

Climatic drivers and BTV1 incursion in Central Italy in 2014

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Reference Laboratory

Bluetonque

INTRODUCTION

In 2014, Central Italy experienced an extensive epidemic of BTV1 never recorded before. More than 1,300 outbreaks were notified in different regions of Central Italy (Lazio, Abruzzo, Umbria, Marche, Molise). The entomological surveillance activities identified species belonging to the Obsoletus and Pulicaris complexes, as the main potential vectors. Two main clusters of infection identified at the beginning of the 2014 epidemic, in Terni and Frosinone provinces, were investigated to identify the climatic drivers possibly associated with the unexpected and exceptional spread of the infection observed in the

MATERIALS AND METHODS

Surveillance data

Outbreaks data refers to both clinical cases and seroconversions notified to the National Information System for Animal Disease Notification (SIMAN https://www.vetinfo.sanita.it/). Entomological data are collected in the frame of the National Entomological Surveillance Plan.

Climatic data

Daily minimum, mean, maximum temperature and rainfall form 2007-2014 were provided by the DEWETRA platform, a real-time for integrated system hydro-meteorological and wildfire risk forecasting, monitoring and prevention from the National Department for Civil Protection.

Figure 1. Study area (yellow boxes): BTV1 outbreaks distribution (red points) from 1st January 2014 to 7th of September 2014. In green the DEWTRA weather stations.



Statistical analysis

The daily data were aggregated at weekly level (average for temperatures and cumulated for rainfall). Weekly anomalies in the period 2007-2014 have been calculated by z-scores :

$$Z_{ij} = \frac{x_{ij} - \overline{x}_{i.}}{0.7413 \cdot IQ_{i.}}$$

Where:

is the climatic value in the ith week in the year j

is the average value in the ith week of all the weather stations

 $\overline{X}_{i.}$ in the entire period 2007-2014

is the interquartile range in the ith week in the period $IQ_{i.}$ is the intervelocity $IQ_{i.}$ 2007-2014

To detect longer periods with values systematically above or below the average, the Rescaled Sum of z-scores values has been calculated for each week i and year j considering a moving window of five weeks:

summer of 2014.





RESULTS

Figure 2a and 2b show the BTV1 distribution in 2013 from its arrival (20th of September) in Central Italy to the end of the year.

Figure 3a and 3b show the BTV1 distribution from January to June 2014 and for the entire epidemic (till 22nd of October 2014) in Central Italy.

Figure 5 and 6 reports the results of the anomalies of rainfall and temperatures in the period 2007-2014.

Figure 2a. BTV1 outbreaks distribution (January -September 2013).



Figure 2b. BTV1 outbreaks distribution (January -December 2013).



Figure 3a. BTV1 outbreaks distribution (January - June 2014).



Figure 5. Anomalies in cumulated weekly rainfall recorded in the period 2007-2014 in the study area.



Figure 4. Epidemic curves in the 2013 and 2014 and mean temperature patterns on the thyrrenian coast and inland - Central Italy.



Figure 6. Anomalies in mean weekly temperature (a. minimum, b. mean, c. maximum) recorded in the period 2007-2014 in the study area.



Figure 3b. BTV1 outbreaks distribution (January -October 2014).









Figure 7. Permanent collection sites in Central Italy and *Culicoides* abundance pattern from 2000 to 2014.

Figure 8. Average number of *Culicoides* specimens found in the permanent collection sites in 2012, 2013, 2014.





DISCUSSION

The study demonstrated the important role played by climate and time of arrival of the virus. The limited spread of BTV1 in 2013 was associated to the late arrival of the virus when temperatures were already dropping down (Figure 4), whereas the great expansion of the virus in the following vector season probably depended on the fact that BTV1 never stopped its activity during the winter 2013-2014, as showed by a few seroconversions recorded between January and June 2014 (Figure 3a).

As proven by the analysis of temperature and rainfall anomalies in the two selected study areas, the 2013-2014 winter season was significantly warmer than the normal trend of the period (especially in the minimum values) while summer of 2014 was characterized by lower temperatures (especially for the maximum values) and higher precipitations. Although these anomalies did not influence the abundance of vector populations in the spring and summer months (Figure 7), they probably did in the winter months of 2014 when the Culicoides abundance monthly average was higher than previous years (Figure 8) allowing the virus to overwinter. The heavy circulation of BTV1 and the severity of clinical outbreaks recorded in the regions of the Central Italy leave however a number of "open questions" that need a deeper investigation with a multidisciplinary approach.

Are they related to:

- b the particular adaptation of the BTV1 strain responsible for the 2014 outbreaks to the vector population of the areas?
- The special characteristic of virulence of the BTV1 strain responsible for the 2014 outbreaks for vertebrate hosts?





the improved vectorial capacity of Culicoides species because of warmer winter and cooler summer?

the particular genetic characteristic of the vector population involved in

