

MOLECULAR DETECTION OF RICKETTSIA PATHOGENS IN ECTOPARASITES OF RED FOXES

Raminta Likšaitė¹, Ugnė Medikaitė¹, Indrė Lipatova¹, Justina Snegiriovaitė¹, Renata Špinkytė¹, Algimantas Paulauskas¹

¹Vytautas Magnus University, Kaunas, Lithuania
raminta.liksaite@stud.vdu.lt

The population of red foxes (*Vulpes vulpes*) has increased rapidly over recent decades, raising concerns about their role as reservoirs of parasites and pathogens of veterinary and medical importance [1,2]. Ectoparasites associated with foxes may contribute to the maintenance and transmission of zoonotic pathogens, including bacteria of the genus *Rickettsia* [3]. However, data on the occurrence of *Rickettsia* spp. in fox ectoparasites remain limited. The aim of this study was to evaluate the presence of *Rickettsia* spp. pathogens in ectoparasites collected from red foxes using molecular methods.

Ectoparasites were collected from nine red foxes and identified morphologically. DNA was extracted from individual ectoparasites, and *Rickettsia* spp. were detected using real-time PCR targeting the *gltA* gene. Positive samples were further analyzed by nested PCR amplifying a 381 bp fragment of the *gltA* gene, followed by sequencing for species identification.

A total of 109 ectoparasites were collected, including fleas (80.73%, n = 88) and ticks (19.27%, n = 21). *Rickettsia* DNA was detected in 9.52% of ticks (2/21) and 1.83% of fleas (2/88). Sequence analysis identified *Rickettsia* spp., *Rickettsia helvetica*, and *Rickettsia conorii* subsp. *raoultii*. These findings demonstrate the presence of several zoonotic *Rickettsia* species in fox-associated ectoparasites. The detection of pathogenic *Rickettsia* species in ectoparasites of red foxes highlights their potential role in the circulation of zoonotic pathogens. These results emphasize the importance of monitoring wildlife ectoparasites to better understand the epidemiology and public health risks associated with *Rickettsia* infections.

Keywords: *Rickettsia*, *Vulpes vulpes*, ticks, fleas

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