

## Hemoparasites of wild living carnivores

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The currently observed changes in natural ecosystems, the ongoing urbanization process and climate change contribute to the increased interaction of wild and domestic animals, as well as the spread of vectors of selected parasites and pathogens, including those with zoonotic potential. In the epidemiology and epizootiology of vector-borne diseases (VBD), apart from the knowledge of individual species of parasites and arthropod species acting as vectors, data on the host and reservoir competences of various animal taxa, including domestic, synanthropic and invasive species, are important, in connection with ecological dependencies (eco-epidemiology).

The aim of the research was to describe the diversity of VBP pathogens in wild living carnivores, with particular emphasis on invasive species, and with regard to the possibility of overcoming host specificity. The area of south-western Poland was selected for the study, where the expansion of invasive species, i.e. raccoon and raccoon dog, has been observed in recent years. The research material consisted of tissue fragments (spleen, liver, skin) collected from co-occurring invasive carnivores (raccoon dog, raccoon) and native (red fox, European badger, beech marten and pine marten). The study material was obtained thanks to the cooperation with the Ruszów Forest District, as a part of the project of capercaillie

reintroduction in Bory Dolnośląskie (grant LIFE11 NAT/PL/428) and the related control of predators. Pathogen detection was carried out using molecular methods (PCR, nested PCR, qPCR), the selection of genetic markers was made on the basis of literature data and own study.

DNA isolated from the tissues of 340 carnivore individuals obtained from the Bory Dolnośląskie 2017-2020 was subjected to molecular analysis. The presence of DNA of vector-borne pathogens belonging to the following genera was found: *Babesia*, *Theileria*, *Hepatozoon*, *Anaplasma*, *Ehrlichia*, *Candidatus Neoehrlichia*, *Borrelia* and *Rickettsia*. In case of hemoparasites, the total prevalence of blood protozoa in the studied animals was 64.3% (from 91.1% in badgers to 31.1% in raccoon dogs), and bacteria of Anaplasmataceae family was 22.7% (from 41.2% in badgers to 9.8% in raccoon dogs). The analysis of the obtained nucleotide sequences allowed for a detailed taxonomic identification of individual isolates, and for determining the specificity of the pathogen-host relationships. The greatest diversity of taxa was found in the raccoon, and the smallest in the badger. However, the badger turned out to be the host for its own specific haemoparasites, unlike the raccoon, which „adopted” pathogens occurring in other animals, not only carnivores.