Towards the identification of potential infectious sites for bluetongue in Italy: a spatial analysis approach based on the distribution of *Culicoides imicola*

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Summary

A geographic information system (GIS) based on grids was developed by the National Reference Center for Veterinary Epidemiology at the Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise 'G. Caporale' (IZS) in Teramo to identify potential infectious sites for bluetongue (BT) disease in Italy. Geographical and climatic variables were used to build a spatial process model (SPM); the different layers were combined by sequential addition. The final grids (with a cell size of 0.0387 decimal degrees) were generated for each season of the year, and the suitability of each cell for the presence of *C. imicola* given a value ranking from 0 to 10. While this model more accurately predicts the presence of *C. imicola* in the Basilicata and Sicily regions, it still over-predicted its presence in the Puglia region. This could be due to the occurrence of calcareous soils which dominate the Puglia landscape. The present SPM is an additive model that assigns an equal weight to each variable. However, the results suggest the existence of hitherto unconsidered variables that significantly influence the prevalence of *C. imicola*. To reflect their importance, these variables should be assigned a higher weighting in future models. However, the decision in regard to precisely what this weighting should be depends on a very thorough knowledge of the ecology of *C. imicola*.

Keywords

Bluetongue – *Culicoides imicola* – Geographic information system – Italy – Spatial model.

Introduction

A significant amount of research on the distribution of bluetongue (BT) and its principal insect vector *C. imicola* in the Mediterranean Basin was generated following incursions of the disease into southern Europe between 1998 and 2003. Special attention has been focused on modelling the spread of *C. imicola* and the effect of climatic and geographic factors on its presence (1, 4). The National Reference Center for Veterinary Epidemiology at the Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise 'G. Caporale' (IZS) in Teramo, developed a grid-based geographic information system (GIS) to identify potential infectious sites for BT in Italy through the analysis of areas found most suitable for the persistence of *C. imicola*. A spatial process model (SPM) (5, 7) was created in an effort to identify areas into which BT virus (BTV) would be most likely to penetrate, but the model is based solely on the principal vector of BT in the Mediterranean, namely *C. imicola*. The recent incrimination of at least two other species of *Culicoides* in the transmission of BTV in Italy (3, 6), the ecologies of which differ from that of *C. imicola*, complicates the epidemiology of the disease, and will require separate spatial analyses in future.

Materials and methods

The SPM was developed in four stages, as follows:

1) datasets input
2) creation of datasets for the generation of new information
3) reclassification of each dataset to a common scale
4) combining datasets for the identification of suitable locations. The analysis considered the

four seasons: spring (March, April, May), summer (June, July, August), autumn (September, October, November) and winter (December, January, February).

Step 1: The following grids and datasets on Italy were considered to explain the spatial interactions:

a) the digitalised elevation model (DEM) built using the isohypse of 1:100 000 topographic map of Italy produced by the Military Geographical Institute (IGM)
b) land use (Corine Land Cover version 12/2 000 European Environment Agency (www.eea.eu.int)
c) the aridity index (European Environment Agency www.eea.eu.int)
d) the lithologic environment (derived from a 1:500 000 map on the humidity retention capacity of soil)
e) the monthly normalised difference vegetation index (NDVI) for 2000-2002 (Royal Netherlands Meteorological Institute (KNMI) Observations and Modelling Department R&D Observations Division)
f) the animal population density
g) the daily minimum temperatures from the 81 weather stations of the Italian Air Force Meteorological Service for 2000-2002.

Step 2: A slope grid indicating the maximum rate of change between each cell and its neighbours was derived from the DEM; four grids of mean minimum temperature (one for each season) were created through Ordinary Kriging Interpolation in ArcGis 8.2 using the data from the 81 weather stations; four mean NDVI grids (one for each season) were calculated also. Through the spatial extension in ArcGis 8.2 each grid was used to extract values for each site where midge catches were made between 2000 and 2002. From the values obtained, frequency distributions were created and the percentage of positive and negative catches calculated (an example is provided in Table I).

Step 3: Each of the suitability factors was reclassified on a common scale from 0 to 10, creating new integer grids for each variable. The risk reclassification was made using the percentage of positive catches/total catches falling in each class (Table I).

Step 4: For each season, the eight grids were combined, assigning the same weight to each layer. The final grids had a cell size of 0.0387 decimal degrees. The following formula, generating a ranking for each cell for *C. imicola* suitability, was adopted:

1/8*elevation + 1/8*aridity + 1/8*landuse + 1/8*density + 1/8*ndvi + 1/8*slope + 1/8* temperature + 1/8*lithologic environment.

Table I
Example of the aridity index reclassification in Microsoft® Excel: percentage of sites positive for *Culicoides imicola* according to various aridity classes

1	A Aridity class	B Positive sites	C Negative sites	D Total sites	E Positive sites (%)	F Risk class
2	<=60	41	161	202	20.3%	4*
3	60-70	49	106	155	31.6%	6
4	**70-80**	**164**	**143**	**307**	**53.4%**	**10**
5	80–90	124	281	405	30.6%	6
6	90-100	59	263	322	18.3%	3
7	100-110	11	217	228	4.8%	1
8	110-120	3	114	117	2.6%	0
9	>120	1	141	142	0.7%	0

* $Fi = round\left(\frac{Ei * 10}{Max(Ei)}, 0\right)$

Results

Examples of input variables included in the model are shown in Figures 1, 2, 3, 4 and 5.

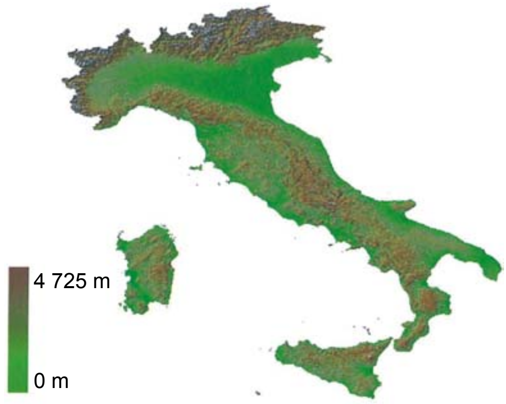

Figure 1
Elevation above sea level

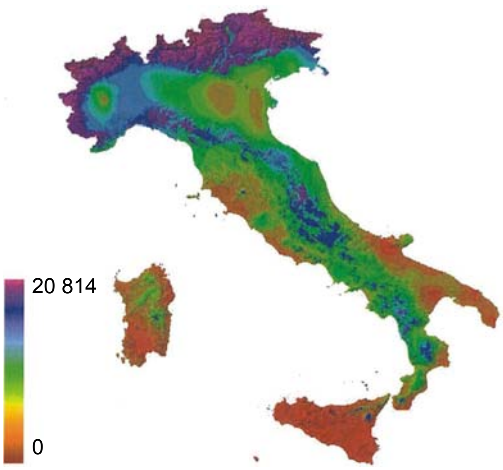

Figure 2
Aridity index

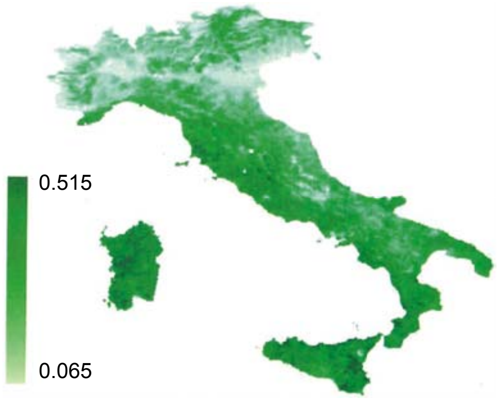

Figure 3
Normalised difference vegetation index in winter

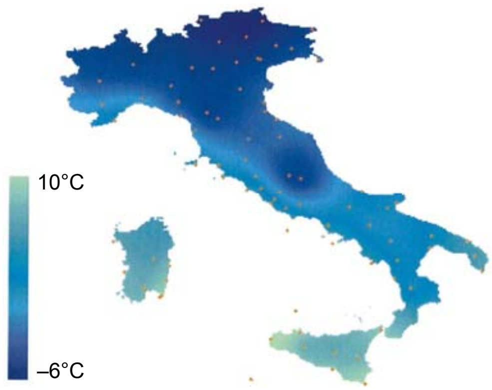

Figure 4
Mean minimum temperature in winter

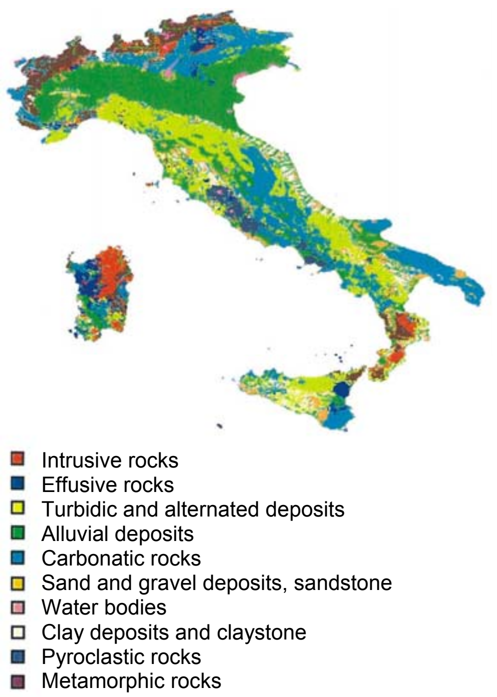

Figure 5
Lithologic environment

The characteristics of territories with the highest percentage of sites positive for *C. imicola* are listed in Table II. The final grids with geographic and climatic characteristics suitable for *C. imicola* are illustrated in Figures 6, 7, 8 and 9, where the risk classes (ranked from 7 to 10) are depicted in shades of red. Figure 10 gives the distribution of *C. imicola* presence from 2000 to 2003 and the distribution of BT seroconversions in cattle in 2002 and 2003.

Table II
Highest ranking values of the eight variables associated with the presence of *Culicoides imicola*

Variable	Risk values
Elevation	0-50 m above sea level
Slope	0-3 degrees
Aridity index	70-80
Landuse	Permanently irrigated land
Animal density	≥250 animals/km²
Type of soil	Intrusive rocks
Temperature (winter)	6°C-7°C
Temperature (spring)	10°C-11°C
Temperature (summer)	19°C-20°C
Temperature (autumn)	14°C-16°C
NDVI (winter)	0.445-0.49
NDVI (spring)	0.195-0.34
NDVI (summer)	0.195-0.25
NDVI (autumn)	0.345-0.39

NDVI normalised difference vegetation index

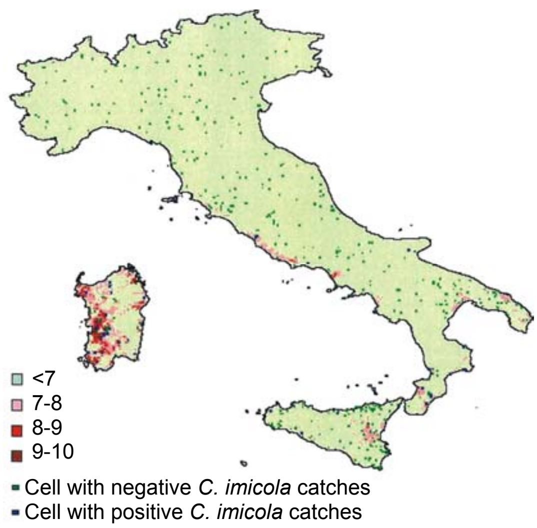

Figure 6
Risk map for *Culicoides imicola* in winter

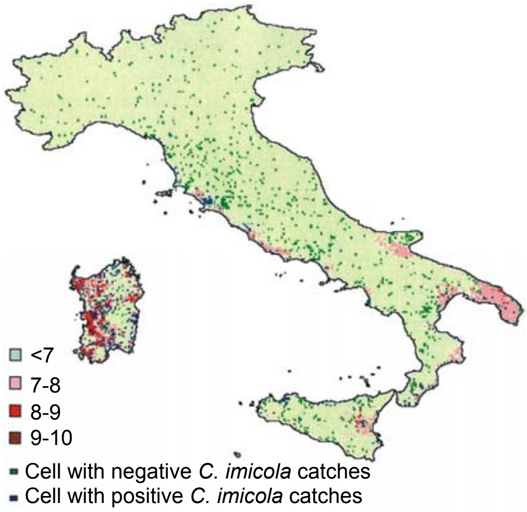

Figure 7
Risk map for *Culicoides imicola* in spring

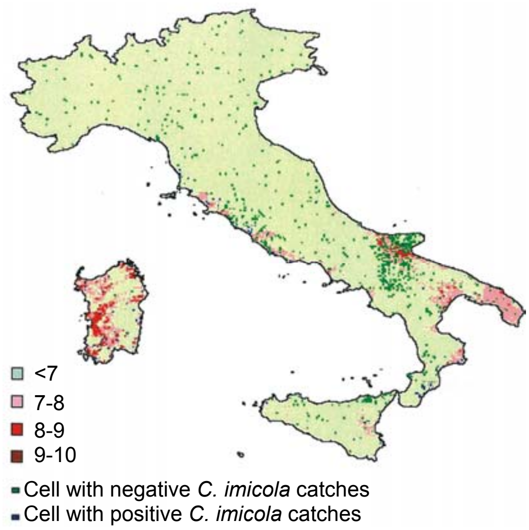

Figure 8
Risk map for *Culicoides imicola* in summer

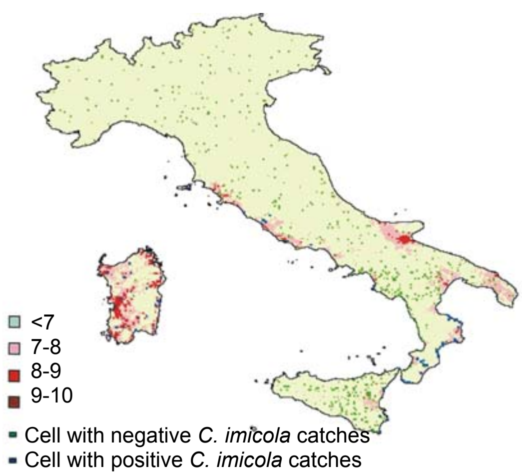

Figure 9
Risk map for *Culicoides imicola* in autumn

Discussion

Previous models have indicated that temperature, elevation, humidity, rainfall and NDVI are the most important variables that predict the presence of *C. imicola* across the Mediterranean Basin (1, 2, 4). The success of these predictions has, however, been partial which indicates that the full range of climatic and geographic variables that determine the presence of this vector have yet to be identified. In an effort to refine these earlier predictions, new variables were taken into consideration, these including the aridity index, lithologic environment and land use. Other adjustments made were to consider the seasons separately since climatic variables and NDVI have a clearly seasonal pattern. In the earlier models, and specifically in those for Italy, the presence of the vector, in a number of areas, was either over-predicted or under-predicted. For example, the model of Conte *et al.* (4), based only on presence/absence data (i.e. not refined to using actual abundances which can fluctuate greatly), over-predicted *C. imicola* along the entire southern coastline of the island of Sicily, and under-predicted it for the mainland region of Basilicata. For both of these areas, the model presented here, and more specifically that for autumn (the period of greatest disease prevalence), shows a marked improvement over our earlier results (4). However, a persistent exception was that the model still incorrectly predicted the vector to be widely present in the Puglia region. However, this is not the case as demonstrated by hundreds of *Culicoides* light-trap collections made over more than one season in the field (Fig. 10).

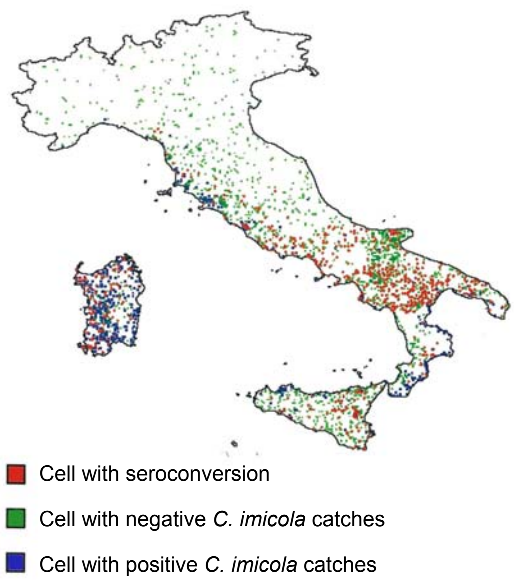

Figure 10
Distribution of *Culicoides imicola* presence from 2000 to 2003 and distribution of bluetongue seroconversions in cattle in 2002 to 2003

In the present model, the disagreement seems to be due to the similarity between Sardinia and the Puglia region for almost all the variables except for lithologic environment. As Figure 11 clearly shows, calcareous soils dominate the landscape in the Puglia region. This principal edaphic difference would suggest that this is a factor that significantly influences the ability of *C. imicola* to persist locally. However, this remains a 'best-fit' hypothesis that requires confirmation through additional testing as the 'heel' of Italy may also experience higher average winds, which could also decrease flight and feeding activity in *C. imicola*. At present, the SPM is an additive model that assigns equal weight to each variable. This would need to be improved as it would appear that a specific variable (such as calcareous soil) has a causal relationship with the total absence of *C. imicola* locally. From the above, it is obvious that gaps exist in the current knowledge and understanding of climatic and geographic factors (and their interactions) that affect the survival and spread of *C. imicola*. Much remains to be done before *C. imicola* can be predicted with greater accuracy around the Mediterranean Basin.

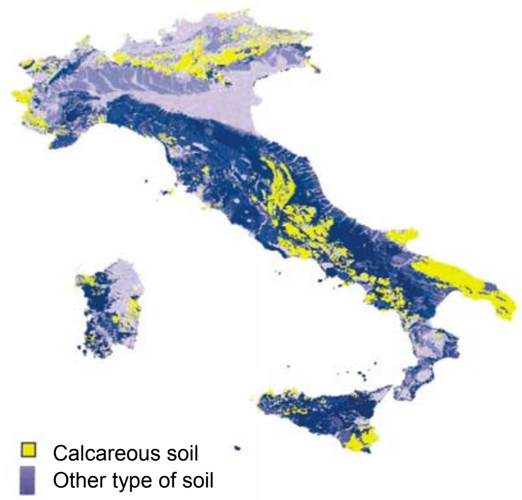

Figure 11
Calcareous areas of Italy

Another serious complication revealed was that during the current incursions of BT into Italy seroconversions in sentinel cattle and outbreaks amongst sheep also occurred in areas in which *C. imicola* was not to be found or, if found, its abundances were very low. In some of these outbreaks, at least two additional species of Palaearctic *Culicoides* were incriminated in the transmission of the disease. By definition, each *Culicoides* species in nature occupies a different niche, and consequently future modelling of these species as novel vectors of BT will necessitate the inclusion of variables different from those used for *C. imicola* in the present study. This in turn demands a fairly detailed understanding of the life-cycles of the new vectors, which, for species in the Obsoletus and Pulicaris Complexes, may be even less well understood than for *C. imicola*.

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