Abstract

Deer keds (syn. louse flies) belong to the genus *Lipoptena* Nitzsch, 1818. These insects are potential vectors of pathogens of epizoonotic importance. Particular attention should be paid to *Lipoptena cervi* (Linnaeus, 1758) - a native insect species and *Lipoptena fortisetosa* (Maa, 1965) - an invasive species spreading across Europe. Deer keds are blood-sucking ectoparasites. Their specific hosts are cervids, including: sika deer, red deer, European fallow deer, European roe deer and Eurasian elk. The aforementioned ectoparasites were also identified in non-specific hosts such as: horse, European bison, cow and dog. Cases of human infestation have also been reported in the literature. Lipoptena spp. bites can cause acute or chronic eosinophilic or lymphocytic dermatitis, alopecia and even anaphylactic shock. Their role in the transmission of pathogens has not been thoroughly investigated so far. Studies on *L. cervi* have shown the presence of genetic material of many pathogens, including: *Anaplasma* spp., *Bartonella* spp., *Borrelia* spp., *Rickettsia* spp., *Theileria* spp. and *Trypanosoma* spp. Environmental conditions affecting the activity of this species in the environment were also determined, but further research on the transmission of pathogens and the biology of this louse fly was discontinued. It should also be noted that similar studies have not been carried out for *L. fortisetosa*. Even the lack of an official Polish name indicates the minor interest in this insect.

In Poland, *L. fortisetosa* was first identified in Lower Silesia in the late 1980s. In the years 2007-2012, the presence of this species was confirmed in southern and northern Poland. This ectoparasite was identified in Greater Poland in 2017.

The aim of the study was to assess the correlation between the abundance of *L. fortisetosa* searching for hosts in the environment and selected time and microclimatic conditions in forests at the beginning of the search for hosts. The aim of the study was also to assess the occurrence of *L. fortisetosa* in north-eastern Poland and to determine phylogenetic relationships with other *L. fortisetosa* sequences obtained in previous studies. Another aim of the research was to identify the genetic material of pathogens with zoonotic potential in *L. fortisetosa* obtained from specific hosts and from the environment. The final aim of the study was to assess genetic differences between *L. cervi* populations and to determine phylogenetic relationships with other *L. cervi* sequences obtained in previous studies.

Data for research on the phenology of *L. fortisetosa* were obtained in the period from May 6 to July 15, 2019 and 2020 in a natural mixed forest. During the study, the number of deer keds collected, the date of sample collection (time in days), temperature (°C), relative humidity (%), air pressure (hPa) and wind speed (km/h) were recorded. The 16S rRNA gene was used for molecular studies on samples of *L. fortisetosa* and *L. cervi* obtained from various regions of Poland. The DNA obtained during the tests was analyzed for the presence of the following pathogens: *Anaplasma ovis*, *Anaplasma phagocytophilum*, *Babesia* spp., *Bartonella* spp., *Borellia* spp., *Coxiella burnetii*, *Francisiella tularensis*, *Mycoplasma* spp., *Rickettsia* spp. i *Theileria* spp. using polymerase chain reaction and sequencing.

The results of the presented study provide additional evidence that the populations of *L. fortisetosa* in Central Europe have different genetic lineages. The results of previous studies indicate that *L. fortisetosa* has formed stable and genetically diverse populations throughout Poland. The population genetics of *L. fortisetosa* should be further studied in order to track the migration of these ectoparasites in northern and western Europe. More research is needed to detect new locations and analyze the genetic lineages of *L. fortisetosa*. The sequences identified in these studies indicate, that the *L. fortisetosa* population continues to spread despite geographic constraints. The presented research reveals the genetic variability in the 16S rRNA gene of *L. fortisetosa* and *L. cervi* populations

in selected voivodeships of Poland. The study regions were colonized by two dominant *L. cervi* haplotypes that were identified in other Central European countries, and local haplotypes were detected in isolated cases. The analyzed samples of *L. fortisetosa*, taken from animals and the environment, contained genetic material of *A. phagocytophilum*, *Babesia* spp., *Bartonella* spp., *Borellia* spp., *Coxiella*-like endosymbionts, *Francisiella tularensis*, *Mycoplasma* spp., *Rickettsia* spp., and *Theileria* spp. Future research may reveal the competence of *L. fortisetosa* as a biological or mechanical vector. However, the role of *L. fortisetosa* as a vector of pathogens requires further, more extensive research due to their new colonization sites and flights on humans and animals. These are important issues that require further attention.

Keywords: deer keds; ecophysiology; ectoparasites; Hippoboscidae; infectious diseases; louse flies; phenology; phylogenetics; temporal-climatic variation; vectors; vector-borne diseases