

Immunology of avian migrations – adaptations and constraints

Long-distance bird migrations are among the most fascinating spectacles in nature. Every year, tens of millions of birds move thousands of kilometres to spend winter in different geographical regions from those where they bred or were born. Millions years of evolution of migratory birds promoted development of numerous adaptations that enhance the process of cyclic migrations, primarily by increasing efficiency and reducing energetic costs of long-distance flight. Despite this, migration still constitutes a huge effort for an avian organism, which may cause limitations in other biological functions not necessarily related to migration. The aim of this project is to investigate both adaptations and constraints of the immune system in migratory birds.

The project is based on several hitherto understudied hypotheses. First, migratory birds are exposed to different types of pathogens and parasites at different times of their annual cycle, and migration induces birds to aggregate in high-density concentrations, increasing the risk of transmitting pathogens between individuals. Hence, it should be expected that evolutionary processes (natural selection) will favour the development of effective immune mechanisms aimed at detection and neutralization of diverse pathogens in long-distance migratory bird species. On the other hand, energetic costs of migration may not allow birds to maintain high activity of the immune system during this critical period. Finally, it remains unknown whether we can expect similar associations at both evolutionary (differences between species) and ecological (differences between individuals within species) level.

The research will focus on a group of shorebird species, which show exceptionally high variation in migratory behaviour. Approximately 400 shorebirds from over 20 species will be captured during autumn migration to collect biological material for analysis. Additionally, a group of individuals from one species will be equipped with satellite transmitters, allowing to accurately track migration routes and determine individual variation in migratory traits. In order to effectively test the hypotheses we plan to examine and quantify the diversity of key genes responsible for recognition of pathogenic agents (the major histocompatibility complex, toll- and NOD-like receptors), activity of basic components of the innate immune system (complement system, natural antibodies), and species composition of basic groups of pathogens and parasites, including gastrointestinal pathogenic bacteria and parasites, haemoparasites, and ectoparasites. Data analysis will be carried out on two basic axes of variation (between and within species).

In consequence, the project has a potential to provide answers to outstanding questions in the evolution and ecology of avian migration, filling existing gaps in our knowledge on the adaptations and constraints associated with this unique biological process. The pioneering nature of the project, combining extensive biological sampling, advanced methodological approaches, complex experimental design, and multi-species analytical framework may yield novel and important results for our understanding of the complex associations between migration and disease resistance. The project may also shed new light on the epidemiological potential of migrating birds (shorebirds), including the potential for transmission of human zoonotic diseases.