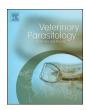
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#### Original article

## Seroprevalence of Fasciola hepatica in cattle in Estonia



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#### ARTICLE INFO

#### ABSTRACT

Keywords: Bovine Distribution ELISA Fasciolosis Liver fluke Serology Fasciolosis, an infectious disease caused by the liver fluke *Fasciola hepatica*, affects grazing cattle world-wide. Liver fluke *F. hepatica* is prevalent and well-documented in cattle in many European countries, but for the Baltic countries such information is limited. This study investigated the seroprevalence and distribution of *F. hepatica* in cattle in Estonia. A total of 2461 individual serum samples from 218 farms distributed throughout all 15 Estonian counties, collected between February 2012 and March 2013, were tested for specific anti-*F. hepatica* antibodies using an in-house enzyme-linked immunosorbent assay (ELISA). In total, 144 individual animals tested seropositive, yielding an animal-level seroprevalence of 5.9% (95% CI 5.0–6.9). The herd-level seroprevalence was 28.4% (95% CI 22.8–34.7) and the herds with at least one seropositive animal were located in 13 of the 15 counties. Of the 62 *F. hepatica*-positive herds, 14 (6.4%) had an in-herd seroprevalence higher than 25%. With respect to production type, the herd-level seroprevalence was 20.2%, 35.6%, and 36.4% in dairy, mixed, and beef herds, respectively. Animals from the two large islands had higher odds of testing *F. hepatica*-seropositive than animals from the mainland. Animals from mixed and beef herds had higher odds of testing *F. hepatica*-seropositive than animals from dairy herds. Mixed and beef herds had higher odds of testing *F. hepatica*-seropositive than animals from dairy herds. Mixed and beef herds had higher odds of testing *F. hepatica*-seropositive than animals from dairy herds. Mixed and beef herds had higher odds of testing *F. hepatica*-seropositive animal. This study provided the first serological evidence of the presence and distribution of *F. hepatica* in cattle herds in Estonia.

#### 1. Introduction

Fasciola hepatica, the causative organism of fasciolosis in ruminants, is a common liver fluke in temperate climate zones world-wide. In cattle, fasciolosis affects growth, fertility and carcass composition and reduces milk yield (Charlier et al., 2014). The annual financial losses due to fasciolosis in the global agricultural sector are estimated to exceed US \$3 billion (Cwiklinski et al., 2016).

Diagnosis and surveillance of *F. hepatica* in cattle at country level are often performed using detection of *F. hepatica*-specific antibodies in bulk tank milk (Salimi-Bejestani et al., 2005). National surveys of fasciolosis in dairy cattle have been performed in a number of European countries, including Belgium (Bennema et al., 2011), Germany (Kuerpick et al., 2013), Ireland (Selemetas et al., 2015), the UK (Salimi-Bejestani et al., 2005), and Sweden (Novobilský et al., 2015a). Although bulk tank milk ELISA (BTM-ELISA) is a convenient and efficient

tool for detecting exposure to liver fluke, its utility is limited to dairy cattle only. In addition, at least 20–27% of the cattle in the herd must be infected to obtain a positive response in BTM-ELISA (Salimi-Bejestani et al., 2005; Duscher et al., 2011). In beef cattle, serodiagnosis is based on individual serum samples (Novobilský et al., 2015b).

In Estonia, *F. hepatica* has been sporadically reported in cattle (Reek, 1963; Estonian Veterinary and Food Laboratory, 2016), but its distribution and current prevalence are not known. The main aims of this study were to estimate the seroprevalence and evaluate the geographical distribution of *F. hepatica* in cattle in Estonia. An additional aim was to evaluate potential risk factors for seropositivity.

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Table 1 Fasciola hepatica seroprevalence in cattle in Estonia, by age, breed, production type, herd size, and farm location. A herd was considered seropositive if at least one of up to 20 serum samples investigated tested positive.

	No. of farms	No. of positive farms	Prevalence % (95% CI <sup>d</sup> )	No. of animals	No. of positive animals	Prevalence % (95% CI <sup>d</sup> )
Age						
< 1 year				1	0	0.00 (0.00-95.00)
$\geq 1 < 2 \text{ years}$				109	10	9.17 (4.61–15.74)
≥ 2 < 3 years				845	39	4.62 (3.35–6.19)
≥ 3 < 4 years				340	18	5.29 (3.27-8.08)
≥ 4 < 5 years				293	22	7.51 (4.89–10.97)
$\geq 5 < 6 \text{ years}$				224	15	6.70 (3.94–10.57)
$\geq 6 < 7 \text{ years}$				216	13	6.02 (3.39–9.82)
$\geq 7 < 8 \text{ years}$				163	10	6.13 (3.16–10.66)
$\geq 8 < 9 \text{ years}$				82	2	2.44 (0.41–7.83) (ref)
$\geq 9 < 10 \text{ years}$				65	5	7.69 (2.87–16.23)
$\geq 9 < 10 \text{ years}$ $\geq 10 \text{ years}$				78	7	8.97 (4.01–16.95)
Breed <sup>a</sup>				76	,	8.97 (4.01=10.93)
Dairy breeds				00.4	40	4.00 (0.15 5.50)
Estonian Holstein				924	40	4.33 (3.15–5.79)
Estonian Red				365	8	2.19 (1.02–4.12)
Other <sup>b</sup>				17	0	0.00 (0.00–16.16) (ref)
Beef breeds						
Aberdeen-Angus				225	16	7.11 (4.27–11.06)
Hereford				391	25	6.39 (4.27-9.16) (ref)
Limousine				258	18	6.98 (4.32–10.60)
Other <sup>c</sup>				236	34	14.41 (10.35–19.33) <sup>e</sup>
Production type						
Dairy	104	21	20.19 (13.30-28.72) (ref)	1309	49	3.74 (2.81-4.88) (ref)
Mixed	59	21	35.59 (24.19-48.38)	591	50	8.46 (6.41–10.91) <sup>e</sup>
Beef	55	20	36.36 (24.50–49.63)	561	45	8.02 (5.98–10.49) <sup>e</sup>
Herd size						(,
≤ 50	107	24	22.43 (15.28-31.05) (ref)	750	36	4.80 (3.44-6.51) (ref)
$50 < n \le 100$	42	14	33.33 (20.39–48.51)	543	41	7.55 (5.55–10.01) <sup>e</sup>
> 100	69	24	34.78 (24.27–46.55)	1168	67	5.74 (4.51–7.18) <sup>e</sup>
Herd size, by production type	0)	2.1	31.76 (21.27 10.00)	1100	0,	3.7 ( (1.31 7.10)
Dairy herds ≤ 50	20	_	16 67 (6 97 99 15)	101	7	2.07 (1.71.7.50)
	30	5 3	16.67 (6.37–33.15)	181	7	3.87 (1.71–7.50)
$50 < n \le 100$	21		14.29 (3.77–34.14) (ref)	244	12	4.92 (2.69–8.21)
> 100	53	13	24.53 (14.38–37.40)	884	30	3.39 (2.34–4.75) (ref)
Mixed herds						
≤ 50	41	10	24.39 (13.11–39.18) (ref)	308	16	5.19 (3.11–8.13)
$50 < n \le 100$	9	3	33.33 (9.27–66.76)	126	5	3.97 (1.47–8.57) (ref)
> 100	9	8	88.89 (56.14–99.44) <sup>e</sup>	157	29	18.47 (12.98–25.12) <sup>e</sup>
Beef herds						
≤ 50	36	9	25.00 (12.94-40.95) (ref)	261	13	4.98 (2.80-8.16) (ref)
$50 < n \le 100$	12	8	66.67 (37.69–88.39) <sup>e</sup>	173	24	13.87 (9.31–19.64) <sup>e</sup>
> 100	7	3	42.86 (12.27–78.40)	127	8	6.30 (2.97–11.61)
Counties						
Northern counties	98	23	23.47 (15.88-32.61)	1132	52	4.59 (3.49-5.93) (ref)
Hiiumaa	6	3	50.00 (14.66-85.34) <sup>e</sup>	90	7	7.78 (3.47–14.78) <sup>e</sup>
Läänemaa	14	7	50.00 (25.13-74.87) <sup>e</sup>	187	24	12.83 (8.59-18.22) <sup>e</sup>
Raplamaa	19	3	15.79 (4.18–37.21)	203	8	3.94 (1.85-7.35) <sup>e</sup>
Järvamaa	18	4	22.22 (7.49–45.31)	197	4	2.03 (0.65–4.82)
Harjumaa	13	3	23.08 (6.23–50.86)	130	5	3.85 (1.42–8.32) <sup>e</sup>
Lääne-Virumaa	17	3	17.65 (4.69–40.89)	205	4	1.95 (0.62–4.64)
Ida-Virumaa	11	0	0.00 (0.00–23.84) (ref)	120	0	0.00 (0.00–2.47) (ref)
Southern counties	120	39	32.50 (24.58–41.26)	1329	92	6.92 (5.65–8.38) <sup>e</sup>
Võrumaa	18	8	44.44 (23.21–67.34) <sup>e</sup>	175	13	7.43 (4.19–12.06) <sup>e</sup>
	15	5	33.33 (13.38–59.21) <sup>e</sup>		7	
Valgamaa				179		3.91 (1.73–7.58) <sup>e</sup>
Põlvamaa	4	1	25.00 (1.25–75.77)	44	1	2.27 (0.11–10.70)
Pärnumaa	12	6	50.00 (23.38–76.62) <sup>e</sup>	154	27	17.53 (12.13–24.15) <sup>e</sup>
Saaremaa	41	15	36.59 (22.99–52.02) <sup>e</sup>	403	32	7.94 (5.59–10.89) <sup>e</sup>
Viljandimaa _	5	2	40.00 (7.35–81.76)	56	8	14.29 (6.86–25.33) <sup>e</sup>
Tartumaa	14	0	0.00 (0.00–19.26) (ref)	208	0	0.00 (0.00–1.43) (ref)
Jõgevamaa	11	2	18.18 (3.17-48.27)	110	4	3.64 (1.17–8.54) <sup>e</sup>
Total	218	62	28.44 (22.75-34.70)	2461	144	5.85 (4.98-6.83)

<sup>&</sup>lt;sup>a</sup> Breeds represented by more than 100 samples investigated are shown.

b Other dairy breeds: Estonian Native.

c Other beef breeds: Blonde d'Aquitaine, Belgian Blue, Charolais, Galloway, Highland cattle, Piedmontese, Simmental.

<sup>&</sup>lt;sup>d</sup> Confidence interval, Mid-P exact.

<sup>&</sup>lt;sup>e</sup> Significantly higher (*P*-value, Mid-P exact < 0.05) seroprevalence than the lowest (ref) seroprevalence within the variable.

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