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BOOK OF ABSTRACTS

4th Belgrade **Bioinformatics** Conference

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FOREWORD

Dear colleagues and friends,

The 4th Belgrade Bioinformatics Conference - BelBi2023, where many high-quality scientific contributions were presented, has just ended. With great thanks to all participants, we now proudly present a book of abstracts that both reflects the scientific abundance and diversity of the conference and serves as a reminder of a memorable event.

Several research institutions, faculties, and scientific societies from Serbia joined forces in organizing this international conference, which covered numerous topics in computational biology, bioinformatics, and biomedical and health informatics. The main goal of BelBi2023 was to foster contact between scientists, both early stage career and senior researchers, allowing them to share experiences and latest advances in their fields. We sincerely hope that BelBi2023 has served as a platform for researchers from around the world to meet, initiate new collaborations, and expand professional contacts, and that all of you would become a part of the growing BelBi community.

We are grateful and proud to have welcomed more than 250 researchers from 21 countries. We have had 28 scientific sessions, consisting of more than 60 lectures (including eight Keynote talks), 47 presented posters, as well as three workshops and one satellite event – COST action. We have also organized seven industry lectures, including the NGS Challenge, two Meet the Expert Sessions, and one Business Coffee Break where ten start-up companies took part. And finally, the future BIO4 campus was presented and first panel on Serbia's resources for storage and analyses of genetic data was organized.

We would like to thank all the members of the International Advisory Board and the International Program Committee for their efforts and help in making this event a success. We are very grateful to the Ministry of Science, Technological Development and Innovation of the Republic of Serbia, SAIGE project, and UNDP-Serbia for their support. Finally, the Local Organizing Committee is very grateful to all the sponsors of the conference - BGI, Illumina & Elta'90MS, PacBio & East Diagnostics, ThermoFisher Scientific & Vivogen, Huawei, Labena, DSP Chromatography, RNIDS, Telekom Srbija, Alfa Genetics, Kefo and Superlab, hoping that they will stay with us for many years to come.

Looking forward to seeing you again at the 5th Belgrade Bioinformatics Conference.

Belgrade, July 2023

Dr. Valentina Đorđević
& Dr. Ivana Morić,
On behalf of BelBi2023
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Evaluating *ND1* and *Cytb* mitochondrial genes as markers for diversity analysis of protected White-tailed eagle species from Serbia

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White-tailed eagle is the biggest bird of prey in Central and Southeast Europe. In Serbia it inhabits the Vojvodina province and the valleys of Danube, Sava, Tisa and Tamiš. Anthropogenic pressure on its habitats in Europe caused a decline in its numbers, but due to the strict laws protecting both species and its habitats, birds' numbers are now steady and increasing. In Serbia, as a strictly protected species it is a subject of different conservation programs. The available genetic data for this population are scarce and it is necessary to assess its genetic diversity to improve the existing conservation efforts. *ND1* and *Cytb* mitochondrial genes can be used to estimate the populations' adaptation to different environmental conditions and their variability can potentially be used to evaluate differentiation between populations.

To assess the genetic diversity of White-tailed eagle in Serbia we used mitochondrial *ND1* and *Cytb* nucleotide sequences from 40 unrelated birds collected in nests. *ND1* and *Cytb* nucleotide sequences variability was evaluated using standard parameters of genetic diversity (PGD). Acquired values were compared with the available data for the variability of the *D-loop* region which showed that combined *ND1/Cytb* nucleotide sequences PGD provide comparable results. Using publicly available sequences we reconstructed haplotype networks for *ND1*, *Cytb*, *ND1/Cytb* and *D-loop* which further showed the applicability of ND1/*Cytb* in population genetics analyses. Phylogeny reconstructed using combined *ND1/Cytb* sequences identified two branches in Serbian white-tailed eagles. Although the majority of substitutions were nonsynonymous, no selective pressure was detected.

Our data suggest that combined *ND1/Cytb* sequence variability provides sufficient information to be used for population comparison, population differentiation analyses and phylogeny reconstruction, but also gives a tool to potentially identify adaptations to different environmental conditions.

Keywords: sequencing, population genetics, genetic markers, genetic diversity, protected species

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