Inferences about the transmission of Schmallenberg virus within and between farms

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Introduction

In the summer of 2011 Schmallenberg virus (SBV), a novel orthobunyavirus, emerged in Germany and the Netherlands and rapidly spread across much of Europe. Despite the short duration of viraemia in cattle and sheep (mean of 3-4 days) the within-farm seroprevalence can reach high levels (>80%). Phylogenetic analysis suggested that *Culicoides* biting midges and/or mosquitoes might be involved in transmission. The potential for other routes (fomites, mechanical transmission) was not known.

To draw inferences about the transmission of SBV we fitted a within-farm model to seroprevalence data for cattle and sheep farms in Belgium and the Netherlands and estimated key transmission parameters using approximate Bayesian computation.

Methods

The within-farm dynamics of SBV were described by a stochastic compartmental model (Figure 1) which was adapted from an earlier model for BTV (Gubbins et al. 2008; Szmaragd et al. 2009).

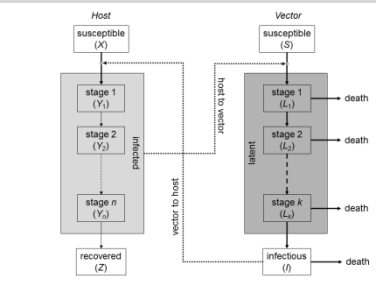

Figure 1. Schematic diagram of the within-farm transmission model

Nine parameters were estimated:

- probability of transmission from vector to host,
- probability of transmission from host to vector,
- mean duration of viraemia in cattle and sheep,
- number of stages for duration of viraemia in cattle and sheep,
- Virus replication rate,
- threshold temperature for virus replication, and
- number of stages for the duration of the EIP.

Parameters were estimated using **approximate Bayesian computation** (ABC) **rejection sampling** (Marjoram et al. 2003; Toni et al. 2009). In this approach, samples from the posterior distribution are generated as follows:

a) Sample a parameter set θ, from the joint prior distribution π(θ).
b) Simulate a data-set D using the model with the sampled parameter set θ.
c) If the simulated data-set, D, is sufficiently close to the observed data, D_{obs}, as judged by an appropriate metric, accept the parameter set, otherwise, reject it.

This allows a joint posterior distribution for the parameters to be generated without specifying the full likelihood for the model (which in this case would be too complex to calculate).
Prior distributions were based on published data relating to SBV where available. Where this was not the case, data for BTV were used instead.

Results

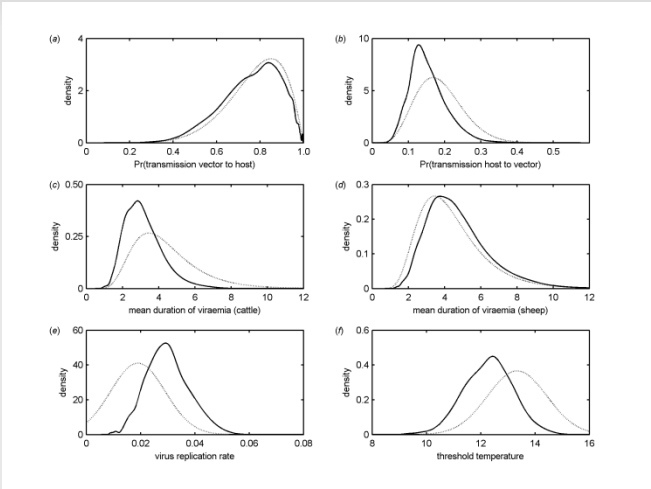

Figure 2. Marginal posterior distributions for epidemiological parameters for Schmallenberg virus (SBV). Each figure shows the prior (dotted black line; Table 2) and posterior (solid black line) densities.

Vector competence for SBV is relatively high (15%) and it is able to replicate quickly (0.03 per day-degree) and at relatively low temperatures (replication threshold 12.3°C).
As a consequence, despite the short duration of viraemia in cattle and sheep (mean of 3-4 days) compared to BTV, the net effect on transmission is a substantial increase in the basic reproduction number (Figure 3).

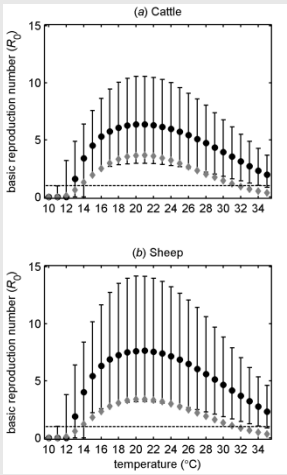

Figure 3. Basic reproduction number (R_0) for SBV and its dependence on temperature. The black dashed line indicates R_0 =1. Grey diamonds indicate the median R_0 for BTV (Gubbins et al. 2012).

Acknowledgements

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