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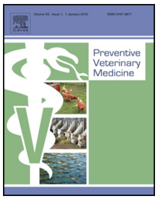

The evolution of the prevalence of classical scrapie in sheep in Great Britain using surveillance data between 2005 and 2012

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ABSTRACT

After the decline of the Bovine Spongiform Encephalopathy (BSE) epidemic in Great Britain (GB), scrapie remains the most prevalent animal Transmissible Spongiform Encephalopathy (TSE) present in GB. A number of control measures have been implemented for classical scrapie, and since 2005 there has been a large reduction in the number of observed cases. The objective of this study is to estimate two measures of disease frequency using up to date surveillance data collected during and after the implementation of different control measures established since 2004, and breeding for resistance schemes that ran from 2001 until 2009. This would enable an assessment of the effectiveness of both the breeding for resistance programme and the compulsory eradication measures in reducing the prevalence of scrapie in GB. Evaluation of the sensitivity of the rapid post-mortem test for scrapie indicated that it detected scrapie in the last 25% of the incubation period. A back-calculation model was developed to estimate the prevalence of infection at animal and flock-level. The results of the model indicated a mean drop of infection prevalence of 31% each year, leading to a 90% drop in infection prevalence between 2005, with an estimate of 5737 infected sheep in GB in 2012.

The risks of classical scrapie infection in animals with genotypes of National Scrapie Plan Types I–IV (all other genotypes), relative to Type V (all genotypes containing V_{136} R_{154} Q_{171} and not A_{136} R_{154} R_{171}), were estimated to be: 0, 0.0008, 0.07, and 0.21 respectively. The model estimated a very low rate of reporting of clinical suspects and a large decline from 2007 of the probability of a sheep being reported as a clinical suspect. The model also estimated that the expected number of sheep holdings with classical scrapie in 2012 was 215 (95% confidence interval: 33–437), out of a total of approximately 72,000 sheep holdings in GB. Model estimates indicate that the prevalence in 2012 has dropped to 10% of that in 2005, showing the effectiveness of the control measures. It also shows a bias in the destination of infected animals, with the majority of infected animals being detected in the fallen stock surveillance stream, and an extremely low proportion of animals detected as clinical suspects; this is very important in terms of the design of surveillance schemes for classical scrapie.

1. Background

After the decline of the Bovine Spongiform Encephalopathy (BSE) epidemic in Great Britain (GB), scrapie remains the most prevalent animal Transmissible Spongiform

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Encephalopathy (TSE) present in the country. The number of clinical scrapie suspects notified by farmers has drastically declined in the last 6 years. Since the disease became a notifiable disease in 1993, 2010 and 2012 have been the only 2 years where no clinical cases of scrapie were confirmed in GB and only three clinical index cases of classical scrapie were confirmed in GB in 2009, and the same number in 2011. The number of clinical cases and the apparent prevalence in the different surveillance streams have shown a continuous decline of classical scrapie over the last 6 years, although no statistically significant differences have been detected year by year (Ortiz-Pelaez et al., 2012).

Although surveillance data provide a trend on the evolution of the incidence of the disease, the actual prevalence of disease at animal and holding level are uncertain. Previous attempts to estimate disease frequency at animal and flock-levels used data generated by surveillance before the eradication measures and the breeding for resistance programmes could have had any impact on the disease frequency. A prevalence estimate ranging from 0.33 to 2.06% using abattoir and fallen stock survey data for 2002 was obtained (Gubbins, 2008). A back-calculation approach was used to estimate the prevalence of sheep infected with classical scrapie, integrating data on reported clinical cases (1993–2007) and the results of fallen stock and abattoir surveys (2002–2007) (Gubbins and McIntyre, 2009). The authors reported an estimated prevalence of 0.6–0.7%, if infected animals could only be detected in the final quarter of the incubation period, and an overall decline between 2003 and 2007 of 40%, independent of the assumptions made about the diagnostic tests.

In terms of holding prevalence, a minimum lower bound for the total number of holdings in GB infected with scrapie was estimated to be 642 (Del Rio Vilas et al., 2005) by applying capture–recapture methodology (CRC) to data from the abattoir and fallen stock surveys. Using data from the Compulsory Scrapie Flocks Scheme (CSFS) and the passive and active surveillance programmes between April 2005 and 2006, the number of scrapie-affected holdings in GB was estimated at around 350 (Del Rio Vilas and Böhning, 2008). The same authors applying one-list capture–recapture approaches to passive surveillance data for the years 2002, 2003 and 2004, estimate a flock prevalence of around 300 holdings per year (Del Rio Vilas and Böhning, 2008).

No estimates of scrapie prevalence have been produced since 2007 and therefore there has been no attempt to assess the effectiveness of the breeding for resistance and the compulsory eradication measures in reducing the prevalence of scrapie in GB. The objective of this study is to estimate two measures of disease frequency using up to date surveillance data collected during and after the implementation of the different control measures established in 2004, and the breeding for resistance schemes that ran from 2001 until 2009. In particular, the two estimates produced were: (i) the animal prevalence (proportion of adult sheep infected with classical scrapie) in the national flock and (ii) the holding prevalence (percentage of holdings with at least an adult animal infected with classical scrapie) in the national flock.

2. Methods

2.1. Model description: estimation of animal level prevalence by genotype group

A back-calculation model was developed to integrate data from the abattoir survey and fallen stock surveys to determine the prevalence of infection in the national flock, taking into account the NSP genotype group of tested and positive sheep. The model is described in full as supplementary material (Appendix A). The model is similar in principle to a previous approach (Gubbins, 2008), except that (i) it estimates prevalence over several years data, (ii) it allows the rate of under-reporting of clinical suspects to vary over time, and (iii) it assumes that animals show overt clinical signs at clinical onset, whereas in (Gubbins, 2008) it is allowed for a large proportion of animals to die at clinical onset prior to overt clinical signs.

2.2. Estimation of the flock-level prevalence

The flock-level prevalence of classical scrapie was estimated from the animal level prevalence, but adjusting for the clustering of infection within flocks (i.e. the within-flock prevalence distribution), and the effect of flock size on the likelihood of a flock being infected, p. The estimation of flock-level prevalence did not take genotype into account. The flock-level prevalence can be estimated from the estimator of animal-level prevalence, as the two are related, since the animal prevalence $P(\mathit{animal\ infected})$ is given by:

$$P(\mathit{animal}\ \inf \mathit{ected}) = \sum_{\mathit{flocks}} P(\mathit{flock}\ \inf \mathit{ected}) \times P\left(\frac{\mathit{within\,flock\,prevalence}}{\mathit{flock}\ \inf \mathit{ected}}\right)$$

The animal-level prevalence ($P(\mathit{animal\ infected})$) was estimated from the 2012 data on scrapie positives, using the back-calculation approach (see supplementary material Appendix A).

The within-flock prevalence distribution ($P(\mathit{within\ flock\ prevalence}|\mathit{flock\ infected})$) was estimated using data from infected holdings culled and tested under the Compulsory Scrapie Flocks Scheme (CSFS) (Ortiz-Pelaez and Del Rio Vilas, 2009). Zero-truncated Poisson model and negative binomial models were fitted to the data on the number of positive sheep from the CSFS flocks with at least one positive sheep, in order to determine the per capita rate of scrapie infection. The per capita rate of infection from the CSFS data was multiplied by 2.2 to account for the ratio between detected positives and within-flock prevalence (Matthews et al., 2001).

The term $P(\mathit{flock\ infected})$ was assumed be depend on holding size, as found in a previous study looking at the