"Schmallenberg" virus: likely epidemiological scenarios and data needs

Summary

Since autumn 2011, a previously unknown virus, provisionally named as "Schmallenberg" virus (SBV), has been reported in ruminants (cattle, sheep and goats) from Germany, The Netherlands, Belgium, the United Kingdom and France. In January 2012, the European Commission requested scientific assistance from EFSA under the provisions of Article 31 of Regulation (EC) No 178/2002. Among others, a preliminary analysis of the likely epidemiological scenarios that could be observed in the next months was requested, based on the existing knowledge of viruses of the Simbu virus serogroup and other vector borne epidemics in the region. This report provides likely epidemiological scenarios and data needed to improve the understanding of the disease spread and impact of SBV.

The report mainly focuses on animal health aspects. Current knowledge suggests that it is unlikely that SBV can cause disease in humans and as stated in the rapid risk assessment carried out by ECDC (ECDC, 2011). No additional information has since become available to invalidate this assessment. However, EFSA and ECDC are closely monitoring the situation in order to address public health concerns should these arise.

There is currently very limited knowledge specifically related to SBV. Available information on the SBV genome suggests that this virus is part of the Simbu serogroup of the Bunyaviridae family. SBV has been detected in ruminants. Main clinical signs observed in cattle are fever, loss of appetite, up to 50 percent reduction in milk yield and, in rare cases, severe diarrhoea, for approximately one week. SBV has also been detected in association with a variety of congenital abnormalities observed in stillborn or newborn lambs and calves.

In the absence of SBV specific knowledge regarding pathogenesis of SBV infection, an analogy was made with knowledge on Akabane virus, another representative of the Simbu serogroup. It is known that the pathogenic effects of infection with Akabane virus are only seen when the virus exceeds the geographical boundaries of the endemic area and infects susceptible animals in early stage of pregnancy. Such a situation is likely to occur at the edges of an endemic area and may be due to the movement of either infected hosts or infected vectors.

Without knowing the susceptibility to SBV in animal populations throughout the EU, and assuming that SBV induces a strong immunity similar to Akabane virus, 3 types of epidemiological situations can be envisaged: i) areas where a recent incursion might have occurred in populations not previously exposed to the pathogen, that is naive populations, causing clinical disease in adult animals and, at a later date as consequence of infection of dams, malformation in foetuses;
ii) areas where incursi on occurred in the past and part of the ruminant population is immune and where congenital malformations are not observed or observed at a low level (mainly not reported); and iii) areas where no virus incursion occurred but a susceptible population is present. Surveillance data, as proposed in this report, should be collected by and shared between Member States in order to assess the immune status of animal populations, the impact of SBV infection, and further spread throughout EU. This should include data from serological surveillance also in areas where SBV has yet not been reported.

Due to limited information on the epidemiology of SBV, EFSA used a bluetongue virus (BTV8) model to assess under which conditions SBV could spread into susceptible populations. BTV8 was chosen because; i) BTV8 is an exclusively vector transmitted diseases as are other Simbu serogroup viruses i i) BTV8 and SBV are circulating in the ruminant population iii) information is available regarding BTV8 in Europe whereas there has only been one case report for viruses of the Simbu serogroup in Europe. Assuming that SBV is a non-direct transmissible, vector borne, infectious disease, that vector parameters for the spread of SBV are those for BTV8, and using indications on SBV viraemia given by a preliminary experimental infection in cattle, the hypothetical scenarios show that, depending on the temperature and the number of vectors, SBV might spread further in susceptible populations. Whenever the number of vectors per host and the temperature are above a specific threshold there is a possibility of a wider disease epidemic affecting more Member States. EFSA proposes a coordinated data collection in all Member States in 2012 on the incidence and prevalence of the disease, number of malformed foetuses, as well as the presence of the virus in dams.