

PREVALENCE OF STRONGYLE GASTROINTESTINAL NEMATODES IN SHEEP IN THE CZECH REPUBLIC

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Background. In sheep, gastrointestinal nematodes (GIN) are an important cause of parasitic gastroenteritis, a disease of great socioeconomic importance worldwide. Typically, all grazing animals are simultaneously infected with several GIN species. Their specific composition in the host and synergic clinical effect determine the severity of the disease.

The high burden of nematodes, together with increasing resistance to anthelmintics, has led us to focus on integrated control with justified and species-dependent use of drugs based on rapid and accurate diagnostics.

Commonly, the diagnosis of GIN is based on traditional coprological methods and morphological/morphometric analyses. Such approach is laborious, time-consuming, inaccurate and requires skilled experts. Modern molecular tools allow reliable and efficient identification of nematode species/genera and can thus be valuable for sustainable parasite control strategies.

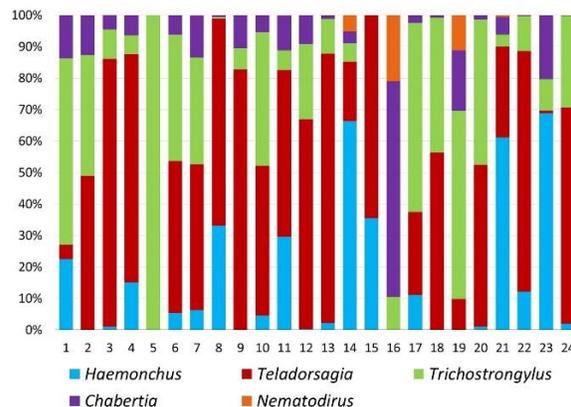


Strongylid type eggs (photo by J. Vadlejch)

Material and methods. During autumn 2019, about 600 individual faecal samples were obtained rectally from 34 farms in the Czech Republic. Samples (approx. 5 g) were collected from 10% of the animals in each flock. Of these, 455 samples have already been subjected to two multiplex real-time PCR assays targeting six species/genera of ruminant GIN (*Haemonchus*, *Teladorsagia*, *Trichostrongylus*, *Nematodirus battus*, *Chabertia ovina*, and *Ashworthius sidemi*) to detect and semi-quantitatively assess the intensity of infection.



Further details on the methodology are provided in the publication by Reslova *et al.*, 2021 (QR code).



Proportional representation of GIN species/genera derived from the sum of EPG values from all positively tested samples for each farm

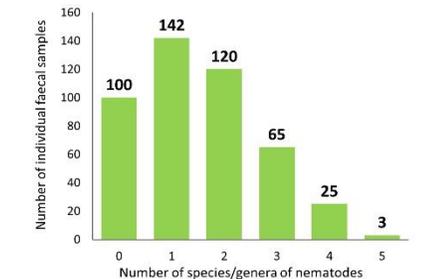
Farm no.	<i>Haemonchus</i>	<i>Teladorsagia</i>	<i>Trichostrongylus</i>	<i>Chabertia</i>	<i>Nematodirus</i>
1 (n=14)	14.3% (1,088)	7.1% (440)	71.4% (281)	78.6% (39)	0.0%
2 (n=20)	0.0%	20.0% (200)	45.0% (33)	25.5% (53)	0.0%
3 (n=18)	27.8% (29)	77.8% (854)	83.3% (117)	44.4% (64)	5.6% (9)
4 (n=21)	61.9% (213)	61.9% (1,287)	28.6% (84)	85.7% (99)	0.0%
5 (n=12)	0.0%	0.0%	8.3% (11)	0.0%	0.0%
6 (n=15)	13.3% (31)	26.7% (138)	53.3% (22)	40.0% (5)	0.0%
7 (n=21)	19.0% (34)	52.4% (113)	85.7% (23)	52.4% (26)	4.8% (5)
8 (n=11)	27.3% (4)	36.4% (515)	63.6% (11)	27.3% (57)	0.0%
9 (n=13)	0.0%	53.8% (223)	23.1% (89)	61.5% (17)	0.0%
10 (n=20)	5.0% (442)	50.0% (97)	95.0% (91)	55.0% (21)	0.0%
11 (n=30)	36.7% (107)	33.3% (230)	20.0% (38)	40.0% (26)	3.3% (5)
12 (n=21)	4.8% (8)	52.4% (37)	76.2% (28)	47.6% (6)	0.0%
13 (n=23)	4.3% (179)	34.8% (229)	65.2% (35)	17.4% (12)	0.0%
14 (n=25)	28.0% (45)	16.0% (104)	32.0% (7)	40.0% (12)	4.0% (169)
15 (n=20)	90.0% (22)	35.0% (100)	0.0%	0.0%	0.0%
16 (n=20)	0.0%	5.0% (1)	25.0% (8)	50.0% (42)	5.0% (161)
17 (n=15)	13.3% (27)	26.7% (26)	66.7% (29)	13.3% (6)	0.0%
18 (n=17)	0.0%	17.6% (109)	35.3% (45)	11.8% (3)	0.0%
19 (n=22)	0.0%	13.6% (245)	72.7% (147)	45.5% (40)	9.1% (321)
20 (n=16)	25.0% (18)	68.8% (292)	81.3% (435)	50.0% (13)	0.0%
21 (n=22)	27.3% (1,431)	27.3% (170)	36.4% (70)	77.3% (36)	13.6% (24)
22 (n=29)	58.6% (290)	69.0% (1,421)	75.9% (374)	44.8% (8)	6.9% (26)
23 (n=15)	26.7% (86)	6.7% (4)	26.7% (12)	26.7% (24)	0.0%
24 (n=15)	6.7% (13)	26.7% (77)	53.3% (22)	6.7% (1)	0.0%

Results. A total of five species/genera were confirmed in faecal samples of sheep: *Haemonchus*, *Teladorsagia*, *Trichostrongylus*, *N. battus*, and *C. ovina*. DNA of nematodes was detected in the range of ten to tens of thousands of eggs per gram (EPG) of faeces in each of the tested farms.

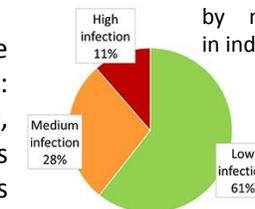
Most animals carry one, two or no tested GIN species/genera. In addition, the majority of sheep have a low infection intensity (up to 100 EPG), while only about 11% show a high infection burden (above 1,000 EPG).

Teladorsagia → *Haemonchus* → *Trichostrongylus*

Percentage of nematode species/genera detected on each farm. Median EPG values calculated from positively tested samples are shown in parentheses. *A. sidemi* DNA was not detected in any of the samples and was therefore not included.



Number of nematodes detected by multiplex real-time PCR assays in individual faecal samples (n=455)



Low (< 100 EPG), medium (100-1,000 EPG) or high (> 1,000 EPG) infection intensity was determined for each animal

Conclusion. To date, 455 individual samples from 24 sheep farms have been analysed by real-time multiplex PCR, which has proven to be a sensitive and reliable approach to identify GIN eggs present in faeces. Our results suggest that *Teladorsagia*, *Haemonchus* and *Trichostrongylus* are the most abundant species (in terms of EPG) being the main causative agents of sheep disease in the studied area.

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