

The effect of interspecific introgression and geographic subdivision on variation of the major histocompatibility complex (MHC) genes

Description for the general public

The immune system allows organisms to detect and destroy pathogens attacking it. Most organisms have only the innate immunity, which acts quickly but with little precision or specificity. Vertebrates have however another branch, the adaptive immunity which acts precisely against a specific pathogen and remembers it, so that another infection will be dealt with quickly and effectively. Understanding the mechanisms driving evolution of the genes underlying adaptive immunity is of major scientific importance and has implications for design of conservation strategies. The Major Histocompatibility Complex genes (MHC hereafter) encode proteins that are a key component of adaptive immunity. MHC are the most diverse genes in the vertebrate genome, i.e. many MHC variants are present in populations. Pathogen pressure resulting in arms race between pathogens and hosts is widely invoked as the main driver of this extraordinary diversity. However the specific mechanisms that generate and maintain MHC diversity are not fully understood. In particular, it is challenging to reconcile rapid turnover of genetic variants expected under arms race (Red Queen dynamics) with an empirical observation of extensive diversity within populations, including numerous apparently old variants.

In this project we will assess the role of the two factors that are potentially important in generating and maintaining MHC diversity: interspecific hybridization and intraspecific geographic subdivision. The project has two main objectives: i) test empirically, whether hybridization leads to an extensive exchange of MHC genes between species and, in consequence, to increased diversity within species, ii) explore theoretically, whether hybridization and subdivision facilitate long-term maintenance of MHC variation within populations and species. The empirical test of the effect of hybridization on MHC diversity will be performed in contact zones between hybridizing, but strongly reproductively isolated species. More than 30 contact zones between species representing ten genera from all major vertebrate classes (teleost fish, amphibians, reptiles, birds, mammals) will be examined. We will test for increased MHC similarity between species close to the contact zone. The global effect of MHC introgression will be estimated by combining results from all systems using a metaanalytical approach. In the theoretical part of the project, the effect of introgression and subdivision on MHC variation will be explored using computer simulations under host pathogen arms race and several models of geographic structure. We expect more diversity in simulations assuming hybridization and subdivision

Because of the crucial role MHC plays in fighting pathogen assault, understanding the evolutionary processes driving their evolution is of both theoretical (mechanisms maintaining genetic diversity) and practical (conservation and management of endangered species, minimizing extinction risks, wildlife epidemiology) importance. In this project we will investigate the effect of two potentially essential factors that have not been sufficiently explored: introgression and subdivision. The combination of empirical and theoretical approaches should allow comprehensive understanding of the effect of these processes, provide a framework to interpret already collected data and help guide future research. Therefore, the results will be of broad interest for conservation biology, evolutionary genetics and wildlife epidemiology.