

## Updates on *Trichinella* species infection in wild boar (*Sus scrofa*) from Southern Romania

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### Abstract

Romanians widely practice hunting; the meat of hunted animals, especially wild boar, can often avoid specific control for various reasons. Consequently, human trichinellosis in Romania is a zoonosis with a high incidence, with the consumption of uncontrolled pork and game being incriminated as the leading cause of human infection. Molecular analysis of *Trichinella* larvae collected by artificial digestion from wild boars hunted in several areas in Vâlcea County, Romania, revealed only one species, *Trichinella britovi*. The obtained results should alarm the human consumer, especially hunters, regarding the significance of veterinary control of the meat from the hunted animals.

**Keywords:** wild boar, Romania, molecular analysis, *Trichinella britovi*

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### 1. Introduction

Trichinellosis, a widespread zoonosis affecting mainly carnivore and omnivore mammals, is produced by species of the genus *Trichinella*. Currently, ten recognized species and three undefined genotypes are taxonomically accepted within the genus [1, 2]. Among them, *Trichinella spiralis* is the most well-known; pigs are most susceptible to infection, followed by carnivores and rodents [1, 3, 4].

Two cycles are defined in the epidemiology of trichinellids; the domestic one involves pigs, horses, synanthropic rodents, and domestic carnivores [5, 6]. The sylvatic cycle associates a large number of omnivorous and carnivorous species, rodents, birds, and reptiles. Of the ten accepted species of *Trichinella*, only *T. spiralis* is transmitted and maintained in the domestic cycle worldwide and can also spread in the sylvatic one [7]. However, it is not excluded that the sylvatic species to invade domestic habitats.

Out of the sylvatic genotypes, *T. britovi* is more specific to carnivores in temperate areas in Europe [8]. The flow of sylvatic *Trichinella* species from wildlife to domestic focus and in the opposite direction of *T. spiralis* from domestic to sylvatic animals is provided by multiple mechanisms [7]. Wild and domestic carnivores, through necrophagy and predation, the synanthropic and sylvatic rodents species, and humans by improper hunting habits, can transfer *Trichinella* species between the two cycles.

In Romania, numerous studies have reported an increased prevalence of *Trichinella* infection in wild species [9]. Of these, the wild boar is a significant source of human contamination [10]. Local and regional studies focused on this game species reported a prevalence varying between 0.1 and 23.5% [9]. Both *T. spiralis* and *T. britovi* were molecularly identified across the country. These studies covered Romania's North-Eastern and North-Western, Central, Western, South-Western, and South-Eastern regions [11].

In wild boars hunted in Southern Romania, we previously reported by artificial digestion a prevalence of 0.21% (3/1364) in a study carried out in Vâlcea County between 2017-2019 [10]. The current research aimed to identify the *Trichinella* species involved in infected wild boars hunted in the mentioned area using molecular analysis.

## Materials and methods

### 2.1. Geographic Location of the Hunting Area

The study was performed between January 2017 and December 2019 in 14 hunting grounds located in Vâlcea County, Southern Romania (Figure 1).

### 2.2. The collecting of *Trichinella* sp. larvae

All wild boars hunted in the period mentioned above were tested by artificial digestion. The method was performed at the County Sanitary-Veterinary Laboratory (CSVL) Vâlcea, according to the EU Regulation 1375/2015, to examine striated muscle tissue [12].

### 2.3. DNA extraction and molecular analysis

Five *Trichinella* sp. larvae isolated from each infected boar were used for DNA extraction. The PureLink® Genomic DNA Mini Kit (INVITROGEN®) was used for extraction according to the manufacturer's instructions. The DNA obtained and purified, free of proteins, nucleases, other contaminants, and inhibitors, was stored at -80°C until molecular analysis through PCR.

Molecular identification was carried out in the Parasitology Department, Faculty of Veterinary Medicine, Timisoara, by multiplex PCR according to the methodology described by Pozio and La Rosa [13]. Five pairs of primers were used to identify nine species/ genotypes of *Trichinella*, namely *T. spiralis*, *T. nativa*, *T. britovi*, *T. pseudospiralis*, *T. murelli*, *Trichinella* T6 genotype, *T. nelsoni*, *T. papuae*, and *Trichinella* T11 genotype (Table 1).

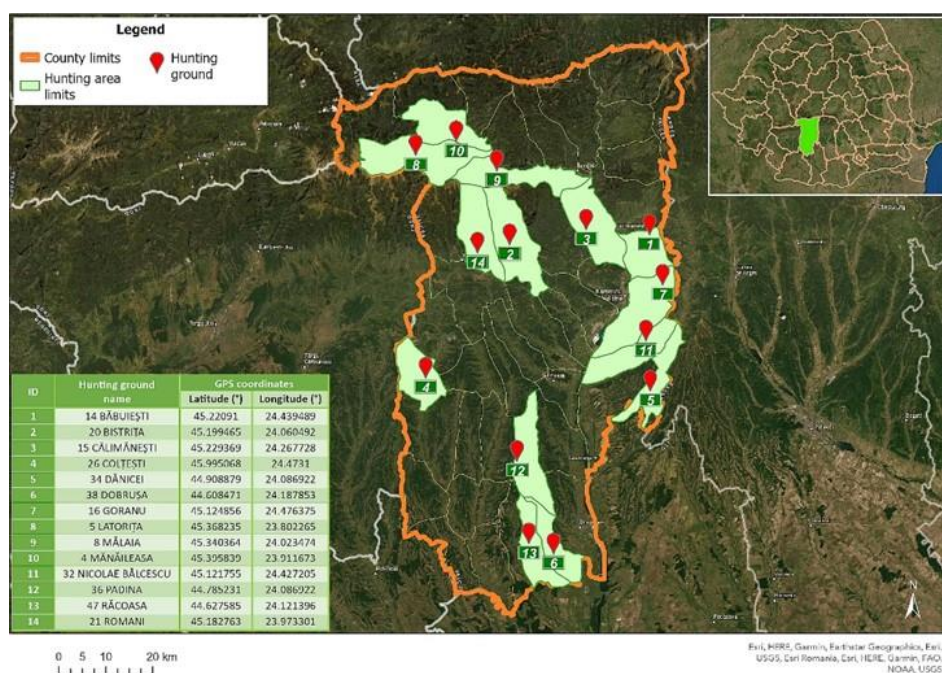


Figure 1. The location of the hunting grounds where the wild boars were collected

Table 1. The pair primers used in the study.

No	Pairs identified	Primer sequences (5'-3')
I.	5'-GTTCCATGTGAACAGCAGT-3'	5'-CGAAAAACATACGACAACACTGC-3'
II.	5'-GCTACATCCTTTTTTTTGT-3'	5'-AGACACAATATCAACCACAGTACA-3'
III.	5'-GCGGAAGGATCATTATCGTGT-3'	5'-ATGGATTACAAAGAAAAACCATCACT-3'
IV.	5'-GTGAGCGTAATAAAGGTGCAG-3'	5'-TTCATCACACATCTTCCACTA-3'
V.	5'-CAATTGAAAACCGCTTAGCGTGTTT-3'	5'-TGATCTGAGGTCGACATTTCC-3'

Master Mix MyTaq™ Red Mix (BIOLINE®) containing the necessary components in a concentrated form 2x was used to achieve the reaction. The final volume of the PCR reaction was 50 µl, of which 39.0 µl was represented by MyTaq™ Red Mix (BIOLINE®), 1 µl primer reverse, 1 µl primer forward of each pair, dilute to a concentration of 10 pmol/µl according to the protocol described by the manufacturer. The remaining components in the reaction were represented by DNA extracted from the sample to be analyzed and ultrapure water. Also, positive and negative controls were included in the reactions for each analysis.

The amplification program was made with the MyCycler thermo cycler (BioRad®). This program included the following steps: DNA denaturation cycle performed at 94°C for 5 minutes; 35 cycles of distortion at 94°C for 20 seconds, hybridization at 58°C for 30 seconds, and extension at 72°C for 1 minute; incubation of samples at 4°C.

The control of the amplicons was achieved by horizontal electrophoresis in a submerged system of electrophoresis in agarose gel 1.5% at 120 V and 90 mA for 60 minutes. HyperLadder IV DNA represented the standard of DNA molecular size - Bioline® 100 bp, which contains ten strips from 100 bp to 1000 bp.

After the samples migrated on the agarose gel, the gel image with DNA fragments was captured using a UV photosystem.

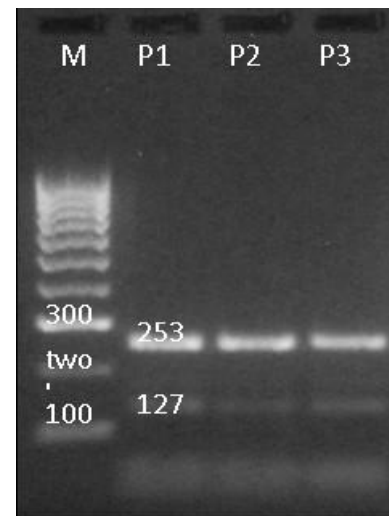
### 3.Results

Multiplex PCR demonstrated the presence of *T. britovi* in all three positive samples, two species-specific bands (127 and 253 bp) being revealed (Figure 2); no mixed infections were confirmed.

### 4.Discussion

Although *T. spiralis* and *T. britovi* are spread in the same environments in Europe, it is colloquially recognized that *T. britovi* is more prevalent in sylvatic carnivores, whereas *T. spiralis* is prevalent in both wild boars and domestic swine [8]. The results of the presented study seem to deny this statement since all three samples isolated from infected wild boars were confirmed as *T. britovi*. However, it is often reported *T. britovi* infects wild boars across Europe.

In Southern European countries, *T. britovi* was recently first reported in a wild boar originating from a defined risk area in Portugal [14].



**Figure 2.** PCR-based detection of *Trichinella britovi* in infected wild boars; M-molecular marker, P1, 2, 3 – analyzed samples

In Northeastern Spain, the species was identified in 0.009% (3/33206) tested wild boars; however, *T. spiralis* was the dominant species (0.32%, 109/33206) in the area [15]. *T. britovi* is also reported in wild boar in Bosnia and Herzegovina [16]. In Bulgaria, *T. britovi* affected 97.83% of the examined wild boars, whereas *T. spiralis*, only 2.17% [17]. In Croatia, *T. britovi* was identified in 14 of the 38 (36.8%) molecularly tested samples from wild boars examined between 2010–2017 [18]. In Greece, even if all examined wild boars hunted during 2019–2020 were negative for *Trichinella* spp., [19] human infections with *T. britovi* are reported, wild boar meat or semi-raw pork being incriminated [20]. In Italy, *T. britovi* is reported in wild boar in different regions [21] being also involved in numerous human outbreaks, with the meat of this species as the source of infection [22, 23, 24]. Additionally, *T. britovi* was isolated from wild boar meat linked to a human trichinellosis outbreak in Serbia, suggesting the significant role of wild boars as reservoirs of this species in the country [25].

*Trichinella britovi* was also frequently reported in wild boars from Northern and Western Europe. Although *T. nativa* is the dominant species in the wildlife of the Nordic countries, an outbreak of human trichinellosis is described in Sweden with the source of wild boar meat contaminated with *T. britovi* [26].

The presence of *T. britovi* in wild boar is also indirectly confirmed in France through reporting some human outbreaks with the meat of this species as the source [27, 28]. A 38-year study in Latvia established an overall prevalence of 2.5% infected wild boar, *T. britovi* being the predominant (90%) species [29]. In Estonia, *T. britovi* has registered a total prevalence of 0.7%, but mixed infections with *T. spiralis* (0.01%) and *T. nativa* (0.02%) were also identified [30]. In Lithuania, 72% (31/43) of the examined wild boars were infected with *T. britovi* [31].

*Trichinella britovi* infection in wild boars is also reported in Central European countries. In Poland, *T. britovi* was identified in 23.8% of the wild boars' infected carcasses [32]. In Hungary, *T. britovi* was dominant in wild boars since 64.7% of the infected animals were infected with mentioned species, only 29.4% with *T. spiralis*, and 5.9% with *T. pseudospiralis* [33]. In Slovakia, *T. britovi* is also the predominant etiological agent of the sylvatic cycle, reported in 99% of the infected wild boars [34].

In Romania, *T. britovi* infection in wild boars is reported in the North-Eastern part of the country, where the recorded prevalence was 1.46% (156/10,695) [35]. Three samples collected from wild boars in Central Romania were confirmed as *T. britovi* [36]. In Eastern and Western Romania, the overall prevalence of *Trichinella* sp. in wild boars was 1.66% (93/5596), with *T. britovi* being identified in 34 (36.5%) of the infected animals [37]. Here, we also confirmed the presence of the species in the southern part of the country.

*Trichinella britovi* is the most widely distributed species within the temperate climate; apart from Europe, it is also spread in Asia and Northern and Western Africa [24]. In hunted wild boars in Northern Iran, the overall prevalence of *Trichinella* spp. infection was 5.7% (2/35), *T. britovi* being the most prevalent species circulating in wild boars of Iran [38]. The human outbreaks caused by consuming hunted wild boars' meat confirmed the presence of *T. britovi* in Turkey [39, 40].

Analyzing the data presented above, the hypothesis of parasitism, to the same extent, of wild carnivores and wild boars by *T. britovi* emerges, thus disproving the statement that this species is more prevalent in wild carnivores. Indeed, following the recognition of *T. britovi* as an independent species, it was initially identified in many wild carnivore

species, leading to the idea of a specific carnivore species. However, equal parasitism of wild boar and carnivores by *T. britovi* demonstrates that the existing inter-relationships within the sylvatic focus are much more complex, requiring further investigations.

## Conclusions

The presence of *T. britovi* in wild boars across Romania is a certainty. Thus, wild boar meat poses a high zoonotic risk, especially for private domestic use and the estrangement of untested meat. Consequently, it is essential to raise hunters' awareness of the risk that the consumption of wild boar meat can represent. Adjusting the health measures to minimize the infection risk of humans appears to be significant in reducing consumer risk. Concluding, the surveillance and control of *Trichinella* infection in wild boars must be maintained and promoted.

**Acknowledgements:** This scientific paper was carried out in the Laboratory of Parasitology and Parasitic Disease at the ULS/Faculty of Veterinary Medicine Timisoara, Laboratory within the Animal Hygiene and Pathology Research Center

**Compliance with Ethics Requirements:** Authors declare that they respect the journal's ethics requirements. Authors declare that they have no conflict of interest and all procedures involving human or animal subjects (if exist) respect the specific regulation and standards.

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