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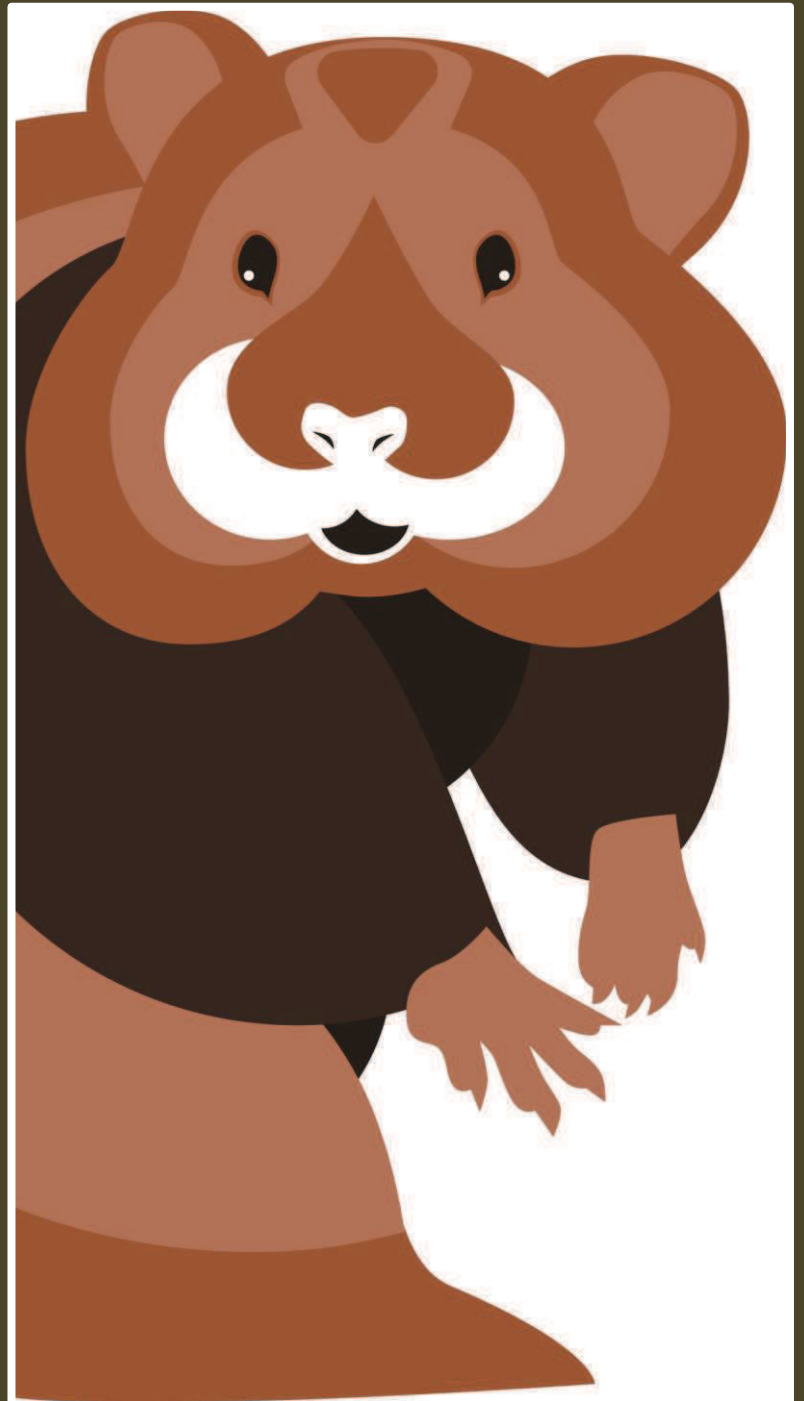
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Abstract Book & Programme

The Future of the Common
Hamster

Regional Conservation,
National Responsibility and
International Cooperation

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**Phylogeography of the Common hamster (*Cricetus cricetus*) in
Romania and western Ukraine**

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The aim of this study was to describe the distribution of the Common hamster (*Cricetus cricetus*) mitochondrial DNA (mtDNA) lineages in western Ukraine and Romania. The research in the Ukrainian part of the range is important as the mtDNA lineages come into secondary contact there and, moreover, the steppe areas of Ukraine were most probably refugial for the Common hamster. The phylogeographic analysis of Romania is necessary to resolve the history of the mtDNA lineages, as eastern Romania served as one of main corridors for hamster dispersal into Central Europe. Samples for the research were collected in late July and early August 2013 in the western parts of Ukraine and in late July and early August 2014 in southern and eastern Romania. We performed non-invasive sampling through the use of hair traps. To verify the distribution of the phylogeographic groups we conducted mtDNA analysis from collected hair samples. Three mtDNA sequences were used: control region (ctr), cytochrome b (cytb), and 16S rRNA (16S). Based on our results, the mtDNA lineage affiliation was defined for each sample. The Common hamsters belonging to the E1 lineage were found in Volyn, Ternopol, Ivano-Frankovsk, Chernovtsy and Khmel'nitskiy oblasts in western Ukraine. The Pannonia lineage is present only in the Lvov oblast in the area of Lvov and Sambir. The phylogeographic analyses of samples collected this year in Romania are still in progress. These results will be presented during the conference.