NEW SEROTYPES/STRAINS OF BLUETONGUE VIRUS (BTV) – ANIMAL HEALTH ISSUES ARISING FROM REPORTS OF NOVEL BTVS

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Bluetongue virus (BTV) is the cause of bluetongue (BT), an arboviral disease of domestic and wild ruminants and certain other mammals that is transmitted by *Culicoides* biting midges. There have been profound recent changes in the global distribution/range of BTV, especially in the Northern Hemisphere. Recent outbreaks of BT in livestock, most notably in Europe, have led to refinement of laboratory diagnostic procedures and increased surveillance for BTV in countries and regions at risk of infection. The traditional methods for BTV detection that involved virus isolation in embryonated eggs or cell culture have largely been replaced by nucleic acid detection assays, specifically quantitative real-time polymerase chain reaction (PCR) assays (BTV qRT-PCR). Recent surveillance has identified three genetically novel BTVs that putatively constitute three new serotypes, in addition to the previously known 24 BTV serotypes. These three new BTVs have all been isolated from small ruminants in Europe and the Middle East, and studies to date show that they have biological properties distinct from "traditional" BTVs e.g. BTV-25 (Toggenberg orbivirus) causes persistent infection of goats and BTV-26 can be spread directly between goats without the requirement for an insect vector. Importantly, the BTV-qRT-PCR assays used routinely in several national diagnostic laboratories did not detect at least one of these viruses (BTV-25). Much remains to be learnt about these, and potentially other novel BTVs, including their global distribution, host range and epidemiology, pathogenesis and virulence to domestic livestock. Furthermore, the considerable genetic diversity of BTV in nature must be accounted for if diagnostic testing is to be internationally harmonised in the future. A logical strategy for harmonised BTV-qRT-PCR testing will require whole genome sequencing of a wide variety of virus strains from throughout the world, as well as comparative evaluation of assays in different laboratories with access to potentially different field viruses. Field strains of BTV are highly heterogeneous genetically, which is consistent with the marked variation in their biological properties including their virulence to livestock. This genetic diversity of BTV arises continuoually in the field as a consequence of: 1. genome segment reassortment between different viruses (genetic shift); 2. Genetic drift as a result of quasispecies evolution and founder effect in either the insect or animal hosts of the virus.