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Bayesian estimation of seroprevalence of small ruminant lentiviruses in sheep from Poland

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ABSTRACT

In Poland, no systematic survey of ruminant lentiviruses (SRLVs) infection was performed, neither at the national nor at the regional level and only limited knowledge exists on the prevalence of SRLVs among sheep. The aim of the present study was to establish the true prevalence of SRLVs infection in sheep from Poland at the animal and herd-levels. The blood samples used for this study were the fraction of samples collected by Veterinary Inspection during an official sampling for the national monitoring program for brucellosis. Under this program the animals and herds were randomly selected using the data available from ARMA (Agency for Restructuring and Modernisation of Agriculture). The sampling unit was the herd and the target population included at least 5% of sheep, over 6 months old, from each of 16 voievodships (provinces) of Poland. Two-stage cluster sampling design was performed in this study offering the possibility to determine the prevalence of SRLVs infection, when only a fraction of herds and a fraction of animals in the herds are tested. In total, 8233 sheep serum samples coming from 832 herds were tested by indirect ELISA. 1474 (17.9%) samples were positive and 261 (31.4%) herds with at least one seropositive animals were identified. The overall true prevalence estimated by the Bayesian framework was 9.3% (95% CI 6.8, 11.3) and 33.3% (95% CI 26.5, 38.2) on the animal and herd level, respectively. Large variation in the animal and herd prevalence between the voivodships was observed. True prevalence on the herd level varied from 0.0% (95% CI 0.0, 0.0) to 71.6% (95% CI 67.6, 75.9) whereas true prevalence on the animal level ranged from 0.0% (95% CI 0.0, 0.0) to 55.3% (95% CI 50.0, 61.2). The true prevalence of SRLVs infection at animal and herd level increased according to herd size as was proved by posterior probabilities (POPR).

1. Introduction

Maedi Visna Virus (MVV) together with Caprine Arthritis Encephalitis Virus (CAEV) belong to the cluster of viruses called small ruminant lentiviruses (SRLVs) within the *Lentivirus* genus of the *Retroviridae* family and infect sheep and goats. In sheep, the multisystem inflammatory diseases like pneumonia, arthritis, mastitis which often lead to chronic wasting, dyspnea and emaciation are the predominant clinical signs of SRLVs infection. Clinical disease tends to occur in adult sheep older than three years (Brodie et al., 1998), however, most of infected animals never develop clinical symptoms. Transmission occurs from an infected ewe to its offspring via colostrum and milk (Blacklaws et al., 2004) and horizontally by respiratory secretions (Berriatua et al., 2003). Other potential sources of virus transmission include milking and tattooing equipment and needles (Ghanem et al., 2009; Christodoulopoulos, 2006). One of the main features of SRLVs is their ability to cross the species barrier (cross-species infection) under field conditions. This gave basis for a new classification of SRLVs, which so far includes five phylogenetic groups (A–E). Genotype A and B, which involve MVV-like and CAEV-like isolates, respectively are the most common and widely distributed. Recent studies have shown that SRLVs isolated from sheep from Poland were classified mainly into the two new subtypes, known as A12 and A13 (Olech et al., 2012a).

Infection with SRLVs occurs worldwide, particularly in European and North America countries (Peterhans et al., 2004). Consequently, World Organisation for Animal Health (OIE) classified SRLVs as pathogens causing the main infectious disease of small ruminants. Considerable economic losses to the sheep industry are due to decreased lamb birth weight, delayed weight gain and increased mortality in offspring before weaning (Keen et al., 1997). In older sheep the infections are also associated with a higher incidence of mastitis, inflammation in the joints and changes in the central nervous system (Benavides et al., 2006; Calavas et al., 1998).

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Since neither treatment nor efficient vaccines are available, the control of disease is very difficult and is generally based on the early detection of the infection, using ELISA tests, and elimination of seropositive animals. However, the high genetic variability of SRLVs and the absence of sensitive diagnostic tools able to detect all local circulating strains are the barriers to successful implementation of eradication programs (Herrmann-Hoesing, 2010; De Andres et al., 2005; Reina et al., 2009).

In Poland, no systematic survey of SRLVs infection was performed, neither at the national nor at the regional level and only limited knowledge exists on the prevalence of SRLVs among sheep. The seroprevalence at herd level at 26.5% was recently reported in sheep from some regions (Olech et al., 2012b). However, the knowledge about the overall prevalence in Poland has not been reported so far. Thus, the aim of this study was to estimate the true prevalence of SRLVs infection in sheep from Poland at the animal and herd levels.

2. Material and methods

2.1. Population tested and sample collection

The blood samples used for this study were the fraction of samples collected by Veterinary Inspection during an official sampling for the national monitoring program for brucellosis. Under this program the animals and herds were randomly selected using the data available from ARMA (Agency for Restructuring and Modernisation of Agriculture). The sampling unit was the herd and the target population included at least 5% of sheep, over 6 months old, from each of 16 voievodships (provinces) of Poland. Two-stage cluster sampling design was performed in this study offering the possibility to determine the prevalence of SRLVs infection, when only a fraction of herds and a fraction of animals in the herds are tested. Serum samples were collected from 8233 sheep, which accounted for 1.6% of the total population of sheep in Poland, as was estimated using the data from ARMA. The animals came from 832 herds (5.0% of the total number of recorded herds), located in all 16 voivodships. An overview of the number of herds and animals per voivodship subjected to this study is given in Table 1.

2.2. Detection of antibodies

For serological survey the sera were separated from blood by centrifugation at 2000 rpm for 10 min and aspirated in Eppendorf tubes and stored at −20 °C until testing. The detection of antibodies against SRLVs was performed using a commercially available ELISA test (MAEDI VISNA/CAEV, IDEXX, Montpelier, France), according to manufacturer's recommendations. This test was based on indirect ELISA which uses an immunogenic peptide of a transmembrane protein and the recombinant p28 capsid protein.

2.3. Statistical analysis

The apparent and true prevalence of infection at the animal and herd level were estimated according to the overall population, voivodship and herd size. The apparent animal prevalence (p^A) was calculated as the number of test-positive animals among the total number of animals tested, while apparent herd prevalence (p^H) was calculated as test-positive herds among the total number of herds tested. A herd was considered positive when at least one animal showed the presence of antibodies in ELISA test. In this study we used beta–binomial models to estimate both the animal and herd prevalence according to a commonly accepted formula (Faes et al., 2011; Skellam, 1948; Kleinman, 1973; Williams, 1982). The estimation of the true animal (π^A) and herd (π^H) prevalence was obtained from apparent prevalence by correction for misclassification of diagnostic test via Rogan- Gladen estimator (Rogan and Gladen, 1978) using the equation:

$$p^A = \mathrm{Se}^A\pi^A + (1 - \mathrm{Sp}^A)(1 - \pi^A) \leftrightarrow \pi^A = \frac{p^A + Sp^A - 1}{Se^A + Sp^A - 1} \tag{1}$$

and

$$\begin{aligned}\pi^H &= \sum_{n_i=0}^{\infty} P(n_i)\left(1 - \prod_{k=0}^{n_i-1}\left[1 - \frac{p^A + Sp^A - 1}{Se^A + Sp^A - 1} + \frac{k(p^A + Sp^A - 1)\rho}{\{1 + (k-1)\rho\}(Se^A + Sp^A - 1)}\right]\right) \\ &= \sum_{n_i=0}^{\infty} P(n_i)\left(1 - \prod_{k=0}^{n_i-1}\left[1 + \frac{(p^A + Sp^A - 1)(\rho - 1)}{(Se^A + Sp^A - 1)\{1 + (k-1)\rho\}}\right]\right).\end{aligned} \tag{2}$$

This equations depends on the apparent animal prevalence p^A, the animal's test sensitivity Se^A and specificity Sp^A and the within-herd correlation of the disease status ρ. Prior estimation for sensitivity (Se) and specificity (Sp) of ELISA, based on published data was 98% and 97% for Se and Sp, respectively, as was estimated by the use of latent class model in Bayesian analysis (Toft et al., 2007). The parameters alpha (α) and beta (β) prior distributions for sensitivity and specificity were calculated using BetaBuster software and the respective values for αSe and βSe and for αSp and βSp were 2.21, 60.36, 329.66 and 11.16, respectively.

Because a two-stage sampling design was used in our study, the following correction was used to estimate herd prevalence, defined as the probability of having at least one infected animal in the herd

Table 1
Overview of the sampling scheme used in this study.

Voivodship	Number of animals	Number of tested animals	% of tested animals	Number of herds	Number of tested herds	% of herds	Weight
Dolnośląskie	25,942	590	2.3%	1042	84	8.1%	**0.6178**
Kujawsko-pomorskie	26,091	614	2.3%	507	26	5.1%	**0.9711**
Lubelskie	34,161	623	1.8%	988	78	7.9%	**0.6308**
Lubuskie	10,180	108	1.1%	369	35	9.5%	**0.5250**
Łódzkie	32,304	650	2.0%	1168	106	9.1%	**0.5487**
Małopolskie	136,694	391	0.3%	4680	126	2.7%	**1.8497**
Mazowieckie	16,631	30	0.2%	683	8	1.2%	**4.2516**
Opolskie	5607	114	2.0%	332	21	6.3%	**0.7873**
Podkarpackie	31,679	624	1.9%	1209	54	4.5%	**1.1150**
Podlaskie	41,518	675	1.6%	1139	81	7.1%	**0.7003**
Pomorskie	30,075	1042	3.4%	769	46	6.0%	**0.8325**
Śląskie	22,941	391	1.7%	1295	39	3.0%	**1.6536**
Świętokrzyskie	9922	691	6.9%	455	24	5.3%	**0.9441**
Warmińsko-mazurskie	25,565	480	1.8%	659	39	5.9%	**0.8415**
Wielkopolskie	46,215	651	1.4%	875	44	5.0%	**0.9903**
Zachodniopomorskie	17,361	559	3.2%	537	21	3.9%	**1.2734**
Total	**512,886**	**8233**	**1.6%**	**16,707**	**832**	**5.0%**	