Immunocompetence, which is the ability of the body to produce an immune response against pathogens, is a key determinant of individual fitness. In general, active immune response is developed by the immune system, which aims to eliminate foreign molecules (antigens) emerging in the body. The first stage of an immune response is the induction phase, in which the proteins of the Major Histocompatibility Complex (MHC) present antigens to lymphocytes to allow their recognition. There are two types of MHC molecules. MHC class I molecules present antigens to the cytotoxic lymphocytes Tc and take part in the defence against intracellular pathogens, while MHC class II molecules present antigens to the helper lymphocytes Th, being responsible for the defence against extracellular pathogens. Each MHC molecule has a special region, which can bind antigens of a specific amino-acid sequence (Antigen-Binding Region, ABR). For this reason, a large diversity of MHC molecules in the organism allows to bind more antigens, and thus, to fight a broader range of pathogens.

The diversity of MHC molecules in the organism is primarily determined by the number of genes (loci), which code for different MHC alleles. In the course of the evolution, the number of MHC genes may be increased in the process of duplication, while some of duplicated loci become lost by deletion or mutation into nonfunctional pseudogenes. As a result, there are large differences in the number of loci (copy number variation, CNV) within and between different groups of vertebrates, and the greatest variation has been reported for birds. In some avian species only one MHC class II gene is present, while in some others species the presence of over 20 different loci was confirmed. However, the evolutionary forces responsible for generating this immense variation are largely unexplained.

The main objectives of this project are to characterize the historical patterns of MHC duplication across the avian phylogeny, as well as to determine the effect of duplication on selection and recombination patterns at MHC. We aim to use Single Molecule Real-Time (SMRT) sequencing to determine the number of MHC loci in a group of passerine species chosen for their class II diversity patterns. To date, the number of MHC loci in passerine birds has mostly been estimated from the number of sequences recovered from targeted genotyping studies of class I or class II exons and very few physical maps of MHC region exist for any passerine species.

An additional goal of the project is to test for intra-specific variation in the number of loci in a passerine, the common yellowthroat *Geothylpis trichas*, by genotyping the MHC region of individuals with low and high number of MHC alleles (determined previously with 454 pyrosequencing). To date, evidence for intra-specific variation in the number of MHC genes has been found only for a few non-passerine species. In passerines, intra-specific variation in the number of MHC loci has only been suggested by large variation in the number of sequences recovered from different individuals, and the largest recorded variation has been reported for the common yellowthroat (10 to 45 class II alleles recorded in different individuals).

Variation in the number of MHC loci is related to disease resistance in humans and lab animals, but it has only recently been studied in wild populations and could be an important contributor to population viability. We expect that this study will help to determine the evolutionary significance of MHC duplication, which may allow us to better understand variation in disease resistance that is observed among different clades of birds and other vertebrates.