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**BROWN HARES IN HUNTING AREAS OF VOJVODINA: GENETIC  
DIVERSITY AS REVEALED BY mtDNA SEQUENCES**

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*Summary:* Brief introduction: Brown hare (*Lepus europaeus* Pallas) represents one of the most important game species in hunting grounds in Vojvodina. Remarkable decline of brown hare populations has been registered in several last decades all around Europe which led to efforts to evaluate genetic diversity of brown hare populations, with main goal to contribute to maintenance of genetic resources and sustainable management of brown hare populations. Previous studies of genetic variability of brown hare populations in Vojvodina showed moderate levels of intra- and inter-population diversity. The main aim of this study was to determine genetic variability of brown hare populations in Vojvodina, after remarkable decline registered before last hunting season, using mitochondrial genome variability, as a part of continuous monitoring of this game species.

*Materials and methods:* Total number of 90 brown hare individuals sampled from 10 localities across Vojvodina during hunting season 2012/13 was included in this study. Hypervariable domain 1 of the mtDNA control region was amplified and sequenced, and sequence variability was analysed using standard population-genetic software.

*Results and conclusions:* Total number of 32 mtDNA haplotypes was found. Haplotype diversity value was  $Hd=0.938\pm 0.012$ , while nucleotide diversity was  $\pi=0.0128$  and average number of nucleotide differences  $k=5.342$ . Three genetically different groups were defined in the study area ( $F_{ct}=0.201$ ,  $p=0.013$ ), even though no geographical barriers were determined ( $r=0.042$ ,  $p=0.421$ ). Detected inter-population diversity points that controlled translocations are required in order to maintain present level of genetic variability. Genetic monitoring represents one of necessary evaluation procedures for sustainable management of brown hare populations in studied hunting grounds.

*Key words:* brown hare, mtDNA variability, Vojvodina

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**EVROPSKI ZEC U LOVNIM PODRUČJIMA VOJVODINE: GENETIČKI  
DIVERZITET NA OSNOVU VARIJABILNOSTI mtDNK SEKVENCI**

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*Sažetak:* Uvod: Evropski zec (*Lepus europaeus* Pallas) predstavlja jednu od najvažnijih vrsta divljači u lovnim područjima Vojvodine. Značajan pad brojnosti populacija evropskog zeca zabeležen je u proteklih nekoliko decenija širom Evrope, što je podstaklo istraživanja genetičkog diverziteta ovih populacija, sa osnovnim ciljem da se doprinese očuvanju genetičkih resursa i održivom razvoju populacija od biološkog i ekonomskog interesa. Prethodna istraživanja genetičke varijabilnosti populacija evropskog zeca u Vojvodini pokazala su srednji nivo intra- i inter-populacione varijabilnosti. Cilj ovog rada je da se utvrdi stepen genetičkog diverziteta populacija evropskog zeca u Vojvodini, nakon značajnog pada brojnosti registrovanog pre poslednje lovne sezone, primenom analize varijabilnosti mitohondrijalnog genoma, i time da se doprinese kontinuiranom genetičkom monitoringu ove vrste divljači. Materijal i metode: Uzorkovano je ukupno 90 jedinki evropskog zeca sa 10 različitih lokaliteta u Vojvodini u toku lovne sezone 2012/13. Hipervarijabilni domen 1 kontrolnog regiona mitohondrijalne DNK je amplifikovan i sekvenciran, a varijabilnost sekvenci je analizirana standardnim populaciono-genetičkim kompjuterskim programima. Rezultati i zaključci: U analiziranom uzorku je nađeno 32 mtDNK haplotipa. Diverzitet haplotipova iznosio je  $H_d=0.938\pm 0.012$ , dok je diverzitet nukleotida  $\pi=0.0128$  i prosečan broj nukleotidnih razlika  $k=5.342$ . Tri genetički diferencirane grupe su definisane na analiziranom prostoru ( $F_{ct}=0.201$ ,  $p=0.013$ ), iako je izostala potvrda prisustva geografskih barijera između njih ( $r=0.042$ ,  $p=0.421$ ). Utvrđeno prisustvo inter-populacionih razlika u genetičkom diverzitetu ukazuje na neophodnost kontrolisane translokacije jedinki na istraživanom području da bi se očuvao prisutan nivo genetičkog diverziteta. Kontinuirani genetički monitoring se pokazao kao neophodna procedura evaluacije u cilju održivog razvoja populacija evropskog zeca sa akcentom na održanje lokalno adaptiranih populacija.

*Ključne reči:* zec, mtDNA Varijabilnost, Vojvodina

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