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/km^2 (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 outbreak[11]. 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 km^2, 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.

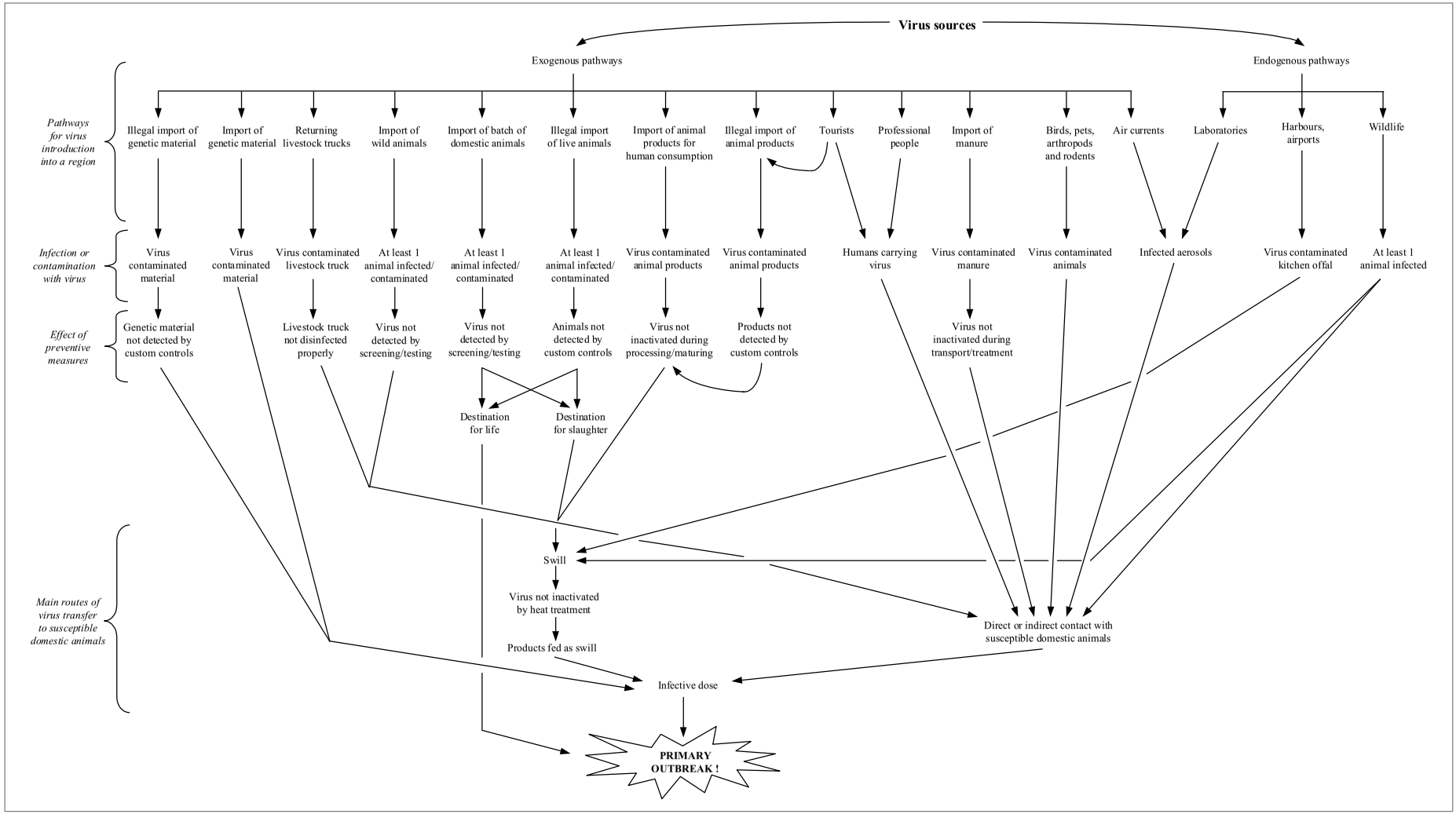
13.3 Pathway diagram

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.

	The Netherlands		Germany		Italy		Belgium		France	
	South	South-West	Süd-oldenburg	Hannover	Mantova	Rovigo	West-Flanders	Namur	Côtes d'Armor	Orne
Type of region[b]	DPLA	SPLA	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

	The Netherlands		Germany		Italy		Belgium		France	
	South	South-West	Süd-oldenburg	Hannover	Mantova	Rovigo	West-Flanders	Namur	Côtes d'Armor	Orne
Type of region[a]	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

	The Netherlands		Germany		Italy		Belgium		France	
	South	South-West	Süd-oldenburg	Hannover	Mantova	Rovigo	West-Flanders	Namur	Côtes d'Armor	Orne
Type of region[a]	DPLA	SPLA	DPLA	SPLA	DPLA	SPLA	DPLA	SPLA	DPLA	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	moderate	low	high	low	high	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):

$$Epidemics_{year} = 1 - \exp(-x/\beta) \quad (1)$$

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 occured 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; Crucière et al., 1998; Kern, 1998). The regions in which infected wild boar roam are the Bundesländer 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 fomites[12] 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
Import of pigs (numbers)[a]					
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
Export of pigs (numbers)[a]					
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
Import of pork products (metric tons)[a]					
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:

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

Figure 13.2 Schematic representation of model calculations for exogenous pathways

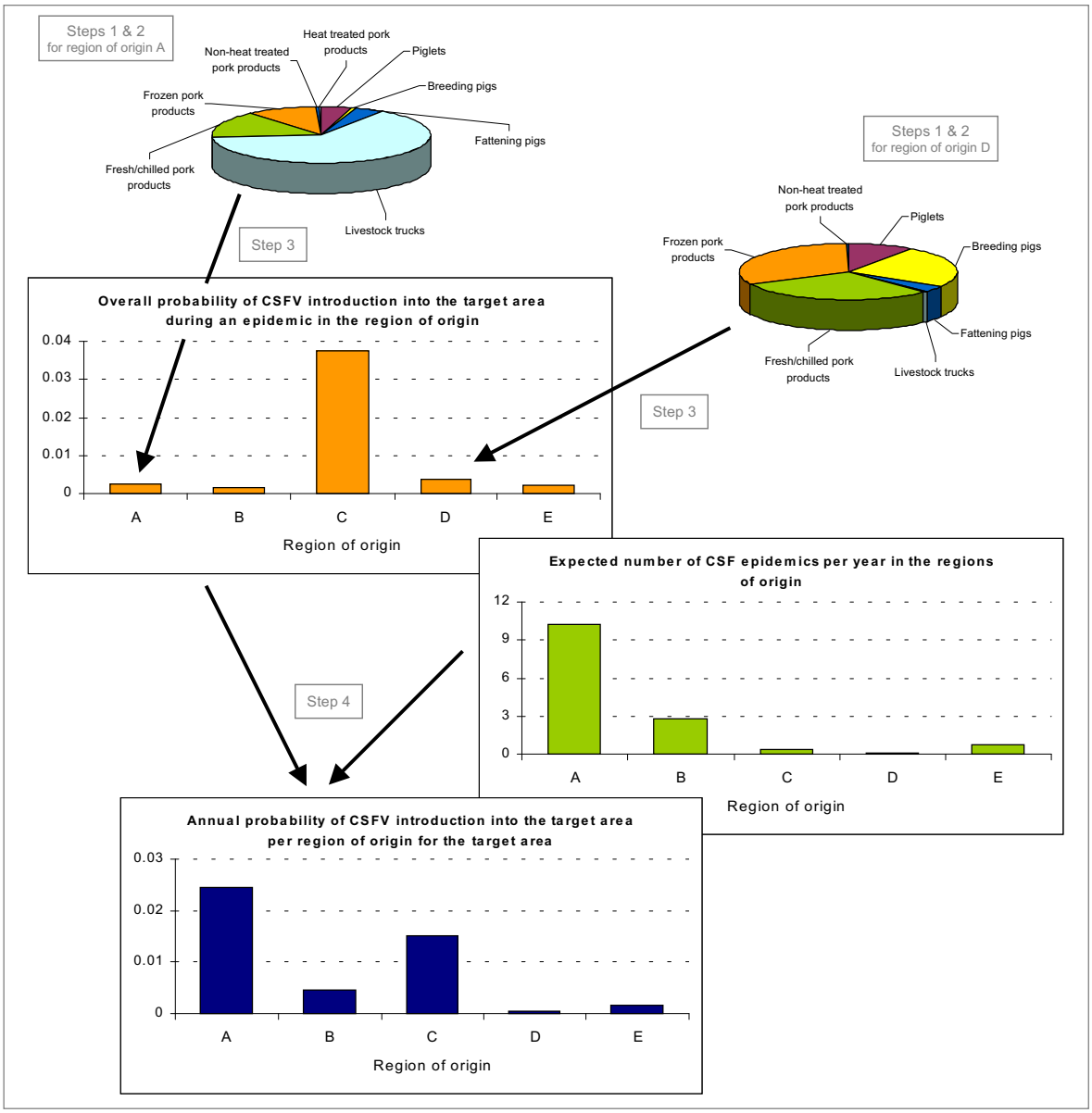
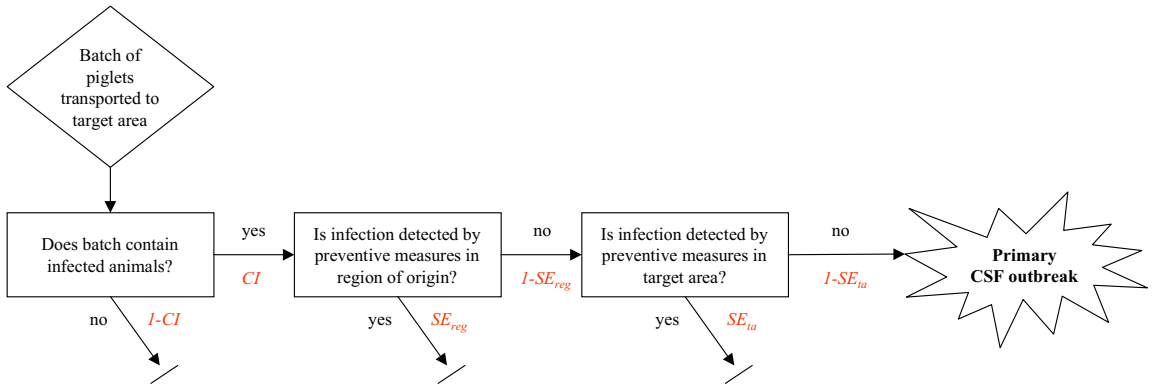


Figure 13.3 Scenario tree for the exogenous pathway 'import of batch of piglets'



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:

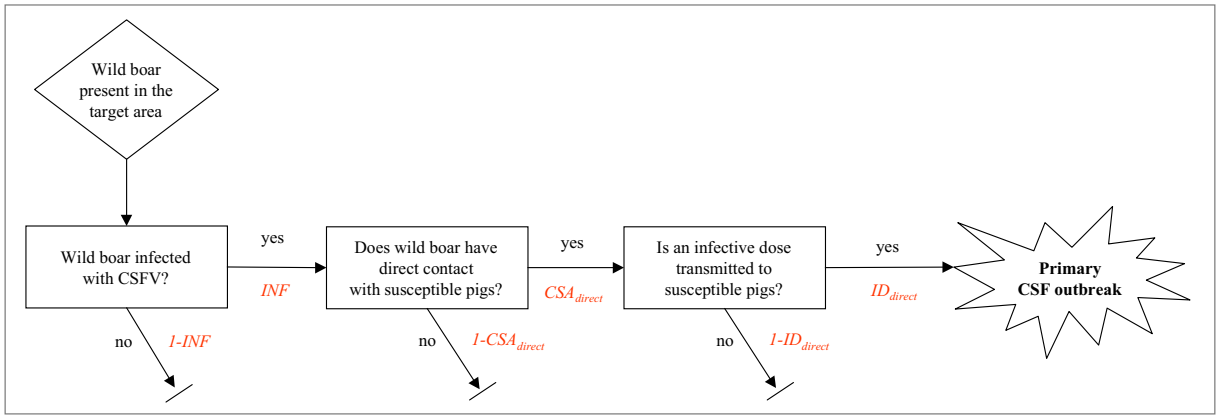
$$P_{\text{boar}} = INF * CSA_{\text{direct}} * ID_{\text{direct}} \quad (4)$$

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):

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

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).

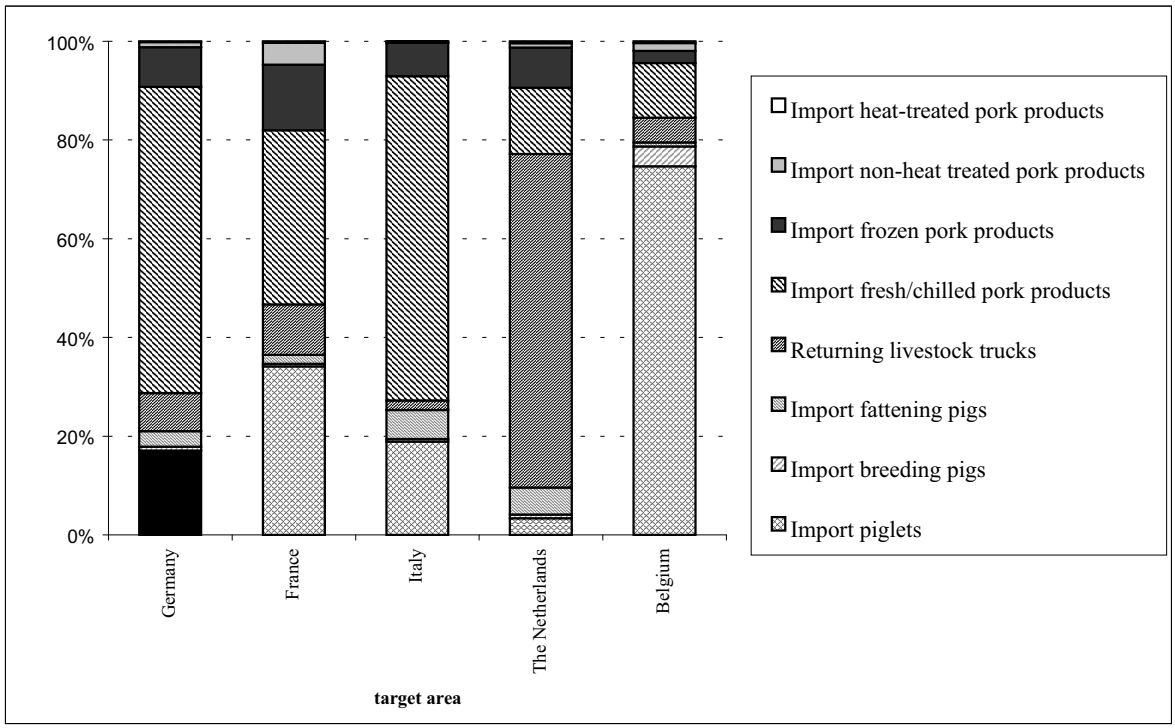
In general, The Netherlands, Belgium and Germany contribute most to the annual probability of CSFV introduction into the target areas (left column of graphs). The probability that CSFV will be introduced into one of the target areas during a single epidemic in Germany is, however, low when compared to 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 life 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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