

SPATIAL ANALYSIS OF CHIKUNGUNYA AND DENGUE EPIDEMIC RISK IN EMILIA-ROMAGNA REGION, ITALY

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Introduction

Outbreak risk for Chikungunya (CHIKV) and Dengue (DENV) viruses is influenced by different parameters among which the distribution and density of the vector population. The basic reproduction number $R_{\scriptscriptstyle 0}$, i.e. the number of secondary cases produced by one initial case in a completely susceptible population, is usually used to create epidemiologic risk maps.

The present study was carried out within the framework of the Emilia-Romagna *Aedes albopictus* monitoring and control program with the aim to create epidemic risk maps and cluster maps for CHIKV and DENV using R₀ model-based and data collected by means of 2606 ovitraps positioned in the urban areas of 248 municipalities. Ovitraps were positioned in each urban area following standard criteria at a mean distance varying in the range 200-600 m, checked weekly from May to October 2009. The statistical model used to calculate the mean egg threshold corresponding to R₀>1 (outbreak risk) was developed on data obtained in a study conducted in 2008 in four cities where a Chikungunya epidemic occurred in the summer 2007

plain municipalities not monitored Adriatic sea Appennini mountains

Padana

administrative borders

Emilia-Romagna region monitoring network 2009.

Matherial and Methods



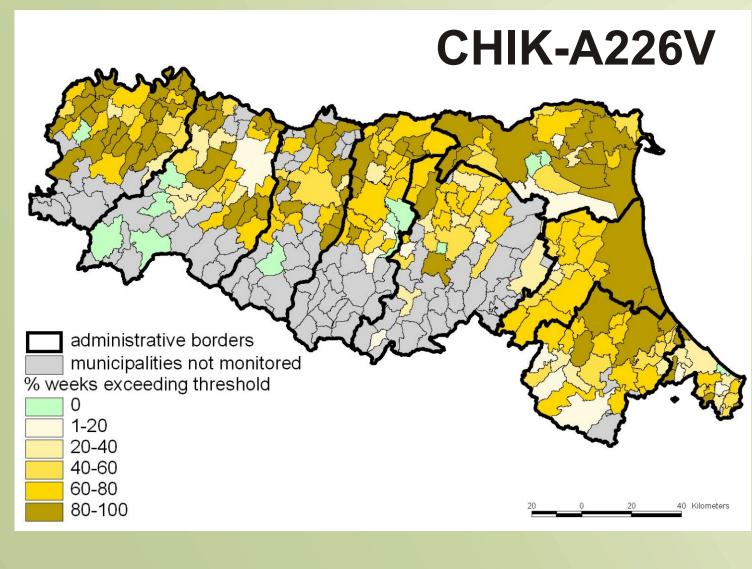
Mean egg density aggregated for each municipality, and mean egg threshold based on R₀ model was calculated for each monitoring week in the period of highest density and diffusion of the species, from week 27 to week 36. Epidemic risk maps (choropleth maps) based on the percentage of weeks exceeding the threshold were produced by using ESRI ArcView 3.3 for: CHIKV, CHIK-A226V mutation, DEN I, DEN II, DEN III and DENV IV (Ae.

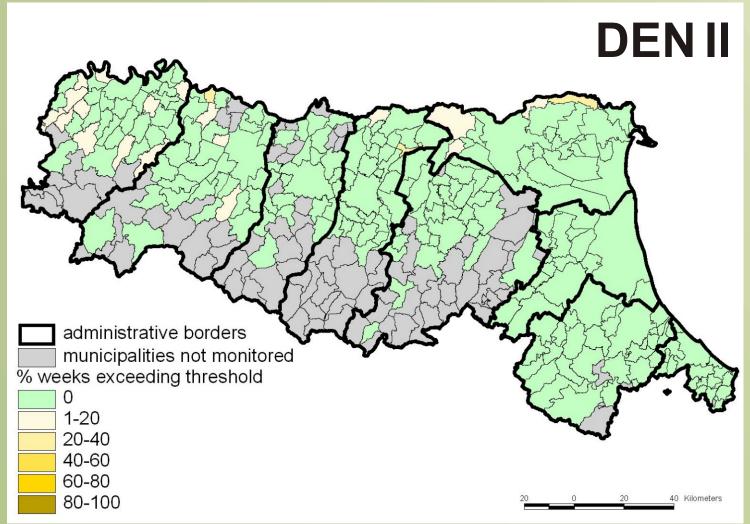
albopictus is a more efficient vector for Dengue virus type

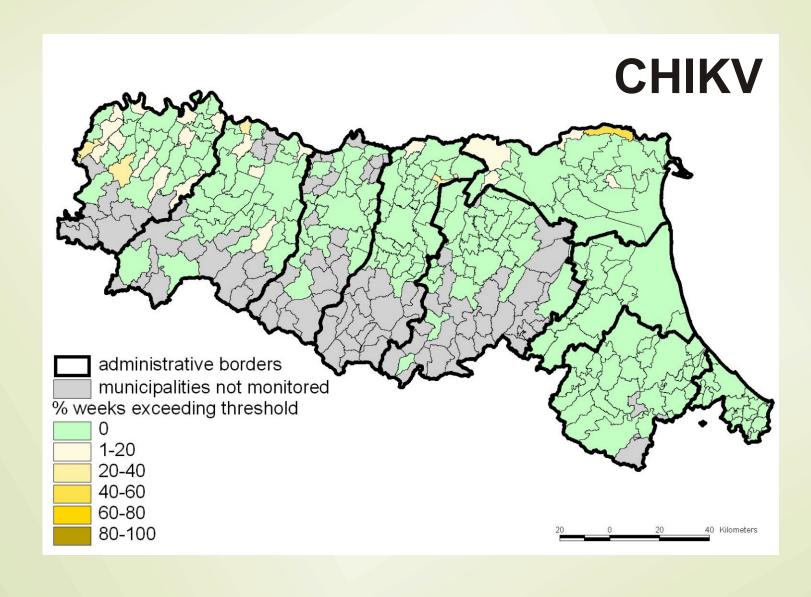
LISA (Local Indicator of Spatial Associations) analysis was used to detect municipality clusters for CHIK-A226V mutation virus, in order to identify large areas with epidemiologic risk. LISA was elaborated by using GeoDa software.

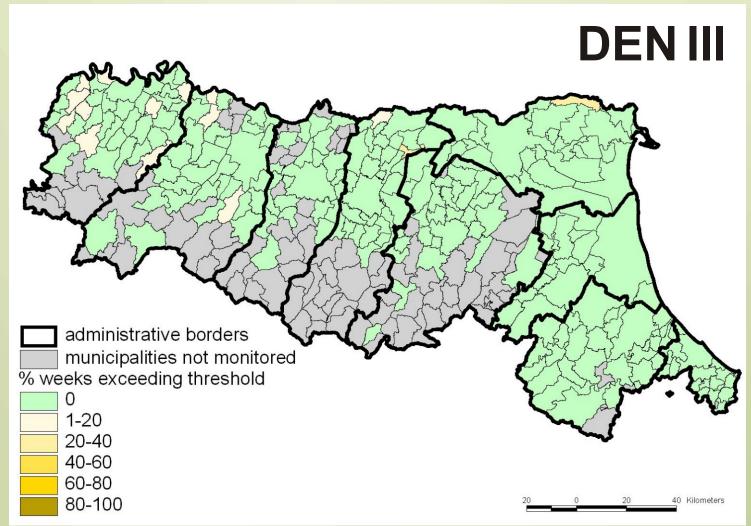
II than for the other types).

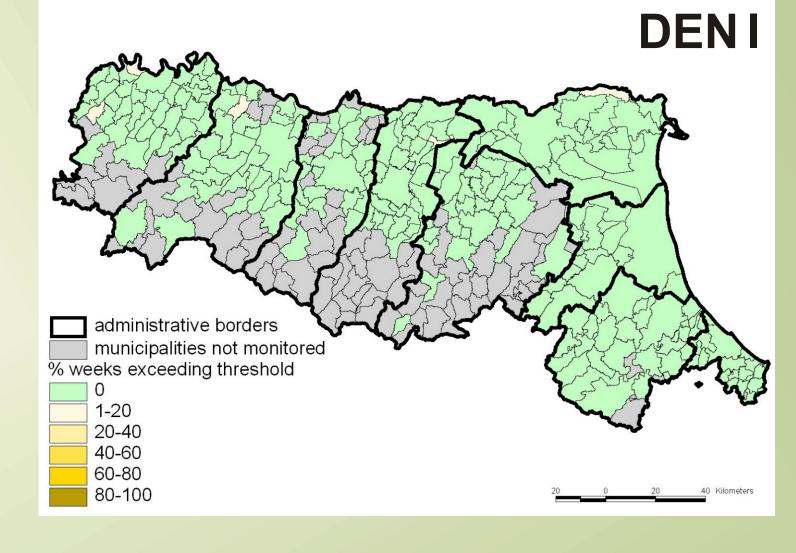
Results and conclusions

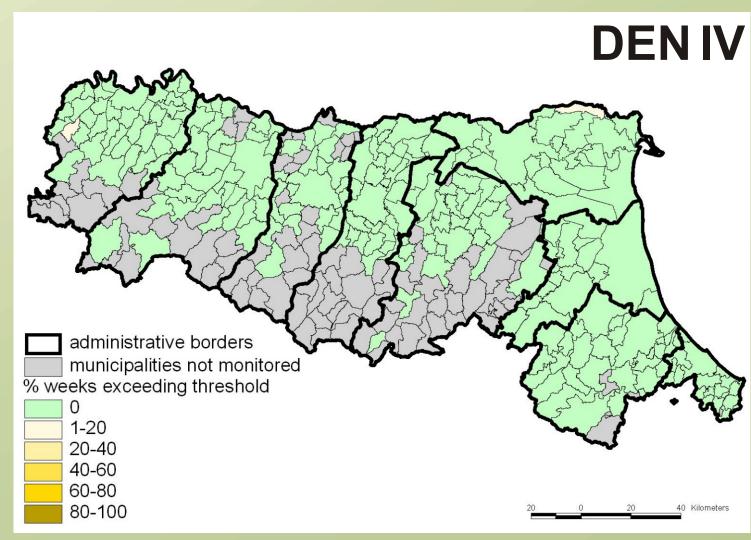




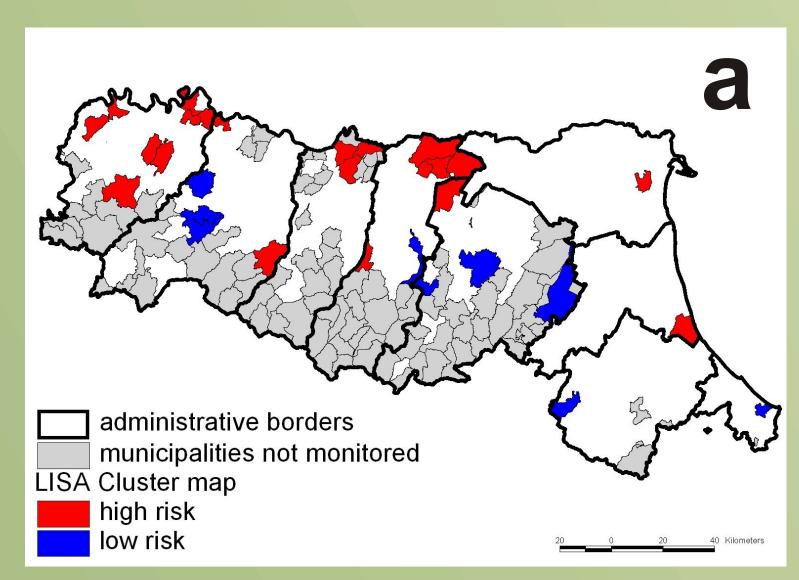


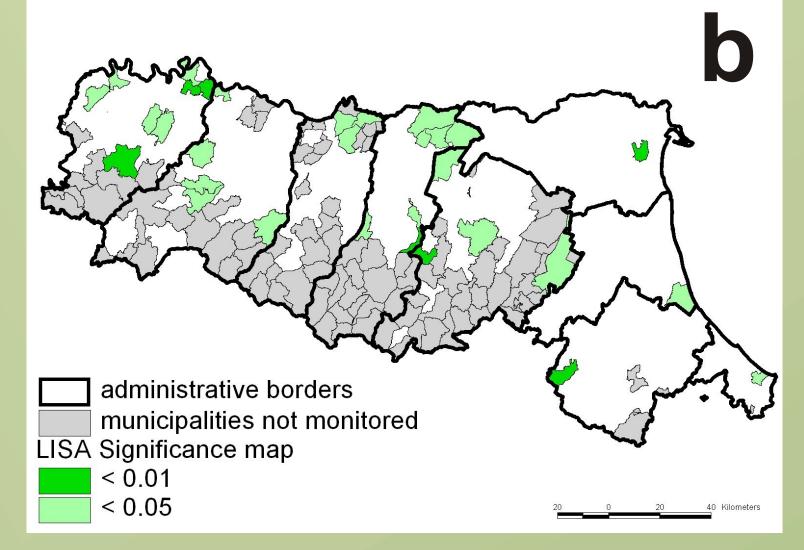






Epidemic risk maps (choropleth) calculated on the percentage of weeks exceeding thereshold during monitoring period (weeks 27-36) for each virus.





Cluster (a) and Significance (b) maps calculated using LISA (Local Indicator of Spatial Associations) for percentage of weeks exceeding threshold for CHIK-A226V mutation virus.

Choropleth maps show high percentages of week threshold exceeding only for CHIK-A226V mutation virus that was the responsible of 2007 outbreak in Italy. LISA Cluster map, that was based on local Moran's I spatial correlation for each municipality, and Significance map, that showed the classification of significant (at p<0.05) municipalities for the Moran's I statistics, were elaborated for percentage exceeding threshold data of CHIK-A226V mutation virus and large municipality areas of high epidemiologic risk (Red color) were identified in the the north of the province of Modena (MO), Reggio Emilia (RE) and Piacenza (PC).

The highly autocorrelated values of these areas could be due to environmental factors, poor mosquito control or other factors that neeeds further investigations.

CHIKV and DENV Epidemic risk maps based on ovitraps data and R₀ model-based are a good tool at low cost for the evaluation of the risk and a possible need to increase mosquito control activities when the mean egg threshold is exceeded.

ACKNOWLEDGMENTS