

BOOK OF ABSTRACTS



CONGRESS

OF THE SERBIAN GENETIC SOCIETY

2019 | October
13–17

VRNJAČKA BANJA • SERBIA





Publisher
Serbian Genetic Society,
Belgrade, Serbia
www.dgsgenetika.org.rs

Editors
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Printing
Serbian Genetic Society,
Belgrade, Serbia

Number of copies printed
300

Design
Ivan Strahinić
Ana Kričko

ISBN
978-86-87109-15-5

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Abstracts of the 6th CONGRESS OF THE SERBIAN GENETIC SOCIETY



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WELCOME TO VI CONGRESS OF THE SERBIAN GENETIC SOCIETY!

Dear colleagues,

Welcome to the 6th Congress of the Serbian Genetic Society. The Serbian Genetic Society (SGS) has been founded in 1968 and the first Congress organized by the SGS was held in 1994 in Vrnjacka Banja. Since then, the Congress of Serbian Genetic Society is held every five years. Over the past years, the Congress has grown from a national to an international meeting.

The experience of the past meetings motivated our efforts to continue with this series with a clear tendency to strengthen the scientific connections among researchers from different European countries.

The Congress will focus on the most recent advances in genetics and on wide range of topics organized in 9 sessions and two workshops. Many of the presentations will be in lecture-like settings, but we hope that there will also be ample opportunities for informal interaction outside the scheduled sessions.

The successful organization of the Congress has required the talents, dedication and time of many members of the Scientific and Organizing committees and strong support from our sponsors. I hope that you will find the Congress both pleasant and valuable, and also enjoy the cultural and natural beauty of Vrnjacka Banja.

Yours sincerely,



Branka Vasiljevic
President of the Serbian Genetic Society

05 – 03 Invited lecture

THE FIRST INTEGRATIVE ASSESSMENT OF THE INVASIVE POPULATION OF *Aedes albopictus* (DIPTERA: CULICIDAE) FROM THE CENTRAL BALKANS

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The Asian tiger mosquito, *Aedes (Stegomyia) albopictus* (Skuse 1984), represents one of the medically most important mosquito vectors. Although native to South East Asia, the species has recently spread globally, and was registered in the city of Novi Sad (Serbia, the Central Balkans) in August 2018. The knowledge about the microevolutionary patterns characterizing the introduced populations can help evaluate the invasion model and the population establishment likelihood, as well as the introduction route. We therefore characterized the invasive population using phenotypic (wing size and shape) and molecular (nuclear, internal transcribed spacer 2- ITS2, and mitochondrial, cytochrome c oxidase subunit I- COI) markers, also including CLIC and GenBank repository data, respectively. The results of phenotypic analyses indicated that the Serbian population was differentiated from the native (Thailand) and invasive (Hawaii and Florida) populations, which might be due to restricted gene flow, founder effect, and supposed different strain origin. Concerning the molecular analyses, the Serbian population showed genetic homogeneity, indicative of a small founder number (bottleneck invasion model). Despite the incorporation of ITS2 GenBank sequences into the data set, neither spatial (Geneland) nor nonspatial (BAPS) genetic structuring analyses helped infer the Serbian population origin. However, the comparison of the retrieved COI haplotype with previously characterized mitogenomes indicated a temperate strain origin, capable of overwintering. Such findings suggest that the newly registered *Ae. albopictus* population could be able to establish itself since previous studies outlined Novi Sad as a suitable area.

ASIAN TIGER MOSQUITO, COI, ITS2, WING GEOMETRIC MORPHOMETRICS

05 – 04 Oral

GENETIC VARIABILITY OF *CHEILOSIA URBANA* (DIPTERA, SYRPHIDAE)

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Cheilosia urbana (Meigen, 1822) (Diptera, Syrphidae) belongs to the genus *Cheilosia* which comprises 445 currently described species worldwide. Despite the lack of morphological differences, previous research has revealed high intraspecific genetic variability of *C. urbana* suggesting the existence of potential hidden or cryptic taxa. In order to provide additional information on this subject, the 5' and 3' ends of the mitochondrial cytochrome c oxidase subunit I gene (COI) were analyzed. In total, 41 *C. urbana* specimens were collected from 14 different localities in 7 European countries (Greece, Spain, Serbia, Montenegro, Hungary, Switzerland, Slovenia) and Turkey. The results have shown high haplotype diversity for both analyzed regions of the COI gene (Hd = 0,96 for both 3' and 5' COI regions). Additionally, the construction of phylogenetic trees revealed that certain specimens from different geographically distant localities are clustered together into monophyletic clades with often moderate to high bootstrap support. Furthermore, in some cases, specimens from the same localities are placed in multiple independent clades (e.g. specimens from Simplon Dorf, Switzerland are placed with those from Greece and Slovenia in one monophyletic clade, with specimens from Hungary and Serbia into a second monophyletic clade, while one of the specimens from Switzerland forms a separate independent branch). Similar cluster formation is observed for specimens from other localities as well. These findings indicate possible presence of cryptic species with overlapping distribution and stress the importance of the application of molecular markers in the assessment of hoverfly species diversity.

CHEILOSIA URBANA, COI GENE SEQUENCES, CRYPTIC SPECIES