Modelling the spread of foot-and-mouth disease virus

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Summary — Foot-and-mouth disease is an economically important viral disease in animals. It is shown that airborne diffusion is one of the main sources of contamination between animals and between herds. Epidemiological data linked to viral particle excretion can thus be used in a predictive model, added to meteorological data related to the few days before the slaughter of animals. The model computes, on a 10 km radius around the outbreak and in every space direction, the quantity of viral particles that a sensitive animal could have breathed. The aim is to define a risk area, and, according to the number and size of farms in the surrounding, to give arguments for the best sanitary decision within the emergency plan.

foot-and-mouth disease / modelling / airborne diffusion

INTRODUCTION

Foot-and-mouth disease (FMD) is a viral disease in domestic animals. Although the situation for FMD may be qualified as good for western Europe, this disease is still the most feared of all domestic animal diseases. The species concerned are even-toed mammals (order Artiodactyla). In European countries, this means cattle, sheep, goat and pig. Further east or south, camel and buffalo, for example, may also be infected (Asso, 1985).

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The consequences of FMD outbreaks are mainly economical. Any case will greatly imperil animals and animal-produce trade, on local, regional and international levels. Whole areas of the world cannot trade with other countries because of a real, or suspected, FMD endemic situation. Besides this economical impact, FMD may also kill young animals, create lesions in the mouth, on the foot, on the udder, and then add a sanitary dimension. This explains why the disease is still of concern to a number of countries, even free of FMD, and why there are still programmes concerning either the virus, or prevention systems against the disease (Anon, 1978; Sanson et al, 1991; Tison and Merlin, 1992).

Many studies have been performed to understand the main routes of transmission of the disease. Since the end of the 1970s, the importance of the airborne transmission of the virus has been documented (Donaldson, 1979; Gloster et al, 1981; Moutou et al, 1987).

The aim of this work is to provide a tool available during an episode of FMD that could help to forecast the risk of new outbreaks. With such a tool, the team in charge of the emergency plan may use the means they have at their disposition with a higher efficiency.

**AIRBORNE TRANSMISSION MODELLING**

The airborne virus is emitted over a 4–5 d period by an infected animal and the excretion of the virus may start 1 or 2 d before the onset of the first clinical signs. Between pigs and ruminants (cattle, sheep and goats), a large difference has been discovered at this level. The peak of excretion in a pig may reach $10^8$ infectious units per 24 h, whereas the same peak is only of $10^5$ in a cow, a sheep or a goat. The evolution of farming over the past 30 yr with a number of large pig units has created new epidemiological conditions in which clouds of FMD virus may be spread around an outbreak (Donaldson, 1979).

The characteristics of particles containing FMD virus are the following. The virus is adsorbed on small drops of saliva or mucus which may reach a diameter of 6 μm. Their falling speed to the ground is only $10^{-3}$ m/s to $2 \times 10^{-2}$ m/s. Thus it is possible to say that there is no substantial transfer of the airborne virus to the ground within about 10 km of the source when over land (a different situation will prevail over the sea, *vide infra*). These characteristics are the same as those known for many other airborne particle transfers, already studied by physicists, for example, the physicists in charge of preventing chemical or nuclear industrial pollution. This is why we have been working on a model developed by the Atomic Energy Agency (Commissariat à l’Energie Atomique: CEA), called ICAIR 3V model (Doury, 1982; Crabol, 1988). In this model, the actual emission is represented by a sequence of instantaneous emissions of individual puffs. The sum of these puffs forms the infectious cloud.

The future of an individual puff depends on 2 factors: the movement of the carrier air (wind speed, and wind direction) determines variations in the position of the center of the puff; and the age of the puff, because if the quantity of infectious particles inside a puff remains constant throughout time, their concentration around the center of the puff decreases, following a 3-dimensional Gaussian dispersion law. The standard deviation ($\sigma$) in each direction of space is a function of the age of the puff (the longer the transfer time, the larger the standard deviation).

Thus, for constant meteorological data, and for a single puff, the volumic concentration of infectious particles in the air, $X$, at the moment $t$ from the beginning of the outbreak and at the position $x$, $y$, $z$, where $x$ is the coordinate along the average direction of
the wind and y and z are the coordinates along orthogonal positions, may be calculated as follows:

\[
X = \frac{2Q}{(2\pi)^{3/2} \sigma_x \sigma_y \sigma_z} e^{-\frac{1}{2} \left( \frac{(x-x_0)^2}{\sigma_x^2} + \frac{(y-y_0)^2}{\sigma_y^2} + \frac{(z-z_0)^2}{\sigma_z^2} \right)}
\]

where \( Q \) is the total quantity of particles leaving the outbreak; \( \sigma_x, \sigma_y, \sigma_z \) are the standard deviations of the distribution of \( Q \) from its average localization with \( \sigma_x = \sigma_y = (A_h t)^{k_h} \) and \( \sigma_z = (A_z t)^{k_z} \); \( A_h, A_z \) are parameters of horizontal and vertical diffusion; and \( k_h, k_z \) are horizontal and vertical diffusion indexes. \( A_h, A_z \) and \( k_h, k_z \) were determined experimentally by the physicists at the CEA. The variables \( x_0, y_0, z_0 \) represent the position of the outbreak and \( \bar{u} \) is the average wind speed.

Figure 1 shows the trace of a single puff. For varying meteorological data, the evolution of each puff (trajectory, dispersion) is calculated separately. The volumic concentration of infectious particles at the moment \( t \) and at the position \( x, y, z \) results from the sum of the concentrations of each of these single puffs (fig 2).

When far enough from the outbreak, i.e. the source, and when the wind speed is over 1 m/s, the puff model will be simplified in a plume model:

\[
X = \frac{Q}{\pi \sigma_y \sigma_z} e^{-\frac{1}{2} \left( \frac{(y-y_0)^2}{\sigma_y^2} + \frac{(z-z_0)^2}{\sigma_z^2} \right)}
\]

The plume model is a simplification of the puff model, used when the meteorological data allow it, and when the length of transfer time is long enough. In this case, dispersion in the direction of the wind is not

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**Fig 1.** Trace of a single puff. As the puff moves away from the source, its volume increases, but the quantity of virus inside remains the same. The grid is made of squares of 1 x 1 km.

**Fig 2.** Traces of different puffs in variable meteorological conditions. The different puffs may have followed different routes. The model computes the contribution of any single puff over the 1 x 1 km grid. The lines can be seen as the tracks of the center of individual puffs.
taken into account. ICAIR 3V will automatically switch to the plume or puff model, depending on the data. The parameters in equation [2] are as in equation [1].

Besides wind speed and direction, another important parameter is relative humidity (RH). The virus will not survive in the air if RH is below 60%. Thus the model should check, at each time, the value of RH.

The model developed here may be used for viral fallout in a 10-km radius around the source, ie outbreak over land. Another model should be used for transfer over sea, because contamination seems to be possible up to 200 km of the source along a shore (Donaldson et al, 1982). When the sea temperature is lower than the air temperature, and when the low layers of the atmosphere are very stable, long-range contamination is possible because the sea surface is smooth compared with any land area where relief, trees and buildings soon clear the air-borne virus. In this study, we have only worked on the overland model.

APPLICATION

The application of ICAIR 3V is a tool for decision making in the case of an outbreak of FMD. Knowing where the virus may have been carried, it is possible to take preventive measures, even before the first clinical sign is detected, in the hope to stop the epidemic at its very beginning. The computer programme that implements the ICAIR 3V model has been written in C language on an IBM RS/6000 workstation in CNEVA/Laboratoire Central de Recherches Vétérinaires. The charts and maps are drawn using the software Mathematica (Wolfram Research, Inc). In the case of an outbreak, or in the case of a suspicion, meteorological data from the nearest meteorological station will be sent by the national meteorological service as soon as they receive the location of the suspected source. We have signed a contract with them. At the same time, epidemiological data will be collected, and the model may be run in less than 15 min. The meteorological data collected are wind speed, wind direction, and relative humidity. Depending on the meteorological station, the periodicity of the data will vary from one set every 15 min to one set every 3 h. The epidemiological data are collected for each outbreak or suspected farm: the probable date and time of the beginning of excretion of the virus and the number of animals for each concerned species. The beginning of viral excretion may be known from the suspected time of introduction of the virus, or by dating the lesions of sick animals.

To analyze the risk of secondary outbreak, we assume that a cow downwind will breathe 100 l air per min, and that a sheep, a goat or a pig downwind of the outbreak will breathe only 5–10 l air per min.

We have tested the model on past Brittany outbreaks (March 1981: last French episode of FMD) and we have recently been asked to use it in real time, in April 1993, in Verona, Italy, during the last EEC outbreak. In the case of Brittany outbreaks, the model confirms that airborne transmission may explain 10 of the 13 secondary outbreaks.

In the Italian case, 4 outbreaks were detected in the Po valley, in the Verona province, between 4 and 29 March 1993. All were fattening beef units with 300 to 1,000 heads in each. They were all within 4–5 km of each other. At the end of March, the question was: is it possible to assess the risk of any other spread of the disease in the area? The model was run using and adding meteorological data from 4 March (time of introduction of infected animals to the first premises) to 29 March (time of destruction of the animals in the last premises), and epidemiological data. Figure 3 shows the result. The area at risk concerns a very small area around each farm, the 50 infectious units average fallout line. The largest area seen here is the 1 infec-
tious unit average fallout line, and it is really theoretical. Furthermore, it was known that 2 large pig fattening units (962 and 1,517 animals) were located very close to the last outbreak. Figure 4 shows what could have happened if these 2 farms had been contaminated and had excreted the virus for the same days as outbreak number 4. Many more farms would have been at risk. Thus, the 2 pigs units were destroyed, although no clinical sign was ever detected on any of them. In this case, the model helped for the difficult political and economical decision of slaughtering animals free of disease.

CONCLUSION

We see this model as a tool for decision making within the emergency plan when

Fig 3. Real virus fallout for cattle, from 4 March to 29 March 1993 around Verona, Italy. Four fallout average lines are shown: 100, 50, 10, and 1. The risk area is very small. Every dark spot is a farm. The 2 arrows show the 2 pig farms.
FMD is suspected. Added to all other information, it may help to decide where to go first, or where to increase vigilance. Using facsimile, it is easy to send the data to run the model. We also see possible theoretical developments in the field of percolation. Could it be possible to predict, knowing where an outbreak is notified, whether the disease may reach epidemic level, from meteorological, epidemiological, geographical and human data? This is under investigation.

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Development of an on-line mastitis detection system within an integrated knowledge-based system for dairy farm management support

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Summary — Some aspects of automated clinical mastitis detection and diagnosis are discussed. Knowledge representation techniques for the different steps in the diagnostic process are presented. The main focus of this paper is on automated early detection, based on data that are automatically collected in the milking parlour. Principal component analysis, logistic regression and back-propagation neural networks were used in the analysis of the automatically collected data. The 3 techniques did not differ greatly in performance. All the techniques performed better when data from milking with observed clinical signs were used, compared with data from milking before clinical symptoms were noticed. Healthy quarters were mostly correctly classified by all techniques. It seems unlikely that all clinical mastitis cases can be detected at milking before visible clinical signs occur.

clinical mastitis / automation / mastitis detection

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