Molecular Epidemiology of An Asian Pandemic Strain of Foot-and-Mouth Disease Type O Virus

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INTRODUCTION

The OIE/FAO World Reference Laboratory for Foot-and-Mouth Disease (WRLFMD) is established within the high security laboratory at the Institute for Animal Health, Pirbright, U.K. Anamoly, over 400 samples are received for diagnosis of foot-and-mouth disease (FMD) from throughout the FMD endemic region, which is predominantly African, Asia and parts of South America. There are seven serotypes of FMD viruses: SAT 1, SAT 2, A, O, C, Asia 1 and Asia 2. Each serotype is further divided into specific subtypes. The movement of FMDV is predominantly associated with the legal and illegal movement of infected animals, although it can spread in animal products, and, under the right conditions, up to 250 km as an aerosol. We describe here a strain of serotype O FMD virus which we have identified as spreading from India westward into South Arabia and then throughout the Middle East and into Europe, and onward through Nepal and Bhutan to mainland China, Taiwan, Korean Peninsula, Japan, and South Korea.

MATERIALS AND METHODS

Total RNA was extracted either directly from epithelial suspensions or from cell culture grown virus using a commercial kit (QIAamp Viral RNA minikit). The PCR amplification was partially sequenced using the universal template and an automated sequencing kit (ALFExpress II; Pharmacia) with M13-labeled primers N72 (5'-GGTAAAACGACGGCCAGT-3') and ARS4 (5'-ATCTGTTAAGAGTACTTTG-3'). The PCR products were sequenced using a commercial kit (fmol, Promega) and the sequences aligned using the PHYLIP package (Felsenstein, 1993). All these techniques are fully described in a laboratory manual (Knowles and Samuel, 1998) which is downloadable from our website: http://www.iah.bbsrc.ac.uk/virus/Picornaviridae/Aphthovirus/Protocol.pdf

RESULTS & DISCUSSION

The pandemic virus was first isolated from outbreaks of FMD in northern India in 1998. It spread into South Arabia, probably with the live trade in sheep and goats. South Arabia supports over 6 million live animals annually to support the requirements of the Muslim festival. During 1999 the virus spread westward in South Arabia and then moved into neighboring countries so that by 1999 it had reached Turkey. From Turkey it crossed the Ussuriysk district of eastern Russia, was also caused by this new strain (report to OIE). FMDV type O topotype normally exists. By April 2000 all mainland South East Asian countries, with the exception of Vietnam and Cambodia had outbreaks of FMD. The cattle on these farms are regularly vaccinated at the point of purchase. The virus moved across international borders. A region of approximately 200 nucleotides of the 1D gene, which codes for the RNA-dependent RNA polymerase, was sequenced using the PHYLIP package (Felsenstein, 1993). These techniques are fully described in a laboratory manual (Knowles and Samuel, 1998) which is downloadable from our website: http://www.iah.bbsrc.ac.uk/virus/Picornaviridae/Aphthovirus/Protocol.pdf

REFERENCES


Fig. 1. Conspicuous spread of the India-90 (PanAsia) lineage of the South Asian topotype of FMDV-O

Fig. 2. Phylogenetic tree showing the relationships between partial VP1 sequences of viruses belonging to the PanAsian lineage with other FMDV type O viruses

Fig. 3. Phylogenetic tree showing the relationships between the complete VP1-coding sequences of some of the FMDV type O virus isolates

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