

BOOK OF ABSTRACTS



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16S rRNA GENE POLYMORPHISM SUPPORTS CRYPTIC SPECIATION WITHIN THE LESSER BLIND MOLE RAT *NANNOSPALAX LEUCODON* SUPERSPECIES (RODENTIA: SPALACIDAE)

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Among 26 genera of Palaearctic mammals, the genus *Nannospalax* has the highest karyotype variability with 74 chromosomal forms (CFs). Taxonomic effects i.e. implications to phylogeny and speciation process of such chromosomal variety are still lacking, especially among 25 reported CFs of South-European *N. leucodon* superspecies. Many cryptic species are under serious threat of complete disappearance, with population declines in Europe. As genetic discrepancies for the majority of them are missing, we analyzed nucleotide sequence polymorphism of the mitochondrial 16S rRNA gene between eight *N. leucodon* CFs and also add for the first time nucleotide sequence data for three CFs: *monticola*, *montanoserbicus* and *syrmiensis*. Further, including 40-57 years old teeth we evaluate the usefulness of the archived samples, e.g. from museums and other old collections as starting material for phylogenetic analysis. The topology of the Bayesian Inference tree is in agreement with the traditional taxonomic separation of recent blind mole rats. Among the three superspecies, the genetic diversity was lowest in *N. ehrenbergi* (0.004-0.031), highest in *N. xanthodon* (0.009-0.063) and intermediate in *N. leucodon* (0.008-0.055). The comparable scale of evolutionary divergence among *N. leucodon* CFs and among species from the genus *Spalax* supports our previous proposal that seven reproductively isolated CFs should be considered to be cryptic species and thus protected from extinction in their natural habitat.

16S rRNA GENE, CRYPTIC SPECIATION, KARYOTYPE EVOLUTION, CONSERVATION, MUSEUM ARCHIVED SAMPLES