

Studies on Modifications of the Sampling Interval and Size in the Framework of CSF Surveillance of Wild Boar

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Abstract

Classical swine fever is a serious viral animal disease affecting pigs and wild boar. In wildlife population surveys data are often reported as small-area counts in time and space. Resources are tremendous to detect low virological prevalence for CSF in wild boar. Nevertheless up to 1.2 / 5.1 samples per sqkm were taken per month / year in some regions of Germany.

A methodology was applied to show, that modifications of the sampling interval and / or the sample size will save resources. The probability of the detection of the infection can only be guaranteed until a certain limit.

Keywords: wild boar, surveillance, Classical Swine Fever.

Introduction

Classical swine fever is a serious viral animal disease affecting pigs and wild boar. It has caused major socio-economic damages in the EU during the last decades [1, 2].

Disease monitoring and disease surveillance systems (MOSS) are of increasing importance to veterinary authorities and policy makers because they allow the detection of changes in the prevalence of infectious diseases at an early stage and can lead to the fast implementation of control measures.

The present work was developed in the framework of the CSF_goDIVA project of the EU. It is part of the work package: early warning systems of CSF and surveillance in domestic pigs and wild boar.

Materials and methods

As study area we used 65 hunting grounds (about 230 sqkm) in the district Euskirchen in the Federal State North Rhine-Westphalia within the municipalities Euskirchen and Bad Münstereifel. We considered a time period of 72 month from 1st January 2004 until 13th December 2009 (state: 15th December 2009). During this time period 4652 virological investigations with 72 virological positive results were recorded.

We conducted a simulation study. We merged the monthly virological investigations into several sampling periods of 2, 3, 4 and 6 month length. Out of these merged investigations we sampled randomly 45 or 90 samples and tested if we found at least one positive sample. We repeated this sampling 100 times to estimate the probability of detection of the infection.

Result

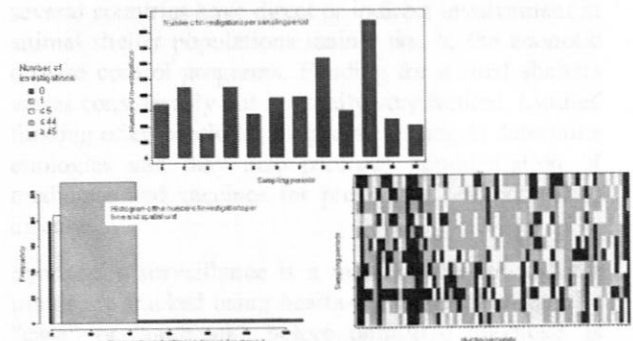
The histogram of the number of investigations per hunting ground shows that 36 of the 65 spatial units sampled more than 45 animals that are necessary to

detect 5% prevalence in a population of 100 animals with a confidence level over 95%. Separated for time and space, the overall numbers of investigations seem to be sufficient and detecting at least one case. But the distribution of the investigations in time and space show only 4 of 4680 fields contain more than 45 samples. Most of the combinations between time and space are empty or poorly investigated (without figures).

To check, if the number of fields with an adequate number of samples taken would increase and still detecting at least one case, we merged in the first step the time periods into several sampling periods of 2, 3, 4 and 6 month length.

Figure 1 shows the results for the 6-months sampling period and consists of 3 plots. The first two plots show the distribution of investigations over time and spatiotemporal as histogram. Furthermore, the number of investigations in time and space were plotted. The grid shows that also for the 6-months period there is a lack of data. Only 6 combinations of time and space reach the required sample size of 45 and higher. Nevertheless, the combinations with more than 5 samples increased significantly.

Figure 1: Distributions of investigations in time and combined in time and space for the 6-months sampling period



In the next step of our study, we simulated the sampling of 45 samples out of the merged investigations. We repeated the sampling 100 times and count the cases with at least one positive result within the sample. During the 2-months sampling period there were only 7 sampling periods with virological positive results. In the sampling simulations we found 3 out of these periods with a probability over 95%. Table 1 shows the results for all merged sampling periods. Only 25.0 to 42.8% of the virological positive sampling periods could be found with a sample size of 45 samples. Therefore, we enlarged the sample size to 90 samples per sampling interval.

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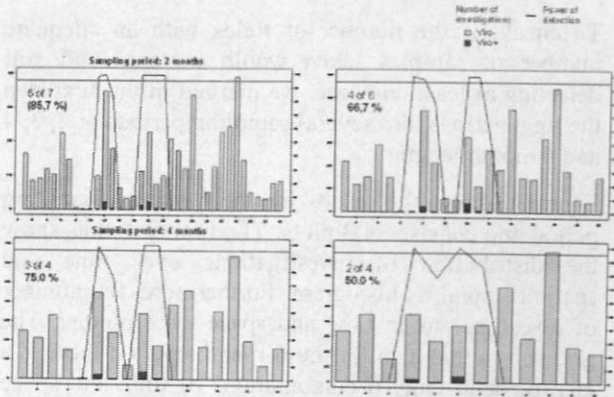
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Table 1: Simulation results with a sample size of 45

Sampling period	Probability of detection > 95%
2 months	3 of 7 viro+ sampling periods (42.8%)
3 months	2 of 6 viro+ sampling periods (33.3%)
4 months	1 of 4 viro+ sampling periods (25.0%)
6 months	1 of 4 viro+ sampling periods (25.0%)

Figure 2 shows the results for this study. With 90 samples per sampling interval we were able to find 50.0 to 85.7% of the positive sampling periods.

Figure 2: Results simulation study concerning the surveillance in the merged sampling periods with a sample size of 90



Discussion

Modifications of the sampling interval and / or size save resources. Nevertheless, the probability of detection of the infection can only be guaranteed until a certain limit.

In the study several sampling intervals and sizes were tested. An optimal scheme could be developed based on assumptions regarding population density and design prevalence. Furthermore, targeted sampling of certain age classes, passive sampling and ecological driven time periods will increase the probability of detection of the disease. In CSF free areas same methods could be applied for targeting serological positive animals.

References

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