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Short Communication

Environmental determinants of the spatial distribution of *Trichinella britovi* and *Trichinella spiralis* in Hungary

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ABSTRACT

Trichinella spiralis and *Trichinella britovi* are the two most common species of the genus *Trichinella* persisting in the European wildlife. To investigate the spatial distribution of these *Trichinella* spp. and the factors influencing their circulation in Hungary, 3304 red foxes (*Vulpes vulpes*) and 0.29 million wild boars (*Sus scrofa*) were tested for *Trichinella* sp. infection in Hungary from 2006 to 2013. *Trichinella* spp. larvae from 68 (2.06%) foxes and 44 (0.015%) wild boars were identified by a multiplex PCR as *T. britovi* or *T. spiralis*. The locality of origin of foxes and wild boars were recorded in a geographic information system database. There was no correlation between environmental parameters in the home range of foxes and wild boars and the *T. spiralis* larval counts, but there was a positive correlation between the boundary zone of Hungary and *T. spiralis* infection ($P < 0.0001$; odds ratio: 24.1). These results indicate that the distribution of *T. spiralis* in the Hungarian wildlife is determined by the transborder transmission of the parasite from the surrounding endemic countries. Multiple regression analysis was performed with environmental parameter values and *T. britovi* larval counts. Based on the statistical analysis, non-agricultural areas (forests, scrubs, herbaceous vegetation and pastures) and the mean annual temperature ($P < 0.0001$; odds ratios: 9.53 and 0.61) were the major determinants of the spatial distribution of *T. britovi* in Hungary. The positive relationship with non-agricultural areas can be explained by the generalist feeding behaviour including scavenging of foxes in these areas. The negative relationship with the mean annual temperature can be attributed to the slower decomposition of wildlife carcasses favouring a longer survival of *T. britovi* larvae in the host carrion and to the increase of scavenging of foxes.

1. Introduction

Nematode parasites of the genus *Trichinella* are among the most widespread zoonotic pathogens in the world (Pozio and Murrell, 2006). In Hungary, *Trichinella britovi* is the most common species circulating among carnivore and omnivore wild animals (Széll et al., 2008, 2012). To assess the consumer risk for *T. britovi* and *Trichinella spiralis* infections, it is important to know the spatial distribution pattern of these parasites and environmental factors (e.g., temperature, land cover) influencing this pattern. Geographical information systems (GIS) represent new tools for studying the spatial distribution of parasites (Rinaldi et al., 2006). To investigate environmental factors which

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can play a role in *Trichinella* spp. transmission in wildlife, red foxes and wild boars, the most important indicator species of these parasites in the European wildlife, were sampled and examined for *Trichinella* spp. infection in Hungary. The pattern of infection in foxes and wild boars, and the relationship of these patterns with landscape and climate was analysed by GIS.

2. Materials and methods

2.1. Sample collection, parasite isolation and identification

From November 2008 to February 2013, carcasses of red foxes killed by hunters in Hungary were sent in individual plastic bags to the National Food Chain Safety Office of Budapest. Carcasses were labelled by the hunters with an identification number reporting the information on the nearest place to killing on the topographic map. Red fox carcasses, representing more than 4% of the total fox population of each county, were randomly selected out of all the foxes from 19 counties and from the Budapest municipality (Fig. 1). Muscle samples were collected and examined as previously described (Széll et al., 2008).

Between June 2006 and September 2013, a total of 0.29 million hunted wild boars were tested at official control laboratories for *Trichinella* sp. larvae during routine meat inspection. When a *Trichinella* spp. positive animal was detected, a 100 g sample was collected from the predilection muscles and sent to the National Food Chain Safety Office, Budapest, Hungary, for the confirmatory diagnosis, evaluation of the worm burden (number of larvae/g, LPG) and parasite isolation (Széll et al., 2012). As the place of killing of uninfected wild boars is not recorded in Hungary, these data could not be included in the analysis.

Trichinella spp. larvae were washed, counted, and forwarded to the Istituto Superiore di Sanità, Rome, Italy, for the species identification as previously described (Széll et al., 2008, 2012).

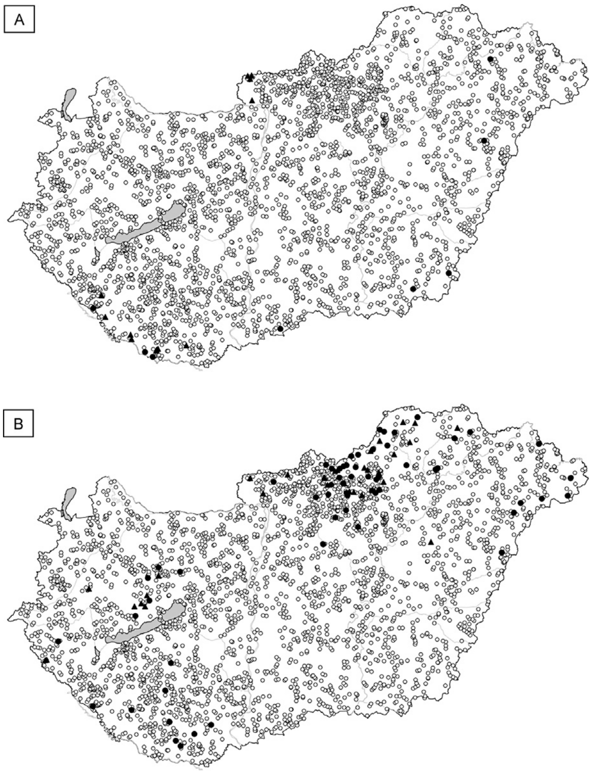

Fig. 1. Map of Hungary showing animals sampled from 2006 to 2013. Panel A: uninfected and *Trichinella spiralis* infected red foxes (*Vulpes vulpes*) (circles) and wild boars (*Sus scrofa*) (triangles). Panel B: uninfected and *Trichinella britovi* infected red foxes (circles) and wild boars (triangles).

2.2. Geographic information system database, spatial and statistical analysis

The locality of origin of foxes and wild boars and the number of larvae/g were marked on a point layer by the Quantum GIS 1.8.0 software QGIS Team (2012). The vector layers of altitude, land cover, permanent water bodies, protected areas according to the Hungarian Law No. LII/1996 (national parks, landscape protection areas, nature conservation areas), soil water retention and soil permeability, were obtained from VÁTI Hungarian Nonprofit Ltd. for Regional Development and Planning (Budapest, Hungary). The vector layers of the mean annual temperature and annual precipitation were created and vector-based analysis was carried out by the Quantum GIS 1.8.0 software on the basis of the georeferenced digital map of the Hungarian Meteorological Service. The spatial resolution of the vector layers varied from 10 m (land cover, country border) to 50–100 m (other layers). The radius around the locality of animal origin was restricted to 2.5 and 3.0 km, which was assumed to represent the average home range of foxes and wild boars, respectively (Staubach et al., 2001; Calenge et al., 2002). Along permanent water bodies, a 100 m wide buffer zone was created, where the probability of the presence of reservoir hosts was high. Along country border, a 10 km wide buffer zone was created to evaluate the transborder transmission of these parasites from neighbouring countries. The digitised home range and the vector data were used to calculate the altitude, mean annual temperature, annual precipitation, areas of land cover types, and the buffer zones of permanent water bodies and country borders. The associations between environmental factors and the larval burden of *T. britovi* and *T. spiralis* infection were analysed by multiple linear regression analysis and logistic regression analysis as previously described (Tolnai et al., 2013).

3. Results

T. spiralis larvae were detected in 8 foxes and 12 wild boars (Table 1). *T. britovi* larvae were identified in 60 foxes and 32 wild boars (Table 1). The spatial distribution of *T. britovi* and *T. spiralis* was highly clumped in Hungary (Fig. 1).

There was no correlation between environmental parameters and the *T. spiralis* LPG. The multiple regression analysis and the logistic regression analysis show a positive correlation (95% CI of odds ratios: 3.81–108.3) between the