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Short communication

Toxoplasma gondii in wild cervids and sheep in Finland: North-south gradient in seroprevalence

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ABSTRACT

A nationwide seroepidemiological study was conducted to estimate the prevalence of Toxoplasma gondii in selected wild and domestic ruminants in Finland. Serum samples from 1367 game cervids collected during the hunting season in 2008-2009 and 1940 sheep sera collected in 2008 were screened with a commercial direct agglutination test at a serum dilution of 1:40. T. gondii-specific IgG antibodies were detected in 116 (9.6%) of 1215 moose (European elk, Alces alces), 36 (26.7%) of 135 white-tailed deer (Odocoileus virginianus), 3 (17.6%) of 17 roe deer (Capreolus capreolus), and 477 (24.6%) of 1940 domestic sheep. Seropositive sheep were found in 74 (76.3%) of the 97 flocks examined. The odds of seropositivity in the adult moose was 2.9 times higher than the odds in calves; in white-tailed deer, the odds ratio was 3.2. The male moose had a significantly lower seroprevalence than the female, whereas the seroprevalence in the male white-tailed deer was higher than in the female; the odds ratios were 0.6 and 2.5, respectively. A clear geographical gradient in the seroprevalence was revealed in moose and sheep. The seroprevalences were lowest (1.6 and 8.6%, respectively) in the north and highest (24.6 and 36.4%, respectively) in the south-western regions, and ranged between these values in the other regions. In fact, the seroprevalence in moose from the south-west was not significantly different from the prevalence in white-tailed deer from the same area. Thus, the Finnish wild cervids and sheep are commonly exposed to T. gondii, especially in the southern part of the country.

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1. Introduction

The protozoan parasite *Toxoplasma gondii* can infect and cause disease in a wide range of animal species, including humans (Hill and Dubey, 2002). The major risk factor for humans is consumption of undercooked meat containing infective *T. gondii* tissue cysts, accounting for up to 63% of human infections (Cook et al., 2000). Cultural differences partly explain the varying seroprevalences in humans reported from different parts of the world, but

mutton and venison are generally regarded as important sources (Cook et al., 2000; Tenter et al., 2001; EFSA, 2007; Kijlstra and Jongert, 2008). Furthermore, not only consumption of meat but contact with the carcasses of wild game animals is among the discussed risk factors (Sacks et al., 1983; Ross et al., 2001; Vikoren et al., 2004).

Game cervids form a noteworthy source of meat in Finland. The annual game bag of roe deer, white-tailed deer and moose have been 3000, over 20,000 and up to 84,000, respectively; the latter forming 75% of the entire game meat yield of 10 million kilograms (Finnish Game and Fisheries Research Institute, 2009). Nevertheless, national estimates of the seroprevalence of *T. gondii* neither in these animals nor in domestic sheep have been tendered. The

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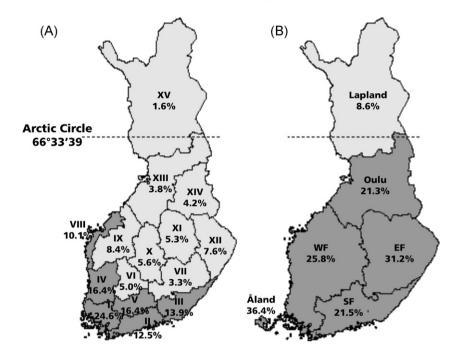


Fig. 1. Maps of Finland showing seroprevalence in moose by game management districts (I–XV) (A) and in sheep by provinces (B); the ones with a seroprevalence higher than 10% are hatched. The game management district was unknown for 27 moose. SF=Southern Finland; WF=Western Finland; FF=Fastern Finland

main aims of this study were to estimate these seroprevalences and to investigate geographical variation within the seroprevalences in moose and sheep.

2. Materials and methods

2.1. Sample sizes

Sample sizes were calculated with the expected seroprevalences of 10–20% for the moose and 30–40% for the deer, and 10–45% for the sheep. The latter was revised with an intra-cluster correlation coefficient of 0.2 and sampling of 20 sheep per flock. Thus, the aim was to screen samples from 700 moose, 350 deer, and 1920 sheep.

2.2. Samples from wild cervids

For the 2008–2009 hunting season, altogether 2917 sampling packages were sent to the 15 game management districts (Fig. 1) to be distributed to hunters. Each package included two plastic blood sample tubes and a short questionnaire covering the game management district and the species, age group (less than 1-year-old calf, or adult), and sex of the animal. Samples arrived at the laboratory within 4 days after the kill, and sera were separated and stored at -20 °C until analyzed.

All of the animals sampled were hunted for human consumption. The samples from 1215 moose (European elk, *Alces alces*) originated from all 15 districts (Fig. 1, Table 1). The deer samples, from 135 white-tailed deer (*Odocoileus virginianus*) and 17 roe deer (*Capreolus capreolus*), were collected only from the south-western districts, where these cervids are most numerous.

2.3. Samples from sheep

Sera of 1940 domestic sheep were included in the study. These samples were taken in 2008 by local veterinarians originally for another disease surveillance program, which restricted the sampling frame to adult animals (over 1 year of age) and flocks with 20 or more ewes. The samples originated from all 6 provinces (Fig. 1), altogether from 97 separate flocks (Table 1).

2.4. Serology

The sera were screened for *T. gondii*-specific IgG antibodies with a direct agglutination test (Toxo-Screen DA; bioMérieux SA, Marcy-l'Etoile, France), according to the manufacturer's instructions. The negative and positive controls provided in the kit were included in all plates. The sera were diluted 1:40, and samples positive at this dilution were defined as seropositive.

2.5. Statistical analysis

Cross-tabulations and test statistics (Chi square or Fisher exact) were used to evaluate unconditional associations prior to the multivariable logistic regression analysis with Stata 9.2 (StataCorp, College Station, Texas, USA). The age group was a dichotomous variable (calf-adult), as was sex (female-male). The game management districts and provinces were included in the models as dummy variables.

3. Results

T. gondii-specific IgG antibodies were detected in 116 (9.6%) of 1215 moose, in 36 (26.7%) of 135 white-tailed

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