



"Modern aspects of sustainable management of game populations"

**Proceedings of
3rd International Symposium on Hunting
with Abstract book**



Organizers



Zemun-Belgrade, 26-28. September, 2014.

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HUNTING**

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MANAGEMENT OF GAME
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PHYLOGEOGRAPHIC POSITION OF BROWN HARES FROM VOJVODINA

Djan, M.¹, Veličković, N.¹, Obreht D.¹

Summary: Previous phylogeographic analyses revealed presence of five different haplogroups in brown hares based on mtDNA variability: ‘Anatolian/Middle East type haplogroup’ (Turkey, Israel, north-eastern Greece, Bulgaria); ‘south-eastern European type haplogroup’ (Greece, Bulgaria, Croatia, Italy); ‘European type haplogroup’, divided into two subgroups: subgroup A (central Europe, the United Kingdom, Spain, France, Netherlands, Germany, Bulgaria) and subgroup B (Greece, Crete, Bulgaria); and ‘intermediate haplogroup’ (Greece, Bulgaria). The postglacial recolonization of central and northwestern continental Europe by the brown hare has started exclusively from the Balkans due to the lack of profound geographical barriers in south-north direction. The aim of this study was to determine phylogeographic position of the brown hare (*Lepus europaeus*) in Vojvodina (the Northern Province of Republic of Serbia) by analyses of control region mtDNA sequence variability. In total, 135 brown hares, sampled in a period 2004-2014, were analysed for mitochondrial DNA variation by sequence analysis of the control region (CR-I). The data were compared with mtDNA CR-I sequences retrieved from GenBank. Genetic diversity was determined using standard population-genetic softwares. Haplotype diversity was $Hd=0.915$ and nucleotide diversity $\pi=0.012$. Phylogeographic analysis revealed two main groups corresponding to ‘Anatolian/Middle East type haplogroup’ and ‘European type haplogroup’, while the second was divided into two subgroups, which corresponded to subgroups A and B. The majority of haplotypes found in brown hares from Vojvodina were grouped in ‘European type haplogroup’ subgroup A, while two were grouped in ‘Anatolian/Middle East type haplogroup’. The presence of these haplotypes is expected in the south-eastern Balkans, and not in the north Balkans. It might be that translocations could be responsible for the presence of unexpected haplotypes in this area.

Key words: brown hare, Vojvodina, mtDNA

¹ Mihajla Djan, PhD, associate professor, Nevena Veličković, MSc, teaching assistant, Dragana Obreht, PhD, associate professor, University of Novi Sad, Faculty of Sciences, Novi Sad, Serbia;
Corresponding author: Mihajla Đan, University of Novi Sad, Faculty of Sciences, Trg Dositeja Obradovića 2, 21000 Novi Sad, Serbia; E-mail: mihajla.djan@dbe.uns.ac.rs; Phone: +381 21 485 2799

FILOGEOGRAFSKA POZICIJA EVROPSKOG ZECA IZ VOJVODINE

Djan, M.¹, Veličković, N.¹, Obreht D.¹

Sažetak: Prethodne filogeografske analize pokazale su prisustvo pet haplogrupa u arealu evropskog zeca na osnovu mtDNK varijabilnosti: ‘Anatolija/Bliski Istok haplogrupa’ (Turska, Izrael, severno-istočna Grčka, Bugarska); ‘Jugoistočna Evropa haplogrupa’ (Grčka, Bugarska, Hrvatska, Italija); ‘Evropska haplogrupa’ podeljena u dve podgrupe: podgrupa A (centralna Evropa, Britanija, Španija, Francuska, Holandija, Nemačka, Bugarska) i podgrupa B (Grčka, Krit, Bugarska); i ‘intermedijalna haplogrupa’ (Grčka, Bugarska). Postglacijalna rekolonizacija evropskog zeca centralne i severozapadne Evrope bila je isključivo sa Balkana zbog odsustva značajnog geografskih barijera u pravci jug-sever. Cilj ovog rada je da se utvrdi filogeografska pozicija populacije zeca Vojvodine (Severna Autonomna Pokrajina Republike Srbije) pomoću analize varijabilnosti sekvenci kontrolnog regiona mtDNK. Ukupno je analizirano 135 jedinki izlovljenih u period 2004-2014 godina i sekvenciran je kontrolni region mtDNK (CR-I). Dobijene sekvence su upoređene sa dostupnim sekvencama preuzetim iz GenBanke. Genetički diverzitet je izračunat pomoću standardnih populaciono-genetičkih softvera. Diverzitet haplotipova bio je $Hd=0,915$ i diverzitet nukleotida $\pi=0,012$. Filogeografska analiza pokazala je prisustvo dve osnovne haplogrupe, koje odgovaraju ranije definisanim ‘Anatolija/Bliski Istok haplogrupi’ i ‘Evropskoj haplogrupi, koja je podeljena na dve podgrupe, koje odgovaraju podgrupama A i B. Većina haplotipova koji su detektovani u populaciji zeca Vojvodne pripada podgrupi A, dok su dva haplotipa grupisana u ‘Anatolija/Bliski Istok haplogrupu’. Prisustvo ovih haplotipova očekivano je u region jugoistočnog Balkana, ali ne i u region severnog Balkana. Najverovatniji uzrok prisustva ovih haplotipova jesu translokacije koje su registrovane u poslednjih pola veka na ovom području.

Ključne reči: evropski zec, Vojvodina, mtDNK

¹ Mihajla Djan, PhD, associate professor, Nevena Veličković, MSc, teaching assistant, Dragana Obreht, PhD, associate professor, University of Novi Sad, Faculty of Sciences, Novi Sad, Serbia;
Corresponding author: Mihajla Đan, University of Novi Sad, Faculty of Sciences, Trg Dositeja Obradovića 2, 21000 Novi Sad, Serbia; E-mail: mihajla.djan@dbe.uns.ac.rs; Phone: +381 21 485 2799