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Control of African swine fever epidemics in industrialized swine populations

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ABSTRACT

African swine fever (ASF) is a notifiable infectious disease with a high impact on swine health. The disease is endemic in certain regions in the Baltic countries and has spread to Poland constituting a risk of ASF spread toward Western Europe. Therefore, as part of contingency planning, it is important to explore strategies that can effectively control an epidemic of ASF. In this study, the epidemiological and economic effects of strategies to control the spread of ASF between domestic swine herds were examined using a published model (DTU-DADS-ASF). The control strategies were the basic EU and national strategy (Basic), the basic strategy plus pre-emptive depopulation of neighboring swine herds, and intensive surveillance of herds in the control zones, including testing live or dead animals. Virus spread via wild boar was not modelled.

Under the basic control strategy, the median epidemic duration was predicted to be 21 days (5th and 95th percentiles; 1-55 days), the median number of infected herds was predicted to be 3 herds (1–8), and the total costs were predicted to be €326 million (€256–€442 million). Adding pre-emptive depopulation or intensive surveillance by testing live animals resulted in marginal improvements to the control of the epidemics. However, adding testing of dead animals in the protection and surveillance zones was predicted to be the optimal control scenario for an ASF epidemic in industrialized swine populations without contact to wild boar. This optimal scenario reduced the epidemic duration to 9 days (1–38) and the total costs to €294 million (€257–€392 million). Export losses were the driving force of the total costs of the epidemics.

1. Introduction

African swine fever (ASF) is a notifiable infectious disease in pigs. It is caused by ASF virus (ASFV), a DNA virus from the family Asfarviridae, genus *Asfivirus* (cited from Gallardo et al., 2009). The disease is endemic in Africa (Chenais et al., 2015), the Russian Federation, and in certain regions of the Baltic countries (Gallardo et al., 2014, 2015b; Olsevskis et al., 2016). It is considered to be a substantial threat for Western Europe (EFSA-Panel, 2014). In countries with a large production and/or export of swine and swine products, an outbreak of ASF may result in devastating economic consequences for the swine industry due to export restrictions. Therefore, it is important to explore the effectiveness and consequences of strategies to control outbreaks of ASF in the industrialized swine populations.

The EU has established a set of strategies that should be followed in the case of an outbreak of ASF in the domestic swine populations (CEC, 2002). To our knowledge, the effectiveness of these strategies and their combination with other strategies, such as pre-emptive depopulation of neighboring swine herds or intensive surveillance in the control zones has never been investigated before. Identifying effective control strategies will assist the national veterinary authorities in the development of national guidelines for ASF control and contingency planning.

Simulation models of disease spread is a widely used tool to assist the national veterinary authorities in contingency planning (e.g. Backer et al., 2009; Martínez-López et al., 2011; Boklund et al., 2013; Halasa et al., 2015). Such models are invaluable for exploring mechanisms of disease spread and control, taking into account the complexities of agricultural systems.

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The objective of this study was to compare the epidemiological and economic effectiveness of different strategies to control a hypothetical epidemic of ASF in industrialized swine populations, where the role of wild boar in ASFV spread is negligible, exemplified by the Danish swine population.

2. Materials and methods

This section describes the simulation of ASFV spread between swine herds using different control strategies. It provides information about the herd data used in the model, ASFV-spread mechanisms, ASFV detection and the control strategies that are simulated. Important input parameters are presented in Table S1 in the Supplementary materials. Details on model parameters and equations can be found in Halasa et al. (2016a).

2.1. Herd and movement data

We used geographical data (UTM coordinates), the number of animals, and specification of herd types for the 8262 swine herds registered in the Danish Central Husbandry Register (CHR) in 2014. Descriptive data on the number of herds, herd sizes and frequencies of outgoing movements was presented in Halasa et al. (2016a). For each herd, the daily frequency of moving animals to another herd was calculated as the sum of all registered herd movements in the period from 01 January 2014 to 31 December 2014 divided by 365, based on the registrations in the Pig Movement Database. For each herd, this frequency was used as the mean (λ) in a Poisson distribution, describing the number of daily outgoing movements (batches) of animals. Similarly, the probability of moving animals to an abattoir was calculated for each herd. By analyzing the distances between source herds and receiving herds, it was found that animals from nucleus herds were moved further than animals moved from other herd types. As a result, two separate distributions for movement distances were used to model the movements of animals from nucleus herds and from other herd types, respectively (Halasa et al., 2016a). The probabilities of animal movements from one herd type to another were calculated based on the Pig Movement Database and are presented in Halasa et al. (2016a).

2.2. The simulation model

The DTU-DADS-ASF model (version 0.15.1) (Halasa et al., 2016a) was used. The model runs in the statistical computing language R (version 3.1.3) (R Core Team, 2015). The parameterization of the model was based on the Georgian strain of ASFV, reflecting the original strain of the epidemics currently running in Eastern Europe as explained earlier (Halasa et al., 2016a).

2.2.1. Modelling ASF spread

ASFV spread was modelled in two processes: 1) spread within a herd; 2) spread between herds by different mechanisms (transmission routes).

2.2.1.1. Modelling ASFV spread within a herd. The infection model for the individual animals is a state transition model with the following states: susceptible-latent-subclinical-clinical-removed (SLSCR model; Halasa et al., 2016b). The infection model for the herd follows the same model, but includes the possibility of an infected herd to become susceptible again, should the infection fade out before all animals in the herd are infected. Infected herds will start as latent and progress to the subclinical and clinical states following infection. The infection is then either detected, and therefore the herd is removed (culled), or it becomes susceptible again.

2.2.1.2. Modelling ASFV spread between herds. ASFV is simulated to spread between herds via animal movements, abattoir movements, via indirect medium-risk contacts (direct contact to animals such as contacts by veterinarians or artificial inseminators) or low-risk contacts (no direct contacts to animals, such as feed trucks and visitors), or via local spread. Each type of contact was modelled as a Poisson distribution. For movements of animals to other herds or to abattoirs, the mean (λ) was calculated for the individual herd, as described above, while for indirect medium and low risk contacts, a Poisson distribution was modelled for each herd type. For animal movements, each movement represented a batch of animals moved from the sending infectious herd to the receiving herd. The probability of transmitting the ASFV from the infectious herd to the receiving herd was dependent on the prevalence of the disease within the infectious herd and the number of animals moved in the batch (Halasa et al., 2016a). Local spread was modelled in a distance up to 2 km around infectious herds, and was assumed to consist of a mixture of unregistered animal movements, shared equipment and tools, and spread via rodents and insects. Detailed information including the equations and steps for modeling each of these mechanisms can be found in Halasa et al. (2016a).

The risk of ASFV spread and/or maintenance through wild boar was not modelled as the number of wild boar in Denmark is limited due to intensive farming in the country, leaving few suitable habitats for wild boar (Alban et al., 2005; Jordt et al., 2016). There is also a Danish legal requirement to eliminate stray wild boar (Anonymous, 2015c).

2.2.2. Modelling ASFV detection

In the model, the ASFV infection can be detected by three different mechanisms: passive surveillance before first detection; passive surveillance after first detection; and active surveillance.

In passive surveillance, before first detection, detection was modelled to occur when 1) the proportion of sick or dead animals (referred to as SIED throughout the paper) reached 2.55% (Halasa et al., 2016a); and 2) the proportion of SIED animals relative to the expected cumulative mortality level within the herd (in the period from the appearance of ASF clinical signs until the current time step) had increased by 2; and 3) the number of SIED animals within the herd was minimum 5 (Halasa et al., 2016a). In passive surveillance, after first detection, the first two conditions were assumed to be the same as before first detection, while the minimum number of SIED animals was set to 1, to represent a higher awareness of the disease in the country (Halasa et al., 2016a).

In active surveillance, detection occurred as a result of surveillance visits to infected herds by official veterinarians, either due to tracing or because the herd was located in a control zone (Halasa et al., 2016a). Herds to be surveyed were set in a queuing system, and visited as soon as resources were available. The daily surveillance capacity is dynamic over time (Table S1 in the Supplementary materials). The active surveillance includes either clinical surveillance alone (clinical signs and mortality), or clinical surveillance combined with serological and/or PCR testing, depending on the control strategy modelled. In case of clinical surveillance only, suspicion was assumed to occur if points 2 and 3 (in passive surveillance) were reached. Suspicions were then followed up by serological and/or PCR testing for confirmation of ASFV (Halasa et al., 2016a). When live animals were sampled for laboratory testing, the sample was dependent on the herd size (see details in Halasa et al., 2016a). For finishers and weaners, it was assumed that 30 animals were sampled per 500 animals in the herd. If sows were present in the herd, it was assumed that 30 of them were tested. If fewer than 30 animals were present in the herd, we assumed all animals were tested.