



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

Abstract ID: 1460

Mitochondrial variant specifically impairs male fertility in seed beetle *Acanthoscelides obtectus*

Lea Vlajnić¹, Uroš Savković², Biljana Stojković¹, Snežana Pešić³, Filip Vukajlović³, Dragana Predojević³, Ana Mitrovski Bogdanović³, Mirko Đorđević²

¹*Institute for Zoology, Faculty of Biology, University of Belgrade, Belgrade, Serbia*

²*Department of Evolutionary Biology, Institute for Biological Research "Siniša Stanković"- National Institute of Republic of Serbia, University of Belgrade, Belgrade, Serbia*

³*Faculty of Science, University of Kragujevac, Kragujevac, Serbia*

Uniparental inheritance of mitochondria leads to asymmetry of mtDNA evolution because selection acts directly on non-neutral mtDNA polymorphisms only through the female lineage. In other words, natural selection will not recognize any mtDNA mutation which is male harming, but neutral, beneficial, or slightly deleterious for females. Ultimately, non-Mendelian inheritance of mitochondria drives the evolution of male-specific mitochondrial mutation loads, an idea known as mother's curse. Naturally occurring mtDNA mutations that impair male fertility, but have no effects on females, have been recognized as an opportunity for the development of the biocontrol of pest species termed Trojan Female Technique (TFT). Namely, females carrying TFT mutations, and their female descendants, could continuously, over multiple generations, produce males that sire fewer offspring than wild-type counterparts. Although the TFT shows promise as a trans-generational, self-sustaining method, its empirical success hinges on the existence of natural TFT mutations that remain uncharacterized in pest insects. In order to identify and test possible TFT candidates for biological control of seed beetle, a common pest in legume storages, three mtDNA haplotypes found in laboratory lines were expressed alongside one outbred nuclear background. We analyzed the effects of specific mitotypes on female and male life history traits, and found a male-only reduction in fertility in one mito-nuclear combination. Specifically, fertility (but not total fecundity and lifespan) of males carrying specific mtDNA variant was reduced by 35% relative to the controls. Our study provides evidence that intergenomic conflict leads to the existence of male-harming mtDNA mutations that segregate within populations.

Abstract ID: 1237

The evolution and genetic mechanism of sex-ratio meiotic drive in *Drosophila affinis*

Wen-Juan Ma, Robert L. Unckless

Department of Molecular Biosciences, University of Kansas, Lawrence, United States

Meiotic drivers are selfish genetic elements that promote their own transmission to the gametes. Sex-ratio (SR) meiotic drive occurs when a selfish genetic element on the X chromosome manipulates gametogenesis to prevent the maturation of Y-bearing sperm in males, resulting in the production of predominant female progeny. The spread of SR meiotic drive can affect host genetic diversity, sex chromosome evolution, and even cause host extinction if it reaches high enough frequency. SR meiotic drivers have evolved independently several times, however, the underlying genetic mechanism is only known in few cases. In this study we use a combination of genomics, transcriptomics,