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Modelling climatic suitability and dispersal for disease vectors: the example of a phlebotomine sandfly in Europe

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Abstract

Climate change is thought to assist spreading vector-borne diseases. During the last years, ecological niche modelling has been increasingly applied to predict the current distribution of disease vectors and their potential responses to climate change. However, sandflies and their transmitted diseases are only scarcely investigated via niche modelling. Here, we propose a methodological approach to combine specific dispersal pathways for a sandfly species (*Phlebotomus perniciosus*) with the shifting climatic niche in the face of climate change. Current climatic suitability for the species was determined. Future projection is based on data of a regional climate change model. We defined a cost-surface assigned by the changing climatic suitability and expert knowledge on species dispersal ability. The derived travel costs correspond to the effort for the species to move across the landscape to climatically suitable habitats. In future steps, least-cost paths will be calculated for this and further sandfly species with assumed spreading tendencies to Central Europe in the 21st century. Challenges are the integration of wind speed and biotic interactions.

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Keywords: global warming; leishmaniasis; MaxEnt; Regional Climate Model; sandfly-borne disease; species distribution model

1. Background: Sandflies as disease vectors in the light of climate change

Globally, vector-borne diseases pose a serious and increasing problem to public health. Today, almost one third of the emerging cases of infectious diseases are vector-borne [1]. Most of the disease vectors are ectothermal arthropods which cannot regulate their body temperature themselves. Therefore, climate change may be associated with spatio-temporal variations in occurrences of vector-borne diseases [2].

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While mosquito-borne diseases such as Malaria and Dengue-fever attract much attention in science and policy, sandfly-borne diseases are often neglected. Nevertheless, especially leishmaniasis constitutes a serious human and animal health concern [3].

In Europe, phlebotomine sandflies have been thought to be restricted to the Mediterranean. However, in recent years a northward spread of the disease vector is documented in Italy [4]. Sandflies have recently even been caught north of the Alps in Central Europe [5], where they have not been recorded before. This may either indicate spreading tendencies from the Mediterranean or range expansions from potential small Central European refugial areas. It is noticed that even moderately increasing temperatures in the 21st century would provide further suitable areas for the infestations of sandflies in Germany [6]. Based on these findings the question arises which regions explicitly could provide suitable climatic habitats in the near future and whether sandflies are capable to disperse to these potential climatically suitable areas.

2. Ecological niche modelling of sandflies and sandfly-borne diseases

Correlative ecological niche models refer to the algorithms relating observed presences (and absences) of a species to values of ecological variables at those sites. The aim is to determine a species' known and inferred distribution in the environmental space. They have become increasingly important due to advanced modelling techniques for determining spatial distribution patterns of species and their potential responses to environmental changes [7]. The organisms (pathogen, vector and reservoir/host) involved in a chain of infection of a vector-borne disease are dependent on a specific environment. Therefore, niche modelling can be expected to be a useful tool for projecting occurrences of vector-borne diseases.

Table 1. Peer-reviewed articles dealing with the topic of sandflies or/and sandfly-borne diseases and ecological niche modelling.

Reviews or reports	Vector/reservoir/disease	Climate change		
Peterson (2006) [8]	Sandflies/further vectors	Effect		
De la Roque et al. (2008) [9]	Leishmaniasis/further diseases	Effect		
Ready (2008) [10]	Sandflies/Leishmaniasis	Effect		
Colacicco-Mayhugh et al. (2009) [11]	Sandflies/further vectors	Effect		
Research	Vector/reservoir/disease	Climate change	Region	Software
Peterson and Shaw (2003) [12]	Sandflies	Positive effect	Brazil	GARP
Peterson et al. (2004) [13]	Sandflies	Not addressed	Brazil	GARP
Nieto et al. (2006) [14]	Leishmaniasis	Not addressed	Brazil	GARP
Chamaille et al. (2010) [15]	Leishmaniasis	Not addressed	France	MaxEnt
Colacicco-Mayhugh et al. (2010) [16]	Sandflies	Not addressed	Middle East	MaxEnt
Gonzales et al. (2010) [17]	Sandflies and reservoir	Positive effect	North America	MaxEnt

We conducted a literature survey (January 2011) in the ISI Web of Knowledge (literature databases: Web of Science, BIOSIS Previews and Medline) to search for peer-reviewed articles dealing with ecological niche models and their application to sandflies and sandfly-borne diseases. We found ten articles addressing explicitly this topic (Table 1). Possible application of niche modelling for leishmaniasis or sandflies without concrete research was found in four articles [8]-[11]. In those reviews or reports, climate change is noticed to affect vector and disease occurrences, but without mentioning whether it will benefit spreading tendencies or not. Concrete modelling approaches are used in six original research papers [12]-[17]. America is addressed in the majority of the research articles as study area. Those authors who

integrate climate change scenarios point out a potential spread of sandflies [12][17]. Nevertheless, for some *Lutzomyia* species (*L. intermedia* and *L. migonei*) endemic in South America only subtle improvements in climatic conditions are projected [16]. Europe is solely addressed in the work of Chamaille et al. (2010) [15]. There, ecological variables refer to the occurrence of canine leishmaniasis. Until today, explicit modelling of the current distribution of *Phlebotomus* species and of their potential shifts in spatial patterns of occurrence in the face of European climate change is missing.

3. Case study: Combining climatic suitability and dispersal ability of *Phlebotomus perniciosus*

3.1. Current and projected climatic suitability for *Phlebotomus perniciosus*

Maximum entropy algorithm implemented in MaxEnt software [18] was used for modelling the current and projected distribution of *Phlebotomus perniciosus* (*P. perniciosus*) in this case study. MaxEnt is found to be superior in performance in comparison to other algorithms that are capable to handle presence-only data [7]. Recently, MaxEnt has successfully been applied to model the ecological niche of leishmaniasis as well as sandflies and substituted GARP as preferred modelling software (Table 1).

Bioclimatic variables [19] were used to predict the current distribution of *P. perniciosus*. The climatic niche was then transferred to the expected climatic conditions for the upcoming time-period (2011-2040; IPCC A1B scenario). The climatic projection is based on data of the regional climate model COSMO-CLM that covers entire Europe and is nested into the global model ECHAM5 [20]. Regional climate models integrate regional structures of land cover and topographical specifics in the dynamically downscaling procedure of their driving model [21]. Hence, studies concerning vector-borne diseases in climate change investigations benefit in particular from applied spatio-temporal highly resolved climate change projections [2][21]. Results are shown using the example of Bavaria (Southeast Germany).

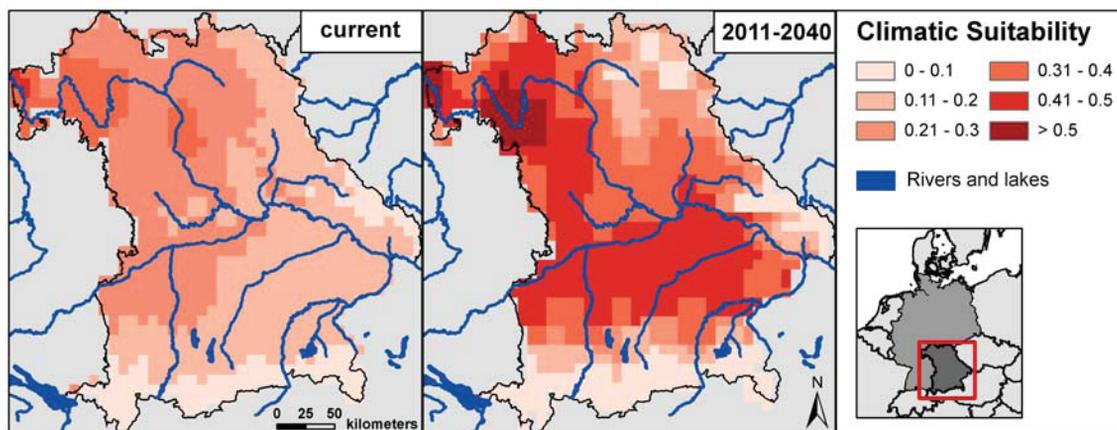


Fig. 1. Current and projected (2011-2040; A1B scenario) climatic suitability for *Phlebotomus perniciosus* in Bavaria (Southeast Germany). Values for climatic suitability range theoretically from zero to one. Establishment generally seems unlikely in regions with unfavourable conditions (values < 0.3). Climatically suitable regions are labelled by values > 0.5. Climatic suitability was modelled with MaxEnt based on a statistical selection of significant bioclimatic variables. 70% of the 271 spatially explicit species presence records were used to train the model. The remaining occurrence points were used to test model quality. The model was run 100 times and the results were averaged. The AUC value for the test data was 0.92 (\pm 0.01) and indicated high model quality. An AUC value of 1 would represent a perfect fit.

Currently, no part of Bavaria provides suitable climatic conditions for *P. perniciosus* (fig. 1). Only in a small region in the outermost Northwest, climatic requirements of the species are almost fulfilled. Applying the A1B scenario for the next time-period (2011-2040), the river valley of the Main in the Northwest of Bavaria offers climatically suitable conditions. Then, also further parts in western Bavaria and central parts along the the river valleys Danube and Isar will almost fulfill climatic requirements. Mountainous regions such as the Alps in the South and the Bavarian Forest in the East will persist to be completely climatically unfavourable for vector establishment.

3.2. Cost analysis and dispersal ability for *Phlebotomus perniciosus*

Least-cost analysis helps to identify the potential dispersal pathway, which is directed to climatically suitable habitats. The path function is based on graph theory and determines the shortest cost distance in a landscape between a specified origin and a target area. In ecology, least costs correspond to the least effort for a species that is moving through a landscape, assuming the species is capable to take the optimal dispersal pathway [22]. We defined a cost surface (fig. 2, a) that must be crossed by *P. perniciosus*. The cost surface includes, firstly, changing climatic suitability between the current conditions and the subsequent time-period (2011-2040; A1B) and, secondly, further expert knowledge on sandfly ecology and ability to disperse, such as flight range, topography and their dependency on landcover [23]. River valleys for instance are attributed as preferred dispersal pathways (no costs), lower mountainous regions exhibit a reduced ability to be crossed (mid to high costs; depending on altitude) and the highest regions above 2000 m above sea level are efficient barriers that exclude dispersal.

Based on the cost surface, we calculated the cost distance (CD) (fig. 2, b) as accumulated shortest weighted distance (“travel costs”) for movement between raster cells with CS_1 as first cost value of the starting grid cell defined by the cost surface and CS_n as end point. For vertical and horizontal movement CD was calculated by:

$$CD_{\text{orth}} = (CS_1+CS_2)/2 + (CS_2+CS_3)/2 + \dots + (CS_{n-1}+CS_n)/2$$

and for diagonal movement in the same manner (but with length correction) by:

$$CD_{\text{diag}} = ((CS_1+CS_2)/2 + (CS_2+CS_3)/2 + \dots + (CS_{n-1}+CS_n)/2) \cdot 1.414214.$$

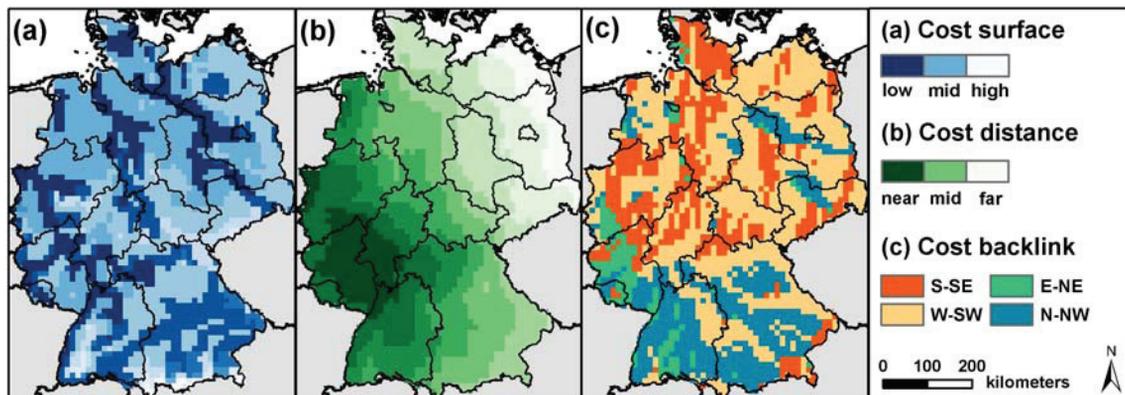


Fig. 2. Cost analysis for *Phlebotomus perniciosus*, aiming to estimate the species' dispersal probability in Germany. Least-cost path requires the following input. Initially, a cost surface is generated (a), where travel costs are indicated. Then, a specific cost distance (b) that is based on defined occurrence points and the cost surface to be crossed is determined. The cost backlink (c) is a qualitative expression and indicates for each raster cell, to which of the neighboring raster grids the costs are lowest. Based on the occurrence points as start, a defined target area and the calculated cost distance and backlink, the final path of least-cost can be defined.

Cost distance and spatial distance are not necessarily similar (fig. 2, b). The cost distance is for instance relatively far to southeastern Bavaria, although *P. perniciosus* is present in northern Italy. Here, the Alps cause high costs to cross. The species is furthermore located in western and southwestern parts of Europe. As a consequence, the cost distance is nearest to western Germany as there are only little cost barriers for species movement. Values of cost distance increases to northeastern Germany. The cost backlink (fig. 2, c) of each raster cell is determined by the neighbouring raster cell to which costs are cheapest and marked in direction to this cell. Central, northern and northeastern Germany mainly show backlinks to western, southwestern and southern directions. Only few southern and northern Bavarian areas indicate a backlink to southern direction, although many records are documented in northern Italy (not presented here). Most parts of Bavaria, especially the central parts, show backlinks to western and northwestern regions. Hence, it is likely that *P. perniciosus* may disperse from western Europe towards Bavaria. A direct northward spread from Italy may be blocked by the Alps.

4. Discussion and outlook

Here, we propose a method to improve conventional niche modelling with integrated species-specific dispersal ability. Based on this, the least-cost path as most likely spatial trajectory of the species dispersing to Bavaria can be calculated on basis of the cost distance and cost backlink for *P. perniciosus*. Climate change alters dispersal and movement patterns of insects. It has to be acknowledged that the direction of movement may not be optimal in all cases. Especially, dispersal behaviour of individuals between populations may differ from the general tendency of the metapopulation level [22].

Nevertheless, ecological niche modelling in combination with least-cost path analysis offers the opportunity to detect whether sandflies are able to occupy their potential suitable habitats by natural dispersal. It is uncertain, if humans assist the migration of sandflies directly. Hence, such potential accidental carry-overs are not considered in this study. Spreading tendencies for other *Phlebotomus* species can be assumed as well. Probably, these species may also disperse to Central Europe. Knowledge concerning biotic interactions and the competitive ability of the species in particular is missing. Therefore, experiments and field observations must be intensified in order to reduce uncertainty. Integrating biotic interactions into environmental niche modelling under climate change conditions would yield more realistic projections [24].

Comparing climate change scenarios and model algorithms will reduce the uncertainties of species range shifts [25]. Moreover, wind speed as well as differences in potential flight ranges have to be considered. Wind is not a mere vector but affects the behaviour of the species. Sandflies reduce their flight activity with increasing wind speed [26]. Generally, future research and in particular modelling approaches will require more knowledge on sandfly ecology and biology. Our approach represents a powerful tool for detecting regions with potential infestations and establishment of disease vectors. Already early stages of risk exposure can be identified. Hence, efficient monitoring and surveillance activities can be specifically directed to these target areas.

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