

**RESEARCH BRIEF:** Modelling the within-herd spread of ASF and implication for the British industry.

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### 1. KEY MESSAGE

Our study, using data from Russia to model ASF spread, has generated important parameters for future modelling work. Based on these data, it appears that ASFV could be circulating in a herd for several weeks before a substantial increase in mortality is observed in a herd, limiting the usefulness of mortality data as a means of early detection of an outbreak.

### 2. MAJOR FINDINGS

- Using data from Russia, the model predicts that ASFV was introduced to herds several weeks before the day on which ASFV was confirmed, varying between 20 days and 43 days (see figures). The mean time between the most likely day of disease introduction and detection was 32 days (see figure).
- The basic  $R_0$  (a measure of disease spread) varied amongst the nine ASFV outbreaks, ranging from 4.4 to 17.3. This between-herd variation in  $R_0$  is primarily a result of differences amongst herds in the transmission rate but is also partly a consequence of differences in the mean duration of the infectious period (ranging from 4.5 to 8.3 days).
- Our estimates are the first parameters inferred from field data from real ASFV outbreaks (rather than from transmission experiments) and suggest that the mean time from infection to infectiousness is longer by 1 or 2 days, and the mean infectious period is shorter by 1–4 days than was inferred from transmission experiments.
- Most of the parameters differed amongst herds, reflecting the impact of herd management and biosecurity practices on spread.

### 3. OBJECTIVES

The objective of this study was to use data from Russia and models to (1) characterise the potential of ASFV to spread in commercial pig herds, and (2) evaluate how long ASF may remain undetected despite active surveillance.

### 4. POLICY IMPLICATIONS

The finding that the average time from infection to detection was 32 days illustrates the difficulties in diagnosing incursions and therefore has implications for ASF surveillance.

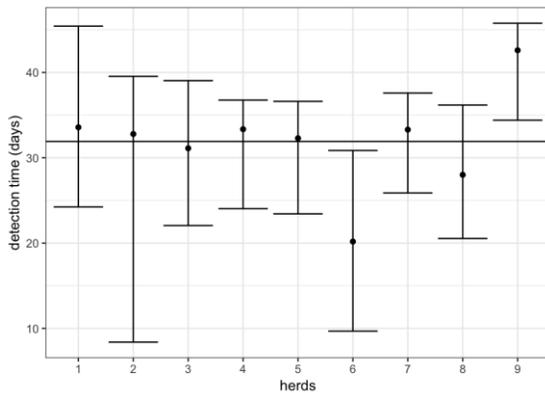
Our results also show that mortality data are a potential source of data from which to infer transmission parameters, at least for diseases, which cause high mortality

### 5. IMPORTANT ASSUMPTIONS AND LIMITATIONS

- We fitted a stochastic model for the within-herd transmission of ASFV to mortality data for nine pig herds in the Russian Federation (RF) affected by confirmed ASFV outbreaks. Parameters were estimated using approximate Bayesian computation.
- The within-herd dynamics of ASFV were modelled using a stochastic SEIR epidemic model, meaning that pigs in herds are divided into three classes: susceptible (i.e., uninfected), S, exposed (i.e., infected but not yet infectious), E, and infectious, I. There is little evidence that pigs recover following infection with ASFV strains circulating in the RF and, consequently, all pigs were assumed to die at the end of their infectious period.

- We have ignored the potential impact of herd structure on transmission in the model. This is principally a consequence of the limited availability of data on how pigs were managed within the farms included in the study. Additional limitations are the small number of herds for which data were available.

## 6. FIGURE



Time between the most likely day of disease introduction and detection (in days) for each of the nine herds from the Russian Federation involved in the study, as inferred by the model. Solid dots and error bars represent the median and 95% credible intervals of the posterior detection time resulting from our fitting exercise, respectively. The horizontal black line represents the mean value of the median herd-level detection time.

## 7. LINKS TO EXISTING PUBLICATIONS OR REPORTS

The work presented in this research brief was published in:

- C. Guinat, **T. Porphyre**, A. Gogin, L. Dixon, D.U.Pfeiffer, S. Gubbins (2017) Inferring the within-herd transmission parameters for African swine fever virus using mortality data from outbreaks in the Russian Federation. *Transboundary and Emerging Diseases*. doi: 10.1111/tbed.12748.