

Abstract

The genera *Haemoproteus* and *Plasmodium* are widespread genera of blood parasites from phylum Apicomplexa. Both genera have a dixerous life cycle and their definitive hosts belong to the order Diptera. Both parasites can be found in birds where asexual division takes place. The infection with genera *Haemoproteus* and *Plasmodium* is usually asymptomatic; during long lasting chronic phase relapses of the infection can occur.

We gained 1 092 blood samples from 29 trapped species of passerines in Milovice forest during seasons 2017-2019. Haemosporidians were detected in 48 % of samples. The prevalence of genus *Plasmodium* was 16 %, the prevalence of genus *Haemoproteus* was 22 % and 10 % we could not specify the parasite. We have found six new lineages of genus *Haemoproteus*, provisionally named *Haemoproteus* lineages coccoc_1, coccoc_2, coccoc_3, coccoc_4, embcit, fricoe which total prevalence was 14 %. Lineage *Haemoproteus* sp. coccoc_1 was the most noticed one and its prevalence was 12 %. *Plasmodium relictum* clone Peng14-121Br2AF and isolate Cc_P1 was the second most prevalent (13 %).

Infection dynamics was studied in samples gained in years 2014-2019. Forty individuals were examined between years and twenty-seven individuals were examined intraseasonally. Three individuals were trapped both intra- and interseasonally. Passerines keep their infection status, in total 82 % retrapped individuals did not change their infection status.

I was comparing microscopy and a diagnostic method nested PCR. Results of both methods were identical in 72 % of investigated samples. Comparison of these methods was done at 745 samples gained in years 2017 and 2018. The PCR method is more effective for detection genera *Haemoproteus* and *Plasmodium* because we have noticed by 20 % more infected birds.