

Experimental foot-and-mouth disease virus serotype O infection in domestic animals: a systematic review

Mardones FO (1), Sanchez J (2), Perez AM (1), AIKhamis MA (1), Carpenter TE (1)

(1) Center for Animal Disease Modeling and Surveillance (CADMS), School of Veterinary Medicine, University of California, Davis, CA 95616, USA (2) Department of Health Management, University of Prince Edward Island (UPEI), Charlottetown, PEI, Canada

Foot-and-Mouth Disease (FMD) is considered one of the most important infectious diseases of livestock. The disease is exotic to North America, and it has been estimated that an FMD epidemic, should it occur in the region, would have devastating social and economic consequences to affected countries. One possible strategy to gain knowledge on the expected dynamics of FMD epidemics in free regions is the use of simulation models. The objective of this work was to estimate the most likely distributions and sources of variation of certain parameters required to formulate a simulation model for spread of serotype O FMD virus, which is considered the most prevalent FMD virus type in the world. A double independent, systematic review of 17 publications reporting results from experimental trials conducted in four FMD reference laboratories was conducted to extract the values of individual records of animals ($n = 273$). Probability density functions were fitted and tabulated for the extracted data. Parametric regression models for survival data including shared frailty (gamma distributed) effect, were used to quantify the association between the duration of the latency (L), subclinical (SC), incubation (IP) and infectious (INF) periods and factors hypothesized to influence their distribution. Average duration of the L, SC, IP, and INF were estimated in 3.8 (95% CI = 3.4, 4.4), 1.5 (95% CI = 1.3, 1.9), 5.2 (95% CI = 4.7, 5.7), and 4.6 (95% CI = 3.3, 5.7) days, respectively. In general, route of exposure (direct or indirect contact), type of animal, sample for detection, and characteristics of clinical signs as indicator of disease, were associated ($P < 0.05$) with these FMD stages. In addition, this study quantified the effect of different strain in the dynamic of a FMDV infection. The distributions of L, S, IP, and INF and the associations reported here will help to improve the accuracy of the predictions of simulation models when especially the intra-herd transmission is evaluated in FMD-free regions of the world.