

Do antigen-processing genes coevolve with MHC class I genes in salamanders?

The immune system allows organisms to detect and destroy pathogens attacking it. Most taxonomic groups 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 designing conservation strategies. In this project we propose to test whether the Antigen Processing Genes (APG) coevolve with the MHC class I (MHC I) genes in salamanders. Proteins encoded by the APG prepare pathogen antigens for presentation by MHC I, which initiates the adaptive immune response. Coevolution would mean that changes in one of the gene types drive changes in another type. The coevolution hypothesis states that an MHC I protein variant presents most efficiently antigens prepared by variants of the APG proteins co-occurring on the same chromosome. Because MHC I genes are usually highly polymorphic, coevolution should result in high APG polymorphism, which has indeed been observed in several species.

Some researchers suggest, that coevolution occurred already in the ancestor of vertebrates and is widespread among vertebrate species, with a notable exception of mammals. However in our opinion, available information on structure and variation of MHC I genes (and, to some extent, although they are less studied, at APG) in several vertebrate group is not really consistent with the coevolution hypothesis. Salamanders are one of such taxa, characterized by a long (ca. 300 million years) independent evolutionary history. Because the coevolution hypothesis generates several predictions which can be evaluated using MHC I and APG sequences, in this project we propose to test this hypothesis studying DNA of 25 species from five salamander families.

Testing the coevolution hypothesis is important because, as suggested by several authors, coevolution may limit efficiency and flexibility of the adaptive immune system. If that is indeed the case, it can be expected that natural selection has acted in various evolutionary lineages to remove this constraint as was the case in mammals. It is however possible that coevolution may occur without a negative effect on efficiency and flexibility of the adaptive immunity, as some data from non-mammalian vertebrates suggest. Addressing these issues would provide fundamental insights into our understanding of mechanisms driving the evolution of the adaptive immune system. Thus the results of the project should be of broad interest for scientists working in fields of evolutionary biology and immunology. Results will also be relevant for amphibian conservation. Amphibians are the most globally threatened vertebrate class, and infectious diseases caused mainly by viruses and pathogenic fungi pose a major threat for them.