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Kolokvij
Zavoda za molekularnu biologiju

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NGS of environmental DNA for monitoring biodiversity and detecting invasive species, and the occurence of copy-number variation in nature

I will discuss 2 separate studies that use molecular methods to address questions in **conservation, evolution and ecological genomics**.

The isolation of DNA from environmental samples offers the opportunity to rapidly characterize local biodiversity in an ecosystem. Metabarcoding is a rapid and sensitive genetic tool that has shown promise for monitoring biodiversity and for the early detection of invasive species. I will present results from mock communities that assess the limitations of metabarcoding to identify species in a sample. With this knowledge, we characterize zooplankton biodiversity from 16 natural communities spanning three oceans and the Great Lakes, and provide a framework for the **application of metabarcoding to monitor biodiversity** and for the early **detection of aquatic invasive species** in environmental samples.

In the second part of my presentation, I will present results from a recently published genomics study on **copy-number variations (CNVs)**. We combine **comparative genomics** with **population genomics** analyses to evaluate the distribution and impact of CNVs across natural populations of an eco-genomic model, the three-spined stickleback. With whole genome sequences of 66 individuals from populations inhabiting three distinct habitats, we find that CNVs generally occur at low frequencies and are population specific. A subset of CNVs however displays copy-number differentiation between populations, showing elevated within-population frequencies consistent with local adaptation. By comparing teleost genomes to identify lineage-specific genes and duplications in sticklebacks, we highlight rampant gene content differences among individuals in which over 30% of young duplicate genes are CNVs. Young genes and CNVs are evolving rapidly at the molecular level and are enriched with functional categories associated with environmental interactions, depicting the dynamic early copy-number polymorphic stage of genes during population differentiation.

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