DESCRIPTION FOR THE GENERAL PUBLIC

One of the major tasks facing evolutionary biology is to explain how populations diverge and maintain their identity in spite of gene flow. Interesting case for the study of these processes is provided by the honeybee *Apis mellifera*. First of all, the honeybee genome is already well studied, which facilitates further analyses. Secondly, within this species, there are several highly distinct evolutionary branches arising from ancient migrations and isolation in refugia during glaciation. Populations of bees that were on the way to speciation due to prolonged isolation, come into contact with one another over large areas of Europe since the end of the Ice Age, but - interestingly – they have not been completely mixed despite gene flow between them. This results in an interesting experimental system in which both pure forms and their hybrids are available for the study. Comparisons of genomes of pure forms and their hybrids genes may help to explain the genetic basis of assortative mating, and also shed light on the effect of diversifying selection.

The research material will include a large sample of bees sampled in the area between northern Poland and southern Hungary. The genome of each individual will be described using the method known as "genotyping-by-sequencing*"* (GBS). This technique consists of reading large number of genome fragments using modern, highly efficient sequencing platforms. Comparisons of reads between individuals will reveal differences between them consisting of changes in single nucleotides (single nucleotide polymorphisms or SNPs). The resulting massive data set (tens of thousands of SNPs, distributed all over the genome) will allow us to test a series of hypotheses.

First of all, we will be interested in the history of hybridization between bees in the Central Europe. This is an area that brings together two distinct evolutionary branches within the species. The first of them, occurring originally on the northern side of the Carpathian Mountains (referred to as "M") include the European dark bee *A. m. mellifera*, and the second, inhabiting areas in the south of the Carpathians (referred to as "C") includes the so-called Carniolan bee *A. m. carnica*. Our aim is to reconstruct the demographic history of bees in the studied area, including the time of contact between forms M and C, changes in their effective population sizes and trends of gene flow across hybrid zones. It is often believed that only M bees occurred north of the Carpathian Mountains, and C bees have been imported by man because of their superior utility in beekeeping. It cannot be ruled out, however, that the earlier gene flow between M and C bees could took place without human intervention. Using a method known as coalescence analysis we will answer the question when the admixtures of the other lineages appeared in the M and C genomes and at what rate the process of introgression (gene movement from one population into the gene pool of another) is going on. It is often believed that bees of various subspecies could interbreed freely, but results of our previous experiments show that bees usually breed within their own subspecies, which implies that reproductive barriers between different evolutionary lineages must exist. Such barriers are presumably heritable but their genetic basis has not yet been investigated. We assume that the regions of the genome which contain genes responsible for reproductive isolation should show a lower introgression than the rest of the genome. By exploring the intensity of introgression along the genome in hybrids between M and C we will identify genes responsible for the reproductive barriers. We will also find out, what the direction of gene flow between M and C bees is, and which sex is more responsible for this phenomenon. The results of previous studies indicate that the gene flow could be asymmetric and there may be significant differences in the rate of gene flow from M to C and from C to M. Another set of research questions that may be answered thanks to the data obtained from the GBS genome scan concerns adaptation to local environmental conditions. We will be particularly interested in whether natural selection pressures related to the different environment conditions (e.g. climate) have led to the evolution of different versions of genes (alleles). By examining the relationship between allele frequencies of and environmental factors we will identify genes responsible for local adaptations in bees. We will also test the links between genetic markers and phenotypic traits used for discrimination of honeybee subspecies.

The results of our research may shed light on important evolutionary issues, especially on the mechanisms of evolution of reproductive isolation in the early stages of species formation. Since the honeybee belongs to the most important organisms for both nature and the economy, we are convinced that our findings will also be of considerable practical importance. Our results will strengthen the scientific basis for beekeeping and protection of genetic resources.