5. Genetic characterisation in FMD and ASF viruses

Improving detection and characterisation methods for FMDV and ASFV for cattle and pigs in the SADC region

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Real-time Polymerase chain reaction for African swine fever virus (ASFV)

The detection of ASF viral DNA is achieved by use of the PCR technique that has been developed to target highly conserved regions of the genome. This allows for the detection and identification of a wide range of isolates belonging to all the known virus genotypes, including both non-haemadsorbing viruses and isolates of low virulence. It is useful for identifying virus DNA in pig tissues that are unsuitable for virus isolation or antigen detection because they have undergone putrefaction, or when it is suspected that the virus may have been inactivated during transport or at any time before samples arrive in the laboratory. Results suggest that the real-time PCR can be used to replace the conventional PCR assays that currently in use at TADP.

Real-time PCR for Foot and mouth disease virus (FMDV)

Recent events in the spread of FMD around the world have highlighted its extremely contagious nature and the disease remains a constant threat to trade and the economies of countries in SADC. Rapid and sensitive laboratory diagnostic tools that can recognise infected animals are imperative for the effective control and elimination of the disease. Automated real-time PCR has become a valuable diagnostic tool for FMD with a diagnostic sensitivity superior to that of Virus isolation/antigen ELISA combined. Results suggest that this real-time can be implemented for fast identification of possible outbreaks.

Genetic diversity of FMD viruses

FMDV evolved separately in geographical regions giving rise to topotypes. Due to the great amount of genetic and antigenic diversity within the SAT types, vaccines prepared from one strain may not provide protection against other strains. FMD molecular epidemiological studies for the SAT type viruses have concentrated on the 1 D-coding region to determine genetic relatedness of isolates. Data on the complete capsid-coding region is inadequate due to the restricted numbers and the fact that the majority are historic isolates that do not shed much light on the current epidemiological

situation. Characterisation of the external capsid-coding region allows for addressing the lack of knowledge for the SAT type viruses addressing the characterisation of possible epitopes which may be important for vaccination. Therefore the genetic variability of the SAT types in Africa was investigated to evaluate the characteristics of recent field isolates from wildlife, as well as livestock. The latest outbreaks of FMD were determined for the whole of Africa, with emphasis on southern Africa. The viruses were chosen to be representative of what is currently in the field and to cover the 3 topotypes found within southern Africa (South Africa, Namibia, Zimbabwe, Botswana, Zambia and Malawi). The viral RNA was amplified by reverse transcriptase-PCR, purified and used for sequencing. The nucleotide and deduced amino acid data was analysed for genetic and phylogenetic comparisons.