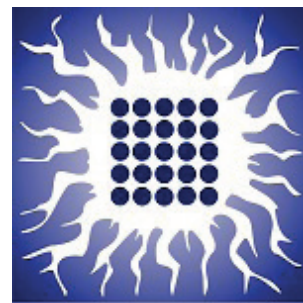


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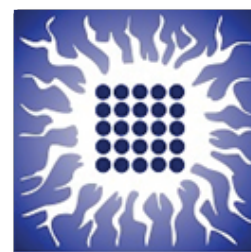
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Genetic diversity analysis of microsatellites and mitochondrial *Cytb* gene, relatedness estimates and *Cytb* phylogeography of protected Griffon vulture species from Serbia

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Abstract

Once a widespread species across the region of Southeast Europe, the Griffon vulture is now confined to small and isolated populations across the Balkan Peninsula. The population from Serbia represents its biggest and most viable population that can serve as an important reservoir of genetic diversity from which the birds can be used for the region's reintroduction programs. The available genetic data for this valuable population are scarce and it is necessary to assess its genetic diversity and inbreeding level if the population is going to be used for restocking and reintroduction.

To assess the genetic diversity we used microsatellite markers from ten loci and mitochondrial *Cytb* nucleotide sequences. The blood samples were collected from 58 unrelated birds during the marking in the nests. We have performed a comparative analysis of newly obtained data on microsatellites and *Cytb* with existing data. Genetic differentiation analysis between different native populations of French Pyrenees, Croatia and Israel identified two genetic clusters that differentiate populations from the Balkan and Iberian Peninsulas. Genetic diversity analysis based on microsatellites demonstrated similar levels among all populations while analysis of *Cytb* detected somewhat lower diversity in the population from Serbia. Further analyses demonstrated that all analyzed populations experienced a recent bottleneck event. Phylogeographic analysis based on *Cytb* sequences showed that the most frequent haplotype is found in all Griffon vulture populations and that each population possesses private haplotypes. Considering the serious recent bottleneck event which the

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