Vaccine strain selection for FMD serotype O viruses in Southeast Asia and East Asia using antigenic and genetic data by measuring the effect of protective viral determinants

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Abstract

Foot and mouth disease (FMD), caused by FMD virus (FMDV) is a highly contagious disease affecting cloven hoofed animals. Although vaccination is one of the most important control measures to prevent FMD outbreaks, the available vaccines may not provide enough cross protection against recent circulating FMDV, mainly due to emergence of new lineages and sub lineages. Therefore, the main aim of this project is to find out a suitable cross protecting vaccine strain by matching (antigenic and genetic characterisation) circulating viruses with existing vaccines and new putative vaccine strains. So in the first year of this study, a total of 50 serotype O (2013-2017) viruses selected from SEA, Far East and EA countries, were characterised by virus neutralisation test and capsid sequencing. O/PanASIA-2 is seen to be the broad cross reacting vaccine for serotype O. However, recent circulating CATHAY topotype viruses are not protected by any of these existing vaccines. Further capsid sequence analysis of these viruses elucidated amino acid changes in the antigenic sites of these viruses. The effect of these amino acids changes are being investigated using reverse genetics technique. This can help to design new vaccines, which can give better cross protection against the circulating viruses.

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