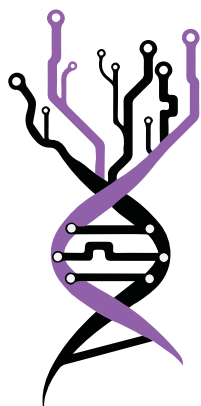


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BOOK OF ABSTRACTS



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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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