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Quantitative assessment of the likelihood of the introduction of classical swine fever virus into the Danish swine population

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Abstract

Classical swine fever virus (CSFV) is a major infectious-disease agent of livestock and causes production losses through increased morbidity and mortality, particularly of young pigs. We identified the pathways for introduction of CSFV into Denmark and assessed the annual probability of introduction (based on a US Department of Agriculture model).

We developed pathways based on material from scientific articles, reports from veterinary agencies and custom officers, and consultations with experts in the field.

Returning livestock trucks and legal meat imports were the most important pathways for CSFV introduction to Denmark from other EU states with predicted overall likelihood of one or more introductions of CSFV within a median of 130 years (46–280) provided mitigating steps, such as cleaning trucks, were maintained to a very high standard. The likelihood would increase dramatically if these activities were abandoned: one or more introductions within a median of 5.2 years (2–14). The predicted risks from live-animal imports and semen were extremely low given the very few imports of these products. The most important countries for Denmark's CSFV risk are Germany and the Netherlands, though this risk is again predicted to be dramatically reduced as long as mitigating activities are maintained. We predicted the risk

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from illegal movements of pork into Denmark to be low because little pork enters through this route and only a small fraction of this pork would be fed to pigs.

Keywords: Risk assessment; Swine; CSFV; Denmark

1. Introduction

1.1. Background

The European Union (EU) is currently considered free of many of the trans-boundary animal infections considered by the World Organisation for Animal Health (OIE) to be of major economic and/or public-health importance including foot-and-mouth disease (FMD), African swine fever and classical swine fever (CSF). However, CSFV outbreaks in the Netherlands and United Kingdom in 2000 and the FMD outbreaks in several EU states in 2001 demonstrate that the EU is at continuous risk of introduction of infection. Clearly, when infection incidence is low or a country is infection-free, the most efficient method of maintaining this status is to prevent the introduction of the infection. For countries to minimise the risks of these infections, the countries must identify high-risk activities and potential pathways for infection introduction.

In order to facilitate trade and to prevent trade barriers, many countries have signed the Sanitary and Phytosanitary (SPS) agreement of the World Trade Organisation (WTO). To justify any trade barriers, a country trying to prevent imports are required to demonstrate that trade in particular animals or plants or their products is likely to put the country at an increased risk of infection introduction. To satisfy international regulations, these risks need to be assessed as part of a clear and transparent risk analysis as set out by the OIE.

1.2. Hazard identification

CSFV has caused the most outbreaks of any of the former O.I.E. list-A diseases in Europe and was therefore considered the first priority for assessment. CSF is caused by a *Pestivirus* in the family Togaviridae. It is a highly contagious viral disease of domestic pigs and wild boar. In Europe it has been controlled for several decades through a stamping-out policy. Moreover, swill feeding is prohibited within the EU, although Germany and Austria were allowed swill feeding under certain conditions until October 2006.

Although 13 states have recorded CSFV outbreaks between 1996 and 2004 (Table 1), it is clear that several countries have on-going problems controlling CSFV. Over this same period, there have been repeated outbreaks of CSFV in pigs states bordering the EU such as Bosnia (257), Bulgaria (66) Romania (203) and Serbia (718). The repeated outbreaks in wild boar strongly suggest they are a reservoir (Artois et al., 2002).

CSFV can be transmitted from infected animals directly or indirectly; recognised routes of transmission include animal movements, movement of animal products such as carcases, human contact due to contaminated clothing, contaminated trucks due to faecal contamination and via genetic material such as semen (Elbers et al., 2001; Guerin and Pozzi, 2005; Ribbens et al., 2004). However, there is often considerable uncertainty about the probability of infection introduction associated with a particular mode of transmission. Moreover, illegal movements of animals and animal products are difficult to quantify (Wooldridge et al., 2006).