An Epidemic Simulation Model Of Foot And Mouth Disease Spread Applied Into A High Densely Populated Area of Lombardy Region (Italy)

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Abstract

This paper is concerned with the developing of a simulation model for space-time behaviour of Foot-and-Mouth Disease (FMD) in a high densely populated area. The data for our model were the spatial coordinates, the dimension and type of the farms in the studied region. We modelled the *Spatial dependence* applying a "gravitational" function, which relates the location of a susceptible (farm) to any infective location (farm) with a distance decay modulation; a SLIR model was adopted for the *Temporal dependence*. We defined a "risk potential" for each farm to become infected as a combination of the gravitational component with some known risk factors like susceptibility, transmissibility, latency, contact rates between farms and a random factor, called "frailty". All risk factors were regarded as random variables with a suitable distribution, except for susceptibility and transmissibility. Through a logistic model, which used the previous "risk potential", we calculated the risk for a farm to become infected. The model defines the infected farms sampling from the upper tail of the distribution of the risk. This process will update each day the suitable random variables, e.g. contact rates will vary every day in different way according to the size, type of farms and according to the day of the week. Moreover we have built a package in R Language performing the simulation here presented.

Introduction

The aim of this study was to develop a simulation model for the spread of FMD Virus in a high-risk area like the Lombardy region, a densely populated area for cattle and swine intensive farms. The availability of a simulation model allows to evaluate *a priori* the best control strategies *vs.* FMD.
The lack of past epidemics data induced us to follow the suggestion of Kitching el al. (2005) - "the mathematical algorithms for FMD models should not be cumbersome" - constructing a simulation model easy to use, requiring only commonly available data and to modify. We defined a "risk potential" as a combination of a gravitational component (interaction between farms size and their distance) on one side and, on the other side, to some known risk factors like: susceptibility, transmissibility, latency, contact rates and a random factor, 'frailty'. All risk factors were regarded as random variables with a suitable distribution, supplemented with expert judgement. Only susceptibility and transmissibility were considered fixed parameters (from literature). The probability for a farm to get infected has been calculated assuming a logistic model for the effect of the "risk potential" on it. We generated randomly an index case and a number of contacts among farms in the area of interest with the index case. In every step of the simulation process we have considered the farm as the statistic unit, without modelling the intra-herd epidemic. New cases of infection were sampled from the upper tail of the risk distribution. In the last step the model, identified the first case, a control basic strategy based on restriction measures was applied to stop contacts and on depopulation of animals in protection areas.

Materials and Methods

We used Geo-coded data of all farms (cattle, swine, sheep & goat) in the selected area, with information about species type and dimensions. The pilot area, a flat land located in Lombardy

Region, has an extension of 3,200 Kmq (80 km x 40 km) with 6,122 farms raising 3,048,786 FMD susceptible animals for 2 farms/Kmq and 953 heads/Kmq densities.
We have also used data collected by a survey in a similar area about the number of daily contacts in the different type of farms (beef and dairy cattle, swine and sheep) and data found in the literature about latency, susceptibility, and transmissibility. These latter were the base to define the distribution of these parameters, with the help of an expert consensus. We assumed that latency, sub-clinical time, daily # contacts had a beta-pert distribution and the frailty parameter, which tries to capture in the model unknown risk factors, have a lognormal distribution.
Our model is a mixture of the approach of Durand et al. (2000) and Gerbier (2002). As central keys, we assumed that the epidemic spread can be modelled first of all using the spatial network of the farms and the network of the contacts ("contact matrix"). The "risk potential" of a farm at time *t* is expressed by the following formula

$$\mathsf{f}_i(t) = \mathsf{q}_{1,t} \sum_{j=1}^{n_{t-1}} \frac{m_i m_j}{d(x_i, x_j)} + \mathsf{q}_k Z_k$$

where $d(x_i,x_j)$ represents the distance between an infected farm *i* and a susceptible one *j*, m_i and m_j are the size of the two farms and the $\bullet_k Z_k$ with $k=1.n$ modelled the effect of the other risk factors (contacts, susceptibility, sub-clinical phase, transmissibility). The lack of sufficient data about past epidemics in Italy didn't allow to estimate the weights of the different factors; however, we have assumed that the $\bullet$'*s* has a beta-pert distribution with $\bullet$=1. Hence, the probability of a susceptible farm at time *t*, given a set of infected farms, is

$$p(Y_i(t)) = \frac{e^{\mathsf{f}_i(t)}}{1 + e^{\mathsf{f}_i(t)}}$$

Using this model, we have simulated an epidemic, extracting a farm as index case. Then the simulation process assigns to each farm its latent period randomising from the suitable distribution in relation of the species in the farm, calculates the distances from the index case and the infection probability for each farm. This process, with a daily updating of the suitable parameters, e.g. contacts, continues as soon as some of the infected farms become infecting; the risk potential of a susceptible farm is the sum of the risk potentials related to each infected farm and/or any farm has ended up his sub-clinical period and is identified. Then, in order to simulate the stamping out policy, the simulation process eliminates from the set of susceptible all farms located in a *radius* of 5 km around the identified infected farms. We have run 1000 plus 1000 iteration to simulate two epidemic scenarios: the first one describing a silent epidemic of 20 days (out of control) and the second consisting in an epidemic under control. We used the statistical open-source language 'R' to construct this simulation (R Development Core Team, 2005). Moreover we are building a package called "epi.afta". This package will assume all information (geo-referenced data, farms, latency) for the simulation process as inputs. This package in its final version will analyse also the role of dairy industry as multiplier of the epidemic process.

Results

The scenario obtained from an epidemic out of control gave a range from 25 to 183 expected outbreaks with a median value of 118.
On the other hand, the scenario obtained from an epidemic under control gave as result from 1 to 4 new outbreaks originating from index case. A sound surveillance could permit the identification of the first case after 7-8 days from the beginning of the spread of FMD virus. In this case, during the following 20 days of simulation we could expect the onset of 25 until to 61 outbreaks with a median value of 42.

In Figure 1 two possible scenarios are compared: epidemic out of control (red line) or under control (blue line).

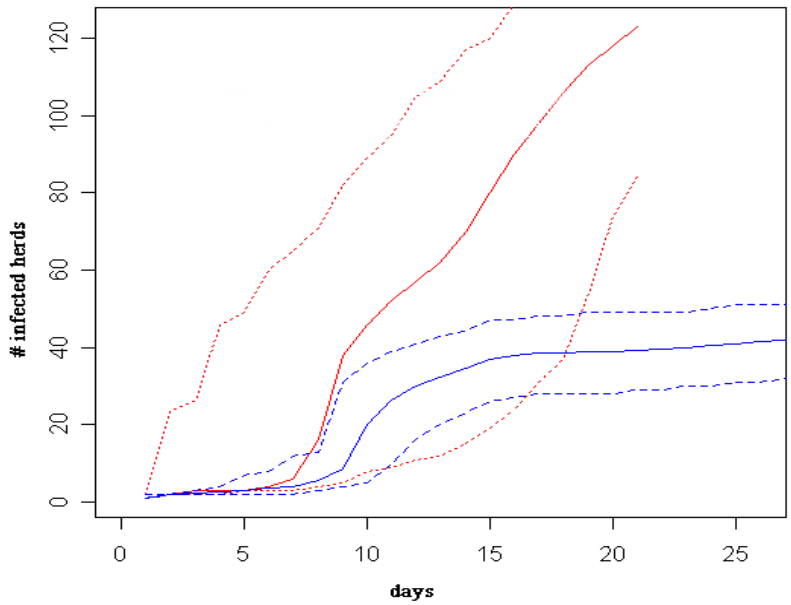

Figure 1 FMD epidemic with or without control strategy

Epidemic under control

Epidemic out of control

We have also performed simulations with a suitable selection of the type and/or size of index-farm (e.g. large *vs.* small cattle or swine livestock) to evaluate possible differences concerning the development of the epidemic. We have not found great differences (data not shown), probably due to the high density of the pilot area.

Discussion and conclusions

The simulation model produced has been for the first time applied in a densely populated area in Italy to elaborate different scenarios of FMD spread.
The greatest advantage of this model is based on the use of the enclosed open-source program in R language, in our opinion a flexible tool regarding to the adopted distributions and/or the selected fixed parameters. A critical point of our model is the lack of estimates of the weights of the risk factors.
However, we think that the model can represent a useful basis upon which to implement further epidemiological application.

References

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