Evaluation of the surveillance programme for Aujeszky's Disease (AD) in Norway

Innhold / Content

Forfattere / Authors
Madelaine Norström, Carl Andreas Grøntvedt, Anne Nordstoga, Petter Hopp

ISSN 1890-3290

Summary

The Norwegian Veterinary Institute have evaluated the surveillance programme of Aujeszky's Disease in Norway from 2004 to 2020 by using a scenario tree modelling approach (1). The results from this model indicates a probability of freedom for Aujeszky's Disease with 99.1% by the so called design prevalence of 0.002 in 2020.The model and assumptions for the model are described in the following.

Background

The EFTA Surveillance Authority (ESA) has recognized Norway's disease-free status for AD since July 1 1994, and has laid down additional measures for the trade of pigs and pork to protect Norway's Disease free status for AD. The additional measures are described in ESA Decision No 160/10/COL.
According to the Animal Health Law, Article 81(3)e, Appendix IV, Part V, Section 2: "The status free from infection with ADV as regards kept porcine animals of a Member State or a zone may only be maintained if:
(a) the requirements defined in points (a) and (c) of Section 1 continue to be fulfilled;
(a) vaccination against AD has been prohibited for kept porcine animals for the previous 12 months;
(c) in case, infection with ADV is known to be established in wild porcine animals, measures have been implemented to prevent any transmission of the ADV from wild to kept porcine animals.
(b) surveillance is carried out annually based on random sampling to allow at least the detection, with a 95% level of confidence, of establishments infected with ADV at a target prevalence rate of 0.2%. The number of blood or meat juice samples to be taken from the porcine animals kept in an establishment must allow at least the detection, with a 95% level of confidence, of seropositive animals at a target prevalence rate of 20%.
In Norway, the point b) applies and in order to evaluate the surveillance program for ADV we used a scenario tree modelling approach as described by Martin et al (2007).

Description of the surveillance program for Aujeszky's Disease in Norway.
The surveillance programme has been run from year 1994 as shown in Table 1. All the 104 nucleus and multiplying herds as well as the nucleus units of all 14 sow pools were included in the programme. Blood samples from ten adult swine in each herd were collected, usually at the farms, but occasionally also at the abattoirs. In addition, a selection of the remaining Norwegian swine herds was included in the programme. Until 2010, the samples from the sows were taken from randomly selected herds with ten samples per herd. The herds were weighted with higher weight on herds from densily populated areas. From 2011, sampling have been taken on animal level from abattoirs. Consequently, the number of herds tested increased even if the total number of samples were relatively stable. At the 16 largest abattoirs where more than 97% of the pig slaughter takes place, blood samples proportional to the number of sows and boars per herd, were collected. The samples were randomly collected from different herds and the sampling periods were evenly distributed throughout the year. Furthermore, at the six largest abattoirs, ten blood samples were collected from 60 randomly selected large fattening herds.

Laboratory analyses
All serum samples are tested for antibodies against ADV using a commercial blocking ELISA from Svanova (SVANOVIR® PRV gB-Ab) at the NVI. The test detects antibodies against glycoprotein B (previously glycoprotein II) found on the surface of the virus. Positive or inconclusive results in the surveillance programme are retested in duplicate with the same test method. Samples are concluded as negative if the retest give a negative result. Until 2017, virus neutralization test (VNT) was used as confirmation test when the retest was positive/inconclusive. Since 2017, positive samples are being sent to Statens Veterinärmedicinska Anstalt (SVA) in Uppsala, Sweden, for a second ELISA (SVANOVIR® PRV gE-Ab). If samples are still positive, VNT is performed.
In cases of positive or inconclusive VNT test results in the surveillance programme, at least 20 new pigs are resampled from the herd in question. If clinical signs of disease are absent in the herd, and all

resampled animals are negative for antibodies against ADV, a single positive or inconclusive sample in the surveillance programme are considered false positive.

Table **1**. Results from the surveillance for Aujeszky's disease (AD), transmissible gastroenteritis (TGE), porcine respiratory corona virus (PRCV), porcine epidemic diarrhoea (PED), porcine respiratory and reproductive syndrome (PRRS) and swine influenza (SI) from 1994 to 2019

Year	Total no. of herds	Herds tested	Animals tested	H1N1pdm		PRCV		Other viruses		Diseases included
				Animals positive[3]	Herds positive	Animals positive	Herds positive	Animals positive	Herds positive	
1994	7 799	1 112	12 010	-	-	0	0	0	0	AD, TGE/PRCV
1995	7 471	956	11 197	-	-	0	0	0	0	AD, TGE/PRCV, PRRS
1996	7 045	468	4 968	-	-	0	0	0	0	AD, TGE/PRCV, PRRS
1997	6 661	512	4 925	-	-	0	0	0	0	AD, TGE/PRCV, PRRS, SI, PED
1998	6 275	491	4 695	-	-	0	0	2[1]	1[1]	AD, TGE/PRCV, PRRS, SI, PED
1999	5 761	470	4 705	-	-	0	0	0	0	AD, TGE/PRCV, PRRS, SI, PED
2000	4 827	458	4 600	-	-	0	0	0	0	AD, TGE/PRCV, PRRS, SI
2001	4 554	472	4 972	-	-	0	0	0	0	AD, TGE/PRCV, PRRS, SI
2002	4 150	492	4 899	-	-	0	0	0	0	AD, TGE/PRCV, PRRS, SI
2003	4 005	483	4 783	-	-	0	0	0	0	AD, TGE/PRCV, PRRS, SI
2004	4 006	492	4 935	-	-	0	0	0	0	AD, TGE/PRCV, PRRS, SI
2005	3 762	468	4 644	-	-	1[2]	1[2]	0	0	AD, TGE/PRCV, PRRS, SI
2006	3 339	457	4 569	-	-	0	0	0	0	AD, TGE/PRCV, PRRS, SI
2007	3 010	456	4 641	-	-	0	0	0	0	AD, TGE/PRCV, PRRS, SI
2008	2 682	487	4 845	-	-	0	0	0	0	AD, TGE/PRCV, PRRS, SI
2009	2 546	452	4 724	131	20	0	0	0	0	AD, TGE/PRCV, PRRS, SI
2010	2 441	459	4 250	940	189	0	0	0	0	AD, TGE/PRCV, PRRS, SI
2011	2 346	730	4 713	2 216	353	0	0	0	0	AD, TGE/PRCV, PRRS, SI
2012	2 213	764	4 961	2 412	378	0	0	0	0	AD, TGE/PRCV, PRRS, SI
2013	2 178	737	5 038	1 417	338	0	0	0	0	AD, TGE/PRCV, PRRS, SI
2014	2 117	622	4 083	1 138	296	0	0	0	0	AD, TGE/PRCV, PRRS, SI
2015	2 141	568	3 764	993	280	0	0	0	0	AD, TGE/PRCV, PRRS, SI, PED
2016	2 180	564	3 824	952	271	0	0	0	0	AD, TGE/PRCV, PRRS, SI, PED
2017	1 955	548	3 804	695	225	0	0	0	0	AD, TGE/PRCV, PRRS, SI, PED
2018	2 038	533	3 598[3]	473	134	126[4]	30[4]	0	0	AD, TGE/PRCV, PRRS, SI, PED
2019	1 853	545	3 838[3]	526	153	532	118	0	0	AD, TGE/PRCV, PRRS, SI, PED
Total			131 985							

1 Two samples from one herd were seropositive for SI H3N2 in 1998 (probably infection from humans)
2 One sero-positive sample for PRCV in 2005 (probably unspecific reaction).
3 Maximum 5 influenza A positive samples per submission were followed up with a HI-test to identify the influenza strain.
4 In addition to routine surveillance for PRCV, NVI also detected 238 positive pigs in 30 positive herds (27 in Rogaland, 1 in Vest-Agder and 2 in Hedmark).

Materials and methods

Terminology

The abbreviations, variables and specific terms and their meaning used in this report are explained in Table 2.

Table 2. Description of abbreviations used in the report.

Abbreviation	Description
SSC	**Scenario tree component**
CSe	**SSC sensitivity**

CSeU	**SSC unit sensitivity (unit herd/flock or group)**
P*	**Design Prevalence**
P*$_H$	**Among group design prevalence**
P*$_U$	**Within group design prevalence**
Pr ()	**Probability of…**
PIntro	**Probability of infection being introduced into the population during a time period.**
PostPFree	**Posterior probability of population being free of infection at P***
PriorPInf	**Prior Pr (population infected at P*)**
PostPInf	**Posterior Pr (population infected at P*)=1- *PostPFree***
PrP	**Proportion of…in the SSC reference population**
***Pr*SSC**	**Proportion of…among the units actually included in the SSC.**
R	**Relative risk**
RR_	**Risk Relative to the lowest risk branch (for which RR_is 1); or**
AR_	**Adjusted relative risk**
EPIH	**Effective probability of infection for a group (=*P*$_H$* x *any applicable AR*)**
EPIU	**Effective probability of infection for a unit within an infected group (=*P*$_U$* x *any applicable AR*)**
SeH	**Group level sensitivity=Pr(positive|infected) for a group in the SSC**
SeU	**Unit sensitivity Pr(detected|infected) for a single unit**
SSe	**Surveillance system sensitivity**
TP	**Surveillance time period**
Unit	**The surveillance unit: the basic unit processed in the SSC (could be individual animal or herd/flock)**
OIE	**World Organization for Animal Health**
RPS	**Registry of Production Subsidies**
SSB	Statistics Norway

Data sources

The following data sources were used to calculate the population size and categorize the Norwegian swine population into production types: the Registry of Production Subsidies (RPS, Norwegian Agricultural Authority, Oslo), Statistics Norway (SSB, Oslo), and the Agricultural Property Register (Norwegian Agricultural Authority, Oslo).

Description of the methodology and assumptions

The probability that the swine population in Norway was free from Aujeszky's Disease by the end of 2020 was calculated using scenario tree modelling (1). In short this approach, can be described as constructing an event tree for each surveillance system component where the testing regimes and the probability of an outcome being positive (infected) are calculated based upon the assumption that the infection is present at the specified design prevalences. The scenario tree for Aujeszky's disease is presented in Figure 1 and the testing regime is presented in Figure 2.

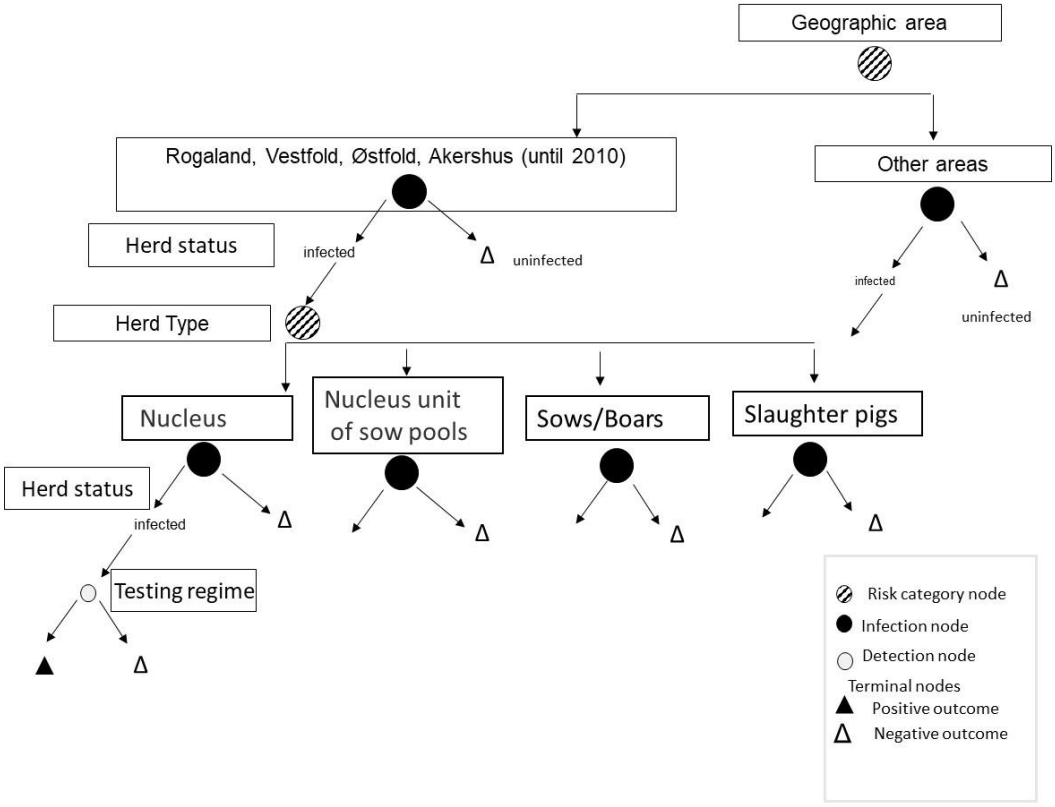

Figure 1. The scenario tree with the categorization of surveillance system components in Norway used in the scenario tree model for the calculation.

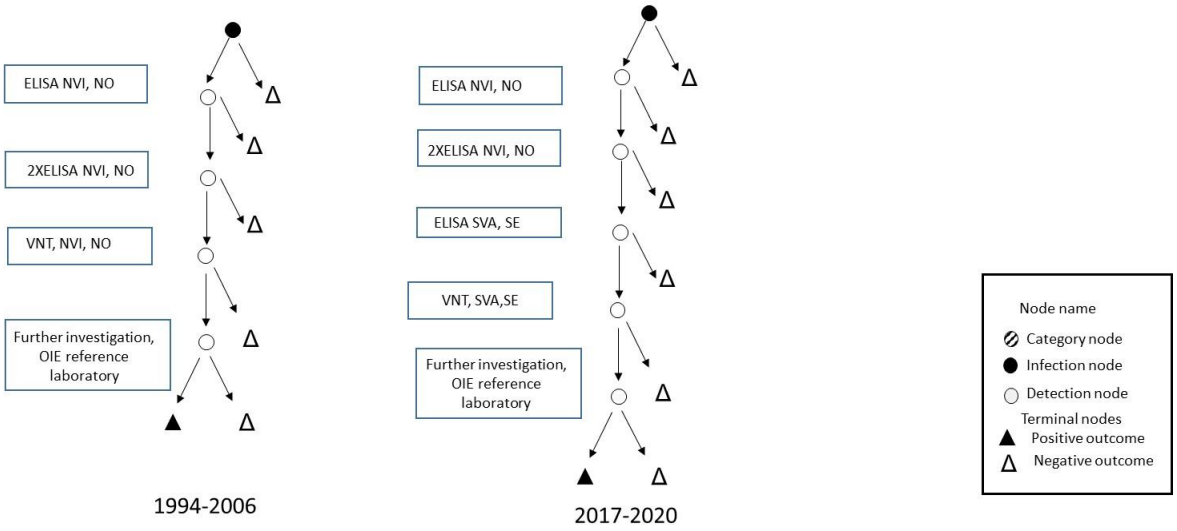

Figure 2. The testing regimes for Aujeszky's Disease, from 1994 to 2006 and from 2017 to 2020, respectively.

The model used a herd design prevalence (P^*_H) of 0.2% and a within herd design prevalence (P^*_U) of 20% (Table 3.); which means that the model will be able to estimate "the freedom from disease" if the disease would be present in the Norwegian swine population in less than 0.2% of the herds and detect seropositive animals within a herd if the prevalence is less than 20%; which is the required design prevalences as described in the background. All the other parameters included in the model are presented in the Table 3. The sensitivity of the different tests are based on the manufactures (SVANOVA.SE) own data.

Table 3. The parameters and their estimates used in the scenario tree model of Aujeszky's Disease in Norway (2004-2020)-

Parameters	Inputs	Distribution	Notation
Herd level design prevalence	0.002	fixed	P*H
Within herd design prevalence	0.2a	fixed	P*U
Relative risk; geographical area*	1.5	fixed	RRGeo
Relative risk, farm type*	2.0	fixed	RRFarm
Sensitivity on individual blood samples ELISA	0.999	Beta (675,1)	SeELISA
Sensitivity on individual blood samples ELISA at SVA from 2017 and onwards	0.999	Beta (675,1)	SeSVAELISA
Sensitivity on virus neutralisation test	0.955	Beta (x,1)	SeVNT
Sensitivity of the further investigations OIE reference laboratory	1	fixed	SeInv
Prior (pre surveillance) probability of infection	0.5	fixed	PriorPInf
Probability of introduction (per year)	0.01	-	PIntro

*The relative risks were set to 1 for each category as well as to 1.5 for the Geographical area and Farm type, respectively to assess the sensitivity of the model.

A set by AHL, Article 81(3)e, Appendix IV, Part V, Chapter 2, Section 2, 1.(b)

B with and without risk factors included

Due to possible differences of risk between different geographical areas based on historical information on traffic and higher density of herds, and between different herd types, we categorized the herds according to their geographical locations as well as in relation to their farm type. The risk categories were divided into Geographical area (high risk (H) vs low risk (L)) as well as farm type (high risk (H) vs low risk (L)). Because there has been some changes in the administrative boarders of both counties and municipalities in 2020, we decided to simplify the analyses by using the new administrative boarders of county to replace the previous ones. Thereby some of the herds (n=) were falsely categorized as high risk herds in relation to geographical location due to this change. Further, the number of farms and number of primary samples tested within each SSC (2004 to 2020) included in the scenario tree model are presented in Table 3.

Table 4 The number of farms and number of primary samples (samples) tested within each surveillance system component since 2004 included in the scenario tree analyses.

	Surveillance system component							
	HGeoHFarm		HGeoLFarm		LGeoLFarm		LGeoLFarm	
	No. of							
Year	herds	samples	herds	samples	herds	samples	herds	samples
2004	48	501	158	1582	166	1640	118	1203
2005	45	446	157	1564	156	1527	110	1107
2006	37	384	163	1641	161	1568	95	962
2007	42	423	174	1841	153	1515	87	849
2008	39	427	186	1848	182	1774	80	793
2009	35	353	164	1689	166	1643	87	1023
2010	33	342	168	1420	171	1627	87	861
2011	29	398	257	1666	368	1881	81	850
2012	27	381	258	1477	389	2155	74	989
2013	25	374	262	1600	377	2088	73	975
2014	28	408	206	1208	313	1541	75	925
2015	24	396	188	1055	283	1491	64	823
2016	37	461	174	1028	289	1412	64	919
2017	16	267	200	1278	260	1373	62	875
2018	22	403	181	971	266	1336	66	988
2019	25	433	184	1048	270	1406	67	952
2020	25	259	169	1025	241	1390	52	496

Simulation
The model was run in R version 4.03 (2).The model were run 1000 iterations for each of the SSCs.

Sensitivity analysis
The sensitivity of the model were tested by varying the parameters; risk of introduction and relative risk estimates in relation to geographical area or farm type.

Results

The total mean sensitivity for each of the SSCs HGeoHFarm, HGeoLFarm, LGeoHFarm, LGeoLFarm were 0.96, 0.78, 092 and 0.70, respectively. The estimated mean value of probability of freedom from Aujeszky's in the swine population was above 99.0 % from 2007 and increased to 99.5 in 2010 and then decreased to 99.1%

(95% Credibility interval: 99.12-99.13) in 2020 (Figure 1). The sensitivity analyses showed that the estimates are rather stable regardless of defining special parts as high risk groups or not. Further, the estimates increased/decreased if the risk of introduction increased substantially.

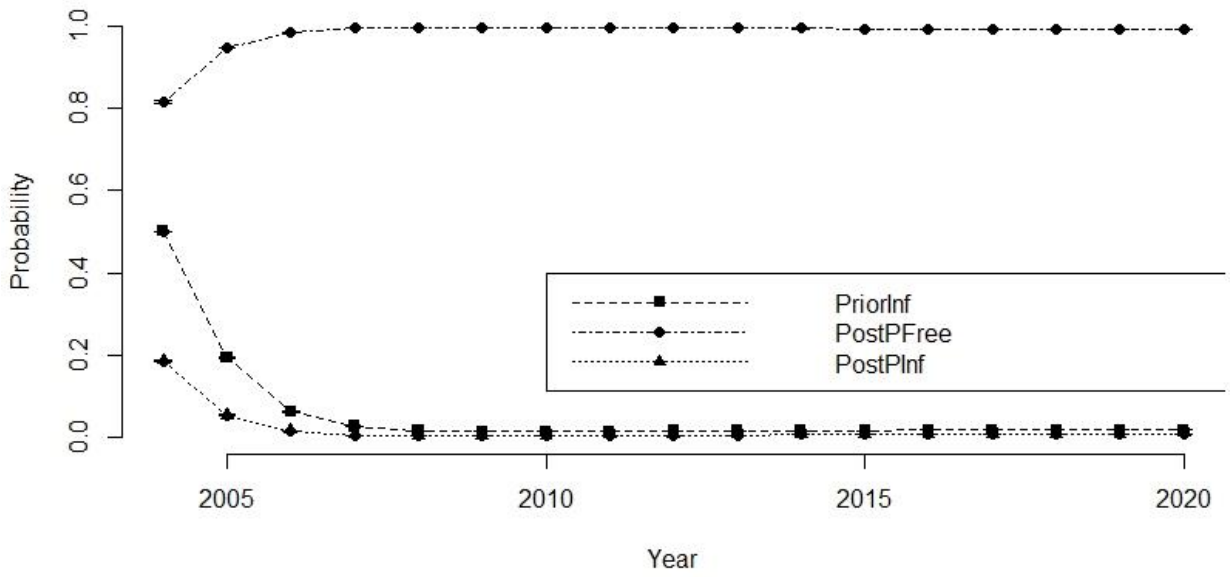

Figure 1. The results from the Scenario tree modelling of Aujeszky's Disease from 2004 to 2020, showing the annual mean Probability of Freedom (PostPFree), the mean Probability of infection being introduced into the population (PriorInf) and the mean Posterior Pr (population infected at a design prevalence of 0.002)=1- *PostPFree*.

Conclusion

The results from the scenario tree model support that the Norwegian swine population is "free from" (i.e below the between herd design prevalence rate of 0.2% and the within herd prevalence rate of 20%) Aujeszky's Disease with 99% confidence

References

1. Martin PA, Cameron AR, Greiner M. Demonstrating freedom from disease using multiple complex data sources 1: a new methodology based on scenario trees. Prev Vet Med. 2007;79(2-4):71-97.
2. Team RC. R: A language and environment for statistical computing. : R Foundation for Statistical Computing,Vienna, Austria.; 2020 [Available from: https://www.R-project.org/.