Analysis of the epidemiological dynamics during the 1982-1983 epidemic of foot-and-mouth disease in Denmark based on molecular high-resolution strain identification

An epidemic of foot-and-mouth disease (FMD) causing a total of 23 cases in 1982-1983, primarily on the island of Funen, Denmark, was subjected to molecular epidemiological investigations. In an attempt to exploit the quasi-species nature of foot-and-mouth disease virus strains for molecular high-resolution strain identification in order to analyse the dynamics of this epidemic, full-length VP1 coding regions were sequenced for 17 isolates collected at different farms during the epidemic. The sequence information together with epidemiological information gathered during the epidemic suggests that the epidemic was caused by at least three introductions across Danish borders and one case of airborne transmission between two islands in Denmark over a distance of 70 km. The assortment of nucleotide markers among the three strains is indicative of common recombination events in their evolutionary history, and the prerequisite of co- or superinfection of animals with variant strains in turn implies that they have a common source or epidemiologically related sources originating from an area with endemic FMD.

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