

## Bluetongue virus serotype 3 in Italy

Bluetongue virus (BTV), genus Orbivirus - family Reoviridae, causes the bluetongue (BT) disease, one of the OIE - listed major diseases of ruminants. BT has a global distribution normally coinciding with that of the corresponding competent *Culicoides* midges, vectors of the virus.

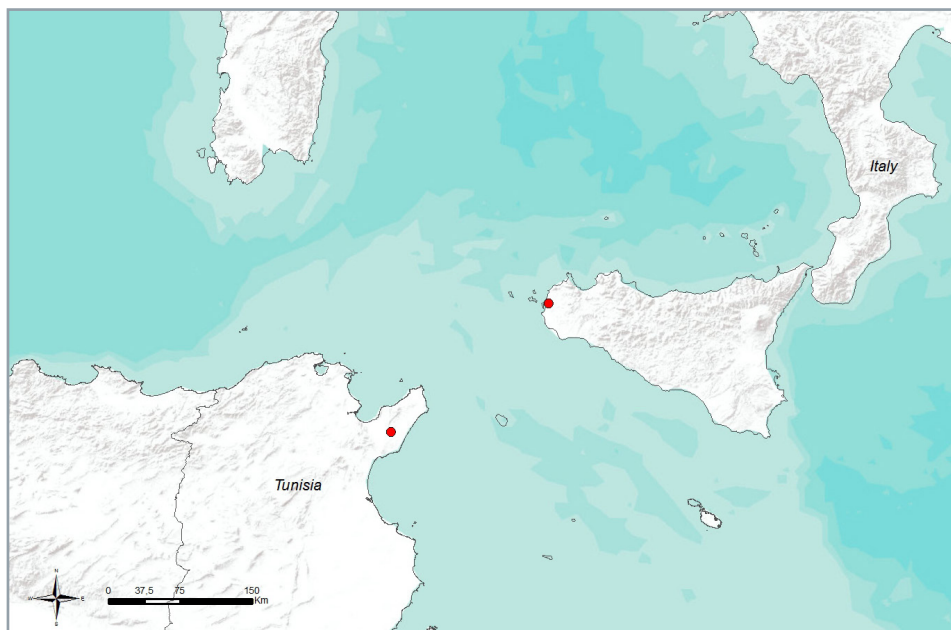
BTV exists into multiple serotypes and two major geographic groups of BTVs have been identified and designated as eastern (e) or western (w) topotypes. They include viruses from Australia and the Middle/Far East, or Africa and the Americas, respectively (Maan *et al.*, 2008).

Since 1998, southern Europe has experienced multiple incursions of different serotypes and topotypes of BTV. Predominantly, BTV incursions have entered southern Europe via two distinct routes. Strains of BTV-1e, BTV-4w, BTV-9e and BTV-16e have all entered the eastern Mediterranean region. BTV-1w, BTV-2w and BTV-4w have entered Europe most likely as a result of wind-blown dissemination of infected midges from Northern Africa. Specifically, the virus had been likely introduced to Europe from Northern Africa via two major gateways: (i) from Morocco to Spain through the Straits of Gibraltar, (ii) from Tunisia to Italy through Sicily or Sardinia (Wilson and Mellor, 2008).

The introduction of BTV from Tunisia to Italy was reported the first time in 2000, when the first BT incursion in Sardinia, was immediately linked with BTV-2w circulation in the northeastern part of Tunisia in 1999 (Calistri *et al.*, 2004). In 2012, a novel reassortant strain of BTV-4w was identified in Sardinia together with BTV-1w (Lorusso *et al.*, 2013). This reassortant BTV-4w was shown to be closely related to BTV-4w isolated in Tunisia in 2007 and 2009. Likewise, BTV-1w Sardinian strain originated from a strain closely related to a BTV-1w isolated in Tunisia in 2011 (Lorusso *et al.*, 2014).

On November 1st 2016, an eight years old red-head Barbarine ewe, located in the Gouvernorat de Nabeul, delegation Beni Khalled, Imada Hannous (36°37059.04"N-10°42039.52"E), in the north-eastern part of Tunisia, in the central area of Cap Bon, showed clinical signs consistent with BTV infection. The animal belonged to a flock composed by 46 sheep, seven goats and eight cattle. The newly identified BTV was typed as western BTV-3 with a clear African origin (NCBI, KY432369-KY432378; Lorusso *et al.*, 2017). Further surveillance activities conducted in collaboration between the Tunisian and Italian authorities, revealed the presence of BTV-3 RNA and antibodies in sheep of some Tunisian regions. Moreover, an additional western BTV-3 strain, named BTV 3 TUN2016/Zarzis (NCBI, MF124292 MF124301) was identified nearby the border with Libya. The two viruses are different by comparative analysis of the genome constellations (Lorusso *et al.*, 2018).

In November 2017, a 3 years old female crossbred sheep belonging to a flock of nearly 400 animals located in the surroundings of Trapani (Western part of the island of Sicily, facing the peninsula of Cap Bon) showed clinical signs consistent with BT infection. Symptoms included fever, oedema of the head, nasal discharge, and depression. The veterinary services of local health unit (ASL) visited the entire flock and collected EDTA-blood and serum samples from the symptomatic sheep. The Seg 2 of BTV-3 identified in Sicily was identical to that of BTV-3 TUN2016, first detected in Cap Bon in November 2016 (Lorusso *et al.*, 2017) (figure 1).



**Figure 1.**  
BTV-3 outbreaks in Italy and Tunisia

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