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Three popular disease spread simulation models were used to simulate the spread of foot-and-mouth disease (FMD) in Denmark. The models’ predictions in term of disease spread, consequence, and the ranking of the applied control strategies were compared. The original Davis Animal Disease Spread (DADS version 0.05) was adapted to DTU-DADS, and this model as well as InterSpread Plus (ISP version 2.001.11) and the North American Animal Disease Spread Model (NAADSM version 3.0.81) were all used to simulate hypothetical spread of FMD in Denmark. Data on Danish herds were used including herd type, movements, and location in the period 1st October 2006 to 30th September 2007.

The three models to the highest possible extend set up to simulate the same epidemics in 3 different control scenarios: 1) A basic scenario representing EU and Danish control strategies, 2) pre-emptive depopulation of susceptible herds in a 500 meters radius around the detected herds, and 3) suppressive vaccination of susceptible herds in a 1,000 meters radius around the detected herds. Depopulation and vaccination started either 14 days following the detection of the first infected herd or following detection of 50 infected herds. Five thousand index herds were selected randomly in which there were 1,000 cattle herds located in high density cattle area and 1,000 in low density cattle area, 1,000 swine herds located in high density swine area and 1,000 in low density swine area, and 1,000 sheep herds.

Generally, NAADSM predicted the largest, longest duration and costliest epidemics. DTU-DADS predicted larger, longer duration and costlier epidemics than ISP, except when epidemics started in cattle herds located in high density cattle area. ISP predicted suppressive vaccination to be less costly than depopulation, while the least costly control strategy predicted by DTU-DADS differed depending on the species and density area of the index herd. It was not possible to run the depopulation scenarios in the NAADSM due to limitations in the model.

Running several models in parallel gives better insight in disease spread, limits typing and coding errors and improves understanding of modeled processes. The chosen control strategy might depend on the chosen model.