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A tool to support the identification of suspect cases of exotic diseases in cattle

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ABSTRACT

Maintaining vigilance with regard to the introduction of exotic diseases is a challenge, particularly because these diseases are numerous, some are not well known, and they are not immediately suspected by people in day-to-day practice, specifically veterinary practitioners. The objective of this article is to present a tool to support the identification of suspect cases of exotic diseases in cattle, based on a Bayesian approach. A list of 22 exotic diseases in mainland France was selected mainly on the basis of their potential consequences if introduced, and the ability to detect them on a clinical basis. In response of a set of epidemio-clinical criteria observed in the field this tool provides a list of exotic diseases by descending order of likelihood. The tool's performance was assessed by simulation. When simulating epidemio-clinical observations of each of the 22 diseases included in the tool with some uncertainty, the right disease was ranked in the first place between 83.8% and 100% of the times, and always in the five most likely diseases. Even when some noise was introduced in the epidemio-clinical observations simulated by addition of criteria non-characteristic of the simulated diseases, the right disease was always in the five most likely diseases. This tool could be usefully included in a global approach aiming to improve vigilance against exotic diseases.

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1. Introduction

After several decades of surveillance and control measures, the health status of livestock concerning infectious diseases, particularly regulated and notifiable diseases, is now very good in a large number of developed countries (Rautureau et al., 2015). For example, in mainland France in 2014, no cases were identified for 24 of the 34 cattle diseases included on the list of the World Organisation for Animal Health (OIE) (Anonymous, 2015). However, there is a real risk of reintroduction, resurgence, or emergence of exotic diseases (Angot, 2009) and these events are hardly predictable, with an economic impact that may be considerable (Stöhr and Meslin, 1997; Vourc'h et al., 2006). Recent examples in Northern Europe include Bluetongue in 2006 and Schmallenberg Disease in 2011.

Because of this, it is essential that we remain vigilant to rapidly detect any cases of exotic diseases (Bronner et al., 2014; Rautureau et al., 2015). This vigilance is primarily clinical and relies on veterinary practitioners. For certain exotic diseases, there may be specific clinical surveillance schemes in place. These are generally diseases that were present historically and that are now under control, such as Foot-and-Mouth Disease or Brucellosis (Bronner et al., 2013). In these cases, maintaining a high level of vigilance in the field is difficult because these diseases are by definition not present in the country (Rautureau et al., 2015). Moreover for most exotic diseases, there is no specific surveillance scheme. In any event, the ability to detect cases relies on the vigilance of veterinary practitioners to identify suspected cases of exotic diseases on the basis of the epidemio-clinical manifestations.

There are many exotic diseases, some of which are not well known to practitioners and do not immediately come to mind since, by definition, the risk of occurrence is very low. Given this problem, we developed a prototype diagnostic assistance tool (DAT) for exotic diseases in cattle in France. This DAT was based on a Bayesian approach, as for most tools of this type. For example in the human field, such DAT have been developed for acute abdominal pain (Gammerman and Thatcher, 1991), abdominal pain of suspected gynaecological origin (Todd and Stamper, 1994), severe head injuries (Titterington et al., 1981), breast cancer recurrence (Mani et al., 1997) or infectious diseases (Berger and Blackman, 1995). In the veterinary field, a DOS-operated tool named BOVID was developed using the NBC approach in Australia in the 1980s.

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Table 1
Results of Simulation 2.

	Reference Disease	Simulation 2a		Simulation 2b		Simulation 2c	
		Rank of Reference Disease according to the algorithm (% based on 1000 simulations)					
		[a]In first place	[b]Among the first 5	[a]In first place	[b]Among the first 5	[a]In first place	[b]Among the first 5
AKAB	Akabane Disease	98.3	100	94.5	100	83.9	99.9
AUJ	Aujeszky's Disease	99.9	100	99.8	100	99.8	100
BAB	Babesiosis	100	100	100	100	99.2	100
BEF	Bovine Ephemeral Fever	99.9	100	99.2	100	97.4	99.9
BHV5	Bovine Herpes Virus 5 Encephalitis	100	100	99.1	100	96.3	99.9
BRU	Brucellosis	98.8	100	98	100	96.2	100
BT	Bluetongue	83.8	100	81.1	100	69.6	99.9
CBPP	Contagious Bovine Pleuropneumonia	99.9	100	99.5	100	95.3	100
COWD	Cowdriosis	99.9	100	99.7	100	98.6	100
EHD	Epizootic Haemorrhagic Disease	99.2	100	99.2	100	97.9	99.9
EHRL	Ehrlichiosis	99.8	100	99.3	100	95.9	100
FMD	Foot-and-Mouth Disease	99.5	100	99.7	100	99.4	100
HSEP	Haemorrhagic Septicaemia	100	100	100	100	100	100
LSD	Lumpy Skin Disease	100	100	100	100	100	100
ONDI	Ondiri Disease	99.9	100	100	100	100	100
RAB	Rabies	100	100	99.8	100	98.8	100
RVF	Rift Valley Fever	99.8	100	99.4	100	99.5	100
RIND	Rinderpest	100	100	100	100	100	100
THEL	Theileriosis	100	100	99.1	100	96.7	100
TRYP	Trypanosomiasis	100	100	99.7	100	99.4	100
VSTO	Vesicular Stomatitis	100	100	99.7	100	94	100
WESS	Wesselsbron Disease	96.8	100	86.2	100	63.1	100

Simulations aimed to study the ability of the algorithm to identify the right disease used to generate the epidemio-clinical pictures. These pictures were generated using the knowledge database adding uncertainty in notations (Simulation 2a), and one to four criteria that are not expected to be observed (Simulation 2b) or five to eight criteria that are not expected to be observed (Simulation 2c).
In Simulation 2a, 1000 vectors of epidemio-clinical patterns were generated for each disease on the basis of the knowledge database.
In Simulation 2b, 1000 vectors of epidemio-clinical patterns were generated for each disease like in simulation 2a but some noise was added.
In simulation 2c, 1000 vectors of epidemio-clinical patterns were generated for each disease like in Simulation 2b but some more noise was added.

[a] For each reference disease, the proportion of times the score of the generated vectors for the reference disease was higher than the score of all others diseases.

[b] For each reference disease, the proportion of times the score of the generated vectors for the reference disease was among the five highest scores of all diseases.

Its database included 1000 cattle diseases and syndromes, both endemic and exotic, and more than 1500 clinical signs (Brightling et al., 1998). This tool was again used in the 1990s, when it was modernised and adapted for use by farmers themselves under the name BOSSS (Bovine Syndromic Surveillance System) (Shephard, 2006a).

Practically, our prototype tool consists of an algorithm that compares an epidemio-clinical picture (e.g. a case observed on a farm) with a knowledge base, to provide a prioritised list of suspected exotic diseases by descending order of likelihood. The aim of this article is to present the method used to develop this tool and its performance assessed through simulations, and to discuss its possible applications to improve surveillance of exotic diseases.

2. Material and methods

Development of the DAT took place in four steps: (i) determine a list of exotic diseases of interest, (ii) design an epidemio-clinical knowledge base using literature data supplemented by consultation of experts, (iii) develop an algorithm to compare an epidemio-clinical picture on a farm with the knowledge base, and (iv) carry out simulations to assess performance of the DAT.

2.1. Defining a list of exotic diseases of interest

As an example, we established a list of exotic diseases of interest in cattle for mainland France based on reference documents (Lefèvre et al., 2003a,b). The inclusion criteria were as follows: (i) a disease that could manifest acutely in the event of introduction to France and that can therefore be identified clinically, (ii) a disease that may take on an epizootic form (minimum requirement: grouped cases on a farm, potential epizootic spread) with major economic and health repercussions, and (iii) an infectious disease caused by a virus, a unicellular organism, or a non-conventional transmissible agent with a marked pathogenic potential.

These inclusion criteria were applied to the reference documents on infectious diseases cited above. A list of 22 exotic cattle diseases was thus established (at the start date of the study, mainland France was officially Bluetongue-free) (Table 1

2.2. Building an epidemio-clinical knowledge base

A list of 119 criteria (116 clinical, 3 epidemiological) was established based on the literature to precisely describe the 22 retained diseases. Among the clinical criteria, 15 were general (e.g. hyperthermia, anorexia, and emaciation). The 101 clinical criteria considered more specific were placed into the following categories: behavioural and nervous, skin and mucosal (type and localisation), mucosal colour, oral cavity signs, oedema, gastrointestinal signs, respiratory signs, reproductive disorders, locomotor disorders, and other signs. The list of criteria is provided in Supplementary material 1.

The frequency of observation for each clinical criterion for each of the diseases was estimated based on the literature. A probability of 0 (sign never observed) to 1 (sign always present) was attributed to each criterion for each disease.

The three epidemiological criteria were as follows: morbidity (proportion of diseased animals among the animals present), lethality in adults (proportion of deaths among diseased adult animals), and lethality in young animals (proportion of deaths among diseased animals under one year). Five modalities were defined to characterise these criteria (<5%, [5–20%[, [20–50%[, [50–80%[, ≥80%). For each disease, the most likely frequency and the possible frequencies for these three criteria were also estimated based on the bibliography.