

Exposure Assessment in the context of the SPARE project: A model to spatially assess exotic diseases incursions and spread throughout Europe

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INTRODUCTION

Aim of the SPARE project (www.spare-europe.eu) is to develop a quantitative risk assessment to describe the spatial introduction and spread of exotic livestock pathogens within Europe, based on the most probable routes of transmission. The risk assessment will be modular with the release, exposure and consequence assessments developed independently. Here we discuss in detail the development of the spatially explicit exposure assessment model, using Bluetongue virus (BTV) in the Piedmont region of North Western Italy as an example. We present one example output of the exposure assessment model: an estimate of the spatial probability that introduction of one infected animal with BTV will lead to at least one other infected animal.

MATERIAL & METHODS

- 1) Exposure risk factors information for 33 diseases listed in the OIE animal code was obtained through an extensive literature search, snowball searching and googling.
- 2) A systematic and structured inventory of exposure risk factors by route of transmission was populated (see Fig 1).
- 3) Scenario tree pathways were developed, detailing the main, and most likely, exposure pathways in terms of probability of a secondary transmission, along with the equations and their most appropriate parametrization based on available data, incorporating variability where relevant (see Fig 2).
- 4) Deterministic and stochastic models were then implemented and run to provide a spatially explicit quantitative assessment of the risk of exposure to livestock of the pathogens at a NUTS 3 level, following the introduction of one infected animal in the period of highest activity of *Culicoides spp* (April-November) (see Fig 3).

RESULTS

Fig 1: Factors affecting the exposure to vector-borne diseases (Bluetongue)

BLUETONGUE	Data availability	Uncertainty
INFECTION EPIDEMIOLOGY		
Case definition		
Incubation period (infectious period before the clinical symptoms)		
Average time to end of infectious period		
Differential diagnosis complexity		
Vaccine availability		
Vaccine efficacy		
DISEASE PREVALENCE IN:		
Bovine		
Sheep		
Goats		
COUNTRY FEATURES		
Vaccine diffusion		
Existence of a surveillance program		
Surveillance efficiency		
Public health authorities awareness		
Farmer awareness		
Proxy of Population awareness		
GEOGRAPHIC RISK		
Infected areas proximity (geographical borders)		
POPULATION DENSITY		
Bovine		
Sheep		
Goats		
POTENTIAL CONTACTS		
Bovine movements in Italy		
Sheep movements in Italy		
Goats movements in Italy		
Importation of bovine in Italy		
Importation of sheep in Italy		
Importation of goats in Italy		
VECTORS		
Vectors distribution (mosquitoes)		
Presence of wetland		

Legend:
■ Very good data/No uncertainty
■ Sufficient data /Medium uncertainty
■ Good data/Low uncertainty
■ Poor data/High uncertainty
Bold Necessary parameter

Fig 2: A fishbone diagram showing the scenario tree pathway for the exposure to vector-borne diseases after the introduction of an infected animal (Bluetongue)

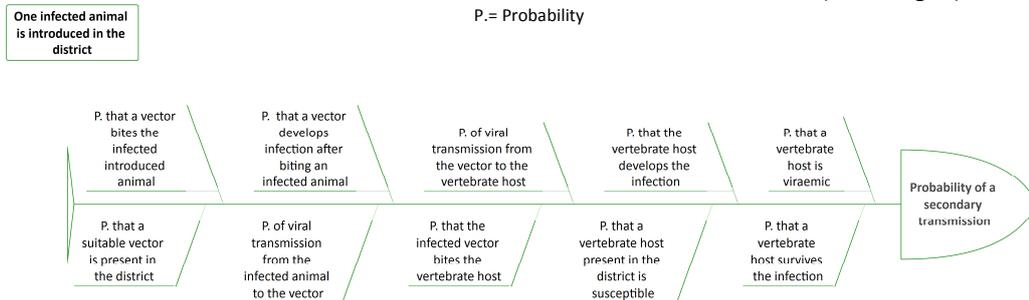
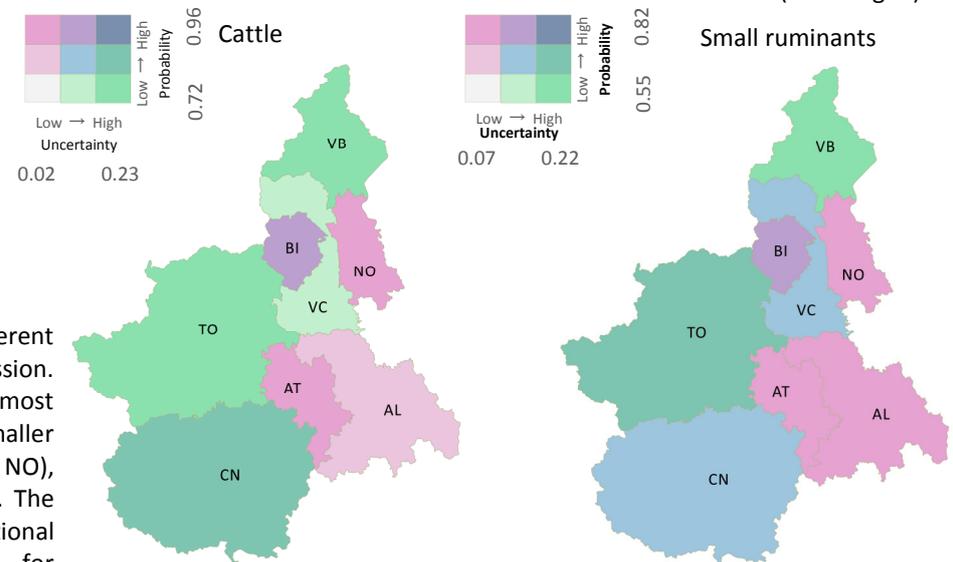


Fig 3: Output of the stochastic quantitative assessment of the probability of exposure to vector-borne diseases after the introduction of an infected animal (Bluetongue)



This map combines two types of information: the probability that a domestic animal is infected after the introduction of a Bluetongue infected animal (shown from bottom to top in the legend) and how certain it is (shown from left to right in the legend).

DISCUSSION

Based on the model we provide maps with a different distribution of the probability of a secondary transmission. This is quite high in the whole Region and the factor most influencing it, is temperature: districts with smaller temperature excursions around 23 °C (AT and NO), showed the highest risk and the lowest uncertainty. The outputs of this assessment can help to inform national surveillance policies, by providing evidence for geographical areas where livestock are more likely to be exposed.