A Step Forward in the Development of a Molecular Database for African Horse Sickness Virus

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African horse sickness virus (AHSV), although largely restricted to sub-Saharan Africa, has occasionally expanded outside this usually endemic zone. It has persisted in the new affected areas for a number of years which suggests that the geographic area suitable for successful AHSV transmission is much greater than that in which AHSV currently occurs. If AHSV became established in Europe, the equine industry could be exposed to great losses, due to the devastating effects of the disease in horses. There has been a number of bluetongue virus introductions from West and North Africa into Europe, including multiple independent introductions of the same serotype. There also have been reports on the possible spread of orbiviruses due to wind transportation of infected adult *Culicoides* from West Africa to the Iberian Peninsula. This establishes that there are multiple effective routes for the introduction of orbiviruses into Europe. AHSV has recently been detected in West Africa (Senegal and Mauritania), involving serotypes 2 and 7, which had not previously been detected in the area. The emergence of BTV in Europe since 1998, and the damage caused by BTV-8 in Northern Europe since 2006 suggest that AHSV has the potential to spread much more quickly in Europe than previously anticipated. In order to prepare for possible introductions of AHSV into new geographical areas, the origin, movement and genetic variations of the virus should be fully understood and monitored. Molecular epidemiology studies are highly effective for this type of surveillance, but depend on the availability of a database containing sequence data for different and well documented isolates of the virus. Such a database has recently been created, linked to a reference collection (http://www.reoviridae.org/dsRNA_virus_proteins/ReoID/BTV-isolates.htm) containing well documented bluetongue isolates, which has been used to identify the likely origins of the European BTV outbreak strains, as well as detection of reassortant field and vaccine strains of the virus.

A primary objective of the study described here is to obtain full-length sequence of the entire genome of the nine reference strains of AHSV, as well as other available field and vaccine strains. The sequence data generated will be linked to a reference collection of specific isolates (http://www.reoviridae.org/dsRNA_virus_proteins/ReoID/AHSV-isolates.htm) to provide an initial basis for a molecular epidemiology sequence database. As more strains and data are added, this will develop into a useful tool to help determine the relationship between different AHSV isolates, belonging to different serotypes, different lineages, strains and topotypes.

These studies will explore the level of variation that exists in the different AHSV genome segments and determine if the restricted distribution of AHSV to a single continent has had any significant impact on its variability and evolution, compared to bluetongue virus and epizootic haemorrhagic disease virus, which have a global distribution. Significant progress has been achieved on these research objectives. Three genome segments of the nine AHSV reference strains (segments 5, 8 and 9) have been sequenced and a comparison of their nucleotide and amino acid sequences is presented.

Keywords: *African horse sickness virus* – Nucleotide sequence – Database.

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