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The opportunistic nature of *Trichinella*—Exploitation of new geographies and habitats

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ABSTRACT

For more than 100 years, *Trichinella spiralis* (former *Trichina spiralis*) was considered a zoonotic parasite of the domestic habitat involving pigs, synanthropic rats and humans. In the last 70 years, there has been increasing evidence that the biomass of nematodes of the genus *Trichinella* is greater in wild animals than in domestic animals. Omnivores and carnivores (mammals, birds and some reptiles), mainly those with cannibalistic and scavenger behaviour, act primarily as reservoirs for the 12 *Trichinella* taxa recognized to date. The distribution areas of *Trichinella* spp. hosts can help to identify the environmental suitability where the different *Trichinella* taxa can be detected. Both the survival of larvae in decaying muscles of their hosts, which is favoured by high humidity and low temperatures, and human behaviour in the domestic and wild habitats play roles in the transmission patterns of these nematodes. Although *Trichinella* taxa develop in different host species circulating in different geographical regions, there is a common denominator among the hosts, namely their scavenging behaviour.

1. Introduction

The great impact of *Trichinella spiralis* on the pork industry and human health in the 19th and 20th centuries has strongly influenced the epidemiological view of this zoonosis. This was mainly related to the domestic habitat where both pigs and synanthropic rats were considered the major participants in the natural cycle (Pozio and Murrell, 2006). In the last 70 years, there has been increasing evidence that the biomass of nematodes of the genus *Trichinella* is greater in wild animals than in domestic animals and that the domestic foci of *T. spiralis* represent only an epiphenomenon of the natural cycle of these helminths. Omnivorous and carnivorous mammals, birds and reptiles, mainly those with cannibalistic and scavenger behaviour, act predominantly as reservoirs for the 12 *Trichinella* taxa recognized to date (Pozio et al., 2009a,b). Over the course of millions of years, nematodes of the genus *Trichinella* have colonized new hosts and geographical regions (Zarlenga et al., 2006), thanks to their opportunistic nature. The aim of the present work was to briefly summarize the distribution areas and the host spectrum of the standing species and genotypes identified in this genus.

2. Materials and methods

The information provided in this work originates from the database of the International Reference Laboratory for *Trichinella* (IRLT), which is the repository of more than 3800 isolates (http://www.iss.it/site/Trichinella/index.asp), and the source of eight published papers which identified a significant number of *Trichinella* sp. isolates from Eurasia and North America (Shaikenov and Boev, 1983; Kanai et al., 2007; Malakauskas et al., 2007; Burke et al., 2008; Masuoka et al., 2009; Pozio et al., 2009a,b; Gajadhar and Forbes, 2010).

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3. Results and discussion

Of the 4644 encapsulated *Trichinella* spp. isolates identified to date at the species or genotype levels, 44.8% were identified as *Trichinella britovi*, 39.9% as *T. spiralis*, and 10% as *Trichinella nativa*; the other six encapsulated taxa only account for 5.16% of the total (Table 1). Since each *Trichinella* taxon, with the exception of *T. spiralis*, has its own distribution area, these data could be biased by the number of hosts investigated on each continent given that most of them originate from Europe. The most representative hosts are those of the Suidae family which account for 51.8% of the total. The second most important hosts are those of the Canidae family, which account for 37.1% of the total (Table 1). All the other nine families of mammals that have been found to host *Trichinella* spp. larvae only account for 11.1%.

Undoubtedly, the quality system concerning the repository of IRLT and data from published papers are biased by the types of investigations. Most investigations focused on domestic pigs and wild boars, with the aim of preventing infections in humans, and on canids (mainly foxes but also jackals, coyotes and wolves), which are at the top of the food chain. As a result, they represent good targets for monitoring the circulation of these zoonotic parasites in any given region or country.

The high prevalence of *T. spiralis* in the Muridae and Equidae families is only an epiphenomenon due to the relationship between synanthropic rodents and horses and the domestic habitat where *T. spiralis* circulates. *T. spiralis*-infected rats or horses have always been found to originate from farms or localities where there was a high prevalence of this parasite in domestic pigs.

The dissemination of *T. spiralis* differs from that of the other encapsulated species with respect to its focal distribution (Fig. 1, panel A), where the other encapsulated species show uninterrupted areas of distribution (Fig. 1, panels B–I). This focal distribution could originate from the passive introduction of *T. spiralis* from Asia to Europe and the Americas (Rosenthal et al., 2008) and could also be influenced by the high adaptability of this zoonotic parasite to the domestic pig.

The number of non-encapsulated *Trichinella* spp. isolates identified to date is too small to have a clear epidemiological picture of this group (Table 2). For *Trichinella pseudospiralis*, swine appear to play a more important role than carnivores as a reservoir (54.2% versus 27.0%). The role of birds in the epidemiology of *T. pseudospiralis* is still undefined given the low numbers of carnivorous and omnivorous birds tested. Undoubtedly, the very broad distribution area of *T. pseudospiralis* encompassing North America, Eurasia, and Australasia can be explained only by its predominant transmission through birds (Fig. 1, panel J). Our knowledge on the distribution area of *Trichinella zimbabwensis* in Africa (Fig. 1, panel K) and of *Trichinella papuae* in Australasia (Fig. 1, panel K) is incomplete. Furthermore, we do not know which of the two host groups, reptiles or mammals, plays a more important role as reservoir in the natural cycle of these parasites. If Nile crocodiles (*Cocodylus niloticus*) in Africa and saltwater crocodiles (*Cocodylus porosus*) in Australasia are the major reservoirs of

Table 1
Relationship between host family and encapsulated *Trichinella* taxa. The first number in parentheses is the percentage of each host family out of the total number of isolates tested for each *Trichinella* taxon. The second number is the percentage of each *Trichinella* taxon out of the total of infected hosts for each family. For the Suidae family, the information is also split between domestic and sylvatic swine (in italics). For the data source, see Section 2.

Host	*Trichinella* species[a]									Total
Family	Ts	Tna	T6	Tb	T8	Tm	T9	Tn	T12	
Suidae	1629 (87.9; 67.8)	7 (1.5; 0.3)	0	767 (36.8; 32.0)	0	0	0	1 (5.9; 0.04)	0	2404 (51.8)
Domestic	*976 (52.7; 93.4)*	*0*	*0*	*69 (3.3; 6.6)*	*0*	*0*	*0*	*0*	*0*	*1045 (22.5)*
Sylvatic	*653 (35.2; 48.0)*	*7 (1.5; 0.5)*	*0*	*698 (33.5; 51.4)*	*0*	*0*	*0*	*1 (5.9; 0.04)*	*0*	*1359 (29.3)*
Muridae	45 (2.4; 83.3)	0	0	9 (0.4; 16.7)	0	0	0	0	0	54 (1.2)
Canidae	128 (6.9; 7.4)	329 (70.9; 19.1)	21 (16.4; 1.2)	1185 (56.9; 68.8)	0	31 (58.5; 1.8)	27 (71.0; 1.6)	2 (11.8; 0.1)	0	1723 (37.1)
Equidae	20 (1.1; 80.0)	0	0	4 (0.2; 16.0)	0	1 (1.9; 4.0)	0	0	0	25 (0.5)
Felidae	17 (0.9; 10.8)	51 (11.0; 32.5)	8 (6.2; 5.1)	63 (3.0; 40.1)	4 (57.1; 2.5)	3 (5.7; 1.9)	0	8 (47.0; 5.1)	3 (100; 1.9)	157 (3.4)
Herpestidae	0	0	0	1	0	0	0	0	0	1 (0.02)
Hyaenidae	0	0	0	0	3 (42.9; 33.3)	0	0	6 (35.3; 66.6)	0	9 (0.2)
Mustelidae	2 (0.1; 1.4)	29 (6.2; 20.0)	96 (75.0; 66.2)	18 (0.9; 12.4)	0	0	0	0	0	145 (3.1)
Procyonidae	0	0	0	0	0	12 (22.6; 54.5)	10 (26.3; 45.4)	0	0	22 (0.5)
Ursidae	11 (0.6; 11.0)	48 (10.3; 48.0)	3 (2.3; 3.0)	31 (1.5; 31.0)	0	6 (11.3; 6.0)	1 (2.6; 1.0)	0	0	100 (2.1)
Viverridae	0	0	0	4 (0.2; 100)	0	0	0	0	0	4 (0.09)
Total	1852 (39.9)	464 (10.0)	128 (2.7)	2082 (44.8)	7 (0.1)	53 (1.1)	38 (0.8)	17 (0.4)	3 (0.06)	4644

[a] Ts, *T. spiralis*; Tna, *T. nativa*; T6, *Trichinella* T6; Tb, *T. britovi*; T8, *Trichinella* T8; Tm, *T. murrelli*; T9, *Trichinella* T9; Tn, *T. nelsoni*; T12, *Trichinella* T12.