

Use of a Montecarlo simulation model for the re-planning of bluetongue surveillance in Italy

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Summary

Since August 2000, Italy has lost almost 500 000 sheep to the largest incursion of bluetongue (BT) yet to affect Europe. The national BT surveillance system includes serological and entomological programmes. The main objective of the serological programme is the early detection of BT virus (BTV) circulation by periodical testing of more than 30 000 sentinel cattle distributed across Italy. The sentinel network has been in force since October 2001 and since its inception has provided accurate and timely detection of viral circulation. However, the repeated testing of such a large number of animals required significant effort from the Veterinary Services and was costly for farmers. Consequently, a Montecarlo simulation model was developed to simulate different sentinel system scenarios and the results from each were compared. The model was validated using data derived from the serological surveillance activities in Sardinia from October 2001 to December 2002.

Keywords

Bluetongue – Italy – Montecarlo simulation model – Sardinia – Sentinel system – Simulation – Surveillance.

Introduction

Since August 2000, Italy has lost almost 500 000 sheep to the largest incursion of bluetongue (BT) yet to affect Europe (1, 2). A vaccination programme was enforced in 2002, in conjunction with strict animal movement controls to reduce the spread of infection (3, 4). A surveillance system was implemented that required the periodical testing of more than 30 000 sentinel animals and included a number of other surveillance activities (5). The sentinel network has been in place since October 2001 and has proved reliable for detecting viral circulation. However, the periodical testing of more than 30 000 sentinel animals across Italy in 2002 required significant effort from the Veterinary Services and was costly for farmers. A strong demand to reduce sentinel animal testing came from representatives of the local Veterinary Services and farmers. To evaluate and refine the Italian serological surveillance system, a model was developed simulating different sentinel system scenarios and the results that could be expected from each.

Materials and methods

A simulation model of a serological surveillance system based on periodical testing of sentinel animals was implemented, with the aim of simulating the following:

- a) expected number of animals to seroconvert and to be detected upon subsequent testing
- b) expected number of herds in which at least one animal seroconverts to BTV and for the animal to be detected upon subsequent testing.

The model neither takes into account the sensitivity and/or specificity of the diagnostic tests used, nor the effects of multiple testing.

Assumptions

The model is applicable to any geographic area, but the probability of the final event (i.e. seroconversion) must be constant and continuous geographically and temporally. In other words, the geographic unit of reference and the time period considered in the model must be selected with care, so as to apply the

proposed model on a homogeneous epidemiological population correctly.

Description of the model

The output of the model is the number of sentinel animals that seroconvert to BT in a specific geographic area, during a specified time unit (week, fortnight, month, etc.).

The input variables are as follows:

- incidence of sentinel herds that seroconvert (P_i) per time unit and in a specific geographic area (a sentinel herd was considered to have seroconverted when at least one of its sentinel animals seroconvert)
- number of sentinel herds tested (N) per time unit and in a specific geographic area
- number of sentinel animals tested in each herd (n) per time unit and in a specific geographic area
- incidence of animals that seroconvert in the same sentinel herd (Ph) per time unit and in a specific geographic area.

The model includes the following calculations:

- expected number of herds that seroconvert
- expected number of sentinel animals that seroconvert.

The expected number of sentinel herds that seroconvert, per time unit and in a specific geographic area, is calculated according to a Poisson probability distribution, as follows:

$$X_A = \text{Poisson}(\lambda * t)$$

Where:

X_A = expected number of sentinel herds that seroconvert, in a given time period and in a specific geographic area

t = time period considered

λ = mean number of herds that seroconvert per time unit and in a specific geographic area. This value is calculated according to the following formula:

$$\lambda = \text{Binomial}(N, P_i)$$

Where:

N = number of tested sentinel herds per time unit in a specific geographic area

P_i = incidence of sentinel herds that have seroconverted per time unit and in a specific geographic area.

The expected number of sentinel animals that will seroconvert in each herd that has seroconverted (as calculated in Step 1 of the model) is calculated as follows:

$$C = \text{Binomial}(n, Ph)$$

Where:

n = number of sentinel animals tested in each herd

Ph = incidence of animals that seroconvert in the same sentinel herd.

Therefore, total number of sentinel animals that seroconvert is calculated by adding the expected number of animals that seroconvert in each herd (C):

Expected number of animals that will seroconvert per time unit and in a specific geographic area

$$= \sum_{i=1}^n C_n \cdot$$

Validation of the model

The model was validated using data stored in the bluetongue national database and that had been collected as part of the serological surveillance plan implemented in Sardinia from October 2001 to December 2002. Monthly data, from the four Provinces in Sardinia (Cagliari, Nuoro, Oristano and Sassari) were analysed separately.

For the validation of the model, P_i was calculated based on the following:

- the incidence of diseased sheep and goat flocks for each province and each month, taking into account also the number of vaccinated flocks that were not susceptible to the disease
- the incidence of infection among bovine herds for each province and each month, taking into account the number of positive sentinel herds. The final estimation was calculated assuming that the incidence of positive sentinel herds was equal to the real incidence of infection in the overall susceptible bovine herds.

Furthermore, in the calculation of the C value, n was calculated as the mean number of sentinel animals tested from each herd during each month, and Ph was considered as the mean value of the incidence of animals that seroconverted in the same herd each month. The model was implemented using Palisade Corporation @Risk[®] software (6). The output of the model (1 000 iterations with Latin hypercube sampling) was compared with the real observed number of animals that seroconverted in each province each month.

Using the model to re-plan the sentinel system

Two scenarios were considered. In the first scenario, the number of sentinel herds tested in the population varied. In the second, the number of sentinel animals tested in each herd was varied, leaving unchanged the number of sentinel herds. As a first step, the expected number of herds that would seroconvert was simulated (1 000 iterations with a Latin hypercube sampling) for each of the different scenarios and the number of herds tested (10, 20, 30 ..., 100 herds tested). For each scenario, the following variables were established:

- P_i = incidence of infected herds = 5%
- P_h = incidence of infection within the infected sentinel herd = 25%.

The chosen value of 25% for the incidence of infection within the herd was inferred from the observed values (Table I). Secondly, the expected number of animals that would seroconvert was simulated (1 000 iterations with Latin hypercube sampling) for each of the different scenarios and number of animals tested for each sentinel herd (4, 5, 6 ..., 12 animals tested). For each scenario, an incidence of 5% of infected herds, 25% incidence of infection within herds and 100 herds tested were considered.

Results

The results of model validation indicate that the model predicted the number of animals that would seroconvert correctly. The comparison between the observed number of animals that seroconverted in each Sardinian Province from October 2001 to December 2002 and the output of the model outputs is shown in Figures 1, 2, 3 and 4. To verify the possibility of refining the sentinel system, different scenarios of herds and animals tested were evaluated. The model outcomes indicate that the reliability of the sentinel system is highly sensitive to the variation in the number of herds tested.

The probability of detecting at least one animal that has seroconverted decreases greatly when the

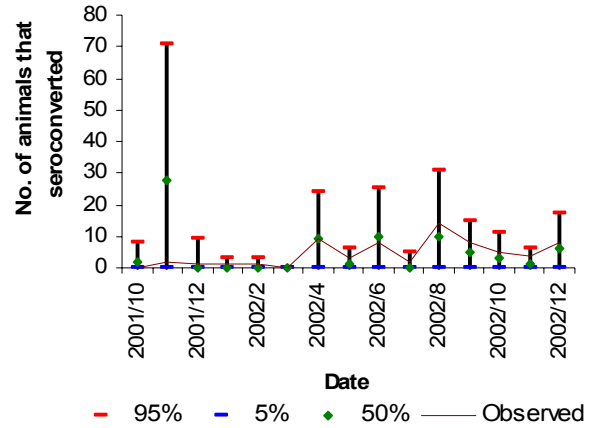


Figure 1 Comparison between the number of animals that seroconverted in the Cagliari Province and the 5th, 50th and 95th percentile of the distribution of the values predicted by the model, October 2001-December 2002

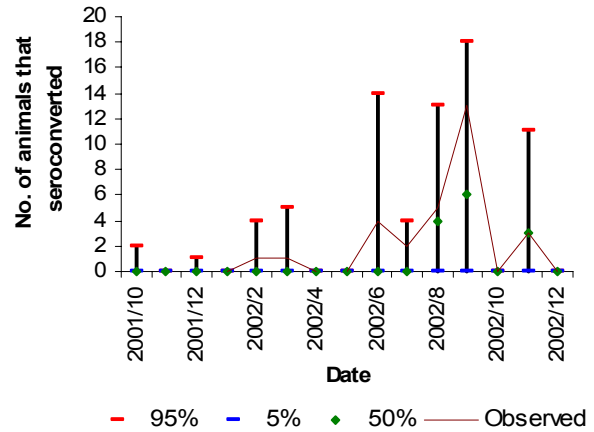


Figure 2 Comparison between the number of animals that seroconverted in the Nuoro Province and the 5th, 50th and 95th percentile of the distribution of the values predicted by the model, October 2001-December 2002

number of herds tested is lowered (Fig. 5). Varying the number of animals tested in each sentinel herd has little effect on the probability of detecting at least one animal that has seroconverted. This means that if either 4 or 12 sentinel animals were tested in each herd, the sentinel system would maintain the same

Table I The mean monthly incidence of infection with bluetongue virus serotypes 2 and 9 in infected sentinel herds in Italy

Serotype	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec	Mean (minimum-maximum)
BTV-2	22.9%	21.4%	17.9%	25.4%	27.3%	25.5%	27.0%	30.9%	24.8%	23.1%	26.5%	27.7%	25.0% (17.9%-30.9%)
BTV-9	27.0%	20.1%	20.9%	26.5%	35.2%	33.6%	28.9%	26.2%	18.1%	19.8%	22.4%	22.7%	25.1% (18.1%-35.2%)

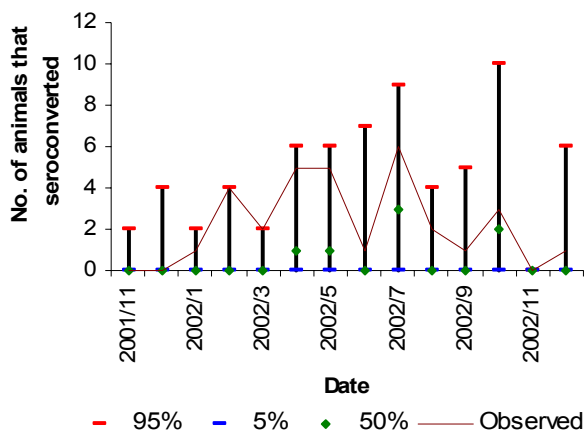


Figure 3
Comparison between the number of animals that seroconverted in the Oristano Province and the 5th, 50th and 95th percentile of the distribution of the values predicted by the model, October 2001-December 2002

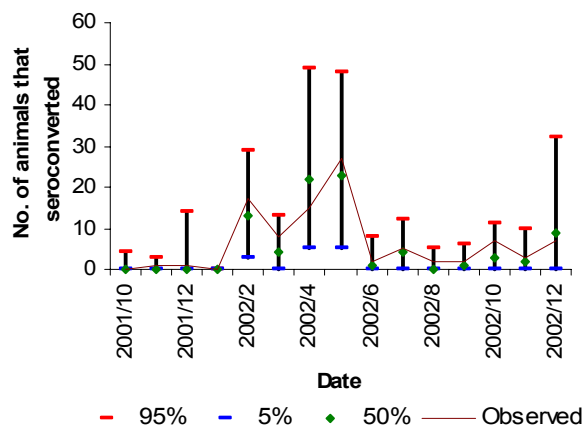


Figure 4
Comparison between the number of animals that seroconverted in Sassari Province and the 5th, 50th and 95th percentile of the distribution of the values predicted by the model, October 2001-December 2002

ability to detect infection if all other variables remain unchanged (Fig. 6). For example, the probability of detecting at least one animal that has seroconverted is 0.914 if four animals are tested in each herd and 0.956 when twelve animals are tested.

Discussion

The current Italian sentinel network is probably the most intensive serological BT surveillance system in

Europe. This network has demonstrated its ability to detect virus both accurately and timeously. However, the repeated testing of a large number of sentinel animals, as prescribed in the surveillance plan, required significant efforts from the Veterinary Services and a heavy commitment from farmers. Therefore, a simulation model was developed to evaluate different sentinel system scenarios in order to develop a new streamlined serological surveillance system.

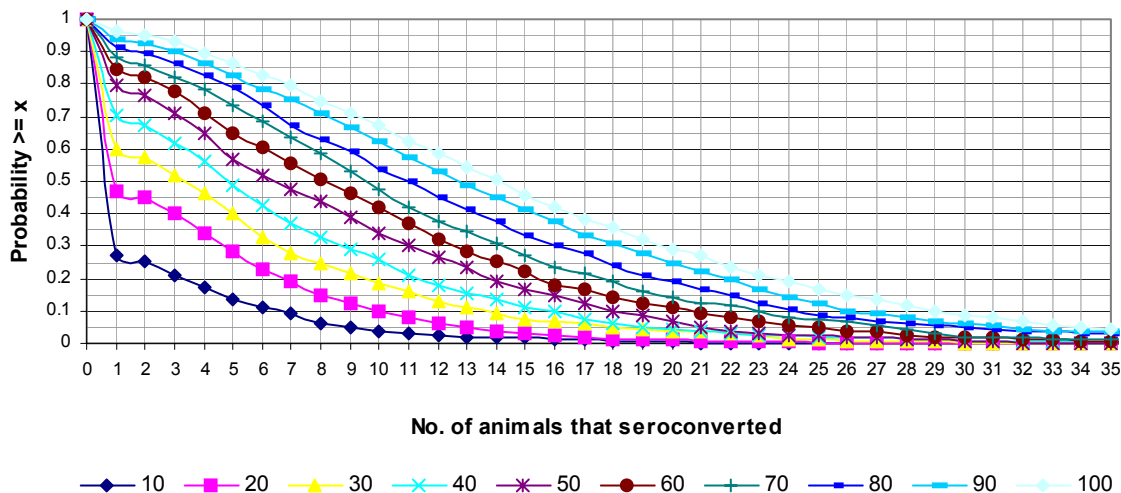


Figure 5
Model outcome: inverse cumulative distribution of probability of having one or more animals to seroconvert
Consideration is made of different scenarios of tested herds (10, 20, 30 ... 100) and the following variables:
5% incidence of infected herds
25% of incidence of infection within herds
12 sentinel animals tested for each herd

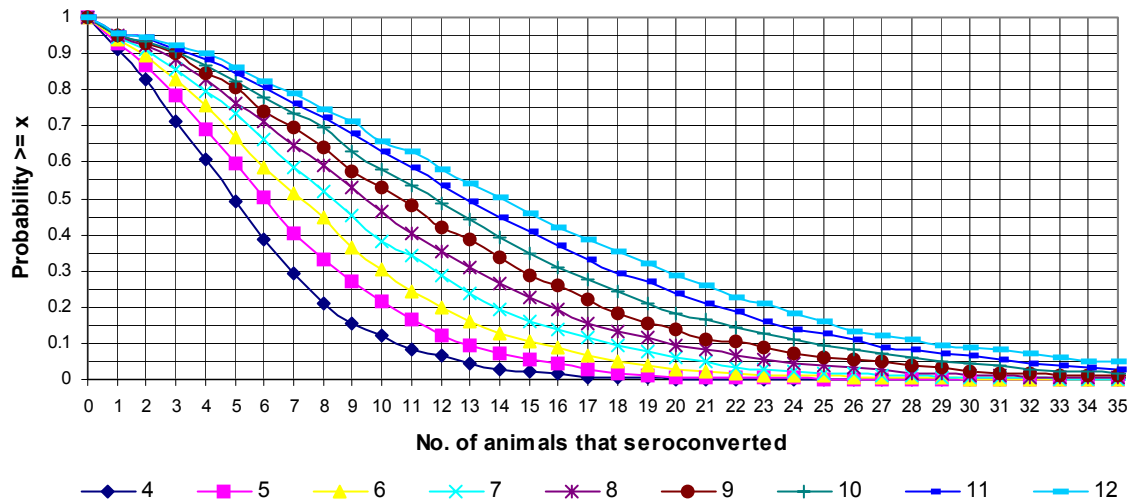


Figure 6

Model outcome: inverse cumulative distribution of probability of having one or more animals that seroconvert

Consideration is made of different scenarios of tested animal for each herd (4, 5, 6 ... 12) and the following variables:

5% incidence of infected herds

25% incidence of infection within herds

100 sentinel herds tested

The simulation model that was developed indicates a significant reduction in the effectiveness of the system to occur when the number of sentinel herds tested is decreased. However, the variation in the number of animals tested within each sentinel herd does not significantly reduce the accuracy of the system. The outcomes of the model are consistent with the expected epidemiological patterns in a vector-borne infection like bluetongue. Consequently, the most effective system for detecting infection would be to use sentinel herds dispersed to form a fine grid mesh. On the other hand, the clustering of infection in positive herds allows the selection of a relatively small numbers of animals to be tested within each herd.

The simulation study, therefore, indicates that the number of sentinel animals within herds could be reduced by one third with significant advantages for livestock owners who can then maintain a lower number of unvaccinated animals in their herds resulting in significant savings for them and for the Veterinary Services.

The simulation model described here was designed and validated using data derived from the Italian serological surveillance plan. Results, therefore, are applicable only to the situation in Italy and cannot be extrapolated to others. However, the mathematical approach used in the present model could prove useful in developing simulation models in countries other than Italy.

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