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Estimation of the probability of freedom from Bovine virus diarrhoea virus in Norway using scenario tree modelling

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ABSTRACT

Disease caused by Bovine virus diarrhoea virus (BVDV) is notifiable in Norway. An eradication programme started in 1992. The number of herds with restrictions decreased from 2950 in 1994 to zero at the end of 2006. From 2007, the aim of the programme has been surveillance in order to document freedom from the infection. To estimate the probability of freedom from BVDV infection in the Norwegian cattle population by the end of 2011, a scenario tree model of the surveillance program during the years 2007–2011 was used. Three surveillance system components (*SSCs*) were included in the model: dairy, beef suckler sampled at farms (2007–2010) and beef suckler sampled at slaughterhouses (2011). The design prevalence was set to 0.2% at herd level and to 30% at within-herd level for the whole cattle population.

The median probability of freedom from BVDV in Norway at the end of 2011 was 0.996; (0.995–0.997, credibility interval). The results from the scenario tree model support that the Norwegian cattle population is free from BVDV. The highest estimate of the annual sensitivity for the beef suckling *SSCs* originated from the surveillance at the slaughterhouses in 2011. The change to sampling at the slaughterhouse level further increased the sensitivity of the surveillance.

1. Introduction

Bovine virus diarrhoea (BVD) is caused by bovine virus diarrhoea virus (BVDV) in the genus pestivirus. The virus is the cause of mucosal disease (MD) and haemorrhagic syndrome, but the economically most important manifestation of the disease is related to infection in pregnant animals, which may result in embryonic death, abortion and congenital defects (Radostitis et al., 2000). If the dam is infected during day 42 and 125 of the pregnancy, persistently infected calves may be born (Radostitis et al., 2000).

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These are considered to serve as the main reservoir of infection to other animals (Baker, 1995). In Norway, BVD/MD is a notifiable disease (Anonymeous, 1989). From 1984 to 1986, preliminary investigations indicated that nearly 30% of the dairy herds had animals with antibodies to BVDV (Løken et al., 1991), whereas for other production types the prevalence was unknown. The annual losses in cattle in Norway due to BVDV infection was estimated to be between 40 and 50 million NOK (Krogsrud and Løken, 1992).

A surveillance and control programme started in December 1992 (Løken and Nyberg, 2013) as collaboration between Governmental institutions and the cattle industry. A cattle herd was considered to be BVDV infected if all sequential tests were positive including virus identification from at least one animal.

The latest BVDV infected cattle herd was identified in April 2005 and the restrictions due to BVDV were lifted in November 2006 (Kampen et al., 2007). As a result, the objective of the control and surveillance programme shifted from eradication of BVDV to surveillance to document freedom from disease. From the beginning of 2007, no BVDV infected herds have been identified in Norway and no herd have been subject to restrictions for BVD (Åkerstedt et al., 2012). The current surveillance program includes dairy as well as beef suckler herds. The only bull station in Norway is approved by the European Union (EU). This requires a testing regime including a several infectious diseases amongst BVD is included (European Commission, 1988). Imported live cattle, semen and embryos undergo additional testing for BVDV in accordance with the cattle industry's own requirements handled by the Norwegian Livestock Industry's Biosecurity Unit (KOORIMP).

The aim of the current study was to estimate the probability of freedom from BVDV infection in the Norwegian cattle population by the end of 2011.

2. Materials and methods

This study was based on the information from the Norwegian surveillance program of BVDV in cattle during 2007–2011, a period where no known BVDV infected herds were reported in Norway. The probability that the cattle population in Norway was free from BVDV by the end of 2011 was calculated using scenario tree modelling (Martin et al., 2007b).

2.1. Data sources and definition of cattle herd production types

The following data sources were used to calculate the population size and categorise the Norwegian cattle 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). As of 01.01.2011, the Norwegian cattle population consisted of 856,349 animals distributed in 16,401 herds.

The herds were categorised into

i) dairy herds defined as herds that delivered milk to dairies, including herds with combined production of dairy and beef (66.6%)
ii) beef herds divided into beef suckler herds defined as herds with more than one breeding cow (23.8%), with one breeding cow (1.0%), and beef finishing herds (8.5%) with no breeding cows
iii) farm stead dairy (0.1%), defined as herds with on-farm production of dairy products and no delivery of milk to dairies (Table 1).

Records on milk delivering cattle were obtained from the dairy industry. Test results and sample information were obtained from the Norwegian Veterinary Institute.

2.2. Surveillance system components

The three surveillance system components (*SSCs*) of the current official Norwegian surveillance program for BVDV during the study period were dairy, beef suckler sampled at farms and beef suckler sampled at slaughterhouses (Fig. 1). Each *SSC* is described below.

2.2.1. Dairy SSC

Annually, 12.5% of all dairy herds were randomly selected for sampling which ensured bulk tank milk (BTM) samples from at least 10% of the herds. The number of herds tested decreased from 1575 in 2007 to 1226 in 2011 (Table 2) due to a decrease in the number of dairy herds in Norway. In 2008, herds selected for BVDV testing the previous year were excluded from the sampling frame, and from

Table 1
Number of Norwegian cattle herds distributed on production types from 2007 to 2011.

Year	Category	No. of dairy delivering milk*[a]	No. of dairy farm stead dairy	No of beef suckler >1 cow*	No of beef suckler 1 cow	No of beef finishing	Total
2007	Herd	140,78	26	3926	213	1634	19,877
	Animal	732,920	1354	131,372	1731	33,273	900,650
2008	Herd	13,227	25	3716	211	1563	18,742
	Animal	725,027	1370	129,247	2257	33,546	891,447
2009	Herd	12,221	23	3834	180	1509	17,767
	Animal	701,310	1320	135,904	1740	35,505	875,779
2010	Herd	11,501	21	3883	176	1491	17,072
	Animal	686,946	1254	141,368	1780	35,082	866,430
2011	Herd	10,928	20	3903	158	1392	16,401
	Animal	672,891	1231	145,707	1491	35,029	856,349

*Included in the surveillance program.
[a] Includes combined herds.

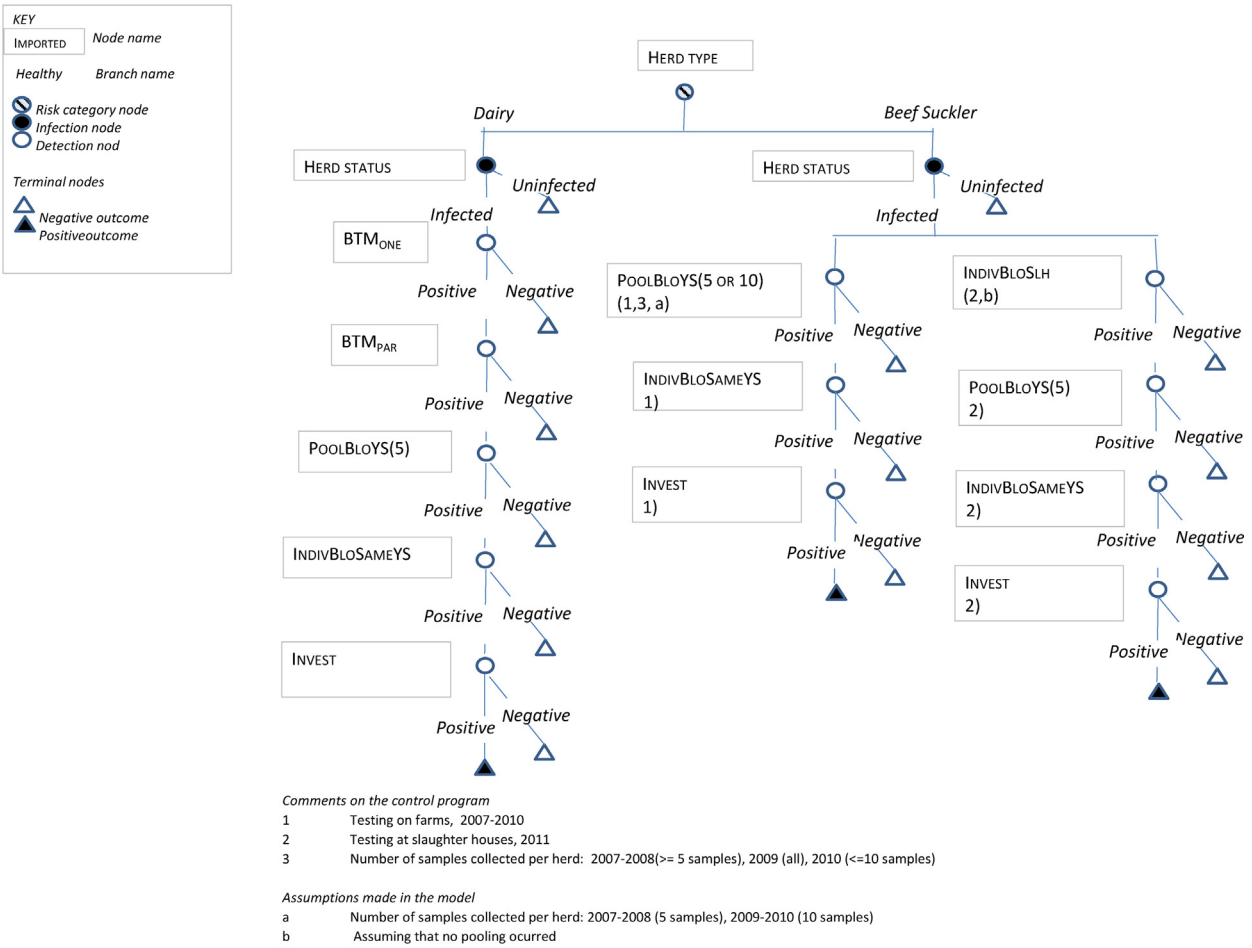

Fig. 1. The scenario tree of the Norwegian surveillance program for BVDV from 2007 to 2011 with the surveillance system components dairy, beef suckler sampled at farms (2007–2010) and beef suckler sampled at slaughterhouses (2011). BTM_{ONE} = bulk tank milk sample; BTM_{PAR} = retest of bulk tank milk samples; PoolBloYS(5) = up to five blood samples in a pool; PoolBloYS(10) = up to ten blood samples in a pool; IndivBloSameYS = individual blood sample collected at the farm; IndivBloSlh = individual blood sample collected in the slaughterhouse; Invest = further investigations.

2009 to 2011, herds tested in the two previous years were excluded from the sampling frame.

2.2.2. Beef suckler SSC at farms

In 2007–2010, 12.5% of the beef suckler herds were randomly selected for sampling. The number of sampled herds varied between 370 and 507 (Table 2). In 2007 and 2008, up to five blood samples from young stock (7–15 months of age) (PoolBloYS(5)) were collected per herd. In 2009 and 2010, the samples were collected from animals older than 24 months. All animals in this age group were sampled in 2009 and in 2010 up to ten animals per herd were sampled. The number of blood samples collected per year varied between 4020 and 5048. For each of the years, those herds that had been tested for BVDV the previous 2 years were excluded from the sampling frame.

2.2.3. Beef suckler SSC in slaughterhouses

In 2011, approximately 5000 samples from adult cattle from beef suckler herds were requested from slaughterhouses, *i.e.* approximately the same sample size as in previous years when beef suckler cattle were sampled at farms. The numbers of samples to be collected at each slaughterhouse were *proportional* to the number of slaughtered adult beef suckler cattle (*i.e.* the carcass categories heifers, cows and bulls) and the samples were equally distributed over working days and months, except for July where no sampling occurred due to reduced number of adult beef cattle delivered to the slaughterhouses. Sampling took place at slaughterhouses that slaughtered more than 500 adult beef suckler cattle in 2010 (12 in total) representing 84% of the total slaughter of adult beef cattle in 2011. In total, 1278 "beef" herds were sampled, however for the present analysis we categorised the herds according to the RPS resulting in 1094 beef suckler herds with more than one cow included in the analysis.

2.2.4. Testing protocol dairy SSC

The first step in the surveillance for dairy cattle consisted of BTM testing for BVDV antibodies (BTM_{ONE}). If BTM_{ONE} was positive, the sample was then retested twice (BTM_{PAR}) with the same test and concluded as positive if at

Table 2
Number of herds or animals included in the surveillance system components 623 for bovine viral diarrhoea in Norway from 2007 to 2011.

Surveillance system component	Year	No of herds	No. of primary samples
Dairy[a]	2007	1575	1575
	2008	1424	1424
	2009	1315	1315
	2010	1328	1328
	2011	1226	1226
Beef suckler sampled at farms	2007[b]	370	1485
	2008[b]	407	1817
	2009[c]	435	4926
	2010[d]	507	4018
Beef suckler sampled at slaughterhouses	2011[e]	1094[f]	4172

[a] One bulk tank milk sample per herd was collected.
[b] Up to five blood samples per herd were collected and pooled.
[c] All cattle in a herd were sampled and pooled with up to ten samples.
[d] Up to ten blood samples per herd were collected and pooled.
[e] Samples were collected from individual cattle at slaughter, only herds categorised beef suckler herds with more than 1 suckling cow is included in the analyses.
[f] Only beef suckler herds with more than one suckling cow were included from the total number of 1278 sampled beef herds.

least one of the tests in BTM_{PAR} were positive. If the BTM_{PAR} was positive, up to five blood samples were collected from young stock in the herd and analysed as a pooled sample (PoolBloYS(5)). When PoolBloYS(5)was positive, the blood samples in the pool were analysed individually (IndivBloSameYS). A herd with positive IndivBloSameYS results would be put under restrictions and further investigations (Invest) were performed to clarify if the herd was infected or not. In order to find persistent infected animals all cattle within such a herd were sampled and samples with a weak positive or negative serological results would be tested for the presence of BVDV using an antigen-capture ELISA (IDEXX Laboratories Inc., Westbrook, Maine, USA). Positive reactions for BVDV in newly infected herds would be verified with the polymerase chain reaction (PCR) and sequence analysis.

2.2.5. Testing protocol beef suckler SSC at farms

Samples from each herd were tested for BVDV antibodies in pools, with a maximum of ten samples in each pool (PoolBloYS(10). If the pool was positive, the individual samples (IndivBloSameYS)forming the pool were analysed separately. If any individual sample was positive, a further investigation (Invest) was performed as described in Section 2.2.4 for dairy SSC.

2.2.6. Testing protocol beef suckler SSC in slaughterhouses

At most five samples were collected from a single herd per day. The samples were analysed individually or in pools comprising the samples collected from the same herd at the same day (IndivBloSlh). If a pooled sample was positive, the individual blood samples were analysed separately. As most herds only had one sample per day, it was assumed that no pooling occurred and retesting of pools was therefore not included in the model (Fig. 1). If this test was positive (IndivBloSlh), young stock samples (PoolBloYS(5)) were collected as described in Section 2.2.4 for dairy *SSC* and the same follow-up procedure was used.

2.2.7. Laboratory analyses and interpretation of the test results

Serum and BTM samples were tested for BVDV antibodies, using an indirect enzyme-linked immunosorbent assay (ELISA, SVANOVIR^{TM} BVDV-Ab; Svanova Biotech AB, Uppsala, Sweden) (Juntti et al., 1987). Results of BTM testing were divided into four groups depending on the levels of antibodies: 0. undetectable, 1. low, 2. moderate, and 3. high (Niskanen, 1993). Until 2009, group 0 and 1 were regarded as negative and group 2 and 3 as positive. From 2010, the groups were reclassified to increase the sensitivity of the programme so that group 0 was regarded as negative whereas group 1, 2 and 3 were considered as positive (Åkerstedt et al., 2012). For blood samples (individual and pooled samples), the cut-off value given by the manufacturer for individual blood samples was used.

2.2.8. Case definition

A herd was considered to be infected if all sequential tests were positive including the further investigations described in Sections 2.2.4–2.2.6 (Fig. 1).

2.2.9. Design prevalence

The probability of freedom from BVDV was calculated using a herd design prevalence P^{*}_{H} of 0.2% (Table 4) *i.e.* the scenario tree model estimated the sensitivity of the *SSCs* as the probability of detecting at least one infected herd if 0.2% or more of the cattle herds in the reference population were infected. The design prevalence of 0.2% was chosen as no international accepted guidelines for design prevalences for BVDV exist, and this design prevalence is used for defining freedom from *Brucella abortus* and enzootic bovine leukosis within the EU (European Commission, 1998).

In the present study, a within-herd prevalence (P^{*}_{U}) of 30% for both dairy and beef suckler herds (Table 4) was used. This is considered as a conservative estimate as other studies have reported higher within herd prevalences both for dairy (Houe and Meyling, 1991; Braun et al., 1997) and beef cattle (Perez et al., 1994; Paisley et al., 1996; Brulisauer et al., 2010).

2.3. Scenario tree model

The scenario tree model (Fig. 1) was used to estimate the probability of getting a positive outcome given that the infection was present at the specified design prevalences. The scenario tree model includes the category node Herd type with two branches, *Dairy* and *Beef Suckler* and the infection node Herd status with two branches, *infected* and *uninfected*. It further includes 12 different detection nodes. The assumptions and calculations of the test sensitivities for the different tests as explained in Section 2.2 are described below. Each *SSC* was assumed to have a specificity of 1, because all samples testing positive are followed up with further testing and investigation.

2.3.1. Test sensitivity on individual serum and milk samples

The manufacturer reported that 99 of 99 individual serum samples positive in the virus neutralisation test (Svanova) also were positive in the ELISA (personal communication, Afsaneh Jalali, Boehringer Ingelheim Svanova). The sensitivity of a serum ELISA (individual sample) (Se_{Blo}) was described by a *Beta* distribution:

$$Se_{Blo} = Beta(100, 1)$$

The sensitivity of the milk ELISA using the serum ELISA as gold standard was evaluated on serum and milk samples from 21 individuals that were positive on serum and 20 of them were also positive when examining milk (personal communication, Afsaneh Jalali, Boehringer Ingelheim Svanova). The total sensitivity of the milk ELISA (Se_{Mi}) was calculated as the product of a Beta distribution, *Beta*(21,2) and the sensitivity of the serum ELISA

$$Se_{Mi} = Beta(21, 2) \times Se_{Blo}$$

The sensitivity of the individual follow up test (IndivBloSameYS) was assumed to be equal to the sensitivity of the individual blood test (Se_{Blo}) assuming only one positive sample would have been included in the pools of five or ten samples although more than one positive sample could have been included.

The sensitivity of the test (IndivBloSlh)was assumed to be equal to the sensitivity of the individual blood test (Se_{Blo}). Although, pooling of samples collected the same day from the same herd occasionally occurred, this was not taken into consideration. The sensitivity of the further investigations (Invest) was assumed to be 1.

$$Se_{Inv} = 1$$

2.3.2. Test sensitivity of bulk tank milk samples

In accord with Niskanen (1993) and manufacturer's information (Svanova, 2012) the BTM ELISA was assumed to have the same sensitivity as the individual milk ELISA for pools with less than 50 animals. This assumption was applicable in Norway as the herd sizes in the Norwegian dairy population rarely exceed 50 dairy cows.

$$Se_{\mathrm{BTMONE}} = Se_{Mi}$$

The sensitivity of the retests of BTM ($\mathrm{BTM_{PAR}}$) interpreted in parallel ($Se_{\mathrm{BTM_{PAR}}}$)was calculated as (Dohoo et al., 2009, page 101–102):

$$Se_{\mathrm{BTM_{PAR}}} = (Se_{\mathrm{BTMONE}} + Se_{\mathrm{BTMONE}}) - Se_{\mathrm{BTMONE}} \times Se_{\mathrm{BTMONE}}$$

2.3.3. Test sensitivity of the pooled samples

The effect of using serum ELISA on pooled blood samples has been evaluated by Cowley et al. (2012). In their study, 90 pools consisting of 30 serum samples each with between 1 and 30 seropositive samples per pool were examined. Of these, 35 of the pools included between 10% and 30% individual ELISA positive samples and all these were positive in the pooled ELISA. Pools with 40% or more positive samples was not included in the sensitivity estimation as the prevalence of positive samples would have exceeded the design prevalence used in this study.

Table 3
The estimated probabilities (min, mode and max values) of selecting at least one infected individual when pooling 5 (a) or 10 (b) individual blood samples from a herd in the surveillance program of BVDV during 2007–2011. The values were obtained by simulation (5000 iterations) including actual herd sizes of the finite population within each production category and within herd design prevalence.

Production type	Year	Min	Mode	Max
Beef suckler[a]	2007	0.819	1.000	1.000
Beef suckler[a]	2008	0.820	1.000	1.000
Beef suckler[b]	2009	0.968	1.000	1.000
Beef suckler[b]	2010	0.967	1.000	1.000
Beef suckler[a]	2011	0.821	1.000	1.000
Dairy[a]	2007	0.817	0.846	1.000
Dairy[a]	2008	0.813	0.843	1.000
Dairy[a]	2009	0.818	0.843	1.000
Dairy[a]	2010	0.816	0.842	1.000
Dairy[a]	2011	0.816	0.843	1.000

Compared to individual blood samples (Se_{Blo}), the sensitivity of a pooled sample (PoolBloYS(10)), (Se_{Po10}) was described with Beta(36,1).

Further, the study from Cowley et al. (2012) indicated that any pool with at least 10% positive samples would be positive. Therefore, we assumed that a pool with one positive out of five samples (20%) would have no loss in sensitivity, *i.e.* the sensitivity when analysing (PoolBloYS(5))was equal to that of individual analysis (Se_{Blo}).

The probabilities of selecting at least one positive animal when sampling five or ten animals, respectively in a herd with 30% infected animals, were estimated using the hypergeometric distribution, This was based on the actual herd sizes in the dairy and beef suckler herd populations for each year *y*, separately. The mode, minimum and maximum values of the probabilities were obtained from simulations with 5000 iterations (Table 3). Using these estimates, the probability that the pool of ten samples ($Se_{Samp10,y}$) and the pool of five samples ($Se_{Samp5,y}$), will include at least one infected animal was described as Pert(min, mode, max) (Table 4). The overall sensitivities of these tests were calculated as

$$Se_{PoolBloYS(5),y} = Se_{Samp5,y} \times Se_{Blo}$$

$$Se_{PoolBloYS(10),y} = Se_{Pol10} \times Se_{Samp10,y} \times Se_{Blo}$$

2.3.4. Repeated tests and interpretation

For each of the *SSCs* there is a sequence of repeated tests that will be performed once a test is positive. Although the repeated tests are likely highly correlated, we choose for simplicity to use the same sensitivity values for the primary test as the repeat test as this would only underestimate the overall sensitivity for each *SSC*.

Table 4
Input values used in the scenario tree model to evaluate the sensitivity of the Norwegian surveillance program of BVDV from 2007 to 2011.

Parameters	Inputs	Distribution	Notation
Herd level design prevalence	0.002	Fixed	P^*_H
Within herd design prevalence	0.3[a]	Fixed	(P^*_U)
Relative risk of beef suckler herds versus dairy herds of being infected	2.59[a]	Fixed	RR_{HR}
Sensitivity on individual blood samples	0.99[a]	*Beta*(100,1)	Se_{Blo}
Sensitivity on bulk tank milk sample	0.91[a]	$Beta(21,2) \times Se_{Blo}$	Se_{BTM}
Sensitivity of pooled blood samples (pools of 10) vs. analyzing individual samples	0.97[a]	*Beta*(36,1)	Se_{Po10}
Probability of selecting at least one infected individual when pooling 5 individual blood samples from a herd[b] in year; *y*	See Table 3	*Pert* (min, mode, max)	Se_{Samp5}
Probability of selecting at least one infected individual when 10 pooling individual blood samples from a herd[b] in year; *y*	See Table 3	*Pert* (min, mode, max)	Se_{Samp10}
Sensitivity of the further investigations	1	Fixed	Se_{Inv}
Prior (pre surveillance) probability of infection	0.5	Fixed	*PriorPInf*
Probability of introduction (per year)	0.1	–	*PIntro*

[a] Expected value.
[b] Dairy or beef suckler herd as described in Table 3.

2.4. Calculation of surveillance system components sensitivities

2.4.1. Adjusted risks

The adjusted risk for each production type category was calculated as described by Martin et al. (2007a) as

$$AR_{LR} = 1/(RR_{HR} \times PrRefPop_{HR} + (1 - PrRefPop_{HR}))$$

where AR_{LR} was the adjusted risk for low risk population, here the dairy herds (*Da*), RR_{HR} was the relative risk for the high risk population, beef suckler herds (*Be*), which was calculated by dividing the proportions of BVDV infected beef suckler herds (20.5%) by dairy herds (7.9%) in 1993. The year 1993 was chosen as it was the earliest year with detailed prevalence data available and the eradication programme was considered to not have had a considerable influence on the prevalence estimates. $PrRefPop_{HR}$ was the proportion of reference population falling into each production type category for each of the years included in the model.

The adjusted risk for the high risk population (AR_{HR}) was calculated as

$$AR_{HR} = RR_{HR} \times AR_{LR}$$

The herd design prevalence and the adjusted risks for dairy herds were used to calculate the effective probability of a dairy herd being infected ($EPInf_{Da}$).

$$EPInf_{Da} = P^*_H \times AR_{LR}$$

where P^*_H is the between herd design prevalence and AR_{LR} is the adjusted risk of a dairy herd being infected. The effective probability of a beef suckler herd being infected was calculated in a similar way.

2.4.2. Annual sensitivity for dairy herds and beef suckler SSC (survey at farms)

The dairy herd sensitivity (Se_{HDa}), *i.e.* the overall sensitivity of the testing including follow up tests (Fig. 1) was estimated by multiplying sensitivities of the five sequential tests in the dairy *SSC*: $Se_{HDa} = Se_{BTM} \times Se_{BTM_{PAR}} \times Se_{PoolBloYS(5),y} \times Se_{Blo} \times Se_{Inv}$

The beef suckler sensitivity ($Se_{Be,y}$), *i.e.* the overall sensitivity of the testing including follow up test (Fig. 1), for the years 2007–2010 was estimated by multiplying sensitivities of the three sequential tests in the beef *SSCs*.

$$Se_{HBe,y} = \begin{cases} Se_{PoolBloYS(5),y} \times Se_{Blo} \times Se_{Inv} & for\ y \in (2007, 2008) \\ Se_{PoolBloYS(10),y} \times Se_{Blo} \times Se_{Inv} & for\ y \in (2009, 2010) \end{cases}$$

The probability of all dairy herds testing negative ($PNeg_{Da,y}$) if $y \in (2007, 2011)$ was calculated as:

$$PNeg_{Da,y} = (1 - EPInf_{Da} \times Se_{HDa})^{nDa,y}$$

where $EPInf_{Da}$ is the effective probability that a dairy herd is infected, Se_{HDa} is the overall sensitivity of the sequential testing done in dairy herds. Further is $n_{Da,y}$ the number of dairy herds tested in year *y*. The annual sensitivity for dairy herds *SSC* ($Se_{SSC\_Da,y}$) is the complementary event of all herds testing negative. The probability of beef suckler herds testing negative and the annual sensitivity of the beef SSC ($Se_{SSC\_Be,y}$) for $y \in (2007, 2010)$ was calculated in a similar way.

2.4.3. Annual sensitivity for beef suckler SSC (survey in slaughterhouses)

For the year 2011, when sampling of beef suckler herds was performed at slaughterhouses, the herd sensitivity was calculated for each herd separately. As herd sizes often were small, the expected number of infected cattle ($no.inf_{HBe,2011}$) in each herd in 2011 was calculated using the Binomial distribution Bin(*n*,*p*), where *n* is the herd size and *p* is the within herd design prevalence (P^*_U). The probability of a herd testing negative was calculated using an approximation of the hypergeometric distribution (MacDiarmid and Hellström, 1988). In 98.5% of the analyses five samples or less were included in the pool and the sensitivity was $Se_{PoolBloYS(5)}$ as described in Section 2.3.3. For simplicity we assumed that the sensitivity was the same for the remaining 1.5% of the analyses. The probability that a beef herd tested negative in 2011, given that it was infected ($PNeg_{HBloBe,2011}$) was calculated as:

$$PNeg_{HBloBe,0=2011} = (1 - (Se_{Blo} \times no.tested/herd\ size))^{no.\ inf\ HBe,2011}$$

where Se_{Blo} is the sensitivity of the individual blood test, *no.tested* is the number of cattle tested in the herd, *herd size* is the number of adult animals in the herd and *no.* $inf_{HBe,2011}$ is the expected number of infected cattle in the herd in

2011. As the number of samples collected from each herd varies between herds, $PNeg_{HBloBe,2011}$ will also vary between herds.

The probability that the infected herd (30%) tested positive is the complementary event:

$$Se_{HBloBe,2011} = 1 - PNeg_{HBloBe,2011}$$

The overall sensitivity for a beef herd (*HBe*) including the sequential testing ($Se_{HBe,2011}$) was obtained by the following calculation:

$$Se_{HBe,2011} = Se_{HBloBe,2011} \times Se_{PoolBloYS(5)} \times Se_{Blo} \times Se_{Inv}$$

where $Se_{HBloBe,2011}$ was the probability that the herd tested positive in the first test; IndivBloSlh and $Se_{PoolbloYS(5)}$ (as defined in the dairy *SSC*) was the probability that it tested positive in the second test PoolBloYS(5), Se_{Blo} was the probability that it tested positive in the third test; IndivBloSameYS and Se_{Inv} is the probability that it tested positive in the further investigation; Invest.

The probability that all beef suckler herds tested negative, ($PNeg_{Be,2011}$) taking into account the effective probability that a beef suckler herd was infected, *i.e.* $EPInf_{Be}$ was calculated as:

$$PNeg_{Be,2011} = \prod_{\forall HBe} (1 - EPInf_{BE} \times Se_{HBe,2011})$$

The probability to detect at least one infected beef suckler herd *i.e.* the sensitivity for beef suckler herds *SSC* in 2011 ($Se_{Be,2011}$) was equal to $1 - PNeg_{Be,2011}$.

2.4.4. The combined annual SSC sensitivity for all SSCs

As the surveillance in dairy and beef suckler herds are mutually exclusive, the probability that both tested negative for $y \in [2007, 2011]$ was calculated as:

$$PNeg_{Da\,and\,Be,y} = PNeg_{Da,y} \times PNeg_{Be,y}$$

The annual sensitivity of the surveillance system in dairy and beef suckler herds, *i.e.* the probability that at least on herd tested positive was calculated as:

$$Se_{Da\,and\,Be,y} = 1 - PNeg_{Da\,and\,Be,y}$$

2.5. Probability of freedom and temporal discounting

The probability of freedom from BVDV was calculated using Bayes theorem (Martin et al., 2007b). The posterior probability of freedom in year *y* ($PostPFree_y$) *i.e.* after the testing that has been done during that year equalled the negative predicted value. Assuming a perfect specificity this was calculated as described by Martin et al. (2007b).

For the first year *PriorPInf* was chosen as a neutral prior probability of 0.5.

The probability of introduction (*PIntro*) was defined as the annual probability of introduction of the disease in a sufficient number of herds to exceed the specified design prevalence (P^*) (Martin et al., 2007b). The probability of introduction of BVDV into Norway for each of the study years was considered to be low. However, we used a conservative approach, i.e. using a higher probability of introduction as we think is realistic and it was therefore set to 0.1 for each year in the model. The most probable sources of introduction were considered to take place due to import of animals, semen or embryo. These imports are strongly regulated both by EU requirements (European Commission, 1964) and voluntary additional requirements by KOORIMP.

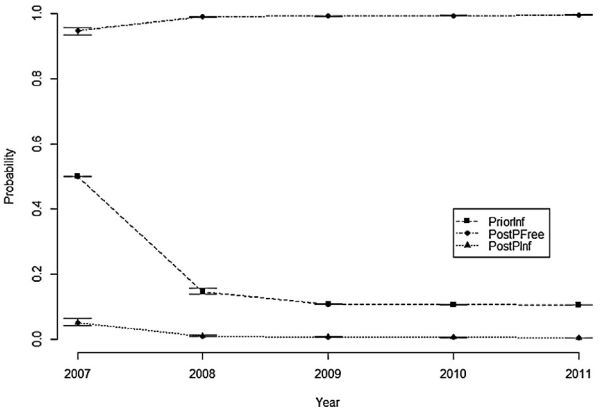

Fig. 2. The probability of infection, (*PriorPInf*), the posterior probability of freedom (*PostPfree*) and the posterior probability of infection (*PostPInf*) of the scenario tree model of the Norwegian surveillance program of BVDV from 2007 to 2011.

PriorPInf at the beginning of the following year and the posterior probability of infection in year *y* ($PostPInf_y$) were both calculated as described by Martin et al. (2007b).

2.6. Simulation

The model was run in R (R Core Team, 2012). There were run 5000 iterations for each of the *SSCs*.

2.7. Sensitivity analysis

The sensitivity of the *PostPFree* to variation in the *PIntro* was assessed by increasing the *PIntro* to 0.2 and 0.3 and by changing the RR to 1.0 and 3.0, respectively.

3. Results

The estimated median value of probability of freedom from BVDV in the Norwegian cattle population was above 0.99 from 2008 and onwards and at the end of 2011, it was 0.996 (0.995–0.997; 90% credibility interval) (Fig. 2).

The estimated median value of annual sensitivity of the dairy *SSC* varied and decreased from 0.811 in 2007 to 0.709 in 2011 (Fig. 3). The estimated median value of annual sensitivity of the suckling beef *SSCs* increased from 0.715 in 2007 to 0.890 in 2011 (Fig. 3). By changing the annual risk of introduction from 0.1 to 0.2 and 0.3 the probability of freedom decreased (median value (90% credibility interval) from 0.996 (0.995–0.997); to 0.991 (0.989–0.992) and 0.985 (0.981–0.987), respectively. By changing the RR the median value of probability of freedom only slightly changed from 0.969 to 0.985 for a RR of 1 and 3, respectively.

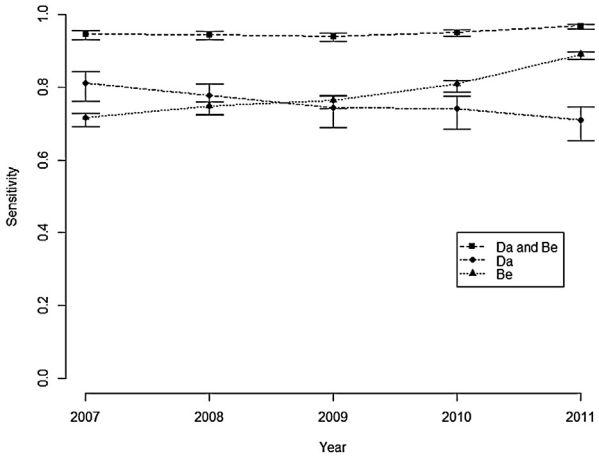

Fig. 3. Sensitivities for each *SSC* with median, lower and upper credibile interval (indicated with horizontal bars) in the Norwegian surveillance program of BVDV from 2007 to 2011; *Da* = Dairy SSC, *Be* = Beef suckler SSC and *Da* and *Be* = Combined Dairy and beef suckler *SSCs*.

Table 5
The estimated herd sensitivities (min, mode and max values) in the surveillance program of BVDV for each of the years 2007–2011 obtained by simulation (5000 iterations).

Production type	Year	Min	Mode	Max
Beef suckler	2007	0.78	0.96	1.00
Beef suckler	2008	0.82	0.96	1.00
Beef suckler	2009	0.75	0.95	1.00
Beef suckler	2010	0.76	0.95	1.00
Dairy	2007	0.90	0.95	0.96
Dairy	2008	0.89	0.94	0.96
Dairy	2009	0.90	0.94	0.95
Dairy	2010	0.91	0.95	0.96
Dairy	2011	0.94	0.97	0.98

The herd *sensitivities*, the probability that an infected herd would have a positive result, varied from 0.60 to 0.93 for dairy herds (Se_{HDa}) as shown in Table 5. For beef herds ($Se_{HBe,y}$) the herd *sensitivities* varied from 0.747 to 0.999 (Table 5). In 2011, the herd sensitivity for beef suckler herds varied from 0.24 to 0.95 (Table 5) with a median value of 0.60 as the number of samples collected per herd varied.

4. Discussion

The results from the scenario tree model support that the Norwegian cattle population is free from BVDV. Surveillance and control programme implemented in the Nordic countries have resulted in either freedom or almost freedom from BVDV. However, to our knowledge, no other countries have been able to quantify the probability of freedom from BVDV in cattle so far. Several other European countries have implemented surveillance and control programme for BVDV (Stahl and Alenius (2012).

The annual sensitivity for dairy *SSC* was lower than for beef suckler *SSCs* from 2009 onwards. Main reasons for this are the lower herd sensitivity for dairy vs. beef, the declining number of dairy sampled and increasing numbers of beef suckler farms sampled and the higher infection risk (EPI) for beef suckler herds. This is partly due to the fact that the sensitivity of the BTM test was lower than the serological test and that more tests were included in the dairy *SSC* than in the beef suckler *SSCs*.

Although the number of analysed samples from beef suckler cattle was comparable with previous years, the sensitivity of the beef suckler *SSC* ($Se_{HBe,y}$) was higher in 2011. This seems reasonable as the sensitivity is expected to increase if more herds and fewer samples per herd are collected since infectious diseases are expected to cluster at herd level. However, the sensitivity of the beef suckler *SSC* of year 2011 was not directly comparable with previous years as the herd sensitivities were calculated in different ways. When sampling was done in individual beef suckler herds (2007–2010), the true number of samples collected in each herd not was taken into account. It was assumed that five or ten samples were collected from each herd. However, when fewer samples were collected, this was due to the herd size being so small that all young stock was sampled, which implies that we have underestimated the sensitivity in those years as this was the case in more than 30% of the included herds. On the other hand, for the sampling at slaughterhouses, the calculation of the sensitivity of the testing in each herd was based on the herd size, the expected number of infected animals in the herd (obtained by simulation) and the number of analysed samples per herd. However, it was assumed that all samples were tested individually despite the fact that pooling of samples collected on the same day from the same herd occurred. Only in 1.5% of the analyses more than five samples were included in the pool. As the extent of this pooling was very small, this was not assumed to affect the output of the model. Furthermore, apart from the component having a higher sensitivity, sampling at slaughterhouses is more cost efficient. Although the number of collected samples was in the same range, the number of analysis increased in 2011. However, the benefits of not having to collect the samples at the farms outweighed the increased costs due to the increased number of analysis in 2011.

Before 2011, beef suckler herds with only one breeding cow were not included in the surveillance system. Even if this subpopulation had been sampled it would have been a seldom phenomenon as this constitutes only a minor proportion of the beef suckler population. Also, introduction and persistence of BVDV in such herds was considered negligible as these herds are very small. In combined herds, *i.e.* herds with both dairy and beef cattle, only the dairy cattle were included in the surveillance. It was assumed that the beef cattle and the dairy cattle had close contact so if the infection had been introduced into the beef suckler cows, the infection would have spread to dairy cattle. Thus, the beef suckler cows on these farms were indirectly surveyed by the BTM sampling. The beef finishing herds were not included in the surveillance programme. No breeding occurs in these herds and the animals were purchased from either dairy or beef suckler herds. Therefore, it was considered unlikely that the infection could establish and persist in these herds. Farm stead dairy herds have not been included in the surveillance after 2006. This population cover less than 0.1% of the total cattle population and the herds are usually small. It is considered unlikely that the infection would establish in these herds, but the inclusion of these herds in the surveillance activities might be

considered in the future to increase coverage of the surveillance programme.

The estimate used for the risk of introduction of BVDV, can be considered conservative. The increase of the probability of introduction performed in the sensitivity analysis only slightly changed the results. Although Norwegian livestock is considered to be free from the BVDV, import of infected animals and unknown wildlife reservoirs may pose a continuous threat to the present status. For the rapid detection of a potential reintroduction and consecutive control of spreading, a surveillance system has to make efficient use of the competence and awareness existing among farmers and local veterinarians. Since the outbreak of bluetongue and the eradication of BVDV, Norwegian farmers have become more aware of introduction of infectious diseases. The probability of introduction of BVDV through illegal import of animals, semen and embryo were considered low because illegal import most likely would be discovered through mandatory registration of herd data for all Norwegian cattle herds into the national individual cattle register. All information regarding origin of animals must be recorded before the animals may be slaughtered. Import of live vaccines contaminated with BVDV might be a potential risk of introduction as well, but to our knowledge there are at present only one such vaccines on the market in Norway (Felleskatalogen, 2014). Other ruminants may pose a risk for introduction of BVDV and pestivirus has been found to be endemic in the roe deer population in Norway (Lillehaug et al., 2003). However, the probability of introduction by wild ruminants can be regarded negligible, as shown in camelids by (Mudry et al., 2010). There is a small population of camelids, such as alpaca and lama in Norway, and a possible introduction of infectious diseases through such populations needs to be considered. Earlier studies (Løken et al., 1991) estimated the mean prevalence at herd level in sheep to 18%. There are no recent prevalence studies performed in Norwegian sheep, but the annual testing of cattle herds since the start of the eradication programme in 1992 have not detected any reinfections due to infected sheep even if BVDV might be present in the sheep population. A recent study from Ireland where a voluntary BVDV control is running (Graham et al., 2013) was not able to identify any risk of having sheep at the farm in relation to BVDV infection in cattle. Hence the risk of introduction through other ruminants can be considered low.

When calculating the overall sensitivity of all tests the formulas used requires that the test are independent, which is not the case when the bulk milk test is repeated on the same sample or when the sera included in the pooled sample were analysed individually with the same test. This was not considered to cause any concern as this lead to the estimated overall sensitivity of the tests to be underestimated. Furthermore, the change in cut-off value for the BTM was not taken into account resulting in a slight underestimation of the sensitivity of the dairy *SSC* after 2010. When considering beef suckler herds, more samples than requested was collected for 1.4% of all the tested herds for the remaining years and in 2009 all adult animals in the beef suckler herds were sampled. This was not taken into account in our analysis and also resulted in underestimation of the sensitivity of the surveillance.

5. Conclusions

The results from the scenario tree model support that the Norwegian cattle population is free from BVDV. A current change to sample at the slaughterhouse level further increased the sensitivity of the surveillance system.

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