

Occurrence and vector role of *Haemaphysallis concinna* in Western Poland

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INTRODUCTION. The relict tick *Haemaphysalis concinna* (Koch, 1844) occurs in Europe and Asia in isolated, limited locations (Rubel 2018). In its areas of occurrence it constitutes, together with *Ixodes ricinus* and *Dermacentor reticulatus* a significant part of human and domestic animals (cats, dogs) ectoparasites. Adult ticks feed on roe deer, red deer and farm animals (cattle, goats, sheep). Larvae and nymphs prey on small rodents, birds and reptiles. Humans can be infested with nymphs and adult stages of this tick.

A single female *H. concinna* was found in close proximity to the German-Polish border and Baltic Sea shore, in Troszyn, N. West Pomerania in 1953, 65 years ago. It was just last year when, unexpectedly, new foci were discovered in SW Poland (Kiewra *et al.,* 2019).

In the same year, during field study aimed to collect juvenile D. reticulatus from rodents, we found a new focus of *H. concinna* in the vicinity of Wolsztyn, wielkopolskie voivodeship. From 39 rodents (*Apodemus* and *Microtus* spp.) a total of 427 *H. concinna* specimens (405 larvae, 22 nymphs) were collected. The highest prevalence and abundance of *H. concinna* was recorded on voles, *Microtus agrestis* and *M. oeconomus*. Prevalence of infestation with *H. concinna* was above 50%, mean abundance exceeded 4 ticks/rodent, mainly due to the high number of *H. concinna* larvae.

There is not much data regarding pathogens vectored by *H. concinna*. It is known, that this tick species may vector *Rickettsia* spp., the etiological agents of TIBOLA/DEBONEL. Haemaphysalis concinna is also known to vector protozoa of *Babesia* genus, including *Babesia canis*, the etiological agent of canine babesiosis. Furthermore, *H. concinna* nymphs infected with *Borrelia* spirochetes were discovered in Hungary.

AIM. Determining the role of the relict tick *H. concinna* as a vector of *Rickettsia*, *Borrelia* and *Babesia* pathogens in Poland.

MATERIALS AND METHODS. Larvae and nymphs were subject to DNA extraction. Larvae were processed in pools, comprising 1–10 larvae from single host, nymphs were processed individually. For DNA isolation the commercially available Genomic DNA MINI AX TISSUE SPIN (A&A Biotechnology) kit was used, according to manufacturer's recommendations. For the detection of Rickettsia spp., the 750 bp gltA gene fragment was amplified in a single-step PCR with CS409 and Rp1258 primers. For the detection of *Borrelia burgdorferi*, the 605 bp fragment of flagellin gene was amplified in a nested PCR. In the first reaction, 132f and 905r primers were used for

amplification of a 774 bp fragment; in the second step 220f and 824r primers were used for amplification of the 605 bp flagellin gene fragment. For the detection of *B. canis*, a 380 bp fragment of mitochondrial COI gene was amplified. Selected PCR products were sequenced, aligned and analyzed. Phylogenetic trees were constructed using the BLAST NCBI and MEGAv6 software.

Results and conclusion: Different prevalence of pathogens was detected in examined *H. concinna* tick. Influence of host species on the frequency of pathogen detection in ticks was observed. Obtained results will contribute to knowledge on *H. concinna* vector role.

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