Transboundary and Emerging Diseases

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ORIGINAL ARTICLE

A Simulation Model to Determine Sensitivity and Timeliness of Surveillance Strategies

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Summary

Animal surveillance systems need regular evaluation. We developed an easily applicable simulation model of the German wild boar population to investigate two evaluation attributes: the sensitivity and timeliness (i.e. the ability to detect a disease outbreak rapidly) of a surveillance system. Classical swine fever (CSF) was used as an example for the model. CSF is an infectious disease that may lead to massive economic losses. It can affect wild boar as well as domestic pigs, and CSF outbreaks in domestic pigs have been linked to infections in wild boar. Awareness of the CSF status in wild boar is therefore vital. Our non-epidemic simulation model is based on real data and evaluates the currently implemented German surveillance system for CSF in wild boar. The results show that active surveillance for CSF fulfils the requirements of detecting an outbreak with 95% confidence within one year after the introduction of CSF into the wild boar population. Nevertheless, there is room for improved performance and efficiency by more homogeneous (active and passive) sampling of wild boar over the year. Passive surveillance alone is not sufficient to meet the requirements for detecting the infection. Although CSF was used as example to develop the model, it may also be applied to the evaluation of other surveillance systems for viral diseases in wild boar. It is also possible to compare sensitivity and timeliness across hypothetical alternative or risk-based surveillance strategies.

Introduction

Animal health surveillance has to be reliable and informative. To ensure that implemented surveillance strategies are effective, the regular evaluation of such measures is advisable. When used for demonstration of freedom from disease sensitivity and the ability to detect an outbreak rapidly (timeliness) are attributes of surveillance systems that need regular evaluation (Drewe et al., 2013). In this study, sensitivity is defined as the probability of detecting a disease at a given level (95%) of statistical confidence if its prevalence exceeds a defined limit (5%) (Drewe et al., 2013). For timeliness, we used the definition given by Hoinville et al. (2013) that timeliness can be defined as the time between the introduction of an infectious agent and disease detection.

The aim of this study was to develop a simulation model to determine the sensitivity and the timeliness of different surveillance strategies for infectious diseases in wild boar. Similar to the study of Sonnenburg et al. (2016), where the possible impact of changes in sample size and sampling intervals on the probability of classical swine fever (CSF) detection was modelled, the present model is non-epidemic. In such a non-epidemic model, the spread of disease is not taken into account, but a static snapshot of an epidemic is considered. Additionally, a non-epidemic simulation is used to evaluate surveillance and not control strategies, as described in previous studies (Klinkenberg et al., 2005; Boklund et al., 2009; Thulke et al., 2011; Lange et al., 2012; Ribbens et al., 2012; Durr et al., 2013; Stahnke et al., 2013).

Classical swine fever (CSF) is a contagious viral disease that can affect all suid species (Kaden et al., 2005; Chander et al., 2014). The occurrence of CSF in a domestic pig population can inflict huge economic losses, which makes it

necessary to prevent the introduction of this virus into disease-free areas (Saatkamp et al., 1997; Meuwissen et al., 1999; Chander et al., 2014). Fritzemeier et al. (2000) found that CSF outbreaks in commercial pig holdings are often due to direct or indirect contact with infected wild boar. It is therefore vital to be aware of the disease status of wild boar populations, which is only possible through effective surveillance.

The strategy currently implemented in Germany for the surveillance of CSF in wild boar was used as a baseline for the model generated in this study. The strategy was developed to fulfil the requirements of Commission Decision 2002/106/EC of 1 February 2002; that is, the sample size for active surveillance required to demonstrate that the wild boar population is free from CSF should be sufficient to detect a seroprevalence of 5% in the population with ≥95% probability. According to Cannon and Roe (1982), at least 59 samples have thus to be examined per year and per defined geographical unit. In Germany, the geographical unit is the district ('Landkreis' or 'Kreis') within a federal state. It is also recommended by Commission Decision 2002/106/EC that both active and passive surveillance strategies should be concurrently implemented. All wild boar found dead, shot when displaying overt clinical signs of disease (termed 'shot sick') or involved in road traffic accidents should thus also be sampled and examined for CSF.

To parametrize the model, we used hunting, infection and population data from two federal states of Germany. These data served as a generic example of wild boar disease and may be replaced by any similar data. This could be data obtained from CSF surveillance in wild boar under different external circumstances or originating from surveillance for other infectious wild boar diseases.

Materials and Methods

Data background (input files) for the simulation model

Figure 1 gives an overview of the model structure and the input files.

Regional information

The modelled study region had an assumed size of 500 km², which reflects the average size of hunting areas in each of the two federal states of Germany (Rhineland-Palatinate and Mecklenburg-Western Pomerania), from where data were obtained to parametrize the model. As variation in the estimates of wild boar population size and density may influence the performance of surveillance, we specified nine different 'regional information' input files. The data used as estimates for wild boar populations and wild boar density are shown in Table 1. The estimations were justified by published information on wild boar density (Kaden et al., 2002; Ebert et al., 2012).

Population structure

To assign an age and gender to each animal, the input file 'population structure' was created on the basis of data published by Von Rueden (2006). The data originated from the

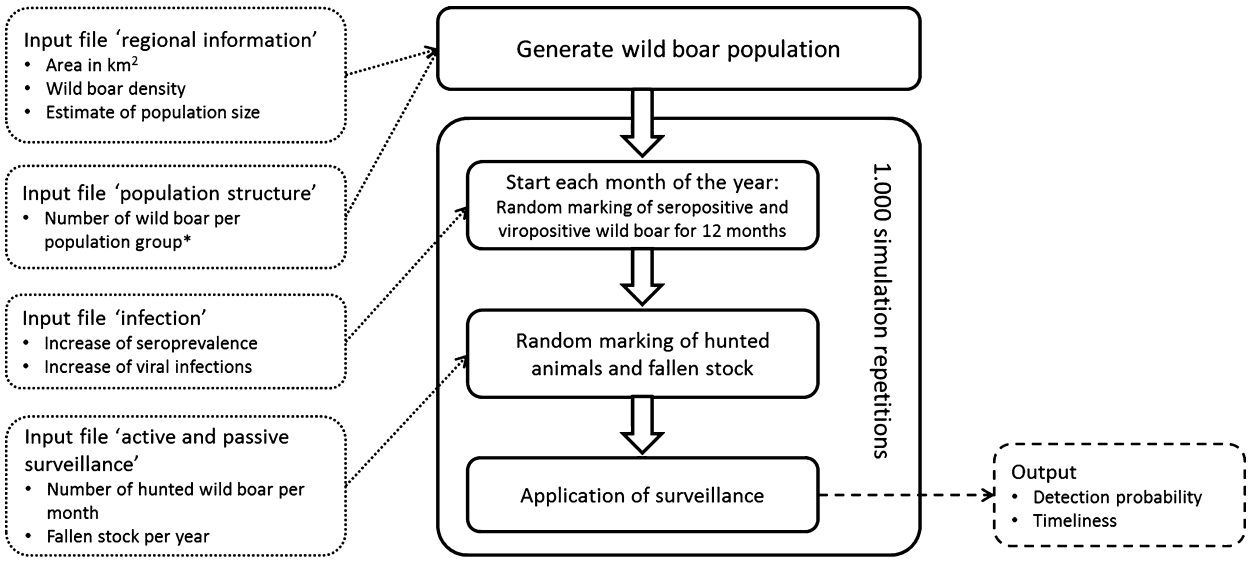

Fig. 1. Structure of the simulation model to estimate sensitivity and timeliness using the currently implemented surveillance strategy for classical swine fever in wild boar in Germany. Solid boxes describe the model flow. Dotted boxes represent input files. The dashed box states the output variables. *population group: number of individuals in each of the combinations of age classes, gender and cause of death.

Table 1. Overview of the nine different assumed wild boar populations and the corresponding wild boar densities with regard to the chosen study area of 500 km² used in the simulation study

Scenario	Assumed population within an area of 500 km²	Assumed density per km²
1	375	0.75
2	500	1
3	750	1.5
4	1 000	2
5	1 500	3
6	2 000	4
7	3 000	6
8	4 000	8
9	5 000	10

'Eifel', a region in Rhineland-Palatinate, Germany, and were collected between 1999 and 2004. The region had been part of a CSF surveillance area such that data for all hunted wild boar were recorded.

In the study of Von Rueden (2006), only the age and sex distributions of actively hunted animals were described. It was assumed that this distribution does not differ significantly within the subpopulation sampled by passive surveillance, and we used these data to determine the structure of the study population for active as well as for passive surveillance (Table 2).

For the proportions of animals in the different categories for causes of death, the estimates based on surveillance data of the federal state of Rhineland-Palatinate were used (Table 3). The data originated from the CSF wild boar surveillance database (http://public.csf-wildboar.eu/Default.aspx), which was collated during the period from 2007 until 2014. Based on these data, it was concluded that more wild boar were involved in road traffic accidents than found dead and that the proportion of wild boar shot sick is very small.

Infection

To estimate the serological and virus prevalence in the simulated infected area, data from the German federal state of Mecklenburg-Western Pomerania were used. Here, CSF had been present for almost two years (from 1993 to 1994) before vaccination started (Kaden et al., 2002). The data were provided by the State Office of Agriculture, Food Safety and Fishery of the federal state of Mecklenburg-Western Pomerania. The processed data set used for the data file 'infection' consisted of 17 492 records and included data from January 1993 to December 1994. Seroprevalence estimates were calculated on a monthly basis. An 11-month period from September 1993 to July 1994 was chosen and interpolated using the R function `spline`. Interpolation was carried out to control for the monthly fluctuations in detection by obtaining an estimate for a smooth increase of the seroprevalence (Table 4). The value of the starting month was set to 5.0% to simulate an outbreak, which would require detection with a probability of 95% by the current surveillance mechanisms according to Commission Decision 2002/106/EG. Due to a lack of CSF virus or genome detection data, we assumed that animals that seroconverted had been virologically positive one month before seroconversion. Therefore, the increase in virus prevalence from 1 month to the next was estimated as the increase in seroprevalence detected 1 month later. The age and sex distribution of the animals marked as serologically positive is shown in Table 5.

Table 2. Assumed population structure for wild boar available for active and passive surveillance as used in the simulation study. The data originated from the 'Eifel', a region in Rhineland-Palatinate, Germany, and were collected from 1999 until 2004

Age (year)	Gender	Percentage
0–1	Female	28
	Male	32
1–2	Female	15
	Male	14
>2	Female	6
	Male	5

Table 3. Assumed distribution of the proportion of animals within the four categories of the cause of death with regard to the simulated population. The distribution is based on surveillance data of the federal state of Rhineland-Palatinate. The data originated from the Classical Swine Fever wild boar surveillance database and comprised a period from 2007 until 2014

	Hunted	Found dead	Shot sick	Road traffic accident
Percentage of simulated population	95.7	1	0.3	3

Active and passive surveillance

To generate the input file 'active and passive surveillance', data from 24 districts of the German federal state of Rhineland-Palatinate were used. Information from the hunting years of 2003/2004 to 2010/2011 was included. Each hunting year starts on 1 April and lasts until the 31 March of the following year. Data on the number of actively hunted wild boar were provided on a monthly basis for each district. Initially, mean values for each month were calculated from the monthly data for the given years for each district. Secondly, hunting data were averaged for each month over the 24 districts and a percentage of hunted out of the estimated wild boar population was calculated for each month (Table 6).

Data on wild boar found dead (animal data available as a result of passive surveillance) were provided on a yearly

Table 4. Prevalence estimates used as a basis for interpolation to estimate the increase of seroprevalence (%). The prevalence estimates and 95% confidence intervals (in square brackets) are based on data from Mecklenburg-Western Pomerania (September 1993 to July 1994). Estimated values for the increase of the seroprevalence are given for months 2 to 12 after the start of infection. An initial seroprevalence of 5% in month 1 was assumed in the simulation model

Month	2	3	4	5	6	7	8	9	10	11	12
Seroprevalence estimates in % based on real data	6.6 [4.7; 9.0]	13.2 [10.1; 16.9]	12.2 [9.6; 15.4]	13.9 [10.6; 17.8]	21.8 [18.3; 25.6]	20.6 [17.0; 24.6]	20.0 [16.5; 23.9]	23.0 [18.8; 27.8]	30.3 [26.6; 34.2]	31.7 [28.2; 35.5]	30.8 [26.7; 35.0]
Interpolated seroprevalence estimates in %	6.6	8.1	9.7	11.4	13.7	15.9	18.1	20.7	23.5	26.3	29.1

basis for each of the districts for the hunting years 2005/2006 to 2008/2009. Values for the given years were averaged for each district. For each district, we divided the number of wild boar found dead by the population estimate per district. Averaging this relation leads to a proportion of 0.3% of the estimated wild boar population found dead. Population estimates were taken from studies of the Research Institute for Forest Ecology and Forestry of Rhineland-Palatinate (Ebert et al., 2012).

Simulation model

A wild boar population was generated in the simulated study region. The number of individuals in this region was given by the input file 'regional information' (Table 1). Each wild boar belonged to (i) one of three age classes (0–1, 1–2, >2 years), (ii) a gender category (male, female) and (iii) one of the four categories of the cause of death [hunted, shot sick, found dead, road traffic accident (RTA)] (Tables 2 and 3). Hunted animals were used to investigate active surveillance, whereas the other three categories pertaining to cause of death were used to investigate passive surveillance strategies. The age, gender and cause-of-death distribution of the generated population is given in the input file 'population structure'.

To compare seasonal variations within a year, we generated an ongoing transmission lasting for 12 months, which started within the study area in each of the 12 months of a year. To this end, individual animals were marked as seropositive and virus positive according to the numbers provided by the input file 'infection' (Table 4).

To simulate hunting, wild boar were randomly chosen for each month according to the proportion of hunted wild boar provided in the input file 'active and passive surveillance' (Table 6). The number of wild boar found dead (yearly estimates) was equally distributed over 12 months, and individuals were again randomly chosen and marked as found dead.

In the last simulation step, current surveillance strategies were applied. For active surveillance, 59 samples were randomly chosen within 12 months from all individuals that had been marked as hunted. Three scenarios were calculated as follows: (i) all samples were examined serologically, (ii) all samples were examined virologically, and (iii) all samples were examined serologically and virologically. For passive surveillance, all samples originating from animals marked as found dead, shot sick or involved in RTA were investigated virologically. The sensitivity and specificity of the diagnostic tests were assumed as perfect.

If a wild boar was marked as seropositive in the simulation matrix and hunted in the same or in a subsequent month, it was still regarded as seropositive after its death. We assumed that antibodies were detectable for life

Table 5. Distribution of the serological test results from Mecklenburg-Western Pomerania with regard to age and sex classes in %; neg: negative serological test results, pos: positive serological test results. The processed data set consisted of 17 492 records and included data from January 1993 to December 1994

Age class 1 (0–1 year)				Age class (1–2 years)				Age class 3 (> 2 years)			
Female		Male		Female		Male		Female		Male	
neg	pos	neg	pos	neg	pos	neg	pos	neg	pos	neg	pos
23.5	1.3	24.7	1.3	14.7	2.7	17.9	2.4	2.7	1.5	5.5	1.8

Table 6. Percentage of animals, which were actively hunted in the individual months based on real hunting data of the federal state of Rhineland-Palatinate. Data from 24 districts of this federal state of Germany were used, and information from the hunting years 2003/2004 to 2010/2011 was included

	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec
%	12.8	5.9	5.3	3.6	6.5	6.6	6.8	7.1	6.5	8.4	16.1	14.4

(European Food Safety Authority, 2009; World Organisation for Animal Health, 2014). For individuals marked as virus positive, a virological diagnosis was only considered possible within the same month as CSF virus is only detectable for 1–3 weeks post-infection (European Food Safety Authority, 2009; Weesendorp et al., 2010).

Detection probability and timeliness of the currently implemented surveillance strategy were then estimated and represent the output variables of the simulation study.

To calculate the detection probability, the number of simulation repetitions, in which the infection was detected within 12 months, was recorded for each starting month of the infection chain. The sensitivity was calculated for three different scenarios of the currently used active surveillance scenario (i.e. random sampling of 59 wild boar per year): (i) serological (ii) virological (detection of the virus, its antigens or genome) and (iii) serological and virological examination of samples. For passive surveillance (i.e. sampling of all wild boar found dead, shot sick or involved in a RTA), only the virological examination of samples was simulated.

A timeliness score was calculated on the basis of all simulation runs in which the infection was detected within 12 months after the start of the infection chain. For every start month, the number of simulation runs, in which the infection was detected within the month of disease introduction or the 11 following months, was recorded. As early detection is preferable, we adjusted for late detection by weighting early detection with higher scores. A weighted average score was calculated for each starting month of the infection chain. Detection within one month of infection was weighted by 12, the second month by 11 and so forth until detection after 12 months, which was weighted by 1. This weighted score was used to compare the timeliness of detection for outbreaks starting in different months. The same weighted timeliness score was calculated for each of the three active surveillance scenarios, that is (i) serological, (ii) virological and (iii) both serological and virological examination. The timeliness score was also calculated for the virological examination of samples resulting from passive surveillance.

Calculations and graphs were generated using the software R (www.r-project.org). Random sampling was performed using the R function sample. The R script can be obtained from the authors upon request.

Sensitivity analyses

We tested the influence of different population estimates (Table 1), different values for the increase of seroprevalence and varied estimates for active and passive surveillance on the outcome variables. The estimated seroprevalence was altered by changing the gradient of the prevalence and by varying the start prevalence from 0% to 7%, and the number of hunted wild boar was increased and decreased by 50%, respectively.

Results

A simulation model was developed to determine sensitivity and timeliness of a surveillance system. CSF in wild boar was used as an example, and the application of the model led to the following results.

Sensitivity

Active surveillance

For the currently used surveillance strategy (examination of at least 59 wild boar samples originating from active surveillance per year and defined geographical unit), we

simulated (i) serological, (ii) virological and (iii) both serological and virological examinations of 59 randomly chosen samples per year for all tested wild boar population estimates (Table 1). Testing samples by both methods (serology and virology) led to high values for the detection probability, ranging from 99.9% to 100.0%. Serological investigations of 59 randomly chosen samples per year led to the same range of detection probabilities, but slightly more cases resulted in a detection probability of 99.9%. Simulating only virological examination of samples led to detection probabilities ranging from 58.4% to 71.9%. The minimum, maximum and average values for this scenario for different wild boar population estimates were calculated on basis of the results for the 12 different starting months and are shown in Table 7.

Passive surveillance

The size of the wild boar population and the detection probability showed a directly proportional relationship when all samples originating from wild boar which were found dead, shot sick or involved in RTA, were analysed (Fig. 2). The values ranged from 1.3% to 35.3% (mean = 14.4%) and were thus clearly lower compared to the values resulting from active surveillance scenarios.

Timeliness

Active surveillance

We calculated the weighted timeliness score of each surveillance strategy and for each starting month of the infection chains. Afterwards, minimum, maximum and mean of the timeliness scores over the starting months of the infection chains were calculated for each surveillance scenario (Table 8). The combination of serological and virological examinations of 59 randomly chosen samples per year led to the highest values for timelines. When new infections started in October, November, December or January, the timeliness resulted in higher values; that is, infections were detected faster (Fig. 3). For active surveillance scenarios, timeliness showed the highest variability in the starting months when samples were examined only virologically (Fig. 3). A significant influence of the population estimates on the values for timeliness was not detected.

Table 7. Minimum, maximum and average detection probabilities for simulation of virological investigation of 59 randomly chosen samples per year. The values are given for the corresponding wild boar population estimates

Wild boar population estimates (number of wild boar)	Minimum (%)	Maximum (%)	Mean (%)
375	66.2	71.9	68.8
500	61.3	69.4	66.3
750	59.2	69.8	65.8
1 000	60.1	69.9	65.8
1 500	60.9	69.1	65.0
2 000	61.2	69.2	65.0
3 000	58.4	69.8	64.5
4 000	59.9	68.6	63.8
5 000	60.0	69.9	64.0

Passive surveillance

With an average weighted score of 0.085, passive surveillance resulted in the lowest values for timeliness (Table 8). However, the variation across the starting months of infection was less pronounced when compared to active surveillance scenarios (Fig. 3).

Sensitivity analyses

The model showed a stable behaviour regarding the outcome variables while performing sensitivity analysis by changing population estimates, the gradient of seroprevalence increase and values for active and passive surveillance (data not shown).

Discussion

A simulation model was developed to determine the detection probability and the period of time that it would take to detect CSF infection (timeliness). The advantage of our newly developed simulation model is its non-epidemic character. We avoid the uncertainty, which goes hand in hand with the use of epidemic spread models (Thulke et al., 2011; Lange et al., 2012; Durr et al., 2013). Instead of using assumptions about the epidemiological characteristics of an outbreak (e.g. contact rates, transmission routes and infectiousness), which are often difficult to define exactly, our model is based on real surveillance data. Most of the existing simulation models regarding CSF evaluate the impact of control measures in the case of an outbreak (Boklund et al., 2009; Thulke et al., 2011; Ribbens et al., 2012). By contrast, our model evaluates surveillance strategies that are implemented to demonstrate freedom from disease. Sonnenburg et al. (2016) also simulated different surveillance approaches for CSF in wild boar in times of disease freedom; however, they only focused on detection probability.

CSF surveillance

When examination of samples by serology alone was simulated, it was shown that detection probability and timeliness were not significantly different to approaches in which both virological and serological methods were employed. These results suggest that evaluating samples by serology is sufficient in times of disease freedom and can thus save

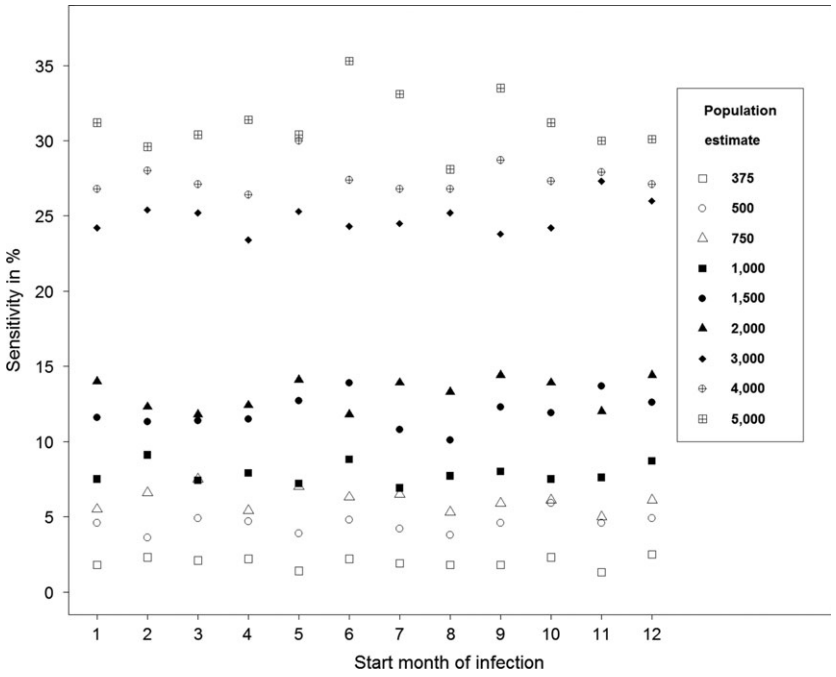

Fig. 2. Detection probabilities of the simulation of virological investigation of samples resulting from passive surveillance for different wild boar population estimates from 375 to 5 000 and for all starting months of infection.

Table 8. Minimum, maximum and average timeliness for the simulated active and passive surveillance scenarios

	Active surveillance			Passive surveillance
	Serological examinations	Virological examinations	Serological and virological examinations	Virological examinations
Minimum	0.113	0.078	0.118	0.053
Maximum	0.136	0.111	0.141	0.112
Average	0.125	0.096	0.129	0.085

resources. This approach is also consistent with the current EU regulations (Decision of the Commission of the 1st of February 2002/106/EG), where the serological examination of all required samples of actively hunted wild boar is recommended. Performing only virological investigations, however, is not advisable due to their low sensitivity and timeliness of detection. These results are probably due to the short time for which virus is detectable in blood and tissue samples (European Food Safety Authority, 2009; Weesendorp et al., 2010). By contrast, antibodies can be detected lifelong in an infected animal (European Food Safety Authority, 2009; World Organisation for Animal Health, 2014).

Sensitivity

Active surveillance

The detection probability of a newly introduced CSF virus infection within one year using the currently implemented surveillance system for CSF in wild boar reached almost 100%. This result shows that sampling on the basis of sample size calculations by Cannon and Roe (1982) yields satisfactory detection probabilities in a field situation. However, we simulated random sampling, which does not correspond to reality, where sampling usually depends on hunting, which is not a random process. Accordingly, it can be assumed that the detection probabilities are probably lower in a real surveillance setting. Nevertheless, the expected hunting bias could also be an advantage. Due to the high infectivity of CSF virus (Artois et al., 2002; Moennig, 2015), the prevalence in areas with a high population density is expected to be higher. Therefore, the probability of shooting more infected animals in a wild boar-dense area is much higher (Zanardi et al., 2003; Moennig, 2015).

Passive surveillance

We found a directly proportional relationship between the wild boar population density and the detection probability. This result reflects the effect of different wild boar population densities which is likely to affect the number of

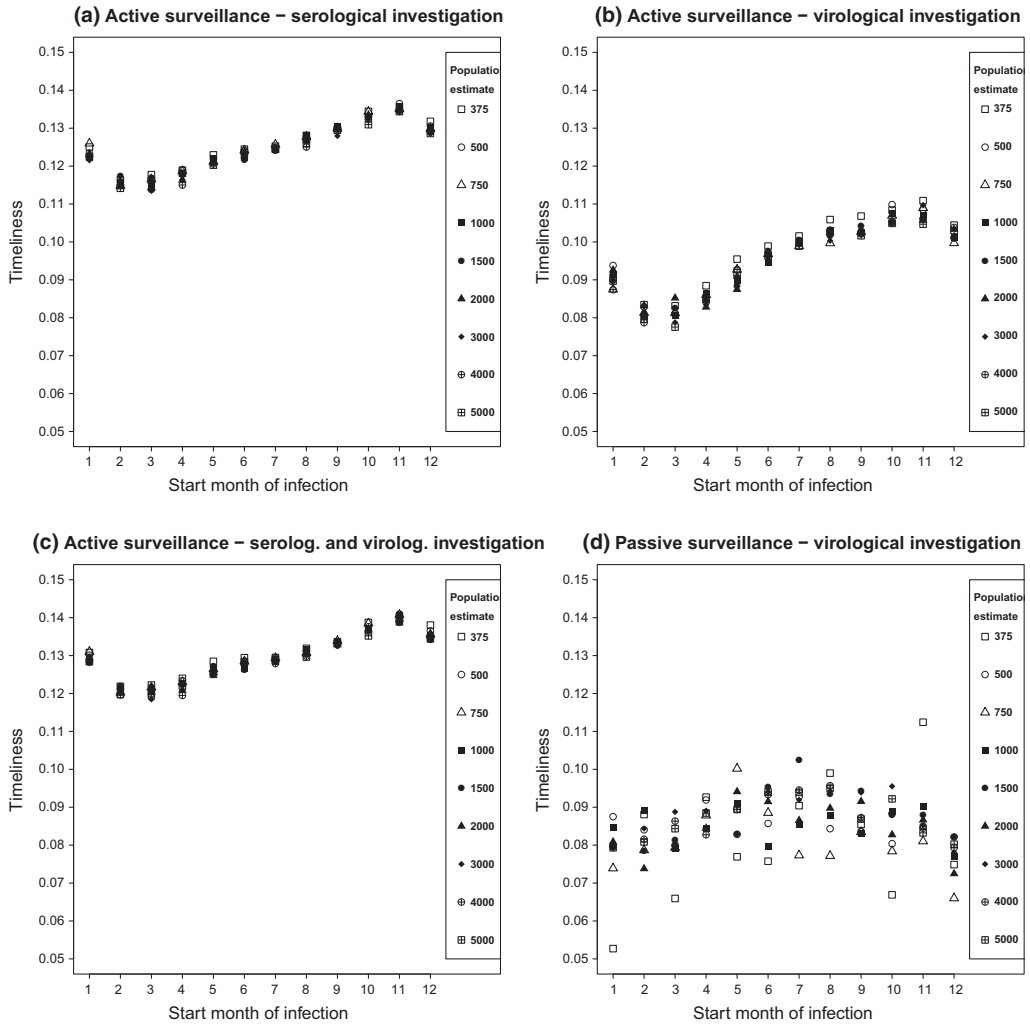

Fig. 3. Results of timeliness calculations for different population estimates for each starting month of infection for (a) serological investigation of 59 randomly chosen samples per year within the study area, (b) virological investigation of 59 randomly chosen samples per year within the study area, (c) serological and virological investigation of 59 randomly chosen samples per year within the study area and (d) virological investigation of samples resulting from passive surveillance.

animals found through passive surveillance as a fixed proportion was assumed to be sampled. Durr et al. (2013) found that for commercial pig holdings, the efficiency of surveillance is higher in areas with a large pig population. Nevertheless, the detection probability by passive surveillance is much lower when compared to active surveillance scenarios.

Timeliness

Active surveillance

When new infections started in October, November, December or January, they were detected faster (Fig. 3). This can be explained by the hunting season. During the hunting season, more samples were investigated, and therefore, infection was detected much faster. In contrast, timeliness showed considerably lower scores if the infection began in the months of February and March. This is due to the very small sample size obtained in the subsequent months. Based on these results, it can be concluded that increasing the number of samples throughout the year would most probably lead to overall better timeliness.

We demonstrated that combining serological and virological investigations is especially beneficial with regard to improving timeliness (Fig. 3). However, when sets of 59 samples per spatial unit were examined by serology only, we showed that the currently applied surveillance achieved the results required to demonstrate freedom from disease.

Passive surveillance

The wild boar population size and structure had no significant influence on the scores for timeliness. This may be explained by the fact that these values reflect the proportion of CSF-positive wild boar per month after the start of the transmission and are therefore independent of the population size.

Our study showed that passive surveillance alone would not be sufficient to meet the requirements of Commission Decision 2002/106/EG for infection detection. Although limited passive surveillance data were available for this study, these findings confirm the results of previous studies (Comin et al., 2012; Sonnenburg et al., 2016), which found that passive surveillance on its own is not enough to detect a disease outbreak reliably.

In general, the results of sensitivity and timeliness analyses showed that passive surveillance efforts may be improved. This might be possible through the implementation of financial incentives for hunters or the application of easier sampling methods. It would be reasonable to expand the evaluation of CSF surveillance in wild boar by including further attributes, for example the acceptability of the surveillance strategies by hunters. An economic evaluation would complete such a study.

Limitations and opportunities of the simulation model

Because all results were subject to the same errors in the performed analyses, we did not estimate exact errors in our study but compared relative performance. The number of iterations was set to 1000 as it led to sufficiently stable averaged results. Increasing the number of iterations would very likely have a negligible effect on the averaged values.

When interpreting the results, it has to be taken into consideration that the model is based on real data from CSF surveillance in wild boar of two federal states of Germany. Accordingly, the results refer to the conditions in these two federal states and do not necessarily hold a universal validity. In areas with different hunting traditions, environments or other wild boar population sizes or structures, the model parameters would have to be adapted and analysed correspondingly. Obtaining reliable data for population sizes in wildlife is difficult. It would be useful to implement more accurate methods for population estimates to improve the results of the model. Ebert et al. (2012) estimated the wild boar population density in some areas of Germany as >11 animals/km², whereas data from hunting bag (number of animals shot in a defined time period) analyses resulted in estimate of 2 animals/km² (Kaden et al., 2002). However, by varying the population density, we took these uncertainties into account.

Assuming that the numbers of wild boar found dead was equally distributed across all months was necessary because of the lack of monthly data. It is likely that more wild boar will be found dead in the hunting season and that sensitivity and timeliness decrease, if a CSF outbreak starts in early spring after the end of the hunting season.

To check the influence of other individual variables and their parameter range on the model, further sensitivity analyses were conducted. This was carried out in a comprehensive evaluation study (K. Schulz, M. Peyre, B. Schauer, J. Sonnenburg, C. Calba, B. Häsler, C. Staubach, and F. J. Conraths, in preparation).

The simulated size of the district was arbitrarily defined as 500 km². As shown by Sonnenburg et al. (2016), the informative value of a surveillance strategy depends on the chosen time period of sampling and on the size of the area. Therefore, our model may be easily adapted to other scenarios using other data sets.

The currently implemented surveillance strategy for CSF in wild boar stipulates a sample size of at least 59 samples per geographical unit and year. This number arises from the Commission Decision 2002/106/EG, which states that the sample size should be large enough so that a seroprevalence of 5% can be detected with a 95% confidence (Cannon and Roe, 1982). However, these calculations are valid for a scenario, in which an infinite wild boar population and the use of perfect laboratory tests are assumed. Neither of these assumptions applies in reality. It can therefore be expected that incorporating the knowledge of a finite population will result in higher detection probabilities or lead to a reduction in sample size without loss of information. Taking realistic data on test performance into account could result in a detection probability of lower than 95% if a sample size of 59 is maintained. However, the sensitivity and the specificity of the usually used tests (ELISA and virus neutralization test) for CSF are described to be above 98% (Langedijk et al., 2001; European Food Safety Authority, 2009). Therefore, the effect is likely to be small. Data on test performance were not considered in our model. The true uncertainty of the model outcome may therefore be higher than expected, as potential false-positive or false-negative test results have not been taken into account. The effect of this simplification is minimal (test sensitivity approximately 98%), consistent across surveillance strategies and therefore has a negligible effect on comparative performance.

Simulation models provide a sound method to evaluate the sensitivity and timeliness of a surveillance strategy in the absence of outbreak data. It is also possible to compare these values across different surveillance strategies. A broader evaluation study has been conducted, where a total of 69 different surveillance strategies for CSF in wild boar were developed and investigated (K. Schulz, M. Peyre, B. Schauer, J. Sonnenburg, C. Calba, B. Häsler, C. Staubach, and F. J. Conraths, in preparation).

The current study used CSF as an example to build a model of surveillance strategies and evaluate their efficacy. The model can be readily used as a template to investigate the two evaluation attributes of surveillance strategies for several diseases. Only the data basis would need adaptation with regard to the disease of interest. In contrast to other models, which are usually tailored towards the specific disease characteristics, only real surveillance data for the relevant disease are needed as input for our model. This allows the easy adaptation of the model to other diseases of wild boar (e.g. African swine fever or Aujeszky's disease).

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