



A generic and spatial risk assessment for animal disease: the COMPARE Project Rachel Taylor, Paul Gale, Robin Simons, Louise Kelly, Emma Snary* Department of Epidemiological Sciences, Animal and Plant Health Agency (APHA)

The aim of this task within COMPARE is to develop a risk assessment framework that can be generic and applicable to a wide range of pathogens. The framework will need to deal with spatial variation, diverse sources of input data at different scales, various transmission routes and distributions of both wild animals and livestock.

Case study: Lumpy Skin Disease Virus

Lumpy Skin Disease (LSD) is a virus of cattle that is transmitted both by direct contact and also mechanical transmission by flies (*Magori-*

Our risk question is:

"What is the risk of infection in area B due to the presence of a hazard

in area A?"

To address this we develop a risk pathway that outlines how disease is

likely to enter and spread within an area:



Cohen et al., 2012). The disease causes severe morbidity in cattle and leads to production loses. It is an OIE notifiable disease and after its introduction in Turkey has spread throughout the Balkan region since 2015 (*Mercier et al., 2017*), increasing the risk of spread to other European countries.

We calculate risk as the probability of at least one infection from species i to species j through a transmission route r, as:

 $R_{ijr}(g) \sim 1 - e^{-V_r \beta_{ijr} S(g) I(g)}$

Risk $R_{ijr}(g)$ in area g is determined by:

- the virus-specific transmission term V_r ,
- the contact rate between the two species β_{ijr} ,
- the number of susceptible animals S(g) in area g,
- the number of infected animals I(g) entering area g based on average prevalence of the disease in the country of import.

Therefore, risk from species *i* to *j* through any transmission route is:

$$R_{ij}(g) = 1 - \prod_{r} \left(1 - R_{ijr} \right)$$

PRELIMINARY RESULTS

INPUTS

We use data on:

- Movement of cattle in 2015: TRACES data
- Livestock abundance in 2015: Cattle Tracings System data
- Direct & mechanical transmission rates (Magori-Cohen et al., 2012)
- Prevalence in other countries pre-2015: Output from release assessment in SPARE project (results used here are preliminary and subject to high uncertainty)

Using England and Wales as proof of concept, we assess risk in 2015 at two spatial scales: farm-level and county-level.



Figure 1: Examples of farmlevel and county-level data. In (A) trade data on movement of cattle to specific farms. In (B), county-level data on livestock abundance in the UK - the average number of cattle per farm. We also use the number of holdings in each county. Our <u>preliminary</u> results include variability in prevalence estimates and uncertainty in transmission rates.

□ -7 to -6
□ -6 to -5
□ -5 to -4
□ -4 to -3

County level: Risk on a log scale of one or more infections of LSD in each county in 2015.





Figure 2: Low, average and high estimates of risk on a log scale, incorporating average number of cattle per farm and number of holdings in each county, livestock entering each county in 2015, variability in prevalence and uncertainty in transmission rates. Note the different axis scales.

Farm level: Risk on a log scale of one or more infections of LSD

occuring at a farm due to trade in 2015.







Conclusions:

- High variation in risk arises from prevalence data.
- Risk is expected to be low no country trading with UK in TRACES dataset had LSD cases for 10 years pre-2015.
- The framework will be improved to include distribution of vectors and survivalibility of species.



Figure 3: Low, average and high estimates of risk on a log scale, incorporating number of cattle at each farm, livestock entering each farm in 2015, variabilioty in prevalence and uncertainty in transmission rates. Note the different axis scales.

<u>References:</u> Magori-Cohen et al., 2012. Mathematical modelling and evaluation of the different routes of transmission of lumpy skin disease virus. *Veterinary Research* **43**:1

Mercier et al., 2017. Spread rate of lumpy skin disease in the Balkans, 2015-2016. Transboundary and Emerging Diseases, 1-4





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