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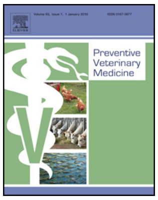

Modelling spatio-temporal patterns of long-distance *Culicoides* dispersal into northern Australia

D. Eagles[a,b,*], P.J. Walker[a], M.P. Zalucki[b], P.A. Durr[a]

[a] *CSIRO Animal, Food and Health Sciences, Australian Animal Health Laboratory, Geelong, VIC, Australia*
[b] *School of Biological Sciences, The University of Queensland, Brisbane, QLD 4072, Australia*

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ABSTRACT

Novel arboviruses, including new serotypes of bluetongue virus, are isolated intermittently from cattle and insects in northern Australia. These viruses are thought to be introduced via windborne dispersal of *Culicoides* from neighbouring land masses to the north. We used the HYSPLIT particle dispersal model to simulate the spatio-temporal patterns of *Culicoides* dispersal into northern Australia from nine putative source sites across Indonesia, Timor-Leste and Papua New Guinea. Simulated dispersal was found to be possible from each site, with the islands of Timor and Sumba highlighted as the likely principal sources and February the predominant month of dispersal. The results of this study define the likely spatial extent of the source and arrival regions, the relative frequency of dispersal from the putative sources and the temporal nature of seasonal winds from source sites into arrival regions. Importantly, the methodology and results may be applicable to other insect and pathogen incursions into northern Australia.

1. Introduction

Culicoides (Diptera: Ceratopogonidae) are one of the smallest known haematophagous insects, measuring between 1 and 3 mm in length. There are over 1400 species worldwide, living in a wide range of habitats from sea level to 4000 m and absent only from the continent of Antarctica and the major island countries of New Zealand and Iceland (Mellor *et al.*, 2000). As a group, *Culicoides* are capable of transmitting bacteria, protozoa and helminth parasites in addition to viruses. In animals the most significant *Culicoides*-borne viral diseases include bluetongue (BT), African horse sickness (AHS) and epizootic haemorrhagic disease (EHD), all caused by orbiviruses (genus *Orbivirus*; *Reoviridae*). Most recently, *Culicoides* have been acknowledged as a vector of the newly identified Schmallenberg bunyavirus (genus *Orthobunyavirus*; *Bunyaviridae*) in Europe (Rasmussen et al., 2012).

Most *Culicoides* movement is over very short distances – usually a few hundred metres, but up to 2 km – from their breeding site (Mellor et al., 2000), but it has been postulated that windborne dispersal can occur over much longer distances. Outbreaks of BT in the Mediterranean, North Africa and northern Europe, AHS in the Middle East and EHD in Israel have been attributed to this means of dispersal (Sellers et al., 1977; Braverman and Chechik, 1996; Ducheyne et al., 2007; Gloster et al., 2008; Agren et al., 2010; Garcia-Lastra et al., 2012). Associating long-distance dispersal of *Culicoides* to these outbreaks has relied on the absence of other possible means of virus introduction and assessment of paths of dispersion through either wind directions ("trajectories") or more complex 3-D atmospheric dispersion models. Several 3-D atmospheric models are available; the Hybrid Single-Particle Lagrangian Integrated Trajectory (HYSPLIT) model used in this study

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[*] Corresponding author at: CSIRO Animal, Food and Health Sciences, Australian Animal Health Laboratory, Private Bag 24, Geelong 3220, VIC, Australia. Tel.: +61 35227 5000.
E-mail address: debbie.eagles@csiro.au (D. Eagles).

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has recently been used to assess the involvement of windborne *Culicoides* in an outbreak of BT in northern Spain (Garcia-Lastra *et al.*, 2012).

Of the *Culicoides*-borne viruses, bluetongue virus (BTV) is of greatest importance to Australia. Whilst a range of ruminants can be infected with BTV, clinical disease is seen predominantly in sheep, less commonly in goats and, rarely, in cattle. Some species of deer and wild ruminants can be severely affected. There are now 26 known BTV serotypes, with serotype 25 (Toggenburg virus) isolated from goats in Switzerland in 2008 and serotype 26 isolated from sheep in Kuwait in 2010 (Hofmann *et al.*, 2010; Maan *et al.*, 2011). Pathogenicity varies between serotypes, while prevailing environmental conditions may contribute to expression of clinical signs in infected animals (Maclachlan, 1994).

In Australia, ten BTV serotypes (1, 2, 3, 7, 9, 15, 16, 20, 21, 23) have been identified since the virus was first detected in 1975 (Boyle et al., 2012). Of these, all have been isolated from the northern region of the Northern Territory (NT), and a number have been detected in Western Australia (WA). On the other hand, only two serotypes (1, 21) have a consistently wider distribution extending along the eastern coast of Australia into Queensland (QLD) and New South Wales (NSW) (Boyle et al., 2012). BTV-2 serotype was detected in QLD in 2010, two years after its first appearance in the NT, but surveillance has not detected any ongoing presence in that state. It has been hypothesised that the presence of these distinct northern and eastern BTV episystems in Australia is a result of the limited vector competence of the more widely distributed *Culicoides* species (Ward, 1994). Experimental studies with Australian BTV serotypes have generally shown mild to moderate signs of disease, but more severe disease has been reported for some of the serotypes restricted to the north, including BTV-16 and BTV-23 (Johnson *et al.*, 1992). Hence, the absence of clinical disease in Australian livestock is primarily attributed to the distribution of the more susceptible ruminants in regions distant from the northern BTV episystem. Novel BTVs, or exotic *Culicoides* with greater vectorial capacity, have the potential to disrupt this status quo, thereby presenting a disease threat to Australian livestock. BTV and its vectors are known to occur in Indonesia, Papua New Guinea (PNG) and Timor-Leste (Gard, 1995).

Recent modelling of *Culicoides* long-distance dispersal has shown that movement to Australia from the island of Timor (to the north-west of Australia) may be possible (Eagles et al., 2012). In this preliminary study the entire island mass of Timor was used as a single source site, and all dates from June 1995-December 2009 were analysed for potential simulated dispersal. The results supported the hypothesis that novel BTVs detected in Australia have arrived via windborne dispersal from regional neighbours (Pritchard *et al.*, 2005). However, the possible source site was limited to Timor, whereas other parts of Indonesia, as well as PNG, are considered potential sources of novel viruses for northern Australia (Eagles et al., 2012). In addition, the effects of rainfall on descent were not accounted for by the migration model used and, by treating the whole area as a single source site, comparison between sites within the putative source area was not possible.

Simulating dispersal from all potential sources is important because the frequency and timing of dispersal, as well as the potential arrival regions, are likely to differ between source sites. Defining both the limits of the likely source region for Australia, and the patterns of movement from within this region, are integral for a complete risk assessment and important for determining future surveillance plans.

2. Methods

2.1. Model

The HYSPLIT_4 (Hybrid Single-Particle Lagrangian Integrated Trajectory) model (Version 4) was used to simulate atmospheric dispersal of *Culicoides* from putative source sites across Indonesia, Timor-Leste and PNG, and to analyse spatial and temporal patterns of arrival in Australia (NOAA, 2011). HYSPLIT has previously been used to model long-distance dispersal of *Culicoides* (Kedmi et al., 2010; Garcia-Lastra et al., 2012) and other insects (Zhu et al., 2006; Feng et al., 2007) as well as its application to the spread of aerosols of diseases of veterinary importance (Garner et al., 2006). The model allows for assessment of both “trajectories” and concentration/dispersion of a particle or pollutant, with the latter based on Eulerian and Langrangian approaches to modelling. The Lagrangian component is used for advection and diffusion calculations, while concentrations are calculated on a fixed grid (Draxler and Hess, 1998). Both trajectory and dispersion model calculations use vertical motion fields directly from the meteorological data.

Calculation of trajectories is based on time integration of an air parcel’s position as it is transported by 3-D winds (McGowan and Clark, 2008). Trajectory calculations do not take into account pollutant or particle (e.g. insect) specific parameters. HYSPLIT allows for clustering of trajectories, by assessing all the trajectories from one location and analysing them objectively to create subsets of trajectories (NOAA, 2011). The choice of which trajectories are clustered together is based on total spatial variance (the sum of the spatial variances of all clusters), with trajectories sequentially combined to achieve the lowest increase in total spatial variance. Often more than one outcome is produced – for example, the same trajectories may be grouped into 3, 7, or 10 clusters, allowing the user to choose the most useful grouping for the desired application. Clusters can, and usually do, contain uneven numbers of trajectories.

For atmospheric concentrations and dispersion, the model can be run in “puff” or “particle” mode. In this study particle mode, which allows for the release of a fixed number of particles, was used. This mode allows for transport of particle with mean wind and a random component to account for turbulence (Garner et al., 2006). The particle source is simulated by the release of a set number of particles (evenly distributed between source sites, when there is more than one) over a specified