Institute of Environmental Sciences

**Topic:** The effect of interspecific introgression on variation of the major histocompatibility complex (MHC) genes

**Supervisor**: prof. dr hab. Wiesław Babik, (Molecular and Behavioral Ecology Group)

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**Background information:**The Major Histocompatibility Complex (MHC) contains the most polymorphic genes in the vertebrate genome. Pathogen pressure is widely invoked as the main driver of this extraordinary diversity. However the actual mechanisms that generate and maintain MHC diversity under pathogen pressure are not fully understood. In particular, it is challenging to reconcile rapid allele turnover, predicted under Red Queen dynamics and suggested by substantial MHC differentiation observed between natural populations, with an observation of extensive variation within populations, including numerous apparently old alleles/allelic lineages.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 assess the role of a factor that is potentially important in generating and maintaining MHC diversity: interspecific introgression.

**The main question to be addressed:**The aim of this project is to test the hypothesis that interspecific MHC introgression is a widespread phenomenon shaping MHC variation – we hypothesize that MHC will be among the last genes to stop flowing between differentiating species, because, initially rare introgressed

alleles will be advantageous in the recipient species.

**Information on the methods.** The empirical test of MHC introgression 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 use zones for which genomic data are already available and genome-wide introgression is known to be limited. MHC will be genotyped in these systems and we will test for an increased allele sharing between species close to the contact zone and compare interspecific admixture in MHC to the genome wide-admixture. The global effect of MHC introgression will be estimated by combining results from all systems using a metaanalytical approach, correcting for phylogenetic relationships between taxa.

**Additional information:** This PhD project is within a recently awarded project *The effect of interspecific introgression and geographic subdivision on variation of the major histocompatibility complex (MHC) genes*. In addition to the regular scholarship funded by the PhD school the student will receive grant-funded stipend up to 4500 PLN/month (tax free) for 3 years. The PhD student, while focusing on the empirical part of the project will collaborate closely with researchers involved in the theoretical part. The candidate will have strong background in evolutionary biology, good knowledge of the Unix/Linux environment, R and a scripting language (Python, Perl or similar).

**Collaborators:** The project will involve close collaboration with prof. Jacek Radwan (UAM Poznań), dr B. Wielstra (Leiden University, The Netherlands) and other researchers studying hybridization in relevant systems.

**References:**

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Hedrick, P. W. (2013). Adaptive introgression in animals: examples and comparison to new mutation and standing variation as sources of adaptive variation. Molecular Ecology, 22, 4606-4618. https://doi.org/10.1111/mec.12415.