

Bartonella spp. distribution assessment in foxes coupling geospatially-based techniques

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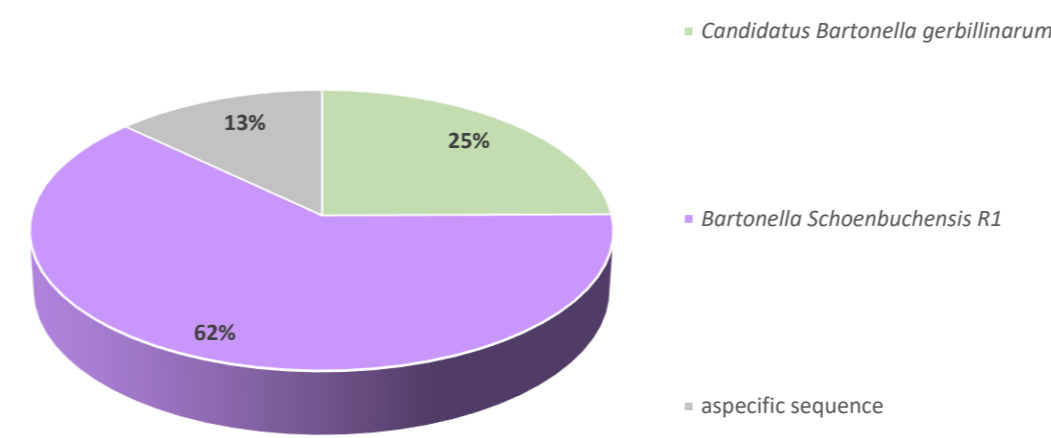
Introduction

Abrupt changes in climate conditions may influence species distribution and pathogens' spreading. Researches on the complex combination between wildlife-diseases dispersion and environmental patterns have to be strengthened, and the assessment of wildlife and zoonotic diseases will represent a key point.

In particular, geospatially-based analysis can help Veterinarians and Public Health Officials to better understand changes in eco-epidemiological factors related to climate changes.

Nowadays, reports on the presence of *Bartonella* spp. in Italy, especially in wild canids, are few in literature. In this study, the prevalence of *Bartonella* spp. was investigated with reference to fox populations (*Vulpes vulpes* L.) culled or found dead in the provinces of Cuneo and Biella (Piedmont) and Aosta Valley (NW Italy).

Results

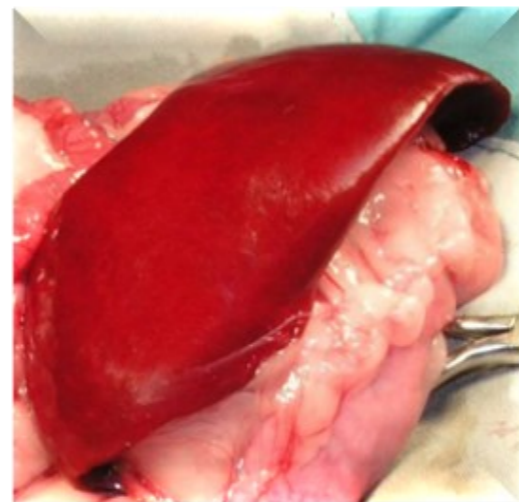


Bartonella schoenbuchensis R1 was found to be the most abundant *Bartonella* species (62.5%, 5/8). *Candidatus* "*Bartonella gerbillinarum*" was found in 25% (2/8) of samples.

Seasonal TCW was positively associated to *Bartonella* spp. infection in foxes as infection was always associated to TCW >0.7. To test the relationship between TCW and *Bartonella* spp. presence, the Moran's index I was calculated per each composite imagery to test the existence of a spatial correlation, and LISA (Local Indicators of Spatial Autocorrelation) maps at the municipal scale were created. Moran I proved to be always ≥ 0.90 , and therefore statistically significant.

Methods

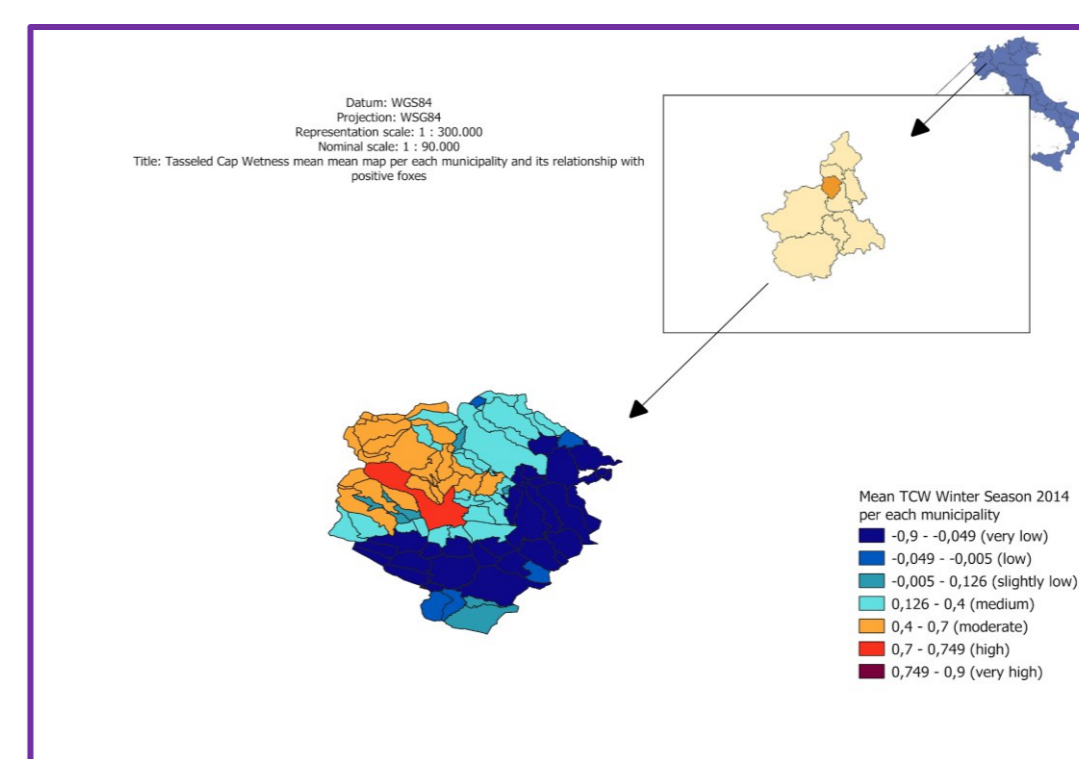
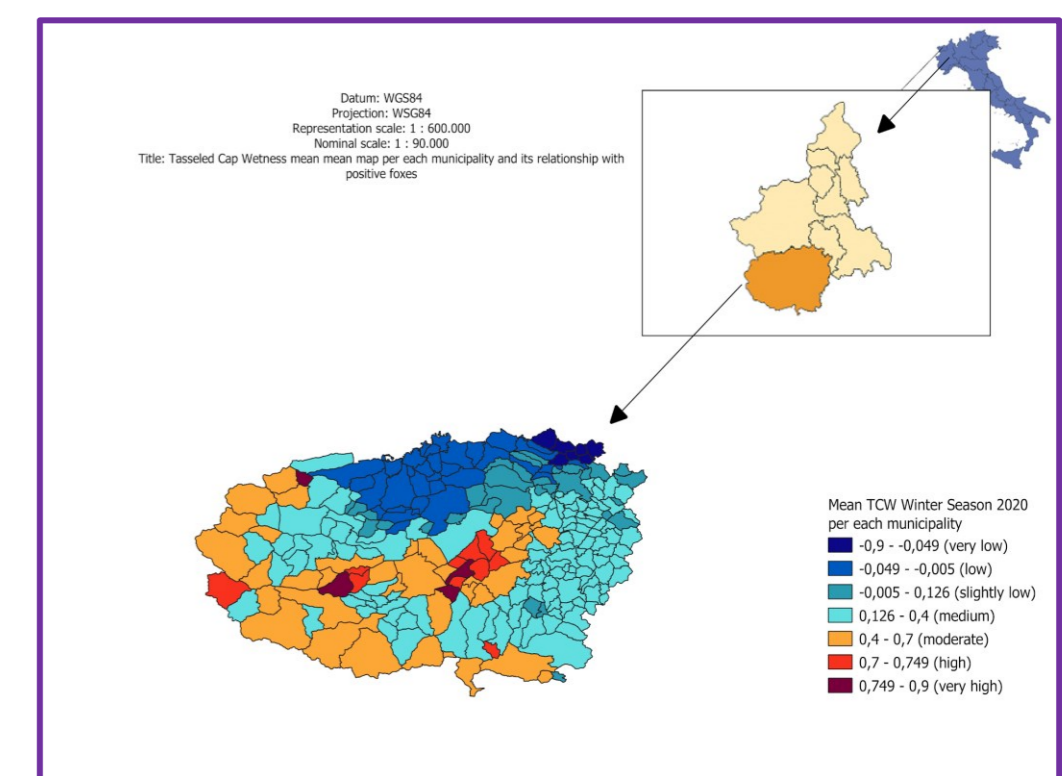
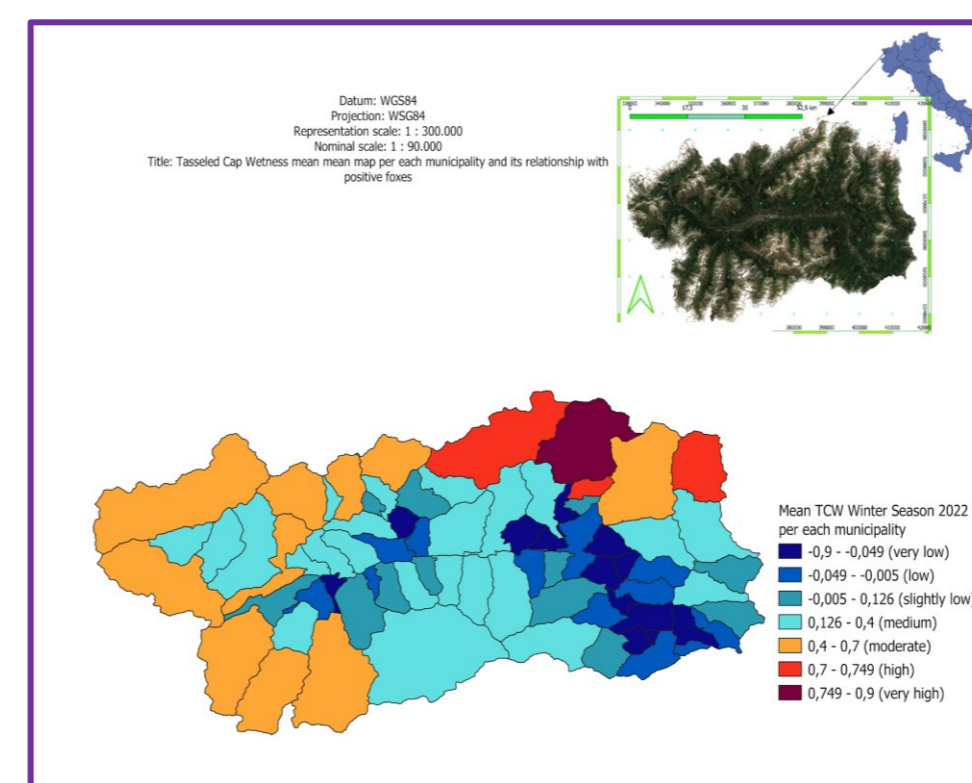
The analysis was carried out at municipality level by coupling molecular diagnostic techniques and satellite remote sensing with the aim of testing possible relationships between pathogen presence and environmental conditions.



The DNA was extracted from the spleen of 114 sampled animals and 7.9% (9/114) of samples yielded *Bartonella* spp DNA by means qPCR (*ssrA* gene).

Positive samples were further analyzed by end-point PCR for *ssrA*, *gltA* and *rpoB* genes of *Bartonella* spp.: PCR products of eight samples were sequenced.

Concerning remote sensing contribution, data from NASA USGS Landsat 4-9 missions (TOA collection), ranging from 2011 to 2022 (ts), were processed in Google Earth Engine. Tasseled Cap Wetness index (TCW) was computed for each date temporal profile consisting of composite images for each meteorological season within ts.



LISA maps show the possible use of TCW as a parameter to facilitate disease management and control.

Conclusion

- A simultaneous spatial correlation between *Bartonella* spp. DNA presence in foxes of the municipalities considered and the TCW was detected.
- Two species of *Bartonella* have been detected in foxes, including *B. schoenbuchensis* R1, capable of causing infection in humans.
- Results show a Remote Sensing One Health application.

Contribution of:

