

Identifying potential hotspots of disease infection of African swine fever virus in European swine

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- We develop a generic and spatial risk assessment framework applicable to a wide range of pathogens
- The aim is to improve hotspot identification of high-risk areas or pathways for exotic disease incursion
- This can inform risk-based surveillance – saving time, money and resources
- We apply this to an African swine fever virus (ASFV) case study

Generic risk question and framework:

What is the risk of infection and spread of a pathogen in Area B due to the presence of that pathogen in Area A?

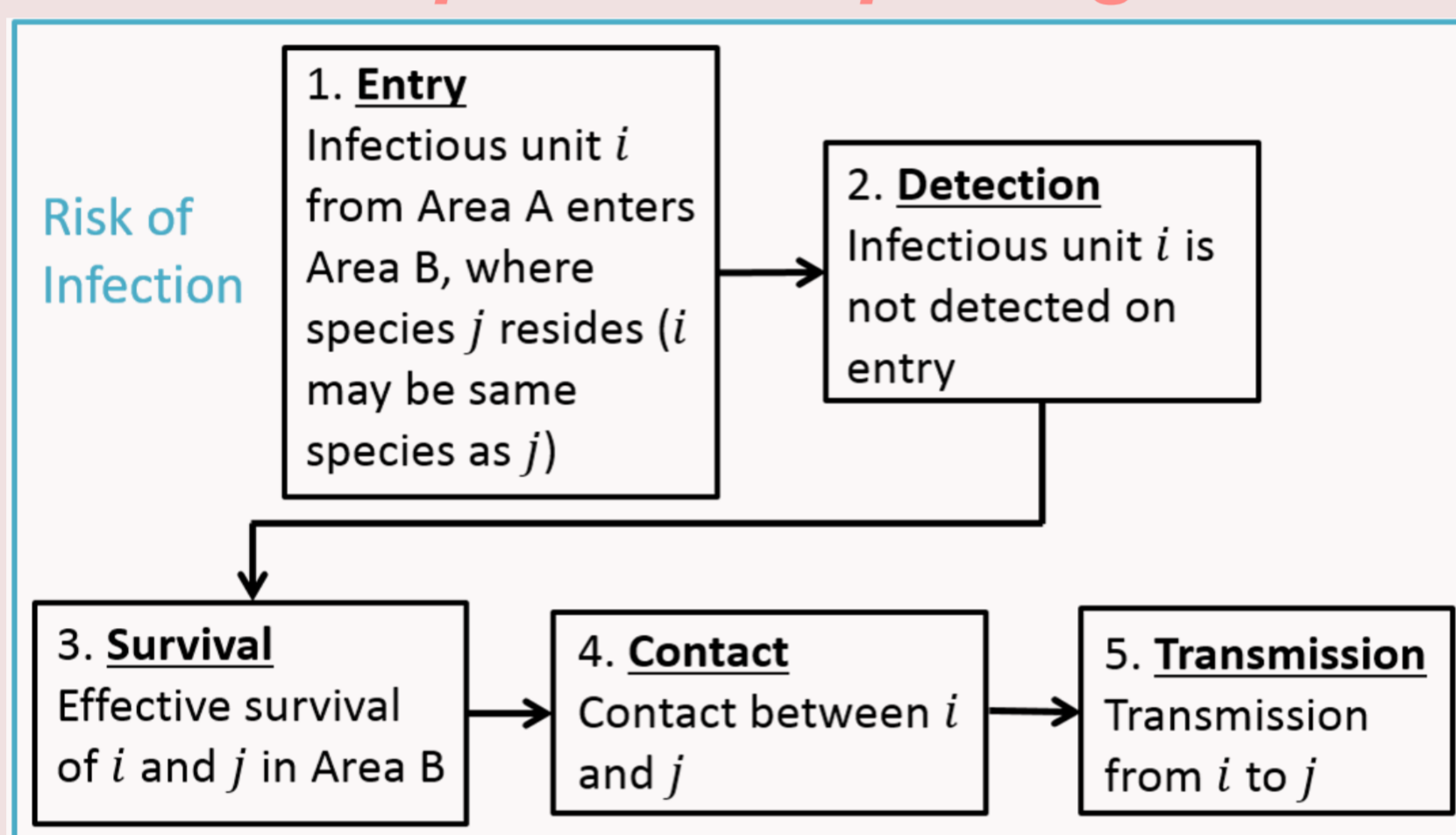


Fig. 1 The five steps of the risk pathway for the generic spatial risk question. The term "unit" in Step 1 refers to a generic source of infection such as species, products or feed, that could have direct or indirect contact with native susceptible hosts, j.

What is the risk of infection of ASFV in Europe in pigs or wild boar?

We predict the probability of at least one infection of ASFV in Europe in 2019 at a 100km² cell level

We consider three risk pathways:

1. Legal Trade of Pigs
2. Legal Trade in Pig Meat Products
3. Terrestrial Movement of Wild Boar

We use data on:

- Boar and pig density maps and estimated numbers of backyard pigs
- Boar habitat suitability maps – to determine direction of boar movement (Alexander et al. 2016)
- Eurostat Comext trade data
- Prevalence in 2018 (Simons et al. 2017 and OIE data)



Fig. 2 Wild boar distribution throughout Europe at a 1km² scale, using data from Alexander et al. 2016. A semi-quantitative scale is used to plot wild boar abundance with 4 representing areas with highest boar abundance.

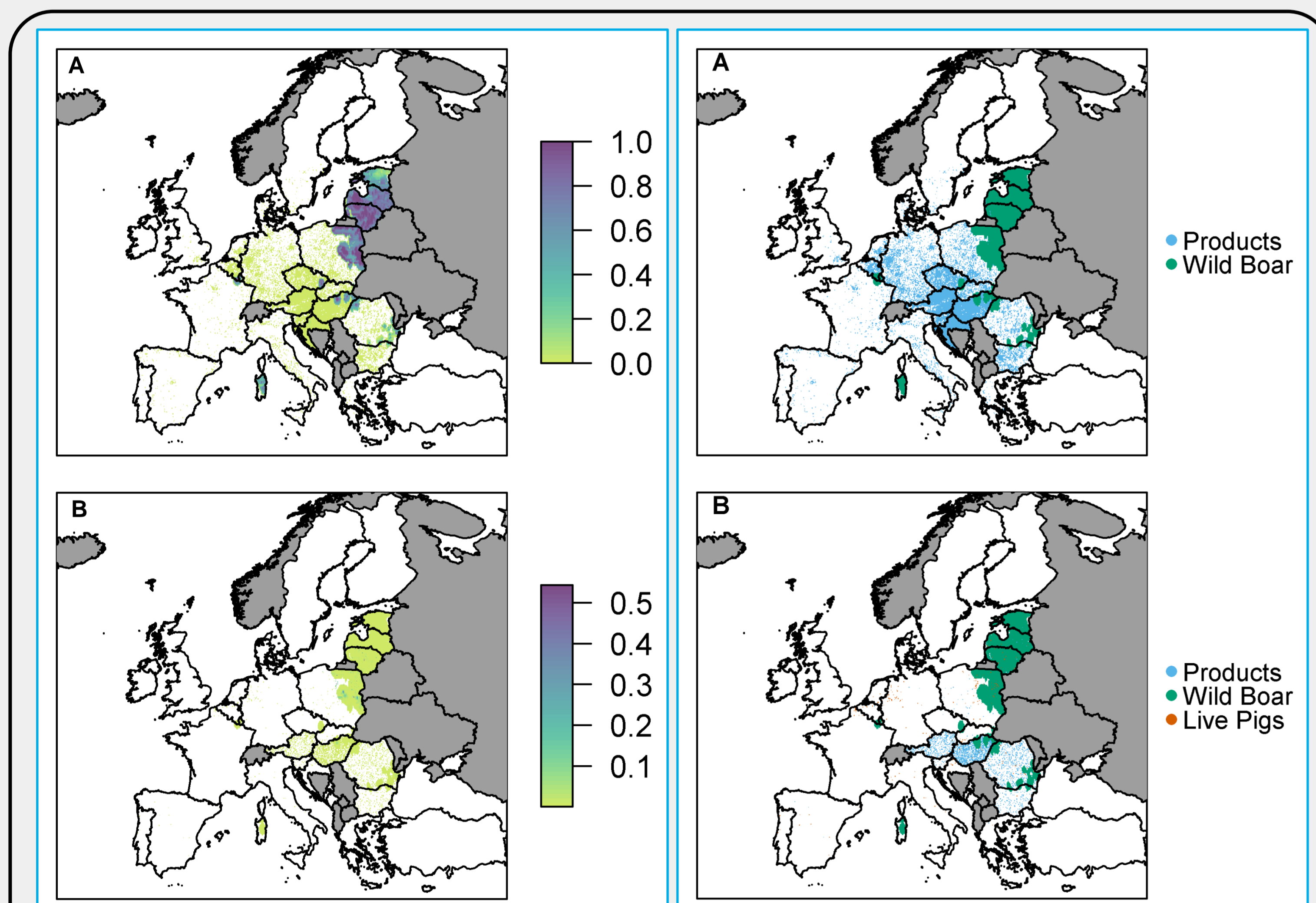
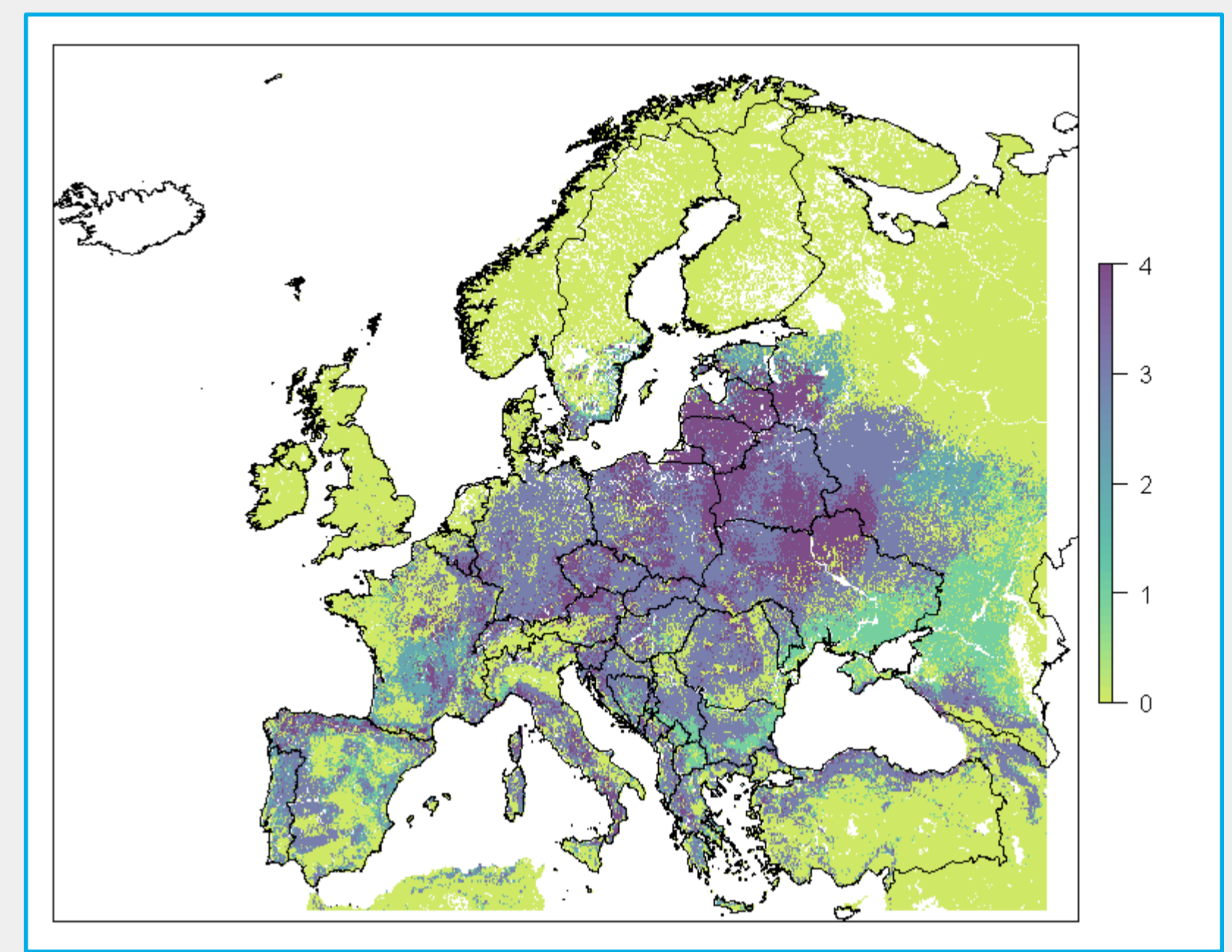


Fig. 3 The probability of at least one infection with ASFV in (A) wild boar or (B) pigs in 2019, plotted at a 100km² cell level across Europe. Countries in grey have insufficient data to complete the risk assessment.

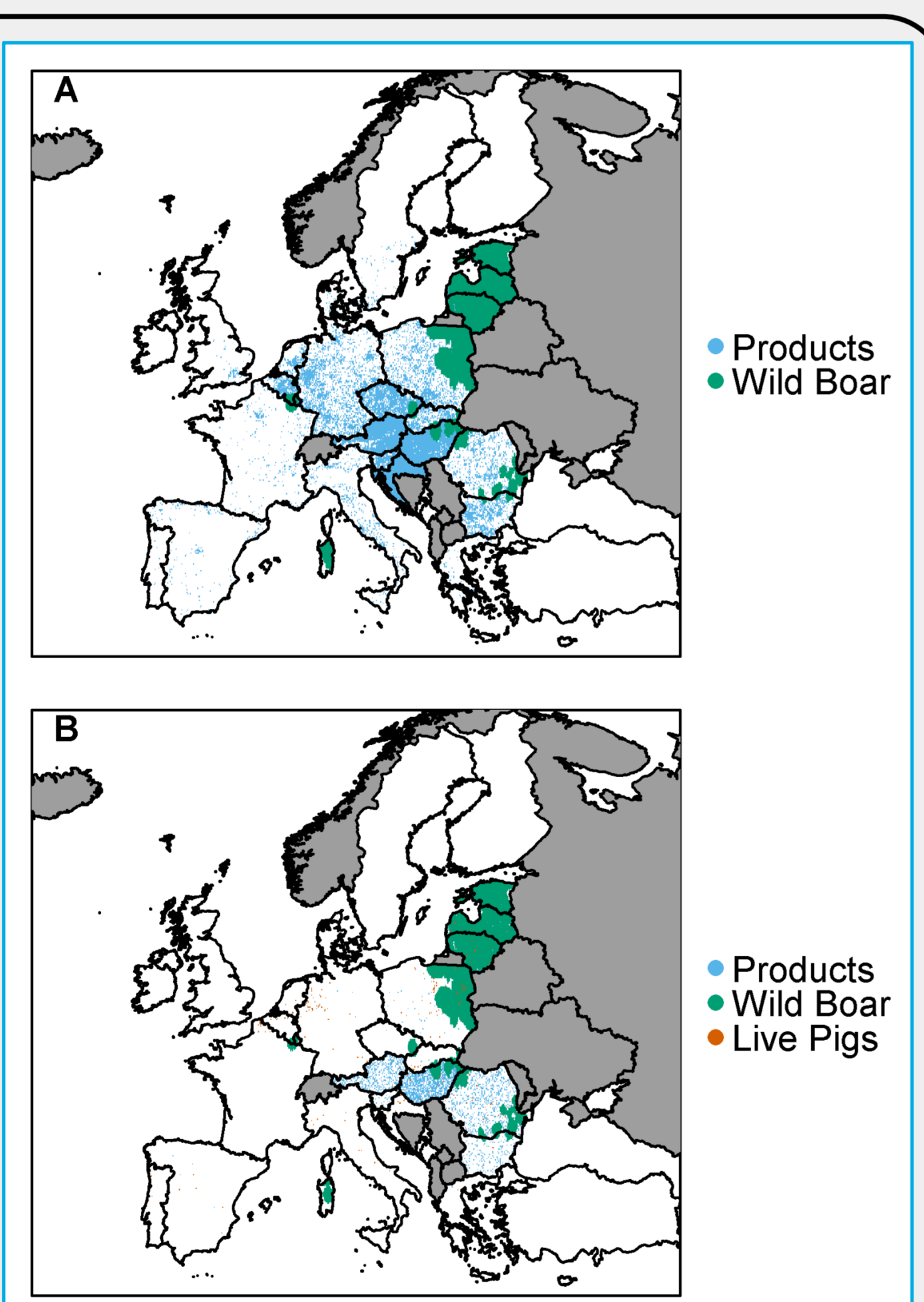


Fig. 4 The pathway which has the highest probability of infection of ASFV for (A) wild boar and (B) pigs is plotted at a 100km² cell level across Europe. Countries in grey have insufficient data to complete the risk assessment.

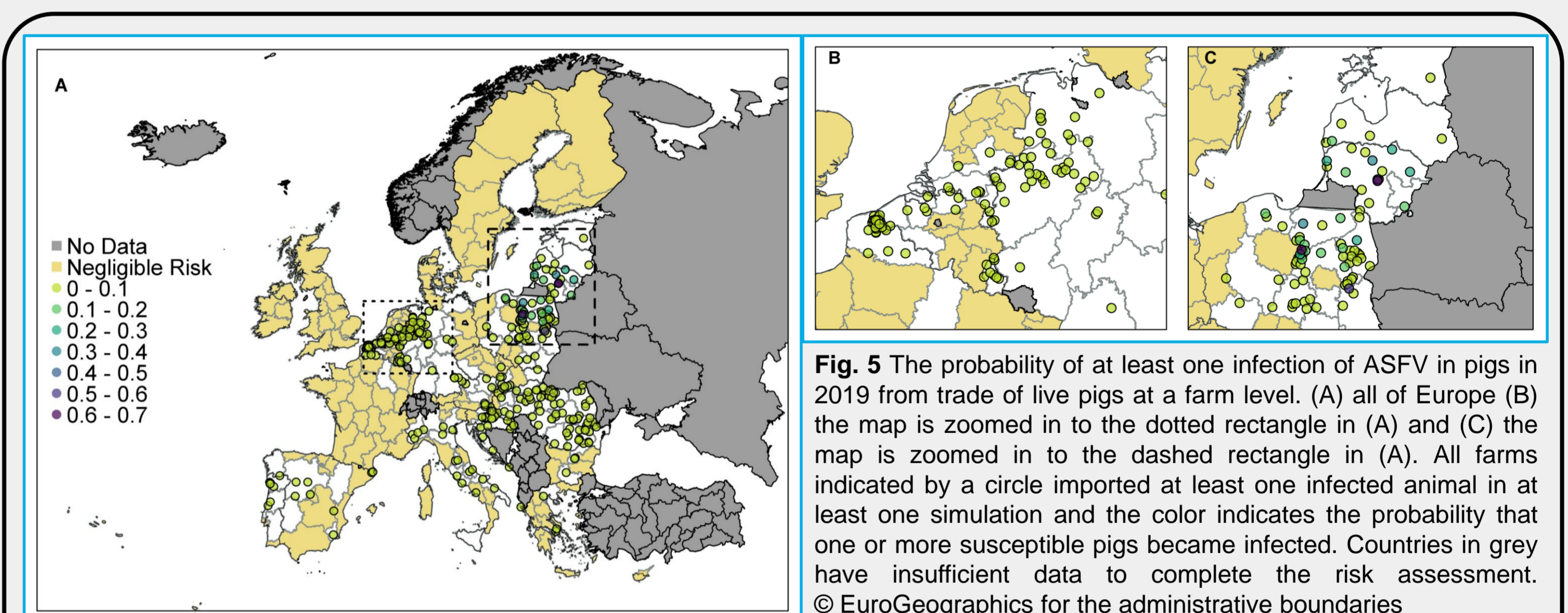


Fig. 5 The probability of at least one infection of ASFV in pigs in 2019 from trade of live pigs at a farm level. (A) all of Europe (B) the map is zoomed in to the dotted rectangle in (A) and (C) the map is zoomed in to the dashed rectangle in (A). All farms indicated by a circle imported at least one infected animal in at least one simulation and the color indicates the probability that one or more susceptible pigs became infected. Countries in grey have insufficient data to complete the risk assessment. © EuroGeographics for the administrative boundaries

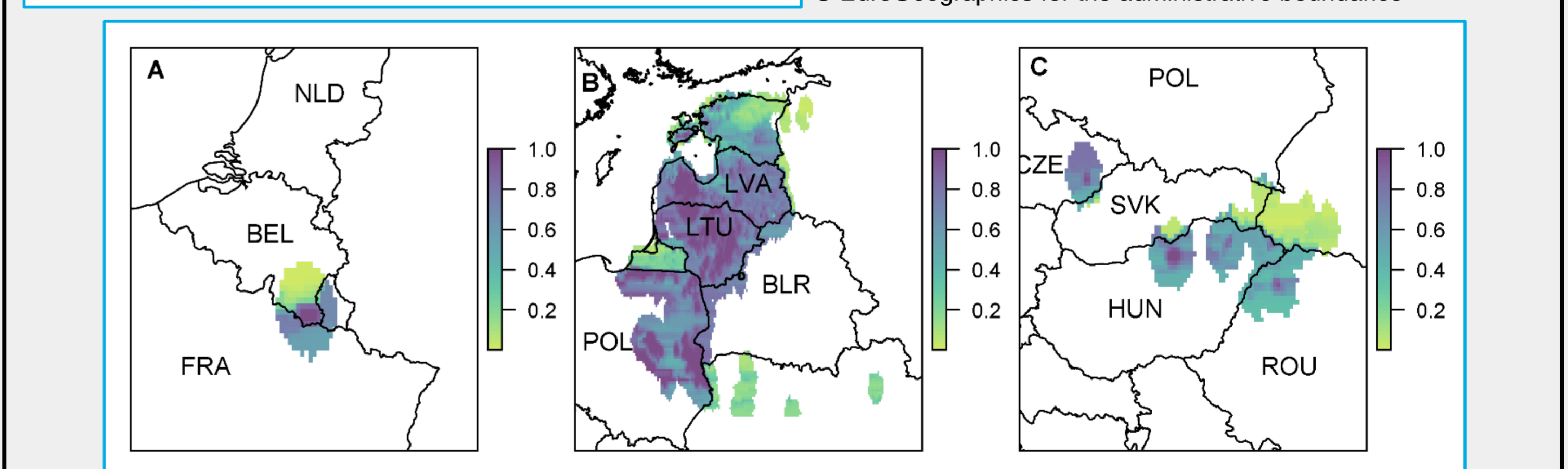
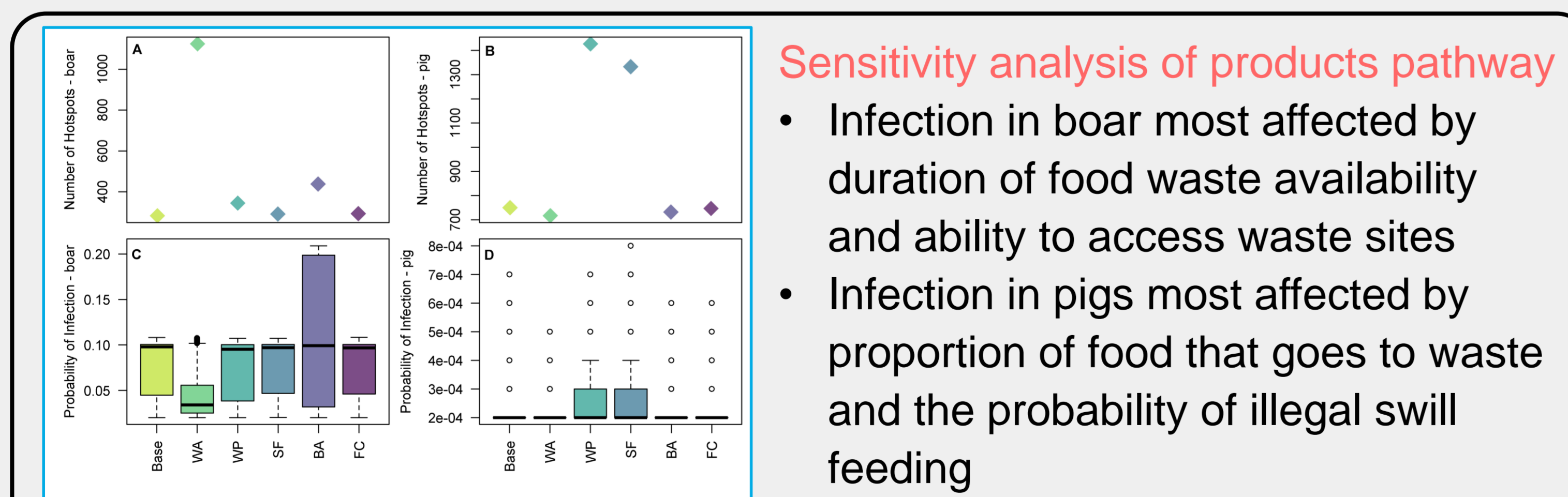


Fig. 6 The probability of at least one infection of ASFV in boar in 2019 due to wild boar movement at a 100km² cell level. We zoom in to three regions where there were cases in 2018 (A) Belgium; (B) Poland, Lithuania, and Latvia; and (C) Hungary, Czech Republic and Romania. Countries are indicated by their ISO3 code.



Sensitivity analysis of products pathway

- Infection in boar most affected by duration of food waste availability and ability to access waste sites
- Infection in pigs most affected by proportion of food that goes to waste and the probability of illegal swill feeding

Fig. 7 The effect of uncertain parameters in the legal trade of pig meat products pathway on hotspots of disease risk across Europe. In (A) and (B) the number of 100km² cells which are hotspots for wild boar infection and domestic pig infection are plotted respectively for the baseline and sensitivity parameters. In (C) and (D) the distribution of the probability of infection across 100km² cells which are hotspots in Europe for wild boar and pig infection, respectively, for the baseline and sensitivity parameters. The sensitivity parameters are: WA, duration of waste availability for boar, WP, proportion of food that goes to waste, SF, the probability of illegal swill-feeding, BA, the probability that boar are able to access waste, and FC, the proportion of food that is cooked sufficiently to kill the virus.

CONCLUSIONS

- Probability of infection is much lower in pigs than wild boar
- Highest risk areas are in E. Europe near current boar cases and results from wild boar movement
- Trade in products has widespread but low probability of infection across Europe
- Trade in pigs has high probability of infection for some farms
- Difficult to predict specific hotspots for sporadic long-distance spread
- Other pathways such as travellers bringing meat products, or trade in pigs within a country likely to be important too

References: Alexander, N.S., et al. (2016). The European Distribution of *Sus Scrofa*. Model Outputs from the Project Described within the Poster – Where are All the Boars? An Attempt to Gain a Continental Perspective. *Open Health Data*, 4(1), p.e1
 Simons, R. R. L., et al. (2017). Mighty models from little data grow: Estimating animal disease prevalence. *Proceedings of the Society for veterinary epidemiology and preventative medicine*, Inverness, Scotland: 166.
 Wild Boar: By Valentin Panzirsch - File:Wildschein, Nähe Pulverstampf.jpg, CC BY-SA 3.0 at, <https://commons.wikimedia.org/w/index.php?curid=4690217>