



Use of a multi-criteria analysis framework to inform the design of risk based general surveillance systems for animal disease in Australia

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ABSTRACT

Australia is a major exporter of livestock and livestock products; a trade assisted by a favourable animal health status. However, increasing international travel and trade, land use changes and climatic change increase the risks of exotic and emerging diseases. At the same time, public sector resources for managing these risks are static or declining. Animal health authorities in Australia identified the need to develop a consistent national approach to surveillance that allocates resources according to risk. A study was undertaken to assess the relative likelihood of occurrence of eight significant diseases of concern to animal health authorities with the aim of producing risk maps to better manage animal disease surveillance. The likelihood of disease occurrence was considered in terms of the likelihood that a disease is introduced and the likelihood that the disease establishes and spreads. Pathways for introduction and exposure and for establishment and spread were identified and data layers representing the factors contributing to each pathway produced as raster maps. A multi-criteria analysis process was used to combine data layers into pathways and pathways into likelihood maps using weightings that reflect the relative importance of each layer and pathway. The likelihood maps for introduction and exposure and for establishment and spread were combined to generate national likelihood maps for each disease. To inform Australia's general surveillance system that exists to detect any disease of importance, the spatial profiles of the eight diseases were subsequently combined using weightings to reflect their relative consequences. The result was a map of relative likelihood of occurrence of any significant disease. Current surveillance activity was assessed by combining data layers for government disease investigations, proximity to vets and wildlife disease investigations. Comparison of the overall risk and current surveillance maps showed that the distribution of current effort was well matched to the distribution of risk.

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1. Introduction

For the past 150 years, Australia's economy has relied heavily on the export of agricultural produce. In 2010–2011, the total value of agricultural production was \$38.4 billion with exports of livestock and livestock

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products worth \$14.8 billion (ABARES, 2011). In the current world trade environment, the capacity to demonstrate freedom from disease is a crucial component in maintaining an export trade in livestock products (OIE, 2011a).

Australia has a favourable animal health status, being free of many of the diseases of concern in other parts of the world (WAHIS, 2011), and is recognised as having a competent surveillance capability and capacity. In recent years, outbreaks of equine influenza, highly pathogenic avian influenza (HPAI) and velogenic Newcastle disease have been detected and successfully eradicated (Garner et al., 2011; Turner, 2011) and emerging infections such as Hendra virus, Australian bat lyssavirus, and Bungowanah virus have been detected and subsequently described (Black et al., 2008). Globally, there is an increasing awareness of the potential threat from animal disease, with concerns including food security, economic impacts of outbreaks of significant diseases, zoonoses and emerging diseases, for which there may be no effective diagnostic test or mitigation immediately available. Within Australia, there is growing recognition by governments and industry (Langstaff, 2008) that Australia needs to strengthen its surveillance arrangements to mitigate these increasing biosecurity threats whilst continuing to facilitate and enhance trade. In the face of static or declining public sector resources there is a need to better understand the threats to ensure that quarantine and surveillance programmes are both effective and efficient.

Of particular relevance to timely detection of exotic and emerging animal diseases is the effectiveness of the general surveillance system. General surveillance can be defined as the background level of passive reporting by animal health professionals, para-professionals, animal owners, producers, processors and others across the livestock industries. Key observation points for livestock include the farm, the saleyard and the abattoir. General surveillance tends to be opportunistic in nature, and most likely to detect diseases associated with unusual or obvious clinical signs. It can be a very effective method of identifying new and emerging diseases (Langstaff, 2008).

One approach to better utilise scarce resources has been the development of risk-based surveillance programmes (Stärk et al., 2006; Alban et al., 2008) where resources are targeted towards subpopulations with a higher risk of infection compared to the whole population or to regions where disease is more likely to occur. In this study, the standard definition of 'risk' – i.e. the likelihood of the occurrence and the likely magnitude of the biological and economic consequences of an adverse event or effect for animal and human health (Murray, 2004) was used. Because the consequences of a disease incursion were beyond the scope of this study, only the 'likelihood' was considered and that is the terminology used throughout this paper. The likelihood of disease occurrence was considered in terms of the likelihood that a disease is introduced and the likelihood that disease subsequently establishes and spreads.

If disease has occurred historically in a country, historical data from surveillance can be collated and used to assess future risk of infection (Alban et al., 2008) however, in the absence of previous experience of the disease,

alternative approaches must be developed to identify populations or geographic regions at greatest risk. Surrogate measures such as population densities, climate patterns, vector distributions and vegetation patterns can be useful in predicting the location of disease outbreaks but have generally been most successful with vector-borne diseases (e.g. Brownstein et al., 2002; Noor et al., 2008) where the vector has particular environmental requirements or breeds in response to certain predictable weather patterns such as rainfall. Despite the rapid adoption of the concepts of risk-based surveillance, this acceptance has outpaced the development of its theoretical and practical bases (Stärk et al., 2006).

Gilbert et al. (2008) constructed an explanatory risk map for highly pathogenic influenza in south east Asia using outbreak data and duck, chicken and human population density together with elevation and rice cropping intensity whilst Wint et al. (2002) used remotely sensed climate and vegetation data to predict the location of outbreaks of bovine tuberculosis in Britain. However, both of these studies involved diseases with a well characterised reservoir species, ducks or badgers, respectively, whose preferred locations can be predicted in a way analogous to predicting preferred habitat or conditions for insect vectors. Studies with diseases lacking an insect vector, intermediate host or wildlife reservoir are less common.

Australia's Animal Health Committee (comprised of the Australian Chief Veterinary Officer and the eight state/territory chief veterinary officers) established the general surveillance epidemiology working group (GSEWG) to examine Australia's general surveillance requirements unconstrained by current and historical capacities and practices among jurisdictions. Their aim was to review the way in which general surveillance is conducted in Australia, to find ways of allocating limited surveillance resources on the basis of risk and make recommendations for future surveillance programmes.

In this paper, we describe the development of maps showing relative likelihood of disease occurrence across Australia, and assess their potential for guiding the development and design of a risk-based general surveillance system. We illustrate the process for each of eight significant diseases: foot and mouth disease (FMD), sheep pox, classical swine fever (CSF), HPAI, Japanese encephalitis (JE), bluetongue, rabies and Hendra virus. These maps are then compared against measures of current surveillance effort, and recommendations are made for enhancement of general surveillance in Australia.

2. Materials and methods

A framework for identifying and assessing the relative likelihood of occurrence for key livestock diseases was developed. Because the likelihood of disease requires consideration of the separate likelihoods of disease introduction, establishment and spread and because there can be multiple pathways by which a disease could be introduced and spread. A multi-criteria analysis (MCA) process was used to combine these data (Hill et al., 2005).

The multi-criteria analysis shell for spatial decision support (MCAS-S) MCAS-S was developed by the Australian

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