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An analysis of a presumed major outbreak of pseudorabies virus in a vaccinated sow herd

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SUMMARY

We describe a major outbreak of pseudorabies virus (PRV) in a sow herd in which the sows were vaccinated simultaneously three times a year with a vaccine containing Bartha strain. Also in the associated rearing herd in which the gilts were vaccinated twice an outbreak of PRV occurred. The outbreak was analysed with mathematical models, statistical methods and Monte-Carlo simulation. Under the assumption that the outbreak started with one introduction of virus the reproduction ratio R_{ind} – as a measure of transmission of PRV between individuals – in the sow herd was estimated with a Generalized Linear Model to be 1·6. Also under the assumption of one introduction of virus R_{ind} in the rearing herd was estimated with a martingale estimator to be 1·7. Both estimates were significantly larger than 1. Mathematical analysis showed that heterogeneity in the sow herd, because of the presence of not-optimally immunized replacement sows could not be the only cause of the observed outbreak in the sow herd. With Monte-Carlo simulations, the duration of an outbreak after a single introduction of virus and $R_{ind} = 1{\cdot}6$ did not mimic the data and thus the hypothesis of a single introduction with $R_{ind} = 1{\cdot}6$ could also be rejected and R_{ind} is thus, not necessarily above 1. Moreover, with statistical analysis, endemicity in the combination of herds as a cause for the observed outbreak could be rejected. Endemicity in the rearing herd alone could not be excluded. Therefore, multiple introductions from outside and most probably from the rearing herd were possibly the cause of the observed outbreak(s). The implications for eradication of pseudorabies virus were discussed.

INTRODUCTION

A major outbreak of pseudorabies virus (PRV) was observed in a sow herd in the period December 1989 to April 1991. The sows were vaccinated simultaneously three times a year with a modified live vaccine containing strain Bartha suspended in an oil-in-water emulsion (O/W). In a previous study, no major outbreaks were observed in 99 sow herds vaccinated three times a year with a vaccine, containing strain 783 O/W [1]. These herds were located in a region in which an area-wide vaccination programme was applied. We concluded, based on a statistical analysis of the observed data, that it was unlikely that major outbreaks would ever occur in herds with similar husbandry conditions.

Possible explanations for the above described discrepancy are that the sow herd with the major outbreak differed from the previously studied sow herds in that: (1) it experienced *a single major outbreak*

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because (*a*) it had many first parity sows with a sub-optimal immunity because rearing stock was vaccinated only twice instead of thrice (heterogeneity in the herd), (*b*) it was vaccinated with vaccine strain Bartha O/W instead of strain 783 O/W and it may be that the Bartha strain O/W vaccine is less effective than the 783 strain O/W vaccine, albeit that the difference in terms of virus excretion after challenge was minimal or absent [2–4], but equality in reduction of virus excretion does not mean equality in reduction of transmission; (2) it experienced *multiple introductions* because it was (*a*) either linked to one rearing herd where PRV was possibly endemic or PRV was endemic in the combination of the two herds or (*b*) situated in an area in which neighbouring herds had outbreaks, because they were not well-vaccinated.

In the present study, we estimated the transmission of PRV within the sow herd and the transmission of PRV within the rearing herd and tested with the help of mathematical models, statistical methods and Monte-Carlo simulation the above described hypotheses.

MATERIALS AND METHODS

Data collection

The sow herd where a major outbreak was observed was a nucleus herd containing about 550 sows. The sow herd had a high annual replacement rate (80%) and a fixed relationship to one rearing herd where only gilts were reared from this sow herd whereas only gilts from this rearing herd entered the sow herd. The gilts were transported at 10 weeks of age to the rearing herd, and at 6 months of age they returned to the sow herd and were placed for 4 weeks in a quarantaine compartment, which also harboured the removed sows.

The vaccination regime applied in the herd in which the major outbreak was observed differed from that applied in a previous study [1]. In this herd, sows were vaccinated simultaneously three times a year with Suvaxyn Aujeszky I.N./I.M.+Suvaxyn O/W emulsion (strain Bartha K61, Fort Dodge Animal Health, Weesp, The Netherlands) intramuscularly instead of three times with Suvaxyn Aujeszky NIA3–783 +Suvazyn O/W emulsion (strain 783, Fort Dodge Animal Health Holland, Weesp, The Netherlands). Rearing gilts were vaccinated twice, at 10 weeks of age intranasally (Suvaxyn Aujeszky I.N./I.M.+Suvaxyn Aujeszky Diluent) and at 14 weeks of age intramuscularly (Suvaxyn Aujeszky I.N./I.M.+Suvaxyn O/W emulsion) and not three times with strain 783 O/W intramuscularly as was the case in the previously described study [1]. From May 1990 onwards vaccine strain 783 was used in the sow herd and in the rearing herd; gilts were now vaccinated twice intramuscularly.

During the study (from 1 Dec. 1989 to 1 Apr. 1991), blood samples were collected from all sows during their stay in the farrowing room and from the gilts when they arrived at the sow herd. The sera were tested in a commercially available gE-ELISA (Eurodiagnostics, Eurodiagnostica, Apeldoorn, The Netherlands). A seroconversion was defined as a positive test result from a formerly negative sow.

Modelling the dynamics of infection

To understand the possible causes of the observed major outbreak, it is necessary to consider in more detail the dynamics of a PRV infection in pig herds, i.e. how PRV is transmitted from pig-to-pig and from compartment-to-compartment. Transmission of an infection can be expressed by the reproduction ratio (R). This ratio is defined as the number of cases infected by one typical infectious case. From the definition, it follows, that an infection will fade out when $R < 1$ and an infection can spread when $R > 1$ [5]. This R can be measured between pigs (R_{ind}), but also between compartments of pigs (R_{comp}) [6]. In the latter case R_{comp} is defined as the total number of compartments infected by one typical infectious compartment during the time that the pigs in this compartment are infectious. When R at a lower level (e.g. individual) is > 1, the infection can still fade out when R at a higher level (e.g. compartment) is < 1.

In a closed group of pigs where R_{ind} is > 1, an introduction of the virus can lead to a major outbreak, but it is also possible that by chance the infection quickly fades out and thus only a minor outbreak occurs. In a closed group where R_{ind} is > 1 only minor outbreaks can occur, i.e. fade out is certain. If there is influx of new susceptible pigs into groups, again, for $R_{\text{ind}} < 1$ only minor outbreaks will occur. In contrast, when $R_{\text{ind}} > 1$ and there is influx of new susceptible pigs, the infection can become endemic, i.e. there is the possibility of a prolonged presence of infectious pigs. For a more extensive discussion of endemicity and extinction, see [7, 8].

The sow herd described in this study in combination with its rearing herd is a population, in which there is

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a continuous influx of new susceptible pigs by the birth of new piglets. The total population consists of several groups of pigs where pigs leaving one group enter other groups (Fig. 1). The following groups can be distinguished: (i) a group of sows in several farrowing compartments with their piglets; (ii) one compartment with sows for breeding and gestation; (iii) a group of weaned piglets in separate compartments per age group; (iv) the rearing herd: a group of replacement gilts in separate compartments.

The infection within compartments was modelled using a stochastic SIR model. In this model, two events can occur when infectious individuals (I) and susceptible individuals (S) are present in a population: infection $(S, I) \rightarrow (S-1, I+1)$ with probability $\beta SI\Delta t/N$ and recovery $(S, I) \rightarrow (S, I-1)$ with probability $\alpha I\Delta t$. It is assumed that pigs had random contacts with each other within the compartments. For a full description of such a model for PRV in pig herds, see [6]. For the modelling, we further assumed that there are also random contacts between the compartments, but there was no contact between the groups, except that animals are moved from one group to the next.

This stochastic S IR model can be studied using Monte-Carlo simulations of the whole model and also parts of the model. In addition, the SIR model can be studied by an analytic approach using reproduction ratios. Given the assumptions there is one R_{ind} value for each group. For the combination of herds, which consists of several groups of animals, R_{ind} is found by studying the next-generation matrix. This matrix describes, on a generation basis, the expected number of new cases that a certain type of newly infected pig causes and how these new cases are distributed over the different groups at the moment of infection. The matrix describes the transmission between individuals and therefore is R_{ind} the dominant eigenvalue of this matrix [9]. Using all information available at this moment [1, 10, 1] regarding transmission of PRV between pigs the matrix for the pig herd under study could be [12]:

To\from	Farrowing sows	Unweaned piglets	Weaned piglets	Breeding and gestation sows	Rearing Pigs
Farrowing sows	0·7	0·7	0·7	0·7	0
Unweaned piglets	0·7	0·2	0·7	0·7	0
Weaned piglets	0·7	0·7	??	0·7	??
Breeding and gestation sows	0·7	0·7	0·7	0·7	0
Rearing pigs	?	?	0	0	1.5

The elements of this matrix are very high estimates for each of the entries and thus it can be expected that the dominant eigenvalue of the actual matrix will be lower than the dominant eigenvalue of this matrix. For example, within a sow herd R_{ind} is estimated to be 0·7. Secondary cases, however, must be distributed over all groups. So, the individual R_{ind}s in the first and fourth row and column for sows in the farrowing and in the breeding and gestation compartments have been overestimated; the totalized number of these rows has to equal 0·7 per row. Moreover, the distribution of the mean number of secondary cases is unknown, because the transmission between compartments and between groups is unknown. Finally, it is possible that the R_{ind} estimated for herds vaccinated with strain Bartha O/W is different from herds vaccinated with strain 783 O/W.

In order to investigate how likely the different hypotheses mentioned in the introduction were as explanation for the major outbreak observed in the herd under study, we have to argue which (measurable) conditions have to be met for the hypotheses to be plausible:

re (1) 'Single major outbreak'

A single introduction of PRV in a pig herd can become a major outbreak when $R_{ind} > 1$. This might be true when the gilts entering the herd were less well protected because they were vaccinated only twice (heterogeneity in immunity). In that case it must be shown by using the next-generation-matrix that the not-optimally-protected first parity sows can bring R_{ind} above 1.

Therefore, we first estimated the transmission rate within the sow herd with a Generalized Linear Model (GLM [13]). In this estimation, it is assumed that the outbreak started with one introduction. The estimator for β (the transmission parameter) is:

$$\beta = \frac{[\text{number of infections per day}] \times N}{S \times I},$$

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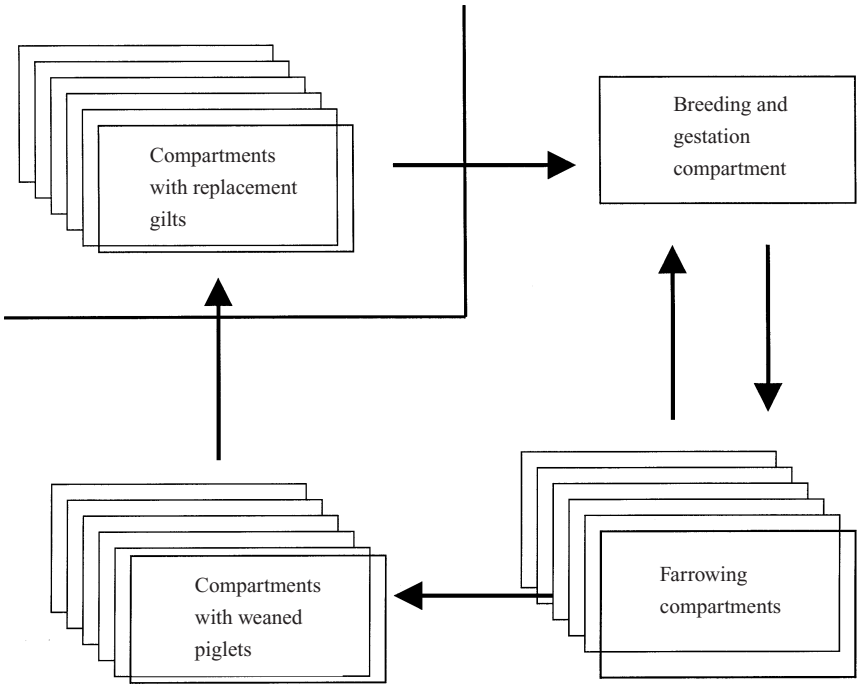

Fig. 1. Visual representation of the different groups of pigs present in the herd. Apart from the gestation and insemination compartment are all other distinct groups housed in separate compartments. The rearing herd is located at a separate site.

in which S is the number of susceptible sows, I the number of infectious sows and N the total number of sows present in the herd. This estimator is linear as a function of the explanatory variables after log transformation, therewith allowing for estimation with a GLM-approach with a log link function. Log $((S \times I)/N)$ is used as offset and the distributions of the error term was assumed to be Poisson. R_{ind} is calculated as β/α, in which $1/\alpha$ is the duration of the infectious period. The duration of the infectious period does not influence the estimate of R_{ind} [7].

A herd of well-immunized sows and not-optimally immunized replacement sows can be considered as a heterogenous population of two types. The R_{ind} of the whole sow population can then be described with the following submatrix [6]:

To\from	First parity sows	Other sows
First parity sows	$\gamma F_g P_g G_g P_g$	$\gamma F_s P_s G_g P_g$
Other sows	$\gamma F_g P_g G_s P_s$	$\gamma F_s P_s G_s P_s$

The symbols are explained in Table 1. The dominant eigenvalue of this matrix [9] is the R_{ind} of the sow herd. By calculating this R_{ind} we can assess the effect of having a not optimally immunized replacement population within the sow herd. One ingredient of this model, the transmission among the gilts in the rearing herd was estimated using a martingale estimator [13] modified by Van Nes et al. [1].

Alternatively, R_{ind} can be > 1, when vaccination with Bartha O/W is less effective than vaccination with strain 783 O/W. In that case the observed number of cases in time should be compatible with a single major outbreak. Therefore, we used Monte-Carlo computer simulation to derive the time course. In this model sows are assumed to have only contacts with sows in the same compartment, i.e. within the breeding and gestation compartment (115 days) and within the farrowing compartments. In this Monte-Carlo simulation there was no stochasticity on demographic processes, and the piglets were not taken into account. This was done because the R_{ind} between piglets is almost 0 and including the piglets would make the model unnecessary complicated. We varied the duration of the infectious period. Moreover, the infection in the simulation was started with a single introduction by making three sows in a randomly drawn compartment infectious, to avoid a large proportion of minor outbreaks. The outcomes of this simulation were the duration of the outbreak and the mean size of the outbreak. It is probable that PRV

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Table 1. *Symbols, meaning of the symbols and, where possible, the used parameter values*

Symbols	Meaning	Used parameter value
α	recovery parameter	
β	transmission parameter	
μ	replacement parameter	
t	time	
γ	effective contact rate	
F_s	infectiousness of sows	
F_g	infectiousness of replacement sows	
G_g	susceptibility of replacement sows	
G_s	susceptibility of sows	
P_g	fraction of the replacement sows in the herd	
P_s	fraction of the sows in the herd $(1-P_g)$	
R_{ind}	the mean number of pigs infected by one infectious pig	0·7 for sows, 1·7 for rearing pigs
l_d	mean duration of a sow in the breeding and gestation compartment	115
l_f	mean duration of a sow in the farrowing compartment	33
frac	fraction of the pigs that leave the farrowing compartment as piglets	0·9
l	expected number of infectious gilts that leave the rearing compartment	estimated by simulations
a	mean duration of infectious period	7 days

entered the herd more often, if the duration and final size after one introduction do not mimic the duration and final size of the data. Moreover, the estimation achieved by GLM is then incorrect and thus R_{ind} is not necessarily > 1.

re (*2*) '*Multiple introductions*'

Supposed that for the sow herd $R_{ind} < 1$ then the observed pattern might be due to multiple introductions of PRV in the sow herd. These multiple introductions might originate either from the rearing herd or from herds in the neighbourhood of the sow herd. The infection can become endemic in the rearing herd, when the R_{comp}, i.e. the transmission between compartments in the rearing herd, is above 1. The relation between the transmission between pigs and between compartments is [6]:

$$R_{comp} = R_{ind} \times \left(\begin{array}{c} \text{total number of infectious} \\ \text{pigs per compartment} \end{array} \right) \times \omega,$$

in which ω is the effective relative contact rate defined as the contact rate of a pig with pigs in a different compartment divided by the contact rate of that pig with pigs in the same compartment. The average total number of infectious pigs per compartment can be calculated from a SIR model. Then the critical value of ω can be calculated for which $R_{comp} \geqslant 1$.

If the infection is not endemic in the rearing herd, it could still be endemic in the combination of the sow herd and the rearing herd. A necessary, but not sufficient, condition for the infection to be endemic in the combination herds is that for this combination $R_{ind} > 1$. In addition, the infection must be able to persist in the combination of herds: this implies that an infection of a young piglet in the sow herd must eventually result in infectious gilt(s) entering the sow herd and also an infectious gilt entering the sow herd must result in infectious piglet(s) leaving the sow herd.

To test the likelihood of the latter hypothesis, we assumed that for the sow herd $R_{ind} = 0{\cdot}7$, the mean duration of a sow in the insemination and gestation compartment is 115 d. (l_d), the mean duration of the infectious period is 5 d. (a), I is the expected number of infectious gilts introduced in the insemination and gestation compartment, the mean duration of a sow in the farrowing compartment is 33 d. (l_f) and the fraction of piglets leaving the farrowing compartment in relation to the pigs present is 0·9 (frac).

For further testing this hypothesis, we also estimated from Monte-Carlo simulations the number of infectious gilts, which would leave the rearing compartment, when an infectious weaner pig was introduced into the rearing compartment. This simulation was done in two ways: (*a*) with a fixed duration of the infectious period, and (*b*) with a stochastically determined duration of the infectious period with the same mean duration. We further assumed that there was no mortality, the duration of the rearing period was 126 days and the pigs had random contact with

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each other. Also in these simulations we varied the duration of the infectious period.

RESULTS

Observed data

The number of seroconversions per week within the sow herd is represented in Figure 2. Because the sows were only sampled in the farrowing unit, the number of seroconverted sows is very variable. R_{ind} was estimated 1·6 (95% CI: 1·3–1·9) during the outbreak. The number of positive gilts at the end of the rearing period is given in Figure 3. R_{ind} in the rearing herd was estimated 1·7 (95% CI: 1·5–1·9).

Modelling the dynamics of infection

re (*1*) '*Single major outbreak*'

At first we tested whether the not-optimally immunized replacement sows could be the cause of this outbreak. R_{ind} of the sow herd in combination with the not-optimally immunized replacement sows derived with the help of a simple next-generation matrix, is

$$R_{ind,s} \times (1 - P_g) + R_{ind,g} \times P_g,$$

in which P_g is the proportion of not-optimally immunized replacement sows. When we assume that for the not-optimally immunized replacement sows $R_{ind,g} = 1{\cdot}7$ (as estimated in this study) and for the other sows $R_{ind,s} = 0{\cdot}7$ [1], the proportion of not-optimally immunized replacement sows has to be 0·9 supposed that $R_{ind} = 1{\cdot}6$ in the sow herd. An estimation of the mean proportion of not-optimally immunized replacement sows is 0·20, based on an annual removal rate of 0·80 and on the fact that a third vaccination is fully effective from 1 month after vaccination. This results means that a single major outbreak cannot be attributed to the not-optimally immunized first parity sows alone.

Furthermore we tested whether strain Bartha O/W was less effective in reducing transmission than strain 783 O/W by stochastic simulation of the outbreak in the sow herd under the assumption that $R_{ind} = 1{\cdot}6$. The results of these simulations are given in Table 2. It can be concluded that the mean number of infected individuals does not depend on the duration of the infectious period (given a same R_{ind}). The duration of the epidemic, however, depends highly on the duration of the infectious period (given a same R_{ind}). In experimental studies the infectious period is about 1 week, but most individuals become infected within the first days of the infectious period of the donor pigs [2], during which most virus is excreted by the infectious pigs. The observed outbreak is much more prolonged than would be expected according to the simulations. Accordingly, it can be rejected, assuming an infectious period of 1 week, that a single introduction can be the cause for this major outbreak and it can also be concluded that the estimation of R_{ind} with the GLM is incorrect and within the sow herd R_{ind} is not necessarily above 1. Moreover the hypothesis that $R_{ind} < 1$ is not rejected by these data.

re (*2*) '*Multiple introductions*'

As stated earlier, the infection in the gilt pool can become endemic, when $R_{comp} \geqslant 1$. The average number of infectious gilts per compartment calculated with a stochastic SIR model is 18. Thus ω must be $\geqslant 0{\cdot}033$. It is, however, not clear how this ω can be estimated in pig populations. From field data, infections of PRV in rearing herds fade out, but exact information on the time course of those infections is, however, not available.

Another hypothesis for explaining this outbreak was endemicity in the combination of herds. For this we calculated the probability whether an infectious weaning piglet could leave the sow herd and enter the rearing herd, when the infection was introduced into the sow herd by infectious gilt(s). The expected number of infectious sows that will leave the breeding and gestation compartment given that one or more infectious gilts from the rearing herd are introduced, is

$$((1/(1 - R_{ind})) - 1) \times I \times (1 - e^{-a/l_d}).$$

(The symbols used and the estimated values are given in Table 1). This is the expected size of the outbreak $(1/(1 - R_{ind}))$ minus the introductory gilt (because she has no chance to go to the farrowing compartment within the duration of her infectious period) times the mean number of introduced infectious gilts (I) times the probability of one infectious sow being transported to the farrowing compartment $(1 - e^{-a/l_d})$. Numerical result of this expected number is 0·14. This means 0·14 infectious sow will leave the breeding and gestation compartment, when 1 infectious gilt is introduced in this compartment.

The probability of an infectious piglet leaving the

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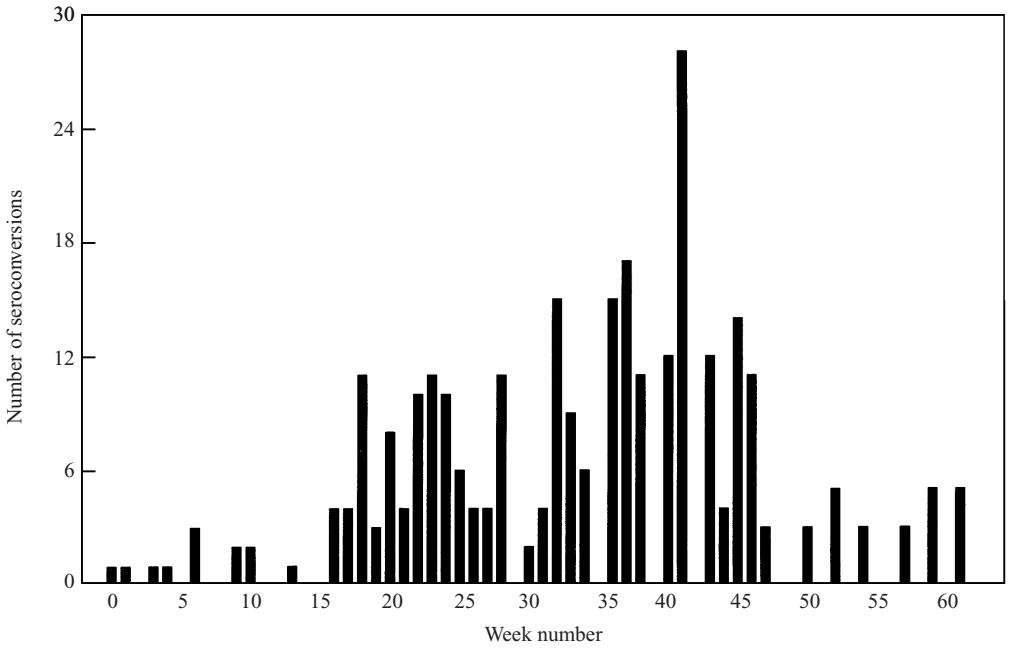

Fig. 2. Number of seroconversions in the sow herd per week. Week 1 is week 50 of the year 1989. Notice that the number of seroconverted sows is very variable, caused by the moment of sampling.

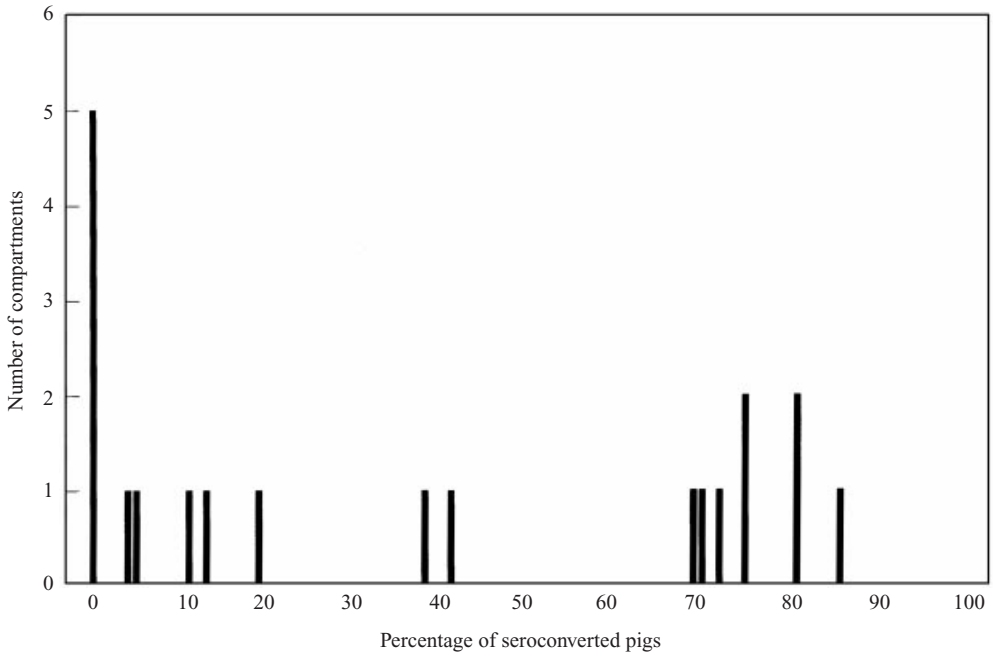

Fig. 3. Observed frequency distribution of the percentage of seropositive gilts at the end of the rearing period. Twenty compartments were sampled with 64 gilts each. Note that the distribution is bimodal, which means that minor and major outbreaks occurred.

farrowing room per infectious sow entering the farrowing room is

$R_{\mathrm{ind}}^{l_f/(0{\cdot}5a)}$ frac.

This is the expected number of pigs in the compartment that will be infectious at the end of the farrowing compartment ($R_{\mathrm{ind}}^{l_f/(0{\cdot}5a)}$), assuming that the other pigs get infected at half time of the infectious period, times the fraction of animals that leaves the compartment as piglets (frac). Numerically the probability one infectious piglet will leave the farrowing room, given one infectious sow entering, is 0·03.

So the total probability, that an infectious piglet will enter the weaned piglets compartment, given one

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Table 2. *Results of 500 simulations of PRV infections with a stochastic model in a sow herd of 529 sows and the relation between the duration of the infectivity and the duration of the epidemic. $R = 1{\cdot}6$ ($\beta/(\alpha+\mu)$) and the infection started with three infectious sows to minimize the percentage of minor outbreaks. The outcomes are the duration of the outbreak (t) and the number of susceptibles at the end of the outbreak (S_{end})*

β (per week)	α (per week)	μ (per week)	$t \pm$ S.E. (weeks)	$S_{end} \pm$ S.E.
0·203	0·125	0·01	180	473
0·42	0·25	0·01	79·8 ± 45·9	384 ± 93
0·82	0·5	0·01	46·7 ± 21·0	371 ± 105
1·6	1·0	0·01	31·5 ± 12·5	390 ± 106
3·2	2·0	0·01	23·9 ± 8·0	420 ± 90

Table 3. *Results of simulations in a rearing compartment with a constant length of the infectious period and an infectious period with exponential decay. Each compartment consisted of 64 gilts and R_{ind} was assumed to be 1·7. End results are the number of infectious gilts leaving the compartment*

No. infected gilts …	0	⩾ 1	Number of simulations
Constant infectious period			
Infectious period			
14	97%	3%	10000
10	> 99%	< 1%	10000
5	100%		10000
2	100%		10000
Length of infectious period with exponential decay			
Infectious period			
14	84%	16%	1000
10	97%	3%	2000
5	100%		2000

infectious gilt entering the breeding and gestation compartment is 0·004. So there is very little chance that a room in the rearing herd will be infected by introduction of an infectious weaned piglet as a result of infection of the sow herd by rearing gilts. Thus it seems highly unlikely that an infectious piglet will leave the farrowing compartment, when a infectious gilt is introduced into the herd.

Moreover, we have simulated a PRV infection in groups of rearing gilts. These results are given in Table 3. It is clear that the assumption for the duration of the infectious period has a great impact. With a fixed duration of the infectious period the epidemic does not last as long as with a stochastically determined duration with the same mean duration. Furthermore, it seems highly unlikely that the rearing herd will deliver many infectious gilts to the sow herd, on account that the infection in the rearing herd is started by introduction of infectious weaned piglets. The latter condition has to be met when there is endemicity of infection within the combination of herds. Moreover, infectious gilts have to be delivered to the sow herd very frequently in case of endemicity of infection.

Finally, multiple introductions can also be caused by the not-well-vaccinated neighbourhood. This is a possibility, because the 99 herds in a previous study were part of an area-wide vaccination programme. Disappointingly, this cause can not be assessed by model analysis or simulation. Moreover, information on these herds was, unfortunately, not available.

DISCUSSION AND CONCLUSIONS

In this article we described and analysed a major outbreak in a sow herd in which all sows were vaccinated simultaneously three times a year against PRV. This observation was, on first sight, in contrast with the study of Van Nes et al. [1] where in 99 vaccinated sow herds only minor outbreaks occurred and R_{ind} was estimated to be significantly smaller than 1. Possible explanations for this discrepancy were that the herd under study experienced (1) *a single major outbreak* caused by (*a*) not-optimally immunized replacement sows or (*b*) failure of the vaccine or (2*a*) *multiple introductions* by endemicity of infection in the combination of herds or by endemicity in only the rearing herd or (2*b*) multiple introductions from the vicinity. Assuming a single introduction, the R_{ind} in the sow herd was estimated with a GLM to be 1·6, R_{ind} in the rearing herd was estimated by martingale to be 1·7, both significantly larger than 1. Mathematical

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analysis showed that the not-optimally immunized first parity sows alone could not be the cause of a single outbreak in the sow herd. Moreover, with simulations, the hypothesis of a single introduction under the assumption that $R_{ind} = 1{\cdot}6$ was rejected, because the observed outbreak is much more prolonged than would be expected according to the simulations. Therefore, it can be concluded that the estimation of R_{ind} with a GLM is not valid and thus R_{ind} is not necessarily above 1. In addition, endemicity in the combination of herds was also unrealistic. Thus, multiple introductions from outside and probably from the rearing herd were the possible cause of these outbreaks. In addition, the analyses gave no indication that vaccination with strain Bartha O/W is less effective than vaccination with strain 783 O/W. In addition, there are no other reports from the field of suspected vaccine failure of the Bartha strain O/W.

Woolhouse et al. [14] described and analysed a supposed vaccine failure in farmed animals, concerning an outbreak of foot and mouth disease (FMD) in a dairy herd. They used a deterministic SLIR model for the estimation of R and, more important, their model was not scaled for population size and thus R increased for increasing population size, which is in reality not the case [15, 16]. A deterministic model simplifies a situation and is in our view only correct when sufficiently large numbers of animals are involved in the analysis, not only a large herd in total, but also both the number of susceptible and infectious individuals at any moment in time during the outbreak must be large. The stochastic SIR model used has advantages above deterministic models, because success of the contacts between pigs (for infection) depends on probabilities and thus when $R > 1$ not only major outbreaks can occur, but also minor outbreaks can occur [10] and the number of pigs in our study was rather small. Lastly, their conclusion, that the vaccination was insufficient is in our view preliminary, because all outbreaks described ceased about 10 days after revaccination and removal of infected cows.

An introduction of PRV into combined herds, i.e. sow herds with finishing and/or rearing pigs herds, can result in more infected pigs than an introduction into herds with only sows. Because $R_{ind} > 1$ in the rearing and/or finishing pigs, a major outbreak within those groups can occur and, moreover, the infection can persist and thus the massive spread of PRV among the rearing and/or finishing pigs can be the cause of repeated PRV-introductions into the sow herd. As it is more difficult to eradicate PRV in such a combined herd, those herds are a threat to eradication campaigns. Nevertheless, it is to be expected that in the future this type of herd will be predominant in The Netherlands.

For eradication it is important that not only the herd in question is well-vaccinated, but also the surrounding herds, because multiple introductions from outside can frustrate an eradication programme for a herd. Moreover, even when finishing herds and rearing herds are well-vaccinated, $R_{ind} > 1$ and thus major outbreaks within compartments can occur. By well-vaccination and reduction of the contact rate between compartments possibly R_{comp} can be < 1 [6]. Thus, by well-vaccination of rearing herds and finishing herds, the transmission within a region is reduced, because the number of infectious herds in a region is reduced, but also the number of infectious pigs within a herd is reduced.

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