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Current distribution and genetic diversity of the common hamster (*Cricetus cricetus*) in central and western Romania

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The Romanian range of the common hamster (*Cricetus cricetus*) is generally considered to cover all parts of Romania except for the mountains, Dobruja and parts of Oltenia. The aim of this work was to update the distribution information, especially since global decrease of the range was stated, and start the genetic analysis of the common hamster populations in Romania. Literature data, museum records, personal reports of field biologists and our own field results were compiled to assess the past and present distribution of the species within Transylvania (central Romania) and the Pannonian Plain (western Romania). Combining available distribution data and the existence of natural barriers we were able to designate four, possibly separate, populations. The 1) *Hungarian Plain population* is a large population distributed in plain areas from Banat region, Crişurilor Plain and Someşului Plain, and showed outbreaks in 2007-2008. The 2) *Transylvanian Plateau population* is a large population distributed mostly in the river valleys of central Transylvania, where so far small-scale agriculture dominates. Outbreaks were observed in 2008-2009 and in 2011-2012. Two smaller populations seem to exist in Transylvania: the 3) *Olt Valley population*, which has the smallest geographic range as it inhabits the plain region of southern Transylvania in the Olt river valley, and the 4) *Braşov Depression population*, which is isolated from the Transylvanian Plateau by forested areas and high elevations. Twenty three individuals were available for the genetic analysis: two from Hungarian Plain, 17 from Transylvanian Plateau, 2 from Olt Valley and 2 from Braşov Depression population. The populations, as expected, belonged to the Pannonia lineage, based on the sequences of 16S rRNA, *cytb* and *ctr* of mtDNA. In total, we found 8 *ctr* haplotypes and very high diversity indices. The most common haplotypes for Transylvanian Plateau were also present in Hungarian Plain population and were also present with high frequencies in populations from Hungary and Slovakia, which indicates recent or even current exchange of individuals. Six *cytb* haplotypes were found, all new and so far specific for Romanian populations, and the diversity indices were also high. We were not able to determine the possible connections between the four putative Romanian populations, as the numbers were too low for any gene flow analysis. We are only able to state that the Transylvanian Plateau population showed high variability levels for 16 microsatellite loci. Summing up, recent mass outbreaks and high levels of genetic diversity, with some indication of current or very recent gene flow, showed that Romanian populations are in a good state, at least compared to many other European countries. As such, these populations should be of particular interest and protection as they could serve as the reservoir of the genetic variability for the European Pannonia lineage.