

## Belgium: Pools of *Culicoides* spp. found positive for Schmallenberg virus by RT-qPCR

Since it was first identified in Germany in Nov 2011, Schmallenberg virus (SBV) has been confirmed in the Netherlands, Belgium, United Kingdom, France, Luxembourg, and Italy. Knowing that related viruses belonging to the same Simbu serogroup of Orthobunyaviruses are generally spread by midges and mosquitoes, it was assumed that these vectors could also spread SBV.

In Belgium, *Culicoides* spp. have been monitored since 2007 through a surveillance program financed by the Belgian Federal Agency for the Safety of the Food Chain (FAVV-AFSCA).

In order to examine the potential role of midges in the spread of SBV, pools of midges were analyzed at CODA-CERVA by RT-qPCR. Midges had been captured outdoors in September and October 2011 with an UV light trap at Betekom (Province of Vlaams Brabant, Belgium) by scientists of the Institute of Tropical Medicine (ITM, Antwerp). The pools consisted of 10 heads of *Culicoides* spp. each identified morphologically at species level. Although only 23 pools have been examined so far, SBV has been detected in 2 of them (by RT-qPCRs detecting S and L segments of SBV according to protocols provided by FLI, Germany). One pool consisted of *C. obsoletus* s.s. caught on 7 Sep 2011 (Ct=34.9 and 37.0 for S and L segment resp.) and another pool consisted of *C. Dewulfi* caught on 4 Oct 2011 (Ct=38.1 for S and negative and L segments). These results strongly confirm the role of biting midges in the transmission and spread of SBV. This indication is strengthened by the fact that the examined pools consisted exclusively of heads, suggesting that midges act as real amplification vectors and were not simply SBV positive after a blood meal on viraemic animals.

More pools collected by the monitoring project will be tested to identify other possible SBV vectors among *Culicoides* species and to shed light on the time of introduction of SBV in this and other regions. Pools of mosquitoes will also be tested to assess their potential role in the spread of SBV.

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*The above information is a welcome additional contribution of the scientific community to the study of the emerging SBV. Scientific fraternity and exemplary transparency have, fortunately, characterised the course of the SBV epizootic since its early stages (as demonstrated also in item 2).*

*The fact that a pool of midges caught on 7 Sep 2011 in Belgium was found SBV-infected is in line with estimates that the virus was already circulating in Aug 2011. Further studies will, hopefully, unravel its earlier history and geographical distribution; most important, its route and mode of introduction.*

*The latter issue is important also in regard to the control measures to be decided upon, including vaccination. Contrary to countries traditionally known to suffer from periodic outbreaks of AH (arthrogryposis-hydranencephaly) caused in susceptible ruminants by the orthobunyavirus Akabane virus (for example, Japan, Australia, Israel), the north western European countries affected by SBV are -- most probably -- not situated on the verge of endemically infected territories, where the virus circulates regularly without clinical expression. The virus "jumped" into north Europe, not gradually, stepwise as would have been expected if climatic changes were at the background, but literally "out of the blue"; similar to the BTV-8 event which started in the same area in 2006. It is assumed that the newly introduced virus(es) encountered a local, receptive, and efficient vector, most probably *Culicoides* population(s), resulting in their extensive and rapid spread. This hypothesis calls for further profound study.*

For the location of Betekom, close to the Dutch and German affected territories, see map at <http://healthmap.org/r/1ZeW>