



2022 Prague – Czech Republic

Congress of the European Society for Evolutionary Biology

August 14–19, 2022

Prague Congress Centre

Book of Abstracts

CONTENTS

TALKS.....4

- S01.** Tug of war between the sexes: The transcriptomic architecture of sex-linked traits
- S02.** Sex chromosome evolution: the canonical model and so much beyond
- S03.** Diversity and evolution in sperm, ova, and other primary reproductive traits
- S04.** The evolutionary ecology of mating systems
- S05.** A combinatorial view on rapid speciation - the role of ancient genetic variants and hybridisation
- S06.** Revisiting chromosomal speciation in the genomic era
- S07.** Chromosome rearrangements in evolution
- S08.** Integrative biogeography: Past, present, future
- S09.** Parallel and repeated evolution in adaptive radiation
- S10.** Eco-evolutionary dynamics in changing environments: insights from models, experiments and case studies
- S11.** Adaptation and evolution across environmental gradients
- S12.** Resurrection ecology as a tool for the study of rapid evolution
- S13.** Evolutionary ecology of chemically-mediated species interactions in plants
- S14.** Ecological drivers and evolutionary consequences of within-population colour variation
- S15.** Rapid evolution of color patterns
- S16.** Predator cognition and the evolution of prey defence strategies
- S17.** Brain, behaviour and cognitive evolution
- S18.** The evolution of behavioural adaptations: Genes, neurons and ecology
- S19.** Eco-evolutionary dynamics and feedbacks in invasive species
- S20.** Unravelling the interplay between plasticity and evolution during rapid global change
- S21.** Epigenetics goes wild! Epigenetic diversity and the evolutionary potential of wild populations.
- S22.** Phenotypic plasticity's importance in evolution: Same old dog or new tricks?
- S23.** The evolution and consequences of non-mendelian inheritance
- S24.** Progress and prospects in adaptation genomics
- S25.** The positives and negatives of whole genome duplication: synthesizing polyploid evolution across organisms and disciplines
- S26.** The biological meaning of SNPs
- S27.** Tandem repeats: their role in molecular evolution and methods
- S28.** Beyond transcription: the role of post-transcriptional gene regulation in adaptation and evolution
- S29.** Comparative genomics: a powerful tool for exploring broad evolutionary questions
- S30.** Characterizing genomic landscapes of recombination and their evolution
- S31.** Limits to adaptation: linking evolution, ecology, and genetics
- S32.** Inferring macroevolutionary patterns from microevolutionary processes: methods and practices
- S33.** Domestication: Fresh insights from ancient genomics
- S34.** How have biomarkers improved our understanding of health and the evolution of senescence?
- S35.** The art of microscopic war: interference competition in microbes
- S36.** Evolution of antibiotic resistance: from lab to clinic

- S37.** Microbiomes in the wild: the drivers and evolutionary consequences of microbiome variation
- S38.** Molecular evolution and trade-offs in host-pathogen interactions and host immunity
- S39.** Mechanisms of host-symbiont coevolution: from genotype to phenotype
- S40.** OPEN SYMPOSIUM

POSTERS.....356

- S01.** Tug of war between the sexes: The transcriptomic architecture of sex-linked traits
- S02.** Sex chromosome evolution: the canonical model and so much beyond
- S03.** Diversity and evolution in sperm, ova, and other primary reproductive traits
- S04.** The evolutionary ecology of mating systems
- S05.** A combinatorial view on rapid speciation - the role of ancient genetic variants and hybridisation
- S06.** Revisiting chromosomal speciation in the genomic era
- S07.** Chromosome rearrangements in evolution
- S08.** Integrative biogeography: Past, present, future
- S09.** Parallel and repeated evolution in adaptive radiation
- S10.** Eco-evolutionary dynamics in changing environments: insights from models, experiments and case studies
- S11.** Adaptation and evolution across environmental gradients
- S12.** Resurrection ecology as a tool for the study of rapid evolution
- S13.** Evolutionary ecology of chemically-mediated species interactions in plants
- S14.** Ecological drivers and evolutionary consequences of within-population colour variation
- S15.** Rapid evolution of color patterns
- S16.** Predator cognition and the evolution of prey defence strategies
- S17.** Brain, behaviour and cognitive evolution
- S18.** The evolution of behavioural adaptations: Genes, neurons and ecology
- S19.** Eco-evolutionary dynamics and feedbacks in invasive species
- S20.** Unravelling the interplay between plasticity and evolution during rapid global change
- S21.** Epigenetics goes wild! Epigenetic diversity and the evolutionary potential of wild populations.
- S22.** Phenotypic plasticity's importance in evolution: Same old dog or new tricks?
- S23.** The evolution and consequences of non-mendelian inheritance
- S24.** Progress and prospects in adaptation genomics
- S25.** The positives and negatives of whole genome duplication: synthesizing polyploid evolution across organisms and disciplines
- S26.** The biological meaning of SNPs
- S27.** Tandem repeats: their role in molecular evolution and methods
- S28.** Beyond transcription: the role of post-transcriptional gene regulation in adaptation and evolution
- S29.** Comparative genomics: a powerful tool for exploring broad evolutionary questions
- S30.** Characterizing genomic landscapes of recombination and their evolution
- S31.** Limits to adaptation: linking evolution, ecology, and genetics
- S32.** Inferring macroevolutionary patterns from microevolutionary processes: methods and practices
- S33.** Domestication: Fresh insights from ancient genomics
- S34.** How have biomarkers improved our understanding of health and the evolution of senescence?

- S35.** The art of microscopic war: interference competition in microbes
- S36.** Evolution of antibiotic resistance: from lab to clinic
- S37.** Microbiomes in the wild: the drivers and evolutionary consequences of microbiome variation
- S38.** Molecular evolution and trade-offs in host-pathogen interactions and host immunity
- S39.** Mechanisms of host-symbiont coevolution: from genotype to phenotype
- S40.** OPEN SYMPOSIUM

Toward proper nomenclature: reassessing honeybee (*Apis mellifera*) mtDNA nomenclature using phylogeny

Pavle Erić¹, Marija Tanasković¹, Katarina Erić¹, Aleksandra Patenković¹, Ljubiša Stanisavljević², Slobodan Davidović¹

¹Department of Genetics of Populations and Ecogenotoxicology, Institute for biological research "Siniša Stanković" – National Institute of Republic of Serbia, University of Belgrade, Belgrade, Serbia

²Center for Bee Research, Faculty of Biology, University of Belgrade, Belgrade, Serbia

The western honey bee (*Apis mellifera*) is one of nature's most important pollinators and domesticated species. Through human management, it has spread all around the world becoming a cosmopolitan species, and its genetic diversity has been shaped over millennia by anthropogenic influence. Six main mtDNA lineages (M, C, O, Y, A and S) with a large number of existing sublineages are recognized, usually associated with appropriate subspecies. Current nomenclature is inconsistent and the naming of newly identified haplotypes is not standardized. Here we reassessed the nomenclature of C lineage using sequences of the *tRNA^{leu}-cox2* intergenic region and complete mitogenomes. Most of the available honey bees' mtDNA haplotypes are based on the sequence variability of this region while available complete mitogenomes are still few. The first complete mitogenome of *Apis mellifera* (NC_001566) was used as the reference genome for haplotype determination. We propose that the naming of the mtDNA haplotypes should be performed based on the differences to the reference mitogenome and according to the phylogenetic relationship between detected haplotypes. Our analyses showed that the current nomenclature of C sublineages is not consistent with the phylogenetic relationships between existing haplotypes and that the reassessment followed by the proper naming of haplotypes is needed. We propose to keep the names of the main lineages but correct the names of sublineages using the same approach as in the identification of human mtDNA lineages. This newly standardized nomenclature will bring more order to the studies of honey bees' genetic diversity.

Abstract ID: 1581

Poster board number:

P636

The dynamic ontogenetic shape patterns of adaptive divergence and sexual dimorphism

Lieke Ponsioen, Marina de la Cámara, Quentin J.B. Horta-Lacueva, Kalina H. Kapralova
Institute of Life and Environmental Sciences, University of Iceland, Reykjavík, Iceland

The interplay between ecological diversification and sexual dimorphism has been largely overlooked in the literature. Sexually dimorphic species which are also undergoing adaptive radiations are ideal for filling this knowledge gap. The Arctic charr in lake Thingvallavatn is one such system: it is a sexually dimorphic species which has recently diverged along the benthic-limnetic ecological axis. In a long-running common-garden experiment we studied the shape variation throughout ontogeny of intra- and inter-morph crosses of a benthic (small benthic SB) and a limnetic (planktivorous, PL) ecomorphs from the lake. We found that shape differences between the ecomorphs had a genetic component. The differences were attributable to adaptations to benthic and limnetic niches, i.e., shorter lower jaws and rounder snouts in the benthic and evenly protruding snouts and pointier snouts in the limnetic. Prior to the onset of sexual