

## Flea community and their role as vectors of *Bartonella* bacteria in three isolated populations of bank voles from the Mazury Lake District

Mohammed Alsarraf<sup>1</sup>, Dina Al-Qazaz<sup>1</sup>, Dorota Dwuźnik<sup>1</sup>, Ewa J. Mierzejewska<sup>1</sup>, Jolanta Behnke-Borowczyk<sup>2</sup>, Maciej Grzybek<sup>3</sup>, Natalia Kartawik<sup>2</sup>, Mustafa Alsarraf<sup>1</sup>, Jerzy M. Behnke<sup>4</sup>, Anna Bajer<sup>1</sup>

<sup>1</sup> Department of Parasitology, Faculty of Biology, University of Warsaw, Warsaw, Poland; <sup>2</sup> Department of Forest Phytopathology, Faculty of Forestry, Poznań University of Life Sciences, Poznań, Poland; <sup>3</sup> Department of Tropical Parasitology, Medical University of Gdańsk, Powstania Styczniowego 9B, 81-519 Gdynia, Poland; <sup>4</sup> School of Life Sciences, University of Nottingham, University Park, Nottingham, NG7 2RD, UK

*Bartonella* gram-negative, vector-borne bacteria, widely distributed among animal reservoirs. Most *Bartonella* species establish a long-term and subclinical infections in their associated reservoir host. *Bartonella* species have been associated with a wide range of domesticated and wild animals, and to date more than 33 known *Bartonella* species and subspecies have been described, and many other *Candidatus* species and uncharacterized genotypes have been documented. The aim of this study is to determine the prevalence and abundance of the fleas from three different populations of bank voles *Myodes glareolus* from the Mazury Lake District and identification of the *Bartonella* species transmitted by these fleas. The bank voles were trapped in August/September 2018 from three sites close to Mikolajki (Urwitałt, Tałty and Pilchy) the sites were distant from each other about 10–15 kilometres. Fleas were identified morphologically using a specific key (N = 259). We identified 5 species of fleas (146 *Ctenophthalmus agyrtes*, 16 *Ctenophthalmus assimilis*, 65 *Megabothris turbidus*, 16 *Megabothris walkeri* and 15 *Hystrichopsylla talpae*). DNA was extracted from the fleas. DNA of *Bartonella* sp. was amplified by PCR using the *rpoB* gene fragment (800bp). The positive samples were sequenced by private company Genomed (Poland). Phylogenetic analysis was conducted for *Bartonella* sp. using the MEGA7 tool and reference sequences from the GenBank. Phylogenetic analysis revealed genetic diversity of *Bartonella taylorii*, *Bartonella grahamii* and several variants of *Bartonella* sp. depending on the site inhabited by the bank voles.

**ACKNOWLEDGEMENTS.** The study was partially supported by National Science Centre (NCN) Sonata Bis grant no. 2014/14/E/NZ7/00153.