

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

Crescio M.I.¹, Maurella C.¹, Bertolini S.¹, Mastrantonio G.², Ingravalle F.¹, Bona M.C.¹, Simons R.³, De Nardi M.⁴, Adkin A.³, Estrada-Peña A.⁶, Ru G.¹

¹ Istituto Zooprofilattico Sperimentale di Piemonte, Liguria e Valle d' Aosta (IZSTO), ² Dipartimento di Scienze Matematiche, Politecnico di Torino, ³ Animal and Plant Health Agency (APHA), ⁴ SAFOSO AG, ⁵ University of Zaragoza (UNIZAR)

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	Very good data/No uncertainty	Low
Incubation period (infectious period before the clinical symptoms)	Very good data/No uncertainty	Low
Average time to end of infectious period	Very good data/No uncertainty	Low
Differential diagnosis complexity	Very good data/No uncertainty	Low
Vaccine availability	Very good data/No uncertainty	Low
Vaccine efficacy	Very good data/No uncertainty	Low
DISEASE PREVALENCE IN:		
Bovine	Very good data/No uncertainty	Low
Sheep	Very good data/No uncertainty	Low
Goats	Very good data/No uncertainty	Low
COUNTRY FEATURES		
Vaccine diffusion	Very good data/No uncertainty	Low
Existence of a surveillance program	Very good data/No uncertainty	Low
Surveillance efficiency	Very good data/No uncertainty	Low
Public health authorities awareness	Very good data/No uncertainty	Low
Farmer awareness	Very good data/No uncertainty	Low
Proxy of Population awareness	Very good data/No uncertainty	Low
GEOGRAPHIC RISK		
Infected areas proximity (geographical borders)	Very good data/No uncertainty	Low
POPULATION DENSITY		
Bovine	Very good data/No uncertainty	Low
Sheep	Very good data/No uncertainty	Low
Goats	Very good data/No uncertainty	Low
POTENTIAL CONTACTS		
Bovine movements in Italy	Very good data/No uncertainty	Low
Sheep movements in Italy	Very good data/No uncertainty	Low
Goats movements in Italy	Very good data/No uncertainty	Low
Importation of bovine in Italy	Very good data/No uncertainty	Low
Importation of sheep in Italy	Very good data/No uncertainty	Low
Importation of goats in Italy	Very good data/No uncertainty	Low
VECTORS		
Vectors distribution (mosquitoes)	Very good data/No uncertainty	Low
Presence of wetland	Very good data/No uncertainty	Low

Legend:
 Very good data/No uncertainty (Lightest green)
 Sufficient data /Medium uncertainty (Light green)
 Good data/Low uncertainty (Medium green)
 Poor data/High uncertainty (Darkest green)

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)

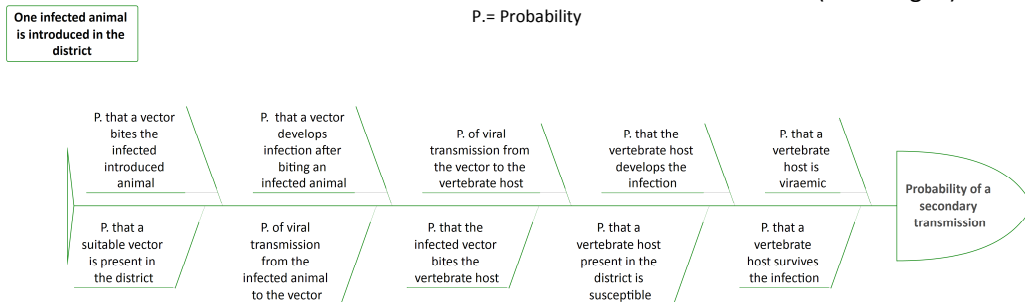
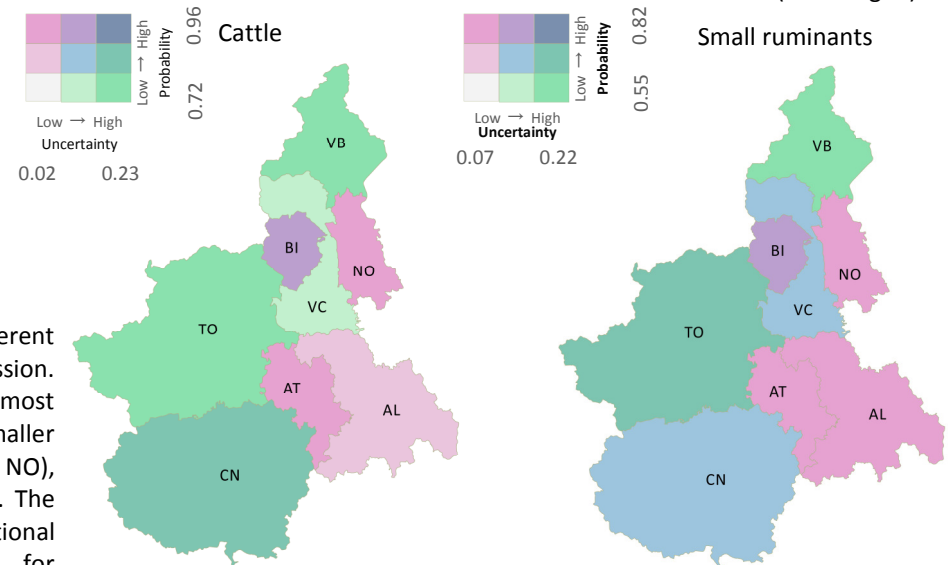


Fig 3: Output of the stochastic quantitative assessment of the probability of exposure to vector-borne diseases after the introduction of an infected animal (Bluetongue)



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.