Molecular characterization of serotype Asia-1 foot-and-mouth disease viruses in Pakistan and Afghanistan; emergence of a new genetic Group and evidence for a novel recombinant virus

Foot-and-mouth disease (FMD) is endemic in Pakistan and Afghanistan. The FMD virus serotypes O, A and Asia-1 are responsible for the outbreaks in these countries. Diverse strains of FMDV, even within the same serotype, co-circulate. Characterization of the viruses in circulation can facilitate appropriate vaccine selection and tracing of outbreaks. The present study characterized foot-and-mouth disease serotype Asia-1 viruses circulating in Pakistan and Afghanistan during the period 1998–2009. Phylogenetic analysis of FMDV type Asia-1 revealed that three different genetic Groups of serotype Asia-1 have circulated in Pakistan during this time. These are Group-II, -VI and, recently, a novel Group (designated here as Group-VII). This new Group has not been detected in neighbouring Afghanistan during the study period but viruses from Groups I and -II are in circulation there. Using near complete genome sequences, from FMD viruses of serotypes Asia-1 and A that are currently circulating in Pakistan, we have identified an interserotypic recombinant virus, which has the VP2-VP3-VP1-2A coding sequences derived from a Group-VII Asia-1 virus and the remainder of the genome from a serotype A virus of the A-Iran05AFG-07 sub-lineage. The Asia-1 FMDVs currently circulating in Pakistan and Afghanistan are not efficiently neutralized by antisera raised against the Asia-1/Shamir vaccine strain. Thus, new Asia-1 vaccine strains may be required to block the spread of the current Asia-1 viruses.

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