Phylogeography and conservation genomics of the Common hamster (*Cricetus cricetus*, Cricetidae) in Central-Eastern Europe

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Abstract

Genetic structure is critical for effective conservation because it clarifies the factors shaping the resilience of threatened populations and guides region-specific management strategies. The common hamster (*Cricetus cricetus*) has undergone severe declines across Europe, yet conservation initiatives have historically focused on long-declining western populations, while eastern ranges—particularly those in Hungary—have remained understudied. In Hungary, where the species was long regarded as an agricultural pest, no comprehensive genetic assessment had previously been conducted despite the region's potential importance as both a historical stronghold and an ancestral source area. To address this gap, we carried out extensive sampling between 2021 and 2025 across the species' key distribution areas in the Pannonian region, stretching from the Vienna Basin to Transylvania, and Russian outgroup samples. Using a RAD-seq approach, we reconstructed the genetic structure and phylogeographic patterns of 161 individuals from the eastern part of the distribution.

Our analyses revealed that most populations formed distinct monophyletic groups with minimal admixture, indicating substantial genetic isolation among regions. Partial intermixing was detected only in geographically adjacent populations. Phylogenetic reconstruction demonstrated that the deepest lineages occur in Transylvania, suggesting a historical refugium there. Whole mitochondrial genome genotyping assured the position of these samples within the previously identified Pannonian lineage. Subsequent westward expansion likely gave rise to a southern Pannonian refugial population, which later split into two major lineages separated by the Danube River. Eastern populations exhibited a clear northward colonisation trajectory, repeatedly crossing the Tisza River and progressively establishing populations further to the north. Nucleotide diversity estimates indicate moderate genetic diversity but strong contemporary structuring consistent with ongoing fragmentation. Together, these findings provide the first high-resolution overview of hamster population structure in Central-Eastern Europe and offer an essential foundation for developing targeted, region-specific conservation measures across the eastern part of the species' range.

Keywords

conservation genomics, reference genome, RAD-seq, genetic connectivity, phylogeography, hamster