



Muséum  
National  
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Naturelle



# ECM 2011

## VI<sup>th</sup> European Congress of Mammalogy

Université P. et M. Curie - Muséum national d'Histoire naturelle

Paris, France - 19 to 23 July 2011

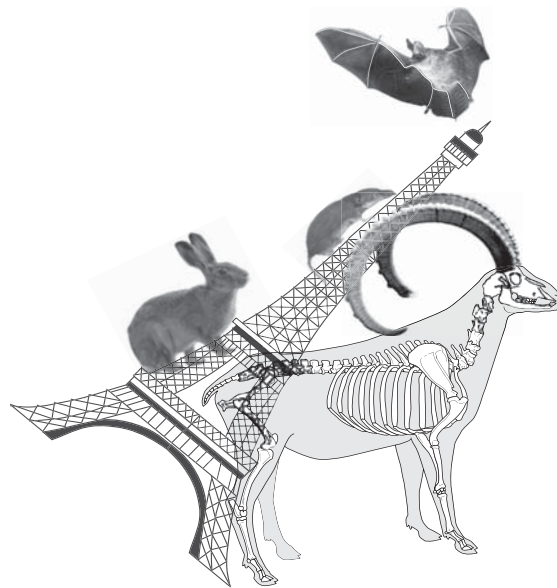
# Abstract volume

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## Comparative estimation of genetic originality of the sable in the East and the West parts of distribution area

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The Kamchatka sable - *Martes zibellina kamtschadalis* - was described in 1918 by A.A. Bjalynitsky-Birula and since then is regarded as a separate subspecies. The complete morphological studies on the Kamchatka sable have been done by some researchers (Kuznetsov 1941; Timofeev and Nadeev 1955; Belov and Monakhov 1970). Analysis of the cytochrome *b* gene restriction polymorphism revealed monomorphy (homogeneity) of the sable population on Kamchatka, and the originality of Kamchatka population versus Sakhalin, Khabarovsk and Magadan populations - so, the genetic data agreed with the Kamchatka sable subspecies status (Balmysheva et al. 2002). Separation of the Ural sable into the subspecies *M. z. zibellina* Linnaeus, 1758 is also undoubtedly for researchers. Although taxonomic status of the Kamchatka and Ural sable is certain enough, the history of existence of these populations differs and can define their genetic originality. The present study was undertaken in order to reveal and estimate the probable genetic differentiation between these two subspecies. We obtained data on mtDNA control region sequences (495 b.p.) and allele frequencies of 11 microsatellite loci for sable samples from Kamchatka and Northern Urals. A total of 13 control region haplotypes ( $H=0.91$ ) was identified among 23 Kamchatka specimens, and 35 haplotypes ( $H=0.96$ ) were found within 67 individuals from Northern Urals. At the same time, a level of nucleotide diversity ( $\pi$ ) of Kamchatka sampling was 0.54 %, and ( $\pi$ ) of Ural sampling was 2.14 %, i.e. 4 times higher. There were no shared haplotypes among two populations, and pairwise  $\Phi_{st}$  value was 0.26 ( $p=0.000$ ). For 11 microsatellite loci for sample set of 37 Kamchatka sables, an average value of expected heterozygosity was 0.706, an average number of alleles for a locus - 7.7. For 71 sables from Northern Urals average expected heterozygosity (0.733), an average number of alleles for a locus (9.4) was evidently higher. Differences between populations were highly significant ( $F_{st}=0.14639$ ,  $p=0.000$ ). Thus, performed analysis confirms not only a high level of genetic differences between the sable populations on Kamchatka and Northern Urals, but also considerably lower genetic variation level of the Kamchatka population. That can be explained by consequences of introduction in Urals of East-Siberian sables in the beginning of 1950th, by high level of natural isolation of a sable on Kamchatka, and, presumably (Balmysheva et al. 2002), by low number of founder individuals, initially inhabited the peninsula. Most probably, all of mentioned factors function simultaneously.

## Variability of mitochondrial DNA in beech marten (*Martes foina*) from central Croatia

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Beech (stone) marten (*Martes foina*, Erx. 1777) is found throughout Europe and Central Asia. This mustelid species prefers open landscape, being less dependent on forested habitats and is often found near human settlements. Although beech martens play a role in controlling rodent populations, in urban areas they are often treated as pests. Probably due to stable and still growing population size throughout its habitat, studies on population genetic of beech marten are quite rare. Most of the data about sequence variation of beech marten mitochondrial DNA comes from research on molecular evolution and research on species-specific primers used for species identification, mostly based on cytochrome *b*, less often on control region sequence variation. We have analyzed 22 beech marten liver/kidney samples, collected in urban areas of central Croatia. In

total, 28 polymorphic sites have been found on 302 base pair mitochondrial DNA control region sequence, representing 8 haplotypes. Two polymorphic sites were a result of insertion/deletion, while other resulted from substitution. The 8 haplotypes showed 2 - 26 pairwise differences resulting in sequence divergences of 0.7%-8.6%. Haplotype diversity ( $H$ ) was  $1.000 \pm 0.0137$ , while the nucleotide diversity ( $\pi$ ) was  $0.0343 \pm 0.0182$ . Clear geographical pattern in the distribution of haplotypes in central Croatia was not found. Comparison of 8 Croatian mtDNA haplotypes found in this study with 3 control region sequences deposited in the GenBank (2 from Iberian Peninsula and 1 from undefined European country) revealed no potential matches between haplotypes.