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Grande salle + visioconférence

SPECIES SPECIFIC POPULATION RESPONSES TO ENVIRONMENTAL STRESS AND POLLUTION. THE STORY OF HONEY BEE AND FRUIT FLY

par

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- A For more than twenty years, the Drosophila Belgrade group has been interested in understanding the association between adaptation and environmental stress/anthropogenic influence, in both natural and laboratory *Drosophila* populations. In recent years, we have expanded our research into conservation genetics with a primary focus on exploring genetic variability in ecologically and economically important species.
- We will present our project on the genetic structure of managed and free-living honey bee population (*Apis mellifera*) in Serbia. To assess the genetic diversity of different types of honey bee colonies, we have analysed mitochondrial tRNAleu-cox2 intergenic region and 14 microsatellite loci in 542 worker bee samples collected from 102 apiaries and 55 free-living colonies in the urban and natural environment throughout Serbia. The analyses of mtDNA and microsatellite loci demonstrate the absence of *A. m. macedonica* subspecies from its historical range of distribution in southern Serbia and significant changes in the genetic diversity of managed honeybees belonging to *A. m. carnica* subspecies due to implementation of modern beekeeping practices. The most concerning result of our analysis is observed population admixture and loss of locally adapted populations previously described in the territory of Serbia. On the other hand, our results confirm the existence of a genetically diverse and distinctive free-living population of honey bees in Serbia, indicating that feral colonies in urban areas exhibit distinct patterns of genetic diversity compared to apiaries in rural parts of the country.
- Furthermore, we will introduce one aspect of our research on heavy metal pollution in *Drosophila* species. The variability in the number of metallothionein (Mtn) genes among species makes the fruit fly particularly interesting, as it possesses six Mtn genes. We analysed the expression of these genes in two *Drosophila* species under various heavy metal experimental conditions and developmental stages. First, we exposed 3rd instar larvae of *D. subobscura* to various concentrations of copper, zinc, cadmium, lead and a combination of lead and cadmium both in short- and long-term treatment assays to determine Mtn genes involved in response to different heavy metal pollutants. We also analyzed the expression of these genes in larvae and adult females and males of *D. melanogaster* and *D. subobscura* exposed to lead for several generations. Our most significant findings indicate that metals predominantly increase Mtn expression, with the exception of the MtnF gene recently discovered through bioinformatic analysis. Mtn expression profiles slightly differ between species and developmental stages, but surprisingly not between males and females. Our results confirmed the primary role of the MtnB gene in response to all non-essential heavy metals, including lead which had not been explored until now in this context.

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