The effect of genetic susceptibility and targeting of sampling on the sensitivity of the surveillance system and certainty-of-freedom for classical scrapie in Finland in 2008–2014

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ABSTRACT

We applied scenario tree modeling to study how the genetic distribution of the sheep population in Finland and the focusing on fallen stock would influence the surveillance sensitivity of scrapie. To incorporate the unevenly distributed susceptibility into the estimation we used data from GB where the genetic distribution and scrapie occurrence have been documented in both normally slaughtered and deceased animals. Finland's sheep population is more susceptible to scrapie than the sheep population in GB and surveillance is concentrated on fallen stock. As a result, there is high systemic sensitivity in Finland even with the moderate number of studied animals. The certainty of the freedom-of-disease status is clearly elevated by the low probability of previous disease occurrence and low probability of introduction. The results highlight the need to change the concept from surveillance system sensitivity to freedom-of-disease status and to also consider the risk of introduction and the cumulative nature of the disease prevalence information due repeated surveillance efforts.

1. Introduction

The transmissible spongiform encephalopathy (TSE) classical scrapie is a naturally occurring neurodegenerative disease of sheep and goats. It is characterized by a long incubation period, most often measured in years, and gradual vacuolar and spongy degeneration of the central nervous system (CNS). As in other prion diseases, there is enhanced accumulation of an abnormal form of a host membrane glycoprotein, prion protein PRNP, in the CNS and variably in other tissues and body fluids (Wood et al., 1997). The type of prion protein defines the susceptibility to scrapie. The primary mode of transmission of classical scrapie is by exposure of susceptible neonates to birth fluids and tissues from an infected animal, usually the mother. Adult animals are less likely to become infected upon exposure to infective tissues (Andreoletti et al., 2002; Race et al., 1998; Tuo et al., 2002). Classical scrapie appears on the list of diseases notifiable to the World Organization for Animal Health (OIE) due to its impact on worldwide trade.

The susceptibility or resistance of sheep to classical scrapie is controlled by the ovine PRNP gene. It is modulated by amino acid polymorphisms at codons 136, 154 and 171. The relationship between different PRNP genotypes and disease susceptibility/resistance has been described in detail elsewhere (Baylis et al., 2004; Goldmann, 2008; Dobly et al., 2013). The National Scrapie Plan (NSP) of the UK classifies allelic variations of the PRNP gene into five NSP types, with Type I being the most resistant and Type V the most susceptible (NSPAC, 2006; Dawson et al., 2008; Goldmann, 2008). Genotypes and NSP types are given in Table 1. Only rams of types I and II are preferred in breeding. On the contrary types IV and V are to be avoided in the British breeding plan.

Arnold and Ortiz-Pelaez (2014) described the observations of classical scrapie in sheep in Great Britain in 2005–2012. The data was reported separately for fallen stock (FS) and animals slaughtered for human consumption (SHC) and grouped according to genetic susceptibility in by the National Scrapie Plan of the UK. The most prevalent groups were NSP types IV and V. The relationship between the allelic distribution of the PRNP gene and resistance/susceptibility to classical scrapie in goats is not as clear cut as in sheep (Vaccari et al., 2009; EFSA, 2010; Corbière et al., 2013; EFSA, 2017).

Classical scrapie has never been diagnosed in sheep in Finland. In goats, four cases were diagnosed in 2002 and four in 2005. No further positive cases have been detected since 2005 (Evira, 2016). Unlike some other EU countries, Finland has never implemented an official breeding program in order to disseminate resistance to classical scrapie in the sheep population.

Since July 2013 the European Commission (EC) has recognized the possibility of Member States (MS) or zones as having negligible risk for

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Table 1
Genetic allelic distribution of NSP groups in the UK breeding programme (NSPAC, 2006).

	NSP type				
	I	II	III	IV	V
Allele combinations	ARR/ARR	ARR/ AHQ	ARQ/ ARH	ARR/VRQ	AHQ/VRQ
		ARR/ ARH	ARQ/ AHQ		ARH/VRQ
		ARR/ ARQ	AHQ/ AHQ		ARQ/VRQ
			ARH/ ARH		VRQ/VRQ
			AHQ/ ARH		
			ARQ/ ARQ		

classical scrapie based on an approved application according to point 2 of Section A of Chapter A of Annex VIII to Regulation (EC) No 999/ 2001 as amended by Regulation (EU) 630/2013. The criteria for approval are based on Article 14.9.3 of the Terrestrial Animal Health Code of the World Organization for Animal Health (OIE, 2012). The criteria include the requirement that "for a period of at least seven years, a sufficient number of ovine and caprine animals over 18 months of age, representative of slaughtered, culled or found dead on farm, have been tested annually, to provide a 95% level of confidence of detecting classical scrapie, if it is present in that population at a prevalence rate exceeding 0.1% and no case of classical scrapie has been reported during that period".

In June 2014 Finland submitted a request to the European Commission to be recognized as a Member State with negligible risk for classical scrapie. The application was approved in 2016.

The aim of this study is to evaluate how the PRNP genotype distribution of the Finnish sheep population and focusing the surveillance on fallen stock contribute to the sensitivity of the classical scrapie surveillance system. We also study the combined sensitivity of the sheep and goat surveillance systems for classical scrapie in Finland and the certainty-of- freedom for classical scrapie.

2. Materials and methods

2.1. The surveillance system for classical scrapie in Finland 2008–2014

Scrapie surveillance in Finland is carried out in compliance with EU legislation and is based on post-mortem screening of sheep and goats. The main focus is on fallen stock (FS), i.e. over 18-month-old animals either found dead or culled. A second surveillance component consists of over 18-month-old animals slaughtered for human consumption (SHC). Table 2 presents sheep and goat population information for 2008–2014 derived from the Finnish national sheep and goat registry administered by Finnish Food Safety Authority Evira.

The national registry was first implemented in 2008. The quality of the data remained incomplete for the first years of use but increased to a reliable level by 2011. For 2008–2010, FS and SHC were estimated using the proportions observed in 2011 and 2012. The Veterinary Virology Research Unit of The Finnish Food Safety Authority Evira acting as the National TSE Reference Laboratory NRL provided the information on scrapie testing (Table 2).

2.2. Finnish sheep and goat populations

The sheep and goat populations in Finland are small. The population of over 18 month old sheep varied between 58 000 and 82 000 individuals and goats between 5000 and 6000 in 2008–2014 (Table 2). Herds are small and far apart with less than 7% of sheep farms and 3% of goat farms having 100 ewes/does or more (Virtanen et al., 2013).

There is very little import of live animals from outside the country that the authorities know. Within the time frame of this study, 2008–2014, 134 sheep and 2 goats were imported to Finland from Denmark (29.4%), Sweden (37.5%), Netherlands (22.1%) and Latvia (11%).

The Finnish sheep and goat populations mainly consist of national breeds and their crosses. The Finnish landrace breed constitutes almost half of all adult sheep in the country. Other important breeds include Kainuu Grey, Aland sheep, Texel and crossbred sheep. The proportional distribution of sheep breeds in Finland (Pr_{breed}) is presented in Table 3. The vast majority of all goats in Finland are Finnish landrace goats. There are also small numbers of British Saanen, British Toggenburg and African pygmy goats.

2.3. Scenario tree – models

We chose scenario tree modeling (Martin et al., 2007a) for the purposes of this study. We created the scenario trees on Excel 2010 spreadsheets and used the Excel add-in, PopTools, to conduct Monte Carlo simulations (Hood, 2011).

All factors influencing the probability of an individual animal being detected as positive for classical scrapie are represented by nodes in the scenario tree. The branches of the nodes represent all possible outcomes

Table 2
Numbers over 18-month-old sheep and goats in Finland in 2008–2014; the absolute and relative size of the two subpopulations: Fallen stock, slaughtered for human consumption and the number of animals sampled and tested for scrapie of both subpopulations.

	Year	Popn	FS	FS/Popn	SHC	FS/(FS + SHC)	SHC/(FS + SHC)	Sampled FS	Sampled SHC
Sheep	2008	51138	2007	0.0392	5545	0,2658	0,7342	1163	0
	2009	57235	2246	0.0392	6743	0,2499	0,7501	1136	5
	2010	59755	2345	0.0392	7488	0,2385	0,7615	946	0
	2011	67508	2625	0.0388	106-05	0,1984	0,8016	1248	3
	2012	67737	2683	0.0389	9854	0,2140	0,7860	1248	9
	2013	75585	3188	0.0422	9113	0,2592	0,7408	1361	11
	2014	82001	3100	0.0378	9677	0,2426	0,7574	1239	6
Goats	2008	4654	297	0.0638	16	0,9489	0,0511	274	0
	2009	4925	349	0.0709	47	0,8813	0,1187	349	0
	2010	4927	314	0.0637	67	0,8241	0,1759	268	0
	2011	4746	269	0.0567	172	0,6100	0,3900	216	1
	2012	4874	335	0.0687	166	0,6687	0,3313	177	0
	2013	5209	368	0.0706	145	0,7173	0,2827	251	0
	2014	5844	253	0.0433	89	0,7398	0,2602	138	0

SHC = slaughtered for human consumption, FS = fallen stock.