Genetic diversity of serotype A foot-and-mouth disease viruses in Kenya from 1964 to 2013; implications for control strategies in eastern Africa

Serotype A is the most genetically and antigenically diverse of the foot-and-mouth disease virus (FMDV) serotypes. Records of its occurrence in Kenya date back to 1952 and the antigenic diversity of the outbreak viruses in this region is reflected by the current use of two different vaccine strains (K5/1980 and K35/1980) and previous use of two other strains (K18/66 and K179/71). This study aimed at enhancing the understanding of the patterns of genetic variation of serotype A FMDV in Kenya. The complete VP1 coding region sequences of 38 field isolates, identified as serotype A FMDV, collected between 1964 and 2013 were determined. Coalescent-based methods were used to infer times of divergence of the virus strains and the evolutionary rates alongside 27 other serotype A FMDV sequences from Genbank and the World Reference Laboratory (WRL). This study represents the first comprehensive genetic analysis of serotype A FMDVs from Kenya. The study detected four previously defined genotypes/clusters (termed G-I, G-III, G-VII and G-VIII), within the Africa topotype, together with a fifth lineage that has apparently emerged from within G-I; these different lineages have each had a countrywide distribution. Genotypes G-III and G-VIII that were first isolated in 1964 are now apparently extinct; G-VII was last recorded in 2005, while G-I (including the new lineage) is currently in widespread circulation. High genetic diversity, widespread distribution and transboundary spread of serotype A FMDVs across the region of eastern Africa was apparent. Continuous surveillance for the virus, coupled to genetic and antigenic characterization is recommended for improved regional control strategies.

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