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**ESTIMATION OF GENETIC VARIABILITY OF WILD BOAR  
POPULATIONS IN VOJVODINA BASED ON MICROSATELLITES**

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*Summary:* Wild boar represents very important and most abundant game species in hunting grounds in Vojvodina. After a strong demographic decline at the end of 19<sup>th</sup> and beginning of 20<sup>th</sup> centuries, wild boar recovered most of its native habitats and nowadays they are worryingly increasing. The main aim of this study was to estimate genetic variability and population structure of wild boars in Vojvodina, using eleven tetranucleotide microsatellite markers.

Total number of 62 wild boars was collected during regular hunts from 14 localities across Vojvodina. Multiplex PCR amplification of 11 tetranucleotide microsatellites was carried out. Genetic variability and population structure was assessed using standard population-genetic softwares.

Total number of 119 alleles in wild boars from Vojvodina was found, with a mean number of 10.82 alleles per locus. Average observed and expected heterozygosity values were 0.69 and 0.77, respectively. Bayesian cluster analysis implemented in STRUCTURE suggested the existence of two genetically different groups in Vojvodina, but there was no strong correlation between individual assignments to genetic cluster and geographical origin of individual. Analysis of molecular variance (AMOVA) showed that genetic variation within defined clusters was significantly higher comparing to variability observed among groups. Detected high genetic diversity together with registered population structuring point that translocations of wild boars in Vojvodina should be controlled and genetic monitoring performed in order to maintain present high genetic diversity of populations.

*Key words:* wild boar, microsatellite variability, population structure, Vojvodina

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**PROCENA GENETIČKE VARIABILNOSTI U POPULACIJAMA DIVLJIH  
SVINJA VOJVODINE NA OSNOVU MIKROSATELITA**

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**Sažetak:** Divlja svinja je jedna od najvažnijih i najzastupljenijih vrsta divljači u lovišima Vojvodine. Nakon lokalnih istrebljenja krajem devetnaestog i početkom dvadesetog veka, populacije divljih svinja ponovo su naselile većinu svojih prirodnih staništa i one su danas prekobrojne u nekim delovima Evrope. Cilj ovog rada je bio da se uradi procena genetičke varijabilnosti i strukture populacija divljih svinja u Vojvodini primenom jedanaest tetranukleotidnih mikrosatelitskih lokusa.

**Materijal i metode:** Ukupno 62 uzorka divljih svinja sakupljeno je u sa 14 lokacija u Vojvodini. Nakon ekstrakcije DNK, urađena je multipleks PCR amplifikacija 11 mikrosatelitskih lokusa. Za procenu genetičke varijabilnosti i strukture populacije korišćeni su standardni populaciono-genetički softveri.

**Rezultati i zaključci:** U analizi genetičke varijabilnosti divljih svinja Vojvodine nađeno je ukupno 119 alela, sa prosečnom vrednošću od 10,82 alela po lokusu. Prosečne vrednosti uočene i očekivane heterozigotnosti iznosile su 0,69 i 0,77, respektivno. Klaster analiza zasnovana na Bajezian statistici urađena je u programu STRUCTURE i pokazala prisustvo dve genetički različite grupe u Vojvodini, ali nije uočena jasna veza između genotipskog prisustva jednom klasteru i geografskog porekla jedinki. Analiza molekularne varijanse (AMOVA) je pokazala da je genetička varijabilnost unutar definisanih klastera signifikantno veća u odnosu na varijabilnost koja je uočena između grupa. Uočene visoke vrednosti genetičkog diverziteta zajedno sa prisustvom struktuiranosti populacija divljih svinja u Vojvodini ukazuju na to da translokacije divljih svinja u Vojvodini moraju biti strogo kontrolisane i zasnovane na genetičkom monitoringu populacija kako bi se održao postojeći visok nivo genetičkog diverziteta.

**Ključne reči:** divlja svinja, mikrosatelitska varijabilnost, struktura populacije, Vojvodina

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