One for all: a generic risk framework for all pathways of disease introduction

Rachel Taylor*, Robin Simons, Roberto Condoleo, Paul Gale, Louise Kelly, Emma Snary
Department of Epidemiological Sciences, Animal & Plant Health Agency (APHA)
*Rachel.taylor@apha.gov.uk

We develop a risk assessment framework that is generic and applicable to a wide range of pathogens. The aim is to improve hotspot identification of exotic disease incursions. The framework will need to cope with spatial variation, diverse sources of input data at different scales, various transmission routes and distributions of both wild animals and livestock.

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

Our framework for the above risk question is outlined in Fig. 1. Major transmission pathways that we consider are:

- Legal live animal trade
- Trade in food products
- Terrestrial movement of wild animals
- Human transportation
- Vector flight
- Bird migration

Risk of Infection: the probability of one or more initial infections in a native species in Area B.

Risk of Spread: the probability of one or more infections at a different location in Area B.

Risk of Infection Calculation

1. Entry: The number of infected hosts, \( I_g \), entering location \( g \) of Area B is defined as

\[
I_g = \sum \Delta \left( N_0 \alpha (P_A) \right)
\]

where \( N_0 \) is the number of hosts entering location \( g \) from sub-region \( A_i \) in Area A and \( P_A \) is the prevalence of infected hosts in \( A_i \).

2. Detection: The number of infected hosts passing any detection controls is

\[
I_g = I_g \left( 1 - p_d (g) \right)
\]

where \( p_d (g) \) is the probability of detection in location \( g \).

3, 4 & 5. Survival, Contact and Transmission

We use \( R_g \) to represent these 3 steps. We use different equations for \( R_g \) depending on the disease and transmission pathways.

Overall our risk of infection \( R_i (g) \) at location \( g \) is:

\[
R_i (g) = 1 - e^{-\lambda (g) / \mu}
\]

Risk of Spread: Calculated using a similar methodology.

Risk of Infection: African Swine Fever (ASF) - PRELIMINARY RESULTS

We predict the risk of infection of ASF in Europe in 2018.

We consider three risk pathways:

1. Trade in Pig Meat Products (Fig. 2)
2. Live Pig Trade (Fig. 3)
3. Terrestrial Movement of Wild Boar (Fig. 4)

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 2017 (Simons et al. 2017 and EMPRES-i data)

Countries predicted to have higher relative risk in 2018 are those which had cases in 2017 (Lithuania, Latvia and Poland), or have now had outbreaks in 2018, such as Romania, Hungary and Bulgaria. Our three risk pathways did not predict sporadic long-distance spread, such as the recent cases in Belgium. In general, the wild boar movement pathway predicted non-negligible risk only near current cases, indicating that natural wild boar movement is not responsible for long-distance spread. The food trade and movement of wild boar pathways were both more likely to cause cases in wild boar than pigs.