

Genetic characterization and molecular epidemiology of foot-and-mouth disease viruses isolated from Afghanistan in 2003-2005

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Abstract

Foot-and-mouth disease virus (FMDV) isolates collected from various geographic locations in Afghanistan between 2003 and 2005 were genetically characterized, and their phylogeny was reconstructed utilizing nucleotide sequences of the complete VP1 coding region. Three serotypes of FMDV (types A, O, and Asia 1) were identified as causing clinical disease in Afghanistan during this period. Phylogenetic analysis revealed that the type A viruses were most closely related to isolates collected in Iran during 2002-2004. This is the first published report of serotype A in Afghanistan since 1975, therefore indicating the need for inclusion of serotype A in vaccine formulations that will be used to control disease outbreaks in this country. Serotype O virus isolates were closely related to PanAsia strains, including those that originated from Bhutan and Nepal during 2003-2004. The Asia 1 viruses, collected along the northern and eastern borders of Afghanistan, were most closely related to FMDV isolates collected in Pakistan during 2003 and 2004. Data obtained from this study provide valuable information on the FMDV serotypes circulating in Afghanistan and their genetic relationship with strains causing FMD in neighboring countries.

Keywords FMDV - VP1 - Phylogenetic analysis - Nucleotide - Amino acid - Afghanistan