of each location of sand fly samples were extracted from topographical and remotely sensed images. Data on elevation, slope, and aspect of the study area were derived from three arc-second resolution shuttle radar topography mission (SRTM) The SRTM radar contained two types of antenna panels, C-band and X-band. The near-global topographic maps of Earth called digital elevation models (DEMs) were made from the C-band radar data. Normalized difference vegetation index (NDVI), enhanced vegetation index (EVI), and land surface temperature (LST) were obtained from Landsat ETM + (path 175, row 34) and MODIS data set. For MODIS data, temperature layers were extracted from MOD11A2 (González et al. 2010) and reflectance layers were extracted from MOD13Q1 files (Didan 2015). The MOD11A2 version six provides an average of 8-d, per-pixel land surface temperature (day land surface temperature, night land surface temperature, Band 31 emissivity, and Band 32 emissivity) in a 1,200- by 1,200-km grid. The MOD13Q1 version six provides a vegetation index (VI) value at a per-pixel basis. There were two primary vegetation layers. The first was the NDVI, referred to as the continuity index to the existing National Oceanic and Atmospheric Administration-Advanced Very High-Resolution Radiometer (NOAA-AVHRR)-derived NDVI. The second vegetation layer was the EVI, which improved sensitivity over high biomass regions. Along with the vegetation layers, there were also MODIS reflectance bands one (Red), two (NIR), three (Blue), and seven (MIR), as well as four observation layers. MOD13Q1 images were generated using the two 8-d composite reflectance granules (MxD09A1) during 16-d period. In addition, reflectance bands were combined to create NDVI vegetation indices by using Landsat ETM + (path 175, row 34) data set for the years 2015 and 2016. A set of 10 measures, or channels, were then processed by a temporal Fourier algorithm: middle infra-red reflectance, day-time land surface temperature, night-time land surface temperature, NDVI (Modis), EVI (Modis), NDVI (Landsat ETM +), Emis31, Emis32, night-time land surface temperature, DEM, and number of the cattle and ovine.

Model Validation

Reported cases of CL between years 2008 and 2015 were obtained from the Ministry of Health (MoH statistics 2015). These data were used for additional verification of the created risk maps. Moreover, the data obtained from the nearest location of 223 CL patients were geopositioned with GIS Technologies by using the ArcMAP 10.2 software.

Statistical Analysis

The relationships between environmental and sand fly fauna data were analyzed using PASW 18.0 software with an univariate regression analysis. Multivariate regression analysis was carried out to determine predictor variables of CL cases.

Formulation of Risk Model

Weighted scoring method was used to create a risk model. The weighted score was calculated for every significant ($P < 0.005$) environmental variable (Ev) derived from the univariate logistic regression analysis.

$$W_i = (1 - p_i)$$

Weighted scores (w_i) were used to determine risk values (Rv). Risk value for each species is independently modeled as follows;

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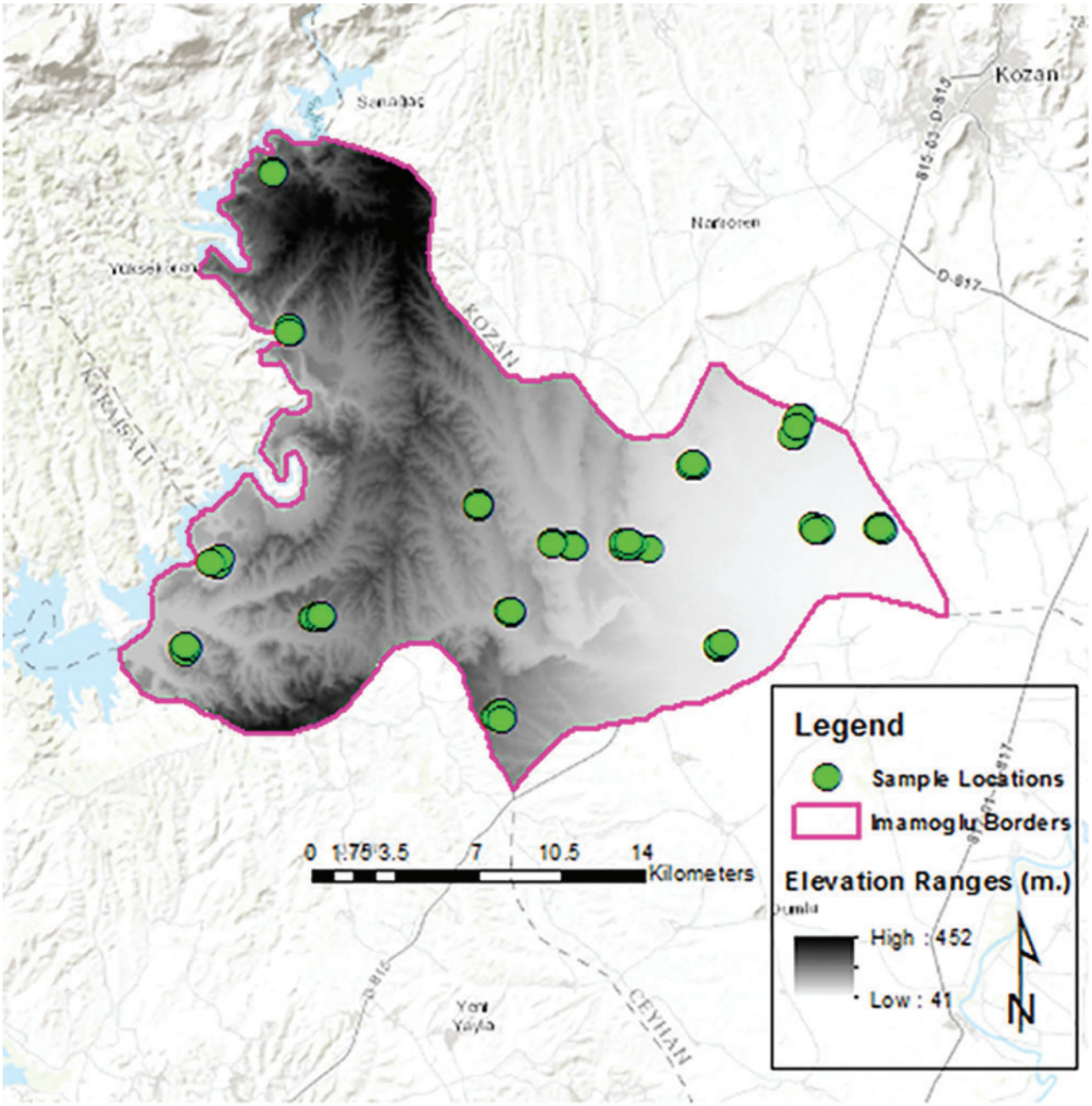


Fig. 2. The location of the light traps in the study area.

$$Rv = 1/\log(w_1Ev_1 + w_2Ev_2 + \ldots\ldots\ldots + w_nEv_n)$$ (Olgen et al. 2012).

The risk map generated for *P. tobbi* in the study area was categorized as 10—high to 1—low, in terms of risk level. *Phlebotomus neglectus/syriacus* and *Phlebotomus perfiliewi* risk map was categorized as 5—high to 4.88—low.

Results

In our field works, our CDC light traps caught 650 sand flies belonging to the *Phlebotomus* genera. Our study area elevations were between 0 and 250 m, as Imamoglu district is located on a small plain in the hills. *Phlebotomus tobbi* was detected as the dominant species. We also identified *P. neglectus/syriacus*, *P. perfiliewi*, and *Phlebotomus sergenti* for other probable vector species (Fig. 3).

Proposed Risk Model

The univariate binary regression analysis of the relation between the presence of CL and various environmental factors is shown in Table 1. The presence of detected probable vectors sand fly species in each station was remarkably correlated with NDVI (MODIS), EVI (MODIS), MIR (MODIS), DEM (SRTM), NDVI (LANDSAT), EMIS31 (MODIS), EMIS32 (MODIS), and LSTNIGHT (MODIS) values.

Multivariate analysis results revealed the correlation between the presence of three vector species and one or more parameters as NDVI, LSTNIGHT, EMIS31, and DEM. The risk model was

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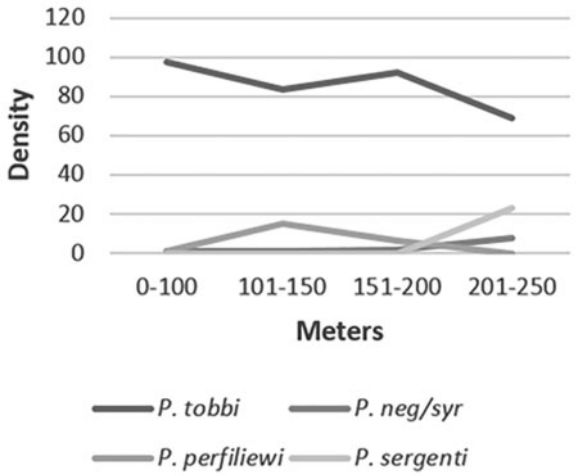


Fig. 3. The density of vector sand fly species according to the altitude in Imamoglu province.

Table 1. Univariate analysis of environmental variables used in the development of the risk map of cutaneous leishmaniasis in the Imamoglu province

Variables	*P*-values			
	P. tobbi	*P. neglectus/ syriacus*	*P. perfiliewi*	*P. sergenti*
MODIS data				
NDVI	0.000***	1.000	0.337	0.087
EVI	0.000***	0.941	0.565	0.208
MIR	0.029*	0.982	0.090	0.026*
LSTNIGHT	0.000***	0.195	0.003*	0.760
EMIS31	0.002*	0.043*	0.001**	0.996
EMIS32	0.005*	0.376	0.438	0.940
Non-MODIS data				
NDVI (LANDSAT)	0.001**	0.501	0.872	0.270
DEM	0.000***	0.855	0.006*	0.076
CATTLE	0.093	0.601	0.534	0.231
OVINE	0.964	0.475	0.980	0.975

***Highly significant (<0.001); **Very significant (<0.002); *Significant (<0.05).

improved based on multivariate logistic regression and spatial weighted overlay analysis, which calculated for every significant ($P < 0.005$) geographical variables (Table 2).

Risk value maps associated with three probable vector sand fly species (*P. tobbi*, *P. neglectus/syriacus*, and *P. perfiliewi*) were produced considering MODIS, non-MODIS, LANDSAT, and SRTM data sets. After statistical and geographical analyses, CL risk level was found to be high owing to the presence of *P. tobbi* in the southeastern part of Imamoglu province. Also, *P. tobbi* was a known probable vector of the cutaneous leishmaniasis in Imamoglu, and it was found to be the dominant species in five of the 15 study areas; Uctepe (78.6%), Malihidirli (59.3%), Corten (50%), Sayca (57.7%), and Sokutas (98.4%) villages (Fig. 4a). The presence of *P. neglectus/syriacus* and *P. perfiliewi* was significantly correlated with the emissivity. These species were detected in nine of the 15 study areas; Yazitepe, Alaybeyi, Uctepe, Malihidirli, Ulucinar, Corten, Sayca, Agzikaraca, and Danacali

Table 2. Multivariate analysis of environmental variables used in the development of the risk map of cutaneous leishmaniasis in the Imamoglu province

Variables	*P*-values			
	P. tobbi	*P. neglectus/ syriacus*	*P. perfiliewi*	*P. sergenti*
MODIS data				
NDVI	0.015**	–	–	–
LSTNIGHT	–	–	0.027*	–
EMIS31	–	0.043*	0.001**	–
Non-MODIS data				
DEM	–	–	0.003*	–

***Highly significant (< 0.001); **Very significant (<0.002); *Significant (<0.05).

(Fig. 4b). *Phlebotomus sergenti* risk maps could not be performed owing to a very low number of specimens. In addition, investigation of *P. sergenti* distribution requires a more comprehensive entomological survey.

Validation

The locations of 223 CL cases were marked on the risk map for the validation. The risk map was created based on the three groups of risk level (high, moderate, and low), and it was tested according to the number of patients in each risk group (Fig. 5).

The high-level risk group in the study area was determined according to the validation map (48.43%). The high-level risk group is followed by moderate (32.28%) and low-level risk groups (19.28%), respectively (Table 3).

Discussion

Geographic information systems can not only provide insights about the factors and mechanisms responsible for the heterogeneous contacts between vertebrate hosts and vectors, but also help to guide science-based programs of disease surveillance, control, and prevention, if it is coupled with rigorous spatial analysis and remotely sensed data (i.e., satellite-derived and spatially continuous proxies of environmental factors; Kitron 1998, Reisen 2010). Spatial epidemiology first studies the epidemiology that is spatially implicit, such as metapopulation models of disease transmission, and then focuses on research on spatial epidemiology that is spatially explicit, such as the creation of risk maps for particular geographical areas (Ostfeld et al. 2005). In our study, we determined that there was a relation between the presence of three probable vector species and the environmental data (MODIS, non-MODIS, SRTM, and LANDSAT). We also observed that the presence of vector species was increasing the risk level of the CL. Produced risk maps in which high CL risk areas are shown in dark can help control programs by emphasizing the priority of these areas in terms of insecticide spraying. There has been an increase in the number of studies on the prediction of the risk level of vector-borne diseases based on multivariate regression analyses, and understanding the epidemiology of CL has become easier than before (Thomson et al. 1999, Baron et al. 2011, Tsegaw et al. 2013).

Phlebotomus tobbi was found to be the dominant species in western part of the Adana In addition, *P. neglectus/syriacus*, *P.*

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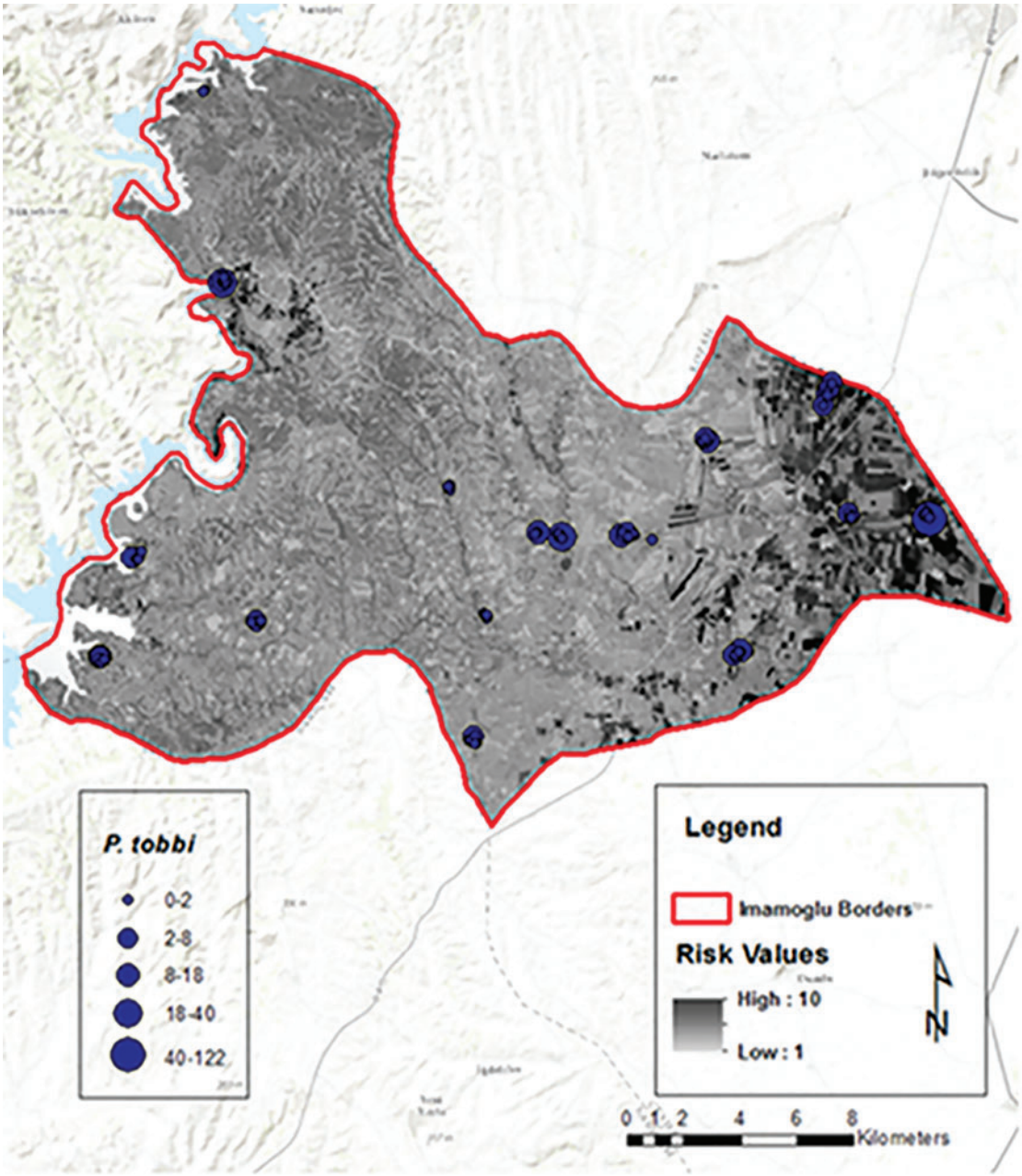


Fig. 4. Risk level map of the cutaneous leishmaniasis (**a**) based on database related to *P. tobbi* and (**b**) based on database related to *P. neglectus/syriacus* and *P. perfiliewi*.

perfiliewi, and *P. sergenti* were detected in the same area (Svobodova et al. 2009). The findings of Belen and Alten (2011) are similar to our findings and showed that *P. tobbi* was the most common species at all altitudinal gradients in the Cukurova Region, Adana. The dominance of *P. tobbi* and *P. neglectus/syriacus* seemed to have been restricted from 100 to 199 m. *Phlebotomus tobbi* was detected rarely in the mountainous areas (Sayedi-Rashdi and Nadim 1992). The abundance of *P. perfiliewi* was the highest between the altitudes of 100 and 299 m. Also, similar to the Olgen et al. (2012), we detected more CL risk in study areas where *P. tobbi*, *P. perfiliewi*, and *P. neglectus/syriacus* were caught (Fig. 4a, b).

In this study, using univariate logistic regression analysis, we determined different statistically significant values related to three vector species in each group of variables (NDVI, EVI, MIR, DEM, EMIS31, EMIS32, and LSTNIGHT) which were meaningful ($P < 0.005$) in the univariate analysis were also used in multivariate logistic regression analysis (Table 1). Multivariate analysis revealed that DEM and LSTNIGHT values were statistically significant for only *P. perfiliewi*. NDVI values were for only *P. tobbi* and EMIS31 values were for *P. neglectus/syriacus* and *P. perfiliewi* (Table 2).

There were six *Phlebotomus* species in the study area, including probable or proven vector species. *Phlebotomus tobbi* known as

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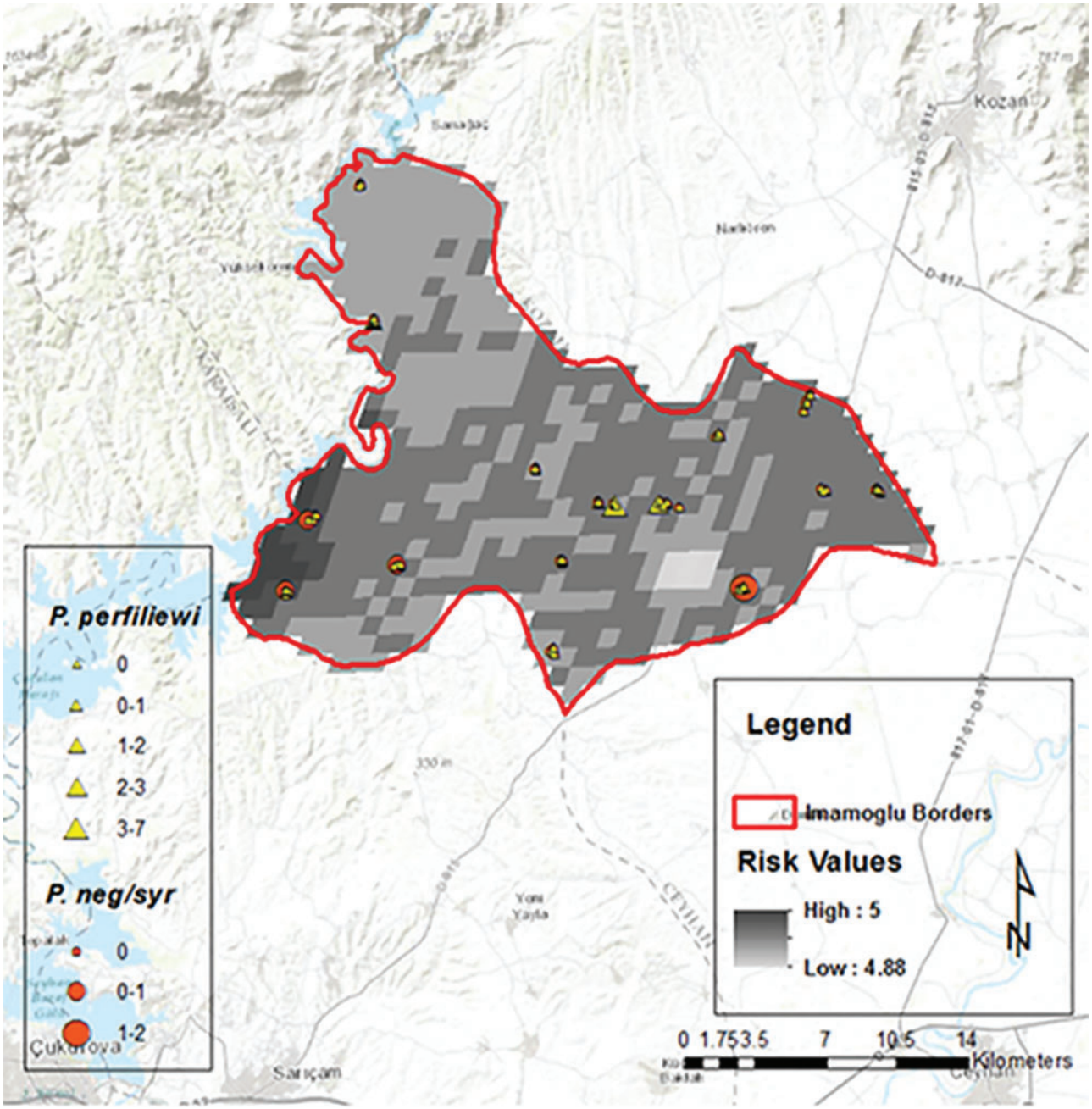


Fig. 4. Continued.

proven vector was clumping at the southeast part of Imamoglu. *Phlebotomus neglectus/syriacus* and *P. perfiliewi* had an equal distribution in the west part of Imamoglu (Fig. 4a, b). There was a consistency between findings reported by Olgen et al and ours which are between significance values of NDVI and *P. tobbi* distribution. Olgen et al. (2012) stated the association between three sand fly species (*P. neglectus*, *P. tobbi*, and *Phlebotomus similis*) and environmental variables (day-time LST maximum, day-time LST phase of biannual cycle, NDVI maximum, NDVI variance in annual cycle, Mean EVI, and EVI phase of biannual cycle) in Aydın province of Turkey.

For the validation of the risk maps, we determined three risk categories (low, moderate, and high) after the correlation of CL case data and the presence of sand fly species. The validation map we created revealed that a high number of CL patients resided or lived in areas associated with high- and moderate-risk level groups (80.58%). The high number of CL cases in high- and moderate-risk level places observed in the present study supports the hypothesis (Table 3).

Using geographical data sets, we developed and created risk maps related to the distribution of vector sand fly species. We assumed that the maps enabled us to predict the future condition of the CL in the study areas. According to the maps, the spatial probability of the presence of *P. tobbi* was higher than the other species. We observed that southwest part of the Imamoglu district had high

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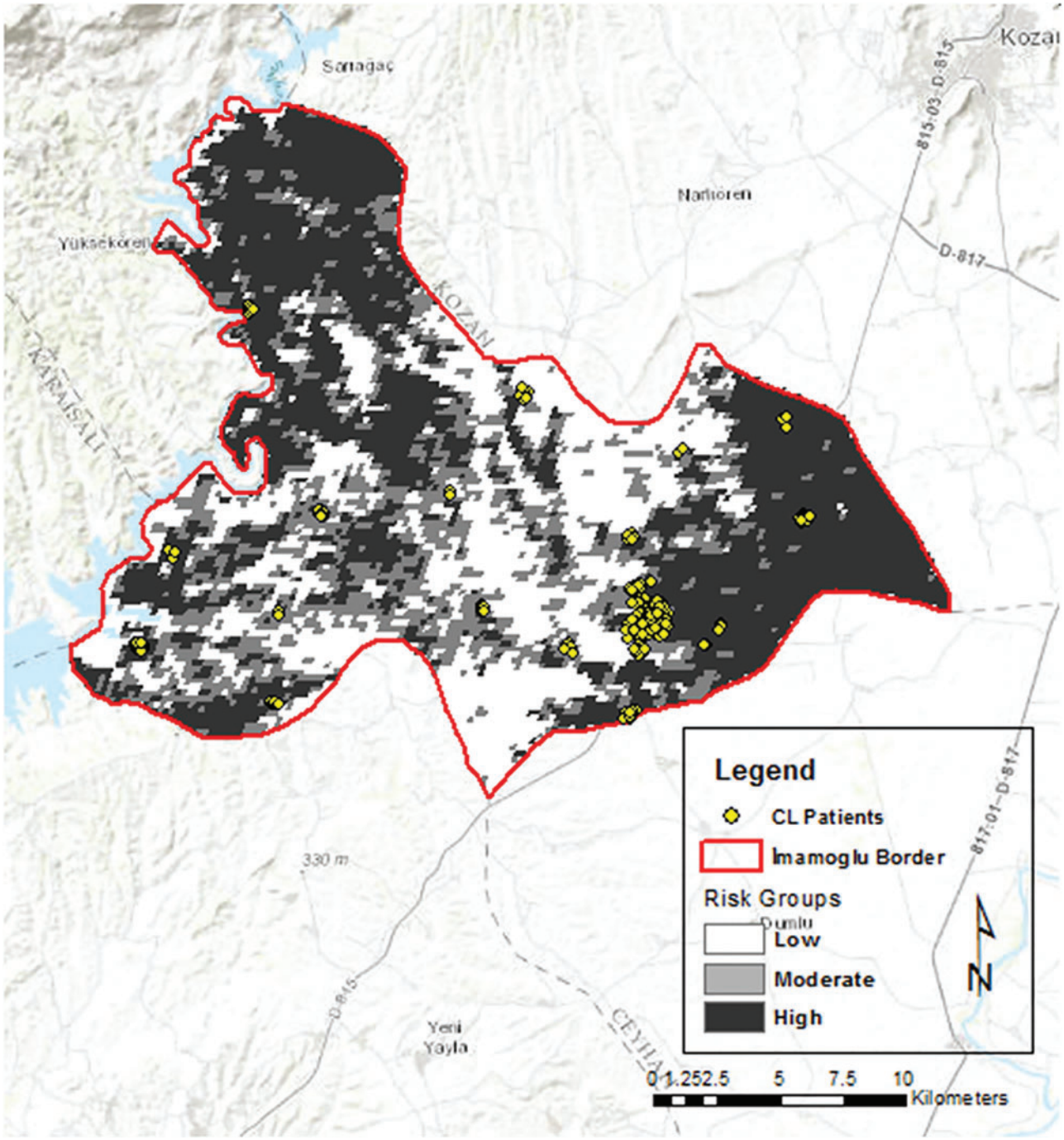


Fig. 5. Validation of risk map based on number of the cutaneous leishmaniasis cases.

Table 3. The rates of cutaneous leishmaniasis cases at different risk levels

Risk levels	No. of CL cases	%
High	108	48.43
Moderate	72	32.28
Low	43	19.28
Total	223	100

level of CL risk owing to the probability of the presence of *P. neglectus/syriacus* and *P. perfiliewi*, which significantly correlated with EMIS31 data (Fig 4b).

In conclusion, GIS tools and mapping technologies are of great importance in analyzing and controlling of vector-borne diseases. Created risk maps enable researchers to control and observe the disease with lower cost in all leishmaniasis-endemic regions in Turkey and other countries.

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