

Parasites are an important evolutionary factor by exerting selective pressure on the host, as well as maintaining its genetic variation. The first line of defense against parasitic infections is the innate immune system which, through pattern recognition receptors (PRRs) is able to detect pathogens and initiate the immune response. The group of pattern-recognition receptors include Toll-like receptors (TLRs) that recognize conserved pathogen-associated molecular patterns (PAMP). Particular groups of toll-like receptors are responsible for the recognition of different ligands. The previous studies showed the relationship between the susceptibility or resistance to various human diseases and the presence of specific alleles of toll-like receptors. In birds the best known species in terms of toll-like receptors is the domestic chicken, but a number of studies in other species is growing. Nonetheless, the relationship between natural parasites and genetic variability of toll-like receptors in wild birds is poorly understood.

In our research we want to verify if there is a relationship between genetic variation of toll-like receptors and the occurrence of infections caused by commonly occurring protozoa (genus *Leucocytozoon*, *Haemoproteus*, *Plasmodium*, *Trypanosoma*). If so, how this relationship looks like. If higher variability of toll-like receptors is associated with resistance to infection / capacity to its total clearance or it may influence only on a reduction of infection intensity? Does this influence varies depending on the genus of the analyzed parasite? Are parasitic co-infections important? It is also interesting if the toll-like receptors, by affecting the resistance / susceptibility to infections, indirectly affect survival and reproductive success of birds which possess them.

We will search for the answers to these questions by conducting research on three species of wild passerine birds (blue tits, great tits and collared flycatchers) and naturally occurring infections with protozoa. For the assessing the parasitic infection and the genetic variability of toll-like receptors we will apply molecular tools: PCR, quantitative real-time PCR, sequencing and next-generation sequencing - MiSeq Illumina. It is also worth noting that it will be the first such a study conducted on wild birds and their naturally occurring parasites and their results will allow for a better understanding of host-parasite co-evolution.