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Simulating risk of bluetongue epidemics in Norway

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Introduction

Cattle positive for bluetongue (BT) virus were detected in four Norwegian herds in February 2009. The BT-virus was probably introduced during fall 2008. No BT epidemic developed. The rate of development of the virus in the midge rEI(T) was given by:

BT epidemics are dependent on

- the density of the vector
- the weather and in particular the temperature
- the density of susceptible animals

Norway has areas belonging to the temperate, continental and polar climatic zones. Therefore, temperature is expected to be a limiting factor of a BT epidemic for at least parts of Norway.

The aim of this study was to evaluate the risk of BT epidemic in Norway by applying a model that simulates the risk of bluetongue transmission under Norwegian temperature conditions based on the effects of temperature on development of the virus in the vector (extrinsic incubation period, EIP) and the biting frequency of *Culicoides*.

rEI(T) = 0.0003*T*(T-10.4057)

The rate of the midge's ovarian development was given by:

rOD(T)=0.000171*T*(T-3.6966)*(41.8699-T)^1/2.7056

where T = temperature (°C).

Epidemics are most likely when the EIP \leq 17 days and the number of ovarian cycles needed for transmission \leq 3.

The model was run with the 1st of August as starting date. Data from 2003 to 2009 for all weather stations south of 61 degrees latitude with hourly observations of temperature (2) were included in the analysis.

Results

The EIP is presented in figure 1. For all locations with EIP \leq 17 days, the number of ovarian cycles needed for transmission was larger than 3.

Material and Methods

A deterministic simulation model was used (1).

The model assumptions were:

- transmission occurs when the midge feeds on blood
- the midge feeds on blood at the start of each ovarian cycle
- the EIP must be completed before transmission can occur
 Model output
- minimum number of days for the EIP
- minimum number of ovarian cycles needed before virus transmission was possible

Conclusions

The results suggest that in certain years a BT-epidemic might develop in areas located along the southern coast or eastern part of Norway.

The fact that the model predicted the possibility of a BTepidemic in Norwegian areas for only two of the seven years included into the simulation, indicates that Norway is on the borders of the extension of BT-virus.

The model is based on data from *C. sonorensis* and data specific for *Culicoides* species transmitting BT in Northern Europe is needed.

Although temperature might be the main factor limiting BT epidemics in Norway, the low density of ruminants in large areas of Norway might reduce the possibility of BT epidemics even further.



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References

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2) Temperature data from Norwegian Meteorological Institute, available at eklima.met.no