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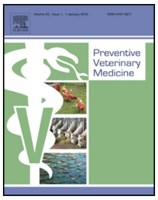

Response to an emerging vector-borne disease: Surveillance and preparedness for Schmallenberg virus

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ABSTRACT

Surveillance for new emerging animal diseases from a European perspective is complicated by the non-harmonised approach across Member States for data capture, recording livestock populations and case definitions. In the summer of 2011, a new vector-borne Orthobunyavirus emerged in Northern Europe and for the first time, a coordinated approach to horizon scanning, risk communication, data and diagnostic test sharing allowed EU Member States to develop early predictions of the disease, its impact and risk management options. There are many different systems in place across the EU for syndromic and scanning surveillance and the differences in these systems have presented epidemiologists and risk assessors with concerns about their combined use in early identification of an emerging disease. The emergence of a new disease always will raise challenging issues around lack of capability and lack of knowledge; however, Schmallenberg virus (SBV) gave veterinary authorities an additional complex problem: the infection caused few clinical signs in adult animals, with no indication of the possible source and little evidence about its spread or means of transmission. This paper documents the different systems in place in some of the countries (Germany and the Netherlands) which detected disease initially and predicted its spread (to the UK) and how information sharing helped to inform early warning and risk assessment for Member States. Microarray technology was used to identify SBV as a new pathogen and data from the automated cattle milking systems coupled with farmer-derived data on reporting non-specific clinical signs gave the first indications of a widespread issue while the UK used meteorological modelling to map disease incursion. The coordinating role of both EFSA and the European Commission were vital as are the opportunities presented by web-based publishing for disseminating information to industry and the public. The future of detecting emerging disease looks more positive in the light of this combined approach in the EU.

1. Introduction

Detecting a new or re-emerging exotic disease is likely to only be made possible by strong collaborations between (state) veterinary and public health services, industry

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and livestock keepers. The challenges posed by new emerging diseases such as BSE, SARS, Highly Pathogenic Avian Influenza, Bluetongue virus serotype 8 (BTV-8) and Schmallenberg virus (SBV) have illustrated the importance of maintaining our animal and public health surveillance systems to identify the truly unusual events, and yet in a restrictive economic environment it is ever more important to share resources and access all the possible early warning and detection systems.

Changes in demographic, economic and environmental factors may lead to new disease risks. A combination of changes in the livestock sector, intensification of farming, proximity to urban centres, trade in livestock, food resource pressures, climate change and changing vector distribution mean emerging and transboundary disease outbreaks may become more frequent. It has been several years since a new emerging disease has been reported from the livestock population of Europe. New epidemics, such as that caused by BTV-8 in North West Europe could not be considered a new disease, simply an incursion into an area where the disease was never introduced before, albeit a rapidly spreading one with significant consequences in naïve livestock populations (van Schaik et al., 2008; Elbers et al., 2009; Santman-Berends et al., 2011). The objective of this paper is therefore to document the way that an emerging new disease of livestock was quickly identified and reported across Europe and how to build on such processes to ensure improved disease surveillance in an ever challenging economic and political environment.

Early identification of unusual animal and/or human health cases is primarily enabled by reporting of farmers and veterinarians of a suspect situation to the competent authorities, an animal health helpdesk or by syndromic surveillance. Syndromic surveillance uses health-related information (clinical signs or other data) that might precede (or may substitute for) formal diagnosis and applies statistical methodology to detect changes from baseline data. This information may be used to indicate a sufficient probability of a change in the health of the population either to deserve further investigation or to enable a timely assessment of the impact of health threats which may require action. This type of surveillance is not usually focused on a particular hazard or pre-established clinical differential diagnoses, so can be used to detect a variety of diseases or pathogens – including new (emerging) diseases. It is particularly applicable for early warning/detection surveillance (Hoinville et al., 2013). Once a baseline is established, for example, the long term mean number of undiagnosed abortions in cattle, then significant increases above the threshold (e.g. a number of standard deviations over the mean during consecutive time periods) may be the basis of an alert system. Statistically derived algorithms, such as the Cumulative Sum or CUSUM algorithm, can be implemented in the R software package and measure when accumulations of extra variance in a timeline occur in order to flag when the statistic exceeds a threshold, which is often set by the user (Chretien et al., 2008; Marceau et al., 2014; Madouasse et al., 2013; Robertson et al., 2010).

While each European Member State has the requirement to collect animal health data in a harmonised manner to ensure food safety and traceability, often-syndromic data is collected at the government or industry level. Commercial sensitivity and incompatible data collection systems means this information is not readily available for Europe-wide surveillance systems (Dupuy et al., 2013). Establishing the initial baseline and acceptable level of variation is often the rate limiting step in setting up syndromic surveillance systems, particularly when comparing across several countries, and in the case of Schmallenberg virus, which caused relatively mild clinical signs in adult animals, different baselines which had been pre-established, were used to identify the first cases: for the Netherlands, an increase in telephone reporting of non-specific clinical signs (diarrhoea and milk drop), and in Germany a decrease in milk yield through an automated system. Reporting through global communication systems (e.g. Promed) allowed other member states to take note of these early warning signs and be vigilant for further incursions. Therefore the emergence and identification of Schmallenberg virus in Europe shows that a combination of collaboration and communication can overcome these shortfalls.

In the summer of 2011 reports started to emerge in the Netherlands and Germany of non-specific, transient clinical signs in dairy cattle (fever, milk drop and sometimes diarrhoea) which could not be linked to detection of possible causative disease agents normally associated with these clinical signs (PROMED, 2011). Affected farms were visited and blood and faecal samples of acute cases were collected. Reports were first made from both the German and Netherlands dairy sector of slightly different clinical signs of a non-specific nature and these reports started to raise awareness. These reports were shared through a network of European partners and through Promed.

Using blood samples collected from clinically affected cattle around the town of Schmallenberg in Germany, metagenomic analysis was used by Hoffmann and colleagues (2012) to identify the presence of a novel Orthobunyavirus, a member of the Bunyaviridae family in the Simbu serogroup, which was consequently named Schmallenberg virus (SBV) (Hoffmann et al., 2012). From the recognition that SBV belonged to the Orthobunyavirus family, it could be deduced that the most likely manifestation of infection in pregnant ruminants would be foetal deformity and congenital malformations. The Netherlands then confirmed that SBV had been the cause of the clinical signs in August/September 2011. In 36% of the samples of 50 acute clinical cases that were collected early September 2011 the PCR tested positive for SBV (Muskens et al., 2012). The viruses in this family are also typically vector borne, so initial expectations were for biting midges (*Culicoides* spp.) to be involved in transmission and this has since been evidenced by identifying SBV in such midges collected during summer and autumn of 2011 (Elbers et al., 2013; De Regge et al., 2012; Rasmussen et al., 2012; Goffredo et al., 2013).

2. Materials and methods

2.1. Passive clinical surveillance

All countries with functioning veterinary services should have in place national legislation requiring farmers

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