Foot-and-Mouth Disease Virus Serotype O Phylodynamics: Genetic Variability Associated with Epidemiological Factors in Pakistan

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One of the most challenging aspects of foot-and-mouth disease (FMD) control is the high genetic variability of the FMD virus (FMDV). In endemic settings such as the Indian subcontinent, this variability has resulted in the emergence of pandemic strains that have spread widely and caused devastating outbreaks in disease-free areas. In countries trying to control and eradicate FMD using vaccination strategies, the constantly evolving and wide diversity of field FMDV strains is an obstacle for identifying vaccine strains that are successful in conferring protection against infection with field viruses. Consequently, quantitative knowledge on the factors that are associated with variability of the FMDV is prerequisite for preventing and controlling FMD in the Indian subcontinent. A hierarchical linear model was used to assess the association between time, space, host species and the genetic variability of serotype O FMDV using viruses collected in Pakistan from 2005 to 2011. Significant (P < 0.05) amino acid and nucleotide variations were associated with spatial distance, but not with differences in host species, which is consistent with the frequent multi-species infection of this serotype O FMDV. Results from this study will contribute to the understanding of FMDV variability and to the design of FMD control strategies in Pakistan. Viruses sequenced here also provide the earliest reported isolate from the Pan Asia IANT-10 sublineage, which has caused several outbreaks in the Middle East and spread into Europe (Bulgaria) and Africa (Libya).

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