

**DEVELOPMENT OF PREVENTION
AND CONTROL STRATEGIES TO ADDRESS ANIMAL HEALTH
AND RELATED PROBLEMS
IN DENSELY POPULATED LIVESTOCK AREAS
OF THE COMMUNITY**



FAIR programme

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Development of prevention and control strategies to address animal health and related problems in densely populated livestock areas of the Community

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Development of prevention and control strategies to address animal health and related problems in densely populated livestock areas of the Community

General introduction

R.B. Huirne

General introduction

R. Huirne

1.1 Introduction and background

Densely populated livestock areas have developed because they have considerable economic advantages for both the farmers involved and the agribusiness industry. Their development gives rise, however, to an increased risk for the introduction and spread of notifiable animal diseases. The cost of dealing with these problems is placing increasingly heavy financial burdens on the commercial and public sectors. Recent outbreaks of Classical Swine Fever (CSF) and Foot and Mouth Disease (FMD) have clearly shown the extent of the problem and the need to reconsider the prevention and control strategies that could best be applied to such regions.

For some important and clear reasons, farmers produce many animals (dairy cows, pigs, poultry, etc) in relatively small areas, known as concentration areas or densely populated livestock areas (DPLAs). Strong material and information links, as they exist in animal production, are often associated with such agglomerations of economic activity. Agglomeration effects that arise from the clustering of activities and which are external to the farm or firm are called external economies of scale. A common distinction can be made between two types of external economy: localisation economies, and urbanisation economies. Localisation economies are cost savings specific to the establishment of a particular industry, such as those that arise from spatial proximity to the units to which they are linked (such as a pig fattening farm and a slaughterhouse). In animal production, face-to-face contacts between producers (such as in study groups) are very important for the exchange of information and experience, possibly focused on innovations, cooperation and sharing expensive production factors (such as transport costs). Moreover, group cohesion, counter-vailing power, and competition to be the best can be stimulated by acting/operating as a group. Urbanisation economies are cost savings to all farms/firms arising from location in an urban area, such as transport facilities, a range of industrial and office premises, or a pool of cheap labour. In this way production costs of all farms/firms involved can be kept low and information can be exchanged easily. These are considerable advantages for DPLAs.

Urbanisation economies are related to settlement size, the larger the settlement the greater the potential economies. Urbanisation diseconomies, such as congestion, rising land prices,

pollution and the escalating costs of providing public services, may also come into operation as the size of urban areas increase. The same is true for localisation diseconomies. Major localisation diseconomies in animal production include competition in obtaining land needed to grow cereals or to spread manure, and the occurrence, spread and control of contagious animal diseases such as CSF and FMD.

The argument for a relationship between linkages and agglomerations is usually based on the cost savings that firms/farms may accrue from local linkages. Although transport costs are an important location factor in pig production, they are only one aspect of the effect of distance on costs. Distance also influences the cost of maintaining contact by exchange of information. This is especially important where non-standardised goods are being produced and close contact between supplier and producers is vital, as is the case with producing pigs or milk according to certain specifications (value-added-chain production). There are also variations in the significance of transport costs between different sized farms/firms (such as feed mills, individual swine producers, the milk processing industry and slaughterhouses).

1.2 Objectives

The main objectives of the project, therefore, are to develop methods of identifying densely populated livestock areas and to develop tools that are necessary in order to reduce risks and help solve problems in such areas. For this, insight is given into the following four key research questions:

1. Which areas of the EU are densely populated with livestock?
2. What are the risk factors for the introduction of notifiable animal diseases into these areas?
3. What are the risk factors for further spread of notifiable animal diseases in these areas?
4. Which specific prevention and control strategies for notifiable animal diseases are possible and what are the costs and benefits?

These key research questions have been discussed frequently in the Commission and in EU member state countries, both formally and informally. However, this did not result in concrete and workable solutions with which the real problems can be tackled. The recent outbreaks of FMD in the UK, France and The Netherlands are a sad example. In order to

ensure definitive and practical results in the current project the key research questions have been translated into the following four working tasks:

Task A: Development and standardisation of data and methods used to identify densely populated livestock areas

Task B: Quantification and classification of the risk of such areas from a disease point of view

Task C: Analysis of recent disease outbreaks of CSF and FMD to test and refine risk parameters

Task D: Cost-benefit analysis of disease prevention and control strategies in such areas

1.3 General organisation of the project and deliverables

The completion of the project makes it possible to identify areas in the EU which are characterised by a high risk with respect to the introduction and further spread of major animal diseases. The results enable the EU to stimulate measures that reduce the risk and to decide what means should be used in particular areas to reduce the cost of an outbreak. Reduced risk factors and improved control strategies help to ensure that measures that are very costly and no longer publicly acceptable, such as the stamping out of a large number of herds that do not show any signs of an infection, are no longer used.

More specifically the major results/benefits from the project include:

- the ability to identify densely populated livestock areas and to characterise the sectoral and spatial structure (pattern) of the livestock industry in such areas
- the development of software tools that allow the analysis of available data sets in order to characterise the risks for densely populated livestock areas and to rank them with respect to the risk of introduction and further spread of major diseases, such as CSF and FMD
- the development of a computerised modelling approach for carrying out cost-benefit analyses of relevant prevention and control strategies for major animal diseases in densely populated livestock areas, aimed at supporting policy makers at EU, national and regional levels
- the possibility of using the data collected and software tools developed for the study of factors other than disease risk, such as environmental problems resulting from the concentration of livestock

In addition, most important technical deliverables include:

- a computerised toolbox for the identification and analysis of densely populated livestock areas
- a method of ranking densely populated livestock areas according to their risk
- an integrated model approach for the evaluation of prevention and control strategies of notifiable diseases in densely populated livestock areas

1.4 Detailed research plan and organisation of the text

The results of the project are presented in this report. The report is organised into four sections: one per task, complemented by an ‘general introduction’ and ‘general summary and conclusions’. Each section is divided into several chapters, as introduced and explained below.

Task A: Development and standardisation of data and methods used to identify densely populated livestock areas

Following discussions in several of the Commission’s workshops, as well as in the Scientific Veterinary Committee’s special sub-group, it became clear that the data available from EUROSTAT could not be the basis for the identification of densely populated livestock areas, as in most cases the spatial reference units are too large. Hence, obtaining data on smaller reference units became necessary. In relation to disease management, especially for notifiable diseases, the areas of protection and surveillance zones defined around an outbreak area are a suitable reference unit because the economic impact of an outbreak is particularly related to these areas. Task A was directed towards obtaining this data in a standardised way and developing methods to make it available for further use through user-friendly software.

The main methodology applied within Task A was the development of a flexible and standardised database that included and was centered on the geographical coordinates of individual livestock holdings. The database has a direct link with geographical information systems software, to allow user-friendly communication and analyses. However, although it is known where the high and low concentrations of livestock are within the EU, there is no clear and unique definition of the term ‘densely populated livestock areas’. Chapter 2 therefore addresses this issue in great detail, i.e. it serves to define densely populated livestock areas, as well as to provide both spatially-oriented methods and indices for identifying such areas - (such as the GINI-index to measure the distribution of herd sizes within an area and the Nearest-Neighbour-Index to characterise the distribution of distances

between livestock holdings). These methods and indices were then calculated and applied to densely populated livestock areas (see Chapter 3). In particular, the so-called Nearest Neighbour Index (NNI), the Lorenz curve for estimating the skewness of animal density distributions, the GINI index and an advanced and detailed kernel tool for density estimation were developed as user-friendly tools for decision-makers (and then) applied to some selected DPLAs. These indices and tools should be seen as a logical next step in analysing animal densities in spatial terms (i.e the next step on from indices such as number of animals per square km, as defined in Chapter 2).

Task B: Quantification and classification of the risk of densely populated livestock areas from a disease point of view

The risk of densely populated livestock areas for the introduction and spread of diseases may depend on factors such as herd size and herd location (analysed in Task A). However, other influencing factors such as management practices of the farmers and trade patterns within, into and out of the area may also be important. Task B, therefore, aims to obtain this, often more qualitative, information, in order to provide insight into what differences in the type of livestock industry exist among and within areas, and whether or not they should result in a modification of the risk rating of the respective areas. First of all an extensive survey on cattle, pig and sheep herds is carried out in order to characterise the structure of sparsely populated livestock areas (SPLAs) and DPLAs in terms of farm management characteristics, animal contacts, vehicle movements, human contacts and biosecurity measures between farms/herds (Chapter 4). Then, as a logical next step, risk analyses are performed referring to the introduction of CSF in SPLAs and DPLAs, using the results and insights obtained from the survey (Chapter 5). For this, a new multiple attribute technique has been developed in which the several underlying risk factors are combined into one overall risk index. Based on the information collected (together with the information from Task A), this method is used to rank densely populated livestock areas with respect to disease risk (Chapter 5 and 6; in close cooperation with Task C – see below).

Additional regression-analysis techniques and epidemiological and mathematical (ratio) techniques were used to analyse the survey data in order to calculate the risk of those areas under consideration and to validate this against the actual outbreaks of notifiable diseases in selected EU countries (Chapters 4-6). Among others, the technique of multivariate analyses was used to define and analyse the importance of (differences in) risk profiles of individual farms in relation to the risk within the region/area. To test for generality, the methods have also been applied to other animal diseases and areas/countries. Chapter 7 deals with

respiratory disease outbreaks in fattening pigs (SPLAs versus DPLAs in France) and Chapter 8 deals with Aujeszky's Disease on pig farms in DPLAs in Belgium.

Task C: Analysis of recent outbreaks of CSF and FMD to test and refine the risk parameters

The major aim of Task C is to validate still further the risk ranking of densely populated livestock areas, as obtained in Task B, using data from recent outbreaks. As shown again by the major outbreaks in Belgium, Germany and The Netherlands, CSF is a major threat to both the private industry and the public sector and hence has been chosen (at the beginning of the project in 1998) as the disease to be used for the validation. Additional analyses, but less detailed, have been carried out for FMD (with recent outbreaks in the UK, France and The Netherlands).

Available data on the CSF outbreaks in the three first-mentioned countries (i.e. Belgium, Germany and The Netherlands) were analysed (Chapters 9 and 10) using similar methods to gain quantitative insight into both the spatial and quantitative dynamics of CSF in densely populated livestock areas, as well as into the underlying factors (i.e., epidemiology). A study on FMD is conducted in Chapter 11. Differences in dynamics and underlying factors between the areas were related to e.g. herd structure, trading patterns, animal contacts, etc. These findings were compared with the risk ranking of the areas as determined in Task B for further validation of the risk ranking tools. The improved understanding of the epidemiology of CSF and FMD in densely populated livestock areas helps to define disease prevention and control strategies that are adapted to specific conditions existing in these areas, resulting in faster eradication and lower costs (see Task D).

To obtain a better understanding of the dynamics of the outbreaks it was considered important in the analyses to include both the spatial pattern of disease outbreaks as well as their diffusion over time. This was made possible by the use of spatial and survival analysis techniques as developed in Task A. Spatial analysis is a relatively new technique in animal health management that allows for the inclusion of the geographical component into more ordinary statistical analyses, such as regression analysis. Survival analysis offers the possibility of studying the diffusion over time. This is explained in Chapters 9-11.

Task D: Cost-benefit analysis of disease prevention and control strategies in densely populated livestock areas

The public increasingly perceives the slaughtering of large numbers of animals and the destruction of their carcasses in the case of an outbreak of a notifiable disease as both

wasteful and ethically unacceptable. It is also a costly measure, a heavy financial burden for both EU member states and producers. There is a need, therefore, to define (i.e., further refine) effective prevention and control strategies, taking into account the specific characteristics of the densely populated livestock area under consideration. This is an area where further epidemiological and economic research is required, and on which Task D was focused. Computer simulation models have been developed that allow cost-benefit analyses of alternative options for disease prevention and control in densely populated livestock areas, taking into account different conditions and scenarios, considering (1) the introduction of the disease into an area, (2) the further spread of the disease, (3) the direct cost of control measures, and (4) the indirect effects due to trade restrictions. These models are described and applied in Chapters 12-14.

Task D made use of stochastic simulation models at herd and regional levels respectively. Computer simulation is a method for analysing a problem by creating a mathematical model of the system under consideration that can then be manipulated by input modification. It is particularly useful where real-life experimentation is impossible, costly or disruptive (as is the case with highly contagious diseases), as well as for exploring new control strategies (Chapter 12 and 14). Specific (conjoint) analyses were used to obtain knowledge from experts as to the relative importance of risk factors for the introduction of a disease into an area as objectively and quantitatively as possible (Chapter 13). Decision analysis techniques were used in evaluating the economic results of different control strategies (Chapter 12). Finally, trade-oriented models have been developed for a broader coverage of all costs involved. These models are described in Chapter 14.

Task A

Development and standardisation of data and methods used to identify densely populated livestock areas

Densely populated livestock areas: Definition and spatial distribution in the European Union – A case study for five member states

I. Michel and H. -W. Windhorst

Veterinary Information System: A GIS based toolbox for handling and analysing epidemiological risk factors in densely populated livestock areas

Manfred Ehlers and Matthias Möller

Densely populated livestock areas: Definition and spatial distribution in the European Union – A case study for five member states

I. Michel and H.-W. Windhorst

Abstract

The centres of animal production in the EU are more or less well known and in most cases named after provinces or natural landscapes. Thus, Brittany is the centre of production in France, the Po valley in Italy, parts of Lower-Saxony and Northrhine-Westphalia in Germany, etc. This description neglects, however, the intensity reached in these areas, as well as the animal density and the exact definition of the boundaries. Considering the fact that these production regions were mentioned again and again in the media in connection with the outbreaks of animal diseases, such a general description is insufficient. As the EU sets the legal framework for a disease outbreak, a more precise definition of densely populated livestock areas at the EU level is necessary, a definition at a national level would be a disadvantage.

The main goal of this paper is to provide a calculation for five member states as a basis for a classification that makes it possible to rank municipalities according to their animal density (animals per km² of land area) in densely and sparsely populated livestock areas (DPLAs and SPLAs). Two parallel calculations were carried out. One deals with ruminants (cattle, sheep, goats) and pigs, animals which would be affected by an outbreak of Food and Mouth Disease (FMD). A second calculation only deals with pigs, for only they would be affected by an outbreak of CSF. DPLAs are defined as municipalities with more than 450 animals/km² or more than 300 pigs/km².

2.1 Introduction

Data from the animal censuses in Belgium, France, Germany, Italy and The Netherlands was used for a definition of DPLAs. To reach a spatial pattern on a small scale, data for cattle, pigs, sheep and goats is needed on the municipality level. A second database was the cadastral area of the municipalities i.e. the density values do not refer to the land in farms, as such a value is irrelevant in case of a disease outbreak. For the same reason, no conversion

tables were used. For the ranking of municipalities according to their disease risk, the risk for an outbreak and the dissemination of an infectious disease would have to be calculated on the basis of each species. Such data is not available, however for an outbreak and the dissemination of a disease the organisation of production is also relevant. As such information cannot be concluded from the animal census, all species are only considered by their number.

2.2 The database

The database developed for FMD and CSF refers to 18,313 and 19,871 municipalities respectively, and an area of 1.10 and 1.13 million km² respectively. The differences are due to the availability of data for the Federal Republic of Germany. In total, Germany has 14,197 municipalities (Fischer Weltalmanach, 2001). For the calculation of animal density on the municipality level, only 5,409 data pairs were available for FMD and 6,964 for CSF. This is due on the one hand to the fact that four of the five states in eastern Germany do not publish animal data at this administrative level, and on the other hand, to disclosed data, when a certain number of farms holds a certain percentage of animals in a municipality. Nevertheless the vast majority of the animal population is contained within the calculations. Of the 15.2 million heads of cattle, 10.2 million are in the database, of the 24.8 million pigs, 20.7 million are in the database and of the 2.3 million sheep, 1.4 million are in the database (all data from 1997).

Another important problem originates from the differences in the animal censuses in the member states. Germany does not count goats because their total numbers are so low. Belgium data cannot be compared to those of other countries in the EU, as it is not the number of pigs that are counted on a certain day, but the number of places. In addition, piglets are not counted. In order to be able to use the Belgium data, a conversion method was used from the “Central Animal Health Association” (Ukkel, Belgium).¹ To avoid further problems, the classification for sows, hogs, piglets etc. was not used, but only the total number of animals for each species.

In addition to the differences in the methodology of the censuses and the general availability of the data, the years for which data sets are available at all, differ considerably. France only publishes data at the administrative level of the canton and the last complete data set is from 1988. Dutch data, on the other hand, stems from 1997. Table 2.1 shows a summary of

the basis_data used. It becomes obvious that this basis is not optimal, but with respect to the differences in the methodology of animal censuses in the EU member states, it is the best possible.

Table 2.1 **Basis data for calculations**

| | B | F | D ^a | D ^b | I | NL |
|-------------------------|------------------------|------------|----------------|----------------|-----------|------------|
| year of census | 1996 | 1988 | 1996 | | 1990 | 1997 |
| Community no. | 589 | 3,644 | 5,406 | 6,964 | 8,102 | 572 |
| area in km ² | 32,419 | 543,860 | 191,442 | 226,066 | 301,976 | 33,883 |
| total no. of cattle | 2,994,981 | 21,217,251 | 10,241,853 | | 7,748,261 | 4,410,635 |
| total no. of pigs | ^c 9,104,474 | 12,212,554 | | 20,676,524 | 8,417,721 | 15,189,064 |
| total no. of sheep | 327,877 | 11,498,746 | 1,358,652 | | 8,691,132 | 1,465,417 |
| total no. of goats | 49,071 | 1,209,302 | no data | | 1,247,606 | 118,549 |

a) For reasons of privacy 4.036 communities are closed.

b) For reasons of privacy 2.478 communities are closed.

c) Calculated pig number

2.3 Definition of DPLAs²

As mentioned before, the animal density was calculated from the number of animals and the area of a municipality. To reach a classification of densely populated livestock areas, density classes were formed: 0 animals/km², 1-50 animals/km², 51-100 animals/km², etc. The same calculation was then carried out for pigs. Figure 2.1 shows that the overwhelming number of municipalities belongs to the classes with low densities. This distribution focussed further considerations on the 5% of the municipalities with highest densities. This percentage was used as we are convinced that the vast majority of the municipalities belong to classes with low or moderate density, if one really wants to identify densely populated livestock areas. Another aspect was the assumption that legal regulations for all member states of the EU, with respect to disease prevention, would only be accepted and could only be applied if the area affected did not surpass 5% of the total land are of the EU.

The appendix shows the tables for both calculations on which the definition of DPLAs is based. Municipalities with more than 450 animals/km² are classified as DPLAs for FMD, in total 1,015 fall into this class. For CSF, the value is more than 300 pigs/km², here, 1,033 municipalities are classified as densely populated. As the remaining municipalities could not be classified as sparsely populated without a buffer, the following classification was used: all

¹ Number of piglets = (number of sow places) x 0.9 x 4.2

² In cooperation with Clazien de Vos, Wageningen Agricultural University.

municipalities that belong to the 80% with lower densities were classified as SPLAs, the remaining as municipalities with a medium density. From Table 2.2 one can see that these percentages have to be understood as a basis for a “rough” classification and that according to the data set they have to be modified. It becomes obvious, however, that the distribution of the percentages is similar for the number of municipalities as well as for the area in these municipalities.

Figure 2.1 Distribution of communities in density classes for pigs and animals

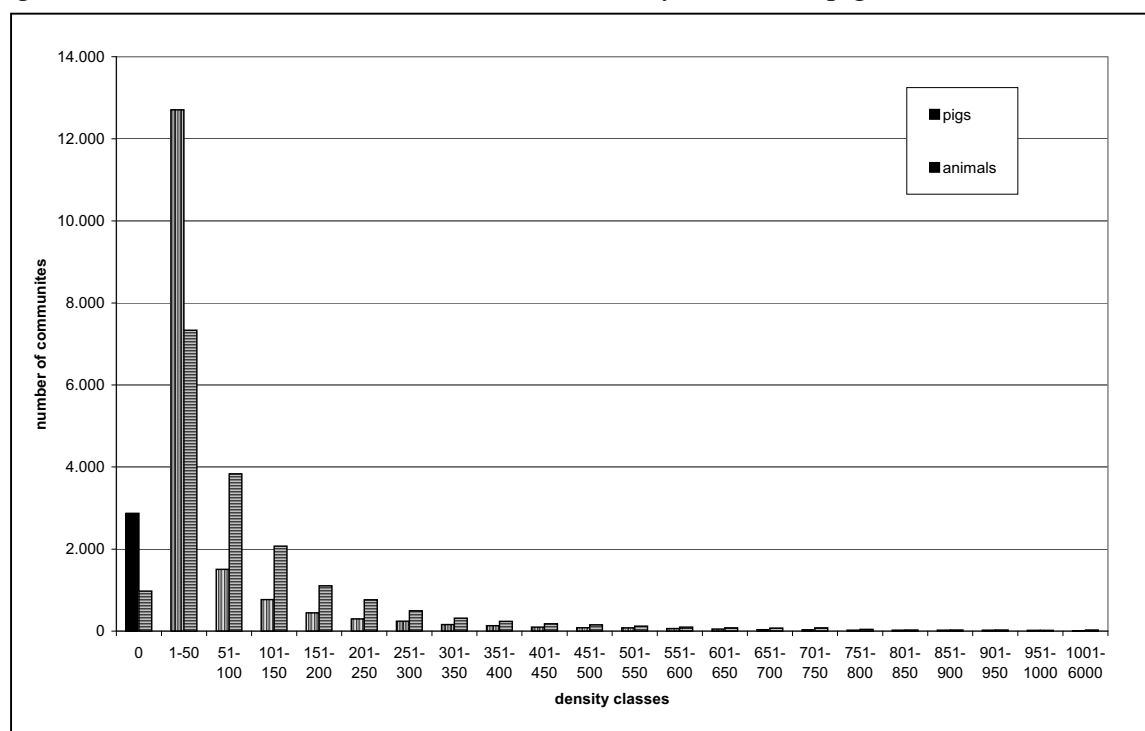


Table 2.2a Marginal values for the classification of DPLAs, MPLAs and SPLAs for FMD and their share (in %) of the number of municipalities and the area

| Class | marginal value animals/km ² | Number of communities | % of communities | % of area |
|-------|---|--------------------------|---------------------|-----------|
| SPLA | 0-150 | 14,219 | 77.64 | 79.35 |
| MPLA | 151-450 | 3,079 | 16.81 | 16.33 |
| DPLA | >450 | 1,015 | 5.54 | 4.32 |

Table 2.2b Marginal values for the classification of DPLAs, MPLAs and SPLAs for CSF and their share (in %) of the number of municipalities and the area

| class | marginal value pigs/km ² | Number of communities | % of communities | % of area |
|-------|--|--------------------------|---------------------|-----------|
| SPLA | 0-50 | 15,578 | 78.40 | 81.71 |
| MPLA | 51-300 | 3,260 | 16.41 | 13.88 |
| DPLA | >300 | 1,033 | 5.20 | 4.41 |

If a municipality reaches a density value of more than 300 pigs/km² but less than 450 animals/km² it would on the one hand be classified as a DPLA for CSF and on the other as a MPLA for FMD. As pigs carry a high risk in the dissemination of FMD, all communities with a density of more than 300 pigs/km² are also classified as DPLAs for FMD. There are 157 respective municipalities, but they are not contained in the figures in Table 2.2a.

2.4 Results

A detailed analysis of the results of the definition for the five countries shows results that differ considerably. Whereas, for example, in The Netherlands more than 30% of the municipalities and in Belgium more than 20% have to be classified as DPLAs, in France less than 2% belong to this class and in Germany and Italy between 5 and 8%. The differences are even higher when looking at the average densities. The Dutch municipality Mierlo shows the highest value with 5,875 animals/km², this is much higher than the highest value that was reached in France in 1988 (1,200 animals/km² in Lomballe). The increase in the pig population in France to more than 15 million in 1997 may, however, have reduced the gap, but the Dutch value is also much higher than the highest value in Germany in 1996 (Damme, 1,838 animals/km²). In Belgium the maximum was attained in Lichtervelde (4,491 animals/km²) in 1996; in Italy, Cumiganao sul Naviglio, reached a medium value with 3,661 animals/km² (c.f. list of the 40 municipalities with the highest animal densities with respect to FMD in the appendix). The maps in the appendices show the differences in the spatial distribution of DPLAs. Whereas The Netherlands and Belgium show continuous areas with an average density of more than 2,000 animals/km², such areas cannot be found in France and Germany at all and only in a few locations in Italy. Only a more recent data set could illustrate how this situation may have changed in France and Italy.

Figure 2.3a and b show another important aspect of the comparison, the percentage of the respective species that are located in the DPLAs. One can easily see that the pig production in the Netherlands and Belgium is almost completely concentrated in regions that have to be classified as DPLAs, whereas in France, Germany and Italy less than 50% of the pig population is located in such areas.

Only in The Netherlands is more than 50% of the cattle population held in DPLAs, followed by Belgium. The same is true for goats. In Italy and France the percentage for goats is less than 10%, even if the values for FMD is used. The number of sheep in DPLAs is highest in

Belgium, followed by The Netherlands. The percentage in Germany, France and Italy remains beneath 10%, as seen before for goats.

Figure 2.3a The share of livestock located in DPLAs for FMD per country

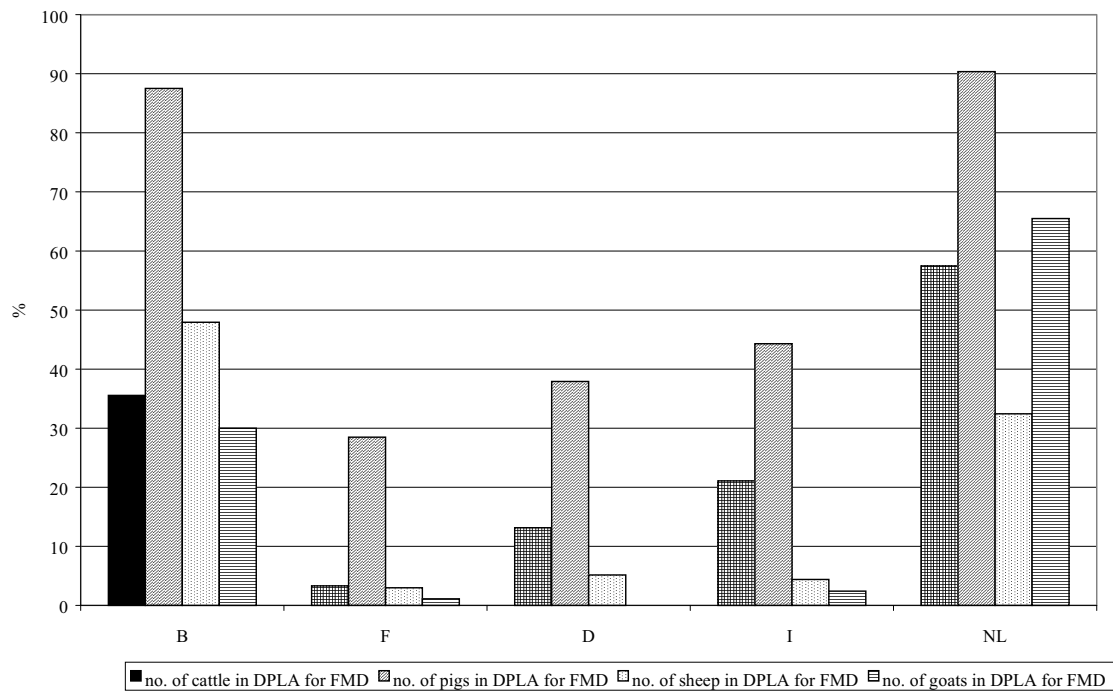
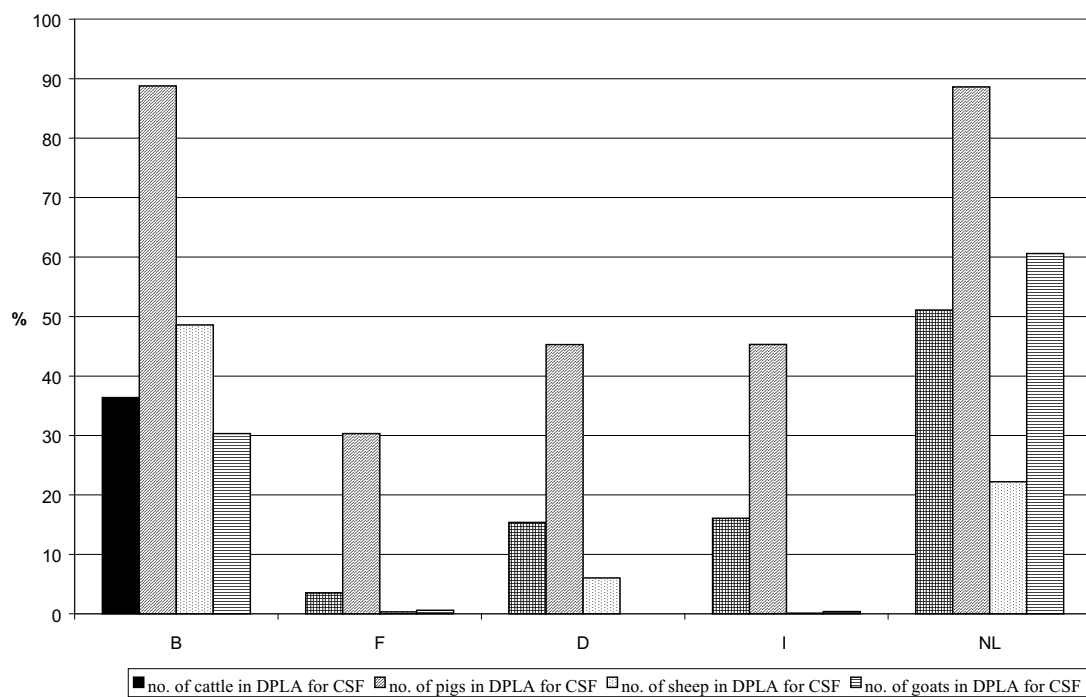
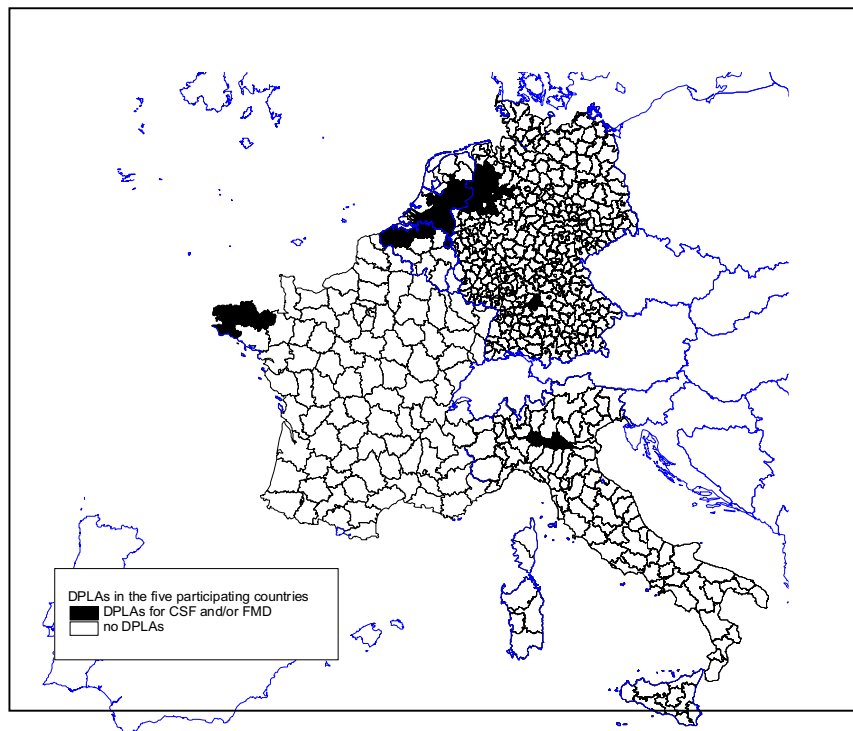


Figure 2.3b The share of livestock located in DPLAs for CSF per country



At a higher administrative level, the result is the spatial distribution pattern as shown in Figure 2.4. Besides the two regions in France and Italy, which are located in a large distance from the other high density areas; a continuous belt can be found reaching from Belgium and The Netherlands to northwestern Germany. In this high-density region about 25% of all pigs of the EU were produced in 1997 (ZMP 1998).

Figure 2.4 DPLAs for FMD and CSF in the five countries participating in the EU project



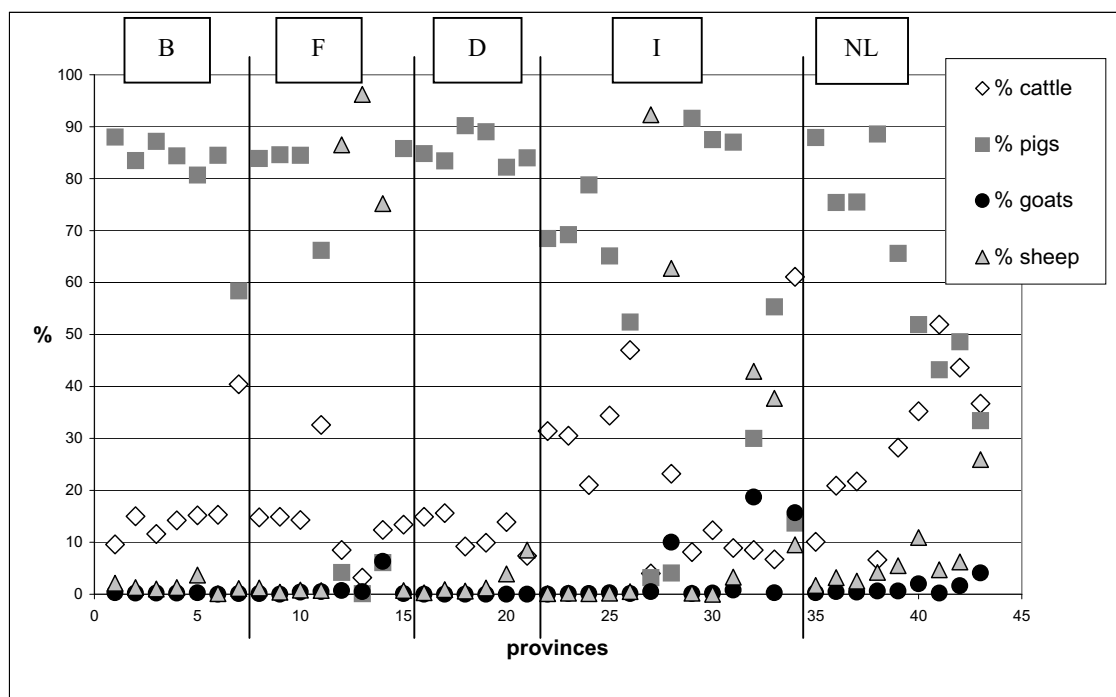
The detailed maps in the appendices show all municipalities classified as DPLAs. When comparing the results on the two administrative levels, one can see that some information is lost in the province³ level. So, for example, the province of Limburg in the Netherlands is classified as a DPLA although the southern municipalities only show a low or medium density. Several other examples can be found. The same is true for the opposite, an example is Cuneo (Piemonte) in Italy. Even though a cluster of DPLAs can be found on the municipality level, the province as a whole is classified as an SPLA for FMD and an MPLA for CSF.

In order to be able to estimate the distribution of the animal species in the DPLAs, the percentage of the species for the provinces in The Netherlands and Belgium, the regions in

³ In Germany: Landkreise (counties), in France: departments

Italy, the states (Bundesländer) in Germany and the departments in France, was calculated (regions with more than 450 animals/km²). From Figure 2.5 one can easily see that pigs are the dominating species in 29 of the 43 provinces. Only in the Italian region of Campagne are cattle the dominant species. On the other hand there are 5 regions on which sheep have a share of more than 60% of the animal population (France: Aveyron, Haut-Vienne, Deux Sevre; Italy: Sardengna, Sizilia). In the remaining 8 regions no dominant species can be found: Liège (B), Veneto (I), Calabria (I), Marche (I), Zuid-Holland (NL), Groningen (NL), Drenthe (NL), and Noord-Holland (NL).

Figure 2.5 Share of animal species at DPLA for FMD provinces



2.5 Final remarks

The presented definition makes it possible to compare municipalities on the EU level and to classify them according to their animal density. The three level classification system is a good and easy way to obtain an insight into the spatial pattern of DPLAs. This also makes it possible to calculate the economic risk in case of a disease outbreak. The classification on the municipality level presents a better and more precise picture than a classification based on the EUROSTAT statistical units. The disadvantage is the inhomogeneous database. This

inhomogeneity leads to sub-optimal results. A calculation based on the location of single farms (c.f. paper of Ehlers and Möller (Chapter3)) will show that in municipalities classified as SPLAs and MPLAs, clusters of farms may also show up that have extremely high animal densities.

One also has to keep in mind that the classification system, presented here, is only based on data sets from five EU member states. To use this definition as a basis for legal regulations, it should be modified on the basis of the data sets from all 15 member states. The presented maps only show the density and do not contain information about the risk of a disease outbreak, nor about the organisation of animal production.

Nevertheless it can be stated that the 5% of the municipalities, classified here as DPLAs are a good means of identifying regions with a very high concentration of animals that could be severely affected by FMD or CSF. This classification is also supported by the fact that the DPLAs cover about 5% of the area. The classification methodology can be transferred to other data sets, either on the EU level in total or for single countries.

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Data sources

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Italy: Istituto National di Statistica, 4th agricultural census 1990

Netherlands: CBS agricultural service, Landbouwtelling 1997

Appendix I.

Table I.A Calculation of DPLAs for FMD

| density classes | no. of communities | Cumulative no. of communities | share per density class | cumulative percentage | share of communities | share of area |
|--------------------|-----------------------|-------------------------------------|----------------------------|--------------------------|-------------------------|---------------|
| | no. | no. | % | % | % | % |
| 0 | 973 | 973 | 5.31 | 5.31 | | |
| 1-50 | 7,338 | 8,311 | 40.07 | 45.38 | | |
| 51-100 | 3,834 | 12,145 | 20.94 | 66.32 | | |
| 101-150 | 2,074 | 14,219 | 11.33 | 77.64 | 77.64 | 79.35 |
| 151-200 | 1,101 | 15,320 | 6.01 | 83.66 | | |
| 201-250 | 757 | 16,077 | 4.13 | 87.79 | | |
| 251-300 | 494 | 16,571 | 2.70 | 90.49 | | |
| 301-350 | 315 | 16,886 | 1.72 | 92.21 | | |
| 351-400 | 238 | 17,124 | 1.30 | 93.51 | | |
| 401-450 | 174 | 17,298 | 0.95 | 94.46 | 16.81 | 16.33 |
| 451-500 | 150 | 17,448 | 0.82 | 95.28 | | |
| 501-550 | 120 | 17,568 | 0.66 | 95.93 | | |
| 551-600 | 95 | 17,663 | 0.52 | 96.45 | | |
| 601-650 | 77 | 17,740 | 0.42 | 96.87 | | |
| 651-700 | 74 | 17,814 | 0.40 | 97.28 | | |
| 701-750 | 77 | 17,891 | 0.42 | 97.70 | | |
| 751-800 | 42 | 17,933 | 0.23 | 97.92 | | |
| 801-850 | 27 | 17,960 | 0.15 | 98.07 | | |
| 851-900 | 26 | 17,986 | 0.14 | 98.21 | | |
| 901-950 | 27 | 18,013 | 0.15 | 98.36 | | |
| 951-1000 | 19 | 18,032 | 0.10 | 98.47 | | |
| 1001-1050 | 26 | 18,058 | 0.14 | 98.61 | | |
| 1051-1100 | 25 | 18,083 | 0.14 | 98.74 | | |
| 1101-1150 | 11 | 18,094 | 0.06 | 98.80 | | |
| 1151-1200 | 24 | 18,118 | 0.13 | 98.94 | | |
| 1201-1250 | 16 | 18,134 | 0.09 | 99.02 | | |
| 1251-1300 | 12 | 18,146 | 0.07 | 99.09 | | |
| 1301-1350 | 10 | 18,156 | 0.05 | 99.14 | | |
| 1351-1400 | 13 | 18,169 | 0.07 | 99.21 | | |
| 1401-1450 | 12 | 18,181 | 0.07 | 99.28 | | |
| 1451-1500 | 6 | 18,187 | 0.03 | 99.31 | | |
| 1501-1550 | 7 | 18,194 | 0.04 | 99.35 | | |
| 1551-1600 | 11 | 18,205 | 0.06 | 99.41 | | |
| 1601-1650 | 6 | 18,211 | 0.03 | 99.44 | | |
| 1651-1700 | 4 | 18,215 | 0.02 | 99.46 | | |
| 1701-1750 | 5 | 18,220 | 0.03 | 99.49 | | |
| 1751-1800 | 8 | 18,228 | 0.04 | 99.54 | | |
| 1801-1850 | 10 | 18,238 | 0.05 | 99.59 | | |
| 1851-1900 | 3 | 18,241 | 0.02 | 99.61 | | |
| 1901-1950 | 1 | 18,242 | 0.01 | 99.61 | | |
| 1951-2000 | 4 | 18,246 | 0.02 | 99.63 | | |
| 2001-3000 | 40 | 18,286 | 0.22 | 99.85 | | |
| 3001-4000 | 19 | 18,305 | 0.10 | 99.96 | | |
| 4001-5000 | 6 | 18,311 | 0.03 | 99.99 | | |
| 5001-6000 | 2 | 18,313 | 0.01 | 100.00 | 5.54 | 4.32 |

Appendix I. - continued

Table I.B Calculations of DPLAs for CSF

| density classes | no. of communities | Cumulative no. of communities | share per density class | cumulative percentage | share of communities | share of area |
|--------------------|-----------------------|-------------------------------------|----------------------------|--------------------------|-------------------------|---------------|
| | no. | no. | % | % | % | % |
| 0 | 2,873 | 2,873 | 14.46 | 14.46 | | |
| 1-50 | 12,705 | 15,578 | 63.94 | 78.40 | 78.40 | 81.71 |
| 51-100 | 1,507 | 17,085 | 7.58 | 85.98 | | |
| 101-150 | 769 | 17,854 | 3.87 | 89.85 | | |
| 151-200 | 445 | 18,299 | 2.24 | 92.09 | | |
| 201-250 | 296 | 18,595 | 1.49 | 93.58 | | |
| 251-300 | 243 | 18,838 | 1.22 | 94.80 | 16.41 | 13.88 |
| 301-350 | 160 | 18,998 | 0.81 | 95.61 | | |
| 351-400 | 131 | 19,129 | 0.66 | 96.27 | | |
| 401-450 | 97 | 19,226 | 0.49 | 96.75 | | |
| 451-500 | 81 | 19,307 | 0.41 | 97.16 | | |
| 501-550 | 78 | 19,385 | 0.39 | 97.55 | | |
| 551-600 | 65 | 19,450 | 0.33 | 97.88 | | |
| 601-650 | 52 | 19,502 | 0.26 | 98.14 | | |
| 651-700 | 37 | 19,539 | 0.19 | 98.33 | | |
| 701-750 | 31 | 19,570 | 0.16 | 98.49 | | |
| 751-800 | 25 | 19,595 | 0.13 | 98.61 | | |
| 801-850 | 23 | 19,618 | 0.12 | 98.73 | | |
| 851-900 | 25 | 19,643 | 0.13 | 98.85 | | |
| 901-950 | 25 | 19,668 | 0.13 | 98.98 | | |
| 951-1000 | 20 | 19,688 | 0.10 | 99.08 | | |
| 1001-1050 | 8 | 19,696 | 0.04 | 99.12 | | |
| 1051-1100 | 18 | 19,714 | 0.09 | 99.21 | | |
| 1101-1150 | 11 | 19,725 | 0.06 | 99.27 | | |
| 1151-1200 | 13 | 19,738 | 0.07 | 99.33 | | |
| 1201-1250 | 6 | 19,744 | 0.03 | 99.36 | | |
| 1251-1300 | 7 | 19,751 | 0.04 | 99.40 | | |
| 1301-1350 | 12 | 19,763 | 0.06 | 99.46 | | |
| 1351-1400 | 2 | 19,765 | 0.01 | 99.47 | | |
| 1401-1450 | 7 | 19,772 | 0.04 | 99.50 | | |
| 1451-1500 | 4 | 19,776 | 0.02 | 99.52 | | |
| 1501-1550 | 8 | 19,784 | 0.04 | 99.56 | | |
| 1551-1600 | 6 | 19,790 | 0.03 | 99.59 | | |
| 1601-1650 | 5 | 19,795 | 0.03 | 99.62 | | |
| 1651-1700 | 3 | 19,798 | 0.02 | 99.63 | | |
| 1701-1750 | 8 | 19,806 | 0.04 | 99.67 | | |
| 1751-1800 | 2 | 19,808 | 0.01 | 99.68 | | |
| 1801-1850 | 0 | 19,808 | 0.00 | 99.68 | | |
| 1851-1900 | 5 | 19,813 | 0.03 | 99.71 | | |
| 1901-1950 | 7 | 19,820 | 0.04 | 99.74 | | |
| 1951-2000 | 1 | 19,821 | 0.01 | 99.75 | | |
| 2001-3000 | 30 | 19,851 | 0.15 | 99.90 | | |
| 3001-4000 | 15 | 19,866 | 0.08 | 99.97 | | |
| 4001-5000 | 3 | 19,869 | 0.02 | 99.99 | | |
| 5001-6000 | 2 | 19,871 | 0.01 | 100.00 | 5.20 | 4.41 |

Appendix I. - continued

Table I.C The top 40 of the DPLA ranking for FMD (>450 animals/km²)

| Community | Province | | total land (km ²) | animals/ km ² | cattle/ km ² | pigs/ km ² | goats/ km ² | sheep/ km ² |
|------------------------|-----------------|----|-------------------------------------|-----------------------------|----------------------------|--------------------------|---------------------------|---------------------------|
| Dentergem | West-Vlaanderen | B | 25.94 | 2,620 | 258 | 2,319 | 8 | 35 |
| San Fiorano | Lombardia | I | 8.95 | 2,645 | 258 | 2,386 | 1 | 0 |
| Casaletto di Sopra | Lombardia | I | 8.59 | 2,650 | 207 | 2,443 | 0 | 0 |
| Kortemark | West-Vlaanderen | B | 55.00 | 2,693 | 187 | 2,463 | 5 | 39 |
| Ichtegem | West-Vlaanderen | B | 45.33 | 2,697 | 227 | 2,413 | 5 | 53 |
| Landerd | N-Brabant | NL | 70.38 | 2,699 | 232 | 2,437 | 0 | 30 |
| Meulebeke | West-Vlaanderen | B | 29.35 | 2,701 | 184 | 2,482 | 7 | 28 |
| Groenlo | Gelderland | NL | 9.29 | 2,710 | 332 | 2,355 | 0 | 22 |
| Pagazzano | Lombardia | I | 5.04 | 2,730 | 272 | 2,458 | 0 | 0 |
| Ambt Delden | Overijssel | NL | 82.81 | 2,818 | 257 | 2,519 | 6 | 37 |
| Someren | N-Brabant | NL | 80.10 | 2,853 | 208 | 2,622 | 6 | 18 |
| Maasdonk | N-Brabant | NL | 37.02 | 2,912 | 295 | 2,541 | 34 | 41 |
| Morengo | Lombardia | I | 10.28 | 2,917 | 54 | 2,863 | 0 | 0 |
| Vottignasco | Piemonte | I | 8.43 | 3,058 | 272 | 2,780 | 1 | 4 |
| Son en Breugel | N-Brabant | NL | 26.09 | 3,079 | 173 | 2,878 | 1 | 27 |
| Koekelare | West-Vlaanderen | B | 39.19 | 3,088 | 222 | 2,844 | 5 | 16 |
| Torhout | West-Vlaanderen | B | 45.23 | 3,180 | 254 | 2,873 | 7 | 46 |
| Gemert-Bakel | N-Brabant | NL | 123.05 | 3,213 | 211 | 2,984 | 3 | 15 |
| Asten | N-Brabant | NL | 70.00 | 3,241 | 257 | 2,969 | 1 | 14 |
| Hooglede | West-Vlaanderen | B | 37.84 | 3,245 | 141 | 3,056 | 5 | 43 |
| Baarle-Hertog | Antwerpen | B | 7.48 | 3,320 | 367 | 2,917 | 6 | 30 |
| Wehl | Gelderland | NL | 23.53 | 3,347 | 251 | 3,054 | 1 | 41 |
| Tielt | West-Vlaanderen | B | 68.50 | 3,533 | 302 | 3,202 | 4 | 25 |
| Sint-Oedenrode | N-Brabant | NL | 64.55 | 3,598 | 348 | 3,201 | 9 | 40 |
| Venray | Limburg | NL | 146.05 | 3,600 | 124 | 3,443 | 3 | 30 |
| Cumignano sul Naviglio | Lombardia | I | 6.63 | 3,661 | 375 | 3,286 | 0 | 0 |
| Reusel- De Mierden | N-Brabant | NL | 78.05 | 3,689 | 198 | 3,466 | 11 | 14 |
| Ardoeie | West-Vlaanderen | B | 34.58 | 3,773 | 159 | 3,561 | 7 | 46 |
| Wingene | West-Vlaanderen | B | 68.42 | 3,774 | 280 | 3,457 | 6 | 31 |
| Veghel | N-Brabant | NL | 78.18 | 3,882 | 374 | 3,470 | 1 | 38 |
| Ruiselede | West-Vlaanderen | B | 30.2 | 3,887 | 268 | 3,590 | 8 | 21 |
| Deurne | N-Brabant | NL | 118.00 | 3,901 | 216 | 3,661 | 6 | 19 |
| Meijel | Limburg | NL | 19.84 | 4,148 | 345 | 3,786 | 0 | 17 |
| Sint Anthonis | N-Brabant | NL | 99.11 | 4,152 | 277 | 3,841 | 8 | 25 |
| Bernheze | N-Brabant | NL | 89.87 | 4,176 | 342 | 3,748 | 36 | 50 |
| Pittem | West-Vlaanderen | B | 34.42 | 4,361 | 180 | 4,159 | 5 | 18 |
| Staden | West-Vlaanderen | B | 46.24 | 4,388 | 116 | 4,239 | 9 | 24 |
| Lichtervelde | West-Vlaanderen | B | 25.93 | 4,491 | 260 | 4,192 | 10 | 30 |
| Boekel | N-Brabant | NL | 34.49 | 5,478 | 329 | 5,112 | 2 | 36 |
| Mierlo | N-Brabant | NL | 17.87 | 5,875 | 142 | 5,712 | 0 | 21 |

Appendix II. – Density classification for Belgium, The Netherlands, Germany, France and Italy

Figure II.A Density classification for Belgium (1996).

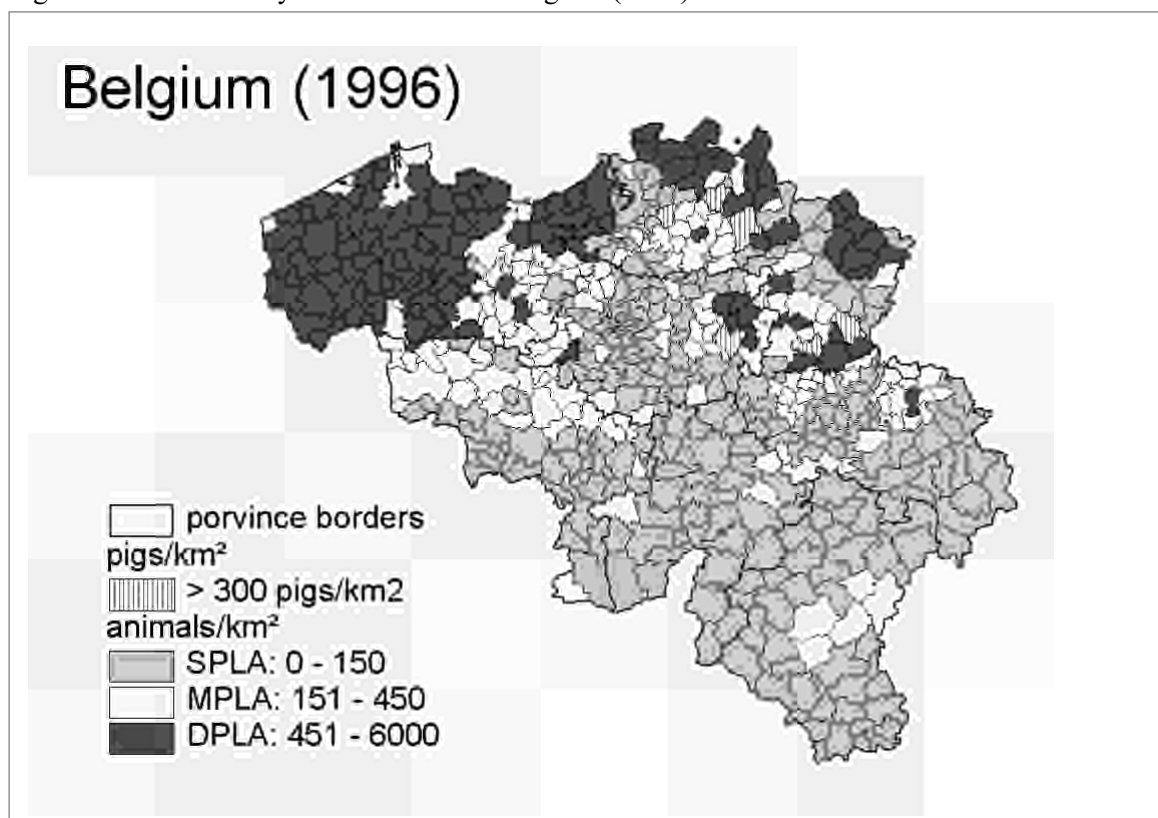
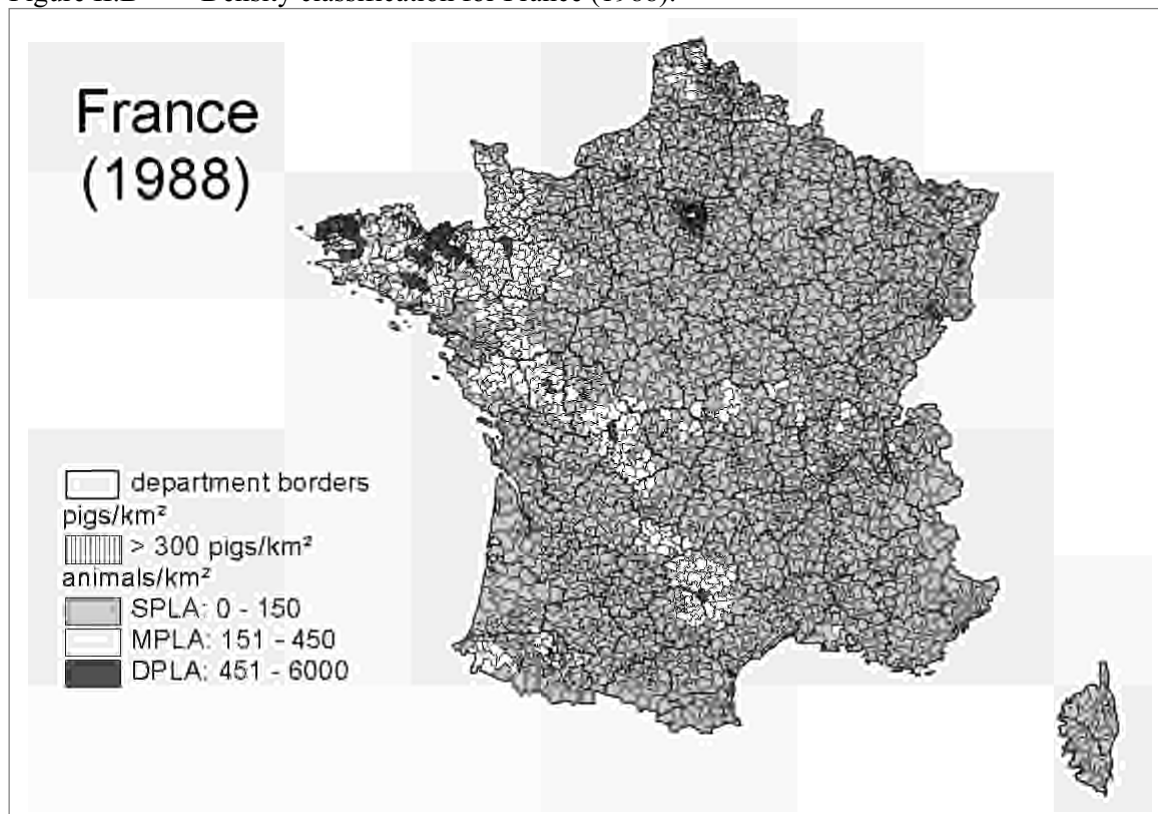


Figure II.B Density classification for France (1988).



Appendix II. - Continued

Figure II.C Density classification for NorthWest Germany (1996).

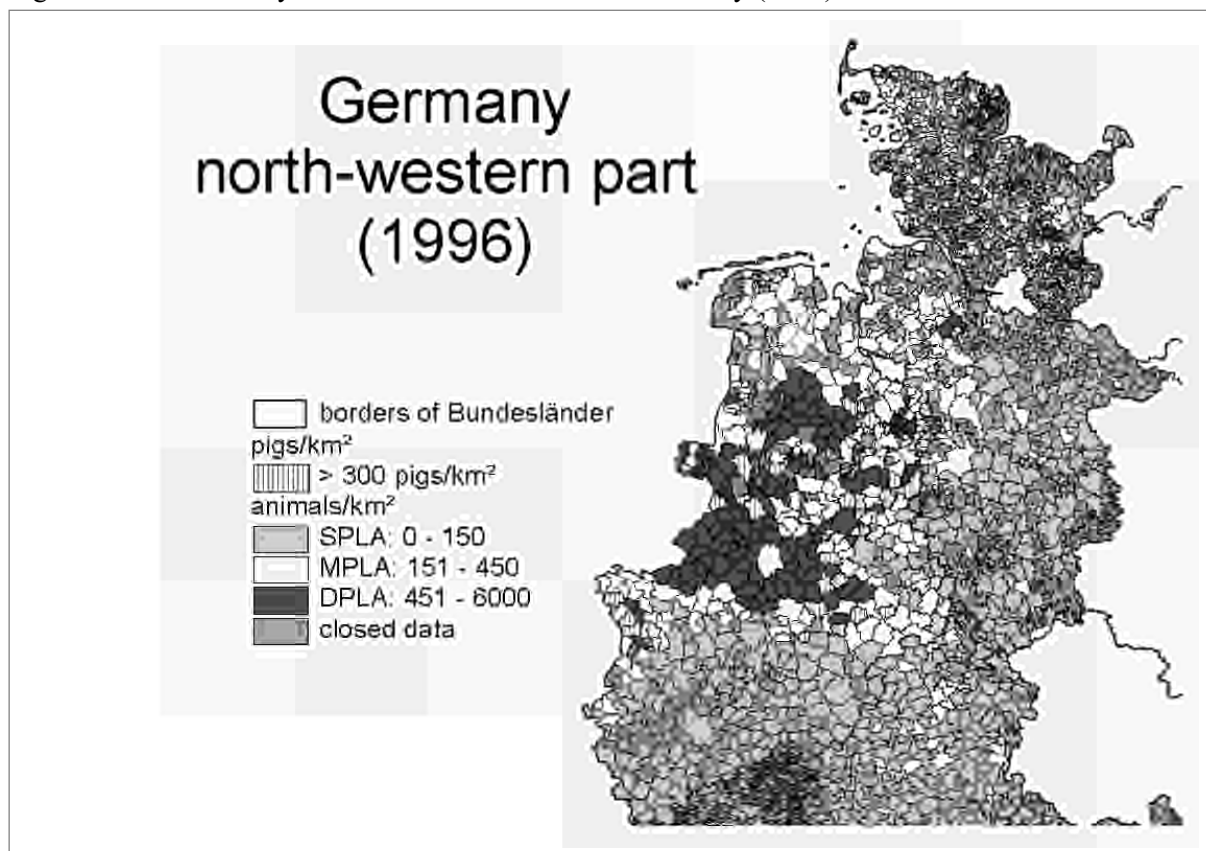
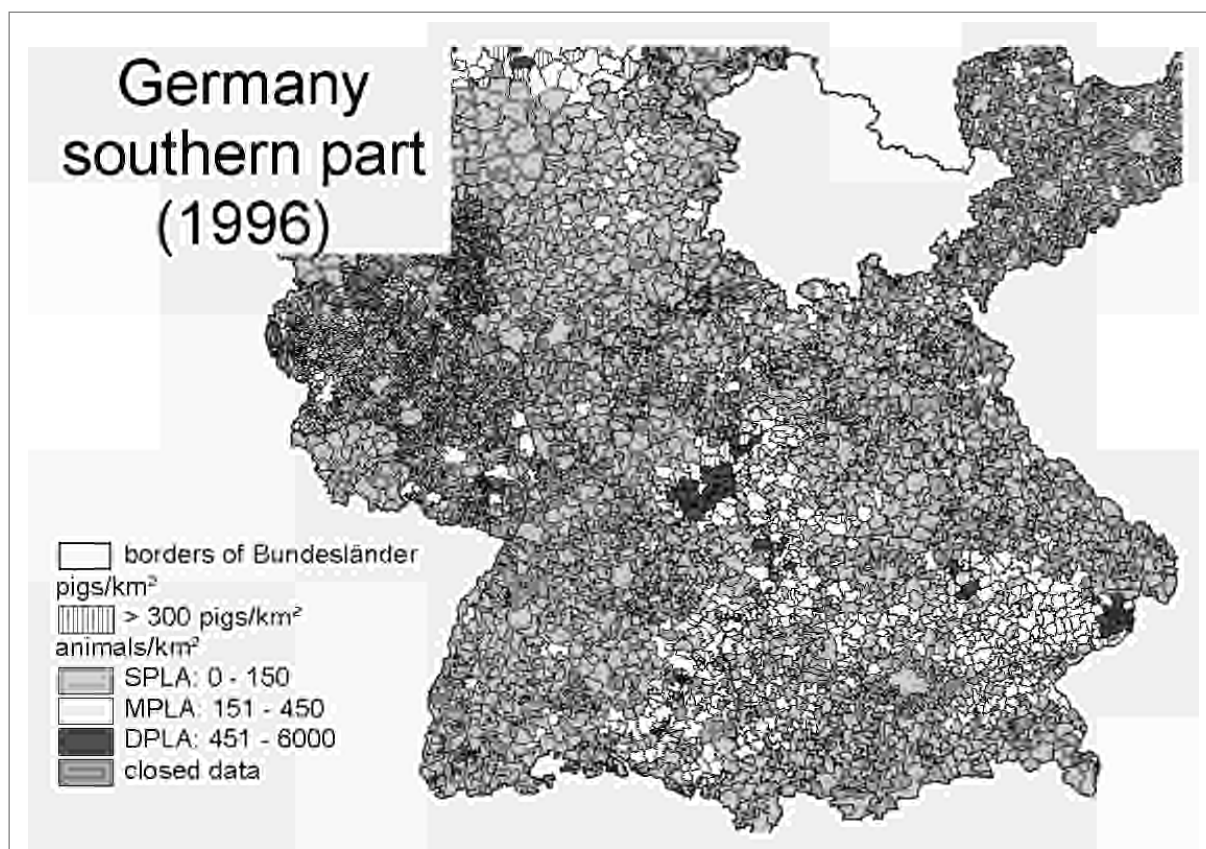


Figure II.D Density classification for Southern Germany (1996).



Appendix II. - Continued

Figure II.E Density classification for the northern part of Italy (1990).

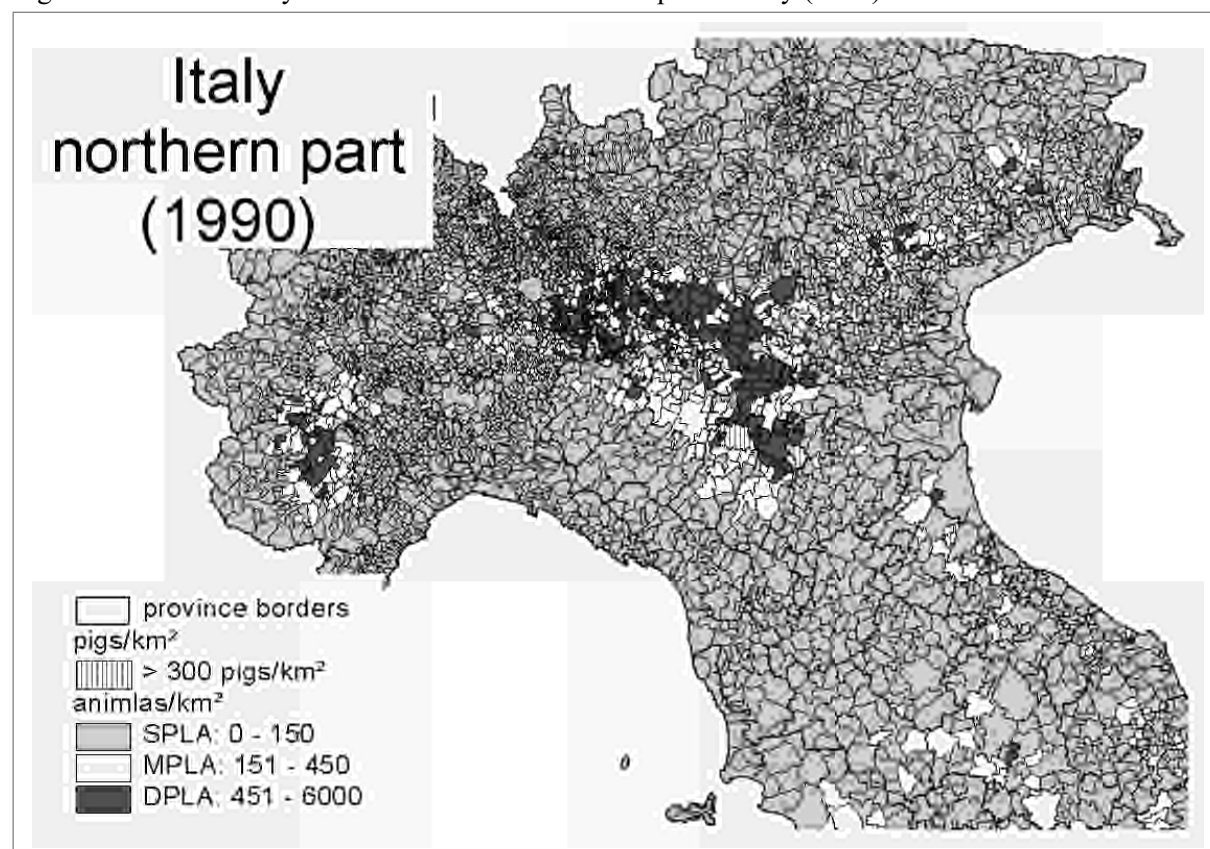
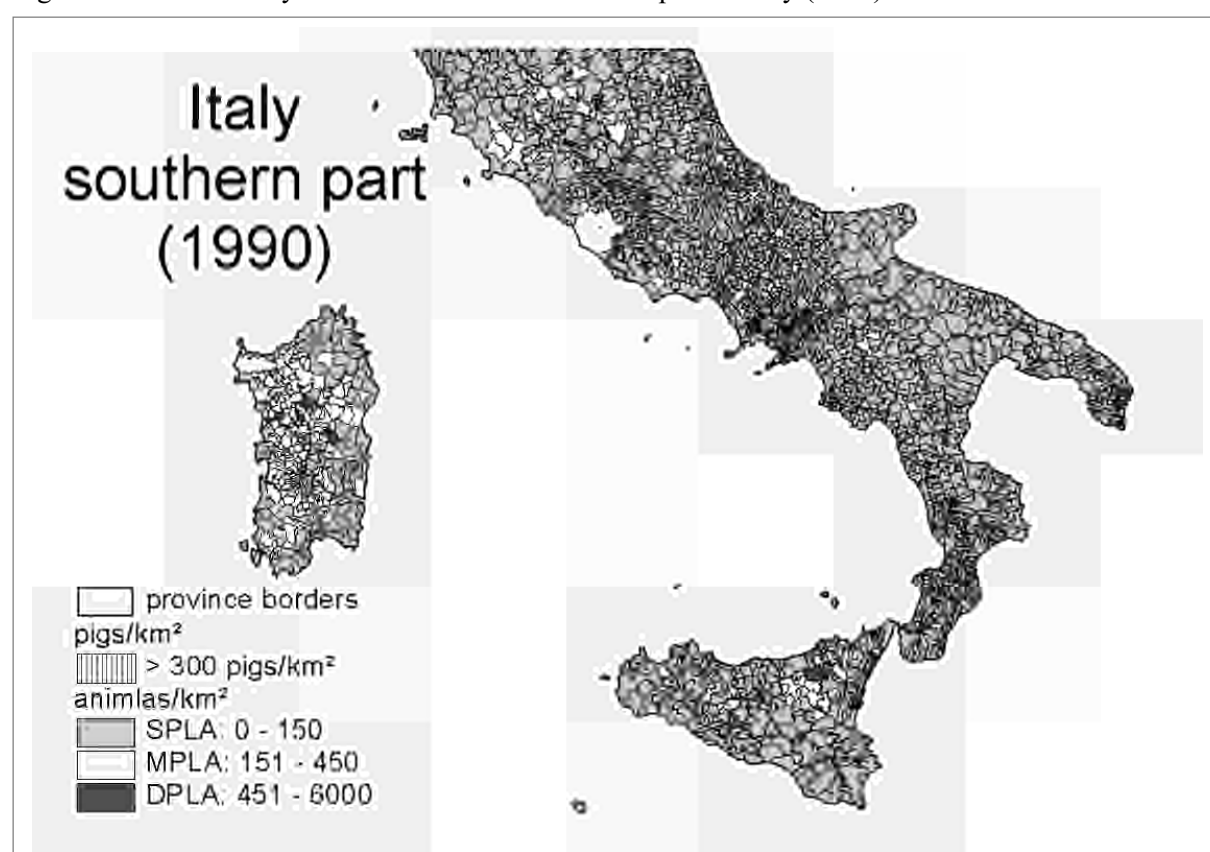
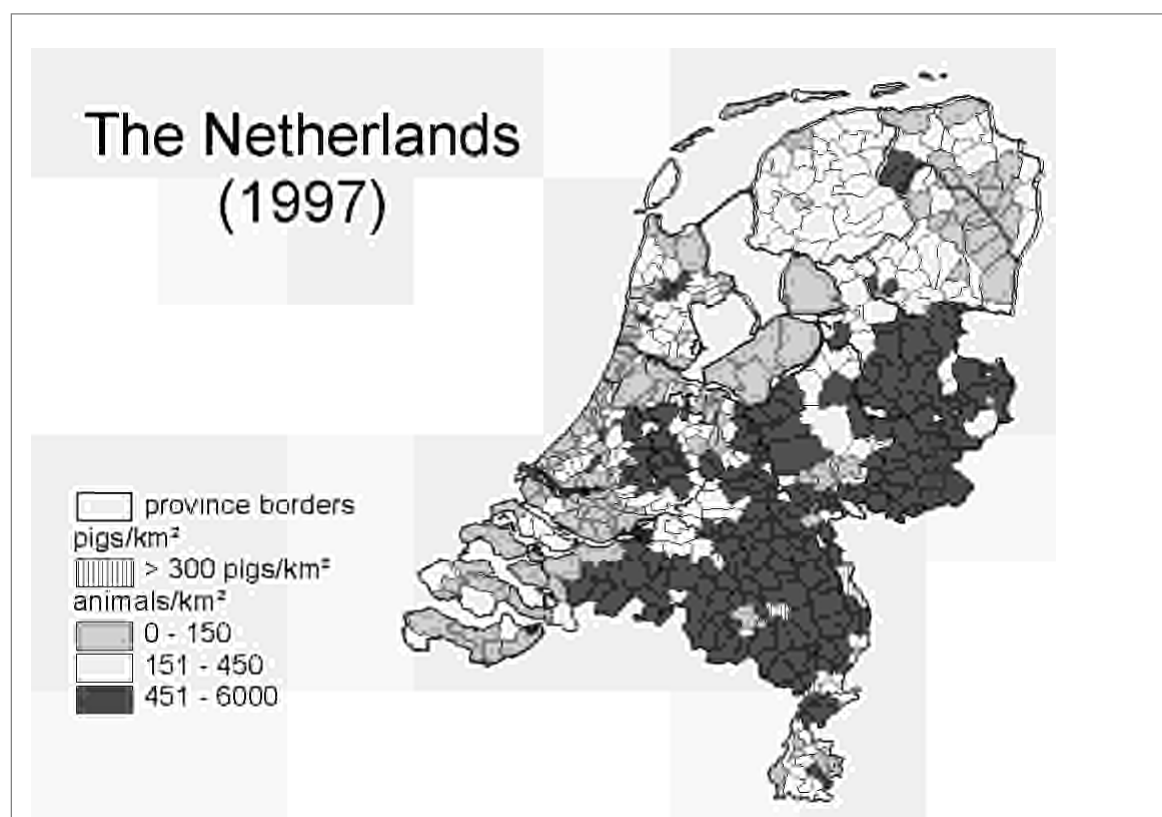


Figure II.F Density classification for the southern part of Italy (1990).



Appendix II. - Continued

Figure II.G Density classification for The Netherlands (1997).



Veterinary Information System: A GIS-Based Toolbox for Handling and Analysing Epidemiological Risk Factors in Densely Populated Livestock Areas

M. Ehlers and M. Möller

3.1 Introduction

Geographic Information Systems (GIS) are very powerful and flexible software tools for the effective management of spatially referenced data (e.g. geodata). Coupling database and GIS technology provides the tools for a detailed analysis of spatial patterns and distributions in veterinary applications. A specific toolbox was developed so that 'GIS laymen' can make use of this powerful technology without having to learn complex Geoinformatics. The complete function, however, as provided by a desktop GIS such as ArcView is still available to the user.

Using a specific script programming language, the toolbox adds statistical features for density analysis and risk assessment to the GIS, most importantly the calculation of indices such as the Lorenz curve, the GINI index and a kernel tool for density estimation. This software was employed for the analysis of livestock data in very densely populated areas of the European Union (EU). The results were used for definition and analysis of animal disease risk areas. The veterinary GIS (VetGIS) toolbox was successfully tested and applied by the contributing partners of the EU project "Development of prevention and control strategies to address animal health and related problems in densely populated livestock areas of the Community" (FAIR CT 97-3566).

3.2 Geoinformatics as a New Discipline

Geoinformatics is the art, science or technology dealing with the acquisition, storage, processing, production, presentation, and dissemination of geoinformation (Ehlers 1993). It consists of two main components, one related to the geographical or spatial content and the other to the basic information technology (IT) disciplines (Table 3.1). Geoinformatics is

highly interdisciplinary, connecting several basic sciences to form a new evolving scientific discipline (Ehlers, 2000). This new field, however, is mainly driven by applications, used in particular to solve spatial problems with its main tool known as a Geographic Information System (GIS).

Table 3.1 Geo and Informatics Components of Geoinformatics

| GEO | INFORMATICS |
|---------------------------------|-------------------------------|
| Geography | Information Technology |
| Cartography | Computer Science & Technology |
| Geodesy & Surveying | Information Theory |
| Photogrammetry & Remote Sensing | Database Management |
| Spatial Planning | Mathematics, Statistics |

3.3 Geographic Information Systems (GIS) for Veterinary Applications

A GIS is used to collect, store, manage, analyse and present geometric information together with its semantic content. Usually, the geometric information is based on geographic or geodetic coordinates (map data). GIS's are powerful software tools for the effective management of spatially referenced data (Aronoff 1989). Coupling digital databases and GIS technology provides the means for a detailed analysis of spatial patterns and distributions. For example, a GIS can be used to calculate the number of animals inside and/or around a specific area as well as to identify their locations. Another problem is the identification of livestock and holders in a specified zone around a location of interest. This is typical for prevention measures in epidemiological veterinary applications. A GIS can handle identification and calculation of animals inside a buffer zone in an automated manner.

Identification and the spatial separation of densely populated livestock areas is a critical task because strategies for fighting animal diseases such as Classical Swine Fever (CSF) or Foot-and-Mouth Disease (FMD) depend heavily on the density and distribution of animals. Typically, circles with appropriate radiuses or general polygonal objects (depending on the risk factors of the disease) are drawn around the location of an outbreak. Within these circles, restrictions are imposed ranging from killing the animals in the inner circle to prohibiting trade in the outer circle. All of these tasks can readily be solved using existing GIS

technology. Density calculation and risk assessment, however, require new solutions that are currently not implemented in standard GIS's. Consequently, they have to be added to address the needs for veterinary applications.

Modern GIS's are flexible software tools that allow the design of user-specific programs or scripts for special analysis tasks. This can be done for virtually any spatial application. These special tools can be incorporated in a user-friendly toolbox, a so-called 'expert shell'. These shells are usually embedded in a Graphical User Interface (GUI) under a common Windows environment. However, access to, and handling of, spatial data can pose some problems as all GIS use different proprietary data formats. But the advent of GIS data translators and more commonly used standards makes data exchange and transfer now feasible even for novice users. For example, in many administrations the surveying and cadastral offices manage digital map data in CAD formats. Using standard translators, this data can now be quickly imported into most current GIS's in order to build an essential spatial database for virtually any application with a geographic component.

3.4 The GIS Part in the FAIR EU Project

Geoinformatics techniques were used in the European Union (EU) project "Development of prevention and control strategies to address animal health and related problems in densely populated livestock areas of the community" (FAIR CT 97-3566). Our subproject focussed on the geographic separation of different spatial densities of European livestock areas.

For an effective spatial and statistical analysis, special GIS techniques were implemented and the underlying basic GIS capabilities had to be modified and extended to address the needs of modelling and simulating spatial patterns of epidemiological risks in livestock. The main target of the project was to generate a user-friendly GIS shell for veterinary applications. This VetGIS toolbox enables the users to define, locate and separate densely populated livestock areas (DPLAs) in the EU and to perform analytical and statistical tasks using their specific data. First investigations were carried out predominantly with pig data but the techniques can be applied to other animals (poultry, cattle) as well (Möller and Ehlers, 2000).

3.5 Design of the VetGIS Toolbox

3.5.1 Program Considerations

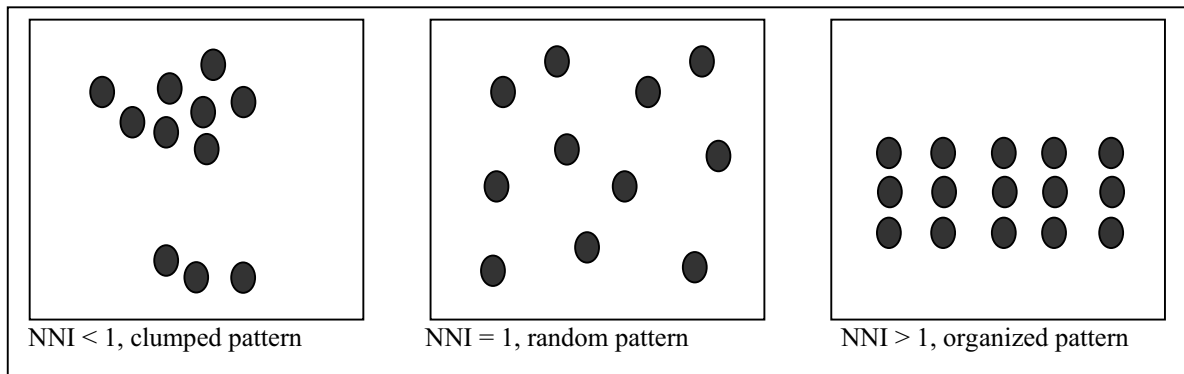
The development of the toolbox was done in the programming environment of the low cost desktop GIS ArcView (ESRI 1996a). ArcView is completely written in the object orientated programming language AVENUE and can be extended using flexible scripts which are also written in AVENUE (ESRI 1996b). Another advantage is the large worldwide user community of ArcView that shares newly developed extensions through the Internet. With a total number of more than 60,000 installed systems, the software of the Environmental Systems Research Institute (ESRI) is the GIS world leader. For all these reasons, we chose ArcView to guarantee future compatibility and sustainability.

Costs for the program itself are quite reasonable and well within most budgets. For the management of very large datasets, however, ArcView as a desktop GIS has its limitations. Therefore a professional GIS and a geodata server environment is strictly recommended for large-scale (e.g. international or EU) activities. ESRI's professional and more expensive GIS software is Arc/Info that cooperates with the desktop GIS ArcView (ESRI 1996a). Both GIS data formats are compatible and provide a very efficient geodata management system.

3.5.2 Nearest Neighbour Index (NNI)

An often-used tool for the calculation of distribution patterns is the Nearest Neighbour Index (NNI). The NNI is expressed in numerical values related to how clustered or dispersed measurements are within a specified area. A value of less than 1 indicates a clumped distribution, a value of 1 indicates a random distribution and an NNI greater than 1 indicates an organised distribution (Figure 3.1). Using additional descriptive statistics like the average animal density for an investigated area, the NNI gives an indication of the accumulation within this region. This is very helpful for the determination of risk factors regarding animal diseases. A small NNI value together with a large number of animals indicates spatially concentrated patterns of large animal densities that may pose a higher risk than indicated by the average density as the only measurement.

Figure 3.1 Distribution Pattern Detected by the Nearest Neighbour Index (NNI)



The NNI is the calculated ratio of observed and expected distances between every point (e.g. stable, herd, etc.) inside an area.

$$NNI = \frac{D_{obs.}}{D_{exp.}}$$

$$D_{exp.} = \frac{1}{2} * \sqrt{A}$$

where:

$D_{obs.}$ = the average of the observed distances between each point (holder, herd) and its nearest neighbour

$D_{exp.}$ = the expected average distance

A = the average density of points (holders, herds) per km² in the region (Güssefeld 1996).

3.5.3 GINI Index and Lorenz Curve

Another VetGIS tool was developed to calculate the GINI index (GI) as a value and plot the results as a chart which is called a 'Lorenz curve' (Güssefeld 1996):

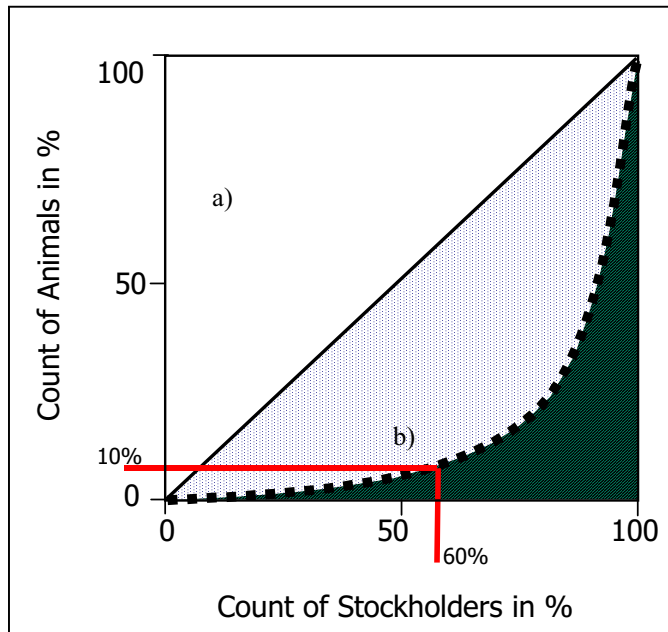
$$GINI = 0.5 \sum_{i=1}^n |x_i - y_i|$$

where y_i and y_i are the cumulative counts of the two parameters to be investigated.

With the Lorenz curve, two related parameters (i.e. herd sizes in livestock production vs. number of herds) can be analysed. If all herds in a particular region were of the same size, the graph would look like the solid line a) in Figure 3.2. For an uneven distribution (e.g. 10% of the animals in a region belong to 60% of the farms and 40% of the farmers own 90% of the animals), the Lorenz curve displays an exponential behaviour as shown in the dotted curve b) in Figure 3.2. The more exponential the distribution is, the smaller the GI will become.

Together with the NNI the GI is another indicator of concentration in an area of intensive animal production.

Figure 3.2 The Lorenz Curve



3.5.4 Kernel Estimation

The Kernel Estimation tool (KE) interpolates the animal density within a specific area of interest, e.g. a circle around a specific herd. The buffer size (radius) of the surrounding circle is determined by the chosen bandwidth of the estimation. For Classical Swine Fever eradication, measures are related to an area within a 1 km radius. Therefore, a default value for the buffer size is set to 1 km. The size is variable, however, according to the user specification. Other geometric buffer features based on interactively drawn polygons are also possible. Ignoring any edge correction the animal density within the buffer is calculated as:

$$\hat{\lambda}_{\tau}(s) = \sum_{h_i \leq \tau} \frac{3}{\pi \tau^2} \left(1 - \frac{h_i^2}{\tau^2} \right)^2$$

with

$\hat{\lambda}_{\tau}(s)$ = estimated density, within a bandwidth τ for a herd of interest s

h_i = distance between the herd on interest and a surrounding herd

τ = bandwidth of the estimation (buffer size)

It is assumed that the risk factor of a potential infection source for a herd of interest decreases with decreasing animal density. The KE value delivers an interpolated ‘average animal

density' for every location. The KE has no dimension; it depends only on the number of animals and the distance of herds in a specified area around a herd of interest. The KE tool, however, can only function when the data is incorporated in the underlying GIS.

All developed VetGIS tools presented in this paper, together with an example demonstration project and a short manual for the use of the tools in the ArcView environment can be found at: <http://www.ispa.uni-vechta.de/projects/fair/germ.html#tools>. The tools are very easy to handle and can be used after a short training period for efficient data analysis. In addition, the whole GIS function as provided by ArcView is also available to the user after installing the tools. A prerequisite however, is the availability of the basic ArcView GIS module. The VetGIS tools are designed to serve the needs of veterinarians.

3.6 Data

The ISPA is located in a densely populated livestock area and its commission is to analyze the region's spatial and economic organizational structure. Veterinarians, on the other hand, are also interested in the results of GIS based statistical spatial analyses. In strong cooperation with the veterinary office of the County of Osnabrück in Lower Saxony we worked with the County's livestock holders database (home address, number and kind of animals, visits of veterinarians, animal diseases, etc.). The area of the county is about 2100 km² separated into 32 municipalities.

Unfortunately, the point data is related to the home addresses of the farmers which may falsify to some degree the results of the spatial analysis (herds and holders are assumed to be at the same geographic location). However, this geographical data is the most exact data available in Germany where privacy laws are strictly imposed and enforced.

3.7 Statistical Risk Analysis

For the identification and ranking of livestock areas, the animal density is an appropriate measure. In our study, for example, we use a simple ratio between the number of pigs and the area of an administrative unit (e.g. a municipality). In the County of Osnabrück, for example, 18 of the 32 inspected municipalities have a density of more than 300 pigs/km² (Figure 3.3).

A density of more than 300 pigs/km² has been found to be a useful threshold for the declaration of an epidemiological risk area (Michel and de Vos, 2000). Table 3.2 presents the threshold values that were determined by the EU project to differentiate between densely, midsize, and sparsely populated regions.

Figure 3.3 Pig Density (pigs/km²) for the County of Osnabrück (1998)

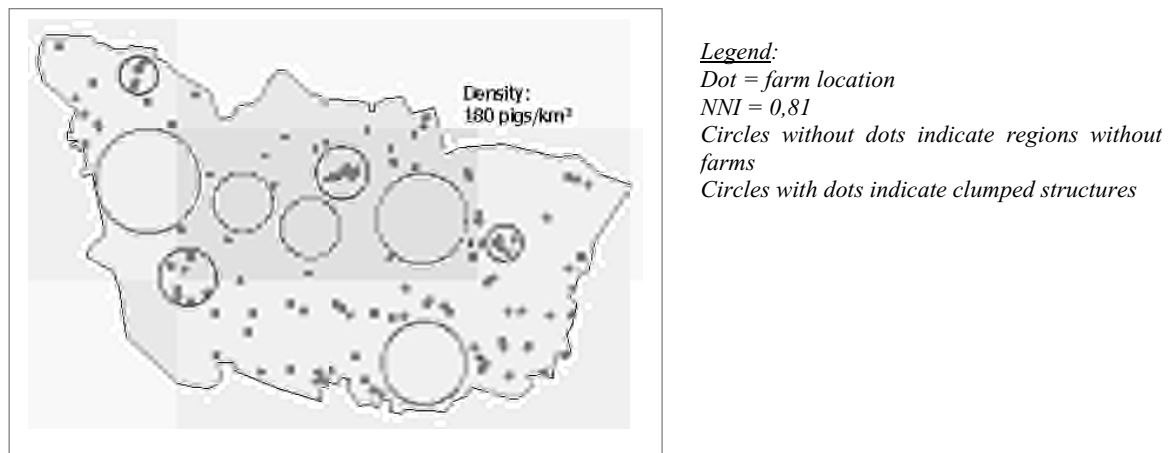


Table 3.2 Differentiation Scheme

| Denomination | pigs/km ² |
|--|----------------------|
| Sparsely populated livestock area (SPLA) | 0 – 50 |
| Midsize populated livestock area (MPLA) | > 50 – 300 |
| Densely populated livestock area (DPLA) | > 300 |

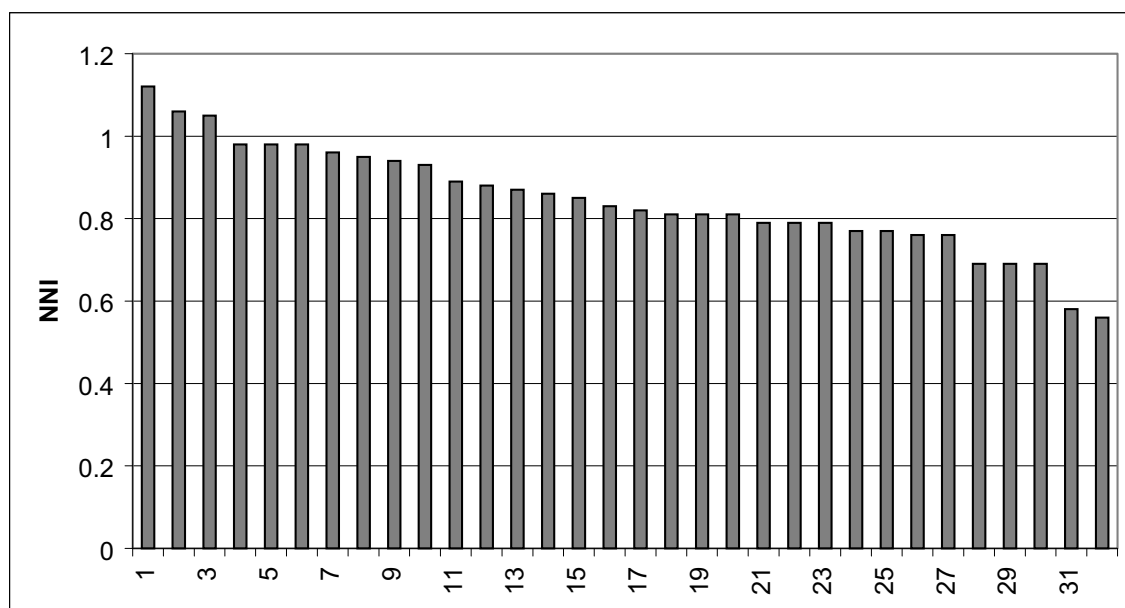
By analyzing the spatial distribution of farms in the municipalities with less than 300 pigs/km² (by definition an MPLA), some clusters and clumps of concentration can be found using the VetGIS tools. The municipality ‘Bramsche’ with an overall density of 180 pigs/km² is a good example (Figure 3.4).

Figure 3.4 MPLA Municipality Bramsche



The NNI for this region is 0.81, which indicates a strongly clumped distribution pattern. Some farms are very close to their neighbours, which leads to densities of more than 4,800 pigs/km² in some areas of this MPLA. This value was calculated inside a buffer zone of exactly 1 km² around every farm location. Figure 3.5 presents the NNI for 32 municipalities in this county. Municipalities 1 – 11 have an NNI of about 1, an indication for a random distribution pattern. All other 21 municipalities display more or less clumped farm location patterns.

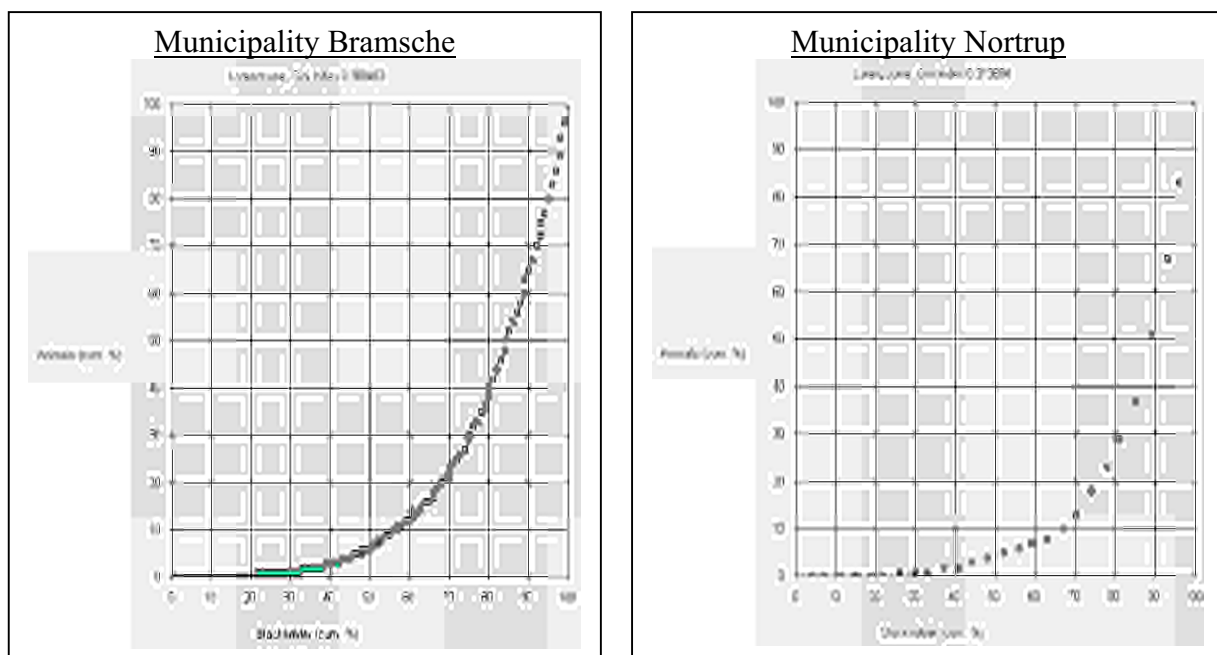
Figure 3.5 NNI's for 32 Municipalities in Osnabrück County



A long-term trend in agriculture is the concentration of large animal herds at a small number of farm locations (Windhorst, 1992). This is especially true for pigs. Mainly economic reasons lead to the development of industrialized pork production in Germany, which is mainly located in the Western part of Lower Saxony. A good measurement instrument for such a concentration is the GINI Index GI (see above). For the municipality Bramsche, an overall GI of 0.38 was calculated using the VetGIS tool.

Figure 3.6 presents the Lorenz curve and the GI for the municipality of Bramsche and illustrates the cumulative distribution of animals and holders in this region. It can be seen that 10% of the holders possess 40% of the animals. On the other hand, 50% of the holders possess only 7% of the animals. An extreme example for an unequal distribution is the municipality Nortrup where 50% of all pigs belong to only 10% of the holders (Figure 3.6). An overall comparison of the GI is given in Table 3.3.

Figure 3.6 Plotted Lorenz Curve and GI for the Municipality Bramsche, respectively Nortrup



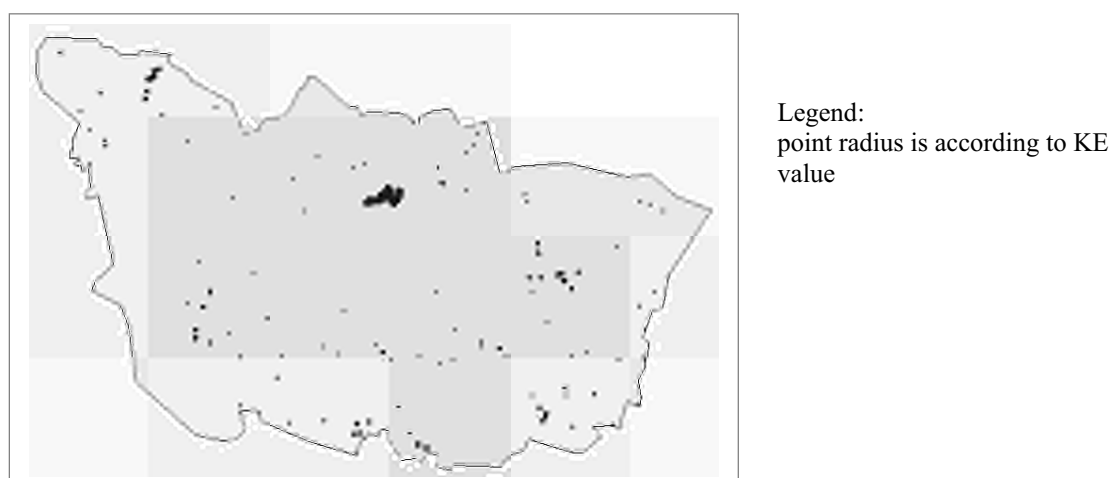
Today, the only operational way to determine the risk factors for densely populated livestock areas is to calculate the ratio of the number of animals per area (see above). As we have shown, a more detailed analysis is necessary and feasible if exact animal numbers and farm locations are known.

Table 3.3 GINI Indices for the County of Osnabrück

| Municipality | N° pig hold. | pigs/km ² | GI | Municipality | N° pig hold. | pigs/km ² | GI |
|----------------|--------------|----------------------|------|---------------|--------------|----------------------|------|
| Nortrup | 27 | 222 | 0,31 | Bad Laer | 100 | 308 | 0,40 |
| Bissendorf | 115 | 216 | 0,32 | Fuerstenau | 131 | 421 | 0,40 |
| Dissen | 18 | 114 | 0,32 | Badbergen | 72 | 316 | 0,40 |
| Melle-Buer | 202 | 470 | 0,32 | Bad Iburg | 72 | 524 | 0,42 |
| Hagen | 46 | 210 | 0,33 | Alfhausen | 66 | 412 | 0,43 |
| Melle-Mitte | 104 | 294 | 0,33 | Ankum | 184 | 552 | 0,45 |
| Ostercappeln | 90 | 191 | 0,34 | Neuenkirchen | 270 | 832 | 0,45 |
| Menslage | 60 | 150 | 0,36 | Melle-Gesmold | 192 | 604 | 0,46 |
| Bad Essen | 146 | 335 | 0,38 | Gehrde | 33 | 249 | 0,46 |
| Hilter | 80 | 420 | 0,38 | Berge | 171 | 302 | 0,46 |
| Hasbergen | 14 | 79 | 0,38 | Glandorf | 152 | 706 | 0,48 |
| Bad Rothenf. | 26 | 327 | 0,39 | Belm | 41 | 235 | 0,49 |
| Bramsche | 122 | 180 | 0,39 | Rieste | 44 | 499 | 0,50 |
| Georgsmarienh. | 75 | 271 | 0,40 | Voltlage | 90 | 773 | 0,51 |
| Wallenhorst | 55 | 351 | 0,40 | Bersenbrueck | 81 | 722 | 0,52 |
| Bohmte | 110 | 261 | 0,40 | Quakenbrueck | 10 | 180 | 0,53 |

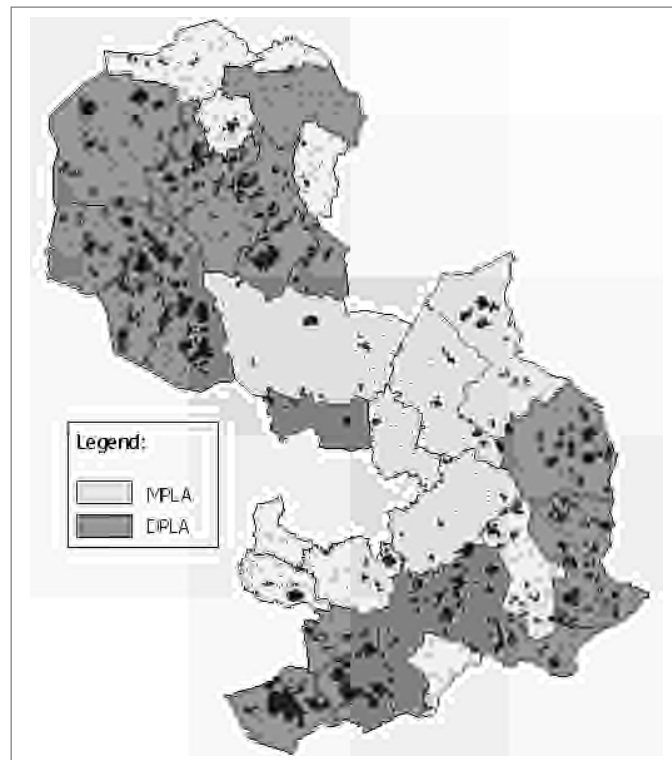
We applied the KE with a radius of 1000 m for each farm location in the County of Osnabrück (see Figure 3.8). Using the same calculation (animals per area), the animal densities can now be linked more precisely to the actual farm locations. It is obvious that clusters do not only exist on the municipality level. In some cases, clusters spread over several neighbouring municipalities in both DPLAs and MPLAs. With this in mind, the VetGIS software provides more accurate measures for identifying risk areas for animal diseases.

Figure 3.7 Kernel Estimation for the Municipality Bramsche regarding pigs



A detailed view of the situation in the municipality Bramsche is illustrated in Figure 3.7; an overview of the whole county is presented in Figure 3.8. The dark patches show the precise location of high animal densities that occur in both DPLAs *and* MPLAs.

Figure 3.8 Kernel Estimation for the county of Osnabrück regarding pigs



3.8 Conclusions

The EU FAIR project has successfully developed new software tools for a detailed analysis and identification of densely populated livestock areas. The tools are easy to use and are implemented in a VetGIS shell based on a low cost GIS.

VetGIS can now be used to perform geostatistical analysis and to enhance the estimation of area-based risk factors. Together with more crude measurements (e.g. DPLA, MPLA, SPLA calculation) it is an operational and accurate tool that can be used by decision-makers for the analysis and assessment of epidemiological risk in regions of the EU. It serves as a basis for the minimisation of epidemiological risks and economic damages.

Acknowledgements

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Task B

Quantification and classification of the risk of such areas from a disease point of view

A survey on cattle, pig and sheep herd characteristics in densely and sparsely populated livestock areas of the European Union

M. Bettio, S. Marangon, N. Ferre, M. Martini, Italy

Risk of introduction of Classical Swine Fever in densely and sparsely populated livestock areas: application of the multiple attribute decision-making method

N. Ferre, M. Martini, C. Pasqual, M. Bettio, S. Marangon, Italy

Ratio of fattening pigs/sow as a movement index: application to the risk analysis in CSF in Brittany

V. Chevalier, G. Gerbier, V. Auvigne, B. Durand, F. Moutou, France

Occurrence of respiratory disease outbreaks in fattening pigs: relation to the features of a densely and a sparsely populated pig area in France

N. Rose and F. Madec, France

Disease risk and factors in relation to management and contact patterns with emphasis on Aujeszky disease on pig farms in a densely populated livestock area

K. Huysmans, J. Hooyberghs, P. Vyt, F. Castryck, G. Verbeke, M. de Becker, R. Geers, Belgium

A survey on cattle, pig and sheep herd characteristics in densely and sparsely populated livestock areas of the European Union

M. Bettio, S. Marangon, N. Ferrè and M. Martini

4.1 Introduction

Over the past decades there has been a significant concentration of livestock production in a limited number of areas in the European Union (EU), because of the considerable economic advantages which derive from these Densely Populated Livestock Areas (DPLAs). Nevertheless, their development has increased the risk for the introduction and spread of major emerging diseases. Recent epidemics of both Classical Swine Fever (CSF) and Foot and Mouth Disease (FMD) in the European Union have clearly shown the need to identify, characterise and classify DPLAs within the EU, with the aim of assessing potential risk factors for the introduction and spread of OIE list A diseases, in farms located in Densely (DPLAs) and Sparsely Populated Livestock Areas (SPLAs). This would allow a review of prevention and control strategies applicable within these regions (Dijkhuizen and Davies, 1995).

In order to provide insight into existing differences in the livestock industry among and within EU countries, a survey on cattle and pig herd characteristics in densely and sparsely populated livestock areas of the EU was carried out.

The main objective of the survey was to collect data about the structure of the livestock production and related industries in the study areas in order to gather information on herd characteristics. These characteristics may give an indication of the risk for the introduction and spread of major disease epidemics, with particular reference to Classical Swine Fever (CSF) and Foot and Mouth Disease (FMD).

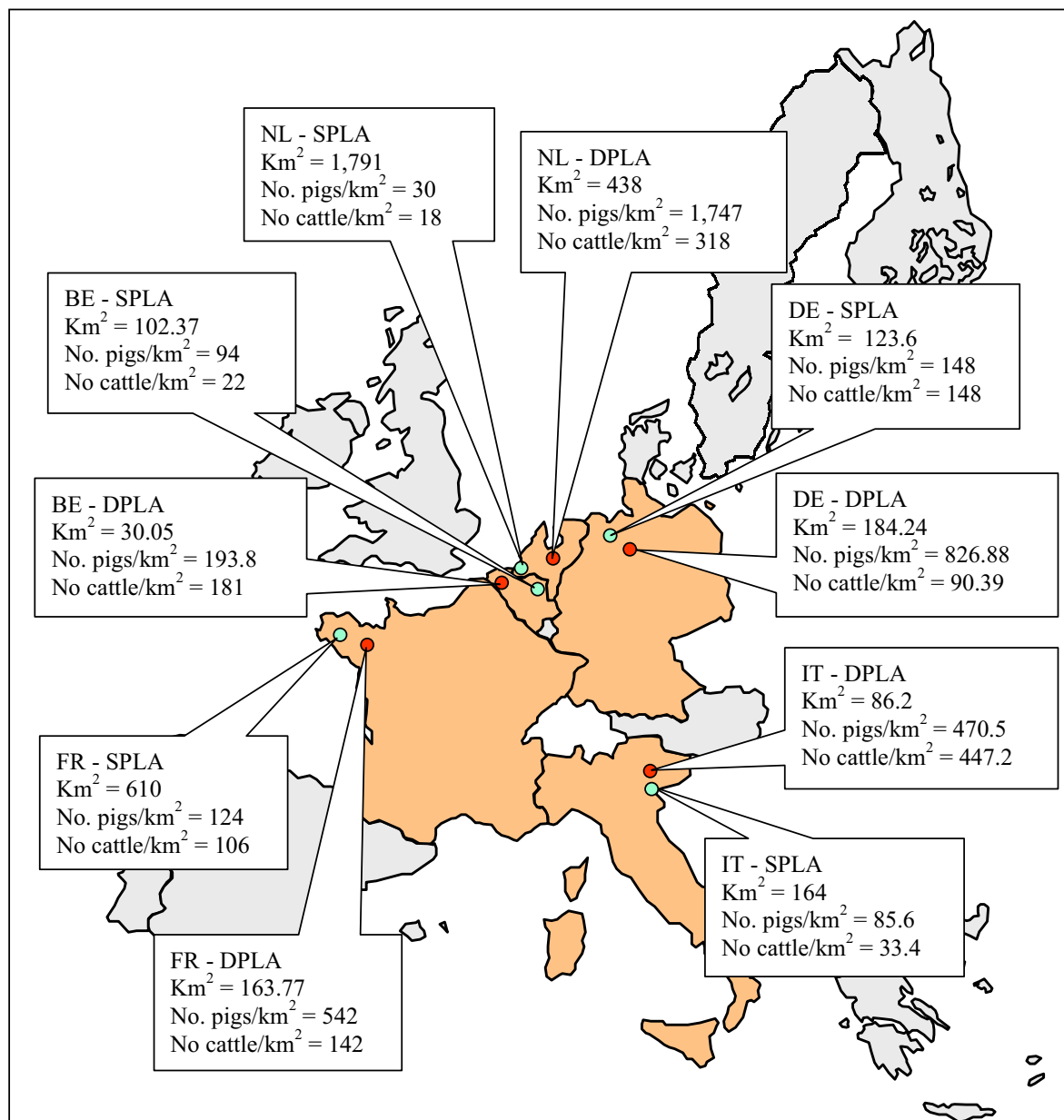
4.2 Materials and Methods

4.2.1 Study areas

The survey was carried out in DPLAs and SPLAs in 5 EU member states. The areas involved in the survey were Flanders (Belgium), Brittany (France), Lower-Saxony (Germany), the Po

Valley (Italy) and the southern part of The Netherlands (Figure 4.1). The study areas were selected at a community level and represent a municipality or a cluster of municipalities with a minimum radius of 3 km. Considering this definition, the size and boundaries of the study areas in different countries were defined on a rather arbitrary basis. Convenience criteria were also taken into consideration. Areas were selected taking into account pig and cattle density: DPLAs had at least 250 pigs/km² and 150 cattle/km², while SPLAs had a maximum value of 150 pigs/km² and 50 cattle/km². This initial definition of DPLAs and SPLAs (Anonymous, 1995) was altered in a later stage of the project (Michel and De Vos, 2000).

Figure 4. 1 Geographical distribution, size and animal density of the selected study areas



4.2.2 Study design

Qualitative and quantitative data on characteristics of farms and related industries located in the selected study areas were collected by means of two questionnaires.

Area questionnaire – The questionnaire was designed to collect data on the type and availability of related industries in each study area. Information was derived mainly from current statistics and existing identification and recording systems. Information on the presence of wild boars was also included.

Herd questionnaire – A questionnaire to gather information on management quality, attitude of farmers, type of trade pattern and related sanitary discipline was drawn up (Czaja and Blair, 1995) (Figure 4.2). The questionnaire was pre-tested following both “formal” (submission to experts) and “informal” (submission to a sample of farmers) techniques (U.S. Bureau of the Census, 1984). To refine the questionnaire under field conditions the pre-test was carried out on 6 farms (2 pig units, 2 cattle herds, 1 sheep flock and 1 mixed herd) in 3 countries (Belgium, Italy, The Netherlands). The pre-test results were evaluated, and the questionnaire was subsequently revised. A document reporting specific comments on the meaning of each question was also prepared and used to train the interviewers.

In 1999, data was collected on 1064 cattle, pig and sheep farms through the submission of the standardised questionnaire to farmers on site, after a previous personal (Italy and Germany) or mail (other countries) contact. In the Belgian study areas all farms were taken into account, whilst in the other countries herds were selected applying a stratified (herd type, size, location) sampling scheme (Italy and France), a systematic sampling (The Netherlands) or a purposive selection (Germany). Trained staff, i.e. veterinarians, university students or scientists involved in the project, interviewed the farmers. On average the questionnaire interview lasted half an hour, with significant variations among different types of farms.

4.2.3 Data analysis

Data was collected and assimilated in order to build up a unique database. In a preliminary stage, data was submitted to an inner validation process, which consisted of checking its consistency and finding out and replacing (where possible, and after consultation with the partner involved) the missing information. A descriptive analysis was carried out on the whole dataset. Contingency tables were obtained and differences in the distribution of predictors between DPLAs and SPLAs were tested using χ^2 and Kruskal-Wallis tests for categorical and continuous variables respectively.

Figure 4.2 Headings of herd questionnaire

| |
|---|
| ⇒ Section A: <i>Interviewee position</i> |
| – experience in farming |
| ⇒ Section B: Farm management |
| – barriers (presence and type) |
| – clean-way/dirty-way at the farm entrance |
| – sharing of farm machinery and equipment |
| – disposal of carcasses |
| – swill feeding (pig units) |
| – veterinary assistance |
| – outdoor facilities |
| – all-in/all-out policy |
| – type of service (natural, artificial) |
| ⇒ Section C: <i>Animal contacts</i> |
| – movements IN – animals and batches (number and origin) |
| – quarantine |
| – movements OUT – animals and batches (destination, etc.) |
| – vertically-integrated production system |
| ⇒ Section D: <i>Vehicles</i> |
| – vehicles (number and type) |
| – disinfecting (incoming/outgoing vehicles) |
| – area for loading/unloading of goods and animals |
| ⇒ Section E: <i>Human contacts</i> |
| – number of workers |
| – contact with other farms |
| – visitors |
| – biosecurity measures (access restrictions, use of overalls/boots, etc.) |
| ⇒ <i>Type and size of the herd</i> |
| ⇒ <i>Historical data on FMD and CSF on the farm</i> |

As far as data collected at a farm level through the herd questionnaire is concerned, the exploratory method of multiple correspondence analysis (Lebart, Warwick and Morineau, 1984) was applied to select herd characteristics that could differentiate DPLAs from SPLAs more effectively. Correspondence analysis is a factorial method that considers relationships between categorical variables, and gives an overview of their dependence pattern in a low-dimensional solution. To apply this method to the current dataset, all continuous variables were categorised on the basis of the distribution percentiles. Region (DPLA vs SPLA) and country (Belgium, France, Germany, Italy and The Netherlands) have been used in the analysis as supplementary variables (not used to find the final solution, but plotted on it), in order to explain their relative position compared with the two-factorial axes solution computed. Different subsets of data were separately considered, according to the different farm characteristics taken into account. The present paper focuses on biosecurity measures applied in all types of herd (analysis A), and on animal introduction practices in pig (analysis

B) and cattle farms (analysis C). For these latter analyses, only pig and cattle holdings which introduce animals, representing respectively 93% and 52% of the total number of surveyed pig and cattle farms, were considered.

4.3 Results

The size of the study areas differed greatly, as their boundaries were defined on a rather arbitrary basis according to convenience criteria. Differences in size could have had a direct influence on the various densities observed among DPLAs and SPLAs (Figure 4.1). In SPLAs pig and cattle densities actually varied from 30 pigs/km² and 18 cattle/km² in The Netherlands, to 148 livestock units/km² for both pigs and cattle in Germany. Taking into account DPLAs, cattle density ranged from 90 to 447 cattle/km² in Germany and Italy respectively, whilst pig density varied from 471 pigs/km² in Italy to 1,747 pigs/km² in The Netherlands.

Table 4.1 illustrates the distribution of the herds included in the study and of the non-response rate for each country. Table 4.2 shows the type and distribution of visited farms in each study area, whilst Table 4.3 reports the median size of cattle, pig and mixed (cattle and pig) holdings.

Table 4.1 Distribution of the number of herds in the study areas and of non-response rates per country

| Country | N. ^o of farms | | | Non-response rate (%) |
|-----------------|--------------------------|-------|-------------------|-----------------------|
| | SPLAs | DPLAs | Total interviewed | |
| Belgium | 92 | 68 | 160 | 30 |
| France | 78 | 117 | 195 | 22 |
| Germany | 70 | 129 | 199 | 5 |
| Italy | 110 | 150 | 260 | 0 |
| The Netherlands | 100 | 150 | 250 | 56 ^a |
| TOTAL | 450 | 614 | 1,064 | 22 |

a) all non-respondents were replaced.

Table 4.2 Type and distribution of the herds included in the survey

| Country | DPLAs | | | | SPLAs | | | |
|-----------------|-------|--------|-------|-------|-------|--------|-------|-------|
| | Pig | Cattle | Sheep | Mixed | Pig | Cattle | Sheep | Mixed |
| Belgium | 13 | 27 | 3 | 25 | 1 | 77 | 1 | 13 |
| France | 22 | 37 | - | 58 | 22 | 23 | - | 33 |
| Germany | 57 | 4 | 1 | 67 | 2 | 44 | - | 24 |
| Italy | 19 | 115 | - | 16 | 19 | 48 | 1 | 42 |
| The Netherlands | 40 | 48 | 1 | 61 | 5 | 49 | 19 | 27 |
| TOTAL | 151 | 231 | 5 | 227 | 49 | 241 | 21 | 139 |

Table 4.3 Median size of cattle, pig and mixed (cattle and pig) holdings included in the survey

| Region | Cattle herds | | Pig holdings | | Mixed farms | | |
|--------|--------------|--------------------------|--------------|--------------------------|-------------|-----------------------------------|---------------------------------|
| | No. | Median size ^b | No. | Median size ^a | No. | Median size (Cattle) ^b | Median size (Pigs) ^b |
| SPLAs | 267 | 38 | 52 | 683 | 109 | 31 | 90 |
| DPLAs | 238 | 53 | 158 | 1,052 | 208 | 57 | 443 |
| TOTAL | 505 | 48 | 210 | 973 | 317 | 52 | 340 |

a) p-value (Kruskal-Wallis test)≤0.05

b) p-value (Kruskal-Wallis test)≤0.001

The presence of wild boars in the selected study areas, the percentage of pig units with a physical barrier around the farmyard, the percentage of those providing outdoor facilities for pigs, and of holdings where swill is fed to pigs are illustrated in Table 4.4. Swill feeding occurred in a total of 8 (1.6%) pig holdings located in 2 countries (Belgium and Germany). The proportion of pig farms that fed the pigs with swill appeared low both in DPLAs (0.8%) and SPLAs (3.3%).

Tables 4.5, 4.6 and 4.7 report the coding and the distribution of predictors included in the multivariate analyses: median, minimum and maximum values and percentages are reported for continuous and categorical variables respectively.

Figure 4.3 shows the final plot of the analysis concerning biosecurity measures in all the 1064 study herds. The variability structure is mainly explained in both its dimensions by quantitative parameters strictly related to herd size. Herds of smaller size are characterised by a lower movement of vehicles, and generally by the application of less strict biosecurity measures. These features are observed more frequently in cattle farms. The same variables

given above identify all herds located in SPLAs. Italy and Belgium are the countries in which herds of a smaller size are most common among those interviewed. On the other hand, larger herds generally adopt more stringent biosecurity measures, and the average number of animal transport lorries entering the farm per month is higher. These parameters define well both mixed and pig units that are mainly located in DPLAs. Germany, France and The Netherlands are the countries in which herds of a larger size are most common among those interviewed.

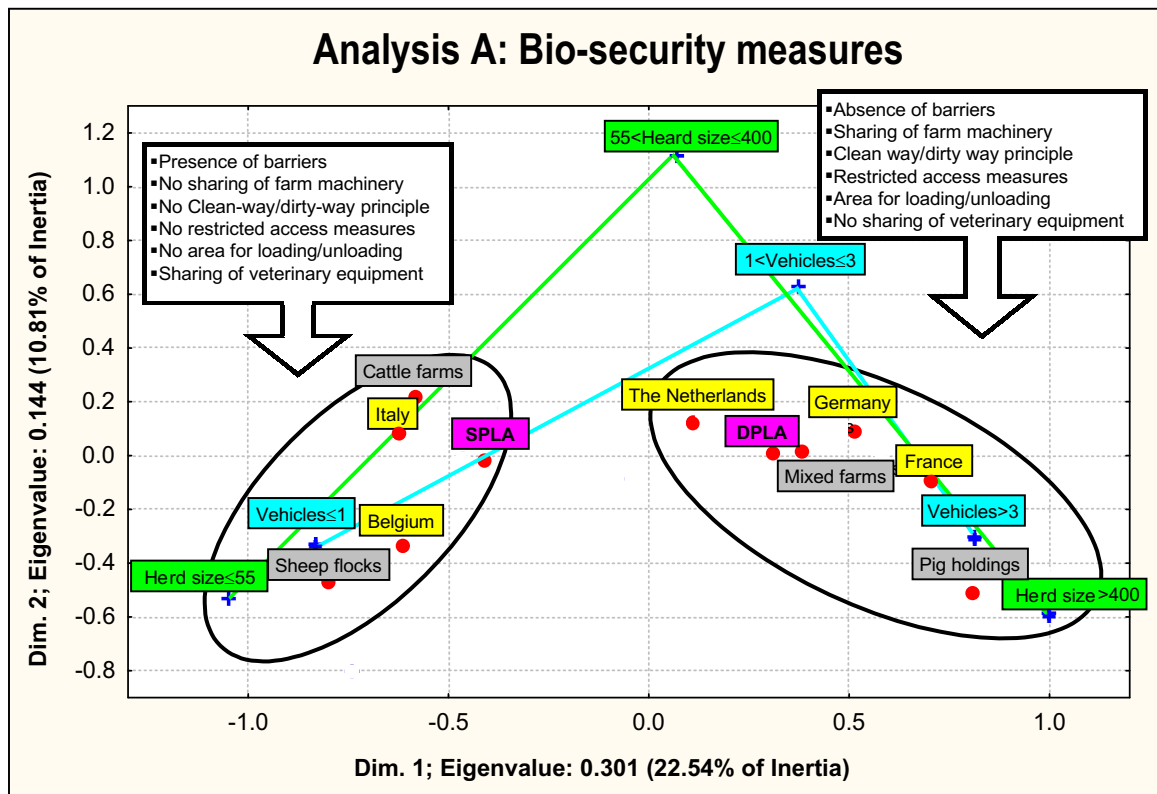
Table 4.4 Presence of wild boar, barriers, outdoor facilities and swill feeding in pig holdings

| Country | Region | Wild boar | No. of farms | Barriers (%) | Outdoor facilities (%) | Swill feeding (%) |
|-----------------|--------|-----------|--------------|--------------|------------------------|-------------------|
| Belgium | SPLA | No | 10 | 60.0 | 20.0 | 50.0 |
| | DPLA | No | 26 | 100.0 | 23.1 | - |
| France | SPLA | Yes | 50 | 88.0 | 4.0 | - |
| | DPLA | No | 75 | 85.3 | 12.0 | - |
| Germany | SPLA | Yes | 22 | 13.7 | 9.1 | - |
| | DPLA | Yes | 118 | 26.3 | 5.2 | 2.5 |
| Italy | SPLA | No | 58 | 91.4 | 12.1 | - |
| | DPLA | No | 33 | 78.8 | 42.4 | - |
| The Netherlands | SPLA | No | 10 | 80.0 | 20.0 | - |
| | DPLA | Yes | 91 | 43.5 | 7.7 | - |

Table 4.5 Distribution of predictors included in analysis A

| Variable | SPLAs (N=450) | DPLAs (N=614) | p |
|--|---------------|---------------|--------|
| Total No. of animals | 58 (1–6000) | 320 (1–15000) | <0.001 |
| No. of animal transport vehicles/month | 1 (0–75) | 2 (0–49) | <0.001 |
| Types of herds: Cattle | 53.6% | 37.6% | |
| Pig | 10.9% | 24.6% | <0.001 |
| Mixed | 35.5% | 37.8% | |
| Presence of barriers | 58.9% | 60.6% | n.s. |
| Clean-way/dirty-way | 6.5% | 21.0% | <0.001 |
| Loading/unloading area | 22.2% | 34.7% | <0.001 |
| Restricted access measures | 20.7% | 32.5% | <0.001 |
| Sharing of farm machinery | 28.9% | 34.8% | <0.05 |
| Sharing of veterinary equipment | 73.3% | 41.6% | <0.001 |
| Veterinary assistance | 79.1% | 98.7% | <0.001 |

Figure 4.3 Analysis A: result of correspondence analysis (two axes solution)



Analysis B suggests the presence of two different types of farms, that are distributed on the two-axes solution plot (Figure 4.4) according to quantitative parameters. The first type of farm is characterised by small units (up to 300 pigs) with a low level of introduction (from 0 to 40 pigs purchased per year). The other type describes larger farms (herd size greater than 300 pigs) with a higher level of animal movement (more than 40 pigs introduced per year). Usually pig units of a smaller size do not belong to a vertically integrated production system; they only purchase pigs from farms located in the neighbourhood without quarantining the introduced animals, and without a separate area for loading and unloading the animals. This type of farm is typical of SPLAs. On the other hand, larger farms have fixed contracts for pig trading and they purchase animals whose provenance is often unknown to the farmer. They are equipped with a distinct area for loading and unloading. This type of farm is commonly represented by breeding and farrow-to-finish units, and is mostly located in DPLAs. Germany, France and The Netherlands are mainly characterised by larger farms, while Italy and Belgium are mostly represented by smaller ones.

With regard to cattle introduction practices, analysis C identifies quantitative variables as the principal discriminating factors between two distinct types of farms. As for pigs, mainly large and small types of herds respectively characterise DPLAs and SPLAs, with the same features previously identified in the analysis concerning pig units.

Table 4.6 Distribution of predictors included in analysis B

| Variable | SPLAs (N=150) | DPLAs (N=343) | p |
|---|---------------|----------------|--------|
| Total No. of pigs | 210 (2–60000) | 633 (10–15000) | <0.001 |
| No. of pigs purchased/ year | 25 (1-10000) | 480 (0-25000) | <0.001 |
| No. of purchased batches per year | 3 (1-50) | 5 (1-100) | <0.001 |
| Types of herds: Breeding | 10.7% | 7.8% | n.s. |
| Fattening | 28.7% | 32.1% | |
| Farrow-to-finish | 60.6% | 60.1% | |
| Presence of cattle | 68.7% | 57.1% | <0.05 |
| Introduction from: known farms | 71.3% | 60.2% | <0.05 |
| other sources | 28.7% | 39.8% | |
| Origin of purchased pigs: regional only | 47.3% | 51.6% | n.s. |
| Other | 52.7% | 48.4% | |
| Quarantine | 29.0% | 22.0% | n.s. |
| Loading/unloading area | 43.3% | 48.1% | n.s. |
| Integrated production system | 14.7% | 35.3% | <0.001 |

Figure 4.4 Analysis B: result of correspondence analysis (two axes solution)

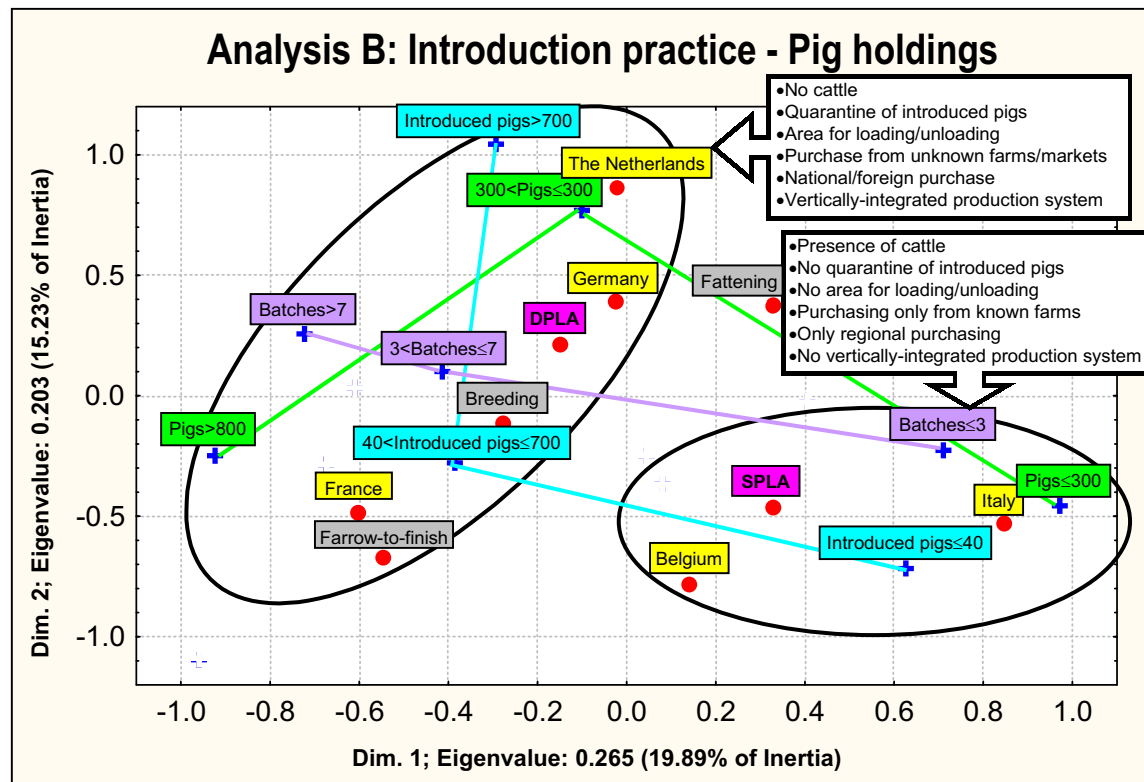
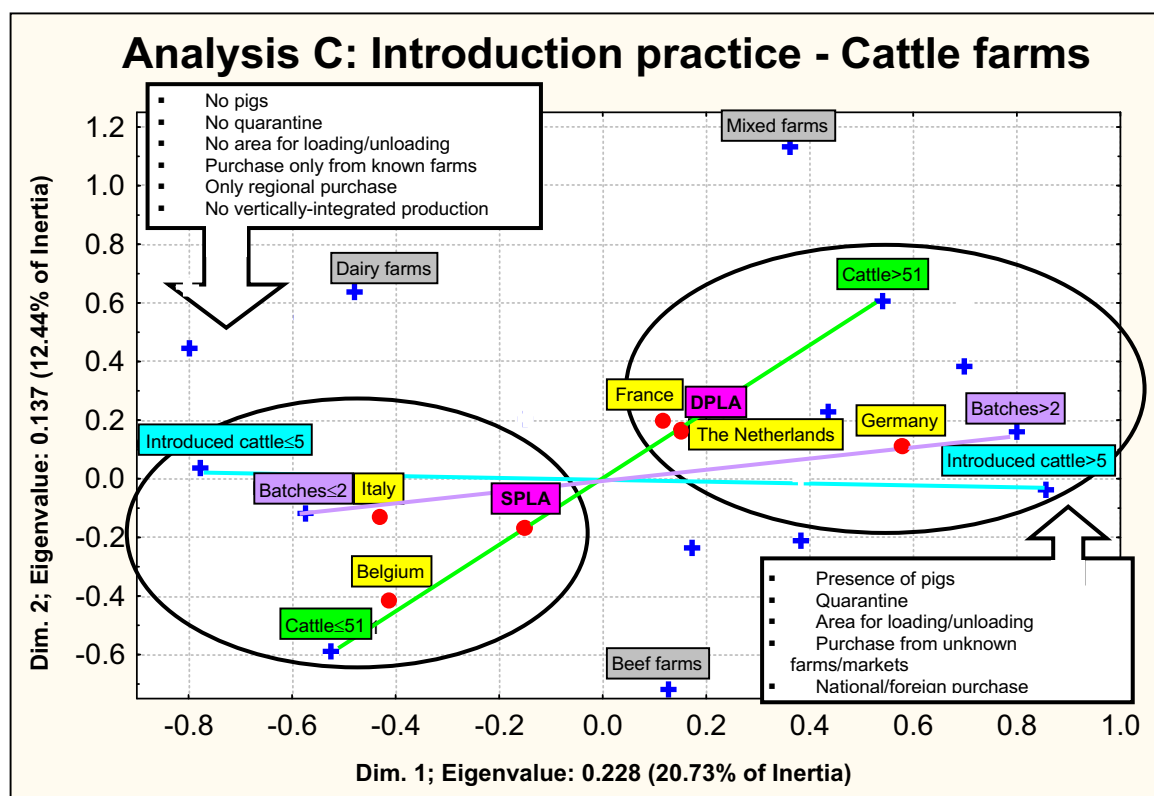


Table 4.7 Distribution of predictors included in analysis C

| Variable | SPLAs (N=212) | DPLAs (N=215) | p |
|---|------------------|------------------|--------|
| Total no. of cattle | 33 (1–1210) | 60 (2–2000) | <0.001 |
| No. of cattle purchased/ year | 4 (1–1810) | 10 (1–4000) | <0.001 |
| No. of purchased batches per year | 2 (1–60) | 2 (1–190) | <0.05 |
| Types of herds: Dairy | 14.6% | 39.1% | |
| Beef | 20.3% | 19.5% | <0.001 |
| Mixed | 65.1% | 41.4% | |
| Presence of pigs | 35.4% | 58.6% | <0.001 |
| Introduction from: known farms | 36.8% | 27.0% | |
| other sources | 63.2% | 73.0% | <0.05 |
| Origin of purchased cattle: regional only | 38.5% | 38.5% | |
| Other | 61.5% | 61.5% | n.s. |
| Quarantine | 24.6% | 17.5% | n.s. |
| Loading/unloading area | 19.3% | 24.2% | n.s. |
| Integrated production system | 6.1% | 17.7% | <0.001 |

Figure 4.5 Analysis C: result of correspondence analysis (two axes solution)



4.4 Discussion and conclusions

The non-response rate of the survey varied from 0% (Italy and Germany) to around 30-50% (Belgium and The Netherlands - in the latter country non-respondents were replaced). The different non-response rate observed in the various study areas could be related to the unwillingness of farmers to cooperate due to the latest CSF epidemics in Belgium and The Netherlands, and to the methods used to approach farmers (personal contact was more successful than contact by mail). Furthermore, it should be noted that professional organisations in France and public veterinary services in Italy took an active part in making farmers cooperative.

With regard to the risk of CSF introduction, swill feeding and the presence of wild boar should be considered. Swill feeding, which also represents a risk factor for FMD (Hyslop, 1970; Sellers, 1971), was identified in a total of 8 (1.6%) pig holdings located in 2 countries (Belgium and Germany). The proportion of pig farms where swill was fed to pigs appeared low both in DPLAs (0.8%) and SPLAs (3.3%), but the percentage of pig farms that made use of swill was much greater in the area. In fact, among the 8 pig holdings where swill was fed to pigs, 5 were located in the Belgian SPLA (half of all pig farms in that area) and 3 in the German DPLA (2.5% of all pig units in the area). This data does not take into account the risk related to illegal swill feeding, which is one of the main causes of CSF virus introduction in the domestic pig population (Fritzmeier et al., 2000).

In 3 countries (Germany, France and The Netherlands) the presence of wild boar was identified in 2 SPLAs and 2 DPLA. In these 4 areas the percentage of pig units where barriers are present varies from 13% to 88%. In geographical areas with a wild boar population, the presence of a physical barrier around farms to reduce the risk of a possible contact between wild boar and domestic pigs should represent one of the minimum requirements to be applied to all pig units in the area. This is of particular relevance for areas where the presence of CSF Virus in wild boar has been detected.

The descriptive and the multiple correspondence analyses suggested that herd size and number of introduced animals and batches per year were the variables mainly associated with the distribution of cattle and pig farms to DPLAs or SPLAs.

One of the main risk factors of disease introduction in a country or a region is the movement of animals. Animal introduction occurred more frequently in pig (93%) than in cattle (52%) holdings, but 50% of pig units and 39% of cattle holdings purchased animals only from farms located in the same region. Furthermore, pig farms were characterised by a higher level (64%) of introduction of animals from known farms, when compared to cattle (33%). A different level of risk was identified in different countries. The practice of purchasing animals

coming from other areas varied from 29% and 49% in Italian pig and cattle holdings respectively, to 97% and 96% in French pig and cattle farms. The introduction of replacement stock from sources at higher risk (holding centres, markets and unknown farms) was much greater in pig (57%) and cattle (90%) farms in the German pilot areas, than in Italian pig (13%) and cattle (53%) holdings. As was also clearly shown during the recent epidemics of CSF and Foot and Mouth Disease in Europe, the discipline on and the traceability of animal movements represent the key points in guaranteeing, on the one hand, a reduction of the risk of introduction of a contagious animal disease in a free area and on the other hand, the success of the eradication measures put into force once it happens. In order to reduce the risk of disease introduction and spread through the movement of animals, animals should be purchased directly from known herds, the access to animals should be restricted and hygienic measures should be regularly applied at farm entrances (Fritzmeier et al., 2000).

DPLAs were characterised by the presence of larger and typically pig or mixed (cattle and pig) farms, with a better sanitary discipline when compared to SPLAs, apart from the practice of sharing farm machinery. Nevertheless, the analysis of variables that describe the sanitary discipline of farms located in the study areas indicated that biosecurity measures were not uniformly applied in farms situated in both DPLAs and SPLAs. To reduce the risk of introduction and spread of contagious animal diseases a minimum set of biosecurity measures and other supplementary requirements should be defined and enforced at the farm level, particularly in DPLAs. Some of these measures should be applicable to all farms, whereas others could apply only to certain types of farms (Terpstra, 1990; Amass and Clark, 1999) (i.e. holding centres).

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Risk of introduction of Classical Swine Fever in densely and sparsely populated livestock areas: application of the multiple attribute decision-making method

N. Ferrè, M. Martini, C. Pasqual, M. Bettio and S. Marangon

5.1 Introduction

Animal density, expressed as the number of livestock units per km², is considered the basic criterion for identifying densely populated livestock areas (DPLAs) (Michel and de Vos, 2000). Evidence exists that these areas are at an increased risk for the spread of notifiable animal diseases such as Classical Swine Fever (CSF) and that the financial consequences of these epidemics in such areas are heavy (Davies and Dijkhuizen, 1995; Meuwissen et al., 1999; Vanthemsche, 1996). It is therefore relevant to evaluate the risk of CSF introduction in densely and sparsely populated livestock areas (SPLAs) considering, besides animal density, more qualitative information on other factors such as farm management, trade patterns, sanitary discipline, and the presence of wild boar. Using this information, a procedure to rank areas according to their risk could be developed to provide insight into what differences exist in the type of livestock industry among and within areas, and whether they should result in modification of their risk rating.

One of the aims of the European Union (EU) research project “Development of Prevention and Control Strategies to Address Animal Health and Related Problems in Densely Populated Livestock Areas of the Community”, was to rank areas in the EU on the basis of information gathered through a questionnaire submitted to farmers. This information was obtained by means of an epidemiological survey on farm characteristics performed in DPLAs and SPLAs in five EU countries in 1999 (Bettio et al., 2000).

Considering that only a limited number of recent CSF outbreaks were identified in a few study areas and that the survey was mainly designed as a cross-sectional study, it was not possible to estimate the relative importance of risk factors to CSF introduction by means of a regression approach. Since this piece of information was essential to rank areas with regard to disease risk, expert judgements were used to provide estimates on the relative importance of the involved risk factors. Expert judgements have been used successfully in many

management decision applications to estimate input variables for which no historical data is available (Horst et al., 1996).

Based on the data collected during the above-mentioned field survey, areas were ranked with respect to the risk of CSF introduction using a multiple attribute decision-making (MADM) method (Hwang *et al.*, 1981). Pioneering surveys on MADM methods were carried out by MacCrimmon, 1968 and 1973. Since then, many methods have been developed by researchers in disciplines as diverse as management science, economics, applied statistics and decision theory. MADM methodology has generally been used to assist in the screening, ranking, prioritisation and justification of proposed schemes.

The present paper describes an application of the MADM method to the veterinary field. The analysis was carried out to identify areas in the EU that are characterised by a high risk of CSF introduction.

5.2 Materials and Methods

A wide range of techniques is included under the general heading of the MADM method, since this covers highly sophisticated methodology techniques based on the application of a simple rating system. According to Hwang and Yoon (1981) taxonomy, among the MADM techniques the hierarchical additive weighting method was applied. The hierarchical additive weighting method is the best known and most widely used MADM method. The method implies the development of a hierarchical tree structure, which is useful in two ways. Firstly, it presents the attributes in an orderly structure. Subsequently, the tree structure can make elicitation of importance weights for twigs much easier than they would otherwise be, by reducing the number of judgements required (Edwards and Newman, 1982).

5.2.1 Study areas

Qualitative and quantitative data on the characteristics of farms located in DPLAs and SPLAs in 5 EU Member States was used (Bettio et al., 2000). The areas involved in the survey were Flanders (Belgium), Brittany (France), Lower-Saxony (Germany), the Po Valley (Italy) and the southern part of The Netherlands.

5.2.2 Attribute generation

Among the farm characteristics taken into account in the field survey, only the main risk factors for CSF introduction were considered in the hierarchical structure. Only attributes that were relevant to the final ranking, exhaustive and non-redundant, were selected. The risk factors of CSF introduction taken into account in the model were hierarchically broken down into three parts (Figure 5.1). All risk factors can be explained by several sub-factors (second level), and some of them by other sub-sub-factors (third level). Each level was confirmed to be nonconflicting, coherent and logical as a set. Independence of the selected risk factors was evaluated using the chi-square statistic and the Bravais-Pearson correlation coefficient for categorical and continuous variables respectively. Nevertheless, even in the absence of full independence the results could be considered a good approximation of the “true” value (Fishburn, 1976).

5.2.3 Data

Relative frequencies of each risk factor (location measures) were obtained using data collected in the survey. Location measures were computed as proportion and as median values for dichotomous and continuous predictors respectively. For quantitative parameters, a linear relationship between each variable and the associated risk was assumed. Curved functions relating quantitative measurements to the output are probably more precise representations than the straight ones, but such curvatures make almost no difference to the final result (Edwards, 1977, Einhorn 1971). A further step consisted of a linear normalisation of the relative frequency values to eliminate computational problems arising from different measurement units (Yoon and Hwang, 1995).

5.2.4 Weights

Not all the attributes were likely to be considered equally important. The function of weights was used to express the relative importance of the involved attributes. The Delphi method was used to generate a vector of weights through the elicitation of expert knowledge (Linstone and Turoff, 1975). A panel of 13 Italian experts on CSF was consulted to assign weights to the identified risk factors. Questionnaires were submitted in four rounds through a web-computer assisted self-administrated interviewing (Fabbris, 2001). The level of agreement among experts was evaluated for each variable through the calculation of the variation coefficient.

The main outcome of the model was represented by a risk index calculated as follows:

$$R(A_i) = \sum_{j=1}^n w_j \times v_{ij}$$

$R(A_i)$ = Risk index of area A_i

w_j = weight of risk factor x_j

v_j = normalised relative frequency of risk factor x_j

In order to assess the stability of the model and to determine which variables mostly contributed to it, a sensitivity analysis was performed using the software @Risk (Palisade, New York, 1997), and applying a BetaPERT distribution (Vose, 1999) for each weight obtained through the expert elicitation.

5.3 Results

The correlation between continuous variables included in the final hierarchical tree structure ranged from 0.12 (number of introduced batches/number of workers) to 0.46 (number of introduced batches/number of introduced pigs). Association among dichotomous variables and between these variables and the continuous ones was low (highest values $\chi^2 = 0.06$ and $\eta^2 = 0.02$, respectively). Given its high correlation with the other continuous variables (lowest $\chi^2 = 0.41$), herd size was the only variable excluded from the model.

In Table 5.1 and 5.2 the outcomes of the Delphi exercise are presented. A high level of agreement among experts was observed after the fourth round (variation coefficient ranged from 0 for human contacts to 0.45 for absence of barriers).

The outcome of the MADM model is shown in Table 5.3, which illustrates the ranking of the selected study areas according to the risk of CSF introduction. The sensitivity analysis indicated a good stability of the model, since the shape of each distribution approximated the normal distribution (kurtosis ranged from 2.8 to 2.9, and skewness ranged from 0.08 to 0.25). Moreover, the sensitivity analysis allowed the identification of those risk factors that mainly contributed to the risk rating in each study area. The relative contribution of each main risk factor to the final ranking of the selected study areas is illustrated in Table 5.4

Figure 5.1 Hierarchical structure of risk factors for CSF introduction.

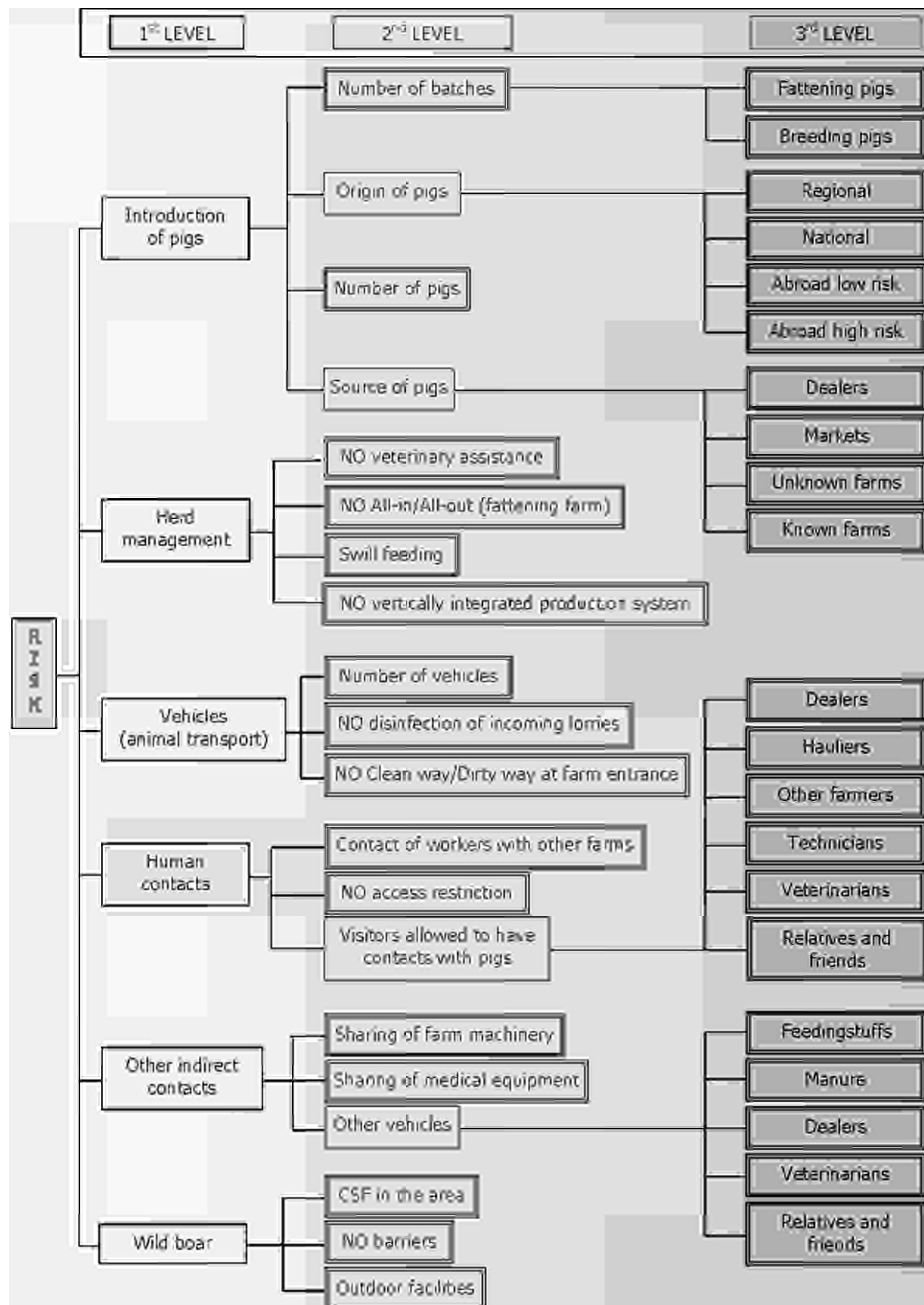


Table 5.1 Relative weights of main risk factors

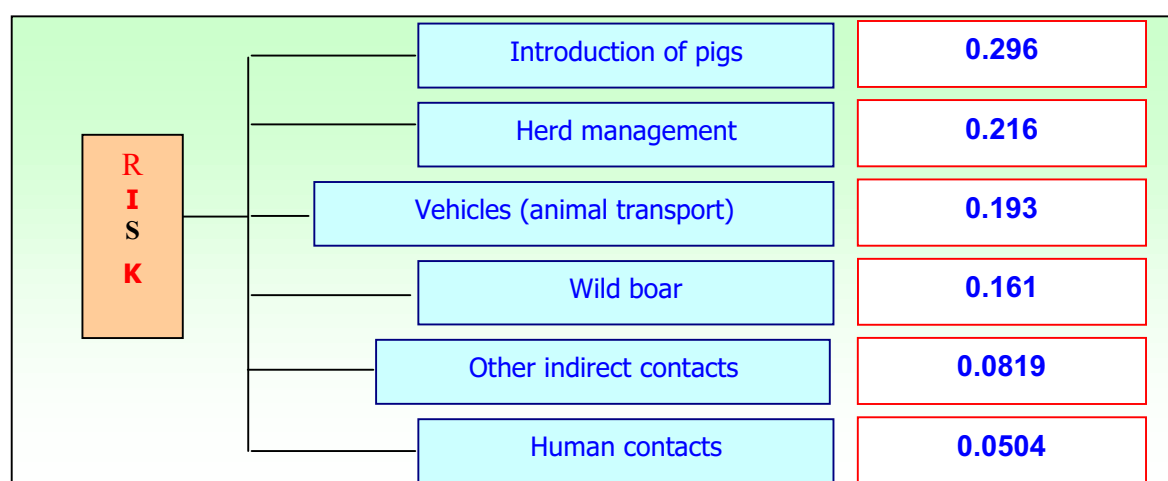


Table 5.2 Second level sub factors: ranking of weights

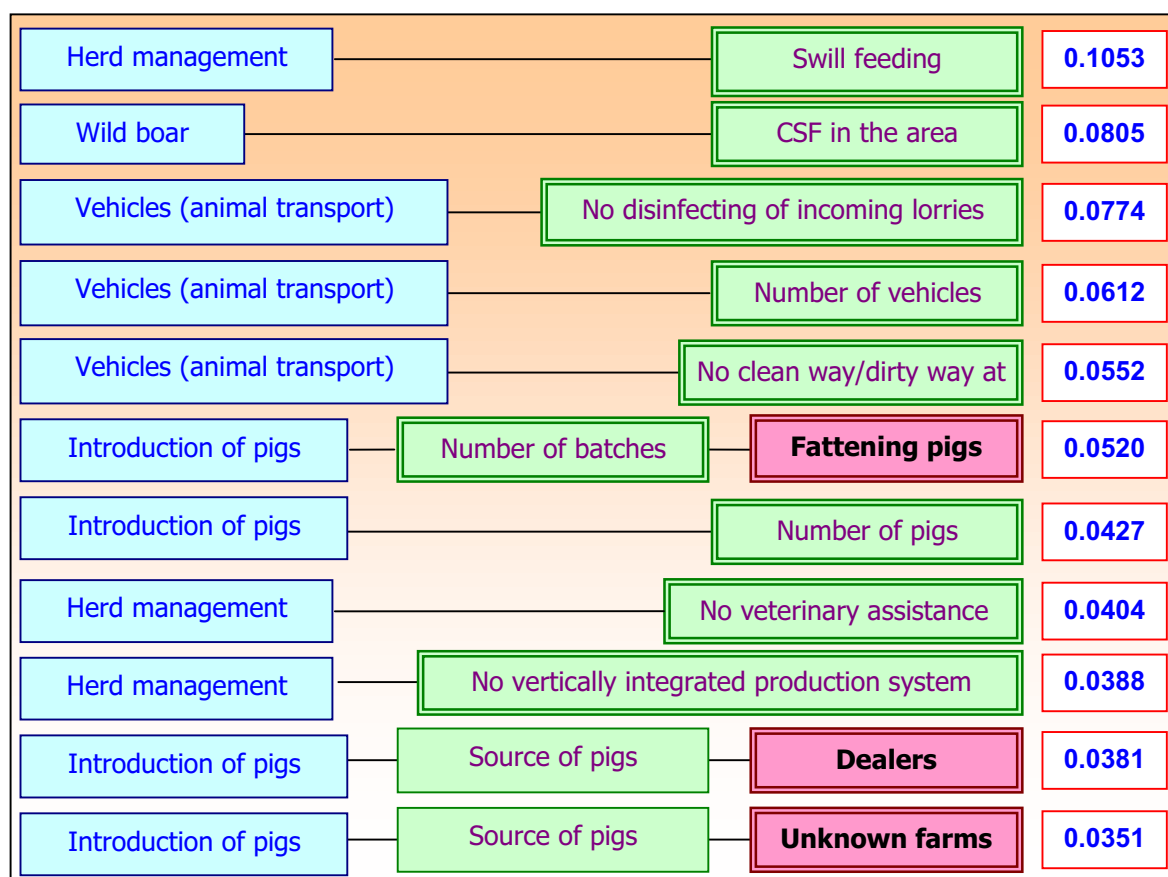
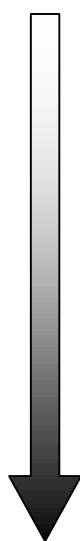


Table 5.3 Ranking of the selected study areas according to the risk of CSF introduction

| | |
|----------------------|--------|
| Belgium DPLA | 0.2675 |
| Italy DPLA | 0.2763 |
| France DPLA | 0.2852 |
| Italy SPLA | 0.2961 |
| Belgium SPLA | 0.3287 |
| The Netherlands DPLA | 0.3320 |
| France SPLA | 0.3346 |
| The Netherlands SPLA | 0.3351 |
| Germany DPLA | 0.3966 |
| Germany SPLA | 0.4460 |

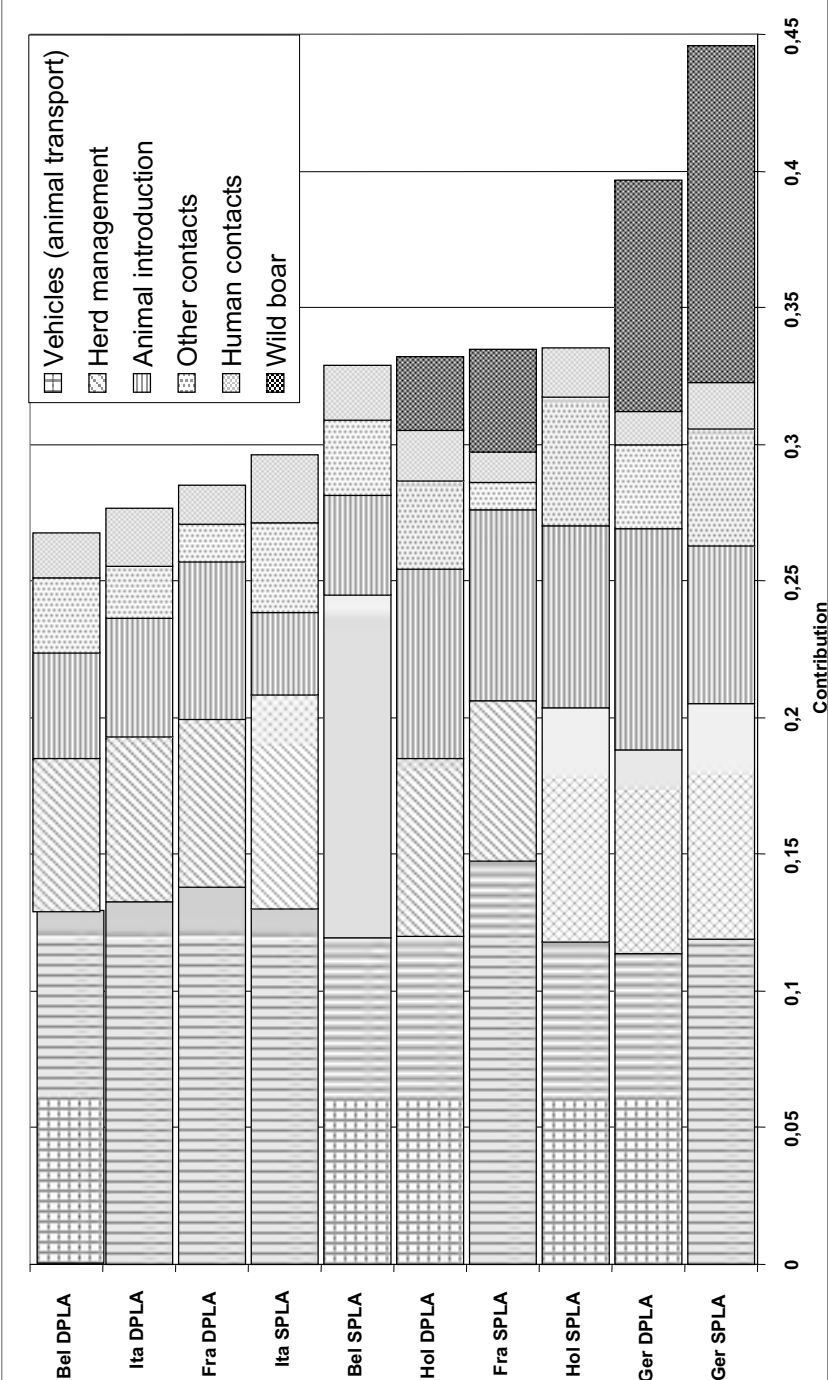


5.4 Discussion and conclusions

The outcome of the Delphi elicitation (Table 5.2) indicated that swill feeding and the presence of infected wild boar represented the main risk factors for CSF introduction in the domestic pig population at area level. These results reflected the knowledge that in some areas of the EU a large proportion of CSF primary outbreaks were due to contact with wild boar or to swill feeding (Kramer et al., 1995; Fritzmeier et al., 2000). The other risk factors for CSF introduction were mainly sub-factors related to both animal trade and herd management. Trade of live animals and returning transport lorries were the presumed source of CSF Virus introduction in free areas (Vanthemsche, 1996; Elbers et al., 1999). The Delphi elicitation assigned a relative weight to the main risk factors of CSF introduction (Table 5.1). Among these, the purchase of live pigs represented almost 30% of the total risk, whilst similar weightings were assigned to herd management (21.6%) and vehicles for animal transport entering a farm (19.3%).

Taking into account the final ranking of the different study areas (Table 5.3) it appears that in each country the risk of CSF introduction is higher in SPLAs than in DPLAs. Therefore, density does not seem to be the only factor associated with the risk of disease introduction in the selected study areas. The epidemiological role that SPLAs may play in the introduction of CSF in the domestic pig population should be emphasised, since the disease could then spread to DPLAs through the movement of live animals or transport lorries (Vanthemsche, 1996; Elbers et al., 1999).

Figure 5.2 Contribution of each main risk factor to the global risk for each study area



The high-risk indices of German SPLAs and DPLAs could be explained by the presence of infected wild boar, associated with the absence of a physical barrier around the majority of pig farms. DPLAs in Belgium, France and Italy showed lower risk index values, due to relatively better herd management and to a lower impact of the risk associated with the introduction of live pigs. The Belgian SPLA risk index value is mainly attributable to herd management, since the percentage of farms where swill was fed to pigs was high.

The application of the MADM method to the dataset on the characteristics of the livestock industry in DPLAs and SPLAs showed that the risk associated with vehicles for animal transport mainly contributed to the risk rating of the study areas (Figure 5.2). Where present, infected wild boar could clearly affect the level of risk with regard to the introduction of CSF in the domestic pig population, whilst herd management and animal introduction were two other factors which influenced the final rating. The MADM outcome could allow the identification of the main factors that contribute to disease risk and the definition of priorities for the adoption of sound preventive measures in each area.

In the European Union, CSF still represents a continuing threat for the pig industry. The financial losses due to the epidemics could be huge for both the commercial and the public sectors, especially once the infection enters a DPLA. The best way to reduce losses from these epidemics is to prevent the introduction of the CSF Virus into the domestic pig population.

There is a need to identify and classify areas according to the risk of disease introduction and to define effective prevention and eradication measures, taking into account the characteristics of the areas under consideration. Michel and de Vos, 2000, have defined the criteria which can be applied to the identification of DPLAs. Expert elicitation techniques could be used to rank areas considering, besides animal density, other qualitative and quantitative information on the characteristics of their livestock industry. The application of such methodologies does, however, require the definition in all the EU countries of a minimum set of data on the main risk factors for disease introduction; such as animal movement and its sanitary discipline, biosecurity measures enforced at the farm level, swill feeding and the presence of (infected) wild boar. Criteria to collect and update this data, which could be partly generated by I&R and ANIMO systems, should be defined and uniformly applied.

The systematic adoption of biosecurity protocols should be enforced to minimise the risk of introducing infectious diseases into pig units (Terpstra, 1990; Amas and Clark, 1999). If this is the case, further information on the compliance of pig farms to these protocols could regularly be collected and used to monitor risk in such areas. This could eventually stimulate

the identification and enforcement of preventive measures aimed at reducing the risk of disease appearance.

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Ratio of fattening pigs/sows as a movement index: application to the risk analysis of CSF in Brittany

V. Chevalier, G. Gerbier, V. Aubigne, B. Durand and F. Moutou

Abstract

Today, and as far as Classical Swine Fever or Foot and Mouth Disease are concerned, densely populated areas are considered as at-risk areas. However, even if the density parameter is synthetic, it does not take animal movements into account. Nevertheless these movements widely contribute to both the introduction and the spreading risks of these two diseases.

The aim of this paper is to show the relevance of using the ratio of fattening pigs/sows, both as a movement index as well as evidence of the import-export status of a given area, to geographically improve the risk analysis of CSF.

6.1 Introduction

The number and importance of DPLAs has significantly increased in recent years. The necessity of adapting the biosafety and fight measures against such diseases as FMD (Foot and Mouth disease) or CSF (Classical Swine Fever) in these areas became evident.

Indeed, the study of previous epizootics showed, on one hand, that the propagation was very fast in these areas and on the other hand, that the economical consequences were very serious. That is why these are considered to be high-risk areas as far as CSF (or FMD) is concerned.

Within the frame of the FAIR project, the proposal was to define the DPLA using the “animal density” criterion: thresholds are 300 pigs/km² for CSF and 450 animals/km² for FMD.

Because it deals with the notions of herd size, herd number and distance between herds, the density parameter is a synthetic one; moreover, density effects on the spreading of FMD or CSF have already been shown (Gerbier 2000; Ferguson et al., 2001; Mintiens et al., 2001).

However, this parameter is obviously inadequate for describing the geographical risk of CSF precisely in a given area. There are several reasons for this:

- the relevant epidemiological unit for CSF is the herd, and the relationship between herd density and animal density is not clear.
- the threshold values were arbitrarily defined
- it does not take animal movements into account, although it was confirmed that these movements were the main transmission factors for infectious diseases between herds (Vannier, 1993).
- lastly, and in a similar way, this parameter does not take the production systems into account. It is obvious that given a density, the import-export status of a country or a region plays an important role in the risk introduction of CSF in this country or region. As an example, Denmark, which has one of the higher densities of EU but which exports 80% of its production, has been free of CSF since 1933 (Anonymous 1999a).

Given this information, the first target for our work was to build a simple tool for describing pig movements in Brittany; using this tool to complete the data given by the density parameter. The second target was to improve the geographical risk analysis of CSF in this area.

6.2 Methodology

The data was extracted from the INFOPORC file (1999). This file was given to us by the UGPVB (our subcontractor). It gives a census of the total number of active pig farms in Brittany as well as their production types, their number of places (sows, fattening pigs, post weaning pigs), and their geographical localisation (coordinates Lambert II Centre).

From this data, we calculated a pig density, a farm density per county (for the French “canton”) on the one hand, then on a grid (10km*10km) on the other hand. Post-weaning piglets were included in the pig density calculation.

Then, we calculated the following ratio per county and on the same grid:

$$Ratio = \frac{\text{number of fattening pigs places}}{\text{number of sows places}}$$

Indeed and by definition, this ratio is an indicator of the import-export status of a given area. If we consider a self sufficient area (neither import, nor export), the number of fattening places in this area, given a year, should be equal to the number of piglets born per sow place minus the total number of dead pigs between birth and sale. Obviously, this value may vary

during the year, according to the economic market and pathologies. However, as far as Brittany is concerned and based on expert opinions, we estimate the value of the ratio at 8. For a higher value, the area will be considered as importing. On the contrary, for a lower value the area will be considered as exporting.

Then using a grid allowed us to calculate the Moran index: this coefficient is used to measure the existence of a spatial autocorrelation.

The formula is:

$$I = \frac{N \sum_i \sum_j W_{ij} Y_{ij}}{\sum_i \sum_j W_{ij} \sum_i Y_{ij}}$$

W_{ij} is a geographical neighbourhood measure

$W_{ij} = 0$ if the two areas are neighbours, 1 if not

Y_{ij} is a measure of proximity of each area value

$Y_{ij} = (y_i - \bar{y}) * (y_j - \bar{y})$ where y_i is the value of the area i , and \bar{y} is the average of the values in the N areas.

If I is significantly positive, we may assume that the cluster is not due to chance. If its value is significantly negative then we may assume that the “chessboard ” repartition is not due to chance.

Analysis was completed using Mapinfo (Mapinfo Corp), and S-plus (Mathsoft).

6.3 Results

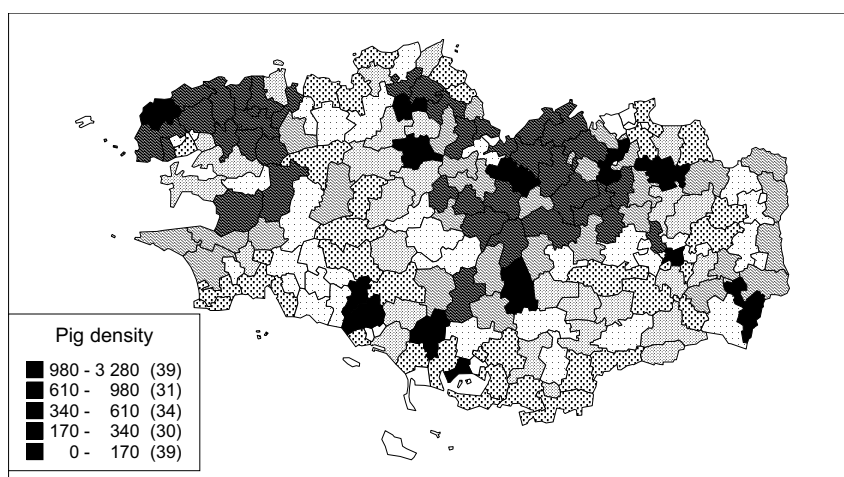
6.3.1 Results per county

The results are presented on maps 6.1, 6.2 and 6.3. The maps 6.1 and 6.2 highlight two big production areas, namely Côtes d’Armor and Finistère Nord. We could superimpose these 2 maps: the value of correlation coefficient herd density-animal density is 0.93.

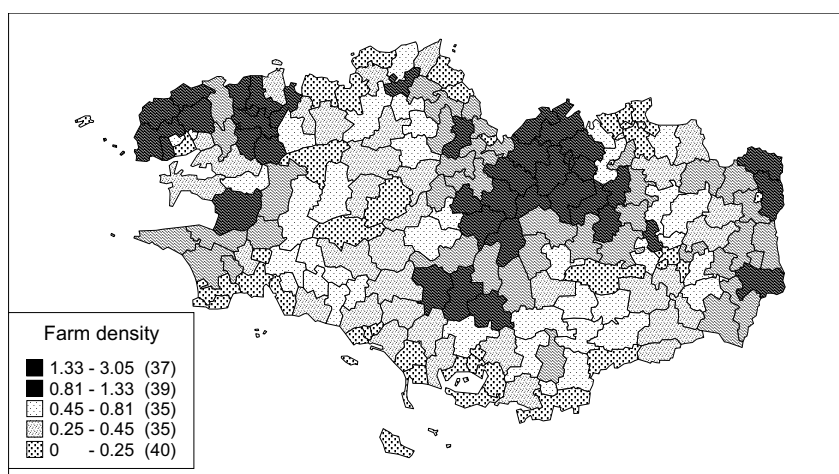
With regards to map 6.3 (ratio map), we notice that the values of the ratio may vary from 0 to 44. Highlighted areas are different from the previous ones. Moreover the “patchwork” shape of the ratio map obviously contrasts with the homogeneity of the production areas highlighted by the density map.

Lastly, the great majority of high-density areas of Brittany seem to be exporting areas.

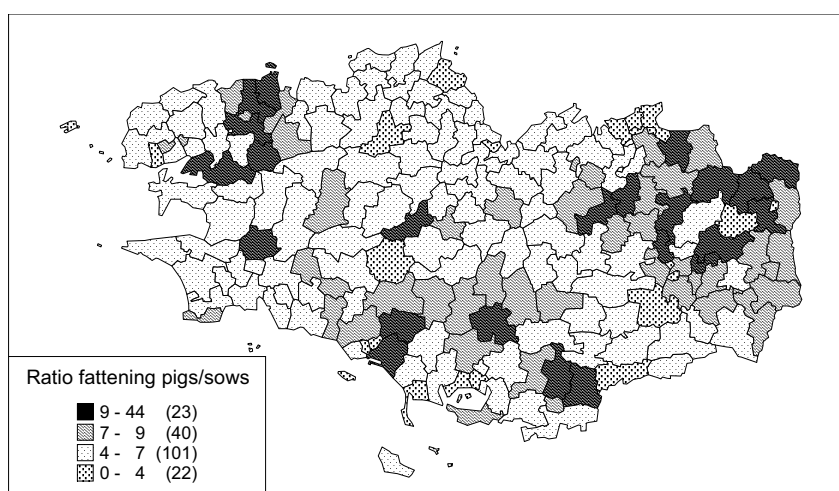
Map 6.1 Pig density on a ‘canton’ level (pigs/km²)



Map 6.2 Farm density



Map 6.3 Ratio of fattening pigs/sows



6.3.2 Results on a grid

The results are presented on maps 6.4 and 6.5.

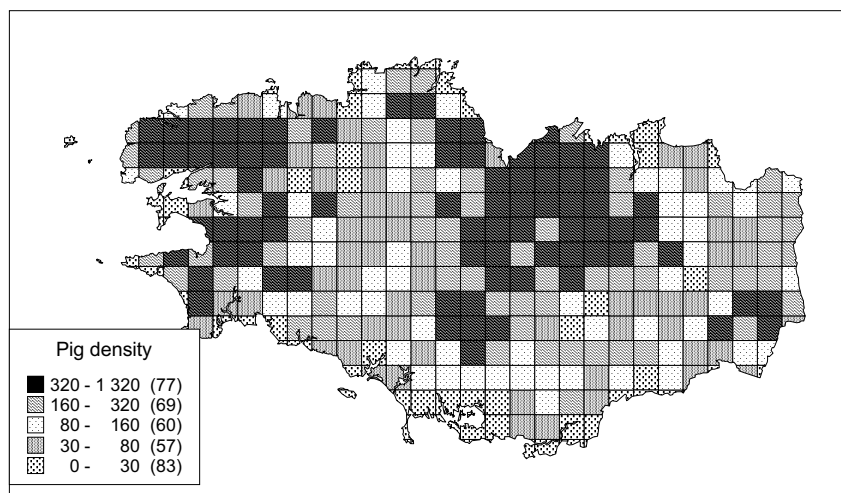
Insofar as animal density and farm density are highly correlated ($r = 0.93$), we decided to keep only one of the two variables to perform the analysis, namely the pig density.

We note again the two big production areas as well as the patchwork shape of the ratio map.

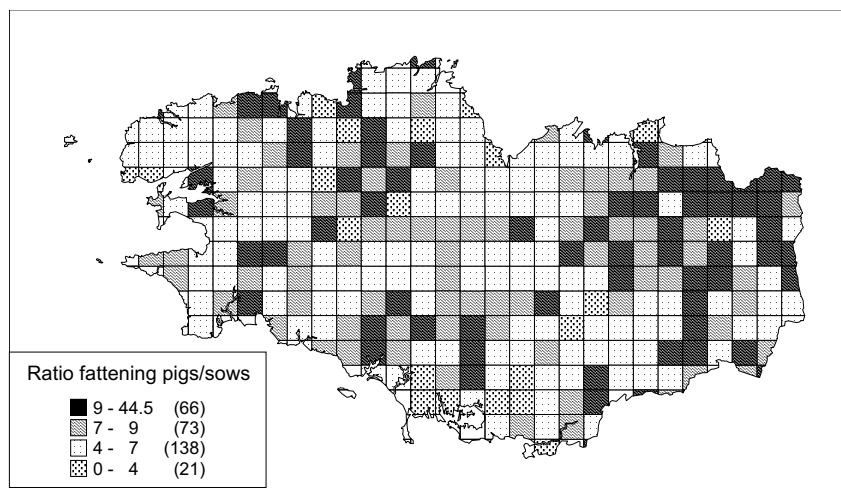
Lastly, the great majority of high-density areas in Brittany again seem to be exporting areas.

The Moran index was calculated for each of the two parameters. Its value is 0.7 for the pig density parameter, meaning that the value of each cell (surface unit) strongly depends on the neighbouring cell's values. On the contrary, the index value for the ratio is 0.15; that means that the self-correlation is low. If this self-correlation exists, we should look for it on a smaller scale.

Map 6.4 Pig density (grid 10km*10km)



Map 6.5 Ratio fattening pigs/sows



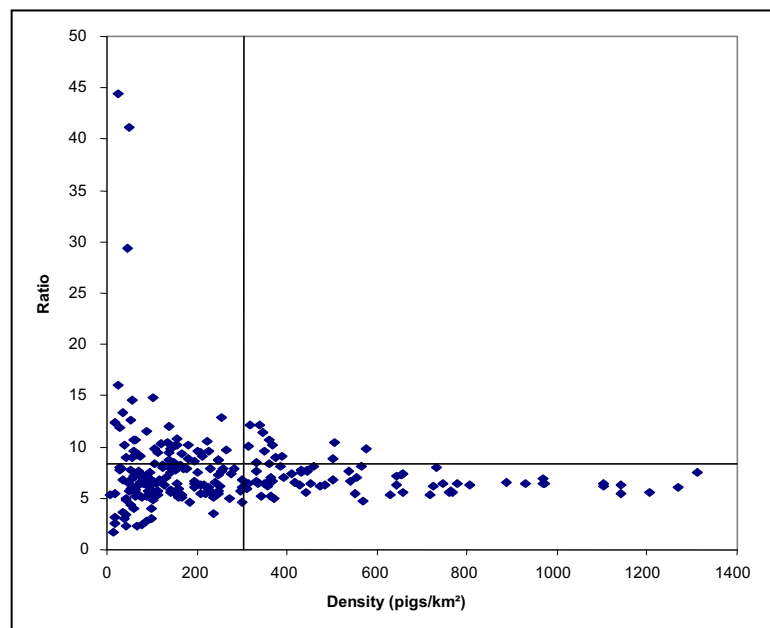
6.3.3 Relationship between ratio and density

Each point of the Figure 6.1 represents a surface unit (a cell of 10 km* 10 km) and gives its position according to its ratio value and its density value.

This figure confirms what the previous maps were suggesting: that the majority of DPLAs are either self-sufficient or lightly exporting (i.e. located on or below the threshold line of the ratio). Moreover, this figure shows that Brittany is quite heterogeneous: densities can be low or high; this is the same as far as ratio values are concerned.

Finally, the average ratio of Brittany is 7.3, which is quite close to 8 and means that this area is globally self-sufficient.

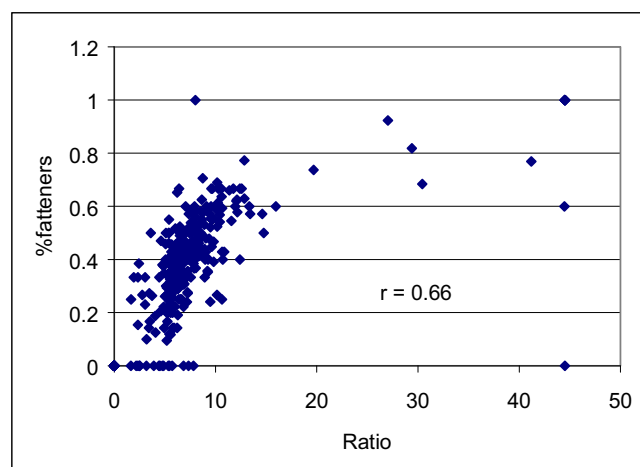
Figure 6.1 Distribution of the surface units according to the pig density and the ratio of fattening pigs/sows (cells of 10 km *10 km)



6.3.4 Relationship between ratio and percentage of fatteners

The analysis of the relation between ratio and percentage of fatteners in the surface units shows that there is a correlation between these two variables ($r = 0.66$).

Figure 6.2 Distribution of the surface units according to the ratio of fattening pigs/sows and the percentage of fatteners



6.4. Discussion

6.4.1 Geographical analysis: administrative units vs. grid

Using a grid allowed us to eliminate the variability of administrative boundaries; consequently we could use this method in other areas as well as in other countries. Moreover, this method allowed us to calculate the Moran index that is an indicator of the spatial correlation between each cell's values.

However, we had to define the cell's size and this choice was made arbitrarily. This implies an approximate and previous knowledge about the carrying-distance of pig movements.

Lastly, and contrary to an analysis based on administrative limits, we need to have accurate data (at farm level) at our disposal in order to perform this kind of analysis.

6.4.2 Animal density vs. farm density

With regard to CSF or FMD, the relevant epidemiological unit is the farm. In the same way, the herd size is an important parameter to consider; this is particularly the case as far as FMD is concerned since it has been shown that the herd size was a risk factor for spread from one herd to another (Hugh-Jones, 1972; Gerbier, 2000).

However, the density parameter takes into account these two variables in an indirect way, and these two variables are not necessarily correlated. Indeed, we could highlight highly

populated animal and sparsely concentrated herd density areas, just as well as we could highlight sparsely concentrated animal and high herd density areas!

Where Brittany is concerned, we could geographically superimpose the two maps of density (pig and herd). That means that there is herd size homogeneity in this area.

6.4.3 Ratio vs. animal density

Density maps show the existence of homogeneous production areas; this is confirmed by the high value of the Moran index (0.7) calculated on densities. On the contrary, ratio maps show a patchwork shape, with a low value of the Moran index (0.15).

As a conclusion, the density allows us to perform a first analysis of the geographical variations of the risk of CSF. Then, the ratio allows us to improve this analysis by inserting a dynamic component. The analysis is thinner and, finally, we may assume that importing areas would be more at risk than the exporting ones.

6.4.4 Relationship between the ratio and the percentage of fatteners

The percentage of fatteners and the ratio are highly correlated ($r = 0.66$). To some extent and because of the lack of relevant data (number of sow places, number of fattening pigs places), we could get closer to the movements notion using a production parameter, namely the percentage of fatteners in a given area.

6.5 Conclusions

The so-called "density" parameter seems to be a good indicator of the geographical risk for CSF. Nevertheless, it could be improved using a second variable: the ratio of fattening pigs/sows. Indeed, this ratio brings additional information; this information deals with pig movements and thus is essential for a more precise geographical risk analysis of CSF. A sparsely populated area may be at risk if it is a strongly importing area.

Moreover, this variable affords some obvious advantages:

- on the one hand, it is very easy to calculate
- on the other hand, it takes the production system into account
- finally, it looks simple and representative of a dynamic whereas the density is heterogeneous and not so easy to understand

Obviously, the significance of this index should be discussed according to the production systems. An internal validation (comparison of the geographical results with movements data of INFOPORC) as well as an external validation of the whole process (comparison with other European countries) should be performed.

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Occurrence of respiratory disease outbreaks in fattening pigs: relation to the features of a densely and a sparsely populated pig area in France

Short title: Respiratory disease outbreaks and pig density

Rose Nicolas and Madec François

Abstract

A survey was carried out in France in 1999 in a Densely Populated Pig Area (DPPA) and a Sparsely Populated Pig Area (SPPA). The two areas were compared regarding the number of respiratory disease outbreaks in fattening pigs on each farm per year with a multiple correspondence analysis and a hierarchical clustering. The two areas exhibited different typologies: in the DPPA, high density was associated with a high proportion of finishing-pig units resulting in a lot of movement of piglets within the area. Farrow-to-finish farms located in the DPPA had many contacts with external vehicles; this was associated with more than two respiratory disease outbreaks per farm per year. There was also a lack of biosecurity measures implemented on these farms. Conversely, the good health status of the farms located in the SPPA was associated with few external contacts and good biosecurity measures. In a second step, risk factors were studied for the occurrence of more than 2 respiratory outbreaks per year. Having more than 4 pig farms within a 2 km radius, more than 30 incoming rendering trucks per year, and storage of the carcasses of dead animals within the farmyard perimeter increased the risk of occurrence of more than 2 respiratory disease outbreaks per year on the farm. This risk was also increased when there were more than 2 animal transport lorries entering the farm per month and more than 1 veterinarian's or technician's vehicle coming in every 2 months. These results were discussed because of possible bias due to the retrospective design of the survey and the sampling scheme (randomisation within two areas).

Résumé:

Syndromes grippaux en porcherie d'engraissement : relation avec les caractéristiques d'une zone à forte et faible densité porcine en France.

Une zone à basse densité (BD) et une zone à forte densité (FD) ont été enquêtées en France en 1999. Les typologies de ces deux zones ont été comparées au regard du statut sanitaire des

élevages (nombre d'épisodes de type grippal en engraissement) au moyen d'une analyse factorielle des correspondances multiples suivie d'une classification ascendante hiérarchique. Les deux zones présentent une typologie différente : en zone FD, la forte densité est associée à un nombre d'élevages plus important de type engraisseur, impliquant une circulation des porcelets plus importante. La forte fréquentation des élevages naisseur-engraisseurs situés dans cette zone par les véhicules extérieurs, peut être interprétée en tant que cause ou conséquence d'une situation sanitaire difficile (nombre de syndromes grippaux en engraissement > 2/an), exacerbée par le manque de précautions sanitaires prises par ces mêmes élevages. En zone BD, la bonne situation sanitaire des élevages à l'égard de la pathologie cible, est associée à une faible fréquentation par les véhicules extérieurs et à la mise en place de mesures de biosécurité. Dans un second temps, les facteurs de risque de l'expression clinique de plus de 2 syndromes grippaux par an ont été recherchés. Le modèle de régression logistique a permis de mettre en évidence que la densité d'élevages porcins autour de l'exploitation (plus de quatre élevages de porcs dans un rayon de 2 km), une fréquentation importante de l'élevage par les véhicules d'équarrissage (> 30 passages par an) et le stockage des cadavres dans le périmètre de l'exploitation augmentent significativement le risque de survenue de plus de deux syndromes grippaux par an chez les porcs à l'engrais. Le risque est aussi augmenté lorsque la fréquentation par les véhicules de transport d'animaux d'une part et par le vétérinaire ou le technicien d'autre part est importante (plus de deux passages par mois et plus d'un passage tous les deux mois respectivement). Ces résultats sont discutés compte tenu de la nature de l'étude (rétrospective) et des spécificités liées à l'échantillonnage (tirage au sort dans deux zones sélectionnées).

7.1 Introduction

Intensification of the pig industry has exerted great pressure on the health status of pigs and respiratory diseases constitute the main cause of economic loss for the farmers (Madec et al., 1992). The classic viral diseases of pigs (Aujeszky's disease, Porcine Reproductive and Respiratory Syndrome [PRRS], Influenza) can be complicated by bacterial agents (*Actinobacillus pleuropneumoniae*, *Pasteurella multocida*, *Mycoplasma hyopneumoniae*) leading to considerable losses in farms with poor rearing conditions. These infectious agents cause acute respiratory disease outbreaks in fattening pigs (Loeffen et al, 1999) (association of anorexia, fever [40°C to 41°C] for at least 2 days, and paroxysmal cough (Madec et al., 1982)). This syndrome can remain subclinical on farms with high standards of hygiene whereas acute clinical outbreaks may be observed on farms with heavy microbial loads. The

severity of a respiratory disease outbreak is an indicator of farm health status (Madec et al., 1987).

Pig density is a risk factor for spreading viral diseases: (1) Aujeszky's disease (Heliez et al., 2000; Leontides et al., 1994; Marsh et al., 1991; Stegeman et al., 1995), (2) PRRS (Albina, 1997; Blaha, 2000), and (3) Influenza (Ewald et al., 1994; Madec et al., 1982; Madec et al., 1987; Maes et al., 1999; Maes et al., 2000). However, the specific features of these densely populated areas might explain the increased risk of spread for the above viral agents. Pig density partly explained the geographical distribution of farms seropositive for Aujeszky's disease in Brittany (Auvigne and Hery, 1997). It suggests that pig density is important but not sufficient to describe the structure of pig production in an area and the crude effect of pig density might be modified by other characteristics of the area (movement of the animals, rearing practices, etc). Thus, the description and comparison of two areas selected for contrasting pig densities might be a useful approach for determining the specific profile of densely populated areas which possibly lead to an increased risk of the introduction and spread of viral diseases.

The aim of our study was therefore to describe and compare the features of a densely populated pig area with a sparsely populated one with regard to management characteristics and pig farm health status measured from the number of respiratory disease outbreaks occurring per year in finishing pigs. In a second part of the study, possible risk factors, adjusted for the geographical area, and related to the occurrence of two or more respiratory disease outbreaks per year in the farm were investigated.

7.2 Materials and Methods

7.2.1 Study sample

The “canton” of Plouguenast (département of Côtes d'Armor) was selected as the densely populated pig area (DPPA) and the “cantons” of Huelgoat and Chateauneuf du Faou (département of Finistère) as the sparsely populated pig area (SPPA) (Table 7.1, Figure 7.1). An exhaustive list of pig farms located in the two areas was obtained from the Veterinary Services of both counties and from the “Farmers Union”, a private organisation (Union des Groupements de Producteurs de Viande de Bretagne). Seventy percent of the pig farms in each area were selected at random, resulting in a sample of 100 farms for the DPPA and 70 farms for the SPPA. Due to refusals and termination of activity, 80 questionnaires were finally obtained from the DPPA and 55 from the SPPA. The proportion of refusals did not

differ between the areas (20% for DPPA vs. 21.4% for SPPA) and was mainly related to a termination of activity.

Table 7.1 General characteristics of selected areas

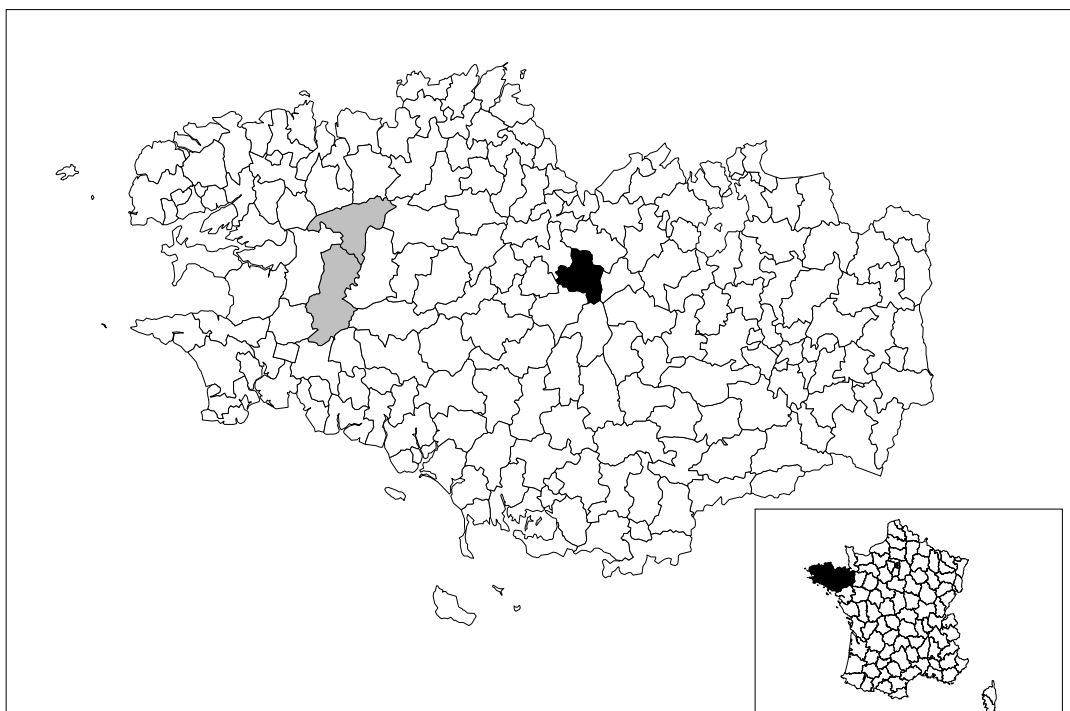
| | DPPA ^a | SPPA ^b |
|---|-------------------|-------------------|
| Agricultural area (km ²) | 169 | 609 |
| Pig density (pigs ^c /km ²) | 780 | 99 |

a) Densely Populated Pig Area (canton of Plouguenast, Côtes d'Armor, France)

b) Sparsely Populated Pig Area (canton of Huelgoat and Chateauneuf du Faou, Finistère, France)

c) Every pig >30kg liveweight

Figure 7.1 Map of Brittany, localisation of the selected areas: ■ densely populated pig area (canton of Plouguenast) and ■ sparsely populated pig area (cantons of Huelgoat and Chateauneuf du Faou).



7.2.2 Data collection

We telephoned the selected farmers in order to explain the aim of the study as well as to make an appointment for an interview. A single interviewer filled in the questionnaire with the farmer at the farm site. It had previously been tested on 15 farms and contained 95 close-

ended questions. All the questionnaires were collected from March to October 1999. The main items included interviewee characteristics, description of the farm site, rearing conditions, animal movements (purchases / sales), incoming vehicles, farm staff and visitors and herd size. The criterion retained as the outcome variable was the number of respiratory disease outbreaks that occurred in 1998. Only typical acute and collective outbreaks were retained that included anorexia, fever for at least 48 hours and paroxysmal cough.

7.2.3 Statistical procedures

7.2.3.1 Features of the DPPA and SPPA

We used a multiple correspondence analysis followed by hierarchical clustering (SPAD-N, 1999). The main objective in this analysis is to detect the associations within a set of categorical variables in a small number of dimensions and to give a low-dimensional (often two-dimensional) graphical representation of these associations (Dohoo et al., 1996). To complete the analysis and to facilitate interpretation of the factorial maps derived from the correspondence analysis, the classification process builds clusters of subjects based on the degree of similarity between the individuals with regard to the variables ((Greenacre, 1993; Lebart et al., 1984). This method is quite similar to principal component analysis. Both methods have the same aim: to build typologies of individuals with data grouped within a table (Individuals X Variables) and where variables are categories, whereas they are continuous in Principal Component Analysis. This typology is based on a distance principle, so that the more the individuals are close to each other, the larger the number of categories they share.

In a preliminary step, an initial screening of the variables possibly related to the area (DPPA vs. SPPA) was performed using the FREQ procedure (SAS, 1989). Only those variables related to the area ($p < 0.20$) were included in the multiple correspondence analysis. Finally 21 active variables (split into 57 categories) were introduced into the analysis. The “area” variable (DPPA vs. SPPA) was included as a supplementary variable so that it was not included in the definition of the factorial axes. In the hierarchical clustering, only those variables that were significantly related (χ^2 -test, $p < 0.05$) to each group were retained to describe the clusters.

Table 7.2 Definition of explanatory variables included in analysis of the occurrence of 2 respiratory disease outbreaks/year or more and percentage of farms for each level of the variables (135 pig farms).

| Definition of variables | Level | Percentage (%) |
|--|-----------------------------------|----------------|
| Rearing of cattle on the farm | No | 34.8 |
| | Yes | 65.2 |
| Fence around the farmyard perimeter | None | 65.2 |
| | For some areas only | 21.5 |
| | All around the farm | 13.3 |
| Sharing of the manure spreader with other farms | No | 45.9 |
| | Yes, without cleaning | 34.1 |
| | Yes, but cleaning before use | 20.0 |
| Storage of carcasses inside the farmyard perimeter ^a | No | 30.4 |
| | Yes | 69.6 |
| Veterinary assistance | Farm veterinarian | 33.1 |
| | Consultant veterinarian | 23.3 |
| | Both | 43.6 |
| Using a quarantine for the introduced pigs | No | 53.3 |
| | yes | 46.7 |
| Pigs are sold to other farms or fattened in other farms | No | 83.7 |
| | Yes | 16.3 |
| Average number of animal transport vehicles entering the farm ^a | ≤ 2 per month | 37.8 |
| | > 2 per month | 62.2 |
| Average number of feed vehicles entering the farm ^a | ≤ 2 per month | 44.4 |
| | > 2 per month | 55.6 |
| Number of veterinarian or technician vehicles entering the farm ^a | ≤ 1 every 2 months | 28.9 |
| | > 1 every 2 months | 71.1 |
| Number of dealer vehicles entering the farm ^a | None | 27.4 |
| | 1 per month at least | 72.6 |
| Number of external manure vehicles entering the farm ^a | < 1 every 2 months | 76.3 |
| | ≥ 1 every 2 months | 23.7 |
| The milk truck comes into the farm | No | 51.1 |
| | yes | 48.9 |
| Number of rendering plant lorries entering the farm ^a | ≤ 30 per year | 69.6 |
| | > 30 per year | 30.4 |
| Use of a vehicle shared with other farms for animal transport | No | 86.5 |
| | Yes | 13.5 |
| Presence of a loading area for pigs | No | 14.8 |
| | Yes, but never cleaned | 43.7 |
| | Yes, cleaned after each operation | 41.5 |

a) Variable retained at screening step to be offered to logistic model (P<0.25)

Table 7.2 (continued)

| Definition of variables | Level | Percentage (%) |
|---|-----------------------------|----------------|
| Number of stock persons on the farm | 1 | 24.5 |
| | 2 | 42.2 |
| | more than 2 | 33.3 |
| Employees: part-time shared with other pig farms | No | 59.3 |
| | Yes | 40.7 |
| Frequency of coveralls laundry | < once a week | 44.4 |
| | once a week | 44.5 |
| | > once a week | 11.1 |
| Employees from feed companies are allowed to enter the facilities ^a | No | 75.6 |
| | Yes | 24.4 |
| Hauliers are allowed to enter the facilities | No | 83.7 |
| | Yes | 16.3 |
| Other farmers are allowed to enter the facilities ^a | No | 84.4 |
| | Yes | 15.6 |
| Disinfection of the boots of visitors before entering the facilities | No | 71.1 |
| | Yes | 28.9 |
| Specific coverall for visitors | No | 18.5 |
| | Yes | 81.5 |
| Visitors wear a cap to enter the facilities | No | 54.8 |
| | Yes | 45.2 |
| Access is restricted if visitors have been in contact with other pig farms before visiting the farm | No | 37.0 |
| | Yes | 63.0 |
| Number of pig farms located in a 2 km radius around the farm under study ^a | ≤ 4 | 67.4 |
| | > 4 | 32.6 |
| Number of fattening places in the farm under study ^a | ≤ 230 | 25.2 |
| |]230 – 400] | 25.9 |
| | > 400 | 48.9 |
| Number of batches of pigs introduced per year ^a | ≤ 4 | 51.9 |
| | > 4 | 48.1 |
| Area ^a | Densely Populated Pig Area | 59.3 |
| | Sparsely Populated Pig Area | 40.7 |
| Farm system ^a | Farrow-to-finish unit | 60.0 |
| | Finishing unit | 40.0 |

a) Variable retained at screening step to be offered to logistic model ($P < 0.25$)

7.2.3.2 Risk factors for the occurrence of 2 or more respiratory disease outbreaks per year

- Outcome and explanatory variables

The unit of observation was the farm. A case was defined as a farm that experienced 2 or more respiratory disease outbreaks during 1998. For possible explanatory variables the number of categories per variable was limited such that the category frequencies were >10% (Table 7.2). The variables under study were selected during a preliminary step to reduce the

chance of obtaining results affected by multicollinearity within the dataset (Dohoo et al., 1996). All bivariable relationships between possible explanatory variables were checked (χ^2 -test). For those relationships between variables that exhibited strong structural collinearity ($P < 0.05$), one of the two variables of interest (the one we believed to be most related to the outcome variable) was chosen.

- Model

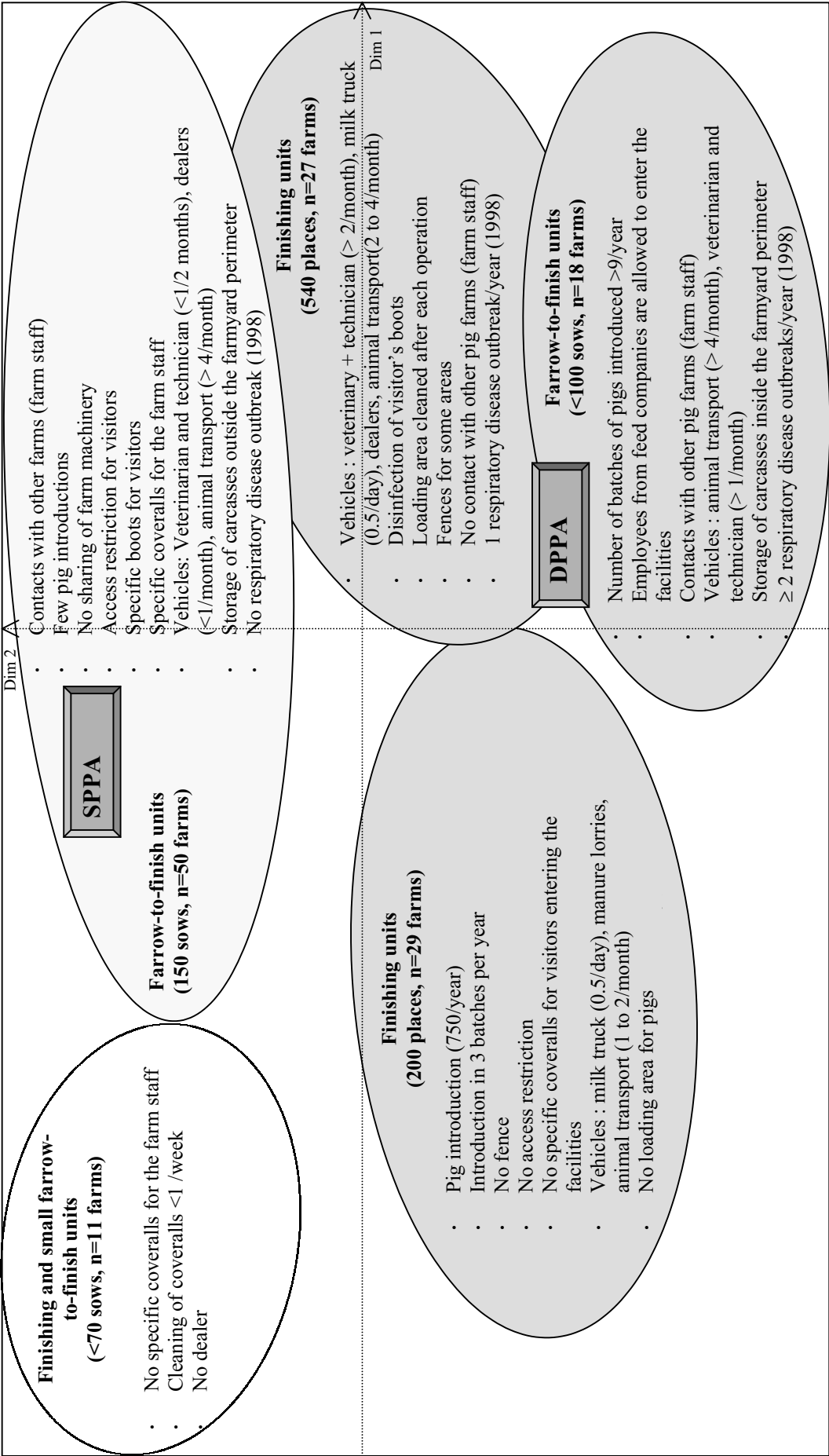
Logistic regression was used (proc LOGISTIC, (SAS, 1989)) according to the method described by Hosmer and Lemeshow (1989). In the first of the two steps, a univariable analysis related the outcome variable to each explanatory variable. Only factors associated with the outcome (likelihood-ratio χ^2 -test, $P < 0.25$) were used in the multivariate model (Table 7.2). The second step involved a logistic multiple regression model that included all factors that passed the first screening. The contribution of each factor to the model was tested using a likelihood-ratio chi-square test (McCullagh and Nelder, 1989). The variable with the highest P was removed and the logistic regression was rerun. This process was continued until a model was obtained with all factors significant at $P < 0.10$ (2-tailed). The variables farm system (Finishing / Farrow-to-finish) and geographical area (DPPA / SPPA) were included in the model in order to adjust the estimation of the odds ratios according to these factors. All possible interactions between these forced variables and other significant factors were tested.

7.3 Results

7.3.1 Profiles of the DPPA and SPPA (Figure 7.2)

One hundred and thirty five farms were included in the analysis and five clusters were obtained according to the hierarchical clustering. The cumulative percentage of inertia for the 3 first dimensions was 24.5%. The DPPA was not homogenous with regard to farm characteristics. Three clusters were related to this area: (1) one group of small finishing units [bottom, left part of the map], (2) one group of larger finishing units [middle, right part of the map], and (3) one group of farrow-to-finish units [bottom, right part of the map]. Finishing units applied few biosecurity measures (no specific coveralls, no access restriction) and introduced a large number of pigs per year but in few batches. The number of vehicles entering the farm per month was moderate to high and these farms experienced few respiratory disease outbreaks per year ($\leq 1/\text{year}$). In contrast, the farrow-to-finish farms that were surrounded by all the previously described finishing units applied very poor biosecurity

Figure 7.2 Multivariate description of the features of the pig farms (135 pig farms) - Dimensions 1-2 of the Multiple Correspondence Analysis. Features related to DPPA □ and SPPA □. 21 active variables, 57 categories, 1 supplementary variable (DPPA/SPPA).



measures and had a high number of vehicles entering the farm per month. They experienced more than two respiratory disease outbreaks per year.

The SPPA was mainly described as a large cluster of farrow-to-finish farms [top, right part of the map] characterised by good biosecurity measures and a low frequentation by vehicles. These farms did not experience any respiratory disease outbreak during the year. Finally, a small group of 11 farms was also related to the SPPA. This was represented by very small, isolated and marginal units where no biosecurity measure was applied.

7.3.2 Risk factors for the occurrence of 2 or more respiratory disease outbreaks per year

Twenty-four (17.8%) of the 135 farms under study experienced two or more respiratory disease outbreaks in 1998. Having more than four pig farms within a 2 km radius (OR=2.9), more than 30 incoming rendering trucks per year (OR=3.2), and storage of the carcasses of dead animals within the farmyard perimeter (OR=3.4) increased the risk of occurrence of more than two respiratory disease outbreaks per year in the farm. This risk was also increased when there were more than two animal transport lorries entering the farm per month (OR=5.1) and more than one veterinarian's or technician's vehicle coming in every 2 months (OR=5.5). Hosmer and Lemeshow's goodness-of-fit statistic indicated a good correlation of the predictive values with the observations ($p=0.83$). Interactions between the forced variables (farm system and geographical area) and the other variables included in the model were not significant.

7.4 Discussion

The random selection of the farms led to a good representation of the farms within each area and made description of the features of each area possible. The proportion of refusals and their reasons did not differ between the two areas so that comparison was possible. However, the 2 areas were not randomly chosen within the densely and sparsely populated areas of Brittany but were selected according to convenience criteria. Therefore, the results should not be generalised to DPPAs and SPPAs in France. Other areas might have been selected as the DPPA but we preferred to choose one with a mean pig density within the cantons exceeding 500 pigs/km².

The pig farms located in the DPPA and SPPA did not have the same profile. Farms located in the DPPA were mainly finishing units, where pig production was often a supplementary activity to dairy cattle. Farrow-to-finish farms located in this area were mainly small units with a rather poor health status and where few biosecurity measures were applied. This

situation might be explained by the presence of many finishing units in the area leading to numerous transfers of piglets that may increase the risk of virus spread as was suggested for Aujeszky's disease (Auvigne and Hery, 1997). In the SPPA, larger farrow-to-finish farms were encountered with better biosecurity measures, fewer vehicle contacts and with a better health status. Therefore, animal movements in association with animal density seem to be involved in the increased risk regarding the occurrence of respiratory disease outbreaks in finishing pigs.

Table 7.3 Final logistic-regression model for risk factors for the occurrence of 2 or more respiratory disease outbreaks per year (135 pig farms).

| Variables | Percentage of farms with ≥ 2 outbreaks/year (%) | Logistic model ^a | |
|--|--|-----------------------------|-----------------------|
| | | OR ^b | (CI ^c 90%) |
| Farm system | | | |
| Farrow-to-finish unit | 20.9 | 1.3 | (0.4, 3.9) |
| Finishing unit | 12.9 | - | - |
| Area | | | |
| DPPA ^d | 22.5 | 2.0 | (0.7, 5.4) |
| SPPA ^e | 10.9 | - | - |
| Number of pig farms in a 2 km radius area around the farm | | | |
| ≤ 4 | 10.9 | - | - |
| > 4 | 31.8 | 2.9 | (1.2, 7.4) |
| Storage of carcasses inside the farm yard perimeter | | | |
| No | 9.8 | - | - |
| Yes | 21.3 | 3.4 | (1.1, 10.4) |
| Number of animal transport vehicles entering the farm | | | |
| ≤ 2 / month | 5.9 | - | - |
| > 2 /month | 25.0 | 5.1 ^f | (1.5, 17.8) |
| Number of rendering plant lorries entering the farm | | | |
| ≤ 30 / year | 10.6 | - | - |
| > 30 /year | 34.2 | 3.2 ^f | (1.3, 8.1) |
| Number of veterinarian or technician vehicles entering the farm | | | |
| ≤ 1 every 2 months | 5.1 | - | - |
| > 1 every 2 months | 22.9 | 5.5 ^f | (1.4, 21.6) |

a) Intercept=-5.65, model deviance=92.5, df=7 ($p<0.001$)

b) Odds ratios

c) Confidence Interval ($p<0.10$)

d) Densely Populated Pig Area

e) Sparsely Populated Pig Area

f) Significant also at $p<0.05$ (likelihood-ratio χ^2 -test)

In order to determine the potential risk factors related to the different health status observed on farms located in the DPPA and the SPPA we decided to use as an indicator the number of respiratory disease outbreaks that occurred on the farm during 1998. Only acute outbreaks were included and the extreme situations defined as those farms in which two or more respiratory disease outbreaks occurred within a year. These were then compared with those with one or no outbreak. The diagnosis was made by the farmer and possible recall bias may have occurred. However farmers are very used to these kinds of respiratory outbreaks and both the fact that the data was collected by only one person and that only extreme situations were retained (≥ 2 respiratory outbreaks/year) may have contributed to a high degree of accuracy of the result. We only took collective outbreaks into account (Loeffen et al., 1999) where more than 80% of the pigs within a batch were affected; thus it was not possible to confuse them with other enzootic respiratory diseases. The outcome was thus defined upon clinical evaluation and the farm could be infected by several viral or bacterial agents responsible for this syndrome: Aujeszky's disease virus, Influenza viruses, Porcine Respiratory Coronavirus, PRRS virus or to a certain extent *Actinobacillus pleuropneumoniae* (Elbers et al., 1992). However, in farms with poor hygiene conditions, infection by these agents is often complicated by secondary infections leading to an acute clinical outbreak: primary infection by Aujeszky's disease virus followed by *Actinobacillus pleuropneumoniae*, or successive contamination by Influenza viruses (Elbers et al., 1990). The severity of the clinical expression of this syndrome in finishing pigs is therefore highly related to a disturbance of the farm ecosystem as influenced by environmental factors.

Pig herd density, measured in our study as the number of pig farms located within a 2 km radius, increased the risk of having more than two respiratory disease outbreaks per year. This observation is in accordance with previous findings concerning Influenza viruses in pig production (Elbers et al., 1990; Ewald et al., 1994; Madec et al., 1982; Maes et al., 1999; Maes et al., 2000). Therefore, a respiratory disease outbreak may be explained by successive or simultaneous contamination by viral agents (Van Reeth et al., 1996) related to considerable microbial exposure due to the high pig herd density. The increased microbial load on a given farm may also result from specific characteristics of that farm that were not investigated in this study (poor ventilation, immune status of the pigs...). However, within a densely populated area some factors related to the large number of pig farms in the neighbourhood might be conducive to successive contamination by viral agents if biosecurity measures are not correctly implemented at the farm level. Our results show that a high number of contacts with vehicles (animal transport, veterinary and technician) were a feature of farrow-to-finish farms located in DPPA (poor biosecurity measures). Elbers et al. (1992) showed that a high number of contacts (visitors associated with pig production) was linked with a high rate of H1N1 Influenza virus seropositivity in these farms. Nevertheless and

because of the cross-sectional design of the survey, we should be careful in interpreting these results as pig herd density is certainly the major factor implying the other conditions such as the number of visits by the veterinarian, technician or rendering lorries. Moreover, these visitors come more often if the health situation on the farm is poor and these factors may be interpreted as consequences rather than causes. Pig herd density is therefore the main factor and affects the features of the area: high number of small finishing units, piglet movements. Biosecurity measures at farm level should be implemented to improve the safety of farms located in these densely populated areas: restricted access for vehicles, location of loading areas outside the farmyard perimeter, and basic hygiene measures for visitors before entering the facilities. Although the pigs remain the main factors for virus introduction via asymptomatic carriage of infectious agents, the above recommendations might help to reduce the risk of introduction of viral and bacterial agents into pig farms.

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Disease risk factors in relation to management and contact patterns with emphasis on Aujeszky disease in pig farms of a densely populated area.

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Abstract

The main objective was to quantify risk for contracting and/or spreading diseases in relation to characteristics of management and/or contact patterns of pig farms within densely (DPLA) and sparsely (SPLA) populated livestock areas. Such information should allow classification of farms according to their disease risk. ADV (Aujeszky Disease Virus) was chosen as a reference because of its prevalence on pig farms in Belgium. Eventually, the selected risk factors have to be compared with those inferred for other important diseases, such as CSF (Classical Swine Fever) and FMD (Foot and Mouth Disease), to define strategies for prevention and eradication. Data was collected in two phases. In phase I a cross-sectional study was carried out on 46 mixed pig farms (23 DPLA, 23 SPLA), which participated in the IQC (Integral Quality Care) system of COVAVEE. In phase II 96 farrow-to-finishing farms (30 cases, 66 controls) were selected within a DPLA for a matched case-control study from the database of the ADV statute programme of the Animal Health Care Flanders.

Important risk factors for respiratory diseases are a high number of animals per unit of area, a high number of contacts and outdoor facilities. Protection factors are good hygiene, use of a spare compartment, application of quarantine and a number of empty days before repopulating the pens (Phase I+ II). Management factors can influence the status for Aujeszky disease on the pig farm (Phase II). Application of all-in/all-out procedures, not regrouping animals, not placing too many animals in one compartment and a good purchase strategy can reduce the chances of a farm testing positive for a disease like ADV. Hence, the disease risk within a DPLA can be reduced by adequate farm management procedures.

8.1 Introduction

The decision to carry out industrial livestock farming within densely populated areas is based on immediate economic benefits, i.e. gaining a higher labour income per unit of arable land on the farm. However, sustainability is endangered in the long term by environmental, animal

health and welfare issues. Epidemic diseases are linked to industrial livestock farming within densely populated areas. However besides sporadic but very expensive epidemics, a lot of additional daily problems are impairing a farmer's income, which may reduce the potential for other investments. Moreover, the health status of farms has to be harmonised within the EU in order to promote the free trade concept.

A case study of farms with fattening pigs showed that (1) between farm variability of management explained about 30% of the observed variability within feed conversion ratio, mortality and carcass quality; (2), there was a high correlation between coughing and air temperature variability as well as the thermal insulation characteristics of the pig house; (3), there was a high concentration of coughing with the mixing of piglets originating from different farms, duration of transport and the effective temperature conditions of the pig house at arrival (Geers et al., 1984,1989). Serological prevalence of four infectious respiratory diseases was found to be related to season, herd size and pig density (Maes et al., 1996). In the mean time a lot of evidence became available to support the implementation of efficient surveillance of the production chain in order to reduce daily production costs.

Therefore, systems for the prevention and surveillance of diseases should allow for the improvement of daily management at farm and sector level. The advantages are: (1) the pay-back of investments through the increase in daily profits; (2) the use of the system will become routine, making it immediately available and operational in case of a disease outbreak. Moreover, the system can be used as an early warning device for all kinds of sanitary problems at farm and sector level. Indeed, farms at risk will be pinpointed very quickly as well as farm-related activities within the sector (insemination centres, market/collection centres, feed suppliers, slaughterhouses, veterinary services, etc.), preventing further spread of the problem. Examples at sector level are already working (Blaha, 1996; Hurnik et al., 1996; Vellenga, 1996). Some countries (Belgium, Denmark, Germany, The Netherlands) are stimulating the implementation of the idea on a voluntary basis or by classifying farms according to hygienic standards for charging sanitary fees (MacDaniel and Sheridan, 2001).

However, the ranking of farms is only possible when an objective measure is available. A Sanitary Risk Index (SRI) may be a possible solution. This can be defined as a quantitative measure for the health status of a farm and/or the risk for contracting and/or of spreading animal diseases on a farm. The SRI is a function of a group of parameters to be measured in the field and their weight factors. It can be used to optimise the health status of individual pig farms as well as the health status of the pig production of a whole country. This SRI strategy should allow for a faster and more specific screening and detection of outbreaks of contagious and notifiable diseases, but it can also be used by the players on the market for the

selection of lower risk contacts. In order to validate the SRI concept, the following objectives were defined:

- Comparison of production and sanitary parameters of pig farms different with respect to management strategy (breeders, fatteners, breeding-fattening, multi-site) within sparsely or densely populated livestock areas (integration with Task B1);
- Inferring relationships between hygienic status, use of drugs on the farm and slaughter line observations in order to provide guidelines for developing an animal health and consumer safety control strategy (Task B3);
- Identification of quantitative risk markers as inputs for epidemiological simulation models to be used in surveillance and control tools (integration with Task D).

The basic research hypothesis to be tested was that pig farms with a good management have less risk of infections whether or not located in a densely populated livestock area, which improves the health status of the farm.

8.2 Materials and Methods

Data acquisition was based on the protocols used by Donham (1991); Elbers (1991); Flesja et al. (1982) and Maes et al. (1996):

- General information was collected by an interview on the farm, and included finding out details about the farmer (age, education level), management (use of PC, general work plan, all in/all out policy, sanitary strategy, vermin control policy), implementation of health programmes, administrative discipline;
- Baseline performance information including number of pigs within each category, breeding strategy, number of weaned piglets per sow and per year, pre- and postweaning mortality, feed conversion rate, growth rate, culling rate, hygienic status of buildings and equipment, veterinary costs, slaughter line information;
- Physical characteristics of the pig houses: engineering of the inside climate, floor type, fly control, feeding equipment, stocking density, cleaning and quarantine facilities, delivery pens, separation between the clean and dirty farm area;
- Import of piglets or breeding stock: origin and number of suppliers, transport conditions, physical condition of the pig house at arrival;
- Evaluation of slaughter pigs: slaughter line findings, serum profiling.

8.2.1 Phase I

8.2.1.1 Study design

A cross-sectional study was carried out on 46 mixed pig farms. They were all members of the Integral Quality Chain of COVAVEE. The selection of farms was based on the region where the farms were located, i.e. 23 farms in a densely populated area (DPLA) and 23 farms in a sparsely populated area (SPLA). Criteria were based on the density characteristics (sow places and fattening places within a radius of 3 km around the farm) of the farms as available from the SANITEL-v (pigs) database (Central Association for Animal Health, Belgium) (Table 8.1), since the criteria defined by Michel (1999) were not yet available. All farm animals, including place of birth and movements, are recorded in the SANITEL database.

Table 8.1 Parameters (mean, standard deviation, minimum, maximum) of the DPLA and SPLA.

| Parameters | SPLA n=23 | | | | DPLA n=23 | | | |
|---------------------------------|-----------|-------|-------|---------|-----------|--------|-------|--------|
| | X | SD | Min | Max | X | SD | Min | Max |
| Farms in a radius of 1 km | 3.6 | 2 | 1 | 8 | 10 | 5 | 3 | 18 |
| Farms in a radius of 3 km | 21 | 9 | 6 | 35 | 62 | 15 | 41 | 93 |
| Farms in a radius of 10 km | 175 | 68 | 60 | 277 | 617 | 148 | 196 | 777 |
| Sow places in a radius of 1 km | 307 | 189 | 90 | 789 | 796 | 432 | 245 | 1554 |
| Sow places in a radius of 3 km | 1357 | 800 | 113 | 2857 | 4558 | 1583 | 2256 | 7514 |
| Sow places in a radius of 10 km | 9144 | 4800 | 1656 | 19036 | 45330 | 11660 | 11622 | 58278 |
| Growing pig places (1 km) | 1771 | 1298 | 585 | 5458 | 5089 | 3186 | 1030 | 12284 |
| Growing pig places (3 km) | 7518 | 4767 | 1210 | 17181 | 30605 | 7714 | 12343 | 47697 |
| Growing pig places (10 km) | 55459 | 25799 | 20750 | 1113175 | 303696 | 100426 | 84196 | 502522 |

The following variables were collected as markers for the health status of a farm: serology for ADV and slaughter line findings (pneumonia (Pn), pleuritis (Plc), lungs with interlobular fissures (Fis) and lesions specific for *Actinobacillus pleuropneumoniae* (App) (Shaw et al., 1999). The blood samples were taken at slaughter from 25 fattening pigs of each participating farm during June and July 1998, while the slaughter line findings were collected during 1998.

All the farms were visited during the spring of 1998 and an interview took place on the farm. This inquiry was based on a list of potential risk factors for respiratory diseases and contagious diseases such as: farm layout, contacts (human, animal, vehicles), artificial insemination, manure and neighbourhood infection. In May and June 1999 an additional inquiry was carried out focussing on structural differences between DPLA and SPLA, and the information was made available to other partners in the project.

8.2.1.2 Statistical analysis

Data was analysed using univariate methods (frequency analysis, Student t-test, Wilcoxon test) taking into account the following class variables: region (DPLA, SPLA), ADV, pneumonia, pleuritis and fissures. Specific lesions for App - *Actinobacillus pleuropneumoniae* - were left out, because of problems with data interpretation. The first two variables were dichotomous, while the others were dichotomised based on the median. After this selection procedure of the most important risk factors, the intention was to quantify their relative importance by means of logistic regression procedures (SAS, 1995).

8.2.2 Phase II

8.2.2.1 Study design

ADV was chosen as a disease model to test the research hypothesis, because farms are still infected (Van Vlaenderen et al., 1999; Hooyberghs, 2001). As for FMD and CSF, air spread and the density of pigs and pig farms in the neighbourhood are also potential risk factors.

Farrow-to-finish farms were selected in a DPLA in Belgium, i.e. West Flanders (1,446 pigs/m²) (Michel, 1999). Data was collected within a matched case-control design, being an observational study (Noordhuizen et al., 1997). Cases were defined as farms testing positive for ADV. On these 30 farms ADV circulation was evident from obvious positive serological results (mean prevalence = 46%). The blood samples were taken for the official eradication programme (Anonymous, 1998). A control farm was a farm that was negative for the different tests for ADV status determination. In order to find differences in management between farms testing positive and negative for ADV, cases and controls were matched for both farm size and density of the area. Besides density other important factors are mentioned in the literature, namely factors on the level of the management of the pig farm and farm characteristics (Table 8.2). The management may be responsible for both limiting the spread and the elimination of the virus on the farm (Table 8.2). In addition, in a further stage of an eradication campaign it is important that farms maintain their free status. When the probability is lower that the virus is spreading on the farm, then the virus spread between farms will also be lower.

Table 8.2 Risk factors for spread of ADV within a pig farm.

| Risk factor | Author(s) |
|------------------------------|--|
| Confinement housing | Anderson (1990); Austin et al. (1993); Norman et al. (1996); Siegel and Weigel (1999) |
| Pig density in the stables | Bouma et al. (1995); Lehman et al. (1994) |
| Farm size | Anderson (1990); Duffy et al. (1991a); Duffy et al. (1991b); Morrison et al. (1991); Siegel et al. (1993); Leontides et al. (1994a); Leontides et al. (1995); Stärk (1999) |
| No compartments | Elbers et al. (1992); Duffy et al. (1991a); Lehman et al. (1994) |
| Production of breeding stock | Lehman et al. (1994); Stegeman et al. (1995); Stegeman et al. (1996) |
| Other respiratory diseases | Anderson (1990); Elbers et al. (1992); Leontides et al. (1994) |
| Not using all-in all-out | Lehman et al. (1994); Weigel et al. (1992) |

For spread between farms the following factors seem to be important (Table 8.3).

Table 8.3 Risk factors for spread of ADV between pig farms.

| Risk factor | Author(s) |
|---|--|
| Purchase of animals | Anderson (1990); Duffy et al. (1991a); Duffy et al. (1991b); Morrison et al. (1991); Siegel et al. (1993); Leontides et al. (1994a); Leontides et al. (1995); Stärk (1999) |
| Aerogen spread | Christensen (1990); Stärk (1999) |
| Density of pigs in the neighbourhood | Leontides et al. (1994a); Leontides et al. (1995); Stegeman et al. (1995); Boelaert et al. (1999); Siegel en Weigel (1999); Stärk (1999) |
| Density of infected pigs in the neighbourhood | Austin en Weigel (1992); Weigel et al. (1992); Norman et al. (1994); Norman et al. (1996) |
| Vehicles, wildlife and persons | Schoenbaum et al. (1991); Stegeman et al. (1994); Austin et al. (1993); Elbers et al. (1992) |

8.3 Matching

In order to find possible differences in management between farms testing positive and negative for ADV, cases and controls were matched for farm size and density.

For each case control farms were selected from the database “SANITEL Pigs” as far as possible. For density the number of pigs per square kilometre on village level was used (Michel, 1999). Farm size was matched by the number of sows, because it is very difficult to find a farm with a comparable number of sows and fattening pigs in the same village. After matching, 15 groups were used in the further analysis. Table 8.4 shows the groups with their characteristics.

Table 8.4 Number of groups, total number of farms, the number of cases, the number of sows or minimum and maximum for the cases, the number of controls, the number of sows or minimum and maximum for the controls and the pig density on village level for each group.

| Group | Total farms | Cases | # sows | Controls | # sows | pigs/km ² |
|-------|-------------|-------|-----------|----------|-----------|----------------------|
| 1 | 3 | 1 | 260 | 2 | 300 – 310 | 1683 |
| 2 | 3 | 1 | 75 | 2 | 100 – 110 | 1683 |
| 3 | 6 | 2 | 120 -200 | 4 | 75 – 265 | 1284 |
| 4 | 3 | 1 | 160 | 2 | 115 – 150 | 1282 |
| 5 | 3 | 1 | 195 | 2 | 120 – 150 | 2463 |
| 6 | 10 | 2 | 200 | 8 | 150 – 280 | 1787 |
| 7 | 7 | 2 | 120 - 170 | 5 | 115 – 160 | 3202 |
| 8 | 7 | 3 | 180 - 300 | 4 | 200 – 260 | 4159 |
| 9 | 3 | 1 | 50 | 2 | 100 – 125 | 3457 |
| 10 | 7 | 1 | 110 | 6 | 52 – 200 | 4192 |
| 11 | 7 | 3 | 60 - 175 | 4 | 80 – 130 | 3056 |
| 12 | 7 | 1 | 200 | 6 | 160 – 230 | 4239 |
| 13 | 6 | 3 | 300 - 380 | 3 | 300 – 350 | 4239 |
| 14 | 16 | 6 | 120 -200 | 10 | 90 – 200 | 3561 |
| 15 | 8 | 2 | 140 - 220 | 6 | 120 – 200 | 1666 |
| Total | 96 | 30 | | 66 | | |

8.4 Risk factors

Information about the farm's management was collected by means of a personal interview on the farm. The controls were selected as mentioned above. They were contacted by a letter and after a week, they were asked for their cooperation by telephone. The response rate from the control farms was 72%. A veterinarian from the Veterinary Service visited the cases instead. All cases detected between July 2000 and February 2001 were visited and all participated in the study. The control farms were visited between December 2000 and February 2001.

The enquiry was the same for both cases and controls. Data about the following potential risk factors for ADV was recorded:

1. Information about the farm (type, purchases of piglets and breeding animals and sales of animals);
2. Farm size (number of sows and fattening pigs);
3. Farrowing compartment (number of compartments, all-in all-out, cleansing, disinfecting, drying period);
4. Piglet compartment (number of compartments, all-in all-out, cleansing, disinfecting, drying period, regrouping of animals);

5. Pre-fattening compartment (number of compartments, all-in all-out, cleansing, disinfecting, drying period, regrouping of animals);
6. Fattening compartment (number of compartments, all-in all-out, cleansing, disinfecting, and drying period, regrouping of animals);
7. Sow compartment (group housing, cleansing, disinfecting, drying period);
8. Breeding animals (purchase of boars/sows, own selection of breeding animals);
9. Quarantine (presence of boars, gilts, cleansing and disinfecting, drying period);
10. Vaccination (type of vaccine, scheme of vaccination, in which stable, needle length, preservation of the vaccine).

The pig houses were visited in order to validate this information. The stables for all cases were inspected as well as 28 of the 60 control farms. Some of the information was also verified using information available from the SANITEL system.

8.4.1 Statistical Analysis

Data was analysed using a simple and multiple conditional logistic regression in order to test the relation between the factors (SAS, 1995).

8.5 Results

8.5.1 Phase I

Results of the frequency analysis between the region and health parameters (class variables) are shown in Table 8.5. In cases where the odds ratio is greater than one (i.e. β -estimate is positive), the disease tested occurred more frequently in the DPLA region.

Table 8.5 Results of the frequency analysis.

| Variable | β -estimate | Confidence interval 95% | P-value |
|----------|-------------------|----------------------------|---------|
| ADV | 7.5 | 0.82 – 68.8 | 0.095 |
| Pn | 3.75 | 1.02 – 13.8 | 0.043 |
| Plc | 3.28 | 0.97 – 11.1 | 0.053 |
| Fis | 22.6 | 4.91 – 104 | 0.001 |

When analysing the results of the two inquiries, the following possible important risk and protection factors for the presence of slaughter line findings and ADV were inferred:

- Risk factors:
 - Higher number of animal places
 - Higher number and frequency of purchase of breeding stock
 - Sharing of equipment with other farms
 - Purchase and sales from a dealer
 - More contacts with neighbouring farms
 - Use of outdoor facilities
- Protection factors:
 - Good hygiene (cleansing of the farm, all in/all out)
 - Presence of a spare compartment
 - Application of quarantine

8.5.2 Phase II

Only the variables with sufficient variation were taken into account for analysis.

Table 8.6 Independent factors with a P – value < 0.25

| Risk factor | p - value | Risk Ratio |
|---|-----------|------------|
| The presence of a prefattening compartment | 0.001 | 4.38 |
| One extra day for drying period in farrowing compartment | 0.007 | 0.74 |
| Drying period in quarantine | 0.03 | 0.25 |
| Drying period in piglet compartment | 0.03 | 0.34 |
| Not using all-in all-out and/or drying period in the piglet compartment | 0.03 | 3.14 |
| One extra pig per compartment | 0.03 | 1.013 |
| Purchase of boars | 0.04 | 3.15 |
| Not using all-in all-out in the fattening compartment | 0.06 | 2.42 |
| Sale of animals | 0.1 | 0.45 |
| Not using all-in all-out in the prefattening compartment | 0.1 | 3.64 |
| Not using all-in all-out in the farrowing compartment | 0.12 | 2.72 |
| Not regularly cleansing the prefattening compartment | 0.14 | 4.49 |
| Three week system | 0.15 | 0.35 |
| One extra day for drying period in prefattening compartment | 0.15 | 0.79 |
| One extra day for drying period in fattening compartment | 0.16 | 0.89 |
| Purchase of gilts | 0.18 | 0.5 |
| Not cleansing the farrowing compartment | 0.19 | 2.49 |
| Regrouping pigs (from battery to prefattening and/or fattening compartment) | 0.2 | 1.99 |
| Not regularly disinfecting the prefattening compartment | 0.2 | 3.89 |

8.5.2.1 Simple univariate analysis

The results from the simple analysis (Table 8.6) indicate that there are some important differences between farms testing positive and negative for ADV.

- The most important factor seems to be the presence of a prefattening compartment for pigs between 20 and 40 kilograms.
- Rest before refilling the compartments seems to be a protecting factor (drying period).
- Not using the all-in all-out principle at different stages seems to be a risk factor for ADV.
- Not regularly cleansing and/or disinfecting stables is a risk factor for ADV.
- A high density on the farm itself (number of animals per compartment) is also a risk factor.
- Regrouping animals at 20 and/or 40 kilograms and/or at a later stage of the fattening period is a risk factor for this disease.
- Sale of animals (piglets and breeding animals) seems to be a protection factor.
- Purchase of boars seems to be a risk factor; whereas purchase of gilts seems to be a protection factor.

8.5.2.2 Multiple univariate analysis

All the variables mentioned in Table 8.6 were used for the multiple analysis. Forward, backward and stepwise/step-by-step selection procedures were used to find the best models.

The following models were selected (models with two significant factors).

Table 8.7 Selected risk factors from the multiple analysis.

| Model | Risk factor | P-value | Risk ratio |
|-------|------------------------------|---------|------------|
| 1 | Prefattening compartment | 0.0333 | 5.199 |
| | Drying farrowing compartment | 0.0253 | 0.736 |
| 2 | Purchase of boars | 0.0395 | 3.934 |
| | Prefattening compartment | 0.0018 | 5.953 |
| 3 | Drying fattening compartment | 0.0241 | 0.735 |
| | One extra pig in compartment | 0.0311 | 1.013 |

The presence of a prefattening compartment, purchase of boars and more animals per compartment are risk factors for ADV.

Allowing the farrowing compartments to remain empty for an extra day after the piglets and sows have left and before new sows enter the compartments is a protecting factor. The first

model seems to be the best from a statistical point of view whereas from a biological viewpoint all three models are valuable.

8.6 Discussion and conclusions

Pig density has already been mentioned several times as an important risk factor for respiratory diseases (Maes, 1998; Boelaert et al., 1999; Stark, 1999, 2000). This is confirmed by the results of Phase I.: A high number of animal places per area, a high number of contacts and the presence of outdoor facilities have to be considered as disease risk factors. These can be minimised by the application of the following protection factors: good hygiene, availability of a spare compartment, application of quarantine and an empty period before repopulating pens. Moreover, the results of Phase II proved that through density the same risk factors could explain an important variation within the health status of pig farms for ADV, confirming the research hypothesis. The management of the pig farms can also play an important role in the risk status of the farm for ADV.

- The presence of a prefattening compartment is a risk factor for ADV. This can have different explanations.

Firstly, a prefattening compartment is more typical for older farms. On older farms, it is not so easy to implement new systems like all-in all-out, cleaning and disinfecting and a period of rest before refilling, because this was not taken into account when the stables were built. When the all-in all-out system is used in the prefattening compartment, the risk of contracting ADV is lower. Therefore it is a protective factor.

Generally the all-in all-out system is only used by 27% of the pig farms in the prefattening compartment compared with 86% in the farrowing compartment and 40% in the piglet and fattening compartment.

Secondly, pigs were probably regrouped or replaced more frequently, which could also be responsible for a lower immune status of the pigs, thus increasing the risk of a disease such as ADV being present on a farm (Harris and Alexander, 1999). The possibility is also greater that pigs of different ages were mixed. This could have an effect on the vaccination programme that is not correctly applied. Mismatching of ages, or vaccinating pigs at the moment when they are moved to a prefattening compartment i.e at a moment when their immune status is lower may lead to the vaccine not working optimally.

- *One days extra rest before refilling the farrowing compartments seems to protect against ADV.* This is one of the parameters of the all-in all-out system. The all-in all-out system with cleansing and disinfecting and a rest before refilling reduces the presence of pathogens in the pig houses (Harris and Alexander, 1999). A three-week system for the breeding stock also allows for the option of implementing an all-in all-out system.

- *Purchase of boars is a risk factor in this study.* It is known that the introduction of animals is a risk factor for the introduction of diseases. Currently all breeding stock needs to be tested before selling. Moreover, boars can be used for the oestrus detection of sows, which can promote the spread of a virus.

- *In contrast, purchase of gilts is a protective factor.* Own breeding stock can be a risk factor for ADV. Breeding one's own stock needs supplementary places and management skills that are not always present on all farms. In these cases it is recommended that breeding stock be purchased from both known and as few as possible sources.

- *Overcrowding* or a high number of animals per compartment is also found to be a risk factor. It is already known from other studies that the more animals in a compartment, the greater the risk that there is spread of a virus, especially when the virus can spread by air.

For density, the number of pigs per square kilometre at village level was used. It is known that the distribution of pig farms is not the same throughout the whole village. Therefore, it would be better to take this distribution into account. This may be possible when working with the kernel estimates (Mintiens, 2000). In a further stage of the research, new groups will be made based on the kernel estimates of each pig farm. Some variables had a P-value below 0.25 but they were obviously a result of the farm being positive for ADV. For example needle length, using quarantine and using a correct vaccination scheme. When a farmer uses a perfect needle length, they seem to have more chance of having ADV. These are the results of an intensive eradication campaign that is held on the positive farms. Namely the negative farms were not controlled on these points because they have no problems; positive farms were strongly controlled on these factors instead. The cases already knew that they were positive for ADV and that they needed to be negative as soon as possible, which can explain these results. These parameters were not taken in consideration for the multivariate analysis.

Despite these discussion points the results are based on a good response rate and a reliable number of farms, so that they can be used to help eliminating ADV from pig farms; certainly when the same factors are confirmed by further analysis with the kernel estimate. Good management such as all-in all-out, not regrouping animals, not too many animals in one compartment and a good purchase strategy can reduce the chances of a farm testing positive

for ADV. These factors are also important when the herd is free, they can help the herd to remain free and ensure the more rapid elimination of a new infection.

The available results demonstrate the possibility of introducing the concept of a sanitary risk index as a rating device at farm level for daily use, and probably also in the case of an outbreak of a notifiable disease when the same risk factors are involved. On-farm sanitary improvement can be established faster than structural changes in the region, thus reducing the risk potential of an area. However, information should be both available on line and accurate. Information on animal numbers and movements are available from the SANITEL-v (pigs) database, while information on slaughter line findings can be collected in a semi-automated way by use of a hand-held computer (Huysmans et al., in preparation). Currently the procedure is on test in the different slaughterhouses of the COVAVEE group. Other important information related to hygiene and contacts on a farm is more difficult to collect, and has to be considered as the farmer's responsibility. Therefore, general hygiene, application of sanitary measures, the number of animal places, number of animals purchased and the frequency of purchase, i.e. contacts in general (Huysmans et al., 2001), may be considered as important risk or protection factors.

8.7 Conclusions

1. DPLA is a risk factor, which can be minimised by the application of appropriate farm management procedures, including reduction of contacts.
2. A list of relevant data to be collected on pig farms as indicators of disease risk is available.
3. A standardised questionnaire and protocol for collecting data are available.
4. A definition of possible risk profiles for ranking individual farms is available, but needs further validation.

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Task C

Analysis of recent disease outbreaks of CSF and FMD to test and refine the risk parameters

Prediction of the likelihood of spread of Classical Swine Fever Virus through ‘neighbourhood infections’ for different regions in Belgium

K. Mintiens, H. Laevens, J. Dewulf and F. Koenen, Belgium

Agreements of communities with dense pig populations and communities with high risk for neighbourhood spread of Classical Swine Fever in Belgium

H. Laevens, K. Mintiens, J. Dewulf, F. Koenen and A. de Kruif, Belgium

Modelling the effect of herd size on the probability of herd infection: application to the infection of airborne FMD

G. Gerbier, V. Chevalier, R. Pouillot, B. Durand and F. Moutou, France

Prediction of the likelihood of spread of Classical Swine Fever virus through ‘neighbourhood infections’ for different regions in Belgium

K. Mintiens, H. Laevens, J. Dewulf and F. Koenen

Abstract

In this study, risk factors associated with the occurrence of ‘neighbourhood infections’ (Westergaard, 1996) during Classical Swine Fever (CSF) outbreaks were examined based on information collected by Veterinary Officers from the Ministry of Agriculture during the CSF epidemic in East Flanders (Belgium) of 1994. Neighbourhood infections were observed in the neighbourhoods of 9 out of 19 primary herds. The only risk factor that was associated with the occurrence of neighbourhood infections was the bivariate kernel estimate of intensity ($P = 0.0553$), i.e. the higher the bivariate kernel estimate of intensity, the higher the risk for occurrence of neighbourhood infections.

In a second part of the study the bivariate kernel estimate of intensity of neighbouring pig herds in a 1 km radius was calculated for all Belgian pig herds based on available geographical coordinates. In a subsequent step, the likelihood for the occurrence of neighbourhood infections within an area with a 1 km radius was predicted for every Belgian pig herd, given that the herd was infected with CSF virus. For the prediction of these likelihoods, the model resulting from the risk factor analysis mentioned above was used. Finally the predicted likelihoods were displayed on a map of Belgium at country level after applying smoothing techniques. As a result, different areas of higher or lower risk for CSF virus spread through neighbourhood infections could be identified on these maps. The areas in Belgium where CSF outbreaks including ‘neighbourhood infections’ occurred in recent decades were all predicted to be of high risk.

9.1 Introduction

In the past, certain areas of the European Union developed highly concentrated livestock populations because of their considerable economic advantages. However, these areas also

appeared to incorporate an increased risk for epidemic diseases and therefore, despite the economic advantages, may have proven to be unsustainable in the long term. In order to estimate the extent to which this livestock concentration is responsible for the increased risk of epidemic diseases, a risk assessment based on real outbreak data is required. This paper presents the risk factors responsible for the spread of Classical Swine Fever (CSF) within the close vicinity of a pig herd on which the CSF virus has been introduced. The risk factors were assessed based on data obtained during a CSF outbreak, which occurred in Belgium in 1994.

In a second part the paper presents a classification of the different regions in Belgium according to the risk for the occurrence of the ‘neighbourhood infections’ they incorporate in the case of a CSF epidemic. This risk was predicted using the probability that pig herds become infected with CSF when located in an area with a one-kilometre radius surrounding a primary CSF infected pig herd, based on the resulting model of the risk factor analysis.

9.2 Materials and methods

9.2.1 Definitions

A neighbourhood was defined as an area with a radius of one kilometre surrounding a primary CSF infected pig herd. A primary CSF infected pig herd (primary herd) was defined as the first herd in which a CSF infection was confirmed in a neighbourhood. A neighbouring herd is a pig herd, other than the primary herd, located in a neighbourhood. A neighbouring herd was considered infected by the primary herd when the estimated day of virus introduction in the neighbouring herd occurred during the infectious period of the primary herd. To avoid dependency of neighbouring herds, no primary herds situated just outside an earlier defined neighbourhood were included in the analysis. Therefore neighbouring herds could only be allocated to one neighbourhood. The infectious period of the primary herd was defined as the period from the estimated day of virus introduction in the primary herd to the day when the primary herd was emptied. In cases where the virus was introduced into the primary herd in pigs housed in a pen housing system, the date of virus introduction was estimated using both the clinical history of the disease on the farm and the logistic regression models from experimental infections, as previously reported (Laevens et al., 1998; Laevens et al., 1999). When the virus was introduced in pigs housed in a sow-box housing system or in a farrowing unit, the date of virus introduction was estimated based on both the clinical history of the infection and the results of the virological and serological examination of the pigs on the farm.

9.2.2 Data

The data set used for the risk factor analysis consisted partially of variables obtained by the Belgian Veterinary Services as was used in the control of a CSF epidemic that occurred in the East Flanders Province of Belgium in 1994. (Koenen et al., 1996). Nineteen predictor variables (Table 9.1) were considered in the analysis, which could be divided into two groups, based on whether they were related to the primary infected herd or to the neighbourhood respectively. Additional 'spatial parameters', i.e. a bivariate kernel estimation of the intensity (Bailey and Gatrell, 1995), a Nearest Neighbour Index (Clark and Evans, 1954) and a Pielou index on non-randomness (Pielou, 1959) were calculated in order to estimate the spatial distribution of herds in a neighbourhood. A gini-index (Pyatt et al., 1980) was calculated to estimate the distribution of the pigs in the neighbouring herds. Categorical variables with n classes were transformed into $n-1$ dummy variables. The CSF infection status of the neighbouring herds served as a dependent variable. The infection status of the pig herds was determined by a virological and serological diagnosis carried out when the herds were depopulated.

9.2.3 Statistical methods

The risk factors for the occurrence of neighbourhood infections were investigated through logistic regression modelling (Neter et al., 1996) using the 'logistic' procedure in the SAS system version 8 (SAS Institute Inc., 1999). The outcome variable was defined as the proportion of infected neighbouring herds and the total number of pig farms in the neighbourhood was used as a weighting variable. The model was built using the forward step-by-step selection procedure with a significance level of $p < 0.25$ of the score chi-square for allowing a predictor variable to enter the model and a significance level of $p < 0.10$ of the Wald chi-square for allowing a predictor variable to stay in the model.

The effectiveness of the resulting model in describing the outcome variable was examined using the Hosmer-Lemeshow goodness-of-fit test (Hosmer and Lemeshow, 1989). Additionally, in a cross-validation procedure, the model parameters were re-estimated after deleting one of the observations (neighbourhoods) from the dataset. The newly obtained model was then used to predict the risk of neighbourhood infections in all neighbourhoods, including the one that was deleted from the dataset. This procedure was repeated for every neighbourhood in the dataset. The Hosmer-Lemeshow goodness-of-fit test was then used to evaluate the ability of the newly obtained models of predicting the risk for neighbourhood infections for all observations included in the dataset.

Table 9.1 List of risk factors and results of the descriptive analysis

| Variables | |
|--|--|
| <i>Independent categorical variables related to the primary herd^a</i> | |
| 1. Type of pig herd: | Fattening herd (n = 2) ^c , breeding herd (n = 2), farrow to finishing herd (n = 7), farrow to finishing herd + purchasing weaner pigs (n = 1), farrow to finishing herd + supply of weaner pigs (n = 7) |
| 2. Type of herd: | Pigs only (n = 10) versus other farm animals (cows) present (n = 9) |
| 3. Employees: | Yes (n = 3) vs. no (n = 16) |
| 4. Virus introduced in fattening unit (n = 12) vs. sow-box or the farrowing unit (n = 7) | |
| <i>Independent continuous variables related to the primary herd^a</i> | |
| 5. Time from virus introduction to stamping out (infectious period (IP)): | 25.8 days (16 - 41) ^d |
| 6. Number of pigs on the day of stamping out: | 1583 pigs (157 – 3433) |
| 7. Number of seropositive pigs on the day of stamping out: | 67 seropositive pigs (0 - 174) |
| 8. Mean number of visits per week by vehicles of the rendering plant during the IP: | 0.67 visits (0 - 1.54) |
| 9. Mean number of visits per week by vehicles of the feed stuff companies during the IP: | 0.84 visits (0.24 - 1.95) |
| 10. Mean number of visits per week by the herd veterinarian during the IP: | 0.83 visits (0.18 - 1.88) |
| 11. Mean number of pigs purchased per week (market support) during the IP: | 32.8 pigs (0 - 103.9) |
| 12. Mean number of times per week that pigs were purchased (market support) during the IP: | 0.35 times (0 - 1.69) |
| 13. Mean number of visits per week during the IP: (= 8 + 9 + 10 + 12): | 2.70 visits (1.19 - 4.27) |
| <i>Independent continuous variables related to the neighbourhood^a</i> | |
| 14. Pig farm density: | 2.51 farms / km ² (0.95 - 3.50) |
| 15. Pig density: | 2140 pigs / km ² (554 - 6229) |
| 16. Nearest neighbour index: | 0.892 (0.425 - 1.417) |
| 17. Pielou index of non randomness: | 0.941 (0.175 - 2.107) |
| 18. Gini index: | 0.478 (0.054 - 0.735) |
| 19. Kernel estimate of intensity: | 2.262 (0.476 - 7.023) |
| a) Descriptive analysis for 19 primary herds and neighbourhoods; | |
| b) Descriptive analysis for the 102 neighbouring herds; | |
| c) Number of observations; | |
| d) Mean (min - max) | |

9.2.4 Risk prediction

Different regions of Belgium were classified according to their risk for the occurrence of ‘neighbourhood infections’, predicted through the obtained model. Firstly, the risk was predicted for every pig herd in Belgium using identification & registration data from 1997 (SANITEL-V) and plotted on a vector map displaying the Belgian municipalities using the ArcView version 3.2 geographical information system. The point estimates of the predicted risk were transferred into a continuous surface variable using an Inverse Distance Weighted (IDW) interpolator (ESRI, 1996).

9.3 Results

9.3.1 Risk assessment

48 CSF herds were identified during the epizootic in East-Flanders in 1994. A total of 19 primary herds and their neighbourhoods, including 102 neighbouring herds, met the inclusion criteria. Twelve neighbourhood infections were detected in 9 neighbourhoods. The other 90 neighbouring herds were classified as uninfected. Seventy-seven of these uninfected neighbouring herds were preventively depopulated. The 13 neighbouring herds that were not depopulated remained free from CSF until the end of the epidemic. The results of the descriptive analysis of the risk factors are presented in Table 9.1.

The bivariate kernel estimate of intensity proved to be the best explaining predictor variable of the variation in the data and was positively associated with the risk for neighbourhood infections (Table 9.2). No significant lacks of fit were observed for the model based on all observations or for the models resulting from the cross-validation procedure (Table 9.3). The parameter was highly correlated ($\rho = 0.77$; $P < 0.001$) with the pig density of the neighbourhood, the second best explaining predictor variable for the available data.

Table 9.2 Parameter estimates for the logistic regression model

| Predictor variable | Parameter estimate |
|--|--------------------|
| Intercept | -2.9580 |
| Bivariate kernel estimate of intensity | 0.2957 |

9.3.2 Risk prediction

For 11,879 (90.8%) out of 13,115 pig herds, which were in registered in Belgium in 1997, the kernel estimate of intensity of neighbouring herds within a one kilometre radius was estimated using geographical coordinates. Of the remaining pig herds, 1,202 (9.1%) did not have other pig herds in their neighbourhood and for 34 (0.3%) herds no geographical coordinates were available. For the pig herds with neighbouring herds within a one kilometre radius, the kernel estimate of intensity varied from 7.7×10^{-8} to 13.022 (mean: 2.306; median: 1.817).

For the pig herds with no neighbouring herds within a one kilometre radius, the risk for 'neighbourhood infections' was set to zero. For the pig herds with neighbouring herds the predicted risk varied from 0.05 to 0.71 (mean: 0.11; median: 0.71). The smoothened predicted risk is mapped in Figure 9.1. Even after smoothening, areas with a potential higher risk, e.g. Tielt-Wingene', 'Kaprijke-Eeklo', can be observed from the map.

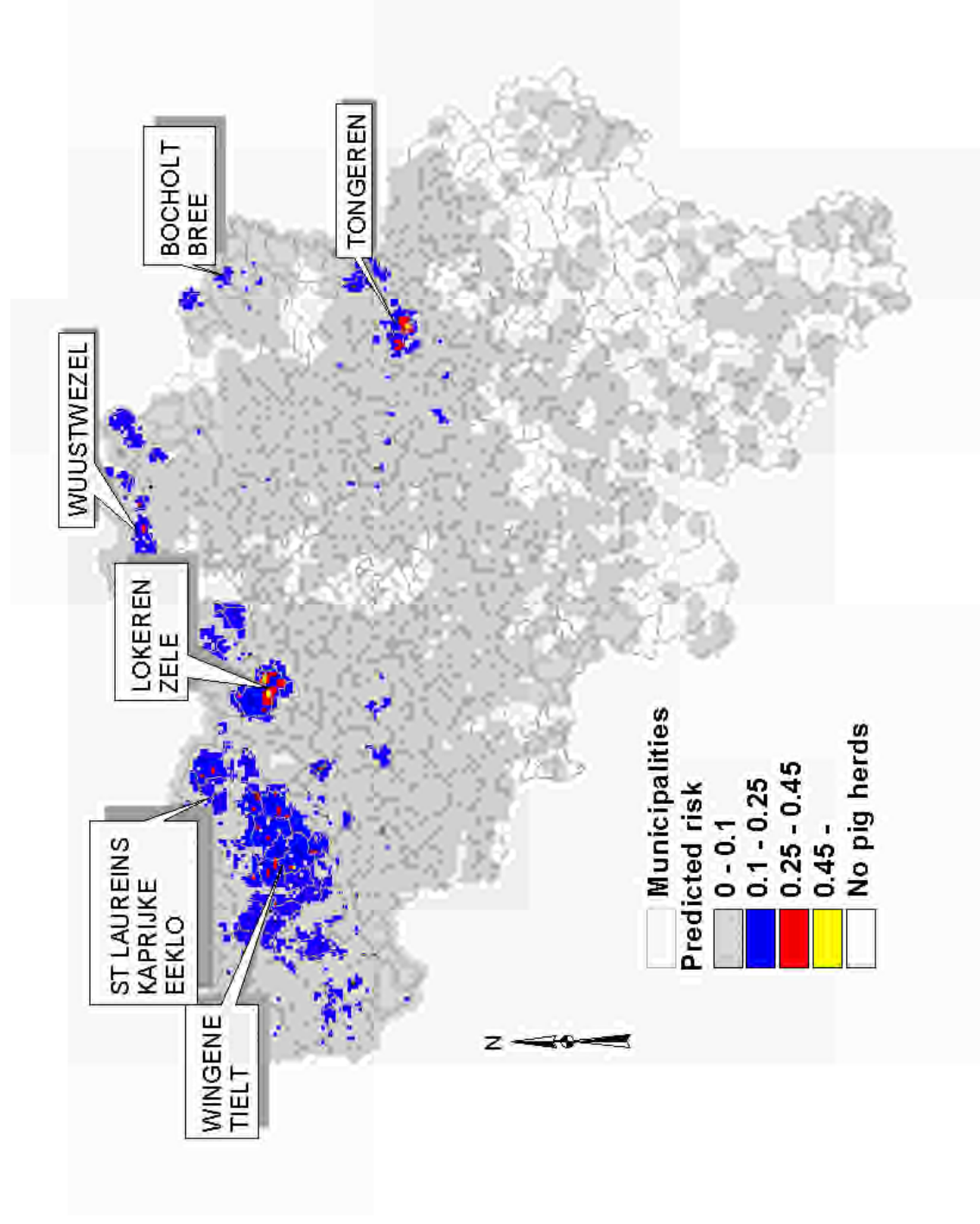
Table 9.3 Assessment of the goodness of fit of the model based on all observations and the models resulting from the cross-validation procedure (Hosmer-Lemeshow goodness-of-fit test)

| Deleted Observation | Chi-square | Degrees of freedom | P-value |
|--|------------|--------------------|---------|
| 1. Model based on all observations | | | |
| None | 2.7289 | 8 | 0.9502 |
| 2. Models resulting from the cross-validation procedure | | | |
| 1 | 2.6665 | 8 | 0.9535 |
| 2 | 2.8479 | 8 | 0.9435 |
| 3 | 2.6987 | 8 | 0.9518 |
| 4 | 2.7324 | 8 | 0.9500 |
| 5 | 3.2546 | 8 | 0.9174 |
| 6 | 3.0836 | 8 | 0.9290 |
| 7 | 2.7000 | 8 | 0.9518 |
| 8 | 2.7105 | 8 | 0.9512 |
| 9 | 2.9601 | 8 | 0.9368 |
| 10 | 3.4355 | 8 | 0.9041 |
| 11 | 2.8236 | 8 | 0.9449 |
| 12 | 2.8619 | 8 | 0.9427 |
| 13 | 2.7249 | 8 | 0.9504 |
| 14 | 2.7128 | 8 | 0.9511 |
| 15 | 2.6713 | 8 | 0.9533 |
| 16 | 2.6762 | 8 | 0.9530 |
| 17 | 2.6784 | 8 | 0.9529 |
| 18 | 2.7161 | 8 | 0.9509 |
| 19 | 2.9361 | 8 | 0.9383 |

9.4 Discussion

The bivariate kernel estimate of intensity is a spatial parameter, which combines the number of herds that are situated within the selected area (one kilometre radius) and the relative distance of these herds to the reference herd (CSF infected herd). The pig density, a parameter assumed to be associated with high risk for the introduction and spread of contagious diseases, did not explain as much variation as the bivariate kernel estimate of intensity did in the final model.

Figure 9.1 Classification of the different regions of Belgium based on the predicted risk for 'neighbourhood infection' during CSF-epidemics



The importance of neighbourhood infections proportionally to the total number of outbreaks was reported by (Roberts, 1995) and (Stegeman et al., 1997) and raised the question whether distance dependent risk factors could be the cause of these neighbourhood infections. The identification of the bivariate kernel estimate of intensity in our study as a possible risk factor may provide evidence for the importance of these distance dependent risk factors. However, this variable does not explain the nature of CSF virus transmission in the neighbourhood.

In the model-building dataset collected during a real CSF outbreak in 1994 the bivariate kernel estimate of intensity varied from 0.426 to 7.203. When predicting the risk for neighbourhood infections for the different regions of Belgium, the kernel estimate of intensity varied from 7.7×10^{-8} to 13.022. This means that the risk predictions for kernel estimates below 0.426 and above 7.203 will not necessarily be correct. Therefore the map presented should be seen as an illustration of a possible methodology for predicting the risk for CSF spread instead of an accurate estimate of the risk. Nevertheless, in a number of the displayed areas of higher risk, CSF outbreaks including 'neighbourhood infections' have occurred in the past, e.g. Wuustwezel (1989-90), Tielt-Wingene (1990-91, 1993), 'Zomergem-Nevele-Kaprijke-Eeklo(1994), and Bocholt-Bree (1997).

One of the recent developments in the control and eradication of epizootic diseases is the implementation of decision support systems (DSS). The DSS allow the prediction, based on epidemiological models containing risk factors for the spread of the disease, of the evolution of a disease outbreak over shorter or longer terms. The presented map with underlying methodology can be used as a DSS as the map can be consulted when a CSF-infection is diagnosed and specific sanitary measures can be taken depending on the displayed risk for neighbourhood infections. The map can also be used when concessions are to be assigned to new pig farms. The assignment can then be based on the predicted risk for neighbourhood infections or the kernel estimate of intensity.

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Health and Related Problems in Densely Populated Livestock Areas of the Community”. The participants in this project are the Wageningen Agricultural University (The Netherlands), the University of Vechta, (Germany), the Regional Centre for Veterinary Epidemiology in Legnaro (Italy), the Ministry of Agriculture (Belgium), the Ghent University (Belgium), the Catholic University of Leuven (Belgium), and AFSSA-Alfort (France).

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Agreements of communities with dense pig populations and communities with high risk for the neighbourhood spread of Classical Swine Fever in Belgium

H. Laevens, K. Mintiens, J. Dewulf, F. Koenen and A. de Kruif

Abstract

The purpose of this study was to estimate the correlation between communities with a high risk of neighbourhood spread of Classical Swine Fever (CSF) and communities with dense pig populations.

Communities were identified as being communities with a high risk of neighbourhood spread of CSF when the risk for ‘neighbourhood infections’ (Westergaard, 1996), as described by Mintiens et al. (this publication), of at least one neighbourhood in the community was above a preset cut-off value. Similarly, communities were classified as being communities with dense pig populations when the pig density of the community was larger than a minimal pig density.

The highest agreement (kappa statistic = 0.74) between the selection of communities with high risk for neighbourhood spread, and the selection of communities with dense pig populations, was observed when the cut-off value for the risk of ‘neighbourhood infections’ was 10% and the minimum pig density was 465 pigs / km². When the cut-off value was 25% or higher, the kappa agreement was only moderate or less than moderate.

For other cut-off values, the choice of the minimum pig density in a community to optimise the selection of communities with a high risk for neighbourhood spread of CSF was not straightforward. The choice will depend on the risk decision-makers want to take.

10.1 Introduction

Outbreaks of Classical Swine Fever (CSF) within the European Union (EU) have been associated with areas of dense pig populations, a high herd density and a high average herd size (Bendixen, 1985; Ellis et al. 1977; Windhorst and Dijkhuizen, 1998). These high risk areas in the EU are West and East Flanders in Belgium, Brittany in France, the Northwestern

part of Germany, Denmark, and the Southern and Eastern parts of The Netherlands (Westergaard, 1996; Windhorst and Dijkhuizen, 1998).

Using the FAIR-project ‘Development of Prevention and Control Strategies in order to Address Animal Health and Related Problems in Densely Populated Livestock Areas of the Community’, densely populated pig areas in the five participating EU countries (Belgium, France, Germany, Italy, and The Netherlands) were identified as being the top 5% of communities with the most dense pig populations (Michel and de Vos, this publication). A community with a dense pig population contained at least 300 pigs / km². These communities are assumed to contain a high risk for the introduction and spread of CSF.

Mintiens et al. (this publication) examined factors associated with the risk of neighbourhood spread of CSF. The only risk factor that was associated with the risk of neighbourhood spread of CSF was the bivariate kernel estimate of intensity of neighbouring herds within a 1 km radius of a primary infected herd. This risk factor was used to calculate the likelihood for ‘neighbourhood infections’ in the neighbourhood of each pig herd in Belgium.

The purpose of this study was to look at whether or not a agreement existed between communities with high risk for neighbourhood spread of CSF and communities with dense pig populations.

10.2 Materials and methods

10.2.1 Data

The initial dataset was made available by Mintiens et al. (this publication). In this dataset, geographical coordinates for each pig herd in Belgium in 1997 were available. Data on the postal codes and on the number of sow and pig places per pig herd in Belgium was obtained from the identification & registration database (SANITEL-V) of the Central Animal Health Organisation in Belgium. After merging these two datasets 1,486 records were deleted because no data was available on the number of sow and pig places. To calculate the actual number of pigs in the herds, a conversion was used (Table 10.1).

With this reduced dataset (number of records = 11,629) the risk for neighbourhood spread of CSF was recalculated for each pig herd as described by Mintiens et al. (this publication) and the pig density per community was calculated as the number of pigs / km² total land area.

Table 10.1 Conversion from the number of sow, and pig places to the actual number of pigs per herd

| Pig category | Actual number |
|--------------|--|
| Sows | # sow places x 0.9 ^a |
| Piglets | # sow places x 0.9 x 4.2 ^b |
| Pigs | # pig places |
| Total | (# sow places x 0.9) + (# sow places x 0.9 x 4.2) + # pig places |

a) 0.9: number of sows actually present;

b) 4.2: number of piglets with the sow during the whole year (J.M. Robijns, Central Animal Health Organisation, Belgium)

10.2.2 Data analyses

For varying cut-off values of risk for neighbourhood spread of CSF (ranging from 5, 10, 15, ... to 60%), communities were identified as being communities with a high risk for neighbourhood spread of CSF when the risk of at least one neighbourhood in the community was above the cut-off value.

Similarly, communities with dense pig populations were identified. A community was classified as being a community with a dense pig population when the pig density in the community was larger than the minimal pig density.

For each cut-off value, the minimum pig density of a community was calculated for which the agreement (kappa statistic) of the selection of communities with high risk for neighbourhood spread, on the one hand, and the selection of communities with dense pig populations, on the other hand, was maximal. Given the cut-off value and the minimum pig density corresponding with the maximum kappa coefficient, the observed proportion of overall agreement was calculated.

The kappa statistic calculates a chance-corrected measure of agreement of two raters, i.e. the proportion of communities with high risk for neighbourhood spread and the proportion of communities with dense pig populations. The interpretation of the kappa statistic is given in Table 10.2.

The observed proportion of overall agreement calculates the fraction of communities both fulfilling and not fulfilling both inclusion criteria, i.e. the preset cut-off value and the minimum pig density.

Additionally, for each cut-off value, a Receiver Operating Characteristic (ROC) curve for pig density was calculated. The ROC curve displays, for all possible pig densities and a given cut-off value for neighbourhood spread, the corresponding sensitivity and '1-specificity' of the identification of communities with high risk for neighbourhood spread of CSF based on the pig density of the community.

Table 10.2 Strength of agreement of kappa statistic

| Kappa value | Strength of agreement |
|-------------|-----------------------|
| 0.00 | Poor |
| 0.01-0.20 | Slight |
| 0.21-0.40 | Fair |
| 0.41-0.60 | Moderate |
| 0.61-0.80 | Substantial |
| 0.81-1.00 | Almost perfect |

10.3 Results

For the reduced dataset, the risk for the neighbourhood spread of CSF varied from 0 to 61.4% (median = 7.5%). Of the 590 communities in Belgium, 91 had no pig herds. The pig density in the remaining communities varied from 0.5 to 3,785.6 pigs / km² (median = 67.8 pigs / km²). The remainder of the analyses was performed only on the 499 communities with pig herds.

The number of communities with a high risk for neighbourhood spread of CSF and the description of the selected communities, given the cut-off value, is shown in Table 10.3. By increasing the cut-off value, the number of communities that fulfill the inclusion criterion decreased. Within these selected communities the number of neighbourhoods increased when the cut-off value increased whereas the total area of land remained constant. This resulted in an increase of the median predicted risk in the selected communities. Although the mean of the median predicted risk increased, the proportion of neighbourhoods with a risk for neighbourhood spread of CSF larger than the cut-off value, decreased.

Table 10.4 shows the minimum pig density for varying cut-off values for which the agreement (kappa statistic) of the selection of communities with a high risk for neighbourhood spread of CSF, and the selection of communities with dense pig populations, was maximal. The agreement was highest (0.74) when the cut-off value was 10%. The corresponding minimum pig density above which a community was classified as a community with a dense pig population, was 465 pigs / km². When the cut-off value was set at 10%, 124 communities with a high risk for neighbourhood spread of CSF and 106 communities with a dense pig population were selected and 92 communities fulfilled both criteria. When the cut-off value was 25% or higher the kappa agreement was only moderate or less than moderate.

Table 10.3 Number of communities with a high risk for neighbourhood spread of CSF^a and description of the selected communities

| Cut-off value (%) | Number of communities | Mean number of neighbourhoods within the communities (range) | Mean total area (km ²) | Mean of median risk for neighbourhood spread of CSF (%) | Mean percentage of neighbourhoods above the cut-off value in the communities (range) |
|-------------------|-----------------------|--|------------------------------------|---|--|
| 5 | 347 | 33 (2 – 253) | 53.1 | 5.9 (0 - 16.8) | 72.7 (10.0 – 100) |
| 10 | 124 | 71 (6 – 253) | 56.4 | 8.5 (2.5 - 16.8) | 31.5 (2.1 – 82.9) |
| 15 | 69 | 94 (17 – 253) | 59.7 | 9.8 (6.0 - 16.8) | 18.5 (0.5 – 57.3) |
| 20 | 41 | 104 (20 – 253) | 61.5 | 10.8 (6.1 - 16.8) | 13.2 (0.9 – 42.3) |
| 25 | 24 | 120 (42 – 253) | 65.5 | 11.7 (7.2 - 16.8) | 11.5 (1.3 – 30.0) |
| 30 | 17 | 109 (42 – 253) | 51.7 | 12.7 (7.2 - 16.8) | 9.0 (1.5 – 23.0) |
| 35 | 12 | 111 (42 – 253) | 59.6 | 12.5 (7.2 - 16.8) | 8.5 (0.7 – 19.0) |
| 40 | 9 | 108 (42 – 253) | 59.1 | 12.7 (7.2 - 16.8) | 5.9 (1.5 – 16.7) |
| 45 | 4 | 153 (42 – 253) | 69.6 | 13.8 (7.2 - 16.8) | 5.8 (1.2 – 9.5) |
| 50 | 2 | 159 (87 – 253) | 78.3 | 12.9 (12.4 - 13.5) | 2.3 (1.1 – 3.5) |
| 55 | 1 | 230 (230 – 230) | 68.9 | 13.5 | 0.4 (0.4 – 0.4) |
| 60 | 1 | 230 (230 – 230) | 68.9 | 13.5 | 0.4 (0.4 – 0.4) |

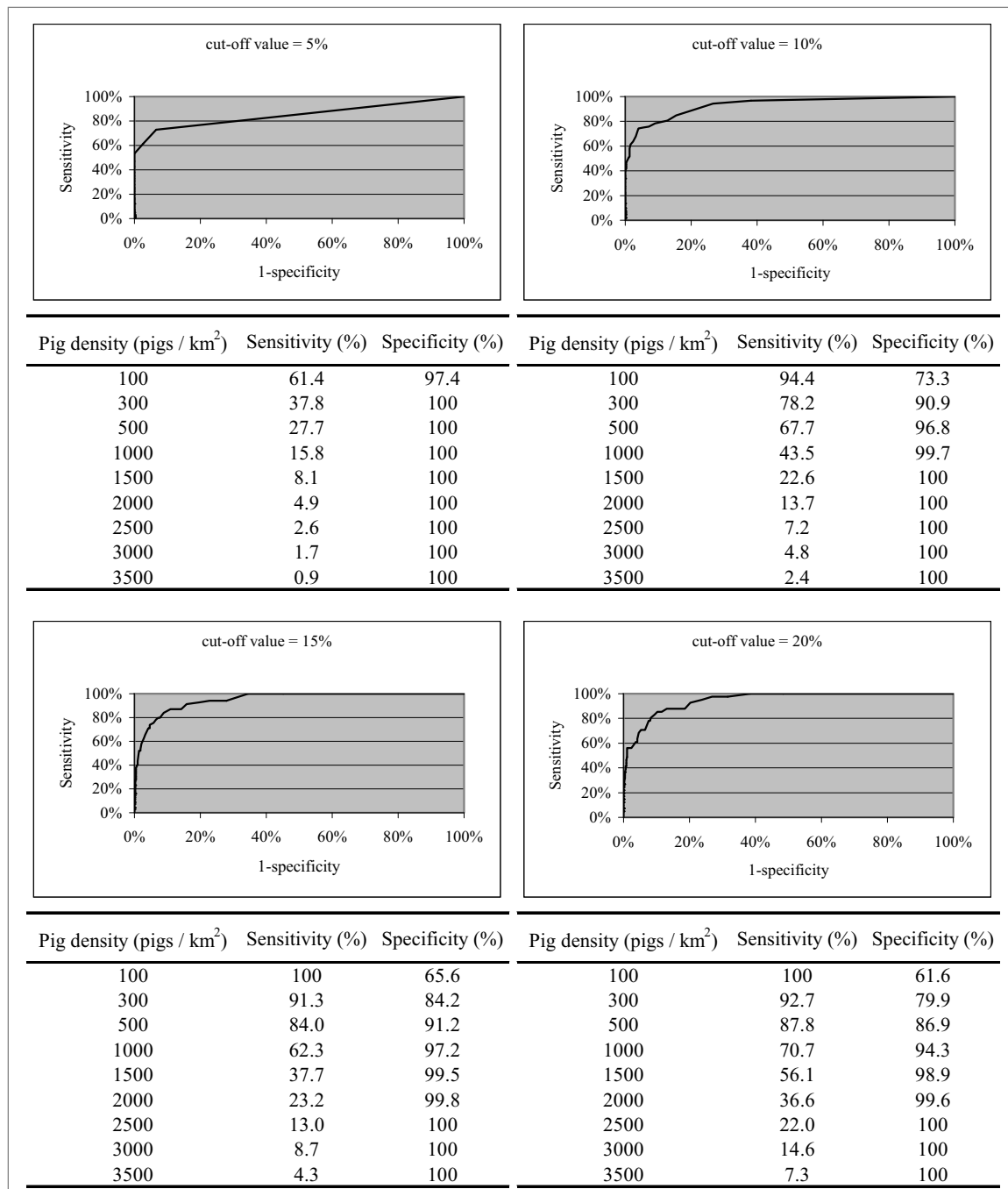
a) A community was classified as a community with a high risk for neighbourhood spread of CSF when the predicted risk for neighbourhood spread of CSF of at least one neighbourhood in the community was above the cut-off value

Table 10.4 Minimum pig density for varying cut-off values for which the agreement (kappa statistic) of the selection of communities with high risk for neighbourhood spread of CSF, on the one hand, and the selection of communities with dense pig populations, on the other hand, was maximal

| Communities with high risk for neighbourhood spread of CSF | | Communities with dense pig populations | | Kappa agreement (95% CI) | Observed proportion of overall agreement |
|--|-----------------------|---|-----------------------|--------------------------|--|
| Cut-off value (%) | Number of communities | Minimum pig density (# pigs / km ²) | Number of communities | | |
| 5 | 347 | 28 | 296 | 0.63 (0.56 – 0.70) | 0.83 |
| 10 | 124 | 465 | 106 | 0.74 (0.67 – 0.81) | 0.91 |
| 15 | 69 | 743 | 72 | 0.69 (0.60 – 0.79) | 0.92 |
| 20 | 41 | 1538 | 28 | 0.64 (0.51 – 0.78) | 0.95 |
| 25 | 24 | 1538 | 28 | 0.51 (0.34 – 0.68) | 0.95 |
| 30 | 17 | 1853 | 20 | 0.52 (0.32 – 0.72) | 0.96 |
| 35 | 12 | 1853 | 20 | 0.36 (0.14 – 0.57) | 0.96 |
| 40 | 9 | 1853 | 20 | 0.33 (0.10 – 0.55) | 0.96 |
| 45 | 4 | 2781 | 8 | 0.33 (-0.02 – 0.67) | 0.98 |
| 50 | 2 | 2781 | 8 | 0.19 (-0.14 – 0.53) | 0.98 |
| 55 | 1 | 2781 | 8 | 0.22 (-0.14 – 0.58) | 0.98 |
| 60 | 1 | 2781 | 8 | 0.22 (-0.14 – 0.58) | 0.98 |

The ROC curves for pig density and for cut-off values ranging from 5 to 20% are given in Figure 10.1. Additionally for each cut-off value, the sensitivity and specificity associated with the identification of communities with high risk for neighbourhood spread is given for varying minimum pig densities.

Figure 10.1 ROC curves for pig density and for varying cut-off values of risk for neighbourhood spread of CSF



10.4 Discussion

This paper only deals with the risk for neighbourhood spread of CSF, which is only one aspect of disease spread during CSF epidemics. However, the importance of ‘neighbourhood infections’ during a CSF outbreak (Miry et al., 1991; Pittler et al., 1996; Stegeman et al., 1997) resulted in the adaptation of control strategies (pre-emptive slaughtering) in order to limit its consequences. The risk assessment for ‘neighbourhood infections’, as described by Mintiens et al. (this publication), may be used by decision-makers as a Decision Support System (DSS) to set priorities during the control of a CSF outbreak. However, the implementation of such a DSS requires detailed geographical coordinates of every pig herd in the affected region (country) and these are not always available. Therefore, the pig density of a community may be an alternative tool for assessing the risk of ‘neighbourhood infections’ in a community.

In this study, a community was considered to incorporate a high risk for neighbourhood spread of CSF when the risk of ‘neighbourhood infections’ of at least one neighbourhood was higher than a preset cut-off value. This criterion implies that not all neighbourhoods in a community have a risk that is higher than the cut-off value. Moreover, the proportion of neighbourhoods having a risk for ‘neighbourhood infections’ higher than the cut-off value decreases when the cut-off value increases.

When the cut-off value is 25% or higher, the Kappa agreement is only moderate or less than moderate (Table 10.4). Therefore, the use of the pig density of a community to select communities for which at least one neighbourhood in the community has a risk of neighbourhood spread of CSF of 25% or higher will not be appropriate. The high proportion of overall agreement observed in these classes (>0.95 : Table 10.4) could be obtained because of the high number of communities that did not satisfy both the inclusion criteria (cut-off value and minimum pig density).

For the other cut-off values (5 to 20%), a substantial Kappa agreement was found. However, the identification of communities with high risk for neighbourhood spread of CSF based on the selection of communities with dense pig populations, results in a number of misclassifications. When, in Belgium, a minimum pig density of 300 pigs / km² is used for the identification of communities with a high risk for neighbourhood spread of CSF, the positive predictive value is 100, 74.0, 48.1, and 29.2% when the cut-off value is 5, 10, 15, and 20%, respectively. Moreover, the positive predictive value for a given cut-off value will differ from country to country because its value will change when the prevalence of communities with a high risk for neighbourhood spread of CSF changes, i.e. the smaller this prevalence the smaller the positive predictive value. On the other hand/Conversely, when

decision-makers are risk averse and want to identify all communities in which at least one neighbourhood has a risk for neighbourhood spread of CSF of at least 5%, the minimum pig density has to be even smaller than 100 pigs / km² because at this density the sensitivity is not yet 100% (Figure 10.1). This also means that communities will be selected that fulfill the minimum pig density but which include no neighbourhoods with a risk for neighbourhood spread of CSF of at least 5% (specificity less than 100%).

In conclusion, the choice of the minimum pig density of a community in order to optimise the selection of communities with a high risk for neighbourhood spread of CSF is not straightforward. The choice depends on the agreement of the selection of communities with dense pig populations and with a high risk for neighbourhood spread of CSF, as well as on the risks decision-makers are prepared to take.

Acknowledgements

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Modelling the effect of herd size on the probability of herd infection: Application to the infection by airborne FMD

G. Gerbier, V. Chevalier, R. Pouillot, B. Durand and F. Moutou

11.1 Introduction

Calculation of the probability of infection is the ultimate goal for the risk assessment of infectious diseases. Several studies dedicated to the study of the spread of airborne Foot and Mouth Disease (FMD) are in fact stopped to the evaluation of exposition (*i.e.* Casal *et al.*, 1997). Up until now the only solution for quantifying the probability of infection is to compare the value obtained from a mathematical model of airborne spread to the minimal doses required to set up the infection experimentally. During an epidemic, each herd belonging to an area where the amount of virus received is greater than this threshold is considered at risk. Nevertheless, in densely populated livestock areas (DPLA), the at-risk area can contain a lot of herds, in particular when the size of the emitter herd is /large/high. Herds may have different sizes and can then represent a variable source of risk. It is then important to be able to categorise these types/kinds of herds.

The infection is set up as the result of interaction between the virus and the animal. For a given strain, virulence is quite constant during an epidemic whereas the susceptibility of the animals may vary according to the species, the age and the immune status of the animals. During an experimental infection, high doses have usually been used and then all the animals are infected (Sellers, 1971). But, if the dose is low, variable reactions are observed (Donaldson, 1987). During an epidemic, the doses received are not high from the outset. Then, the risk of infection to a herd is more difficult to predict. We propose to derive this alea at the herd level from a model of the reaction at the herd level.

11.2 Model

At the individual level, reaction variability can simply be modelled using a dose-effect function. Usually, the relation is modelled using a logistic function:

$$\text{Logit}(p) = a + b * \text{dose} = \eta \quad (1)$$

η is a linear predictor with some variables measured at the individual level such as the individual inhaled dose.

A herd is infected when only one animal is infected. All the animals being assumed independent, the herd probability of infection equals the probability that at least one animal is infected. Then for a herd of size N receiving a given dose:

$$P(\text{herd infected}) = 1 - (1 - P(\text{animal infected}))^N \quad (2)$$

Let us define the following notations:

- P probability of herd infection,
- p probability of individual infection,
- N herd size.

Equation (2) can be written:

$$P = 1 - \left(\frac{1}{1 + \exp(\eta)} \right)^N \quad (3)$$

The choice of the logistic function is arbitrary and is often justified by the fact that the logistic function is the natural link function for binomial data. Nevertheless, another function from the exponential family: the complementary log-log function (*cloglog*) leads to more tractable results. Figure 11.1 shows the comparison between *cloglog* and logistic function (Collet, 1991).

With a *cloglog* function, the dose-effect individual curve is written:

$$\text{cloglog}(p) = \log(-\log(1 - p)) = a + b * \text{dose} = \eta \quad (4)$$

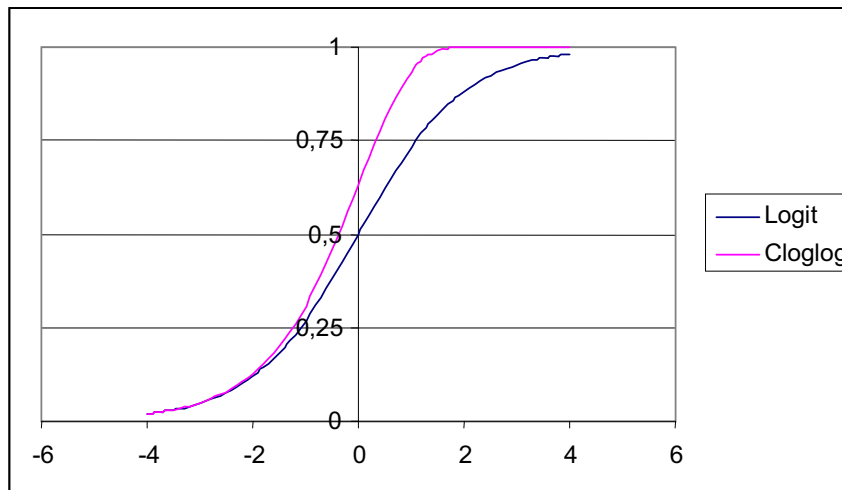
$$\text{then } p = 1 - \exp[-\exp(\eta)]$$

Equation (2) becomes:

$$P = 1 - [1 - (1 - \exp(-\exp(\eta)))]^N$$

$$P = 1 - [\exp(-\exp(\eta))]^N$$

Figure 11.1: Comparison of logistic and complementary log-log function.



$$P = 1 - \exp(-N \exp(\eta))$$

$cloglog(P)$ is obtained as follows:

$$\text{Log}(1 - P) = -N \exp(\eta)$$

$$\text{Log}(-\text{Log}(1 - P)) = \text{Log}(N \exp(\eta))$$

Then :

$$cloglog(P) = \log(N) + cloglog(p) \quad (5)$$

Relation (5) enables us to link in a simple way the herd and individual probability of infection with herd size.

- At the logarithm complementary log-log scale, herd probability of infection is linearly linked to the logarithm of herd size.
- At the logarithm complementary log-log scale, herd size modifies the intercept of equation (4).
- In equation (4) $\log(N)$ is an *offset* variable (variable without parameter).
- Several combinations (dose, herd size) lead to the same value for the herd probability of infection P . As the parameter for the dose is by definition positive, and as is *a priori* the size parameter, for a given P , when the size increases the dose needed to set up an infection decreases.

11.3 Validation

Data on herd attack rates observed during the 1967-68 epidemic (Hugh-Jones, 1972) were used to validate the model. Number of outbreaks per herd size class were extracted from a database kindly provided by ME Hugh-Jones after selecting only the dairy herds infected in Cheshire and Shropshire (Figure 11.2). Number of outbreaks divided by the attack rates give the number of herds in the area. For Shropshire data, one class (70-79 dairy cattle) was excluded as only 23 herds belong to this class. The last class (more than 80 animals) was also excluded as no median size could be obtained.

Individual probability was estimated using the following equation: $\text{cloglog}(p) = \text{cloglog}(P) - \log(N)$. Variance of p is calculated from the derivative of equation (2) according to P (Dacunha-Castelle and Duflo, 1983):

$$\text{Let } p = 1 - (1 - P)^{\frac{1}{N}} \quad \text{with: } \hat{P} = \frac{m}{M} \quad \begin{array}{l} m : \text{number of outbreaks of size } N \\ M : \text{number of herds at risk of size } N \end{array}$$

$$\text{Derivative of } p \text{ is } \frac{\partial p}{\partial P} = \frac{1}{N} (1 - P)^{\frac{1}{N}-1}$$

$$\text{As } \hat{P} \xrightarrow{M \rightarrow \infty} P \text{ and } \frac{1}{\sqrt{M}} (\hat{P} - P) \rightarrow N(0, P(1 - P))$$

$$\text{Then } \left\{ \begin{array}{l} \hat{P} \xrightarrow{M \rightarrow \infty} P \\ \frac{1}{\sqrt{M}} (\hat{P} - P) \rightarrow N\left(0, \frac{1}{N^2} (1 - P)^{\frac{2}{N}-2} P(1 - P)\right) \end{array} \right.$$

$$\text{So :} \quad \text{var}(\hat{p}) \cong \frac{1}{N^2 M} \frac{m}{M} \left(1 - \frac{m}{M}\right)^{\frac{2}{N}-1}$$

Table 11.1 Herd attack rates in Cheshire and Shropshire in 1967-68 (from Hugh-Jones, 1972)

| Herd size class | Middle of the class | Cheshire | | | Shropshire | | |
|-----------------|---------------------|--------------------|---------------------|---------------------------|--------------------|---------------------|---------------------------|
| | | Attack Rate | Number of outbreaks | At risk herds (estimated) | Attack rate | Number of outbreaks | At risk herds (estimated) |
| <10 | 5 | 6.8% | 42 | 618 | 3.8% | 35 | 921 |
| 10-19 | 15 | 5.3% | 45 | 849 | 5.5% | 52 | 945 |
| 20-29 | 25 | 7.7% | 62 | 805 | 9.1% | 59 | 648 |
| 30-39 | 35 | 12% | 99 | 825 | 9.1% | 45 | 495 |
| 40-49 | 45 | 19.7% | 84 | 426 | 17.3% | 52 | 301 |
| 50-59 | 55 | 26.1% | 71 | 272 | 22.2% | 47 | 212 |
| 60-69 | 65 | 31.9% | 73 | 229 | 19.5% | 54 | 277 |
| 70-79 | 75 | 49.6% | 62 | 125 | 83.3% ^a | 19 ^a | 23 ^a |
| >80 | - | 68.3% ^a | 166 ^a | 243 ^a | 40.4% ^a | 68 ^a | 168 ^a |

a) Data not used in the analysis

Table 11.2 Individual probability of infection after transformation

| Herd size class | Middle of the class | Cheshire | | Shropshire | |
|-----------------|---------------------|--------------|-----------------------|------------|-----------------------|
| | | of \hat{p} | $\text{var}(\hat{p})$ | \hat{p} | $\text{var}(\hat{p})$ |
| <10 | 5 | 0.0140 | $4,59 \cdot 10^{-06}$ | 0.0077 | $1.69 \cdot 10^{-06}$ |
| 10-19 | 15 | 0.0036 | $2,91 \cdot 10^{-07}$ | 0.0038 | $2.72 \cdot 10^{-07}$ |
| 20-29 | 25 | 0.0032 | $1,65 \cdot 10^{-07}$ | 0.0038 | $2.45 \cdot 10^{-07}$ |
| 30-39 | 35 | 0.0036 | $1,34 \cdot 10^{-07}$ | 0.0027 | $1.64 \cdot 10^{-07}$ |
| 40-49 | 45 | 0.0049 | $2,81 \cdot 10^{-07}$ | 0.0042 | $3.41 \cdot 10^{-07}$ |
| 50-59 | 55 | 0.0055 | $4,24 \cdot 10^{-07}$ | 0.0046 | $4.42 \cdot 10^{-07}$ |
| 60-69 | 65 | 0.0059 | $4,79 \cdot 10^{-07}$ | 0.0033 | $2.06 \cdot 10^{-07}$ |
| 70-79 | 75 | 0.0091 | $1,37 \cdot 10^{-06}$ | - | - |

Figure 11.2 Dairy herd attack rates in Cheshire and Shropshire according to herd size

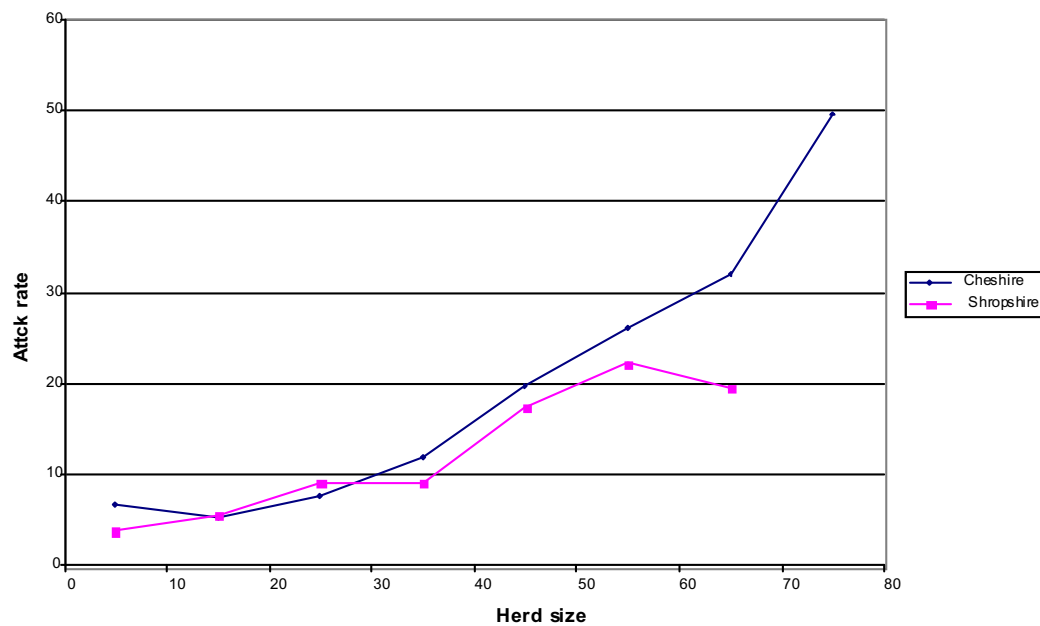
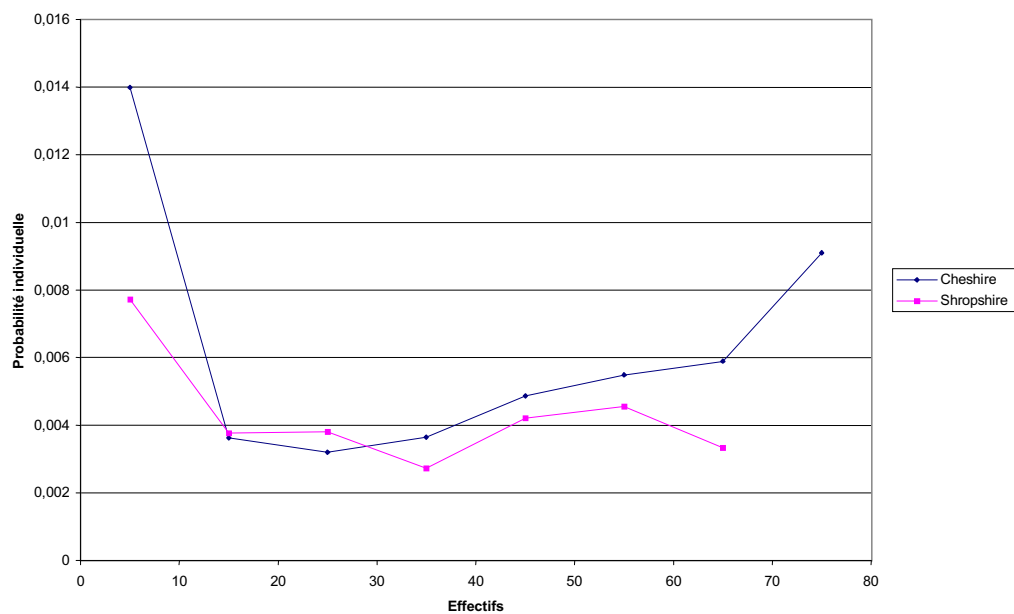


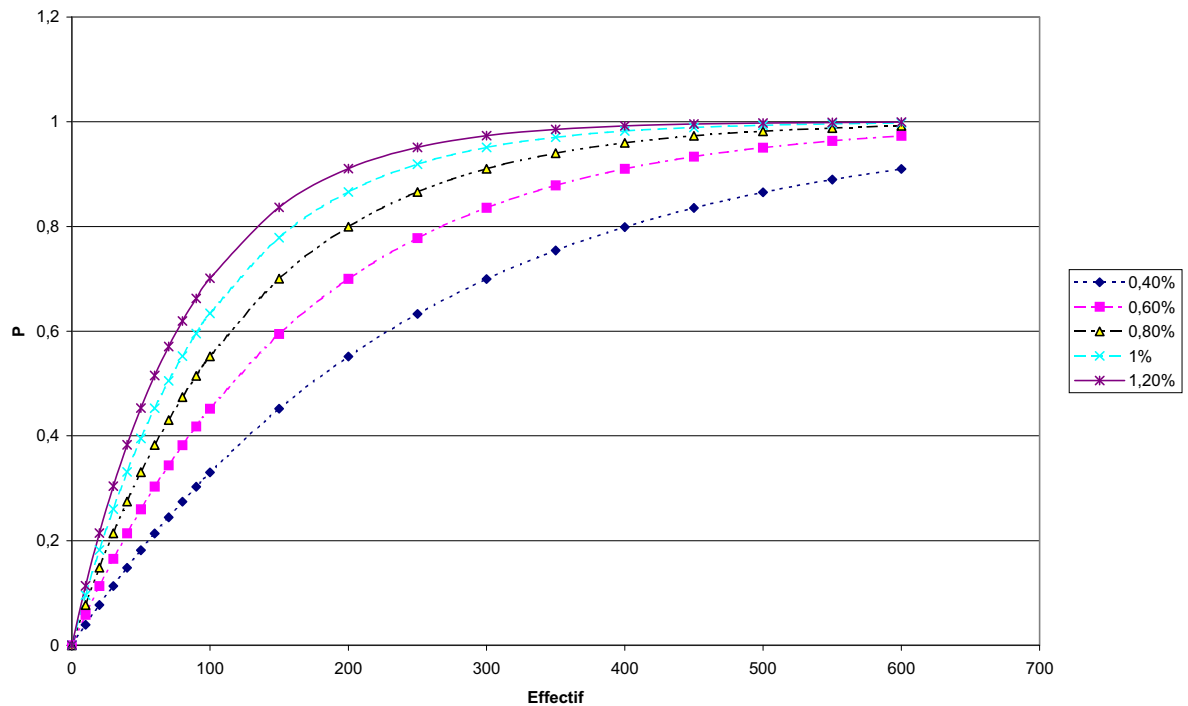
Figure 11.3: Individual probability of infection after transformation



Individual probability of infection fluctuates around 0,4%, minimum 0,3% maximum 1,4% (Figure 11.3). Even if extrapolation is problematic, this figure is interesting as a magnitude. Generally, people use the average values to build a model. This quite low value shows that

for infectious diseases this is probably misleading. Reasoning may rely more on the more susceptible animal than on the average one.

Figure 11.4 Herd probability of infection according to herd size for different individual probabilities of infection.



11.4 Discussion

Herd size is described as a risk factor increasing the herd probability of infection for many respiratory diseases (Stärk, 1998). Usually, parameters related to herd size are treated as nuisance parameters. So, more often, herd size is introduced as a random factor in regression models that deal with individual probability of infection. In the case of respiratory diseases such as FMD or pseudorabies, the herd is the level of interest. At this level, Hugh-Jones (Hugh-Jones, 1972) demonstrated that attack rates are linked to herd size. Our model gives an analytical explanation of this result.

Assuming that FMD is heterogeneously distributed in the air, Casal (1997) suggests another explanation. If a Poisson distribution could be used to describe the quantity of virus inhaled by one animal, some animals may have received a large amount of virus even if the average

amount of the virus is low. Therefore, herd size will increase the probability that at least one animal received a large amount of virus. We assumed that the animals received the same dose but that the susceptibility of the animals varies. Assuming this, herd size increases the probability that an animal susceptible to low doses of the virus is present in the herd. The two approaches lead to the same conclusions but there is no data to distinguish between them.

After the airborne spread of pseudorabies had been demonstrated (Gloster et al., 1984), Danish and American groups studied the effect of neighbourhood and the spatio-temporal distribution of outbreaks respectively (Mortensen et al., 1994, Norman et al., 1996). In the Danish studies, the effect of herd size - directly introduced in a Cox model – was found significant. Following this, Willeberg (1994) proposed a simple model to describe the effect of herd size in pig diseases. If all the animals are free from the disease and with an individual probability of infection p , the herd probability of infection P is, for a herd of size N :

$$P = 1 - (1 - p)^N$$

For low values of p , P is approximately Np . Then, relative risk and odds-ratio are equal to

$$\frac{N_1}{N_2}$$

As a consequence, the logarithm of the size should be included in logistic regression models. It can be shown that in this case, the effects of the "size" variable and the other individual variables are mixed up because of the approximation. Transformation using complementary log-log function (cloglog) does not require such an approximation and should then allow a better estimation.

The principal point for discussion is then the choice of the *cloglog* function for the individual dose-effect curve. This function is implemented in almost all the statistical packages including Generalised Linear Models. Comparison of the results using the logistic or *cloglog* link should then be easy. Unfortunately, available data on FMD experimental infection is sparse and does not cover all the range of variation of the dose (*cf.* Donaldson *et al.*, 1987). The fit of a logistic or *cloglog* function cannot then be used.

11.5 Conclusions

Although theoretical, this model is useful in order to derive conclusions about the behaviour of FMD. It can for example partially explain why all the herds receiving the airborne virus are not infected. Several combinations of doses and herd size give the same risk of infection.

As the inhaled dose is linked to the distance to an infected source, the former relation implies that a big herd located far from an outbreak could have the same probability of infection as a small herd located close to the source. Moreover, a very low dose could be sufficient to set up the infection if a lot of animals have been exposed. Conversely, this implies that many animals are required to evaluate the minimal dose to set up the infection. As the experimental infections often involved few animals, current minimal doses are probably overestimated.

If the parameter of the individual dose-effect curve were known, herd probability of infection could be directly estimated. As these parameters are unknown, equation (5) suggests using the logarithm of the product of the individual dose and the herd size (*log size*individual dose*). This could be a way of ranking the herds according to the risk of airborne contamination.

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Task D

Cost-benefit analysis of disease prevention and control strategies in such areas

A decision tree for optimising control measures during the early stages of a Foot and Mouth Disease epidemic

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Probability of Classical Swine Fever virus introduction in the European Union: analysis and modelling

C. de Vos, H. Saatkamp and R. Huirne, The Netherlands

Spatial and stochastic simulation to compare two emergency vaccination strategies with a marker vaccine in the 1997/98 Dutch Classical Swine Fever epidemic

M.-J. Mangen, A. Jalvingh, M. Nielen, M. Mourits, D. Klinkenberg and A. Dijkhuizen, The Netherlands

A decision tree for optimising control measures during the early stages of a Foot and Mouth Disease epidemic

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Abstract

A decision tree was developed as a tool to support decision-making concerning control measures in the first few days following the declaration of an outbreak of Foot and Mouth Disease (FMD). The objective of the tree was to minimise direct costs and export losses of FMD epidemics in several scenarios. These scenarios were based on important determinants in the development of epidemics and therefore defined by livestock and herd density in the outbreak region, the possibility of airborne spread, and the time between first infection and first detection.

The starting point of the tree was an epidemiological model based on a deterministic Susceptible-Infectious-Recovered approach. The effect of four control strategies on FMD dynamics was modelled. In addition to the standard control strategy of stamping-out and culling high-risk contact herds, strategies were assessed involving ring culling within 1 km of an infected herd, ring vaccination within 1 km of an infected herd, and ring vaccination within 3 km of an infected herd. An economic model converted outbreak and control effects of farming and processing operations into estimates of direct costs and consequential export losses.

Results showed that animal density within the outbreak region is a very important determinant in deciding upon the economically optimal control strategy. Ring vaccination is the economically optimal control strategy for **densely** populated livestock areas whereas ring culling is the economically optimal control strategy for **sparsely** populated livestock areas.

12.1 Introduction

Foot and Mouth Disease (FMD) is a highly contagious disease that infects many cloven-footed mammals, including cattle, pigs, sheep, goats and deer. The virus has the potential to

spread rapidly in susceptible populations. From previous economic studies it is clear that FMD outbreaks generate considerable losses due to costs of disease control and productivity losses as well as to constraints on the international meat and livestock trade (Power and Harris, 1973; Krystynak and Charlebois, 1987; Berentsen et al., 1992b; Garner and Lack, 1995; Mahul and Gohin, 1999; Mahul and Durand, 2000). Recent examples of the devastating consequences of FMD are the epidemics in Great Britain and The Netherlands in 2001. In Great Britain nearly four million animals were slaughtered and the disease spread to over 2030 livestock farms (Department for Environment, Food and Rural Affairs, 2001). During the Dutch epidemic about 265,000 animals had to be slaughtered and 26 farms were actually infected (Ministry of Agriculture, Nature Management and Fisheries, 2001). Another example is the epidemic which occurred in 1997 in Taiwan, in which more than four million pigs had to be slaughtered (Yang et al., 1999).

FMD is a difficult disease to control and eradicate because of the various mechanisms by which the virus can be transmitted (Sellers, 1971). The most common mechanism is the movement of infected animals to susceptible animals (Donaldson et al., 2001). Other mechanisms of spread include the movement of contaminated animal products such as meat, offal and milk. The FMD virus can also be transmitted mechanically, for example, by contaminated milking machines, by vehicles, especially those used for transporting animals, and by people. Another mechanism is airborne spread. Under certain epidemiological and climatic conditions the FMD virus can be spread by the wind. Of all mechanisms, spread by air is least controllable (Donaldson et al., 2001; Ferguson et al., 2001a; Sørensen et al., 2000 and 2001).

The objective of this study was to develop a tool to support decision-making on control strategies during the early stages of an FMD epidemic. The early stage means the first few days after the declaration of an outbreak. Successful eradication of an epidemic mainly depends on the selected control strategy and on the time interval between the diagnosis and implementation of the control strategy. Selecting an inadequate strategy may cause large additional economic losses (Mahul and Durand, 2000). Delayed implementation of control measures may cause extensive spread of the disease (Garner and Lack, 1995; Howard and Donnelly, 2000; Ferguson et al., 2001b). This means that it is very important for animal health authorities to make the right decision immediately following the initial diagnosis. Usually there is no time to gather additional data in order to support decision-making. Therefore, it is absolutely essential to have an overall analytical structure for these kinds of situations beforehand. This paper presents such an analytical structure, comprising a decision tree modelling approach using all information available in the first three days following the declaration of an outbreak. Using this approach the efficacy of disease control measures was evaluated in all kinds/types of scenarios. The efficacy was determined by modelling the

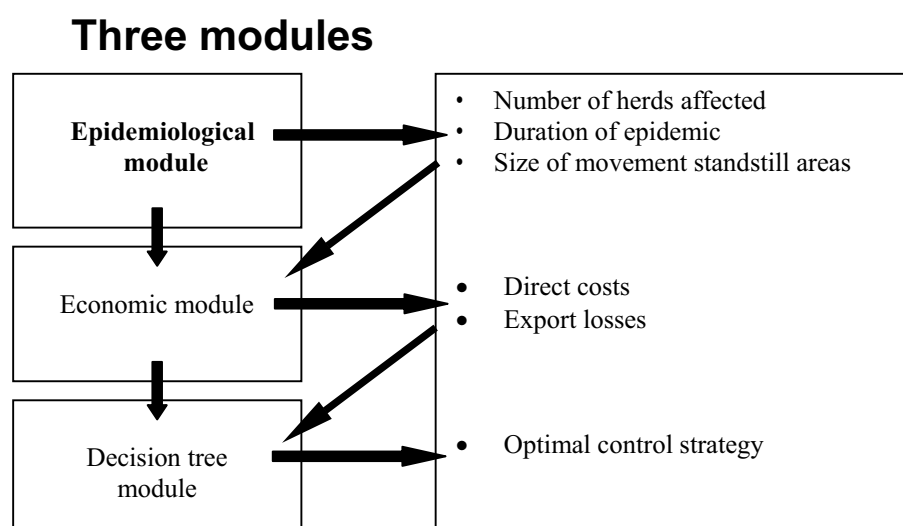
epidemiological consequences and calculating the resulting direct costs and export losses. Scenarios were defined by important determinants in the development of epidemics that were found in the literature.

The objective of the decision tree was to be able to calculate the economically optimal control strategy for each scenario. Economically optimal meant that direct costs and export losses were minimised. The results from the decision tree may be used as yardsticks for deciding on control measures during possible FMD epidemics in the future.

12.2 Materials and methods

The modelling approach consists of three modules (see Figure 12.1): an epidemiological module to simulate the disease dynamics, an economic module to convert outbreak and control effects into estimates of direct costs and export losses, and a decision tree module to optimise decisions on control strategies. These modules are described in sections 12.2.5 to 12.2.7. Firstly the choice of virus strain, control strategies, regions and scenarios are outlined in sections 12.2.1 to 12.2.4.

Figure 12.1. An overview of the modelling approach



12.2.1 Choice of virus strain

There are seven immunologically and serologically distinct types of FMDV: A, O, C, SAT1, SAT2, SAT3 and Asia 1. Within each serotype there are several subtypes. The disease caused by different serotypes is clinically indistinguishable, although they vary somewhat in their epidemiological patterns (Sanson, 1993). Some strains of FMDV show a degree of natural adaptation to an animal species, with the result that the other species of animals appear to be more difficult to infect. An example of a pig-adapted virus strain was the strain that caused the Taipei China epidemic in 1997. No outbreaks were detected in cloven-hoofed animals other than pigs (Chen et al., 1999).

This study also confined attention to FMDV outbreaks in pigs, which is the source of most available data (Sellers, 1971; Salt et al., 1998; Yang et al., 1999). This data made it possible to quantify the FMD transmission between pigs and to estimate the efficacy of vaccination.

12.2.2 Control strategies

The size and duration of an epidemic depend largely on the control strategy implemented and on its effectiveness. In 1990/91 the EU decided to cease routine prophylactic vaccination. The control procedures are now total stamping out⁴ of the disease in affected herds and movement control⁵ in the surrounding area. These measures are laid down in Council directive 85/511/EEC. However, in certain circumstances these measures may need to be supplemented by other interventions such as ring culling⁶ or ring vaccination⁷. In particular, outbreaks in areas containing high densities of susceptible animals and inadequate resources of manpower or plants for the slaughter and disposal of animals may spread out of control without additional control measures. In this context, ring culling and ring vaccination strategies target infection hotspots by reducing the density of susceptible herds in the vicinity of diagnosed infections, thereby removing the “fuel” essential to maintaining the epidemic (Scientific Committee on Animal Health and Animal Welfare, 1999; Ferguson et al., 2001a).

Findings from simulated FMD outbreaks in The Netherlands, Australia and France demonstrated that the strategy of stamping out and movement control alone (as laid down in 85/511/EEC) is rarely/almost never the economically optimal strategy. Extension of this strategy with culling of dangerous contact herds⁸ generally reduced the epidemiological and

⁴ slaughtering of all the affected and in-contact susceptible animals of the infected herd

⁵ prohibition of movement of animals and manure within a radius of 10 km of an infected herd

⁶ slaughtering all susceptible animals within a certain radius of every newly diagnosed case of infection

⁷ vaccinating all susceptible animals within a certain radius of every newly diagnosed case of infection

⁸ slaughtering of herds that, although not showing FMD symptoms, are considered to be at high risk of spreading the disease because of proximity or contact with infected herds.

economic consequences (Berentsen et al., 1992b; Garner and Lack, 1995; Mahul and Durand, 2000).

Previous research, based on the Dutch Classical Swine Fever (CSF) epidemic of 1997-1998, showed that ring culling can also be an effective strategy for reducing the size of a CSF epidemic, if begun at an early stage (Elbers et al., 1998; Nielen et al., 1999; Stegeman et al., 1999). These studies suggested that 1 kilometre was an optimal radius from an epidemiological as well as from an economic point of view. A model analysis of the recent FMD epidemic in Great Britain (GB) showed that both ring culling and ring vaccination are potentially highly effective strategies if implemented sufficiently rigorously (Ferguson et al., 2001a). It was also concluded that ring vaccination policies need to be more extensive than comparable culling policies. In the case of infected but undiagnosed animals, culling eliminates virus replication by removing these animals. Vaccination only reduces the virus replication thereby limiting the transmission of the virus less effectively than culling (Sobrinho et al., 2001). Another analysis of the British epidemic (Donaldson et al., 2001) concluded that ring culling is not always effective because of the very wide variation between different species in terms of the quantities of virus excreted, their susceptibility to infections, and the routes by which they are likely to be infected.

Based on the current EU legislation and previously discussed experiments and analyses of recent epidemics, the following interesting control strategies were considered in this study:

- (1) Stamping out infected herds (85/511/EEC) and culling of high-risk contact herds (SO);
- (2) SO extended with ring culling of all susceptible animals within a radius of 1 km of an infected herd (RC1);
- (3) SO extended with ring vaccination of all susceptible animals within a radius of 1 km of an infected herd (RV1);
- (4) SO extended with ring vaccination of all susceptible animals within a radius of 3 km (RV3).

All four strategies include movement control. The last three strategies also took into account the possibility of airborne spread outside implemented rings. Susceptible animals outside a ring but downwind of a virus plume were culled or vaccinated respectively. Vaccinated animals were culled as quickly as possible to keep the necessary period for regaining the status of an FMD-free country without vaccination as short as possible (see 2.6). Here, culling and destruction capacities were the restricting factors.

12.2.3 Regions

Studies have shown that a densely populated livestock area (DPLA) can give rise to the risk of major disease epidemics (Dijkhuizen and Davies, 1995). For this study The Netherlands

has been divided into seven regions according to Stegeman et al.'s (1997) division method based on pig density per municipality. This method was useful for the epidemiological module, which calculated the transmission of a pig-adapted FMDV strain (see 12.2.1). Statistics were used from the year 1999 and pig densities were based on agricultural land area (Statistics Netherlands, 2001). According to this method, municipalities with more than 1000 pigs per km² were combined to form a pig-dense region. Municipalities that have fewer than 1000 pigs per km², but that are surrounded by densely populated municipalities were included in the pig-dense regions. Figure 12.2 shows the seven regions that could be distinguished. The very dark-coloured regions (regions 1, 2 and 3) have more than 1000 pigs per km². The other four areas are less densely populated.

Figure 12.2 Subdivision of The Netherlands into seven regions, showing density of pig population



Table 12.1 lists the densities of susceptible livestock species, herds and flocks per region and the mean sizes of herds and flocks per region. According to Michel et al.'s definition (2000)⁹ the regions 1 through 4 are classified as DPLAs.

⁹ A DPLA for FMD contains >300 pigs per km² or >450 susceptible animals per km² (total land area).

Not only do animal densities vary between regions but the number of pig and cattle herds per square km also vary strongly. Region 2 has by far the most pig and cattle herds per square km. In this region the mean size of pig herds is small but the mean size of cattle herds is large because of a high concentration of veal calves in this area.

Table 12.1 Descriptive statistics for the regions

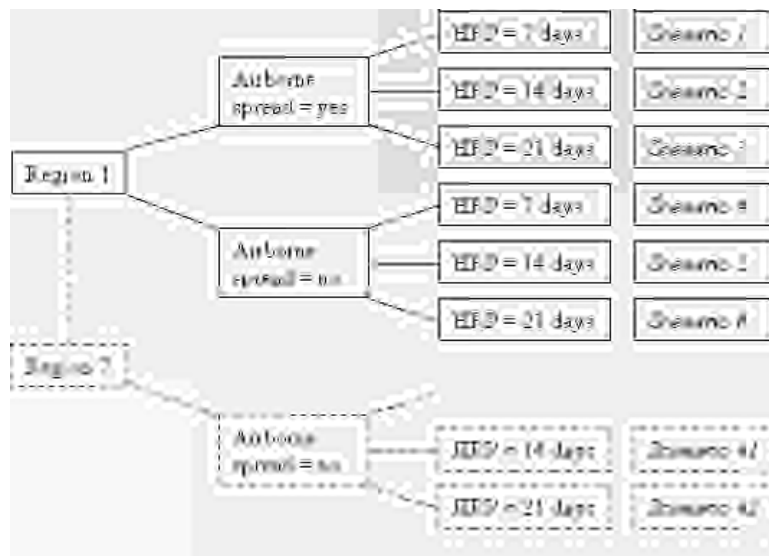
| Region | 1 | 2 | 3 | 4 | 5 | 6 | 7 |
|-----------------------------------|------|------|------|------|------|------|------|
| <i>Total livestock per:</i> | | | | | | | |
| km ² agricultural land | 3019 | 2641 | 1633 | 1353 | 563 | 389 | 384 |
| km ² total land | 1272 | 701 | 920 | 615 | 275 | 236 | 148 |
| <i>Pigs:</i> | | | | | | | |
| Pigs/km ^{2 a} | 2691 | 1736 | 1290 | 916 | 346 | 152 | 175 |
| Herds/km ^{2 a} | 2.30 | 4.56 | 2.32 | 1.24 | 0.41 | 0.19 | 0.31 |
| Herd size | 1171 | 381 | 555 | 738 | 851 | 798 | 559 |
| <i>Cattle</i> | | | | | | | |
| Cattle/km ^{2 a} | 279 | 838 | 305 | 336 | 166 | 178 | 129 |
| Herds/km ^{2 a} | 3.28 | 7.29 | 4.69 | 4.42 | 2.72 | 2.05 | 2.05 |
| Herd size | 85 | 115 | 65 | 76 | 61 | 87 | 63 |
| <i>Sheep</i> | | | | | | | |
| Sheep/km ^{2 a} | 30 | 47 | 31 | 84 | 42 | 55 | 76 |
| Flocks/km ^{2 a} | 1.11 | 2.24 | 1.48 | 2.55 | 1.56 | 1.20 | 1.77 |
| Flock size | 27 | 21 | 21 | 33 | 27 | 46 | 43 |
| <i>Goats</i> | | | | | | | |
| Goats/km ^{2 a} | 19 | 19 | 7 | 16 | 10 | 4 | 5 |
| Flocks/km ^{2 a} | 0.22 | 0.41 | 0.35 | 0.55 | 0.15 | 0.31 | 0.30 |
| Flock size | 85 | 46 | 20 | 29 | 65 | 13 | 15 |

a) per km² agricultural land

12.2.4 Scenarios

Scenarios were defined using important determinants in the development of epidemics that were found in literature. These determinants were: (a) livestock and herd density in the outbreak region (De Vos et al., 2000; Gerbier, 1999), (b) the possibility of airborne spread (Donaldson et al., 2001), and (c) the high-risk period (HRP) which is defined as the time interval between first infection and first detection (Horst, 1998). In Figure 12.3 each scenario is described by a region (which was described by livestock density and herd density), the possibility of airborne spread and the HRP.

Figure 12.3 Scenarios in the module



12.2.5 Epidemiological module

A mathematical model was constructed to estimate the effect of control strategies in the separate regions. A previously described deterministic Susceptible-Infectious-Recovered (SIR) model (De Jong, 1995; Stegeman et al., 1999) was applied to describe the transmission of FMDV between herds. In this model, S is the number of susceptible herds, I the number of infectious herds and R the number of recovered herds. Because herds are depopulated upon detection, $R = 0$ at all times in this study. In the model, the rate at which susceptible herds become infected can be described as: $C = \beta * SI/N$, in which C is defined as the number of virus introductions per unit of time into a susceptible herd, β as the infection rate parameter and N as the total number of herds. Furthermore, infected herds are depopulated at the rate $D = \alpha * I$, in which D is defined as the number of infected herds depopulated per unit of time and α as the depopulation rate parameter. The parameter α is the inverse of T, the average period that a herd is infectious. The transmission of FMDV between herds can be expressed as the herd reproduction ratio R_h , which is defined as the average number of outbreaks caused by one initial infected herd. The R_h can be estimated from $R_h = \beta / \alpha$ (Stegeman et al., 1999). From the definition of R_h it follows that if R_h is <1 , the epidemic will fade out automatically. On the other hand, if R_h is >1 , the virus will continue to spread (De Jong, 1995; Diekmann and Oosterbeek, 2000).

Knowledge and factual information about the precise transmission routes of FMD are scarce. This is in contrast to CSF (for example, see Stegeman et al. (1999) and De Vos et al. (in press)). Both diseases are list A diseases and spread via approximately the same transmission routes (Elbers et al., 1999; Donaldson et al., 2001; De Vos et al., in press). Therefore, to

estimate the R_h , data collected during the Dutch CSF epidemic in 1997-1998 was used (Stegeman et al., 1999). Five transmission routes were distinguished by which the virus could be transmitted from one herd to another: animal transport, persons, neighbourhood, artificial insemination (AI), and rendering (Elbers et al., 1999; Stegeman et al., 2000). Three types of herds were defined: breeding herds, farrow-to-finish herds and finishing herds. The infectiousness of a herd was determined by the virus transmission within the herd (Van Nes et al., 1998). The parameters were adjusted to FMD using data collected from recent FMD outbreaks as well as data from transmission experiments (Sellers, 1971; Salt et al., 1998; Yang et al., 1999).

For each transmission route a transmission matrix was compiled in order to model the transmission from one herd type to another (Stegeman et al., 2000). These matrices combined the number of contacts with the estimated chance of transmission by a contact. The values in the transmission matrices were made dependent on herd density and mean herd size in the outbreak region concerned, as previously applied in Aujeszky and CSF control studies (De Koeijer and Stegeman, 2000; Stegeman et al., 2000).

Because the transmission routes were independent from each other, the five matrices could be added to one total transmission matrix. Subsequently the R_h was determined by calculating the dominant eigenvalue of the matrix. The matching eigenvector reflects the proportion of each herd type that became infected (Diekmann and Heesterbeek, 2000). The R_h was determined for each control strategy and each region. In the case of ring vaccination the assumption was made that transmission continued for one week following vaccination and that subsequently transmission ceased in vaccinated herds. The model was programmed in Mathematica 4.0 (Wolfram Research).

The main difference between transmission routes of FMD and CSF is that the FMD virus could be spread by wind over long distances under certain weather conditions¹⁰ (Gloster et al., 1982; Donaldson et al., 2001), although opinions differ about the range of airborne spread. Air currents play a minor role as a transmission route between herds for CSF (Elbers et al., 1999; De Vos et al, in press). Therefore, airborne transmission was calculated separately, and was subsequently added to the R_h for the scenarios with airborne spread. (Gloster et al., 1982) For each combination of control strategy and region a worst case scenario of airborne spread was modelled (Gloster et al., 1981).

The calculated herd reproduction ratios were used in order to determine the number of herds affected, the duration of epidemics and areas subjected to movement restrictions for the

¹⁰ Most favourable conditions for airborne spread are a constant wind direction, a wind speed of 5 m/second, a high atmospheric stability, no precipitation, and a relative humidity above 55 % (Donaldson et al, 2001).

defined scenarios (see section 12.2.4). These outputs were then used as inputs to the economic module (see Figure 12.1).

12.2.6 Economic module

The purpose of the economic module was to quantify payoffs that could then be used in the decision tree module as the economic consequences of control strategies (see 12.2.7). Payoffs were defined as the direct costs and consequential export losses of the spread and control of an FMD epidemic. The direct costs were defined as the economic implications for (1) producers in the entire livestock value chain whose income depends on the livestock sector (e.g. farmers, abattoirs, hauliers and meat processors) and for (2) the government that is organising the disease control. Direct costs are generated by the implementation of control measures, such as costs of animal slaughter and vaccination, compensation payments and costs due to movement restrictions as well as idle production factors (Berentsen et al., 1992b). An epidemic could also have consequential export losses (Berentsen et al., 1992b; Garner and Lack, 1995; Mahul and Durand, 2000). These losses were defined as the value of livestock and livestock products that could not be exported because of trade restrictions due to the FMD epidemic.

In this module, the direct costs and consequential export losses were calculated in a rather objective way using several statistical databases (Statistics Netherlands, 2001; Product Boards for Livestock, Meat and Eggs, 2000; Product Board for Dairy, 2000). The module was programmed in Excel 97 (Microsoft Corporation).

12.2.6.1 Input data for direct costs

The economic module used the outputs from the epidemiological module (see Figure 12.1). To calculate the direct costs it used the number of affected herds, the duration of epidemics and the size of areas subjected to movement restrictions. The number of culled or vaccinated animals was also calculated. These calculations were based on livestock and herd densities in the outbreak region and the estimated number of contact herds, based on the calculated R_h , during the period between first infection and first detection. The duration of epidemics was longer when the culling and rendering capacity was not sufficient. The culling and rendering capacity was set at 16 farms per day for the SO and RC1 strategies and at 36 farms per day for the RV1 and RV3 strategies.

For each scenario, the direct costs were calculated as costs per dairy cow, sow or fattening pig that was either culled or put under movement restrictions. Input values for calculating the direct costs are represented in Table 12.2. These values were calculated based on statistics

from the [Agricultural Information and Knowledge Centre and Research Station for Animal Husbandry](#) (2000) and estimates of the National Inspection Service for Livestock and Meat (Meuwissen et al., 1999). Organisation costs refer to costs of diagnosis, valuation of the animals, killing, cleansing and disinfecting of stables and equipment and surveillance in the protection and surveillance zones. Compensation payments are governmental payments to farmers whose animals were culled. These payments were calculated as the replacement values of the animals and feed supplies. Costs from idle production factors were calculated as the fixed costs decreased by released labour that could have been deployed elsewhere. The costs of movement restrictions were calculated as the costs for additional feed for maintenance and other supply and delivery problems because of the restrictions. Vaccination costs include labour and material costs of the vaccination teams (Mangen et al., 2001). For sheep and goats only the replacement values were included because a large number of these animals are kept as pets.

The losses for supplying, processing and distribution companies were calculated as half of the gross value added of agricultural production that did not take place due to the implemented control strategies. The distribution of the gross value added within the livestock production chain is shown in appendix III (Koole and Van Leeuwen, 2000).

Table 12.2 Input values for calculating the direct costs per dairy cow, sow and fattening pig (in €)

| | Dairy cow (incl. young stock) | Sow (incl. piglets) | Fattening pig |
|-------------------------|-------------------------------|---------------------|---------------|
| Organisation costs | 136 | 68 | 18 |
| Compensation payments | 1190 | 349 | 66 |
| Idle production factors | 4.95/day | 0.66/day | 0.14/day |
| Movement restrictions | 0.07/day | 0.15/day | 0.02/day |
| Vaccination costs | 9 | 7 | 2 |

12.2.6.2 Input data for consequential export losses

The extent of the consequential export losses depends on the duration and size of the epidemic and the reactions by importing countries during and after the epidemic. The studies of Mahul et al. (2000) and Berentsen et al. (1990) showed that import bans implemented by the importing countries play a key role in the evaluation of economic consequences of an FMD epidemic.

The duration and size of the epidemic resulted from the epidemiological module. For the possible reactions of importing countries two scripts were formulated. One script was based on OIE guidelines (see Table 12.3a).

According to the OIE International Animal Health Code, countries recover their status of FMD-free zone without vaccination after: (i) 3 months after slaughtering of the last infected herd when there is no vaccination strategy implemented but only stamping out and preventive slaughter or (ii) 3 months after slaughtering of the last vaccinated herd if a campaign of emergency vaccination is applied (Office International des Epizooties, 2000).

However, reactions of importing countries during and after epidemics in the past have indicated that these countries did not respect the OIE guidelines. For this reason, a more realistic script (REA) was defined, based on international trade restrictions applied during epidemics in the past (e.g. Italy, 1993; Greece, 1994; Great Britain and The Netherlands, 2001). The assumed import bans are mentioned in Table 12.3b. Assumptions on the duration of import bans were based on results of previous studies of Berentsen et al. (1990) and Mahul et al. (2000) and experiences of recent outbreaks (Commission Decisions 2001/172/EC and 2001/223/EC).

In both scripts three export product groups were distinguished: (1) livestock, (2) meat products and (3) dairy products. The importing countries were divided into a group of EU-countries and non-EU countries. Next, for each combination of product group and country group it was determined how long an import ban would be effective and whether the ban would be at a national or regional level. A regional import ban means an import ban for products coming from regions around infected farms in radii of 10 km. Because regional export data was unavailable, the assumption was made that exports were proportional to the regional production (Mahul and Durand, 2000).

Table 12.3a Import bans during and after an FMD epidemic in the OIE-script (OIE)

| During epidemic | | | After epidemic (days) | |
|-----------------|----------------|----------|-----------------------|-------------------|
| | | | Regional | National |
| <i>EU</i> | Livestock | national | 90 | n.a. ^a |
| | Meat | regional | 90 | n.a. |
| | Dairy products | regional | 0 | n.a. |
| <i>Non-EU</i> | Livestock | national | 90 | n.a. |
| | Meat | regional | 90 | n.a. |
| | Dairy products | regional | 0 | n.a. |

a) Not applicable

Table 12.3b Import bans during and after an FMD epidemic in the more realistic script (REA)

| | | During epidemic | After epidemic (days) | |
|---------------|----------------|-----------------|-----------------------|-------------------|
| | | | Regional | National |
| <i>EU</i> | Livestock | national | 180 | n.a. ^a |
| | Meat | regional | 180 | n.a. |
| | Dairy products | regional | 0 | n.a. |
| <i>Non-EU</i> | Livestock | national | n.a. | 360 |
| | Meat | national | n.a. | 360 |
| | Dairy products | regional | 90 | n.a. |

a) Not applicable

12.2.7 Decision tree module

Rational economic decision-making models assume perfect markets and perfect information (Mileti, 1999). However, in reality animal health authorities are faced with sparse information about the probable efficacy of proposed control strategies. A decision tree analysis offers a formal, structured approach to decision-making, taking into account elements of uncertainty (Marsh, 1999). The aim is to make the chronological decision process explicit and to arrive at the best decision given the available information.

In this study the objective of the decision tree was to optimise early decisions for controlling FMD epidemics by calculating the economically optimal control strategy. A multi-attribute decision tree was built using the expected value criterion (Winterfeldt and Edwards, 1986). The two attributes were the direct costs and the consequential export losses and were weighted equally. For each scenario (see Figure 12.3) these attributes were calculated by means of the epidemiological and economic module.

In the early stages of a possible epidemic information is available on the outbreak region (livestock density and herd density) and the possibility of airborne spread (weather conditions). Information on the high risk period (HRP) is often sparse, because the source of introduction of FMDV in the primary-outbreak herd is often unknown and the analysis of virological and serological samples takes time (Horst, 1998). The decision tree method is used in two different situations: (1) if the HRP is known (see Figure 12.4a), and (2) if the HRP is unknown (see Figure 12.4b). In this last situation the probabilities of the HRPs were weighted equally. The trees were built in Data 3.5 (TreeAge Software, Inc.)

Figure 12.4a Decision tree if the HRP is known

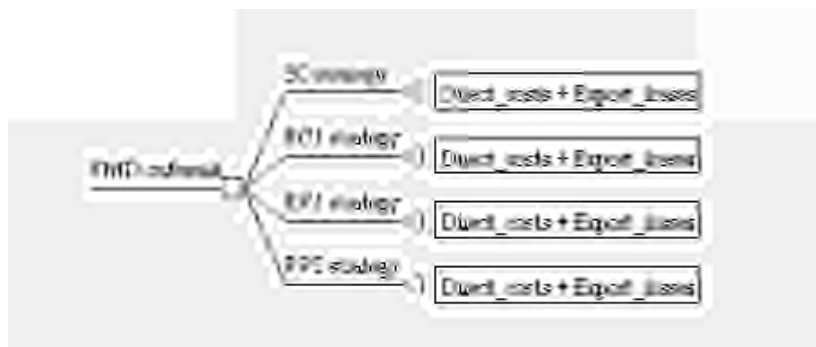
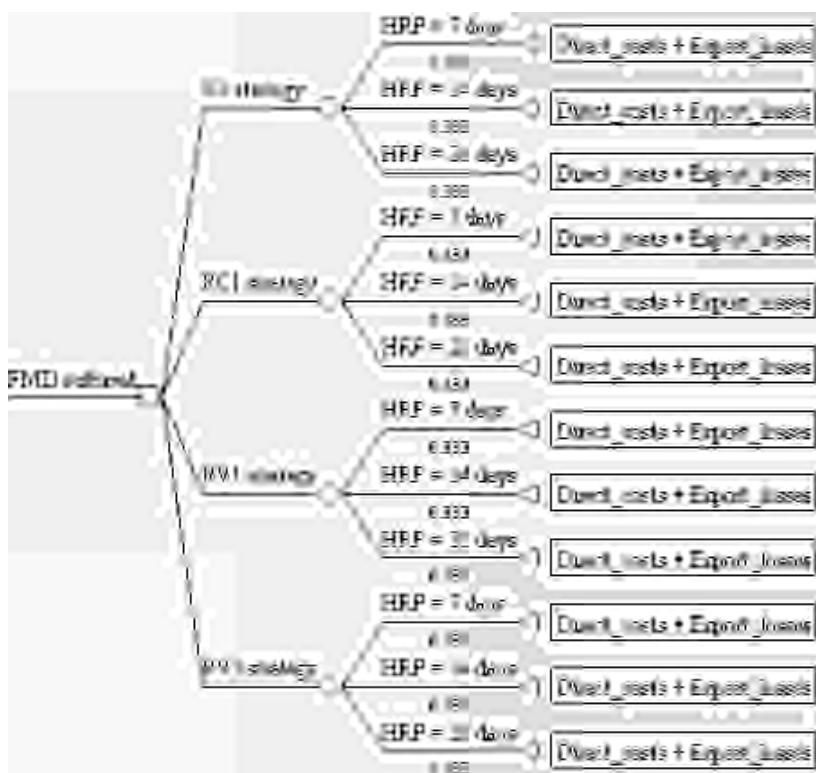


Figure 12.4b Decision tree if the HRP is unknown



12.3 Results

The epidemiological module simulated the disease dynamics, the economic module converted outbreak and control effects into estimates of direct costs and export losses, and finally a decision tree module optimised decisions on control strategies.

12.3.1 Epidemiological results

The epidemiological module generated the herd reproduction ratios (R_h) for each combination of region, control strategy and the possibility of airborne spread (see Table 12.4). When the $R_h < 1$, exact numbers are not shown because the epidemic will fade out automatically. The results indicate that the SO-strategy is not adequate for stopping the epidemic in the regions 1, 2, 3 and 4 in the scenarios with airborne spread because the R_h is > 1 . Additional measures are necessary. In the other three regions the SO-strategy eradicates the virus because R_h is < 1 . With additional measures the R_h could be reduced and likewise the number of infected farms and the duration of the epidemic. In the case of airborne spread, the RC1-strategy is not very effective in region 2 either because of the high livestock and herd densities as well as the limited culling capacity. Ring vaccination is then the only option in this region for eradicating the virus.

Table 12.4 R_h for each region, control strategy and the possibility of airborne spread

| Region | | 1 | 2 | 3 | 4 | 5 | 6 | 7 |
|------------------------|--------------------|-------|-------|-------|-------|-------|-------|-------|
| <i>Without control</i> | | 5.8 | 3.9 | 4.0 | 3.9 | 4.4 | 3.2 | 4.0 |
| SO | airborne spread | 2.0 | 2.7 | 1.7 | 1.1 | < 1 | < 1 | < 1 |
| | no airborne spread | 1.0 | 1.0 | < 1 | < 1 | < 1 | < 1 | < 1 |
| RC1 | airborne spread | < 1 | 1.0 | < 1 | < 1 | < 1 | < 1 | < 1 |
| | no airborne spread | < 1 | < 1 | < 1 | < 1 | < 1 | < 1 | < 1 |
| RV1 | airborne spread | < 1 | < 1 | < 1 | < 1 | < 1 | < 1 | < 1 |
| | no airborne spread | < 1 | < 1 | < 1 | < 1 | < 1 | < 1 | < 1 |
| RV3 | airborne spread | < 1 | < 1 | < 1 | < 1 | < 1 | < 1 | < 1 |
| | no airborne spread | < 1 | < 1 | < 1 | < 1 | < 1 | < 1 | < 1 |

12.3.2 Economic results

The economic module calculated 336 times (42 scenarios per region * 4 control strategies * 2 scripts for possible import bans) the direct costs and consequential export losses of an FMD epidemic. To give an indication of the main results, the extremes in sizes and economic consequences within these 336 calculations are presented in Table 12.5.

In the regions 1, 2, 3 and 4 in the worst case scenarios the epidemic becomes endemic. These results also indicate that the export losses are much higher than the direct costs. This is valid for both scripts, although export losses in the OIE-script were lower than in the REA-script.

Table 12.5 Extremes in sizes and economic consequences of FMD epidemics in each region

| Region | | 1 | 2 | 3 | 4 | 5 | 6 | 7 |
|----------------------------|-----|-------------------|------|------|------|-------|------|------|
| Duration (days) | Min | 75 | 72 | 54 | 46 | 47 | 41 | 45 |
| | Max | end. ^a | end. | end. | end. | 180 | 123 | 119 |
| No. infected herds | Min | 11 | 8 | 7 | 6 | 6 | 4 | 5 |
| | Max | end. | end. | end. | end. | 494 | 159 | 245 |
| Movement control | Min | 518 | 483 | 432 | 411 | 416 | 393 | 407 |
| surface (km ²) | Max | end. | end. | end. | end. | 10874 | 1500 | 2066 |
| Direct costs | Min | 83 | 60 | 36 | 24 | 16 | 4 | 5 |
| (in million €) | Max | end. | end. | end. | end. | 1478 | 63 | 110 |
| Export losses (REA) | Min | 563 | 443 | 453 | 407 | 314 | 315 | 339 |
| (in million €) | Max | end. | end. | end. | end. | 3051 | 678 | 926 |
| Export losses (OIE) | Min | 255 | 183 | 179 | 144 | 90 | 81 | 99 |
| (in million €) | Max | end. | end. | end. | end. | 2305 | 389 | 573 |

a) end. = the epidemic became endemic (duration > 1 year)

12.3.3 Results decision trees

The decision tree module was used in two different situations: (1) if the HRP is known and (2) if the HRP is unknown (see Figures 12.4a and 12.4b).

12.3.3.1 If HRP is known

The economically optimal and next-to-optimal control strategies for each region and HRP are shown in Table 12.6a (with airborne spread) and Table 12.6b (without airborne spread). These tables also present the Δ costs + losses, which is defined as the difference in direct costs and export losses between the optimal strategy and the next-to-optimal strategy.

These tables show that ring vaccination is always the economically optimal strategy in regions 1 and 2. The optimal radius of the ring vaccination depends on the length of the HRP. Ring culling is always the economically optimal strategy in regions 6 and 7. For the regions 3, 4 and 5 the economically optimal strategy depends on the length of the HRP and the presence of airborne spread.

The results of the two scripts of possible reactions of importing countries show almost the same rankings of economically optimal and next to optimal strategies. The differences in costs and losses between the economically optimal and next to optimal strategy generally increase as the HRP is extended.

Table 12.6a Optimal and next-to-optimal control strategies and the differences in costs and losses (in million €) between these strategies in the scenarios with airborne spread

| Region | 1 | 2 | 3 | 4 | 5 | 6 | 7 |
|------------------------|-----|-----|-----|-----|-----|------------------|------------------|
| <i>HRP = 7</i> | | | | | | | |
| optimal strategy | RV3 | RV3 | RV1 | RC1 | RC1 | RC1 | RC1 |
| next to opt. strategy | RV1 | RV1 | RV3 | RV1 | RV1 | RV1 ^a | RV1 ^a |
| Δ costs + losses (REA) | 51 | 11 | 5 | 61 | 35 | 49 | 49 |
| Δ costs + losses (OIE) | 35 | 9 | 3 | 52 | 32 | 45 | 44 |
| <i>HRP = 14</i> | | | | | | | |
| optimal strategy | RV1 | RV3 | RV3 | RC1 | RC1 | RC1 | RC1 |
| next to opt. strategy | RV3 | RV1 | RV1 | RV1 | RV1 | RV3 | RV1 |
| Δ costs + losses (REA) | 30 | 55 | 176 | 24 | 14 | 51 | 47 |
| Δ costs + losses (OIE) | 29 | 44 | 134 | 20 | 13 | 46 | 41 |
| <i>HRP = 21</i> | | | | | | | |
| optimal strategy | RV1 | RV3 | RV1 | RV3 | RV1 | RC1 | RC1 |
| next to opt. strategy | RV3 | RV1 | RV3 | RV1 | RV3 | RV1 | RV3 |
| Δ costs + losses (REA) | 405 | 766 | 241 | 90 | 5 | 134 | 61 |
| Δ costs + losses (OIE) | 404 | 746 | 236 | 71 | 3 | 62 | 51 |

a) OIE-script: SO

Table 12.6b Optimal and next-to-optimal control strategies and the differences in costs and losses (in million €) between those strategies in the scenarios without airborne spread

| Region | 1 | 2 | 3 | 4 | 5 | 6 | 7 |
|------------------------|-----|-----|-----|------------------|-----|-----|-----|
| <i>HRP = 7</i> | | | | | | | |
| optimal strategy | RV1 | RV1 | RC1 | RC1 | RC1 | RC1 | RC1 |
| next to opt. Strategy | RV3 | RV3 | RV1 | SO | SO | SO | SO |
| Δ costs + losses (REA) | 7 | 10 | 51 | 46 | 24 | 14 | 24 |
| Δ costs + losses (OIE) | 5 | 7 | 42 | 33 | 20 | 11 | 39 |
| <i>HRP = 14</i> | | | | | | | |
| optimal strategy | RV1 | RV1 | RV1 | RC1 | RC1 | RC1 | RC1 |
| next to opt. Strategy | RV3 | RV3 | RV3 | RV1 | RV1 | SO | RV1 |
| Δ costs + losses (REA) | 31 | 34 | 9 | 73 | 26 | 30 | 51 |
| Δ costs + losses (OIE) | 28 | 32 | 7 | 61 | 21 | 25 | 45 |
| <i>HRP = 21</i> | | | | | | | |
| optimal strategy | RV1 | RV3 | RV1 | RV3 | RV1 | RC1 | RC1 |
| next to opt. Strategy | RV3 | RV1 | RV3 | RV1 ^a | RV3 | SO | RV3 |
| Δ costs + losses (REA) | 259 | 471 | 96 | 83 | 9 | 62 | 90 |
| Δ costs + losses (OIE) | 219 | 451 | 33 | 63 | 6 | 48 | 76 |

a) OIE-script: RC1

12.3.3.2 If HRP is unknown

The economically optimal and next-to-optimal control strategies for each region when the HRP is unknown are shown in Table 12.7. Ring vaccination is always the optimal strategy in the regions 1, 2 and 3 because ring vaccination reduces the number of infected herds and the duration of the epidemic.

Table 12.7 Optimal and next-to-optimal control strategies and the differences in costs and losses (in million €) between these strategies

| Region | 1 | 2 | 3 | 4 | 5 | 6 | 7 |
|-------------------------------|-----|-----|-----|------------------|-----|-----|-----|
| <i>Airborne spread:</i> | | | | | | | |
| optimal strategy | RV1 | RV3 | RV1 | RV3 | RV1 | RC1 | RC1 |
| next to opt. Strategy | RV3 | RV1 | RV3 | RV1 | RV3 | RV3 | RV3 |
| Δ costs + losses (REA) | 128 | 268 | 23 | 25 | 4 | 81 | 56 |
| Δ costs + losses (OIE) | 132 | 256 | 38 | 21 | 1 | 69 | 48 |
| <i>No airborne spread:</i> | | | | | | | |
| optimal strategy | RV1 | RV3 | RV1 | RC1 | RC1 | RC1 | RC1 |
| next to opt. Strategy | RV3 | RV1 | RV3 | RV3 ^a | RV1 | RV3 | RV3 |
| Δ costs + losses (REA) | 94 | 142 | 28 | 13 | 7 | 65 | 66 |
| Δ costs + losses (OIE) | 110 | 12 | 7 | 42 | 8 | 57 | 56 |

a) OIE-script: RV1

Ring culling is always the optimal strategy in regions 6 and 7. In these regions, ring vaccination prolongs the epidemic and enlarges the surface of movement standstill areas.

For regions 4 and 5 the optimal strategy depends on the presence of airborne spread.

The results of the two scripts of possible reactions by importing countries show almost the same rankings of optimal and next-to-optimal strategies.

12.3.3.3 Expected value of HRP information

Two extreme situations were examined; a situation with no HRP information at all and a situation with perfect HRP information. This made it possible to calculate the expected value of perfect information (see Table 12.8). The expected value of perfect information provides an upper limit for the expected value of information in general (Clemen and Reilly, 2000). The results in Table 12.8 emphasise the importance of retrieving information on the length of the HRP for the situations in which the expected value of perfect information is not zero. Gathering HRP information leads to better decision-making, particularly in regions 3, 4 and 5.

Table 12.8 Optimal strategies when HRP is unknown and known and the expected value of perfect HRP information (in million €)

| Region | Airborne spread | HRP unknown | HRP known | | | Expected value of information |
|--------|-----------------|-------------|-----------|------------|------------|-------------------------------|
| | | | 7 days | 14 days | 21 days | |
| 1 | Yes | RV1 | RV3 (-51) | RV1 | RV1 | 17 |
| | No | RV1 | RV1 | RV1 | RV1 | 0 |
| 2 | Yes | RV3 | RV3 | RV3 | RV3 | 0 |
| | No | RV3 | RV1 (-10) | RV1 (-9) | RV3 | 6 |
| 3 | Yes | RV1 | RV1 | RV3 (-176) | RV1 | 59 |
| | No | RV1 | RC1 (-51) | RV1 | RV1 | 17 |
| 4 | Yes | RV3 | RC1 (-65) | RC1 (-33) | RV3 | 33 |
| | No | RC1 | RC1 | RC1 | RV3 (-121) | 40 |
| 5 | Yes | RV1 | RC1 (-35) | RC1 (-14) | RV1 | 16 |
| | No | RC1 | RC1 | RC1 | RV1 (-85) | 28 |
| 6 | Yes | RC1 | RC1 | RC1 | RC1 | 0 |
| | No | RC1 | RC1 | RC1 | RC1 | 0 |
| 7 | Yes | RC1 | RC1 | RC1 | RC1 | 0 |
| | No | RC1 | RC1 | RC1 | RC1 | 0 |

12.4 Discussion

12.4.1 Epidemiological module

This study used available knowledge to illustrate the epidemiological and economic consequences of an outbreak. For this reason, the model was restricted to a pig-adapted FMD virus strain. There was limited knowledge available on virus transmission in the field between other susceptible species. This means that the results can be interpreted as the optimal strategies for pig-adapted FMD virus strains. These results can be roughly extrapolated to other FMD virus strains. Control approaches for other strains would not differ much from the control approaches used in this study because all susceptible species were included in the control measures. Therefore, the economic results are likely to follow a comparable pattern as the results in this study.

12.4.2 Economic module

The economic module converted outbreak and control effects into estimates of direct costs and consequential export losses for producers in the livestock value chain and the government. An epidemic could also have effects on the Dutch economy as a whole because of the side effects of disease control measures (e.g. the closure of footpaths harms the tourist

sector) and interactions between economic sectors (e.g. price drops for livestock products favours consumers) (Berentsen et al., 1992a; Garner and Lack, 1995; Mahul and Durand, 2000). These ‘non-agricultural’ effects have not been quantified because the aim was not to carry out a full social cost-benefit analysis. This analysis provides a framework for comparing disease control strategies but includes also difficulties. Many costs and benefits are by their nature difficult to quantify (e.g. emotional problems of farmers whose animals had to be culled). Assigning monetary values to these costs and benefits is a major problem of cost-benefit analysis and involves making subjective judgements (Ramsay et al., 1999).

A knowledge gap was found in the possible reactions of importing countries. Reactions do not always respect the OIE guidelines. This problem was solved by using two scripts for possible reactions. The model showed that varying lengths of import bans had only limited influence on the economically optimal control strategies. A limitation of the calculations is that these were based on changes in quantities due import bans. Price and substitution effects were excluded in the economic calculations. Therefore, the results provide upper bounds for the economic costs of an epidemic.

12.5 Conclusions

The decision tree is a useful tool for structuring and optimising early decisions concerning the control of FMD epidemics in different regions in The Netherlands. The outcomes can be used as yardsticks for deciding on control measures during possible FMD epidemics in the future. The results showed that not selecting the economically optimal strategy could cause large additional economic losses.

Animal density within the outbreak region is an important determinant in deciding on the optimal control strategy. The results show a considerable regional variation in the size of impacts. Ring vaccination is the economically optimal strategy for densely populated livestock areas because this strategy reduces the number of infected herds and the duration of the epidemic compared to the other strategies. Ring culling is the economically optimal strategy for sparsely populated livestock areas. For livestock areas that are neither very densely populated nor very sparsely populated, the optimal strategy depends on the length of the HRP and the presence of airborne spread.

The duration of an epidemic was one of the most important parameters, which determined the economic impact of an epidemic. This was consistent with previous research (Horst et al., 1999; Mahul and Durand, 2000). In densely populated livestock areas the culling and

rendering capacity was the limiting factor, causing delays in culling and extension of the epidemic. Therefore, ring vaccination is the optimal strategy in these areas because it reduces the number of infected farms and likewise the duration of the epidemic.

The results of this study stress the importance of retrieving information on the expected length of the HRP as soon as possible after an outbreak of FMD has been declared, especially in regions that are neither very densely nor very sparsely populated.

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Appendix III

Table III.1 Distribution of the gross value added (in billion €) within the livestock production chain (mean value of 1995 and 1998)

| | Grassland based livestock farming | | Intensive livestock farming | | Total | |
|-----------------------|--------------------------------------|-------|--------------------------------|-------|-----------|-------|
| | Billion € | % | billion € | % | billion € | % |
| Livestock farms | 3.0 | 41 | 0.7 | 22 | 3.7 | 35 |
| Supply industry | 1.4 | 19 | 0.7 | 22 | 2.1 | 20 |
| Processing industry | 2.2 | 30 | 1.3 | 40 | 3.5 | 33 |
| Distribution industry | 0.7 | 10 | 0.5 | 16 | 1.2 | 12 |
| Total | 7.3 | 100 % | 3.1 | 100 % | 10.5 | 100 % |

Probability of Classical Swine Fever virus introduction in the European Union: analysis and modelling

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13.1 Introduction

Recent Classical Swine Fever (CSF) epidemics in the European Union (EU) incurred high economic losses. In 1993/94 Germany and Belgium were severely hit by a CSF epidemic, 217 farms being affected in Germany (Kramer et al., 1995; Pittler et al., 1995) and 55 in Belgium (Laevens et al., 1998; Koenen et al., 1996; Vanthemsche, 1996). Even more disastrous was the 1997/98 CSF epidemic in the Netherlands, which affected 429 farms, while more than 10 million pigs were destroyed preventively and for welfare reasons (Anonymous, 1998). The costs of this epidemic (i.e. direct costs and consequential losses to farms and related industries) were estimated at US\$ 2.3 billion (Meuwissen et al., 1999). The import of infected piglets from The Netherlands also lead to a major epidemic in Spain, 99 farms being infected in 1997/98 (Edwards et al., 2000; Greiser-Wilke et al., 2000).

The introduction of CSF is a continuing threat to the pig production sector of the EU. The disease is still present in some central and eastern European countries (Edwards et al., 2000). Besides, CSF occurs in an endemic form in wild boar populations in some areas of Germany, France and Italy (Laddomada, 2000), representing a permanent CSF virus (CSFV) reservoir. The disease can thus easily be reintroduced into free regions if no proper measures are taken. Prevention of CSFV introduction should therefore be given the highest possible priority.

Most outbreaks in the major CSF epidemics mentioned above occurred in the so-called densely populated livestock areas (DPLAs) that have an average pig density of more than 300 pigs/km² (Michel and De Vos, 2000). These areas came into being due to economic factors, such as the availability of cheap feed and reasonably priced land as well as the proximity of urban markets (Dijkhuizen and Davies, 1995; Huirne et al., 1995). The concentration of pig production in these areas is supposed to be correlated with the risk of introduction and spread of epidemic diseases (Dijkhuizen and Davies, 1995). Pig and pig farm densities are, however, not the only determinants in the risk of virus introduction. Insight into all factors contributing to the risk of virus introduction is a prerequisite for taking preventive actions that are both

epidemiologically effective and economically sensible, and is therefore of utmost importance in supporting policy-making.

This study focuses on the probability of CSFV introduction for several regions in the EU. The main objective was to gain more insight into the major factors contributing to this probability. Two approaches were used: (i) a qualitative assessment that provides a tool for a quick analysis that can be performed with relatively little information and (ii) a quantitative approach using a computer model, that provides more detailed insight into the factors that contribute to the probability of CSFV introduction, but for which a lot of quantitative data is needed.

The paper starts with an overview of some relevant definitions. Then a pathway diagram giving an overview of all pathways possibly contributing to the probability of CSFV introduction is presented. This was used as the basis for both the qualitative assessment and the computer model. Results of the qualitative assessment are given for five densely and five sparsely populated livestock areas (SPLAs) in the EU. Model results are presented for five EU member states. The paper concludes with discussion of the approaches used and the results obtained.

13.2 Definitions

As not all definitions in the field of animal health risk analysis are yet standardised, a brief overview of key terms used throughout this paper is given first of all.

Virus introduction is defined as the entrance of a virus into the livestock production sector of a region free of the disease, causing a primary outbreak¹¹. The definition of a primary outbreak was derived from the EU Council Directive 82/894/EEC: ‘an outbreak not epizootiologically linked with a previous outbreak in the same region of a member state, or the first outbreak in a different region of the same member state’ (CEC, 1982). The regions used for this definition are areas with a surface of at least 2000 km², that must be controlled by competent authorities and at least comprise one of a certain, member state-dependent, administrative area, e.g., provinces in Belgium, Italy and Spain, counties in the United Kingdom and Ireland and departments in France (Council Directive 64/432/EEC, Article 2 (CEC, 1964)). Using the EU definition of a primary outbreak, more primary outbreaks can

¹¹ The focus in this article is on CSFV introduction into the domestic pig population of a region. Virus introduction into the wild boar population has not been considered, because prevention and control strategies used are different (CEC, 1980), as well as the economic consequences of such an introduction.

occur within one epidemic if the virus is spread from one region to another. This was the case, for example, during the 1997/98 CSF epidemic in The Netherlands, in which four primary outbreaks were recorded.

Introduction of the virus is induced by so-called pathways. These are the carriers and mechanisms that can transmit a virus from an infected to a susceptible animal. Pathways can either be exogenous or endogenous. Exogenous pathways are linked with virus sources outside the region where they might cause a primary outbreak, whereas endogenous pathways reside within the region affected. The regions where exogenous pathways may come from are called regions of origin, whereas the region affected is called the target area.

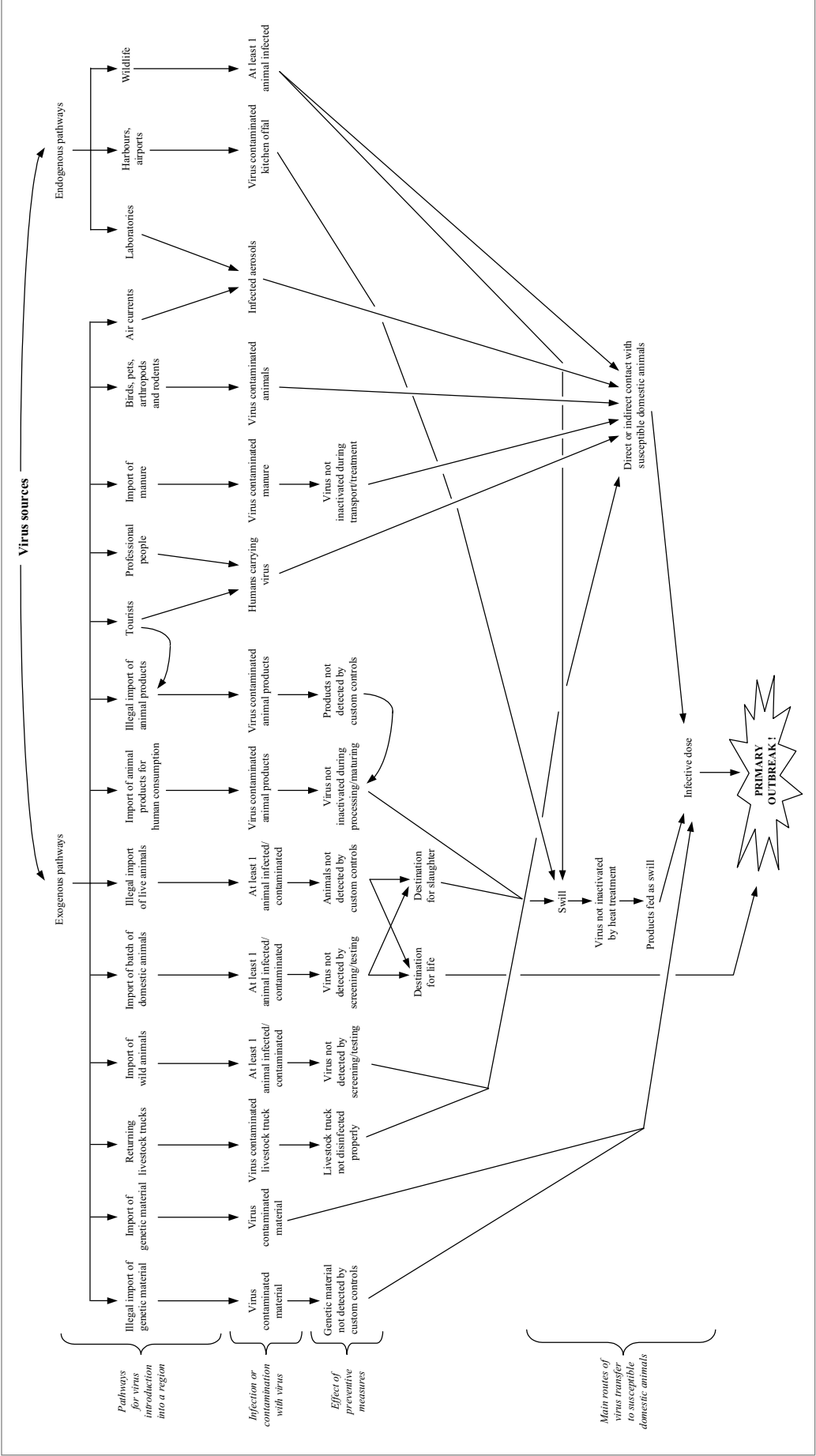
13.3 Pathway diagram

To obtain more insight into the probability of CSFV introduction, a so-called pathway diagram was constructed to show all possible pathways for CSFV introduction, including their main events and interrelations (Figure 13.1). A pathway diagram is a tree-like approach that provides insight into all possible causes of an adverse event (De Vos et al., 2001). In order for the adverse event to occur, all contributing events of a certain pathway have to be true. Assigning probabilities to all events in the diagram makes it possible to estimate the probability of occurrence of the adverse event.

The pathway diagram consists of four levels. Starting at the top of the diagram, the first level comprises the pathways for virus introduction into a region, including both exogenous and endogenous pathways. A pathway can only contribute to the probability of virus introduction if it is present. The extent of presence is expressed in pathway-units, which are the units in which a pathway is measured, e.g., an animal, a metric ton of animal products or a returning livestock truck.

Whether or not any pathway-units are present that are infected or contaminated with a virus is determined at the second level. Obviously, exogenous pathways only constitute a risk if they originate from an area where the disease is prevalent. Endogenous pathways only pose a risk if they contain a virus reservoir. Some exogenous pathways can only contribute to the probability of virus introduction if they originate from a neighbouring area, e.g., air currents and birds, pets, arthropods and rodents. These pathways play a minor role in virus introduction because they only transport the virus over short distances.

Figure 13.1 Pathway diagram containing all pathways that contribute to the probability of CSFV introduction in the European Union



Whether or not preventive actions succeed in detecting and/or inactivating the virus is evaluated at the third level. Only a selection of preventive measures is given in the diagram. Most additional preventive measures that can be taken by a region, e.g., testing or quarantine, can be added to the pathway diagram at this level.

If the virus is still present after passing the third level, virus transfer to susceptible domestic animals can occur by two main routes: swill feeding to - or direct or indirect contact with - susceptible animals. Which route is relevant depends on the pathway for virus introduction. Virus transfer will only result in an outbreak if the virus conveyed constitutes an infective dose. There is, however, one exception to this general pattern: import of an infected live animal, legally or illegally, will always lead to an outbreak if the animal survives and infection is not detected in time. In such cases, swill feeding or contact with susceptible animals is not required in order to cause a primary outbreak, since the imported animal becomes part of the livestock population.

For each pathway, the main events leading to a primary CSF outbreak are shown in the pathway diagram. Theoretically, each event in the pathway diagram can be assigned a probability that it will occur. These are all conditional probabilities, i.e., the probability of occurrence of a certain event given that all previous events have occurred. To give an example, virus introduction by the pathway 'returning livestock trucks' will only occur if a livestock truck returns to the region after visiting an infected region, if this truck is contaminated with virus, if it is not disinfected properly, if it comes into contact with susceptible animals and if the virus dose conveyed is at least the minimum infective dose.

13.4 Qualitative assessment of the probability of CSFV introduction into densely and sparsely populated livestock areas

The pathway diagram in Figure 13.1 was used to qualitatively assess the probability of CSFV introduction for five densely and five sparsely populated livestock areas in the EU. Information about the presence of pathways (level 1 of the pathway diagram) and the possibility of pathways passing the virus to susceptible domestic pigs (level 4) was used to classify the regions according to their probability of CSFV introduction.

Basic information available for each region is presented in Table 13.1-A. This information was used to calculate pig and farm density and to derive an estimate of the number of pigs exported or imported by the region (Table 13.1-B). The estimates derived are the minimum

numbers of pigs imported or exported. Obviously, in most cases these will be an underestimate of the gross imports and exports.

Table 13.1-B indicates that regions with a high pig density have larger net imports or exports of pigs than regions with a low pig density. Südoldenburg (GE), Mantova (IT), and West-Flanders (BE) are major net importers of piglets, whereas South (NL) and Côtes d'Armor (FR) are major net exporters. Südoldenburg (GE) has a net import of fattening pigs, whereas South (NL), Mantova (IT), West-Flanders (BE), and Côtes d'Armor (FR) have a net export of fattening pigs due to a shortage of slaughter capacity. Regions with a high pig density also have a high pig farm density, with the exception of Mantova (IT) where pigs are concentrated in large intensive farms. The number of airports with regular flights is highest in the Côtes d'Armor (FR) which has four. The number of laboratories working with CSFV is highest in Hannover (GE) which has three, including the EU Reference Laboratory for CSF. The number of wild boar is highest in Orne (FR) which has an estimated population of 5,500 animals. No CSF infections in wild boar were, however, detected in recent years in the regions listed in Table 13.1-A (Laddomada, 2000). Swill feeding is forbidden in all but the German regions. In Germany swill feeding is still allowed, but only after adequate heat treatment. Hence, if all regulations were observed, none of the regions of Table 13.1-A would suffer from primary CSF outbreaks caused by swill feeding.

To classify the regions as having a low, moderate or high probability of CSFV introduction, eight criteria were used (see left column of Table 13.2). These criteria were based on (i) the (extent of) presence of pathways and (ii) pig and farm density and swill feeding, which are indicators for the probability that CSFV will reach susceptible domestic pigs once the virus has been introduced. If a region meets none or only one of the criteria, it is denoted as having a low probability of CSFV introduction. If a region meets two or three of these criteria, it is denoted as having a moderate probability of CSFV introduction, and if it meets four or more, it is indicated as having a high probability of CSFV introduction. On the basis of these criteria, the regions South (NL), Südoldenburg (GE), Hannover (GE), West-Flanders (BE), and Côtes d'Armor (FR) were classified as having a high probability of CSFV introduction. South-West (NL), Mantova (IT), and Orne (FR) were considered to have a moderate probability of CSFV introduction, whereas the remaining regions – the SPLAs of Italy and Belgium – were considered to have a low probability of CSFV introduction (Table 13.2).

Table 13.1-A Basic information^a on five densely and five sparsely populated livestock areas used for the qualitative assessment of the probability of CSFV introduction.

| Type of region ^b | The Netherlands | | | Germany | | Italy | | | Belgium | | | France | |
|---|-----------------|------------|-------|---------------------|----------|---------|--------|---------------|---------|---------------|------|--------|--|
| | South | South-West | | Süd-oldenburg | Hannover | Mantova | Rovigo | West-Flanders | Namur | Côtes d'Armor | Orne | | |
| | DPLA | SPLA | DPLA | DPLA | SPLA | DPLA | SPLA | DPLA | SPLA | DPLA | SPLA | | |
| Surface area (km2) | 7,050 | 4,544 | 2,230 | 2,290 | 2,339 | 1,922 | 3,293 | 4,418 | 6,878 | 6,103 | | | |
| Number of sows (*10 ³) | 777 | 26 | 85 | 12 | 47 | 5 | 349 | 3 | 189 | 8 | | | |
| Number of fattening pigs (*10 ³) | 4,095 | 198 | 1,395 | 67 | 625 | 41 | 2,747 | 27 | 1,168 | 53 | | | |
| Total number of pigs (*10 ³) | 8,754 | 336 | 1,636 | 105 | 797 | 55 | 4,413 | 43 | 2,200 | 90 | | | |
| Total number of pig farms | 7,688 | 957 | 3,400 | 695 | 1,101 | 1,364 | 5,376 | 261 | 7,381 | 1,170 | | | |
| Annual number of pigs slaughtered (*10 ³) | 7,225 | 600 | 4,676 | 178 | 1,352 | 208 | 4,639 | 5 | 2,598 | 21 | | | |
| Number of airports with regular flights | 2 | 1 | 0 | 1 | 0 | 0 | 2 | 0 | 4 | 1 | | | |
| Number of laboratories working with CSFV | 0 | 0 | 0 | 3 | 0 | 0 | 0 | 0 | 2 | 0 | | | |
| Estimated number of wild boar | 136 | 0 | 120 | >1,170 ^c | 0 | 0 | 0 | 1,250 | 700 | 5,500 | | | |
| Estimated number of infected wild boar | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | | | |
| Swill feeding allowed? | no | no | yes | Yes | no | no | no | no | no | No | | | |

a) Information was derived from the database described by Michel and De Vos (2000) and from research groups participating in the EU Research Project FAIR5-PL97-3566, see e.g. Anonymous (2000)

b) DPLA: densely populated livestock area; SPLA: sparsely populated livestock area

c) No estimate of the wild boar population was available. In the period 1 April 1999 – 31 March 2000 1,170 wild boar were killed

Table 13.1-B Calculated data for five densely and five sparsely populated livestock areas used for the qualitative assessment of the probability of CSFV introduction

| Type of region ^a | The Netherlands | | Germany | | Italy | | Belgium | | France | |
|--|-----------------|------------|---------------|----------|---------|--------|---------------|-------|---------------|------|
| | South | South-West | Süd-oldenburg | Hannover | Mantova | Rovigo | West-Flanders | Namur | Côtes d'Armor | Orne |
| | DPLA | SPLA | DPLA | SPLA | DPLA | SPLA | DPLA | SPLA | DPLA | SPLA |
| Pig density (pigs/km2) | 1,242 | 74 | 733 | 46 | 341 | 29 | 1,340 | 10 | 320 | 15 |
| Pig farm density (farms/km2) | 1.09 | 0.21 | 1.52 | 0.30 | 0.47 | 0.78 | 1.63 | 0.06 | 1.07 | 0.19 |
| Fattening pig/sow ratio | 5.27 | 7.69 | 16.39 | 5.55 | 13.38 | 8.58 | 7.88 | 8.00 | 6.19 | 6.51 |
| Net number of imported piglets per year ^{bc} (*10 ³) | -1,622 | 9 | 769 | -22 | 281 | 6 | 182 | 2 | -220 | -7 |
| Net number of imported fattening pigs per year ^{bd} (*10 ³) | -4,272 | 45 | 758 | -11 | -402 | 94 | -3,075 | -71 | -681 | -129 |

a) DPLA: densely populated livestock area; SPLA: sparsely populated livestock area

b) A negative net number of imported animals signifies a net number of exported animals

c) Net piglet imports were estimated on the basis of the fattening pig/sow ratio of the region, assuming that with a ratio of about 7.4 theoretically no net import or export of piglets is required. Figures used: weaned piglets per sow per year: 22; replacement rate: 0.4; percentage mortality from weaning to slaughter: 4%; fattening period (20 kg to slaughter weight): 130 days

d) Slaughter capacity in the region was used to estimate the net import or export of fattening pigs

Table 13.2 Qualitative classification of five densely and five sparsely populated livestock areas for their probability of CSFV introduction

| Type of region ^a | The Netherlands | | | Germany | | | Italy | | Belgium | | France | | |
|---|-----------------|------------|------|---------------|----------|----------|--------|---------------|---------|---------------|--------|----------|----------|
| | South | South-West | | Süd-oldenburg | Hannover | Mantova | Rovigo | West-Flanders | Namur | Côtes d'Armor | | | |
| | DPLA | SPLA | DPLA | DPLA | SPLA | DPLA | SPLA | DPLA | SPLA | DPLA | DPLA | SPLA | SPLA |
| Net number of piglets imported > 1 * 10 ⁵ per year | - | - | ✓ | ✓ | - | ✓ | - | ✓ | - | - | - | - | - |
| Net number of pigs exported > 5 * 10 ⁵ per year | ✓ | - | - | - | - | - | - | ✓ | - | ✓ | - | - | - |
| Airports with regular flights present | ✓ | ✓ | - | - | ✓ | - | - | ✓ | - | ✓ | ✓ | ✓ | ✓ |
| Laboratories working with CSFV present | - | - | - | - | ✓ | - | - | - | - | ✓ | - | - | - |
| Wild boar present | ✓ | - | ✓ | ✓ | ✓ | - | - | - | ✓ | ✓ | ✓ | ✓ | ✓ |
| Pig density > 50 pigs/km ² | ✓ | ✓ | ✓ | ✓ | - | ✓ | - | ✓ | - | ✓ | ✓ | - | - |
| Pig farm density > 1 farm/km ² | ✓ | - | ✓ | ✓ | - | - | - | ✓ | - | ✓ | ✓ | - | - |
| Swill feeding allowed | - | - | ✓ | ✓ | ✓ | - | - | - | - | - | - | - | - |
| Expected probability of CSFV introduction | high | Moderate | high | high | High | moderate | low | high | low | high | high | moderate | moderate |

a) DPLA: densely populated livestock area; SPLA: sparsely populated livestock area

13.5 Computer model for assessing the probability of CSFV introduction quantitatively

A computer model was developed to calculate the probabilities of CSFV introduction for individual regions in the EU quantitatively and in more detail. The main aim of this model is to analyse which pathways contribute to the probability of CSFV introduction for a particular region, the so-called target area, and from where, i.e., which regions of origin, these pathways originate. Furthermore, the model provides insight into differences between target areas with regard to the ranking of causative pathways and regions, and their interactions, and hence the need for diversification of preventive measures.

13.5.1. Modelling approach

The model calculates the probability of CSFV introduction into the domestic pig population of a target area by different pathways (see Figure 13.1). The probability of virus introduction by endogenous pathways depends only on the situation in the target area, whereas the probability of virus introduction by exogenous pathways depends on conditions in their region of origin as well as in the target area. Most probabilities calculated in the model are very low, as they are calculated per epidemic in each region of origin as well as separately for each exogenous pathway. Therefore, the scenario pathway approach was used as a modelling technique, and not simulation, because it requires relatively little computing time and can easily calculate extremely low probabilities (Vose, 1997). The model was constructed in Microsoft Excel 97 with the add-in program @Risk 4.0.5 (Palisade Corporation).

For each pathway in the model, a scenario tree was constructed in which the sequence of events that ultimately leads to the introduction of CSFV into the domestic pig population of the target area is determined (Miller et al., 1993). Only those events that are decisive in determining whether an infected pathway-unit will transmit virus to susceptible animals were included in the scenario trees. Each event in the scenario trees was assigned a probability that it would occur. These were all conditional probabilities. To get the probability of CSFV introduction by a certain pathway, all probabilities along its scenario tree were multiplied. The scenario trees for the exogenous pathways were calculated separately for each region of origin. Combining the outcome of all scenario tree calculations gave insight into the relative contribution of regions and pathways to the probability of CSFV introduction for the target area.

Calculations were performed for five EU member states, i.e. Germany, France, Italy, The Netherlands and Belgium. These are the so-called target areas. All EU member states were included in the model as possible regions of origin. No third countries were included.

13.5.2. Input

13.5.2.1. Occurrence of CSF

CSF is not endemic in the domestic pig population of the EU, except for the island of Sardinia, Italy (Anonymous, 1997). The disease situation with regard to CSF in the EU member states was obtained from the Animal Disease Notification System (ADNS). This is an EU computerised database in which all primary and secondary outbreaks of highly contagious animal diseases are recorded. ADNS does not, however, provide information on links between outbreaks, hence the number of CSF epidemics that occurred in the member states could not be directly derived from this database. Therefore, the number of regions experiencing at least one primary outbreak was used to estimate the average number of epidemics per year. Data was used from the period 1990-1999 because from 1990 onwards mass vaccination against CSF was no longer applied in the EU (Terpstra and De Smit, 2000)., The minimum, average and maximum number of regions with primary outbreaks per year for this 10-year period is given in Table 13.3. The average number was used as the expected number of epidemics per year in the model's calculations. For those member states that did not suffer from CSF at all during this period, the expected number of epidemics per year was set at 0.095 using the exponential distribution (Vose, 1997):

$$\text{Epidemics}_{\text{year}} = 1 - \exp(-x/\beta) \quad (1)$$

With x = time interval used for the calculations (i.e. 1 year) and β = minimum interval between two epidemics (i.e. 10 year). This is the highest possible value since it assumes that (i) the event is possible and (ii) it occurred before the first moment of observation and will occur again immediately after the last moment of observation, i.e., in the eleventh year (which is 2000).

Furthermore, the disease situation in the wild boar populations of the target areas was considered. CSF is endemic in parts of the wild boar populations in Germany, France and Italy (Laddomada, 2000). The prevalence of infection varies per metapopulation of wild boar and is monitored using sampling programmes (e.g. Elbers and Dekkers, 2000; Cruci re et al., 1998; Kern, 1998). The regions in which infected wild boar roam are the Bundesl nder of Lower Saxony, Mecklenburg-Vorpommern and Brandenburg in Germany, the departments of Moselle and Bas-Rhin in France, and the provinces of Nuoro, Sassari and Oristano (all on the island of Sardinia) and Varese in Italy (Laddomada, 2000).

Table 13.3 The minimum, average and maximum number of regions per year in each country that experienced primary CSF outbreaks for the period 1990-1999 (source: ADNS)

| Countries | Minimum | Average | Maximum |
|-----------------|---------|---------|---------|
| Germany | 2 | 10.2 | 25 |
| France | 0 | 0.5 | 2 |
| Italy | 0 | 2.8 | 6 |
| The Netherlands | 0 | 0.6 | 4 |
| Belgium | 0 | 0.4 | 1 |
| Luxembourg | 0 | 0 | 0 |
| United Kingdom | 0 | 0 | 0 |
| Ireland | 0 | 0 | 0 |
| Denmark | 0 | 0 | 0 |
| Greece | 0 | 0 | 0 |
| Spain | 0 | 0.7 | 5 |
| Portugal | 0 | 0 | 0 |
| Austria | 0 | 0.2 | 1 |
| Finland | 0 | 0 | 0 |
| Sweden | 0 | 0 | 0 |

13.5.2.2. Pathways in the model

All pathways that possibly contribute to the probability of CSFV introduction were included in the pathway diagram in Figure 13.1. A selection of these pathways was made for inclusion in the computer model for virus introduction on the basis of two criteria: (i) expected importance for CSFV introduction on the basis of historical data and scientific literature and (ii) availability of knowledge and data to quantify the underlying probabilities.

The major routes for CSFV introduction in the EU since the prohibition of mass vaccination were feeding of improperly heated swill, direct or indirect contact with wild boar and animal movements (De Vos et al., 2000; Fritzemeier et al., 2000). Information from ADNS gave similar results, indicating that purchase of animals, waste food feeding, and spread by fomites¹² caused the majority of primary CSF outbreaks for which the origin of disease was given in ADNS (De Vos et al., 2001).

Therefore, the exogenous pathway import of a batch of domestic animals and the endogenous pathway of wildlife were included in the model for virus introduction. Furthermore, the pathway of import of animal products for human consumption was included, as it is one of the major routes that could contribute to (illegal) swill feeding. Illegal imports of animals and animal products could be even more dangerous with regard to the probability of CSFV

¹² Spread by fomites is all virus spread caused by objects that are contaminated with the disease agent and hence covers those indirect contacts between animals that are not included in other transmission routes distinguished in ADNS (Laddomada, personal communication). It also includes spread by wild boar (Pittler et al., 1995).

introduction, because there are no checks on either where these imports come from or their disease status. These pathways were, however, not included in the model, as no data was available on their numbers. The pathway of returning livestock trucks was included in the model, because data could be derived from the total number of animals exported and experts considered it to be an important risk factor for the introduction of CSFV into The Netherlands (Horst et al., 1998). Although CSFV can potentially be transmitted over long distances by the distribution of virus-contaminated semen (De Smit, 2000), the pathway of genetic material was not included in the model due to lack of data. All other pathways displayed in the pathway diagram were not included in the model as they were considered to contribute only marginally to the probability of CSFV introduction and data available for quantification was extremely limited.

13.5.2.3. Occurrence of pathways

In Table 13.4, data on the occurrence of pathways included in the model is given for the five target areas. Imports from and exports to all EU member states are shown. In the model, these numbers were subdivided according to their regions of origin. The numbers of pigs imported and exported were divided by the average batch size to give estimates of the number of batches of domestic animals imported and returning livestock trucks, respectively.

Germany is a major importer of pigs, whereas The Netherlands is a major exporter. Italy exports hardly any pigs. With regard to pork products, it can be seen that most trade is in fresh and chilled products. The wild boar populations of Germany and France are much bigger than the populations in The Netherlands and Belgium. No data on the number of wild boar in the country was available for Italy. In Germany, wild boar are spread all over the country, whereas in the other countries they are more regionally distributed (Anonymous, 1999).

The pathways were divided into subgroups to perform the model calculations. The imports and exports of pigs were subdivided into three categories, i.e., piglets, breeding pigs and fattening pigs. It was assumed that the risks of CSFV introduction might differ between these categories. Fattening pigs are brought to slaughterhouses, whereas piglets and breeding pigs become part of the pig population in the target area. Furthermore, it was assumed that more preventive measures would be in use for the import of breeding pigs than piglets. The import of pork products was subdivided into four categories, i.e., fresh or chilled, frozen, non-heat treated, and heat-treated pork products, because the probability that CSFV will survive maturing and processing differs between those categories. CSFV can survive up to 4-5 years in frozen pork products (Farez and Morley, 1997) and up to several months in fresh or chilled pork products (Terpstra, 1991; 1986). In non-heat treated pork products, i.e., salted, in brine, smoked or dried, CSFV can survive up to three months (Terpstra, 1986). In heat-treated products, CSFV will not survive if the combination of temperature and duration of heat treatment is sufficient.

Table 13.4 Quantification of pathways included in the model for virus introduction

| | Germany | France | Italy | The Netherlands | Belgium |
|--|-----------|---------|-------------------|-----------------|-----------|
| <i>Import of pigs (numbers)^a</i> | | | | | |
| Piglets | 1,416,941 | 283,049 | 306,213 | 31,735 | 702,767 |
| Breeding pigs | 132,633 | 14,805 | 11,753 | 16,319 | 61,418 |
| Fattening pigs | 1,261,402 | 164,555 | 715,212 | 390,452 | 68,494 |
| <i>Export of pigs (numbers)^a</i> | | | | | |
| Piglets | 684,326 | 177,581 | 1,773 | 1,633,211 | 84,531 |
| Breeding pigs | 5,484 | 64,456 | 18,545 | 107,770 | 11,923 |
| Fattening pigs | 371,897 | 72,106 | 7,749 | 1,427,590 | 1,012,768 |
| <i>Import of pork products (metric tons)^a</i> | | | | | |
| Fresh/chilled | 725,832 | 296,606 | 633,062 | 68,997 | 83,836 |
| Frozen | 114,365 | 97,759 | 73,167 | 40,759 | 19,038 |
| Non-heat treated | 32,380 | 60,150 | 8,778 | 10,058 | 25,435 |
| Heat treated | 42,109 | 25,548 | 12,721 | 31,032 | 33,662 |
| Wild boar (head) ^b | 600,000 | 450,000 | n.a. ^c | 3,600 | 10,000 |

a) Imports from and exports to all EU member states in 1999. Source: EUROSTAT COMEXT database

b) Sources: Elbers and Dekkers (2000), Anonymous (1999), and Anonymous (1997)

c) No data available

13.5.3. Calculations

The model calculations were subdivided into three main groups, i.e., region of origin, exogenous pathways, and endogenous pathways.

13.5.3.1. Region of origin

This group contains all calculations of parameters related to the CSF situation in the region of origin, e.g., the annual number of CSF epidemics, the length of these epidemics, the length of their high risk period (HRP), i.e., the period from first infection with the virus to first detection (Horst et al., 1998), the cumulative incidence of disease in the region, etc. The values of these parameters will vary from year to year and epidemic to epidemic due to inherent randomness. Average values were used in the current model calculations.

13.5.3.2. Exogenous pathways

This group contains all calculations for the probability of CSFV introduction by exogenous pathways. The calculation of this probability is performed in four steps. In the first step, the probability that a single pathway-unit will cause CSFV introduction into the target area is calculated, given that CSFV is present in the region of origin. The scenario trees described in section 13.5.1. are used in this step. The Point of Departure in the scenario trees is that CSFV is present in the region of origin. The three main events that can be distinguished in all scenario trees are:

- is the pathway-unit infected or contaminated with CSFV?
- is the infection or contamination detected or eliminated by preventive measures?
- does the infected or contaminated pathway-unit come into contact with susceptible pigs in the target area and transmit an infective viral dose?

In the second step, the probability that CSFV is introduced by a particular pathway is calculated, combining the probability of step 1 with the total number of pathway-units going from the region of origin to the target area, during the period that CSFV is present in the region of origin in a binomial distribution (Vose, 2000). Steps 1 and 2 are repeated for all exogenous pathways in the model. In the third step, the probabilities of step 2 are added together to obtain the overall probability of CSFV introduction into the target area during an epidemic in the region of origin. In the fourth step, the probability of step 3 is multiplied with the expected number of CSF epidemics in the region of origin to obtain the annual probability of CSFV introduction into the target area from this particular region of origin. This whole procedure is repeated for all regions of origin in the model. A schematic representation of the steps can be found in Figure 13.2.

The calculations for the pathway ‘import of batch of piglets’ are described in more detail to illustrate the model calculations in the first two steps. The scenario tree used in step 1 is given in Figure 13.3. The first event in this scenario tree is whether or not the batch of animals transported from the region of origin to the target area contains infected piglets. This probability was set as being equal to the cumulative incidence (CI) of disease in the region of origin. The second event is whether or not the infected animals will be detected by preventive measures taken in the region of origin, such as clinical inspection of pigs before issuing a health certificate. This probability was set as being equal to the sensitivity of preventive measures (Se_{reg}). The third event is whether or not the infected animals will be detected by preventive measures taken in the target area. This probability was also set as being equal to the sensitivity of preventive measures (Se_{ta}). These sensitivities depend on the kind of preventive measures taken as well as the quality of veterinary services. Their values can be changed in order to calculate the effect of more or different preventive measures. In this scenario tree, no event was included for the probability of contact with susceptible pigs and transmission of an infective viral dose. This is because the import of an infected piglet will always lead to a primary outbreak if the infection is not detected in time and the piglet is brought onto a farm in the target area. The probability that a batch of piglets causes CSFV introduction if coming from a region where CSFV is present is hence calculated by the following equation:

$$P_{\text{batch of piglets}} = CI * (1 - Se_{reg}) * (1 - Se_{ta}) \quad (2)$$

Figure 13.2 Schematic representation of model calculations for exogenous pathways

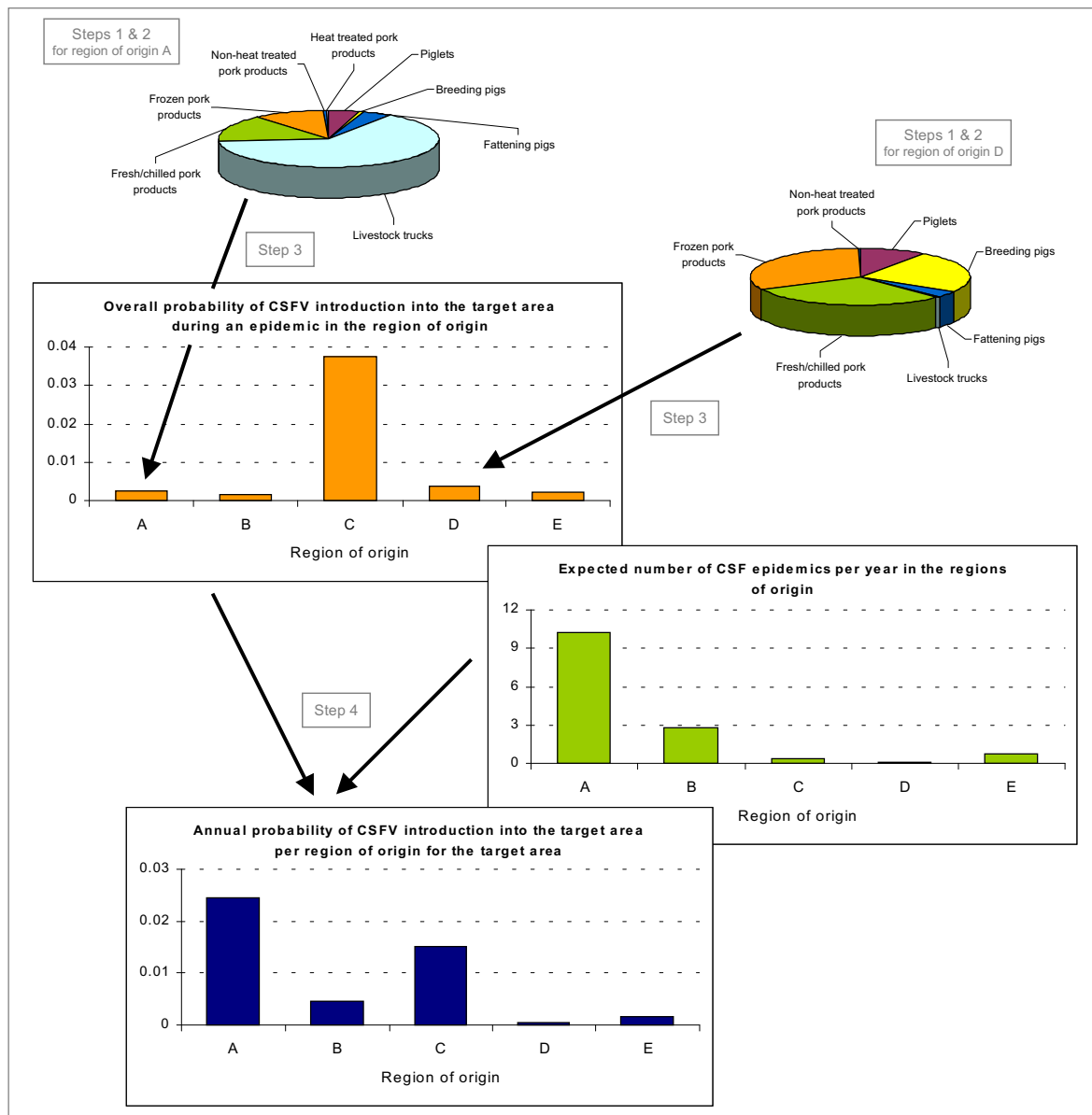
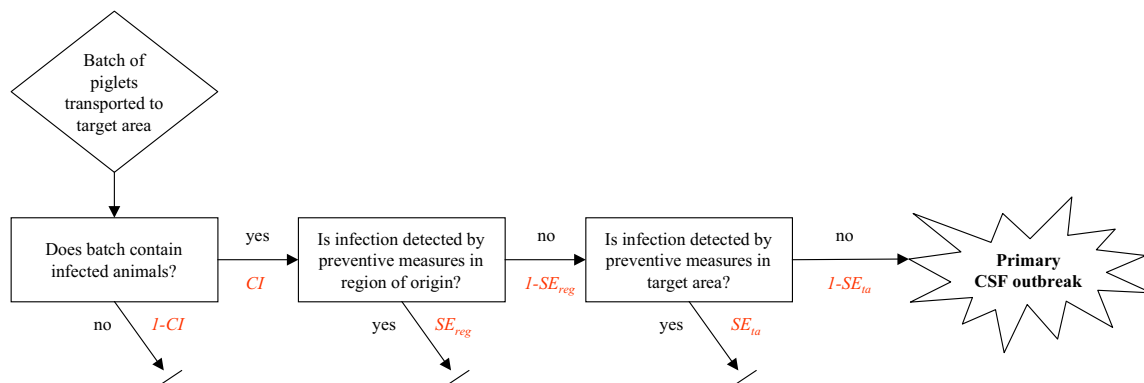


Figure 13.3 Scenario tree for the exogenous pathway 'import of batch of piglets'



In the second step the probability that the pathway import of batch of piglets causes CSFV introduction is calculated as shown:

$$P_{\text{pathway batch of piglets}} = 1 - (1 - P_{\text{batch of piglets}})^n \quad (3)$$

with n = number of batches transported during the period that CSFV is present.

The probabilities used in the scenario tree may be different for the HRP and the remainder of the epidemic (PostHRP). Therefore $P_{\text{batch of piglets}}$ will have different values for the HRP and PostHRP and the calculations have to be performed separately for each period and then added.

13.5.3.3. Endogenous pathways

This group contains all calculations for the probability of CSFV introduction by endogenous pathways. Only the pathways of direct and indirect contact with wild boar were included in the model (as explained previously). The three main events in the scenario trees for these pathways are:

- is an individual wild boar infected with CSFV?
- does this wild boar come into contact with susceptible domestic pigs?
- has an infective viral dose been transmitted to those pigs?

To illustrate the model calculations for endogenous pathways, the scenario tree for the pathway direct contact with wild boar is given in Figure 13.4. The probability of infection (INF) was estimated using results from serological surveys (e.g. Elbers and Dekkers, 2000; Kern, 1998). The probability of direct contact with susceptible pigs (CSA_{direct}) was estimated using information about the geographical distribution of wild boar and domestic pig production, whether wild boar are restricted in their movements by, for example, fences, and the proportion of pig farms with outdoor facilities. The probability of transmitting an infective dose if direct contact occurs (ID_{direct}) was assumed to be rather high and therefore set at 0.9. The annual probability of CSFV introduction by direct contact with a single wild boar is hence calculated by:

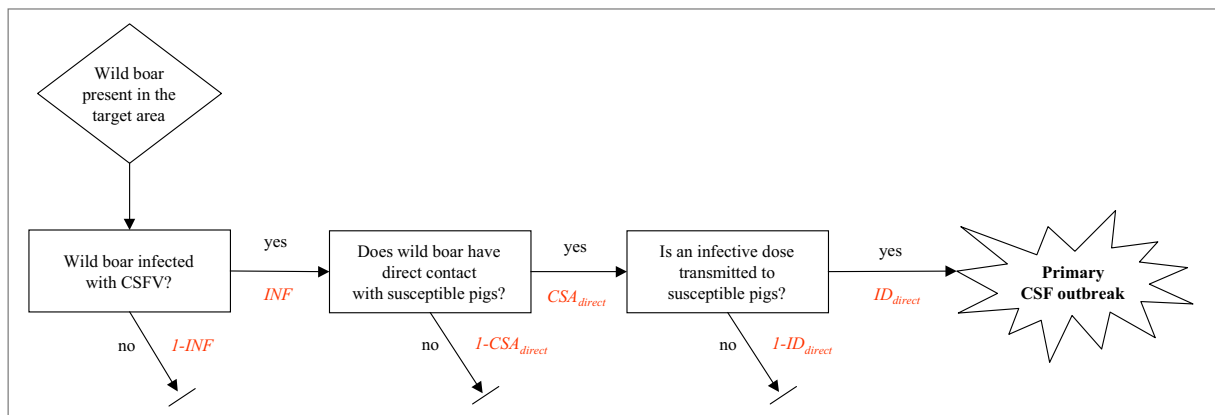
$$P_{\text{boar}} = \text{INF} * CSA_{\text{direct}} * ID_{\text{direct}} \quad (4)$$

To determine the annual probability of CSFV introduction by this pathway, this probability is then combined with the total number of wild boar in the target area using a binomial distribution (Vose, 2000):

$$P_{\text{pathway boar}} = 1 - (1 - P_{\text{boar}})^n \quad (5)$$

with n = total number of wild boar in the target area.

Figure 13.4 Scenario tree for the endogenous pathway ‘direct contact with wild boar’



13.5.4. Results

The annual probabilities of CSFV introduction for the target areas are given in Table 13.5. Results are given for the exogenous pathways and separately for the endogenous pathways for direct and indirect contact with wild boar. The annual probability of CSFV introduction by exogenous pathways is highest for Germany with 0.2. Germany can thus expect CSFV introduction by exogenous pathways on average once every five years. For the other target areas the annual probability of CSFV introduction by exogenous pathways is about 0.05. They can thus expect CSFV introduction by exogenous pathways on average once every twenty years. The annual probability of CSFV introduction due to direct or indirect contact with wild boar is zero for The Netherlands and Belgium, as no infected wild boar populations are present. The probability that Germany and Italy will experience CSFV introduction due to either direct or indirect contact with wild boar is very high. This indicates that it may happen almost every year or even several times per year.

Table 13.5 Annual probability of CSFV introduction for five member states by three groups of causes: exogenous pathways, direct contact with wild boar, and indirect contact with wild boar

| | Germany | France | Italy | The Netherlands | Belgium |
|---------------------------------|---------|--------|-------|-----------------|---------|
| Exogenous pathways | 0.20 | 0.04 | 0.06 | 0.05 | 0.04 |
| Direct contact with wild boar | 0.78 | 0.08 | 0.81 | 0 | 0 |
| Indirect contact with wild boar | 0.81 | 0.21 | 0.37 | 0 | 0 |

13.5.4.1. More detailed results for exogenous pathways

The regions of origin (all EU member states except the target area) determine the annual probability of CSFV introduction by exogenous pathways as well as the exogenous pathways included in the model. Figure 13.5 gives insight into the main regions of origin contributing to this probability for the target areas. In the left-hand column a graph is displayed for each target area in which the annual probability of CSFV introduction is shown per region of origin. In the right-hand column a graph is also displayed for each target area, but in these graphs the probability of CSFV introduction during a CSF epidemic in the region of origin is shown. To give an example, the annual probability that CSFV is introduced from The Netherlands into Germany is almost 0.1 (left upper graph), whereas the probability that CSFV is introduced into Germany during an epidemic in The Netherlands is 0.16 (right upper graph). The probability per epidemic is higher than the probability per year, as the expected number of epidemics in The Netherlands is less than 1 (Table 13.3).

In general, The Netherlands, Belgium and Germany contribute most to the annual probability of CSFV introduction into the target areas (left column of graphs). The probability that CSFV will be introduced into one of the target areas during a single epidemic in Germany is, however, low when compared to epidemics in The Netherlands and Belgium (right column of graphs). The relatively high annual probability of CSFV being introduced from Germany is thus mainly due to the high average number of epidemics per year in this region of origin. Furthermore, it can be concluded that a CSF epidemic in Luxembourg constitutes a considerable risk of CSFV introduction for Belgium and France, whereas an epidemic in Denmark constitutes a considerable risk of CSFV introduction for Germany, France and Italy.

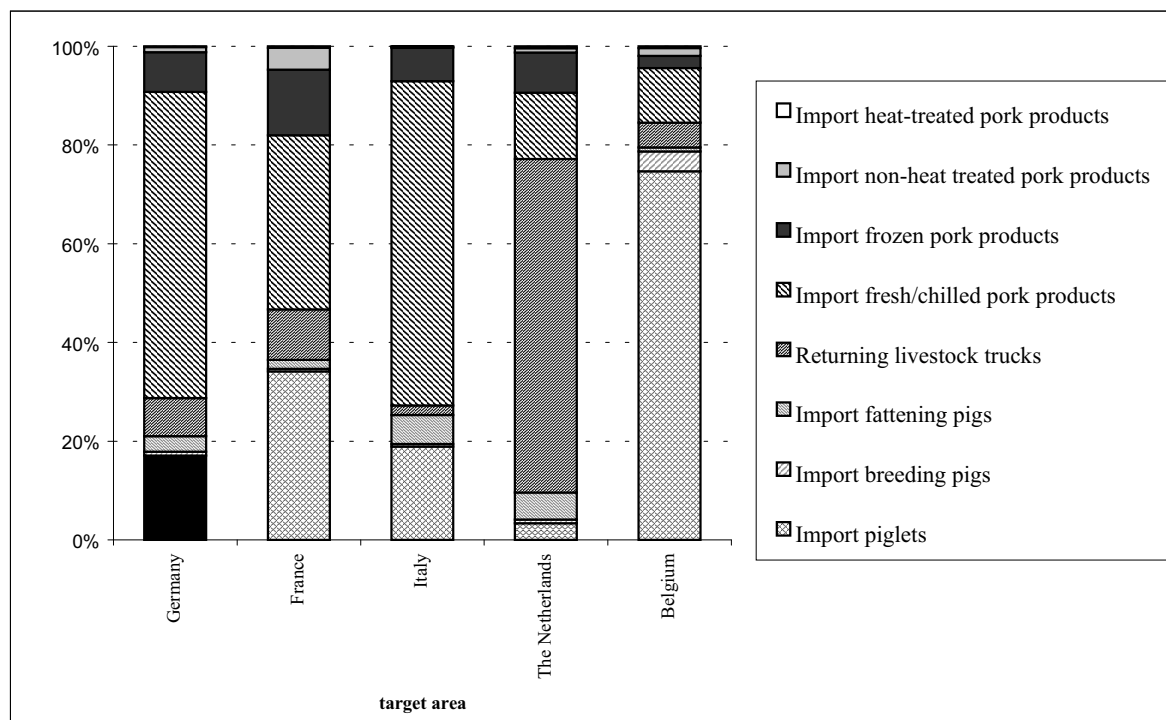
Figure 13.6 gives an overview of the relative contribution of exogenous pathways to the annual probability of CSFV introduction by exogenous pathways into the target areas. In general, the pathways contributing most are the import of piglets, returning livestock trucks and the import of fresh or chilled pork products. Their relative contribution differs per target area and depends both on the number of pathway-units present (see Table 13.4) and the probability of CSFV introduction per pathway-unit. The latter is, for example, quite high for

Figure 13.5 Contribution of regions of origin to the probability of CSFV introduction into the target areas



pork products imported into Germany in comparison to the other target areas, as this is the only target area where swill feeding is still allowed (see Table 13.1-A). This explains the relatively high contribution of this pathway to the annual probability of CSFV introduction into Germany. On the basis of the number of pathway-units present only, one would expect a much bigger contribution from the import of piglets and fattening pigs. For Italy, the relative contribution of imported pork products to the probability of CSFV introduction is also high, which is mainly due to the large amount of fresh and chilled pork products imported. For The Netherlands, returning livestock trucks contribute most to the annual probability of CSFV introduction. This is due to the huge number of pigs exported. Belgium also exports quite a lot of pigs. Returning livestock trucks do not, however, contribute much to the annual probability of CSFV introduction, as in Belgium almost 60% of farmers disinfect incoming vehicles. This reduces the probability of CSFV introduction per pathway-unit, whereas in all other member states, this percentage varied between 0 and 12.5% (data obtained from a questionnaire conducted during the EU Research Project FAIR5-PL97-3566, (Bettio et al., 2002)). For Belgium the import of piglets is the most important pathway which is explained by the large number of piglets imported. For France, both the importing of piglets as well as pork products contributed substantially to the annual probability of CSFV introduction.

Figure 13.6 Relative contribution of each exogenous pathway to the annual probability of CSFV introduction into the target areas by exogenous pathways



13.5.5 Sensitivity analysis

Sensitivity analysis can indicate the impact of input parameters on a model's outcome. For this purpose, increasing and reducing them with a factor of 2 changed the values of some important input parameters. The parameters changed were: (1) the average length of the HRP per epidemic in the regions of origin, (2) the number of live pigs imported, (3) the number of live pigs exported and hence the number of returning livestock trucks, and (4) the probability that swill feeding is practised, which affects both the probability of CSFV introduction by import of pork products and by indirect contacts with wild boar. Furthermore, the probability of CSFV introduction was calculated for the hypothetical situation that no swill is fed at all. Results of the sensitivity analysis for the probability of CSFV introduction by exogenous pathways are presented in Table 13.6 and for the endogenous pathway indirect contact with wild boar in Table 13.7. The sensitivity analysis performed did not change the probability of CSFV introduction by direct contact with wild boar.

Table 13.6 Relative change (in percentages) of the probability of CSFV introduction by exogenous pathways (sensitivity analysis)

| Input parameter | Change | Target area | | | | |
|---|------------------|-------------|--------|-------|-----------------|---------|
| | | Germany | France | Italy | The Netherlands | Belgium |
| Length of HRP | * 2 | +15 | +25 | +13 | +47 | +47 |
| | * 0.5 | +2 | -5 | +3 | -21 | -22 |
| Number of life pigs imported | * 2 | +21 | +36 | +25 | +9 | +78 |
| | * 0.5 | -10 | -18 | -13 | -5 | -40 |
| Number of life pigs exported | * 2 | +8 | +11 | +2 | +67 | +5 |
| | * 0.5 | -4 | -5 | -1 | -34 | -2 |
| Probability that swill feeding is practised | * 2 | +66 | +53 | +72 | +23 | +15 |
| | * 0.5 | -35 | -27 | -36 | -11 | -8 |
| | = 0 ^a | -71 | -53 | -73 | -23 | -15 |

a) To mimic the hypothetical situation that no swill is fed at all, the probability that swill feeding is practised was set to zero

Table 13.6 gives the relative change of the probability of CSFV introduction by exogenous pathways. The effects of changing the above mentioned parameters differ largely between the target areas. The impact of changing the average length of the HRP in the regions of origin was biggest for The Netherlands and Belgium. The impact of changing the number of imported live pigs was biggest for Belgium, whereas the impact of changing the number of exported live pigs was biggest for The Netherlands. This is in accordance with the results presented in Figure 13.6, showing that the import of pigs contributes most to the probability of CSFV introduction into Belgium and returning livestock trucks to the probability of CSFV

introduction into The Netherlands. The impact of changing the probability of swill feeding was high for Germany, France and Italy.

In general, the probability of CSFV introduction by exogenous pathways increased when the values of the input parameters were multiplied by 2, and diminished when these values were multiplied by 0.5. The only exceptions are the changes in probability of CSFV introduction for Germany and Italy when reducing the average length of the HRP in the regions of origin. This is due to the fact that the total length of the epidemic was not changed in this calculation and that therefore the probability of CSFV introduction by the import of pork products during the PostHRP was increased as the PostHRP lasted longer. Import of pork products was the major pathway contributing to the probability of CSFV introduction for these target areas (Figure 13.6).

Table 13.7 Relative change (in percentages) of the probability of CSFV introduction by indirect contact with wild boar when changing the probability that swill feeding is practised

| Change | Target area | | | | |
|------------------|-------------|--------|-------|-------------------|---------|
| | Germany | France | Italy | The Netherlands | Belgium |
| * 2 | +13 | +42 | +35 | n.a. ^b | n.a. |
| * 0.5 | -12 | -23 | -21 | n.a. | n.a. |
| = 0 ^a | -30 | -47 | -44 | n.a. | n.a. |

a) To mimic the hypothetical situation that no swill is fed at all, the probability that swill feeding is practised was set to zero

b) Not applicable

Table 13.7 gives the relative change of the probability of CSFV introduction by indirect contact with wild boar when changing the probability that swill feeding is practised. This increases or reduces the probability of indirect contact per individual wild boar. The impact of changing this input parameter was largest for France and Italy. For Germany it also had an impact, but due to the large wild boar population present in this country, the annual probability of CSFV introduction due to indirect contact with wild boar was changed to a lesser extent. Indirect contact with wild boar did not constitute a risk of CSFV introduction for the domestic pig population in The Netherlands and Belgium and hence changing the probability of swill feeding had no impact on the model's outcome for these target areas.

13.6 Discussion and conclusions

13.6.1 Pathway diagram

Insight into all factors contributing to the risk of CSFV introduction is needed in order to decide upon preventive actions that are cost-effective, i.e., achieve considerable risk reduction at reasonable costs. In this study both a qualitative and quantitative approach were used to estimate the probability of CSFV introduction for several regions in the EU and to evaluate which factors contribute most to the probability of CSFV introduction. Both approaches were based on a pathway diagram especially constructed for CSFV introduction into regions of the EU under a non-vaccination policy.

Constructing such a pathway diagram provides more insight into all possible pathways and events contributing to the occurrence of an adverse event. It is therefore recommended as part of hazard identification, which is the first step in risk analysis (Wooldridge et al., 1996). The more pathways involved, the more complex the diagram becomes. Therefore only the main events leading to the occurrence of a primary CSF outbreak were included in the pathway diagram in Figure 13.1. Scenario trees were used to describe each pathway in more detail.

13.6.2 Qualitative assessment of the probability of CSFV introduction into densely and sparsely populated livestock areas

The qualitative assessment of the probability of CSFV introduction into DPLAs and SPLAs demonstrated that DPLAs generally had a higher probability of CSFV introduction than SPLAs, although this could not be attributed to pig density only. The results should be interpreted with care, because information on their presence was not available for all pathways in the diagram. Furthermore, the contribution of pathways to the overall probability of CSFV introduction will differ, but it was not known to what extent. Some pathways play a more important role in introducing CSFV to a region than others. The criteria of Table 13.2 were, however, given equal weight in the qualitative assessment. The relative contribution of the pathways will also differ per region, because it depends on the number of pathway-units present, the region of origin of the pathway-units and their use. Horst et al. (1998) obtained expert estimates of the relative importance of pathways for CSFV introduction. These were, however, specifically for CSFV introduction into The Netherlands and could therefore not be used for different European regions. To estimate the probability of CSFV introduction for regions in the EU more adequately, quantitative information on the presence of pathways and their main events is thus necessary.

13.6.3 Computer model to assess the probability of CSFV introduction quantitatively

The computer model used to estimate the probability of CSFV introduction quantitatively gave a much more detailed insight into the factors determining this probability for a target area. It shows which regions of origin and which exogenous pathways contribute most to the annual probability of CSFV introduction by exogenous pathways as well as giving separate estimates for the probabilities of CSFV introduction by wild boar. This information is very useful for policy-makers as it helps to set priorities for preventive measures. The computer model can estimate the impact of preventive measures as well by changing relevant input parameters.

13.6.3.1 Modelling approach

The computer model developed has a clear structure. Calculations were subdivided into three main groups, which makes it easy to add or change input parameters. For each target area results can be obtained as aggregates (probability of CSFV introduction per year), as well as separately for each combination of exogenous pathways and regions of origin.

Not all pathways that may contribute to the probability of CSFV introduction could be included in the model. The model structure is, however, such that additional pathways can easily be included if new information and data should become available. Some of the pathways that were not included are considered to contribute only marginally to the probability of CSFV introduction, e.g., import of manure, birds, pets, arthropods and rodents, air currents and laboratories. Others might contribute considerably to the probability of CSFV introduction, but no quantification was possible. This was the case for, e.g., import of genetic material, illegal imports, tourists and professional people. To obtain a more comprehensive overview of the major causing pathways of the probability of CSFV introduction into the target areas, their contribution to the probability of CSFV introduction may be estimated qualitatively.

No third countries were included in the model as regions of origin. Therefore their contribution to the probability of CSFV introduction for the target areas could not be calculated. In order to include third countries into the model without an exponential increase in the number of calculations, third countries could best be grouped/clustered taking into account their geographical situation and disease status with regard to CSF (e.g. endemic, free with vaccination, free without vaccination).

For most regions of origin, i.e., EU member states, the expected number of CSF epidemics per year is less than one. For Germany and Italy, however, the average number of epidemics per year over the last ten years exceeds one (Table 13.3). Simply multiplying the probability per epidemic with the expected number of epidemics in step 4 of the calculations for

exogenous pathways, may in this case lead to an overestimation of the annual probability if the total epidemic period (which also depends on the average length of the epidemics) exceeds a year. Therefore the model may have overestimated the annual probabilities of CSFV introduction into the target areas from these regions of origin. The contribution of Italy to the annual probability of CSFV introduction for the target areas was rather small, but the contribution of Germany was quite large, mainly due to the high average number of epidemics per year (see Figure 13.5).

The target areas for which model calculations were performed were EU member states, and not densely and sparsely populated livestock regions. Calculating the probability of CSFV introduction for regions in the EU appeared to be impossible due to lack of data. Attempts were made to derive data on the imports and exports of live animals per region from the animal movement system (ANIMO), but this data was not readily available. Furthermore, data on the animal movements within the member states is needed in order to perform model calculations at regional level. For this purpose, national identification and recording systems (I&R) should be used, but data from such systems was not available in all EU member states. Estimating the probabilities for the scenario trees is also much more difficult at regional level.

13.6.3.2 Results

The annual probabilities of CSFV introduction by exogenous pathways were quite low when compared with expert estimates (Horst et al., 1998). In addition, comparing the model results with the average number of regions with primary outbreaks in Table 13.3 suggests that the model underestimates the probability of CSFV introduction by exogenous pathways, although for Germany, France and Italy, wild boar may also contribute considerably to the probability of CSFV introduction. The probability of CSFV introduction by direct and indirect contact with wild boar was indeed quite high, especially for Germany and Italy. This is in accordance with reality, as many primary outbreaks in these countries can be attributed to direct or indirect contacts with wild boar. Fritzemeier et al. (2000) concluded that 59% of all primary outbreaks in Germany in the period 1993-1998, which amounted to about 90, were due to direct or indirect contacts with infected wild boar. Additionally, many of the CSF outbreaks in Italy reported to ADNS were in the infected regions of Sicily.

The model probably underestimates the probability of CSFV introduction by exogenous pathways. It should be kept in mind that not all pathways contributing to the probability of CSFV introduction were included in the model and neither were third countries. Absolute values of model outcome should therefore not be considered as true values for the probability of CSFV introduction. The model can, though, be used to rank the target areas for their probability of CSFV introduction. The ultimate aim of the model was not to give exact

estimates of the probability of CSFV introduction, but to gain more insight into the pathways and regions of origin contributing most to this probability. The probability of CSFV introduction by exogenous pathways was, for example, much higher for Germany than for the other target areas. Although Germany is importing millions of live pigs, this pathway contributed less to the probability of CSFV introduction than the import of pork products (Figure 13.6). Analysing the model output explains that this is due to the fact that swill feeding is still permitted in Germany.

The contribution of the import of pork products to the annual probability of CSFV introduction for the target areas was rather high, especially for Germany and Italy (Figure 13.6). This is not in accordance with historical data on the most important sources of CSFV introduction (see e.g. De Vos et al., 2000; Fritzemeier et al., 2000). It could be that some of the underlying probabilities used to calculate the probability of CSFV introduction by pork products were estimated too highly. The import of infected pork products may, however, easily lead to CSFV introduction if fed as swill. This was, for example, seen in the CSF epidemics in the United Kingdom in 1986 and 2000 (Sharpe et al., 2000; Williams and Matthews, 1988).

13.6.3.3 Sensitivity analysis

Sensitivity analysis was performed in order to gain insight into the impact of input parameters on the model's results. Only some of the most important input parameters were screened. Further sensitivity analysis may be performed to estimate the impact of preventive measures on the probability of CSFV introduction for the target areas. Figures 13.5 and 13.6 already give a good indication of the regions of origins and exogenous pathways at which preventive measures should be directed. The model provides all data to make more detailed pictures of the exogenous pathways contributing most to the probability of CSFV introduction per region of origin. Prevention of CSFV introduction may be achieved by changing either (i) the CSF situation in the regions of origin, (e.g. the average number of epidemics per year, the length of the HRP, the number of infected premises), (ii) the number of pathway-units coming from certain regions of origin, or (iii) the preventive measures taken to reduce the probability of CSFV introduction per pathway-unit. The model can provide information on which type of measures will be most effective. In order to calculate the costs and benefits of such measures, as well as their impact on the spread of CSFV once introduced into a target area should be taken into account. For this purpose simulation models can be used (e.g. Jalvingh et al., 1999; Saatkamp et al., 1996).

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Spatial and stochastic simulation to compare two emergency vaccination strategies with a marker vaccine in the 1997/98 Dutch Classical Swine Fever epidemic*

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Abstract

Two alternative emergency vaccination strategies with a marker vaccine that could have been applied in the 1997/98 Dutch Classical Swine Fever (CSF) epidemic were evaluated in a modified spatial, temporal and stochastic simulation model, InterCSF. In strategy 1, vaccination would only be applied to overcome a shortage in destruction capacities (killing and rendering). Destruction of all pigs on vaccinated farms distinguishes this strategy from strategy 2, which assumes intracommunity trade of vaccinated pig meat.

InterCSF simulates the spread of CSF between farms through local spread and 3 contact types. Disease spread is affected by control measures implemented through different mechanisms. Economic results were generated by a separate model that calculated the direct costs (including the vaccination costs) and consequential losses for farmers and related industries subjected to control measures. The comparison (using epidemiological and economic results) between the different emergency vaccination strategies with an earlier simulated preventive slaughter scenario led to some general conclusions about the Dutch CSF epidemic. Both emergency vaccination strategies were barely more efficient than the non-vaccination scenario. The intracommunity trade strategy (vaccination strategy 2) was the least costly of all three scenarios.

14.1 Introduction

When all regular measures to eradicate an CSF epidemic fail, paragraph 14 of the directive 80/217/EEC of the EU legislation foresees an emergency-vaccination (CEC, 1980). In the case of

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an emergency vaccination, the same directive forces the member state to exclude all meat originating from vaccinated pigs (except when heat treated) from the regular pork market. Within the last decade, some severe CSF epidemics occurred in the EU, but no emergency vaccination programme was applied. In 1994, the German proposal for an emergency vaccination programme was refused by the European Commission (Blaha, 1994). During the 1997/98 Dutch CSF epidemic (hereafter referred to as the Dutch CSF epidemic) in The Netherlands, emergency vaccination was only proposed at national level (Jorna, 1997) mainly on ethical grounds.

The use of a marker vaccine to help control a CSF outbreak seems to be technically feasible (Van Oirschot, 1994; Leopold-Temmler, 1996; Vågsholm, 1996; Jorna, 1997), including serological testing to distinguish infected pigs from vaccinated pigs. Changes in the swine herd structure combined with high-density pig populations incur logistic and organisational problems, as well as high costs, when adopting a regular stamping-out policy in order to eradicate an epidemic. Public objections to the destruction (killing and rendering) of healthy animals also increase. These factors are in favour of emergency vaccination. On the other hand, EU policy aims towards a high animal health status and therefore has adapted a non-vaccination policy for the control and eradication of animal diseases of major importance for international trade. In brief, the use of vaccine “means” the presence of disease (Westergaard, 1996).

Epidemiological, political and economic advantages and disadvantages need to be analysed and clarified before it is possible/being able to decide whether or not the use of a marker vaccine is a realistic and attractive option. We improved the simulation model InterCSF, which was developed to simulate the Dutch CSF epidemic, (Jalvingh et al., 1999) by adding emergency vaccination as a disease-control mechanism. InterCSF was specifically developed to answer “what-if” questions (Nielen et al., 1999). Vaccination costs were incorporated in EpiLoss (Meuwissen et al., 1999) for the present study, in order to be able to calculate the direct costs and consequential losses for farmers and related industries subjected to control measures.

The main goal of this paper is to analyse the epidemiological and economic consequences of two possible emergency vaccination campaigns that could have been used in the Dutch CSF epidemic. They are compared with an earlier simulated preventive-slaughter strategy (Nielen et al. 1999), which we will call (in this paper) the “non-vaccination” (NV) scenario.

14.2 Materials and methods

14.2.1 General outline

InterCSF is a spatial, temporal and stochastic simulation model (Jalvingh et al., 1999). InterCSF simulates day to day disease spread from infected farms through 3 contact types

(animals, vehicles, persons) and through local spread up to 1000 m. All Dutch pig farms are known by their geographical coordinates. The main disease control mechanisms that influence the disease spread in InterCSF are: diagnosis of the infected farms, depopulation of infected farms, quarantine zones¹³, tracing and preventive slaughter (see Appendix IV for more details).

Emergency vaccination was incorporated into the base scenario such that it reflected the starting situation of the real epidemic as closely as possible. This involved incorporating historical data from 37 farms with an infection date before February 4 1997 (detection date of first farm) and fixed detection and herd destruction dates later. New infections were only simulated after this date. In our simulations we assumed that after 5 detections in the first week, emergency vaccination would be ordered. In a densely populated area epidemiologists expect a large epidemic if there are at least 5 detections in the first week. In 1997, the first outbreak happened in a very densely populated pig area and 9 outbreaks were notified in the first week following the initial detection (Elbers et al., 1999). In our simulation, the emergency vaccination campaign was initiated 5 days after the decision on day 6 (assuming 5 days of preparation for a vaccination campaign). When the decision to commence the emergency vaccination campaign was taken, all earlier-detected farms from the previous week were identified. In the base vaccination scenarios, a vaccination zone with a radius of 3 km was defined for each detected farm. To mimic restricted vaccination capacities, all defined vaccination zones were put on a vaccination list and all further-defined vaccination zones were also listed. If more than one new vaccination zone was defined on the same day, they were ranked depending on their pig-farm density, starting with the highest pig-farm density. Furthermore, we assumed that emergency vaccination would be stopped based on certain criteria (defined later on in this paper).

Vaccination zones are vaccinated one after another – i.e not simultaneously - by 150 vaccination teams. Each vaccination team (1 veterinarian and 4 helpers) was supposed to handle about 2000 pig places (fatteners¹⁴ and gilts¹⁵) or 465¹⁶ farrowing places per day (or various equivalent combinations).

¹³ Hereafter “quarantine” zones refer to all restricted zones/areas (protection zone (0-3 km) and surveillance zones (3-10 km) in which movement restrictions and control measures are imposed.

¹⁴ A fatterer is a finishing or fattening pig, also called hog (from 45 kg until killed).

¹⁵ A gilt is a female pig from 20-30 kg live weight until first insemination.

¹⁶ Assuming 21.5 piglets/breeding sow/year, which is equal to 0.059 piglets born/breeding sow/day. We assume that a piglet will stay on a sow farm for 70 days. Because pigs need to be 14 days old for vaccination, we will have $(0.059 \times 56 \text{ days}) = 3.30$ piglets/farrowing place and 1 sow/farrowing place to vaccinate

14.2.2 Vaccination effects

Vaccination has two effects: reduction in virus spread on an infected farm and protection against infection of a susceptible herd.

For virus reduction on an infected farm, two kinds of infected farms were distinguished. The first category consisted of infected farms that were never vaccinated and of farms that were firstly infected and later vaccinated. The second category was farms that were vaccinated and became infected later on.

For the first category of infected farms, we assumed no reduction in virus spread. All parameters remained as described in Jalvingh et al. (1999). In short, the infectious period began between 5 and 10 days following infection. The infection level of the farm remained the same for the total infectious period, which ended on the day that the farm was depopulated. The interval between infection and detection was modelled using a single probability distribution, based on observations of the real Dutch CSF epidemic. The selected interval could be influenced downward by certain events (see Table 14.1). The detection probabilities of non-vaccinated farms were used as a base in order to estimate the detection probabilities for all vaccinated farms (Table 14.1). Vaccination as such could also influence detection because infected farms could be detected earlier due to clinical inspection on the vaccination day. The detection probability depended on the time since infection and the source of infection (Table 14.2). For a direct animal contact we defined a higher probability of detection for the first weeks after infection than for all other contacts. If an infected farm was not detected during vaccination, we assumed that the virus was spread mechanically and massively over the farm during vaccination. After the incubation period of 1 week, the large number of sick animals could again lead to a possible earlier detection (Tielen; Personal communication). In both cases, we assumed that the diagnosis was established two days after suspicion. For all other events, more time consuming tests are necessary; so, we defined 7 days after suspicion before a diagnosis would be given (de Smit et al, 1999). For vaccinated farms infected after vaccination (the second category), a reduction in virus spread was expressed by a reduction factor. This reduction factor depended on the time interval between vaccination and infection and was modelled with a probability distribution, based on EU experiments (Appendix V). The reduction factor was multiplied by the probabilities of transmission for a simulated contact and for local spread.

For the farms in the second category, we assumed no change in the latent period but the infectious period was reduced to at most one month. Typically, only small outbreaks are expected on vaccinated farms. Assuming that vaccinated pigs show no or few clinical signs when infected, detection could only be by serological screening (Table 14.1).

Table 14.1 Probability of detection based on a control event (such as traced contacts, surveillance, preventive slaughter, end-screening and animal welfare slaughter) depending on the time since infection and the farm specific vaccination status in a quarantine zone

| Time since infection (days) | Probability of detection by control event (diagnosis date 7 days after event) | | | | | | | | | | | | | | |
|---------------------------------------|---|-----|-----------------|--|-----|-----------------|-------------------------------------|-----|-----------------|----------------------------|-----|-----------------|--------------------------------|-----|-----------------|
| | Traced contacts ^a | | | Surveillance (3 km radius) ^a | | | Preventive slaughter ^{a,b} | | | End-screening ^b | | | Welfare slaughter ^b | | |
| | NV ^c | | IV ^d | NV ^c | | IV ^d | NV ^c | | IV ^d | NV ^c | | IV ^d | NV ^c | | IV ^d |
| | VI ^e | | | VI ^e | | | VI ^e | | | VI ^e | | | VI ^e | | |
| 0 – 14 | 0 | 0.9 | 0 | 0 | 0.9 | 0 | 0 | 0.9 | 0 | 0 | 0.9 | 0 | 0 | 0.9 | 0 |
| 15 – 28 | 1 | 1 | 0 | 0 | 1 | 0 | 1 | 1 | 0.5 | 0.25 | 1 | 0.5 | 0 | 1 | 0.5 |
| 29 – 42 | 1 | 1 | 0 | 0.25 | 1 | 0 | 1 | 1 | 1 | 0.5 | 1 | 1 | 0 | 1 | 1 |
| > 42 | 1 | 1 | 0 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |

a) Based mainly on clinical inspection.

b) Based mainly on serology.

c) NV: No vaccination; farm already has an (undetected) infection (Jalvingh et al., 1999).

d) IV: Vaccination of a farm already infected (but not yet detected).

e) VI: Vaccination of a farm that later becomes infected.

Susceptible farms were also classified into two categories: non-vaccinated and vaccinated. We defined a non-vaccinated susceptible farm as one without protection against a possible infection, whereas a vaccinated susceptible farm was partly protected. The degree of protection depended on the time interval between vaccination and a possible infection and was expressed as a protection factor, modelled using a probability distribution (Appendix V). As for the reduction factor, the protection factor was multiplied by the probabilities of transmission for a simulated contact and for local spread. However, if an infectious pig was moved to a susceptible vaccinated farm, the protection factor was not considered. We assumed that this farm always became infected but could rarely become infectious.

Table 14.2 Probability of detection due to vaccination, relative to the time since infection on an (undetected) infected farm and depending on the source of infection

| Time between infection entrance and vaccination (days) | Probability of detection related to vaccination (diagnosis date 2 days later) | | |
|---|---|------------------------------|-----------------------------|
| | Vaccination day ^a | Vaccination day ^b | 1 week after vaccination |
| 0 – 14 | 0.25 | 0.05 | 0.9 |
| 15 – 28 | 0.9 | 0.5 | 0.95 |
| 29 – 42 | 0.99 | 0.9 | 1 |
| > 42 | 0.99 | 0.99 | 1 |

a) Farm infected by direct animal contact.

b) Farm infected by transport or person contact.

In the EU field experiments, horizontal transmission was significantly reduced for both marker vaccines 3 weeks after vaccination (Anonymous, 1999). In our base emergency vaccination scenarios, we assumed that maximum protection and reduction was reached after 21 days. For sensitivity analysis, this time interval was reduced by 5 days to 16, as well as increased by 5 days to 26 days (Appendix V). In an additional analysis, only 1 week was assumed necessary in order to build up the maximum protection level (simulating a live-virus vaccine).

14.2.3 Delayed-destruction alternatives

The first emergency vaccination strategy (called "delayed-destruction" (DD)), assumed no political acceptance of vaccinated pig meat as fresh meat (i.e. the current EU policy). Vaccination would only be applied to overcome a shortage in destruction (killing and rendering) capacity, created by regularly applied control measures. Because vaccination will reduce the risk of virus spread, the destruction of vaccinated farms may be postponed until

destruction capacity is available. All pigs in the vaccination zone needed to be destroyed (slaughtered and rendered) before the final screening could be applied in order to declare the region CSF free once more. All pigs older than 14 days were vaccinated once. We assumed that vaccinated pigs had maximum protection for at least 6 months. If they were not slaughtered within 6 months, the pigs would be re-vaccinated to maintain maximum protection levels.

As soon as a vaccination zone was defined, all farms within this vaccination zone were put on the preventive slaughter list. Priorities were set to deal with insufficient destruction capacities. Firstly, all farms located within the regular preventive slaughter radius (1 km) as well as contact farms were destroyed. This group was split further. Farms not predestined for vaccination were given the highest priority, followed by farms where vaccination was not yet applied and finally vaccinated farms. In the category of the vaccinated farms, higher priority was given to farms without maximum protection. The second category consisted of farms lying in the vaccination zone (0-3 km), but outside the regular preventive slaughter zone (0-1 km). Here again, the highest priority was given to non-vaccinated farms, followed by vaccinated farms without maximum protection and finally farms with maximum protection. Those priorities were applied to all zones, whereby within a subgroup, the farms of an older zone had priority for animal slaughtering. The decision criterion for stopping emergency vaccination depended on the delay caused by destruction capacities. The number of farms notified for preventive slaughter (including vaccinated farms) was divided by the daily destruction capacity to obtain the number of days needed for destruction of all the farm animals concerned. When the delay was ≤ 3 days within a period of 14 days, no new vaccination zones were installed.

The installation of a breeding prohibition in a defined vaccination zone and the culling of newborn piglets on the vaccinated farms (not simulated as such) allowed the assumption that the pig population on vaccinated farms retained maximum protection. The implementation costs for both control measures were considered when calculating the costs and losses.

In the base scenario (DD-0), we assumed maximum vaccine protection in 21 days, 5 days of preparation, a 1 km preventive slaughter zone and a vaccination radius of 3 km for each detected farm. In alternative scenarios (Table 14.3), we assumed that time to build up maximum protection was reached within 1 week, 16 days or 26 days. In a further sensitivity analysis, the time needed to prepare the emergency vaccination campaign was changed from 5 days to 2 days (alternative I), to 8 days (alternative II) or to 25 days (alternative III). In alternative IV, the vaccination radius was reduced to 1 km instead of the 3 km, and alternative V assumed a 500 m regular preventive slaughter radius.

Table 14.3 An overview of the various alternatives for both emergency vaccination strategies: the Delayed Destruction strategy (DD) and the Intracommunity Trade strategy (ICT)

| Assumption | | DD - x ^a | ICT - x ^a |
|-------------------------------|---------------|---------------------|----------------------|
| Preparation time | 5 days | 0 (base) | 0 (base) |
| | 2 days | I | I |
| | 8 days | II | II |
| | 25 days | III | III |
| Vaccination radius | 3 km | 0 (base) | 0 (base) |
| | 1 km | IV | IV |
| Preventive-slaughter radius | 1000 m | 0 (base) | - |
| | 500 m | V | - |
| Applying preventive slaughter | No | - | 0 (base) |
| | Yes | - | VI ^b |

a) x stands for 21 (base) respectively 7, 16 or 26 days needed to build up maximal protection.

b) Preventive slaughter is only applied to non-vaccinated farms in a radius of 1 km.

14.2.4 Intracommunity trade alternatives

For the second emergency vaccination strategy (the intracommunity trade strategy (ICT)), we assumed that after removing the quarantine zone, pig meat originating from vaccinated pigs could be sold on the EU market. However, we assumed that for the vaccination zones, a so-called “post-vaccination zone” would be installed for 4 months at the moment the quarantine zone was lifted. All movements were allowed, except that live pigs could leave this zone only directly to slaughter in specific slaughterhouses. This supplementary measure should convince all trading partners that no live carrier piglets could leave the vaccination zone to spread the disease, in case an infected sow was overlooked during the serological screening. In the ICT strategy, emergency vaccination was stopped when there were less than two new detections within the previous 4 weeks.

In the ICT strategy, all pigs older than 2 weeks in a vaccination zone (0-3 km) were vaccinated once as for the DD strategy. In addition, we imposed (for the duration of the quarantine zone in a vaccination zone) the re-vaccination of all newborn piglets as well as all breeding sows. These measures would assure a maximally protected pig population. The emergency vaccination capacities were not influenced by the continued vaccination, because we assumed that the local veterinarians carried out the re-vaccinations. A further assumption was that maximum protection of vaccinated farms would last for the total duration of a post-vaccination zone. Once the post-vaccination zone strategy was lifted, all farms lost their protection.

With the ICT strategy, vaccination reduces the susceptible pig population so that preventive slaughter is optional and not applied in the base scenario. If preventive slaughter were applied, only non-vaccinated farms would be destroyed (alternative VI, Table 14.3).

For the base scenario (ICT-0), maximum protection was attained in 21 days, no preventive slaughter was applied, a vaccination radius of 3 km was installed for each detected farm and 5 days of preparation were needed before the emergency vaccination campaign began. Alternative scenarios were simulated for sensitivity analysis, similar to DD (Table 14.3).

14.2.5 Vaccination costs

Related to the vaccination costs were various additional control costs, over and above the cost per dose of vaccine per pig. They consisted of preparation, travel and biosecurity costs for the vaccination teams, as well as costs for the application of the vaccine. In the case of the ICT strategy, the continued vaccination also resulted in some additional costs. Table 14.4 summarises all vaccination-related costs in detail.

All sows on vaccinated farms should be tested to reduce the probability of a carrier piglet going undetected before an area may be declared CSF-free. Despite this, we used the same lump sum (for comparison reasons) for serological costs as Meuwissen et al. (1999). Furthermore we assumed that the discriminatory test would cost the same as the conventional one.

14.2.6 Comparison of alternatives

To compare the alternatives, both epidemiological and economic parameters were used. InterCSF simulated the spread and control of the epidemic, whereby different events (summarised in Appendix VI) related to economic costs and losses could occur. Vaccination was added as a new event. Breeding prohibition and the killing of newborn piglets were applied only for the DD strategies. For each individual farm subjected to control measures, InterCSF recorded events each day in an event-output file. This event file was used as input for EpiLoss, which calculated the total costs and losses for the epidemic (Meuwissen et al., 1999). Vaccination related costs (actually direct costs) were considered as a separate cost factor for reasons of comparison.

Similar to Nielen et al. (1999), a two-tailed, two-sample Student's t-test with unequal variance was performed on mean final outcomes of the 100 replications per scenario, in order to test whether alternatives varied significantly from each other or from the non-vaccination scenario (NV). To correct for multiple comparisons, a Bonferroni correction was applied using a significance level of 0.05 (Jones and Rushton, 1982). Final outcomes that were compared were the mean total losses and the mean total number of infected farms, detected

farms, preventively slaughtered farms and vaccinated farms. Testing was performed using SPSS software (version 8.02).

Table 14.4 The vaccination-related costs

| Description of the costs | € /farm or pig |
|---|--------------------------|
| 1. Biosecurity cost and transport during the emergency vaccination: | |
| - Material needed for a farm visit (Overalls, sterile materials (no re-use)) ^a | ~ 45.4 € /farm |
| - Preparation needed for a farm visit (1/2 h * (25.0 € /h + 17.5 % B.T.W.) ^a | 16.8 € /farm |
| - 1 hour for transport and hygiene measures (4 helpers (33.6 € /h ^a) and 1 veterinarian (74.4 € /h ^b)) | 213.3 € /farm |
| Total: | ~ 272 € /farm |
| 2. Vaccine and vaccination application during the emergency vaccination: | |
| - Vaccine | 2.27 € /pig |
| - Application (2000 pigs/ vaccination group/ 8 hours) (4 helpers * 33.6 € /h ^a * 8 h + 1 vet. * 74.4 € /h ^b * 8) | 0.83 € /pig |
| Total: | 3.10 € /pig ^c |
| 3. Costs for continued vaccination (only for ICT) ^d : | |
| - Vaccine | 2.27 € /pig |
| - Vaccination application | 0.45 € /pig |
| - Veterinary visit (20.42 € /farm ^b) | 0.07 € /pig |
| - Biosecurity cost (no helpers) (45.4 € /farm ^a) | 0.16 € /pig |
| Total: | 2.95 € /pig ^e |

a) Consulting specialist from Animal Health Service, Boxtel, The Netherlands (1999).

b) Royal Netherlands Veterinary Association (1998).

c) It will be 3.10 € /fattener or gilt place and 13.34 € /farrowing place (1 breeding sow + 3.30 piglets).

d) Assuming an average sow herd of 150 breeding sows. Vaccination of newborn piglets and re-insemination of breeding sows will probably only happen once per month. In that case 292 pigs (piglets and breeding sows) will be re-vaccinated each month.

e) $2.95 \text{ € /treated pig} * 0.065 \text{ treated pigs/day} = 0.19 \text{ € /farrowing place/day}$; $0.065 \text{ treated pigs} = 0.006 \text{ breeding sow/ day} + 0.059 \text{ newborn piglets/sow/day}$.

14.3 Simulation results

Nielen et al. (1999) compared the real Dutch CSF epidemic with various alternative eradication strategies, all simulated with the InterCSF model (Jalvingh et al., 1999). All simulated strategies were performed 100 times, in which the simulation time was set at a

maximum of 1 year. The most effective scenario according to Nielen et al. (1999) was to commence preventive slaughter within a radius of 1 km from the day of the initial detection (the so-called “preventive slaughter scenario”; referred to in this paper as the “non-vaccination scenario” (NV)). Complete results were shown in Nielen et al. (1999) and are partly shown in Tables 14.5 and 14.7. In the real epidemic, preventive slaughter of the neighbouring farms was only applied for the first two detected farms and stopped and recommenced two months later for all newly detected farms (LNV, 1998). Table 14.5 recalls the most important key features of the real epidemic, the simulated epidemic and the NV. We chose the NV as the base scenario with which to compare all emergency vaccination strategies. In the future, preventive slaughter would most likely be applied from the beginning making this scenario the best comparison for our simulated emergency vaccination scenarios. In Table 14.6, we compare the two base emergency vaccination strategies with both the NV scenario and with each other. Furthermore, all emergency vaccination alternatives were compared to the corresponding base emergency vaccination strategies. In total, 38 t-test comparisons were performed, which set the P-level for a significant difference between means to 0.001316 (0.05/38).

Table 14.5 Some key features of the real Dutch CSF epidemic, the median of the simulated epidemic and the median of the non-vaccination scenario ^a (Jalvingh et al., Nielen et al., 1999)

| Real Dutch CSF epidemic or simulated scenario | Key features (median for simulations) | | | | |
|--|---------------------------------------|------------------|------------------|-----------------------|-------------------------------|
| | Number of farms | | | Duration (in days) | Costs (10 ⁶ €) |
| | detected | infected | Preventive sl. | | |
| Real Dutch CSF epidemic | 429 | ? | 1247 | >365 | 2124 |
| Simulated Dutch epidemic | 374 ^b | 464 ^b | 743 ^b | 306 | 1137 ^c |
| Non-vaccination scenario | 70 | 99 | 450 | 164 | 590 ^c |

- a) The preventive slaughter scenario from Nielen et al. (1999) is in this paper called the “non-vaccination scenario” (NV).
- b) Numbers differ slightly from Jalvingh et al. (1999), due to some minor adaptations of InterCSF.
- c) Numbers are slightly higher than in Jalvingh et al. (1999) and Nielen et al. (1999), because quarantine zones had been erroneously lifted 1 day too early for some farms in the initial EpiLoss.

14.3.1 Delayed destruction alternatives

Compared to the NV scenario, DD strategies (Tables 14.6 and 14.7) reduced both the number of infected and detected farms, but not significantly. The duration of the epidemic was sharply reduced (for example, the median decreased from 164 days to 108 days for DD-21-0).

The number of preventively slaughtered farms was significantly increased by a factor of almost four. The total costs and losses were comparable, except for the extreme replications. In the case of DD, the worst cases showed smaller epidemics. The composition of the cost factors varied between the NV scenario and the DD scenario. The direct costs for preventive slaughter in the case of the DD vaccination scenario were nearly three times higher. The consequential losses for the farmers increased, but the direct costs for animal welfare slaughter measures were sharply reduced. Compensation paid to the farmers for the breeding prohibition, as well as vaccination costs, were extras/additional costs compared with the NV scenario.

The results of the different DD alternatives, including the base version (DD-21-0) of this scenario, are shown in Tables 14.6-14.9. There was no significant difference in the size of the epidemic, when maximum protection was changed from 21 days to 7, 16 or 26 (Tables 14.6 and 14.8). The effect of preventive slaughter according to the vaccination-related priorities was apparently greater than the vaccine efficacy.

In the base DD scenario (DD-21-0), we assumed 5 days of preparation before the emergency vaccination actually began. In alternatives I, II and III, we assumed that it took 2, 8 and 25 days respectively to prepare an emergency vaccination campaign, following the decision on day 6. A longer preparation time only showed a larger epidemic for the worst iterations (Table 14.8). There was no significant difference in the number of detected farms, the number of infected farms, the number of preventively slaughtered farms or in the costs when comparing the simulated alternatives with the base DD scenario (Tables 14.6 and 14.8). Comparing alternatives I, II and III with the NV scenario, the number of preventively slaughtered farms was always significantly higher.

By changing the vaccination radius from 3 km to 1 km (alternative IV), the number of detected farms was slightly but not significantly higher compared to the base DD scenario (Tables 14.6, 14.8 and 14.9). Except for the worst iterations, the duration of the epidemic was the same (results not shown), but the number of preventively slaughtered and vaccinated farms was significantly lower leading to lower costs (compared to the base DD scenario). The 1 km vaccination alternative was significantly less costly than the NV scenario (1 km preventive slaughter) mainly due to the shorter duration of the epidemic.

Table 14.6 Results of multiple comparisons (t-tests) between the results of the base scenario, non-vaccination and different emergency vaccination alternatives as calculated in InterCSF. The compared mean outcome parameters were: the number of infected farms (I), the number of detected farms (D), the number of preventive slaughtered farms (P), the number of vaccinated farms (V) and the total losses (C), applying the Bonferroni corrected significance level ^a. Significantly different parameters are shown for comparison.

| Scenario | 97/98 simulated CSF epidemic | NV | DD-21-0 | ICT-21-0 ^b |
|--|---------------------------------|------------------------------------|---------------------|-----------------------------------|
| Non-vaccination scenario | | | | |
| NV ^c | I,D,P,C | - ^d | - | - |
| <i>Delayed destruction alternatives</i> | | | | |
| DD-21-0 | I,D,P,V,C | I ^e ,P,V | - | - |
| DD-7-0 | - | I ^e ,P,V | n.s. ^f | - |
| DD-16-0 | - | I ^e ,P,V | n.s. | - |
| DD-26-0 | - | I ^e ,P,V | n.s. | - |
| DD-21-I | - | I ^e ,P,V | n.s. | - |
| DD-21-II | - | I ^e ,P,V,C ^e | n.s. | - |
| DD-21-III | - | I ^e ,P,V | I ^e | - |
| DD-21-IV | - | V,C | P,V, C ^e | - |
| DD-21-V | - | I ^e ,P,V | n.s. | - |
| <i>Intra-community trade alternatives</i> | | | | |
| ICT-21-0 | I,D,P,V,C | I ^e ,P,V,C | P,C | - |
| ICT-7-0 | - | I ^e ,P,V,C | - | I,D,C |
| ICT-16-0 | - | I ^e ,P,V,C | - | n.s. |
| ICT-26-0 | - | I ^e ,P,V,C | - | n.s. |
| ICT-21-I | - | I ^e ,P,V,C | - | n.s. |
| ICT-21-II | - | I ^e ,P,V,C | - | n.s. |
| ICT-21-III | - | P,V,C ^e | - | I,D,V,C |
| ICT-21-IV | - | I ^e ,P,V,C | - | I ^e ,D ^e ,V |
| ICT-21-VI | - | I ^e ,P,V,C | - | P |

a) Bonferroni corrected significance level for the two-tailed test was 0.001316, based on 38 comparisons for $P < 0.05$.

b) In case of ICT, preventive slaughter is with one exception (alternative VI) never applied.

c) Vaccination was not applied in the simulated Dutch CSF epidemic and in the NV scenario.

d) Not tested.

e) If the Bonferroni corrected significance level was not applied, this parameter would have been significant at $\alpha = 0.05$.

f) None of the compared parameters were significant for $\alpha = 0.05$ (n.s. = not significant) or for the Bonferroni-corrected significance level $\alpha = 0.001316$.

Table 14.7 Comparison of the non-vaccination NV strategy with the two base emergency vaccination strategies, delayed destruction (DD-0) and intra-community trade (ICT-0) (maximum protection is reached on day 21)

| Epidemiological and economic characteristics | Scenario | | | | | | | | | | | |
|---|----------|-----|-----|------|---------|------|------|------|----------|------------------|------------------|------------------|
| | NV | | | | DD-21-0 | | | | ICT-21-0 | | | |
| | Mean | 5% | 50% | 95% | Mean | 5% | 50% | 95% | Mean | 5% | 50% | 95% |
| <i>Number of farms :</i> | | | | | | | | | | | | |
| Detected | 120 | 47 | 70 | 232 | 68 | 48 | 58 | 92 | 74 | 57 | 68 | 133 |
| Infected | 166 | 69 | 99 | 349 | 76 | 54 | 64 | 113 | 75 | 57 | 68 | 133 |
| Preventive slaughtered ^a | 566 | 342 | 450 | 1210 | 1335 | 1084 | 1177 | 1930 | - | - | - | - |
| Duration of epidemic (days) | - | 114 | 164 | 344 | - | 99 | 108 | 177 | - | 236 ^b | 258 ^b | 322 ^b |
| <i>Route of infection:</i> | | | | | | | | | | | | |
| Local | 107 | 29 | 54 | 222 | 32 | 15 | 25 | 52 | 32 | 18 | 29 | 63 |
| Animal contact | 2 | 0 | 0 | 9 | 1 | 0 | 0 | 4 | 0 | 0 | 0 | 4 |
| Transport contact | 12 | 0 | 4 | 41 | 4 | 0 | 1 | 18 | 3 | 0 | 1 | 14 |
| Personal contact | 8 | 0 | 4 | 19 | 2 | 0 | 2 | 6 | 2 | 0 | 2 | 6 |
| # Vaccinated Farms | - | - | - | - | 1240 | 958 | 1038 | 1602 | 1243 | 1043 | 1135 | 1961 |
| # Infected farms vaccinated | - | - | - | - | 32 | 20 | 28 | 38 | 32 | 21 | 30 | 56 |
| # Vaccinated farms infected | - | - | - | - | 7 | 3 | 6 | 12 | 10 | 5 | 9 | 19 |
| Start of vaccination ^c | - | - | - | - | - | 11 | 11 | 11 | - | 11 | 11 | 11 |
| Decision to stop with vaccination ^c | - | - | - | - | - | 96 | 102 | 154 | - | 78 | 101 | 164 |
| <i>Direct costs in 10⁶ € :</i> | | | | | | | | | | | | |
| Stamping out infected herds | 10 | 5 | 7 | 14 | 7 | 5 | 7 | 10 | 11 | 8 | 10 | 15 |
| Preventive slaughter ^a | 69 | 45 | 59 | 116 | 153 | 130 | 141 | 184 | - | - | - | - |
| Animal welfare slaughter | 347 | 226 | 290 | 677 | 201 | 157 | 169 | 250 | 305 | 253 | 290 | 423 |
| Breeding prohibition | - | - | - | - | 6 | 4 | 5 | 7 | - | - | - | - |
| Costs of organisation | 59 | 39 | 49 | 112 | 44 | 36 | 39 | 54 | 46 | 39 | 44 | 66 |
| <i>Consequential losses in 10⁶ € for :</i> | | | | | | | | | | | | |
| Farmers | 73 | 43 | 61 | 157 | 88 | 70 | 78 | 106 | 31 | 24 | 29 | 51 |
| Related industries | 154 | 103 | 127 | 277 | 141 | 115 | 123 | 170 | 114 | 99 | 107 | 155 |
| Vaccination costs in 10 ⁶ € | - | - | - | - | 3 | 3 | 3 | 4 | 5 | 5 | 5 | 8 |
| Total losses in 10 ⁶ € | 712 | 465 | 590 | 1349 | 644 | 522 | 567 | 769 | 514 | 429 | 484 | 708 |

a) In case of DD, preventive slaughter includes all vaccinated farms.

b) Includes 120-day post-vaccination zone.

c) The criterion to start or to stop respectively, installing new vaccination zones was fulfilled (days after 1st detection).

Table 14.8 Number of farms detected and preventive slaughtered for different simulated emergency vaccination scenarios

| Scenario | # Detection | | # Preventive slaughter ^a | | Costs 10 ⁶ € | |
|--|-------------|---------------|-------------------------------------|----------------------|-------------------------|-----------------|
| | 50 % | 5% - 95% | 50 % | 5% - 95% | 50 % | 5% - 95% |
| <i>Delayed destruction scenarios^b</i> | | | | | | |
| DD-21-0 | 58 | 48- 92 | 1177 | 1084-1930 | 567 | 522- 769 |
| DD-7-0 | 57 | 49-111 | 1174 | 1086-2051 | 560 | 522- 988 |
| DD-16-0 | 58 | 48-135 | 1176 | 1084-2860 | 568 | 522-1155 |
| DD-26-0 | 58 | 48- 93 | 1176 | 1084-1925 | 567 | 522- 806 |
| DD-21-I | 54 | 45- 79 | 1161 | 1076-1845 | 561 | 519- 831 |
| DD-21-II | 60 | 50- 80 | 1189 | 1088-1518 | 566 | 522- 751 |
| DD-21-III | 58 | 47-141 | 1267 | 1107-3049 | 595 | 530-1617 |
| DD-21-IV | 63 | 51-193 | 422 | 374-1082 | 451 | 405- 812 |
| DD-21-V | 59 | 49-110 | 1175 | 1083-2279 | 573 | 526- 962 |
| <i>Intracommunity trade</i> | | | | | | |
| ICT-21-0 | 68 | 57-133 | - ^c | - | 484 | 429-708 |
| ICT-7-0 | 59 | 50-95 | - | - | 370 | 330-538 |
| ICT-16-0 | 66 | 56-102 | - | - | 477 | 420-687 |
| ICT-26-0 | 69 | 58-133 | - | - | 486 | 434-710 |
| ICT-21-I | 64 | 53-117 | - | - | 481 | 415-720 |
| ICT-21-II | 73 | 61-125 | - | - | 489 | 432-702 |
| ICT-21-III | 113 | 92-169 | - | - | 554 | 487-909 |
| ICT-21-IV | 77 | 61-146 | - | - | 500 | 428-747 |
| ICT-21-VI ^c | 66 | 55-100 | 258 ^c | 237-307 ^c | 491 | 443-669 |

a) In case of DD, preventive slaughter includes all vaccinated farms.

b) All farms in a defined vaccination zone (0-3 km) will be slaughtered from day 6 onwards, if destruction capacities are available, independent of the vaccination preparation time. Except for alternative I until III this will be always 5 days extra. It will be 2 days for alternative I, 8 days for alternative II and 25 days for alternative III.

c) In case of ICT, preventive slaughter is only applied in strategy VI, where only non-vaccinated farms can be preventively slaughtered.

14.3.2 Intracommunity trade alternatives

The results of the different ICT alternatives, including the base version (ICT-21-0) of this scenario, are shown in Tables 14.6-14.9. In comparison to the NV scenario, the ICT base scenario was significantly cheaper (assuming no cost and losses for the post-vaccination zone). Preventive slaughter was not applied in the ICT scenario avoiding the large compensation costs. Furthermore, the consequential losses of the farmers were smaller compared with the NV scenario. No difference could be found for the number of detected and

infected herds, except for the worst iterations. The same was true for the duration of the epidemic, when deducting the 120 days post-vaccination zone (Tables 14.6 and 14.7). Comparing the ICT base scenario with the DD base scenario, no farms were preventively slaughtered. Furthermore, the costs were significantly lower.

There was no significant difference in the size of the epidemic when the maximum protection level was varied from 21 days to 16 or 26 days (Tables 14.6 and 14.8). However, when maximum protection was reached in 7 days, the epidemic was shorter with a significantly lower number of infected and detected premises. This alternative was consequently less costly than the simulated base ICT. In comparison with the NV scenario, all three alternatives were significantly less costly.

There was no significant difference when comparing alternatives I and II of the intracommunity trade with the base ICT (Tables 14.6 and 14.8). A slight (not significant) tendency of a decreased (increased) epidemic was found if the preparation time decreased (increased) by 3 days. However, alternative III (25 days preparation time) caused a significantly larger epidemic with significantly more detected, infected and vaccinated farms (as well as increased costs and losses). Alternatives I and II were significantly cheaper when compared with the NV scenario in contrast to scenario III.

Table 14.9 Comparing direct costs and losses of the base scenario with alternative IV for the intracommunity trade strategy (ICT) and for the delayed destruction strategy (DD).

| Scenario | DD-21-0 | | DD-21-IV | | ICT-21-0 | | ICT-21-IV | |
|---|---------|---------|----------|---------|----------|---------|-----------|---------|
| | 50% | 5- 95% | 50% | 5 - 95% | 50% | 5 - 95% | 50% | 5 - 95% |
| <i>Direct costs in 10⁶ € :</i> | | | | | | | | |
| Stamping out infected herds | 7 | 5-10 | 8 | 6-12 | 10 | 8-15 | 12 | 9-18 |
| Preventive slaughter ^a | 141 | 130-184 | 56 | 48-89 | - | - | - | - |
| Welfare slaughter | 169 | 157-250 | 202 | 181-391 | 290 | 253-423 | 301 | 255-443 |
| Breeding prohibition | 5 | 4-7 | 0.5 | 0.5-0.5 | - | - | - | - |
| Costs of organisation | 39 | 36-54 | 36 | 33-68 | 44 | 39-66 | 45 | 39-69 |
| <i>Consequential losses in 10⁶ € for :</i> | | | | | | | | |
| Farmers | 78 | 70-106 | 44 | 38-97 | 29 | 24-51 | 31 | 24-59 |
| Related industries | 123 | 115-170 | 103 | 95-178 | 107 | 99-155 | 111 | 99-160 |
| Vaccination costs | 3 | 3-4 | 0.5 | 0.5-0.9 | 5 | 5-8 | 1.4 | 0.9-2.3 |
| Total losses | 567 | 522-769 | 451 | 405-812 | 484 | 429-708 | 500 | 428-747 |

a) In case of DD, preventive slaughter includes all vaccinated farms.

A 1 km vaccination radius significantly reduced the number of vaccinated farms (for example the median decreased from 1135 vaccinated farms to 284 (result not shown)). The number of infected and detected farms was slightly higher (not significantly) compared to the base (Tables 14.6, 14.8-14.9).

Applying preventive slaughter in ICT alternative VI showed no difference in the epidemiological parameters and did not increase the total costs significantly (Tables 14.6 and 14.8).

14.4 Discussion

Although the EU regulations currently prohibit routine vaccination against CSF, it is expected that the development of a marker vaccine will lead to a reassessment of the non-vaccination principle (Laddomada and Westergaard, 1999). Therefore, the main goal of our simulations was to analyse different possible emergency vaccination campaigns, which could have been applied in the Dutch CSF epidemic. The vaccination alternatives were compared with the NV scenario discussed in Nielen et al. (1999). The NV scenario was considered to be the most effective that could have been achieved using the regular control measures.

14.4.1 Comparison of vaccination strategies

The results of the significance testing should be used with caution, as with more replications even smaller differences between alternatives would have become significant. The duration of the epidemic could not be tested in the current simulations because the epidemics were always stopped at 365 days. Other useful parameters not tested (such as the cost factors) could largely be explained by changes in underlying parameters.

The main goals of any emergency vaccination strategy (reduced number of infected herds) were reached in both emergency vaccination scenarios compared to the NV strategy. The DD strategy seemed to be the most effective strategy for reducing duration and size of an epidemic. A shorter epidemic would lead to a reduction in direct costs paid for animal welfare slaughter measures and for organisation. For the DD strategy the reduction was countered by the higher preventive depopulation costs (all vaccinated farms) as well as the higher consequential losses for farmers. Vaccination costs were only of minor importance. Except for the 95th percentile (DD was less costly), no overall difference could be found between a DD scenario and the NV strategy.

ICT relies entirely on a reliable and easy-to-handle serological test. Presuming no hindrance on the EU market for pig meat originating from vaccinated pigs and no extra cost and losses for the post-vaccination zone, ICT was significantly cheaper than NV or DD. The vaccination

costs were more than compensated for by the reduction in the direct costs paid for preventive slaughter and in the consequential losses. Furthermore, the numbers of infected and detected farms were on average smaller (but not significantly) for ICT than for NV. The worst-case iterations for ICT were never as severe as for the NV scenario. An ethical as well as an economic advantage of this strategy, compared to NV and also to DD, is that (except for animal welfare slaughter in the quarantine zone) no healthy pigs need to be destroyed.

The effectiveness of the DD strategy was mainly due to the applied preventive depopulation of the vaccination zones in which farms with the highest risk had the highest priority. When simulating an NV scenario with a 3 km preventive slaughter radius but without a classification into risk types, the average epidemic increased from 120 to 209 detected farms (results not shown). Therefore, the effectiveness of the DD scenario was partly the result of the classification into risk types and partly based on the reduced virus spread due to vaccination. The latter effect is mainly of importance in large epidemics and severely limited destruction capacity.

A small change in the effectiveness of the vaccine (16, 21, 26 days to maximum protection) had no extra influence on the epidemic for either emergency vaccination strategy. Only a very effective vaccine (maximum protection in 7 days) significantly reduced the epidemic for the ICT scenario. The 7 days refers more or less to the effectiveness of the conventional non-marker CSF vaccine, as has been used historically in Dutch epidemics (Brus, 1976; Tielen, 1977).

We presumed a fast implementation based on clear criteria about where and when to begin an emergency vaccination campaign (≥ 5 detections in the 1st week) combined with a short preparation time of 5 days. A longer delay (alternative III) had a negative effect especially in the case of the ICT alternative. This effect was much lower for the DD alternative because this scenario also depended on risk-based depopulation as a control measure from day 6 onwards.

Changing the preventive slaughter radius from 1000 m to 500 m in the DD scenario had no negative effect, because the 500 m preventive slaughter was only applied in the first week of the epidemic, followed by a 3 km vaccination and preventive slaughter zone.

Applying preventive slaughter as an additional measure in the ICT scenario showed no significant effect on the course of the epidemic. The main effect was to change the composition of total costs: higher consequential losses for farmers; extra depopulation costs; lower costs for animal welfare slaughter.

A reduction in the vaccination radius from 3 km to 1 km was significantly cheaper than the NV scenario, for DD due to a reduced number of preventively slaughtered farms, for both DD and ICT due to reduced vaccination costs. However, potentially the control of the post-vaccination zone could become more difficult (thus, more costly) for ICT.

14.4.2 Model constraints

A discriminatory diagnostic test with a specificity of less than 1 could lead to the detection of false positive farms. As a consequence, new quarantine zones would be installed and healthy pig farms would be slaughtered out. A high level of sensitivity is required because we want to detect all infected farms. In the current simulations, we assumed a specificity of 1 (simplification reasons) whereas the sensitivity was based on the current conventional diagnostic test. So in our simulation, we detected nearly all infected farms but we would never “find” false positive farms.

The addition of vertical transmission (the sow conveys the infection to its unborn offspring) would have meant a complete overhaul of the transmission structure in the model (Jalvingh et al. 1999), and was excluded. In the case of ICT, vertical transmission could lead to an underestimation of the epidemic. We assumed an infectious period of only 1 month for vaccinated and later-infected farms i.e farms infected at a later stage (which does not take into consideration the birth of carrier piglets) whereas all other infected farms remained infectious until slaughtering took place.

We assumed that only vaccinated and later-infected farms would show a reduction in virus spread (further research is needed). Infected farms and those vaccinated at a later stage were supposed to stay infectious until detection without any reduction in infection levels. Because these farms had a high probability of being detected earlier due to vaccination, their effect on the outcomes is rather small. Vaccination activities could also lead to earlier detection of infected farms, but the effect on the simulation outputs was rather small (results not shown).

We assumed maximum protection of all vaccinated farms during the 120 day post-vaccination zone. This is an over estimation because the number of non-vaccinated pigs will increase in that period. The duration of maternal immunity against transmission was not modelled, but would reduce the above overestimation. At the removal of a post-vaccination zone, the protection level of all vaccinated farms was set to zero, leading to an underestimation of the vaccination effect.

No reduction in the effectiveness of the vaccine was assumed in the case of maternal immunity of the piglets. For simulation at the animal level, the effect of maternal immunity against virus transmission needs to be quantified. InterCSF simulates at the herd level.

Vaccination has some disadvantages and possibly hazards as it may engender a false sense of security (leading to relaxation of other control measures and/or less-strict sanitary behaviour of people involved) (Anonymous, 1997). In our simulations, we presumed no relaxation.

The high number of required diagnostic tests could lead to a delay in diagnosis. This effect was not considered as such in our simulation model. We assumed a minimum 49 days instead of 42 days before removing the standstill, to mimic a waiting period for the laboratory results.

In simulating the actual Dutch CSF epidemic, we knew in advance that we would have a large epidemic in a very densely populated area. Thus, the decision to begin an emergency vaccination campaign was based on only a single criterion in the current study (i.e. 5 detections in the first week). In a more generic model, further criteria may be compared (such as pig density or the total number of outbreaks in relation to the length of the epidemic).

14.4.3 Economic model constraints

Breeding prohibition was not simulated but the compensation paid to the farmers was calculated in EpiLoss. Because a decreasing pig population was only considered for fattening farms in a quarantine zone (Meuwissen et al., 1999), the total depopulation costs could have been overestimated (especially in large epidemics) in the case of DD. In order to make comparisons with NV we accepted this slight overestimation by not adapting EpiLoss.

Serological costs were only incorporated as a lump sum per tested farm derived from the Dutch CSF epidemic. Serological cost calculations based on farm size and type would allow better and more detailed comparisons of different simulated alternatives.

The direct costs for animal welfare slaughter measures were based on average pig prices over the year 1997 because no market reaction was simulated. In a real epidemic, compensation paid for animal welfare slaughter measures is based on slaughter prices, which fluctuate weekly. In the case of a large epidemic, the demand and the supply of growers¹⁷ and fatteners will certainly be interrupted or distorted (which would lead to large price movements (see Asseldonk et al., 2000)). Large price changes would mainly influence the direct costs of animal welfare slaughter measures as well as the consequential losses of the farmers subjected to control measures (such as higher repopulating costs). Consumer behaviour is not always rational and a severe reaction against vaccinated meat could lead to a drastic price drop (not simulated).

EpiLoss is based on partial budgeting and calculates only the cost and losses of farms and related industries subjected to control measures. Benefits were not considered (such as higher profits for pig farmers outside the quarantine zones or profits for the pharmaceutical industry).

To control a post-vaccination some organisational costs will be involved. Farmers situated in a post-vaccination zone may be restricted in their choices for selling their pigs resulting in lower weekly pig prices than paid outside the zone. The current zero cost assumption is therefore too optimistic.

¹⁷ A grower is a piglet of 20-45 kg

14.5 Conclusions

Emergency vaccination (assuming a reliable diagnostic test and no relaxation of other control measures) seemed to be an effective strategy for reducing the size of an epidemic. Emergency vaccination alternatives were at least as effective as the optimal NV scenario. The worst iterations were never as severe as in the case of the NV scenario. The large number of preventively slaughtered farms in the DD strategy is a negative aspect of the DD strategy compared to the NV strategy. This effect mainly reduces the positive effect of a shorter epidemic. If we compare the ICT strategy with the NV strategy, emergency vaccination is certainly the tool to choose. Vaccination costs (which are of minor importance compared to all other costs and losses) are mainly in competition with the cost of preventive slaughter, assuming no extra costs and losses for the post-vaccination zone. ICT avoids the destruction of a large number of healthy pigs that can still be used for human consumption.

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Appendix IV Chronological order of all control measures except vaccination in case of a newly detected CSF outbreak in InterCSF (Jalvingh et al., 1999)

| Time | Measure |
|---|---|
| Day of detection | <ul style="list-style-type: none"> - Infected farm will be put on slaughter list and destroyed (slaughtered and rendered) as soon as capacities are available (highest priority) - Movement standstill is imposed on the protection (0-3 km) and on the surveillance zone (3-10 km) ^a; fewer <u>personal</u> contacts (50%) are allowed. Animal contacts and vehicles contacts are forbidden. - Farms within a certain radius could be subjected to preventive slaughter, limited by destruction capacity (killing and rendering capacities). Preventive slaughter could lead to earlier detection. |
| Start on 2 nd day | <ul style="list-style-type: none"> - Surveillance (clinical inspection) of all farms in the protection zone (0-3 km), which may lead to earlier detection. - Tracing farms that had contact with the infected farm. Traced farms are put on surveillance (clinical inspection), which may lead to earlier detection, or may be subjected to preventive slaughter. |
| Start on day 28 th | <ul style="list-style-type: none"> - Start buying-out schemes of fatteners and growers for animal welfare reasons (referred throughout the paper as animal welfare slaughter) in the quarantine zone until the quarantine zone is lifted. Welfare slaughter may lead to earlier detection. |
| Earliest on day 35 th | <ul style="list-style-type: none"> - Start of serological final screening of all farms situated in the quarantine zone, if no additional farm was detected during those last 35 days. |
| Earliest on day 49 th ^b | <ul style="list-style-type: none"> - If there is no new detection in a quarantine zone, the quarantine zone is lifted up. |

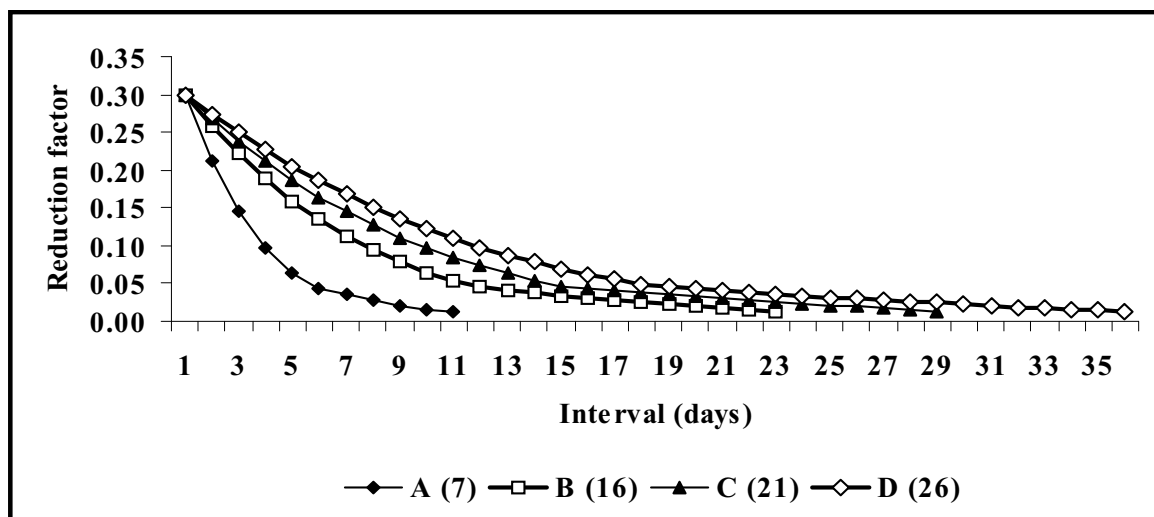
a) Surveillance and protection zones with imposed movement restrictions (movement standstill) are referred to throughout the paper as quarantine zones.

b) We assumed 49 days instead of 42 days, to mimic a waiting period for the laboratory results.

Appendix V The calculated reduction and protection factors

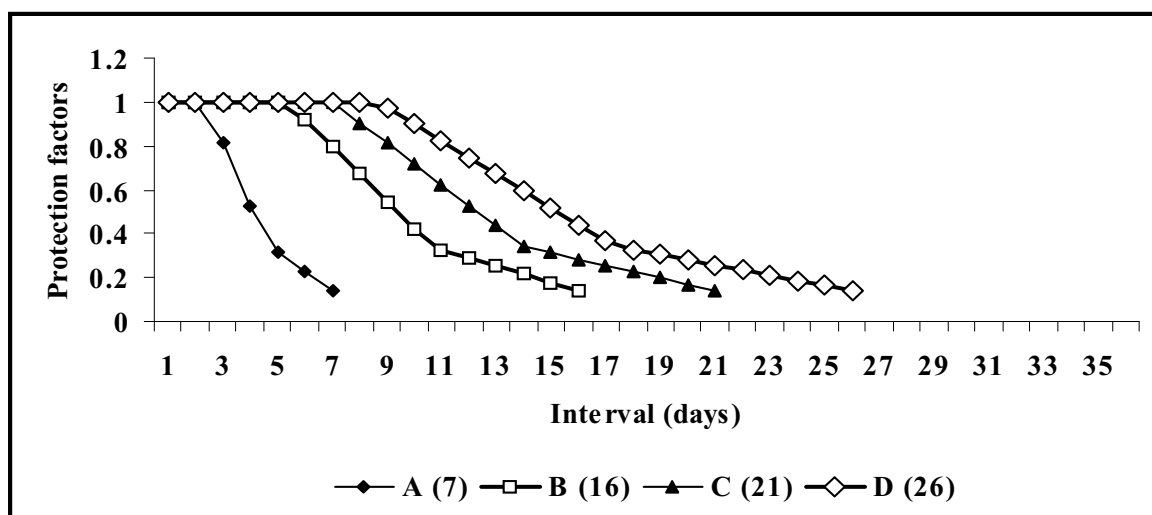
In horizontal transmission experiments coordinated by the EU, animals in groups of 10 were vaccinated with one of two alternative vaccines and 5 of each group were inoculated with CSF 7, 10, 14 or 21 days after vaccination. From the data generated by these experiments, parameters of the standard SIR model were estimated (Klinkenberg et al., 2000). These parameters were used to calculate the reduction in total infection levels for a herd depending on the time between vaccination and infection. Results showed that for both vaccines, 21 days was the time period from vaccination until maximum protection of the individual animal. The relative decline of the estimated between-animal transmission parameter was used as a protection factor. In order to determine what a faster or slower working vaccine would do, time scales of protection and reduction curves were changed. A reference point for these changes was the maximum protection date of the individual animals (21 days) which was changed to 7, 16 or 26 days. Because the vaccines do not differ in their ability to reduce horizontal transmission, we used the average of the estimated parameters from both vaccines. The applied reduction and protection factors are shown in Figures V-1 and V-2.

Figure V-1 Reduction factor for the probability of transmission from a vaccinated farm, related to the time interval between vaccination and subsequent infection. Maximum vaccine efficacy was at 7 (A), 16 (B), 21 (C) or 26 (D) days after vaccination.



Appendix V The calculated reduction and protection factors (suite)

Figure V-2 Reduction factor (called "protection factor") for the probability of a vaccinated farm becoming infected, related to the time interval between vaccination and a possible infection. Maximum vaccine efficacy was at 7 (A), 16 (B), 21 (C) or 26 (D) days after vaccination.



Appendix VI Control measures, related events in EpiLoss, and implications of the events

| Control measures | Related events | Implications |
|------------------------------------|------------------------------|--|
| <i>Compulsory measures</i> | | |
| Stamping-out | - Depopulation | - Herd is destroyed, buildings empty till restocking |
| | - Restocking | - Restarting the farm |
| Quarantine zone | - Start quarantine zone | - No supply and delivery of animals allowed |
| | - End quarantine zone | - Supply and delivery of animals allowed |
| Preventive slaughter | - Depopulation | - Herd is destroyed, buildings empty till restocking |
| | - Restocking | - Restarting the farm |
| <i>Additional measures</i> | | |
| Animal welfare slaughter | - Start welfare slaughter | - Animals for which measure applies are destroyed |
| | - End welfare slaughter | - End of destruction of animals under consideration |
| Breeding prohibition | - Start breeding prohibition | - Prohibition of insemination of sows |
| | - End breeding prohibition | - Insemination of sows allowed |
| <i>Vaccination measures</i> | | |
| Vaccination | - Apply vaccination | - All pigs on the farm older than 14 days are vaccinated once, which may be repeated after 6 months |
| | | - Continued vaccination may be included during the time of the quarantine zone for breeding sows and newborn piglets (only applied in the ICT strategy). |
| | - End quarantine zone | - Vaccination stops |

Development of prevention and control strategies to address animal health and related problems in densely populated livestock areas of the Community

Shared cost research project -- FAIR5-PL97-3566

Overall summary and conclusions

R.B. Huirne and H.-W. Windhorst

Overall summary and conclusions

R.B. Huirne and H.-W. Windhorst

15.1 Research objectives

The main objectives of the project were to develop methods of identifying densely populated livestock areas and to develop tools that are necessary in order to reduce risks and help solve problems in such areas. The major research questions were:

- 1.) What areas of the Community are densely populated?
- 2.) What are the risk factors for the introduction of notifiable diseases into these areas?
- 3.) What are the risk factors for the further spread of notifiable diseases in these areas?
- 4.) What specific prevention and control strategies for notifiable diseases are possible and what are the costs and benefits?

In order to ensure both theoretically and practically useful results, these research questions have been translated into the following four tasks:

- Task A: Development and standardisation of data and methods used to identify densely populated livestock areas
- Task B: Quantification and classification of the risk of such areas from a disease point of view
- Task C: Analysis of recent disease outbreaks of CSF and FMD to test and refine the risk parameters
- Task D: Cost-benefit analysis of disease prevention and control strategies in such areas

15.2 Overall results and deliverables

The project made it possible to identify areas in the EU which are characterised as having a high risk with respect to the introduction and further spread of major animal diseases. The results enable the EU to stimulate measures that reduce the risk and to decide what means should be used in particular areas to reduce the costs of an outbreak. Reduced risk and improved control strategies can help to make measures redundant/obsolete that are both very

costly and no longer accepted by the public, such as the stamping out of a large number of herds that do not show any signs of an infection.

More specifically the major results/benefits from the completion of the project were:

- the ability to identify densely populated livestock areas and to characterise the sectoral and spatial structure (pattern) of the livestock industry in such areas
- the development of software tools that allow the analysis of available data sets in order to characterise the risk factors for densely populated livestock areas and to rank them with respect to the risk of introduction and further spread of major diseases, such as CSF and FMD
- the development of a computerised modelling approach in order to carry out cost-benefit analyses of relevant prevention and control strategies for major animal diseases in densely populated livestock areas, aimed at supporting policy makers at EU, national and regional levels
- the opportunities for using the data collected and software tools developed for the study of purposes other than disease risk, such as the environmental problems resulting from the concentration of livestock

The most important technical deliverables were:

- a computerised toolbox for the identification and analysis of densely populated livestock areas
- a method of ranking densely populated livestock areas according to their risk
- an integrated modeling approach for the evaluation of prevention and control strategies of notifiable diseases in densely populated livestock areas

The results of the project were disseminated:

- to the European Community via partner meetings, progress reports and a final report
- to the scientific community via scientific publications and reports, presentations at congresses and seminars, and teaching in regular (university) curricula and on postgraduate courses
- to disease control authorities of both the public and private sector via computer software:
 - the software toolbox that will be developed to identify densely populated livestock areas will be coupled with low cost PC-based systems that are affordable for small organisations, private industry and municipal organisations. This enables all kinds of possible users to do their own analysis

- the computer simulation models to evaluate the effectiveness and cost/benefits of prevention and control strategies for notifiable disease outbreaks in densely populated livestock areas will run on a PC and will be made available for use by policy makers and others
- a special workshop/seminar organised (on September 26, 2001) following completion of the project in order to demonstrate the practical application of the major outcome and software tools developed

The following research milestones were realised:

Task A:

- Review and synthesis of available databases in densely populated livestock areas
- Ranking of densely populated livestock areas according to their livestock density
- Review and synthesis of existing conversion tables for animals
- Calculation of spatial indices
- Design of a spatial database, integrated with other farm characteristics
- Characterisation of the sectoral and spatial structure of the livestock industry in the study areas
- Design of disease-related conversion tables for the various animal species
- Integrated toolbox with computer software
- Outline training sessions with the approach and software developed

Task B:

- Review of relevant additional data to be collected on farms and related industries as indicators of disease risk
- Design of a standardised questionnaire in order to obtain more qualitative risk factors from farms and related industries
- Database on the more qualitative risk factors using questionnaires and expert consultation
- Procedure for risk ranking of densely populated livestock areas based on quantitative indices
- Added value of qualitative risk factors for animal disease
- Definition of possible risk profiles of individual farms
- Ranking of densely and sparsely populated livestock areas according to their risk
- Validate risk ranking of areas using general data on notifiable disease outbreaks and farm-specific risk profiles
- Redefinition of risk ranking algorithms based on the outcome of undertaken validation (together with Task C)

Task C:

- Design of datasets for the spatial analysis of real outbreaks of CSF in Belgium, Germany and The Netherlands
- Design of the spatial analysis of real outbreaks of CSF
- Procedure for spatial analysis of real outbreaks of CSF
- Design of a procedure to compare the results of the analysis of real outbreaks and the risk ranking of the areas
- Validation of risk ranking with results of spatial analysis of real outbreaks
- Redefinition of risk ranking algorithms based on the outcome of undertaken validation (together with Task B)

Task D:

- Simulation model for introduction and spread of CSF into a region
- Spatial and stochastic simulation model to evaluate disease control strategies for CSF
- Design of a procedure in order to integrate the simulation models for introduction and spread of CSF with economic models
- Definition of interesting prevention and control strategies for CSF
- Cost-benefit analysis of prevention and control strategies for CSF
- Generalised model approach to other notifiable diseases, beginning with FMD
- Cost-benefit analysis of prevention and control strategies for FMD
- Redefined prevention and control strategies appropriate for densely populated livestock areas

The following technical deliverables were produced:

- Report with an extensive review and synthesis of relevant data in densely populated livestock areas (Task A)
- Report of the proposed new approach and databases to identify densely populated livestock areas, including conversion tables for animals to calculate animal density (Task A)
- Computerised toolbox for the identification and analysis of densely populated livestock areas (Task A)
- Data collection system for qualitative and on-farm animal disease risk factors (Task B)
- Quantitative procedure to rank densely populated livestock areas according to risk (Task B)
- Method for analysing data sets on real outbreaks focusing on spatial patterns of real outbreaks (Task C)
- Report on spatial and time patterns of real outbreaks of CSF in different countries and assumptions with respect to steering factors that cause these patterns (Task C)

- Model approach for the economic evaluation of strategies for preventing the introduction of notifiable diseases into a densely populated livestock area (Task D)
- Model approach for the economic evaluation of control strategies for notifiable diseases in densely populated livestock areas (Task D)

15.3 Summary of results and conclusions per research question

QUESTION 1: What areas of the Community are densely populated?

Based on both spatially oriented and veterinary-oriented methodologies, categories of animal density are considered to be disease dependent. For FMD, areas (municipalities) with less than 150 animals (dairy cows, beef animals, sheep, goats, pigs) per square km are classified as SPLA (sparsely populated livestock areas). Those with between 151 and 450 animals are classified as MPLA (medium populated livestock areas) and those areas with more than 450 animals per square km as DPLA (densely populated livestock areas). For CSF, these categories are slightly different, i.e. areas below 50 pigs per square km are defined as SPLAs, with 51-300 pigs as MPLAs and areas with more than 300 pigs per square km as DPLAs. This corresponds to approximately 80% of the areas in the studied EU member states being sparsely populated, about 15% being medium populated and about 5% being densely populated.

The DPLAs are concentrated mainly in the western part of Germany (Lower Saxony), the eastern and southern parts of The Netherlands, the western part of Belgium (Flanders), the western part of France (Brittany) and the northern part of Italy (Po region) (Chapter 2). Detailed maps are provided with the classified areas for FMD and CSF.

Further analyses with advanced spatially oriented techniques in Chapter 3 showed a more detailed picture. The SPLAs, MPLAs and DPLAs defined in Chapter 2 do not seem to be very homogeneous. In SPLAs, for example, there are smaller sub-areas with high densities, and within DPLAs there are smaller sub-areas with low densities. Therefore we need more advanced methods for classifying such areas. This is because the *average* density of an area or municipality is not the most important factor for the introduction and spread of an animal disease, but the spread in density *within* the areas is indeed the most important factor. Detailed maps have been developed using these advanced indices, such as the Nearest Neighbour Index (NNI), the Lorenz curve, the GINI index and a kernel tool, for use in some selected EU areas.

QUESTION 2: What are the risk factors for the introduction of notifiable diseases into these areas?

With regard to the risk of CSF introduction, the use of swill feeding and the presence of wild boar populations in the areas of interest are important risk factors. The use of (highly risky) swill feeding has been identified on 1-5% of pig holdings. However, swill feeding is observed much more frequently in SPLAs compared to DPLAs. In many countries (for instance Germany, France and The Netherlands) the presence of wild boars has been identified both in SPLAs and DPLAs. In these areas the percentage of pig units where barriers are present varies from 13% to 88%. In geographical areas with a wild boar population, the presence of a physical barrier around the farms to reduce the risk of possible contact between (infected) wild boars and domestic pigs should represent one of the minimum requirements to be applied in all pig units in the area (Chapter 4).

Another main risk factor for the introduction of a contagious animal disease in a country or a region is the movement of animals. Animal introduction occurs more frequently in pig (93%) than in cattle (52%) holdings, but 50% of pig units and 39% of cattle holdings purchase animals only from farms located in the same region. Furthermore, pig farms are characterised by a higher level (64%) of introduction of animals from known farms, when compared to cattle (33%). In the areas under study a different level of risk has been identified. For instance, the practice of purchasing animals from other areas varies from 29% and 53% in Italian pig and cattle holdings respectively, to 97% and 96% in French pig and cattle farms. The introduction of replacement stock from higher risk sources (holding centres, markets and unknown farms) is much greater in pig (57%) and cattle (90%) farms in the German pilot areas, than in Italian pig (13%) and cattle (53%) holdings. In addition, as was clearly shown during the recent epidemics of CSF and FMD in Europe, both the discipline regarding animal movements and the traceability of such movements represent the key points for guaranteeing a reduction of the risk of introducing a contagious animal disease into a disease-free area. The success of the eradication measures put in force should a disease outbreak occur (Chapter 4) also depends on these key points.

Further analysis with multiple attribute techniques stress the importance of swill feeding and the presence of wild boar as main risk factors for CSF introduction in domestic pig populations (Chapter 5). These results reflect the knowledge that in some areas of the EU a large proportion of CSF primary outbreaks was due to contacts with wild boar or to swill feeding. Other important risk factors for CSF introduction were mainly factors relating to both animal trade and herd management. In particular the trade of live animals and returning transport lorries are risk factors for CSF introduction. In each country, the risk of CSF introduction is higher in SPLAs compared to DPLAs. Therefore, animal density as such does

not seem to be the only factor associated with the risk of CSF introduction in the selected study areas. The epidemiological role that SPLAs may play in the introduction of CSF in the domestic pig population is that the disease could then spread to DPLAs through the movement of live animals or transport lorries. Good herd management (including proper biosecurity measures) is a very important factor in lowering the risk of the introduction and spread of CSF. Application of the multiple attribute techniques shows clearly that CSF represents a continual threat for the EU pig industry. Systematic adoption of biosecurity protocols at all levels (international, national, herd level) should therefore be enforced to minimise the risk of CSF introduction into pig units (Chapter 5).

These conclusions are also confirmed in a few follow-up studies in France and The Netherlands (Chapters 6, 11 and 13). Chapter 6 shows that the ratio ‘fattening pigs over sows’ is a good indicator for the geographical risk of CSF (tested in Brittany, France). This ratio combines several underlying indices such as pig movements between herds and net import or export of piglets to or from other areas. The ratio is an easy-to-use index for CSF because it does not require a lot of information to work it out. It is a valuable index for calculating over time, in order to represent the dynamics in pig populations.

Several studies dedicated to the study of airborne FMD spread (and introducing FMD into new areas) do not explicitly consider herd size to be a risk factor (Chapter 11). Up until now the only solution for quantifying the probability of infection has been to compare the value obtained from a mathematical model of airborne spread to the minimal doses required to set-up the infection experimentally. However, herds can have different sizes that possibly represent a variable source of risk. Our analytical model (partially) explains why not all the herds exposed to the airborne virus are infected. Several combinations of doses and herd size give the same risk of infection. As the inhaled dose is linked to the distance from an infected source, the former relation implies that a big herd located far from an outbreak could have the same probability of infection as a small herd located close to the source. Moreover, a very low dose can be sufficient to set up an infection if a lot of animals are exposed (Chapter 11).

Insight into factors contributing to the risk of CSF introduction, which is needed in order to decide upon preventive actions that are cost-effective, i.e., that they achieve considerable risk reduction at reasonable costs, is also given in (part of) Chapter 13. In this study both qualitative and quantitative approaches were used to estimate the probability of CSF introduction for several regions in the EU and to determine which factors contribute most to the probability of CSF introduction. Both approaches were based on a so-called pathway diagram (i.e. a combination of risk factors) especially constructed for CSF introduction into regions of the EU under a non-vaccination policy. The qualitative assessment of the probability of CSF introduction into DPLAs and SPLAs demonstrated that DPLAs generally had a higher probability of CSFV introduction

than SPLAs, although this could not be attributed to pig density only. CSF introduction through wild boar was again concluded to be highly probable (Chapter 13).

QUESTION 3: What are the risk factors for the further spread of notifiable diseases in these areas?

The occurrence of ‘neighbourhood infections’ (combination of risk factors associated with the proximity of herds) during CSF outbreaks were examined based on information collected by Veterinary Officers of the Ministry of Agriculture during the CSF epidemic in East Flanders (Belgium) of 1994 (Chapter 9). Neighbourhood infections were observed in the neighbourhoods of 9 out of 19 primary herds. The only risk factor considered that was associated with the occurrence of neighbourhood infections was an index called the bivariate kernel estimate of intensity, i.e. the higher the bivariate kernel estimate of intensity, the higher the risk for occurrence of neighbourhood infections. The bivariate kernel estimate of intensity is a spatial parameter, which combines the number of herds that are situated within the selected area (one kilometre radius) and the relative distance of these herds to the reference herd (CSF infected herd). The pig density, a parameter assumed to be associated with a high risk for the introduction and spread of contagious diseases did not explain as much variation as the bivariate kernel estimate of intensity did in the final model. However, the bivariate kernel estimate of intensity resulted in being the best explaining predictor variable of the variation in the CSF data and was positively associated with the risk for neighbourhood infections (Chapter 9). No significant lacks of fit were observed for the model based on all observations or for the models resulting from the cross-validation procedure. The parameter was highly correlated with the pig density of the neighbourhood, the second best explaining predictor variable for the available data (Chapter 9). In the model-building dataset collected during a real CSF outbreak in 1994, the bivariate kernel estimate of intensity varied from 0.426 to 7.203. Unfortunately, the kernel estimate is not a perfect predictor for neighbourhood infections in the different regions of Belgium. Therefore the presented maps in Chapter 9 should be seen as illustrations of a possible methodology for predicting the risk of CSF spread instead of as an accurate estimate of the risk.

The purpose of the follow-up study in Chapter 10 was to estimate the agreement between communities with a high risk for the neighbourhood spread of Classical Swine Fever (CSF) and communities with dense pig populations. A community was considered to incorporate a high risk for the neighbourhood spread of CSF when the risk of ‘neighbourhood infections’ for at least one neighbourhood was higher than a preset cut-off value. This criterion implies that not all neighbourhoods in a community have a risk that is higher than the cut-off value. Moreover, the proportion of neighbourhoods having a risk of ‘neighbourhood infections’

higher than the cut-off value decreases when the cut-off value increases. When the cut-off value is 25% or higher, the kappa agreement is only moderate or less than moderate. Therefore, the use of the pig density of a community to select communities for which at least one neighbourhood in the community has a risk of neighbourhood spread of CSF of 25% or higher would not be appropriate. A substantial kappa agreement was found for the other cut-off values (5 to 20%). However, the identification of communities with a high risk for the neighbourhood spread of CSF, based on the selection of communities with dense pig populations, results in a number of misclassifications. The positive predictive value for a given cut-off value differs from country to country because its value changes when the prevalence of communities with a high risk for the neighbourhood spread of CSF changes, i.e. the smaller this prevalence the smaller the positive predictive value. The major conclusion was that the choice of the minimum pig density of a community to optimise the selection of communities with a high risk for the neighbourhood spread of CSF is not straightforward. The choice depends on the correlation of the selection of communities with dense pig populations and with a high risk for the neighbourhood spread of CSF, as well as on the risk that decision-makers wish to take (Chapter 10).

To test for generality, the methods have been tested on other animal diseases as well as in other areas/countries. Chapter 7 deals with respiratory disease outbreaks in fattening pigs (SPLAs versus DPLAs in France) and Chapter 8 deals with Aujeszky's Disease in pig farms in DPLAs in Belgium. In contrast to CSF and FMD, these diseases are currently commonly present in the pig population, so the risk factors for *spread* (in contrast to the introduction of the disease) may be studied. Respiratory diseases (and their spread) in finishing pig herds were associated with (smaller) herd sizes, more frequent animal movements and with higher densities of the animal population. Therefore, in DPLAs there are more problems with respiratory diseases than in SPLAs. However, within a DPLA some factors related to the large number of pig farms in a neighbourhood might be conducive to successive contamination by viral agents if biosecurity measures are not correctly implemented at the farm level. Results show that a high number of contacts with vehicles (animal transport, veterinary and technician) was a feature of pig farms located in the DPLAs in France (poor biosecurity measures) (Chapter 7). Chapter 8 deals with risk factors for Aujeszky disease in Belgium. The most important risk factors for Aujeszky disease were (SPLA versus DPLA): a high animal density, a high number of contacts between herds and outdoor facilities. Protective factors are good hygiene, use of a spare compartment, application of quarantines and number of empty days before repopulating the pens/compartments. Management factors that are relevant included the disease status of the herd, application of all-in-all-out systems, not regrouping or mixing animals and a maximum limit on the number of animals within one compartment (Chapter 8).

QUESTION 4: What specific prevention and control strategies for notifiable diseases are possible and what are the costs and benefits?

A decision tree was developed in Chapter 12 as a tool to support decision-making concerning control measures during the first three days following the declaration of an outbreak of FMD. The objective of the tree was to minimise direct costs and export losses of FMD epidemics in all kinds of scenarios. Scenarios were defined by livestock and herd density in the outbreak region, time between first infection and first detection, and the possibility of airborne spread. The starting point for the tree was an epidemiological model based on an epidemiological FMD model. The effects of four control strategies on FMD dynamics were modelled. In addition to the standard control strategy of the stamping-out and culling of high risk contact herds, strategies involving ring culling within 1 km of an infected herd, ring vaccination within 1 km of an infected herd, and ring vaccination within 3 km of an infected herd were assessed. An economic model converted outbreak and control effects of farming and processing operations into estimates of direct costs and consequential export losses. Results showed that animal density within the outbreak region is an important determinant in deciding on the economically optimal control strategy. Ring vaccination is the economically optimal control strategy for densely populated livestock areas and ring culling is the economically optimal control strategy for sparsely populated livestock areas (Chapter 12).

Chapter 13 dealt with obtaining insight into all factors contributing to the risk of CSF introduction that are required in order to decide upon preventive actions that are cost-effective, i.e., they achieve considerable risk reduction at reasonable costs. In this study both a qualitative and a quantitative approach were used to estimate the probability of CSF introduction for several regions in the EU and to determine which factors contribute most to the probability of CSF introduction. Both approaches were based on a pathway diagram (i.e. a combination of risk factors) constructed for CSF introduction into regions of the EU under a non-vaccination policy.

The annual probabilities of CSF introduction by exogenous pathways (risk factors) were quite low when compared with expert estimates. The probability of CSF introduction by direct and indirect contacts with wild boar was quite high, especially for Germany, France and Italy, as is the case for transport of live animals and swill feeding. Prevention and control measures should be developed based on these risk factors. This is in accordance with reality, as many primary outbreaks in these countries can be attributed to contacts with wild boars, contacts with other live animals and/or swill feeding (Chapter 13). The major cost and benefits of CSF introduction into (free) EU areas are unclear because (for many areas) the underlying (import/export) data are not available. Therefore, the 1997/1998 Dutch CSF outbreak was used for economic calculations (Chapter 14).

Two alternative emergency vaccination strategies with a marker vaccine that could have been applied in the 1997/98 Dutch CSF epidemic were evaluated in a modified spatial, temporal and stochastic simulation model, InterCSF. In strategy 1, vaccination would only be applied in order to overcome a shortage in destruction capacities. Destruction of all pigs on vaccinated farms distinguishes this strategy from strategy 2, which assumes the intracommunity trade of vaccinated pig meat. InterCSF simulates the spread of CSF between farms through local spread and 3 contact types. Disease spread is affected by control measures implemented through different mechanisms. Economic results were generated by a separate model that calculated the direct costs (including the vaccination costs) and consequential losses for farmers and related industries subjected to control measures. The comparison (using epidemiological and economic results) between the different emergency vaccination strategies with an earlier simulated preventive slaughter scenario led to some general conclusions about the Dutch CSF epidemic. Both emergency vaccination strategies were barely more efficient than the non-vaccination scenario. The intracommunity trade strategy (vaccination strategy 2) was the least costly of all three scenarios.

In particular, emergency vaccination (assuming a reliable diagnostic test and no relaxation of other control measures) seemed to be an effective strategy for reducing the size of an epidemic. Emergency vaccination alternatives were at least as effective as the optimal non-vaccination scenario. The worst iterations were never as severe as in the case of the non-vaccination scenario. The large number of preventively slaughtered farms in the delayed destruction strategy is a negative aspect of this strategy compared with/to the non-vaccination strategy. This effect mainly reduces the positive effect of a shorter epidemic. If we compare the intracommunity trade strategy with the non-vaccination strategy, emergency vaccination is clearly the tool to choose. Vaccination costs (which are of minor importance when compared to all other costs and losses) are mainly in competition with the cost of preventive slaughter, assuming no extra costs and losses for the post-vaccination zone. The intracommunity trade strategy avoids the destruction of a large number of healthy pigs, which can still be used for human consumption (Chapter 14).

Final comments and outlook

This chapter ends with some general remarks that relate to the entire project:

1. It is important to note that outbreaks of notifiable animals diseases could also have effects on other parts of the economy as a whole, due to both the side effects of disease control measures (e.g. the closure of footpaths harms the tourist sector) as well as interactions between economic sectors (e.g. price reductions for livestock products favour consumers). These ‘non-agricultural’ effects have not been quantified in our studies

because we did not aim to carry out a full social cost-benefit analysis (CBA). A full social CBA provides a framework for comparing disease control strategies but also includes difficulties. Many costs and benefits are by their very nature unquantifiable (e.g. the emotional problems of farmers whose animals had to be culled). Assigning monetary values to these costs and benefits is a major problem for a CBA and involves making subjective judgements.

2. The very inhomogeneous nature of the underlying data (such as in EUROSTAT) limited DPLA methods and indices for performing basic spatial analyses. The statistical (data definitions, size of municipalities, aggregation of data, etc.) harmonisation of this database is an urgent requirement. For some member states there is not enough data of sufficient quality to perform any spatial analysis whatsoever. Lack of detailed data on the exact location of animals hampers the calculation of *more advanced* indices that are necessary to define the regional concentration of animal densities still further. User-friendly software, linked to sound scientific methods are available but their application is severely limited because of the poor quality of the underlying data necessary as input to these systems.
3. This study used available knowledge to model the epidemiological and economic consequences of an outbreak. For this reason, the model was restricted to specific FMD and CSF strains. There was only limited knowledge available on the FMD and CSF virus transmission in the field between other susceptible animals. The FMD results can probably be roughly extrapolated to transmission in cattle however this is not valid for transmission in sheep and goats.
4. Another obvious knowledge gap concerned the possible reactions by importing countries. Our study showed that varying lengths of import bans had only a limited influence on economically optimal control strategies. Possible reactions by importing countries showed almost identical rankings of economically optimal and next-to-optimal strategies. The main limitation of these calculations is that they were based on changes in quantities due to import bans. Price and substitution effects are usually excluded in most economic calculations. Therefore, these results must be considered as the upper limits of export losses due to import bans.

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Valley (Italy) and the southern part of The Netherlands (Figure 4.1). The study areas were selected at a community level and represent a municipality or a cluster of municipalities with a minimum radius of 3 km. Considering this definition, the size and boundaries of the study areas in different countries were defined on a rather arbitrary basis. Convenience criteria were also taken into consideration. Areas were selected taking into account pig and cattle density: DPLAs had at least 250 pigs/km² and 150 cattle/km², while SPLAs had a maximum value of 150 pigs/km² and 50 cattle/km². This initial definition of DPLAs and SPLAs (Anonymous, 1995) was altered in a later stage of the project (Michel and De Vos, 2000).

Figure 4. 1 Geographical distribution, size and animal density of the selected study areas

