

ORIGINAL ARTICLE

Assessing the Risk of African Swine Fever Introduction into the European Union by Wild Boar

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Summary

The presence of African swine fever (ASF) in the Caucasus region and Russian Federation has increased concerns that wild boars may introduce the ASF virus into the European Union (EU). This study describes a semi-quantitative approach for evaluating the risk of ASF introduction into the EU by wild boar movements based on the following risk estimators: the susceptible population of (1) wild boars and (2) domestic pigs in the country of origin; the outbreak density in (3) wild boars and (4) domestic pigs in the countries of origin, the (5) suitable habitat for wild boars along the EU border; and the distance between the EU border and the nearest ASF outbreak in (6) wild boars or (7) domestic pigs. Sensitivity analysis was performed to identify the most influential risk estimators. The highest risk was found to be concentrated in Finland, Romania, Latvia and Poland, and wild boar habitat and outbreak density were the two most important risk estimators. Animal health authorities in at-risk countries should be aware of these risk estimators and should communicate closely with wild boar hunters and pig farmers to rapidly detect and control ASF.

Introduction

African swine fever (ASF) is considered to be one of the most devastating diseases of swine. In June 2007, ASF was first reported in the Caucasus region of Georgia, and since then, it has spread to four neighbouring countries. Since the beginning of the epidemic, direct contact between infected wild boars and domestic pigs has played a central role in the spread of the disease (Gogin et al., 2013; Oganessian et al., 2013). Most of these domestic pigs range freely in backyard farms, which usually have poor or no biosecurity measures. Wild boars have played a similarly significant role in past ASF epidemics (Louza et al., 1989; Mannelli et al., 1998; Sánchez-Vizcaíno and Arias, 2012). Nevertheless, evidence indicates that the ASF virus does not persist for a long time in isolated wild boar populations unless the boars become re-infected through contact with domestic pigs or they feed on contaminated swill (Mur et al., 2012a).

Given the uncontrolled spread of ASF north-west across the Caucasus region and the Russian Federation, concerns have increased that ASF will spread to European countries through wild boar incursions (Roberts et al., 2011; Sánchez-Vizcaíno et al., 2012, 2013; Costard et al., 2013). This may have devastating economic consequences, as pig production makes up the largest part of livestock and meat production in the EU, with 22 million tons of pig meat produced in 2010 (EUROSTAT). To prevent this from happening, countries along the eastern border of the EU need to develop and implement appropriate surveillance and warning systems for early detection and rapid response against the disease.

To date, research about risk of ASF introduction into the EU has focused on introduction through legal import of live pigs (Mur et al., 2012b), animal transport routes (Mur et al., 2012c) and imports of illegal animals and animal products (Costard et al., 2012). Most studies have not

assessed in detail the risk of ASF introduction through wild boar movements.

The scarcity of studies assessing risk of ASF introduction into the EU through wild boars is in large part due to the lack of data on wild boar abundance and distribution in Europe. Indeed, research on diseases shared by domestic livestock and wildlife is often limited by a lack of information on the abundance of susceptible wildlife populations in the area under study. To fill this gap, the model developed by Bosch et al. (2012a) for estimating wild boar density and distribution may be useful. As the authors suggest, the method may be applied for wild boar density in other territories of the European Union.

The objective of this study was to develop a semi-quantitative approach to evaluate the risk of ASF introduction into the EU through wild boars from non-EU countries along the EU border. This method has been applied to generate risk estimates of ASF introduction into the EU countries. This approach may make surveillance systems more effective at early detection of ASF cases in the EU. To explain the method and facilitate its adaptation to other infectious diseases, countries, and regions where the wild boars may play a role, we discuss the assumptions and parameterization of the model.

Materials and Methods

Study area

The study area (Fig. 1) included the following non-EU countries of origin: Russia, Belarus, Ukraine, Moldova and Turkey. It also included the following EU target countries: Finland, Estonia, Latvia, Lithuania, Poland, Slovakia, Hungary, Romania, Bulgaria and Greece. The study area covered the wild boar distribution range described by Genov (1981), extending from 35 degrees South to 65 degrees North, with a surface of 19 940 836 km². The administrative unit of analysis was defined to be the country.

Studies using the capture–mark–recapture technique indicate that 75–90% of wild boars are recaptured within 10 km of where they were first captured (Boisaubert and Klein, 1984; Spitz et al., 1984; Keuling et al., 2010). Therefore, we assumed that only EU countries sharing borders with non-EU countries containing wild boars were at risk of ASF introduction.

Model details

The semi-quantitative methodology developed here to analyse the risk of ASF introduction into the EU by wild boars is similar to that used to assess risk of ASF introduction into the EU through pathways not involving wild boars (Costard et al., 2012; Mur et al., 2012b). The method here assigns values to several risk estimators to generate an index that

can be used to compare different European countries. Data were gathered on the following seven risk estimators: the susceptible population of (1) wild boars and (2) domestic pigs in the country of origin; the outbreak density in (3) wild boars and (4) domestic pigs in the countries of origin; the (5) suitable habitat for wild boars along the EU border; and the distance between the EU border and the nearest ASF outbreak in (6) wild boars or (7) domestic pigs. Data on these estimators were converted to a ranked risk and combined in the model to obtain the relative risk value for each country. We assumed that wild boar would first become infected either (i) by contact with wild boars infected during an ASF outbreak among wild boars or (ii) by contact with domestic pigs infected during an outbreak among domestic pigs. Subsequently, the infected wild boar would leave the country of origin and enter the target EU country.

The following paragraphs describe in detail the principal model inputs.

Wild boar population density in the countries of origin (WBD)

The mean wild boar density (number of heads/km²) was obtained for each country of origin from the FAO (Eroglu, 1995; Melis et al., 2006; FAO EMPRES WATCH, 2010). Data were available down to the first level of the country subdivision for all countries except the smallest one, Moldova, for which only national-level data were available.

Domestic pig population density in the countries of origin (DPD)

Mean backyard pig density (number of heads/km²) was obtained for each country of origin from the FAO (FAO Empress Watch). The spatial resolution of the data was approximately 5 km.

Density of ASF outbreaks in wild boars in countries of origin (WBO)

Data on wild boar ASF outbreaks were gathered from the OIE (WAHID) for the period 2007–2012. The outbreak locations were transformed into a density map using kernel smoothing techniques (Spatial Analyst Kernel Density in ArcMap 9.3.1. GIS software, ESRI[®], Redlands, CA, USA), and the mean outbreak density in each country of origin was redefined as the density of ASF outbreaks in wild boars (WBO) in that country. As transmission of infectious disease is more likely if the at-risk individuals are close in both space and time (Pfeiffer et al., 2008), we applied a radius of 15° to expand the outbreak density across the non-EU countries of origin and generate a mean WBO value for each country of origin. We assumed that the higher the outbreak density and the shorter the distance between the infected and at-risk individuals were, the higher was the risk of wild boar infection. Geographical areas where physi-

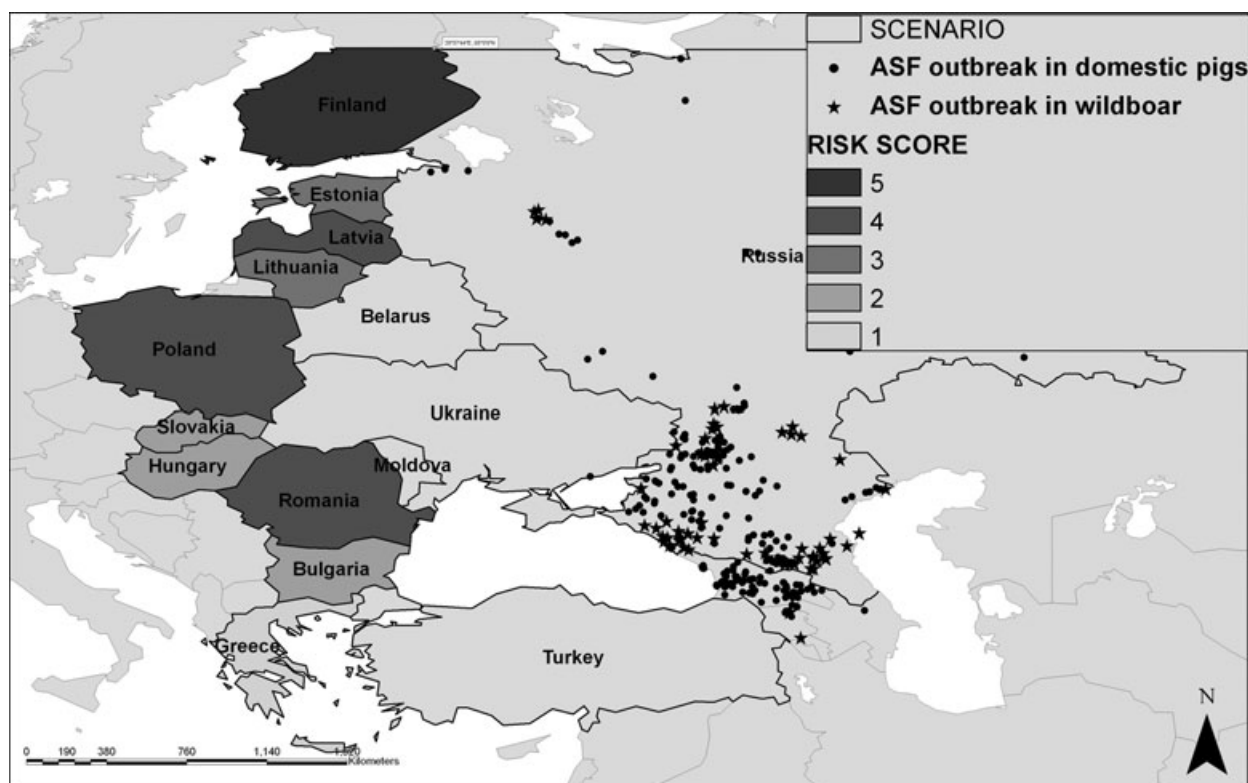


Fig. 1. Probability of ASFV introduction into EU by wild boar. Risk value of 0 should be expected for other EU countries not included in the scenario of study.

cal barriers prevent wild boar movement were not considered; for example, we did not consider Turkey because we assumed the probability to be negligible that a wild boar would cross the Bosphorus or Dardanelles straits or the Marmara Sea. The Bosphorus strait, with a width of 3329 m, acts as a natural barrier that prevents contact between the wild boar populations on either side.

Density of ASF outbreaks in domestic pigs in countries of origin (DPO)

Data on domestic pig outbreaks were gathered from the OIE (WAHID) for the period 2007–2012. The spatial distribution of ASF in domestic pig outbreaks was modelled using kernel density estimations with a radius of 15°, leading to estimates of the mean density of ASF outbreaks in domestic pigs in each country of origin (DPO). We assumed that the higher the outbreak density and the shorter the distance between the infected and at-risk individuals were, the higher was the probability of domestic pig infection by a wild boar.

Wild boar-suitable habitat along the border (SH)

The area of the wild boar-suitable habitat (SH) along the EU border between non-EU countries of origin and EU target country was calculated as described by Bosch et al.

(2012a). Suitable habitat was defined as the surface area (km²) with vegetation that acts as a ‘potential resource’ to provide food and/or shelter to wild boars. It included a buffer area extending 10 km from the border into the EU target countries, which was based on the average movement of 10.38 ± 2.84 km for wild boars at least 17 months of age (Keuling et al., 2010). Geo-referenced information about vegetation coverage was obtained from CORINE 2000 (Coordination of Information on the Environment, Land Cover 2000, European Commission, EEA 2008; cell size = 0.01 km²). Our analysis considered the same land uses that Bosch et al. (2012a) identified after reviewing the literature: homogeneous agricultural areas, such as pastures, and heterogeneous agricultural areas, such as areas including annual crops together with permanent crops, agro-forestry areas and areas of mainly agricultural land containing extensive areas of natural vegetation in complex cultivation patterns (Grid codes 18–22); forests, including coniferous, broad-leaved and mixed (Grid codes 23–25); and semi-natural areas containing scrub and/or herbaceous vegetation, such as natural grasslands, moors and heathland, sclerophyllous vegetation and transitional woodland–shrub, beaches/dunes/sands, bare rocks, sparsely vegetated areas, burned areas, glaciers and areas with perennial vegetation (Grid codes 26–34).

Distance from an EU target country to the nearest ASF outbreak in wild boars (DWBO) or domestic pigs (DDPO)

The distance of each EU country to the nearest ASF wild boar or domestic pig outbreak was measured by Euclidean distance using point distance measurement in ArcGIS 9.3.1 (ESRI®). The Euclidean distance gives the ‘ordinary’ distance between two points based on the Pythagorean formula. We assumed that risk of infection was inversely proportional to the distance from the outbreak, that the ASF virus was transmitted directly during contact between infected animals and non-infected wild boars and that the average movement of wild boars was 10 km (Keuling et al., 2010).

The semi-quantitative modelling was carried out in Excel 2010 (Microsoft, Redmond, WA, USA). Each parameter for each country was assigned a score from 0 to 5 based on natural breaks in the original data adjusted by the Jenks method (Jenks, 1967) in ArcMap 9.3.1. (Tables 1, 2 and Table S1). Then the risk of wild boar infection was estimated for each country as a result of (a) contact with infected wild boars from a wild boar outbreak or as a result of (b) contact with infected domestic pigs from a domestic pig outbreak. This overall risk was defined as the product of the various risk estimators incorporated in the model, as risk depends on the simultaneous occurrence of these risk factors:

- 1 Risk per target country (j) of wild boar infection through contact with infected wild boars from a wild boar outbreak = $RWB_j = \sum_{n=i} RWB_j = [(WBO * WBD)]_i * [(SH_{i-j} * DWBO)]$ and
- 2 Risk per target country (j) of wild boar infection through contact with infected domestic pig from a domestic pig outbreak = $RDP_j = \sum_{n=i} RDP_j = [(DPO * DPD)]_i * [(SH_{i-j} * DDPO)]$,

where j is the target country and i is each country of origin with which target country j shares a border.

Finally, the relative risk of a given target country was calculated as the sum of the risk of both routes of wild boar

infection, as the occurrence of one does not affect the occurrence of the other:

$$3 \text{ Overall risk per target country } (j) = \sum_{n=i} RWB_j + \sum_{n=i} RDP_j$$

Results were once again categorized into scores from 0 to 5 based on the natural breaks in the data adjusted by the Jenks method (Jenks, 1967) using ArcMap 9.3.1. Risk values of 0 were assigned to EU countries not included in the model.

To identify the most influential critical risk estimators, a jackknife sensitivity analysis (Unkel et al., 2012) was performed using @RISK 6 (Palisade Corporation, Newfield, NY, USA) in Excel 2010. The modelling was repeated, and one risk estimator at a time was discarded. The impact of deleting each risk estimator on countries’ overall risk scores was assessed after 10 000 iterations.

Results

Modelling suggests that the highest risk of ASF introduction into a given target country via wild boars occurs in Finland (5.00), Romania (3.01), Latvia (2.98) and Poland (2.45). These results are displayed in a choropleth map in which risk values have been categorized from 0 to 5 (Fig. 1). Figure 2 shows not only the overall risk assessments (in white) but also the risk assessment for each source of wild boar infection, whether by (a) contact with infected wild boars (in black) or (b) contact with infected domestic pigs (in grey). Each target country has a different risk for each source of infection. Finland, Romania, Latvia and Poland are at highest risk of both infection sources.

Ukraine and Russia are the countries of origin at risk of the greatest density of outbreaks among wild boars (0.07 and 0.06 outbreaks/km², respectively); the corresponding values for outbreaks among domestic pigs are 0.34 (Turkey), 0.23 (Ukraine) and 0.21 (Russia). Belarus is the country of origin at risk of the greatest animal population

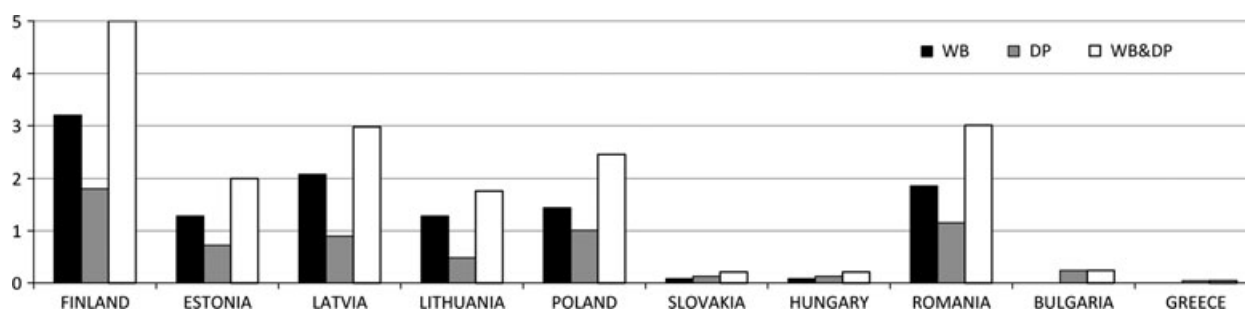
Table 1. Source data and relative rankings (in parentheses) for estimators of the risk of African swine fever (ASF) introduction by wild boar from various non-EU countries of origin

Country of origin	Risk estimator			
	Density of wild boar outbreak (WBO) (no. of outbreaks/km ²)	Density of wild boar population (WBD) (no. of wild boar/km ²)	Density of domestic pig outbreaks (DPO) (no. of outbreaks/km ²)	Density of domestic pig population (DPD) (no. of domestic pigs/km ²)
Russia	0.06 (4)	0.12 (4)	0.21 (3)	8.72 (3)
Belarus	0.01 (2)	0.26 (5)	0.04 (1)	17.98 (5)
Ukraine	0.07 (5)	0.08 (2)	0.23 (4)	10.99 (4)
Moldova	0.02 (3)	0.09 (3)	0.05 (2)	8.47 (2)
Turkey	ND	ND	0.34 (5)	0.002 (1)

ND, not done (see Materials and Methods).

Table 2. Source data and relative rankings (in parentheses) for estimators of the risk of African swine fever (ASF) introduction by wild boar into various EU target countries

Target country	Surface of wild boar-suitable habitat (SH) along border with indicated non-EU country (km ²)	Distance to the nearest wild boar outbreak (DWBO) (km)	Distance to the nearest domestic pig outbreak (DDPO) (km)
Finland	4757.09 (Russia) (5)	579.05 (5)	208.03 (5)
Estonia	814.88 (Russia) (2)	652.66 (5)	152.52 (5)
Latvia	827.38 (Russia) (2)	657.50 (5)	321.15 (4)
	697.66 (Belarus) (2)		
Lithuania	1886.42 (Belarus) (4)	843.72 (4)	548.53 (3)
Poland	1204.85 (Belarus) (3)	1238.26 (3)	911.04 (2)
	1182.46 (Ukraine) (3)		
Slovakia	352.90 (Ukraine) (1)	1591.71 (1)	1407.16 (1)
Hungary	136.37 (Ukraine) (1)	1641.67 (1)	1493.88 (1)
Romania	2109.02 (Ukraine) (4)	984.21 (4)	612.02 (2)
	402.58 (Moldavia) (2)		
Bulgaria	1173.13 (Turkey) (3)	1131.77 (3)	1049.13 (2)
Greece	210.56 (Turkey) (1)	1417.17 (2)	1321.88 (1)

**Fig. 2.** Results of the risk of ASFV introduction into EU by wild boar – a) by contact with wild boar from a wild boar outbreak (WB) (in black); b) by contact with domestic pigs from a domestic pig outbreak (DP) (in grey); or c) sum of both probabilities (WB&DP) (in white).

density: 0.26 wild boars/km² and 17.98 domestic pigs/km² (Table 1).

Among EU target countries, Finland falls into the highest risk category of 5 for the three risk estimators (Table 2), a result of the fact that it shares the largest wild boar-suitable area with countries of origin (4758 km²), and it lies closest to the nearest wild boar outbreak (579 km) and domestic pig outbreak (208 km). Estonia and Latvia are also at high risk because of their distance from outbreaks among wild boars (653 and 658 km, respectively) and domestic pigs (153 and 321 km). Poland and Romania shared the largest suitable area (2387 and 2512 km², respectively), reflecting their shared border with numerous countries of origin. Slovakia, Hungary and Greece showed the lowest risk values for all three risk estimators.

Sensitivity analysis in which the calculations were repeated with each of the risk estimators deleted in turn

showed that wild boar-suitable habitat was the most influential, explaining 51.3% of the results. The density of domestic pig outbreaks explained 38.7%; density of domestic wild boar outbreaks showed 32.7%.

Discussion and Conclusions

The method proposed here to assess risk of ASF introduction into the EU by wild boars is part of a European Community project aimed at comprehensively analysing all pathways of ASF introduction to identify EU areas at high risk. Thus, the model here was developed in the same way as previous models to assess risk of introduction through legal import (Mur et al., 2012b), illegal import (Costard et al., 2012) and fomite transport (Mur et al., 2012c). Together with these previously published models, the present study helps provide a comprehensive understanding of

ASF introduction risk of EU member states, allowing them to carry out cross-country comparisons.

Our model suggests that risk of ASF introduction is similar whether the source of wild boar infection is contact with infected wild boars or contact with infected domestic pigs. Finland, Romania, Latvia and Poland are predicted to be at highest risk, while Estonia and Lithuania are at relatively low risk, and Slovakia, Hungary, Bulgaria and Greece are at lowest risk. Consistent with our results, a national risk assessment based on possible routes of ASF entry into Finland (Oravainen et al., 2011) reported the wild boar pathway to be a threat. The authors of that study hypothesized that wild boars could migrate to Finland from areas where ASF outbreaks have occurred, just as we do here, although those authors suggested that such migration would occur slowly. Although infected wild boars are unlikely to traverse such long distances on their own, habitat continuity favours the spread of ASF among the populations occupying land up to the border with Finland. Such gradual 'migration' to the border would be facilitated by difficulties in detecting infection in wild boars, which can lengthen the time needed to identify an epidemic to more than 100 days (Boklund et al., 2008). We do agree with the authors of the Finland report (Oravainen et al., 2011) that transmission from infected wild boars to domestic pigs at the border would be difficult because of high biosecurity on farms in Finland. Nevertheless, the risk of ASF introduction identified in our model and theirs is epidemiologically plausible, and Finland has already been identified as a 'super-spreader' of ASF during high-risk periods (Nigsch et al., 2013).

In addition to Finland, the target countries Latvia, Lithuania and Poland are also at higher relative risk of ASF introduction via wild boars. These countries border on Belarus, which is close to regions in the Tverskaya Oblast, where ASF appears to be at high risk of spreading from the secondary endemic zone to central Russia (Oganesyan et al., 2013). Indeed, Belarus represents the highest threat scenario. It not only contains the highest density of susceptible animals among the countries of origin examined, but it also shares extensive wild boar-suitable habitat with Latvia, Lithuania and Poland that covers, respectively, 89%, 74% and 65% of the total surface of those countries. Indeed, the risk estimator of SH was identified as the single most important factor in our risk assessment model. Its impact could be biologically and reasonably explained by the fact that only when wild boar habitat is shared between the infected country and the country at risk, wild boar populations are connected through the continuity of the habitat and then the 'hazardous' infected country poses a real risk. This would be consistent with a recent European Food Safety Authority report on animal health and welfare (EFSA, 2010), which suggested that the disease could

spread only in areas with a dense, uniform wild boar population.

Despite the insights obtained from our model, its predictions of disease spread should be interpreted with caution because it is based on limited data and a relatively poor understanding of ASF transmission in wild boars. Therefore, users of the model should be aware of its assumptions and parameterization. One of the most important assumptions is a bandwidth of 15° for the kernel analysis. This analysis served to identify broad trends in the risk of ASF outbreaks among wild boars and domestic pigs as a function of distance from an infected area. Our model assumes that oversmoothing is not a consequence of long-range movement of individual wild boars, but of successive contacts between animals in different populations moving short distances. Our choice of bandwidth differs from the 100-km radius chosen by Gulenkin et al. (2011) and Oganesyan et al. (2013) when they analysed the density surface of ASF cases in the Caucasus region and the Russian Federation. Their smaller radius was useful for defining risk zones within the affected area and estimating the probability of new cases arising from current outbreaks in the Russian Federation. Such a small radius was not appropriate for our study because we wished to discern broad trends and to look in countries along the EU/non-EU border. Even though the work of Gulenkin et al. (2011) and Oganesyan et al. (2013) differed in scale and scope from ours, their findings are consistent with ours. The ASF epidemic in the Russian Federation appears to be moving towards central Russia, and diffusion to Ukraine from the secondary endemic zone appears likely (Oganesyan et al., 2013). This supports our risk assessment that Ukraine is likely to show the highest density of wild boar outbreaks (0.07 wild boar outbreaks/km²).

Our model does not take farm biosecurity directly into account for the lack of detailed information available. Some data are available to distinguish between high and low biosecurity of swine-keeping systems in the Russian Federation (FAO, 2012; Khomenko et al., 2013; Oganesyan et al., 2013), but they do not provide farm-level information. As a result, we used outbreak density as a risk parameter in the model. Kernel density estimation converts outbreak intensities to densities, producing a smooth density surface of outbreaks over the study area. In this way, areas with a high outbreak density, presumably corresponding to low-biosecurity areas, are weighted heavily in the kernel estimation, whereas single outbreaks, such as those occurring on high-biosecurity farms, are weighted weakly.

The lack of available data on ASF spread via wild boars made it difficult to assess the relative importance of each risk estimator in the model, which might have allowed us to weight the estimators differently in the analysis or even differently for the different countries. In such cases of

insufficient data about the factors included in the model, the best approach may be to assume that they all carry the same relative importance (Malczewski, 2000). Nevertheless, we did perform sensitivity analysis in which the modelling was repeated after deleting each of the risk estimators in turn. The results suggest that the area of wild boar-suitable habitat near the EU/non-EU border is a more influential risk factor than are the densities of ASF outbreaks among wild boars or domestic pigs. Further research should examine the relative importance of these risk factors in greater detail.

More complete, accurate and up-to-date data would improve this risk assessment significantly. This is particularly true of data on wild boar populations in the study area. For example, the risk estimator of wild boar-suitable habitat at the European border could be estimated only for EU target countries, as data on vegetation coverage were not available for the non-EU countries of origin. It may be possible to improve estimates of wild boar-suitable habitat by using maximum entropy models based on ecological parameters (Bosch et al., 2012b), which can capture biological variability and uncertainty (Elith et al., 2006). Incorporating recent FAO data on wild boars obtained with hunting bugs (Khomenko et al., 2013) may also improve models of suitable habitat.

In conclusion, this study describes a simple, semi-quantitative approach to assessing the risk of ASF introduction into the EU by wild boar movements. The model developed here can serve as the basis for detailed national assessments whenever accurate and complete data are available. The insights from this model complement those of risk models for other modes of ASF introduction, providing a comprehensive picture of the risk of disease entry into the EU. Communicating this risk appropriately to wild boar hunters and pig farmers in high-risk countries, particularly backyard pig farmers, is crucial to rapidly detect and control ASF. The method proposed here may also prove useful for estimating the risk of entrance of other infectious disease transmitted by wild boars in other territories as well as for optimizing the surveillance of wildlife diseases involving wild boars.

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Supporting Information

Additional Supporting Information may be found in the online version of this article:

Table S1. Break values employed for each risk parameter and overall results.