

BOOK OF ABSTRACTS



CONGRESS

OF THE SERBIAN GENETIC SOCIETY

2019 | October
13–17

VRNJAČKA BANJA • SERBIA





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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 – 13 Poster

GREY WOLVES IN SERBIA – GENETIC DIVERSITY AS INFERRED FROM MICROSATELLITES

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In the past, grey wolf (*Canis lupus*) was widespread throughout Europe but at the end of the 19th century, following the habitat destruction and decline in prey abundance due to human influence, their numbers have dwindled and large continuous population became fragmented. Drastic reduction in their population size has continued in the 20th century after which the need for protection has become apparent. Grey wolf represents a highly important species in Serbia, whose conservation efforts largely depend on genetic monitoring. The main objective of this study is to evaluate the present genetic diversity in grey wolf population from Serbia. For this purpose the panel of microsatellite markers was used. Genomic DNA was extracted from 59 grey wolves muscle tissue samples collected during 2019. Individuals were genotyped by panel of 19 markers, 18 autosomal microsatellite markers and amelogenin sex determination locus (The Canine Genotypes™ Panel 1.1 kit). Genetic variability parameters were calculated in GENEPOP and ARLEQUIN. The number of alleles per locus varied between 16 in the case of AHT121 and 7 alleles for loci REN54P11, REN162C04 and INRA21, with the average number of alleles per locus at 10.278. Overall expected heterozygosity (0.772) was higher than the observed heterozygosity (0.693). The highest observed heterozygosity was found at AHT171 (0.84746), while the lowest value was detected at INRA21 locus (0.424). Estimated effective population size calculated in LDNe was 120.9 (with exclusion of rare alleles 107.7). Comparison to previous results from the genetic monitoring of the same population, it can be concluded that this population shows high level of genetic diversity and constant effective population size.

GREY WOLF, GENETIC DIVERSITY, MICROSATELLITES

05 – 14 Poster

WHOLE MITOCHONDRIAL GENOME DIVERSITY IN SERBIAN POPULATION: PHYLOGENETIC AND FORENSIC ASPECTS

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Mitochondrial DNA (mtDNA) is used in forensics for over three decades and is particularly suitable when STR profiling cannot be performed due to the degraded and/or scarce nuclear DNA. Traditionally, mtDNA typing is based on ~600 bp of the hypervariable segments I and II (HVS-I and HVS-II) of the control region (CR, ~1100 bp). Nowadays, it is possible to use variability of complete mtDNAs which enables maximum resolution of distinct maternal lineages. However, the number of complete mitogenomes in reference databases such as EMPOP is still insufficient, and that hampers their wider usage in forensic casework. In order to fill in the gap in the reference database, which, considering Slavic-speaking populations, currently comprises only mitogenomes of East and West Slavs, we present population data for 226 Serbian mitogenomes, representatives of South Slavs from the Balkan Peninsula. We support previous findings on both high levels of genetic diversity in the Serbian population and patterns of genetic differentiation among Serbian and ten studied European populations. However, increased genetic differentiation was observed among Serbian and two European populations (Russians and Poles) with our high resolution data. We demonstrate that the inclusion of indel polymorphisms into analysis contributed towards nearly complete resolution of mtDNA haplotypes (97.1% vs. 86.3% without indels), and that the random match probability was as low as 0.53%. Bayesian skyline analysis of Serbian mitogenomes revealed population expansion after the Last Glacial Maximum and during the Migration period (IV-IX century A.D.). Phylogenetic analysis of the Serbian and relevant West Eurasian haplotypes contributed towards the improvement of the worldwide mtDNA phylogeny to the certain extent, which is essential for the interpretation of the mtDNA casework. Lineages of a putative Balkan origin as well as those shared among Serbian and other European populations were observed.

COMPLETE MITOGENOMES; DEMOGRAPHIC CHANGES; MOLECULAR PHYLOGEOGRAPHY; SERBIAN POPULATION