

Avian malaria parasites and other haemosporidia in the Scarlet Rosefinch (*Carpodacus erythrinus*)

We studied Avian malaria parasites and other Haemosporida in the Scarlet Rosefinch (*Carpodacus erythrinus*) using both molecular (nested PCR) and traditional microscopic techniques (blood smears) in Bohemian Forest Mountains. Bird blood samples were collected during 8 years (from 2000 to 2008). Haemosporidian parasite prevalence exceeded 61 %. 24 unique *cytochrome b* lineages of three haemosporidian genera (*Plasmodium*, *Haemoproteus*, and *Leucocytozoon*) were recorded in the host species. While the most common lineage *Haemoproteus* ROFI2 reached 53 % of prevalence, the other lineages were far less abundant. The prevalence slightly varied between years; however, the proportion of lineages remained almost stable in the whole studied period. We compared the methods of prevalence estimates and we found the nested PCR more efficient than investigating blood smears. We suppose that extremely low parasitemia is the main cause of the lower efficiency of the traditional detection methods. We have not found any significant effect of parasites on host characteristics (body mass, reproductive success and male ornamentation), however, the *Mhc* allele diversity and genetic variability measured as standardized heterozygosity at 17 microsatellite loci correlated with the *Plasmodium* prevalence. Potential insect vector of haemosporidian parasites were also investigated using the nested PCR method. Our results suggest *Culicoides* spp. as *Haemoproteus* vectors, *Culex pipiens* as *Plasmodium* and suprisingly *Haemoproteus* vector and *Eusimulium securiforme* as *Leucocytozoon* vector at the studied locality.