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Bluetongue surveillance system in Belgium: A stochastic evaluation of its risk-based approach effectiveness

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ABSTRACT

Background: The aim of this study was to assess the sensitivity of the four major bluetongue surveillance components implemented in Belgium in 2007 for farmed animals and prescribed by the European Union regulation; winter serological screening, sentinel system, passive clinical surveillance, export testing. Scenario tree methodology was used to evaluate the relative sensitivity of detection and targeted approach of each component in terms of early detection and freedom of infection substantiation. Field data collected from the previous year's outbreaks in Belgium were used to determine the risk groups to be considered.

Results: The best sensitivities at herd level, taking into account the diagnostic test sensitivity, design prevalence and the number of animals tested within a herd were obtained with the winter screening and sentinel component. The sensitivities at risk group level, taking into account the obtained herd sensitivity, effective probabilities of infection and number of herds tested were high in all components, except for the export component. Component sensitivities ranged between 0.77 and 1 for all components except for the export component with a mean value of 0.22 (0.17–0.26). In terms of early detection, the probability of detection was best using the passive clinical component or the sentinel component. Sensitivity analysis showed that the passive clinical component sensitivity was mostly affected by the diagnostic process and the number of herds sampled. The sentinel and export components sensitivity were mainly affected by the relative risk estimates whereas the winter screening component was mainly affected by the assumptions about the design prevalence.

Conclusions: This study revealed interesting features regarding the sensitivity of detection and early detection of infection in the different surveillance components and their risk based approach as requested by the international standards.

1. Introduction

Bluetongue is an arthropod-borne viral disease affecting both wild and domestic ruminants. The distribution of the bluetongue virus (BTV) is therefore limited to those regions

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where competent vector species are present and its transmission to those times of the year when climatic conditions are favourable for the cycle of transmission (Mellor et al., 2008; Wilson and Mellor, 2009). The vast majority of BTV infections are subclinical. Though cattle are more likely to be infected by a biting midge, clinical signs are more apparent in sheep (Elbers et al., 2008a,b; Saegerman et al., 2010). BTV can cause mild to spectacular outbreaks and has an adverse impact on worldwide trade. Thus, it appears on the list of diseases notifiable to the World Organization for Animal Health (OIE).

Following the epidemics of BTV-8 in 2006, 2007 and 2008, Commission Regulation (EC) No 1266/2007 (EC, 2007) last amended in May 2012, prescribed the implementation of mandatory surveillance systems composed of (i) passive clinical surveillance, (ii) sentinel surveillance, (iii) a combination of serological and/or virological surveillance, as well as targeted risk-based monitoring. More and more, rather than prescribing fixed guidelines, the aim of these current regulations are oriented towards minimum requirements to be fulfilled. As a consequence, regulations are more flexible and allow each member state to adapt its own surveillance activities and prove the effectiveness of its system towards the required objectives. The present study was carried out in this context. The four major BTV surveillance components implemented in Belgium in 2007 (winter screening, sentinel, export, and passive clinical) were evaluated for the relative efficacy in terms of their risk-based design, early detection and substantiation of infection freedom.

The scenario tree methodology, developed by Martin et al. (2007a,b), was used to conduct this study, as it has already proven its efficacy in similar contexts (Frossling et al., 2009; Hadorn et al., 2009; Knight-Jones et al., 2010; Stark et al., 2006; Welby et al., 2012). In the present study, key parameters such as the risk nodes affecting the probability of infection or detection were estimated using historical data as a first step. The obtained sensitivities of detection at herd and risk group level were estimated for each component. In turn, the estimated component sensitivities enabled the computation of the monthly posterior probabilities of freedom, given different probabilities of introduction. Different scenario simulations provided insight about the impact of changes in the key input parameters on the components sensitivity results.

2. Materials and methods

2.1. BTV surveillance system in Belgium in 2007

At the time of the study, 38805 cattle herds and 31777 sheep flocks were present in Belgium.

The four major components for BTV surveillance in Belgium in 2007 were:

- Passive clinical (Clinical): Clinical surveillance and notification of all ruminant case herds (sheep, cattle) (defined as positive as soon as at least one clinically infected animal was serologically confirmed in the herd);
- Sentinel (Sentinel): Monthly serological surveillance in 266 seronegative cattle herds during the vector high activity period (in 2007: April until December) to detect seroconversion (EC, 2007; FASFC, 2012);
- Winter screening (WS): Yearly cross-sectional serological survey in 344 cattle herds during the winter season (December until February) to detect if there has been past infections during the last vector season and to estimate the disease prevalence;
- Export (Export): Serological testing of all exported cattle and sheep (equivalent to 120 herds) all year round.

In each component, in case a positive serological result was found a virological isolation test was carried out.

2.2. Design of the complete disease process in a scenario tree

2.2.1. Design

A scenario tree was designed for each surveillance component (WS, Sentinel, Clinical and Export) in different Excel spread sheets (Fig. 1). Each risk factor affecting the probability of infection was represented by a node and a node had different branches illustrating all possible outcomes. Each outcome had a certain probability of occurrence. For each risk group, defined by the combination of nodes and branches, a detection node was entered. The risk nodes retained to influence the probability of infection at herd level were “Risk Zone” (low/high), “Vector Activity period” (low/high) and “Species” (bovine/ovine). These were the infection risk nodes in the following study for each component. The detection node “Diagnostic Process” was characterised by the different diagnostic tests used with its corresponding sensitivity and differed for each component.

The combination of each probability determined the probability of infection and detection for each risk group. The population at risk and sampled population were partitioned according to these risk nodes and groups in order to estimate the relative effectiveness of the targeted surveillance approach of each component.

2.2.2. Assumptions

All surveillance system components were assumed to be independent. Information of one surveillance component was not taken into account in the other component.

The country was assumed to be free of infection. For the Sentinel, Export and Clinical components, a conservative value of 2% was used as minimum design between-herd prevalence (DPh) and within-herd prevalence (DPa) (EC, 2007). For the WS component, a 20% DPh was assumed and a 23.8 (20.1–28.1)% DPa was assumed (EC, 2007; Méroc et al., 2008). For the Clinical component, it was assumed that all animals and all herds were susceptible to be infected and show clinical signs. However, in order to take into account situations with lower disease awareness or situations where animals would no longer show clinical signs (i.e. vaccinated or naturally immunised animals), additional simulations were performed where only a fraction of the herds and animals were looked at.

The risk nodes retained to influence the probability of infection (zone, vector activity period, species) were considered independent of each other and constant over time.