

AN APPROACH FOR QUANTITATIVE RISK ANALYSIS OF CONTAGIOUS ANIMAL DISEASE INTRODUCTION INTO DENSELY POPULATED LIVESTOCK AREAS OF THE EUROPEAN UNION

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Risk is defined as the likelihood and magnitude of an adverse event (1). An important risk for the livestock production sector is the introduction of a contagious animal disease into an area free of disease and its epidemiological and economic consequences. Classical swine fever (CSF) and foot-and-mouth disease (FMD) are contagious animal diseases which can spread rapidly and may have devastating effects not only for the infected farms, but also for other partners in the livestock chain and the national economy. The losses caused by these diseases are considered to be positively related with the density of farms and animals in the affected area.

In the European Union (EU) so-called densely populated livestock areas (DPLAs) can be distinguished, that have a high concentration of livestock farms and domestic animals (6). Economic factors such as availability of feeding stuffs, reasonably priced land, and local consumer demand have led to the development of these areas (2). Producers in these DPLAs have the advantage of a good infrastructure, availability of know-how, economies of scale, etc. Recent outbreaks of CSF have, however, shown the vulnerability of DPLAs to introduction of highly contagious animal diseases, the most striking example being the Dutch 1997/98 CSF epidemic (3). More insight into the specific causes of virus introduction into DPLAs might help to develop strategies that reduce the risk of future epidemics for these areas, and hence their vulnerability.

Quantitative risk analysis (QRA) can be used to calculate the likelihood of CSF and FMD virus introduction into DPLAs. Application of QRA to estimate the risk of contagious animal disease introduction has increased rapidly in recent years. Most of the risk analyses performed focus, however, on one single pathway along which the disease agent can be brought into an area free of disease (e.g. 7). But in order to prevent outbreaks of highly contagious animal diseases, comprehensive insight into all pathways contributing to the risk of virus introduction is a prerequisite. In this paper an approach to explore all pathways is presented.

Risk network

In QRA, graphical methods are commonly used to obtain more insight into how the various pathways contribute to the occurrence of an adverse event, such as virus introduction. To identify all pathways of CSF and FMD virus introduction and to show their interrelationships a so-called risk network was constructed (figure 1). In this risk network only the events that lead to the undesired outcome, i.e. virus

introduction, are taken into account. Theoretically, each event in the network can be assigned a probability that the event will happen. Subsequent events are only relevant if the preceding events did occur, and therefore most probability parameters are conditional. The starting events for each pathway of virus introduction are indicated bold in the risk network. These will, of course, only constitute a risk if they originate from an area where the disease is prevalent.

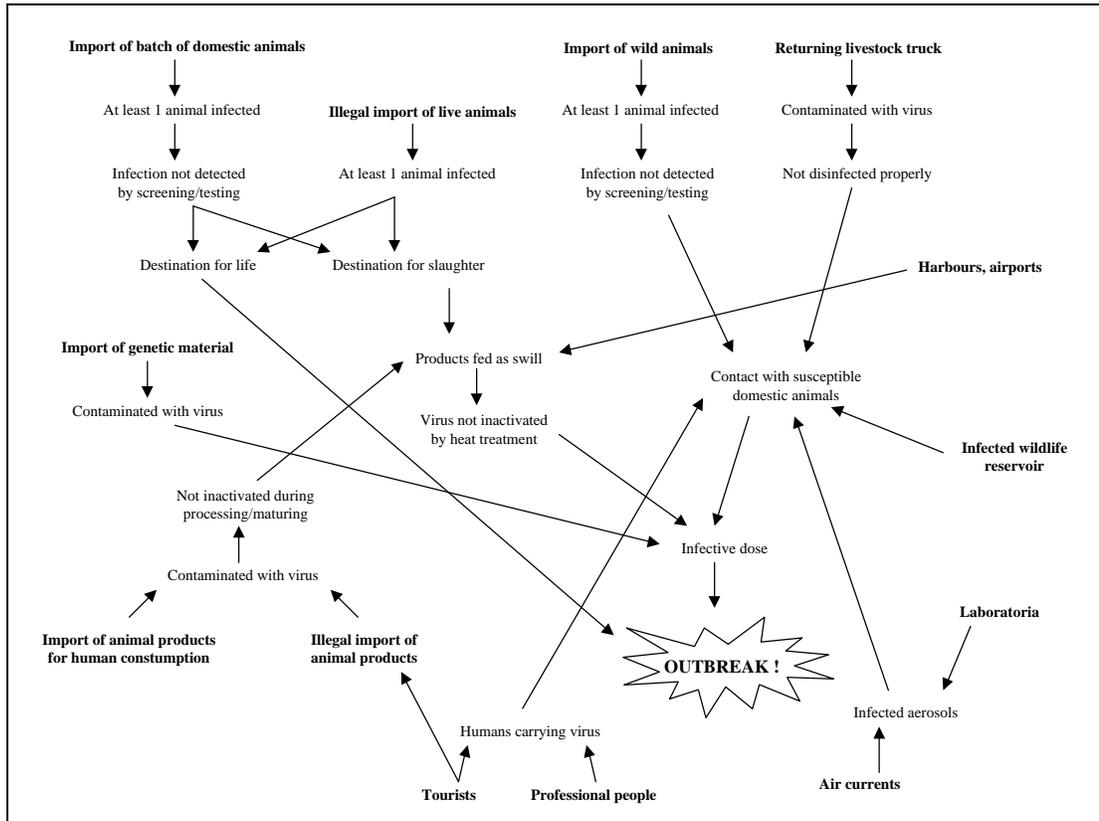


Figure 1. Risk network containing all pathways and events that contribute to the likelihood of CSF and FMD virus introduction into DPLAs of the EU.

Simulation modelling

The risk network is used to quantify the contribution of all pathways to the likelihood of virus introduction. Basically, to calculate the likelihood of virus introduction, (i) the number of units entering the livestock production sector of a DPLA along each pathway should be known, and (ii) the probabilities that these units are infected or contaminated and convey an infected dose to susceptible animals. A prototype simulation model is currently under development to perform these calculations. Monte Carlo simulation is used to account for natural variation of and uncertainty about input parameters (8). The model simulates virus introduction on a daily basis. Once a target DPLA and time horizon have been set, the model calculates how often virus is introduced into the target DPLA. For all introductions the model indicates from where the virus originated and the pathway along which it was introduced. A database is linked to the model, providing information about disease prevalence world-wide, the extent of presence of each pathway in the target DPLA (e.g. number

of animals imported) and the riskiness of each pathway (e.g. probability of virus introduction per imported animal). The riskiness of a pathway is determined by the events that occur along the pathway, as indicated in the risk network.

The model will be used to evaluate the epidemiological and economic efficacy of measures aimed at reducing the risk of virus introduction. For this purpose, the model will be linked with an epidemiological model that simulates virus spread once virus has been introduced (4) and an economic model that calculates the economic losses of such a simulated epidemic (5).

Discussion

A combination of simulation modelling and QRA seems to offer a good perspective to gain more insight into the main pathways of virus introduction into DPLAs of the EU. However, a lot of quantitative information is needed to perform the calculations in the simulation model. Caution should be observed in the process of collecting data and building the model. The risk calculations in the simulation model can only be as sound as the basic data and probability structure used.

Not all information needed for the model is readily available from literature and databases, all the more since the calculations are to be performed on a regional level (DPLAs are regions, not whole countries). Expert elicitation will be used to obtain lacking information. Sensitivity analysis of the model should indicate which parameters particularly influence the likelihood estimates. Research should be dedicated to quantifying those parameters more precisely, if possible.

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