

## ABSTRACT

Parasites causing avian malaria belong to the group Haemosporida, which represents a monophyletic group of dixenic protists within Apicomplexa. Their asexual reproduction takes place in a vertebrate intermediate host, and the formation of gametes and sporogony occur in blood-sucking dipteran insects, which are the definitive hosts of these parasites. Three main genera (*Plasmodium*, *Haemoproteus* and *Leucocytozoon*) are found mostly in their avian hosts.

We focused on the Haemosporida of wild birds and their transmission by insect vectors in natural populations, which had previously been a neglected area. Our results were obtained both by traditional methods (investigation of infections by microscopy of blood smears) and mainly by molecular methods (e.g. nested PCR) centered around work with unique haplotypes of the haemosporid lineages. The aim of our work was to determine the range of possible insect vectors of avian haemosporidians in the territory of the Czech Republic, taking into account the specificity of the parasites within these vectors, and to describe the diversity of haemosporidians in the populations of their bird intermediate hosts. We chose four different species of birds from four orders (Passeriformes, Strigiformes, Accipitriformes, and Galliformes).

As potential vectors of avian blood haemosporidians in the Czech Republic, we identified the biting midges of the species *Culicoides kibunensis*, *C. segnis* and *C. festivipennis*, mosquitos of the *Culex pipiens* complex and black flies of the species *Eusimulium angustipes* and *Nevermannia vernum*. In the vectors we found a total of 12 haemosporid lineages; four of them were new. These results represented some of the very first publications dealing with avian malaria vectors using molecular methods (especially for biting midges as *Haemoproteus* vectors and for black flies as *Leucocytozoon* vectors). Later on, our results were followed by numerous further studies, corresponding to an expansion of molecular detection methods. Prevalence in the bird intermediate hosts ranged from 12 % in Grey Partridge (*Perdix perdix*) to 86 % in Tengmalm's owls (*Aegolius funereus*). We detected a total of 27 lineages (unique haplotypes) of all three major avian haemosporidians (*Plasmodium*, *Haemoproteus* and *Leucocytozoon*), of which 8 were completely new.