

The number of Norwegian sheep flocks with classical scrapie estimated by simulation modelling

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### Summary

Since 1981, scrapie has been diagnosed in 84 Norwegian sheep flocks. The majority of the scrapie cases have been of the classical type. Our aim was to estimate the maximum prevalence of sheep flocks with classical scrapie from data collected at the individual level in the active scrapie surveillance programmes. Preliminary results when using a Monte Carlo simulation model, estimate the maximum flock level prevalence of classical scrapie to approximately 1%.

### Introduction

Scrapie, a transmissible spongiform encephalopathy, is a fatal neurological disease of sheep and goats. Scrapie was first diagnosed in indigenous Norwegian sheep in 1981 and altogether 84 sheep flocks with scrapie have been detected. It seems that scrapie in Norwegian sheep can be classified within to groups, the classical type, and the Nor98 type (1). The majority of the scrapie cases have been of the classical type, i.e. comparable to scrapie as described in cheviots. In the 1990s, there was an increase in the number of detected flocks culminating with 31 flocks detected in 1996. Strict control measures were implemented including slaughtering of 600-700 contact flocks. Thereafter, 1-2 sheep flocks with the classical scrapie type have been detected annually.

Norway has implemented active scrapie surveillance programmes in accordance with EU Regulations (Regulation (EC) Nos 999/2001 with amendments, 2-4). In the period from July 2001 to June 2003, 22,300 sheep have been examined in abattoir surveillance and from January 2002 to June 2003, 4,500 sheep have been examined in surveillance of found-dead animals (fallen stock). The primary test has been an ELISA (Platelia BioRad®) on samples from *medulla oblongata*. No classical scrapie case has been found by the active surveillance programmes.

The aim of this study was to estimate the maximum prevalence of sheep flocks affected by classical scrapie, at the flock level, exploiting data collected, at the individual level, in the active surveillance programmes, using simulation modelling.

### Material and methods

The model for simulation of the scrapie surveillance programmes, presented previously by Hopp et al. (5), uses sheep flock as the unit and year as the time step. In short, the model consists of two distinct stages. First, an artificial sheep population with demographic properties similar to the current sheep population in Norway is created. Thereafter the scrapie surveillance programmes are mimicked with sampling and examination of sheep.

As input into the model were used sheep demographic data (5), properties of the surveillance programmes (6), properties of scrapie and specificity and sensitivity of the diagnostic test. The scrapie properties were estimated as described by Hopp et

al. (5) changed as follows according to the experience we have acquired with the Norwegian flocks with classical scrapie: i) mainly two prion-protein genotypes (ARQ/VRQ, VRQ/VRQ) are susceptible to scrapie; ii) the prevalence of susceptible genotypes in these flocks are higher than in the general population. We chose to use the genotype frequency in the Rygja breed, in which most classical scrapie cases have been found (Table 1). The test sensitivity, estimated based upon expert opinion, was described by a cumulative beta(4.67,5.33) distribution with the lower bound of 15 months before death due to scrapie and increasing to 1 at the time of death. For the animals younger than 30 months, the distribution was modified so that the lower bound was set to 15 months. The test specificity was set to 1.

The prevalence of scrapie positive flocks in the Norwegian sheep population is not known, and the simulation model was run with prevalences varying from 0.5% to 3%. The maximum prevalence that gave no detected flocks in 95% of the outputs was considered as the maximum prevalence of classical scrapie positive flocks.

Genotype	Mean PrP-genotype frequency within infected flocks (%)	Scrapie susceptibility per PrP-genotype in infected flocks (%)	Incubation period (months) (Input to betapert distribution)		
			min	median	max
VRQ/VRQ	2.5	76	16	31	96
VRQ/ARQ'	15	52	19	38	74
VRQ/ARR	11	1	79	86	94
ARQ'/ARQ'	23	5	24	38	84
ARQ'/ARR	35	1	Treated as VRQ/ARR		
ARR/ARR	13	0 (resistant)	NA	NA	NA

Table 1. PrP-genotype-specific parameters used as input to the model of scrapie surveillance of Norwegian sheep. PrP = prion protein, NA = Not applicable.

## Results

Given the input, the prevalence of sheep flocks with classical scrapie in the Norwegian sheep population was estimated to be less than 1,3% and 0.5% when simulating the abattoir surveillance and the surveillance of fallen stock, respectively. The sensitivity analysis shows that by increasing the prevalence of susceptible genotypes within scrapie flocks and/or increasing the susceptibility of these genotypes, the estimated prevalence is reduced. When reducing the test sensitivity, the estimated prevalence of detected scrapie flocks is increased in the simulated abattoir surveillance, but when simulating surveillance of fallen stock the sensitivity of the diagnostic test is not important for the result.

## Discussion

The simulation results indicate that the maximum prevalence of sheep flocks with classical scrapie in the Norwegian sheep population is approximately 1%, which corresponds to a maximum of 200 sheep flocks out of 20,000. In Norway, classical scrapie has until now only been detected in certain geographical areas, representing approximately 50% of the sheep flocks. We therefore consider it unlikely that the true number of scrapie flocks is as high as the estimated maximum found by this model.

The sensitivity analysis of the simulation model shows that both the prevalence of the susceptible genotypes and the scrapie susceptibility of the

susceptible genotypes, were important for the simulation results. The model uses a simplified simulation of the within-flock dynamics of scrapie (5, 7). With the current knowledge of scrapie dynamics, we think this might be justified, though this highlights the need for advanced models describing the within-flock dynamics of scrapie. The test sensitivity was important for the result of the abattoir surveillance but not for the surveillance of fallen stock. This effect is explained by the within-flock model for scrapie dynamics, which predicts that of the scrapie-infected found-dead sheep in scrapie flocks, a large proportion die because of scrapie and therefore are easier detected. However, the sensitivity analysis shows that input parameters, of which available data are sparse, are important for the simulation results. The result should therefore be interpreted with caution.

All the scrapie cases of the classical type until now have been identified as animals with clinical signs, flock mates of scrapie cases or found in flocks which have been depopulated because of close contact with scrapie flocks. We believe this indicates that the passive surveillance of scrapie is more efficient for detecting scrapie flocks than the current active surveillance programmes on the condition that the farmers are motivated to report suspect cases.

#### References

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