

Characterization of Late Pleistocene European small hamsters (subfamily Cricetinae) based on aDNA analysis

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Introduction

The main paleobiogeographic hypothesis suggests that many steppe and steppe-tundra taxa currently found in Central Asia spread to Europe during Pleistocene glacial periods, when open habitats dominated. One of such species was the narrow-headed vole (*Stenocranius gregalis*), which currently inhabits the steppes of Central Asia and parts of the northern Siberian tundra, was once the dominant member of the rodent community in Central and Western Europe. Recent analysis of mitochondrial DNA of the Late Pleistocene European narrow-headed voles have shown that they separated from Asian populations over 200,000 years ago (ka) and belong to a separate species, *Stenocranius anglicus*. To test whether this represents a widespread pattern or rather an exception, we investigated the evolutionary history of small hamsters, which share an ecological niche and overlap in range with narrow-headed voles. **Did small hamsters have a similar evolutionary history with the narrow-headed vole?**

Results

- Partial mitogenomes were obtained from 33 ancient samples from 20 paleontological sites morphologically classified as small hamsters (subfamily Cricetinae), and three modern samples.
- The Late Pleistocene samples were grouped into two species (**Fig. 1a**): the gray dwarf hamster (*Nothocricetulus migratorius*) and the hairy hamster (*Cricetiscus sungorus*), which occurred in the Balkans or Central and Western Europe, respectively (**Fig. 1b**).
- Divergency between two main lineages of *Cricetiscus* sp. (*C. sungorus* and *Cricetiscus campbelli*), is approximately 85 ka BP (95% HPD: 140–49 ka BP). The ancient *C. sungorus* samples formed three highly supported clades that were sister to all modern *C. sungorus* individuals (**Fig. 2a**).
- We revealed the existence of seven major lineages for *N. migratorius* (**Fig. 3a**). The estimated age for the ancient samples ranged from 29.7 ka BP to 17.1 ka BP. European Late Pleistocene samples from the Balkans formed a separate clade that was sister to all modern lineages. The divergence of the European Late Pleistocene lineage from the modern ones was relatively recent and estimated to be ~51 ka BP (95% HPD: 61.7–41.7 ka BP), while the divergence of the main lineages representing modern eastern, western, and Quarma populations was estimated to be between 44.5 and 39.5 ka BP.

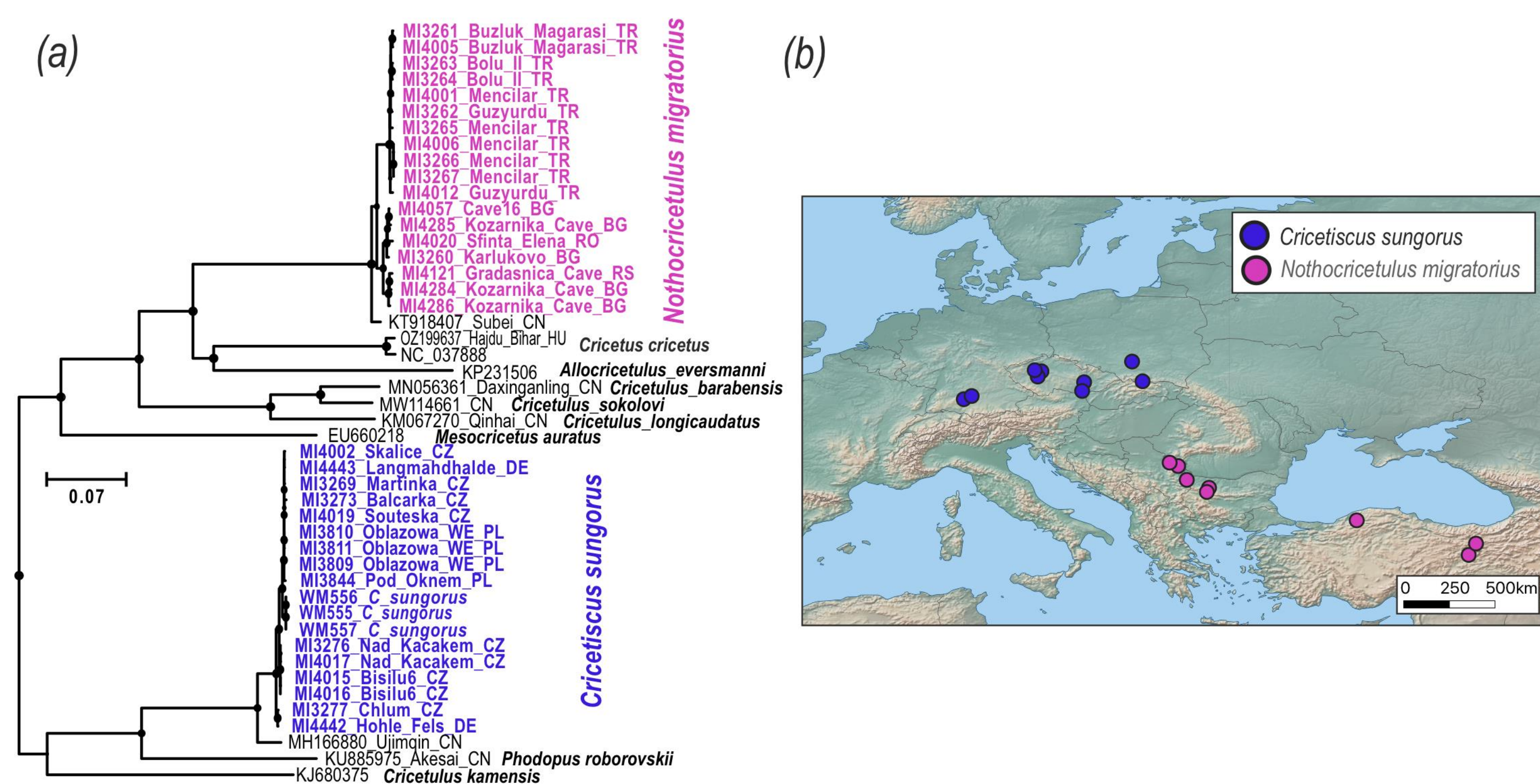


Fig. 1 Mitogenomic phylogeny of Cricetinae (a) with map showing the sampling sites of ancient specimens (b). Black dots at nodes indicate ultrafast bootstrap support >0.95.

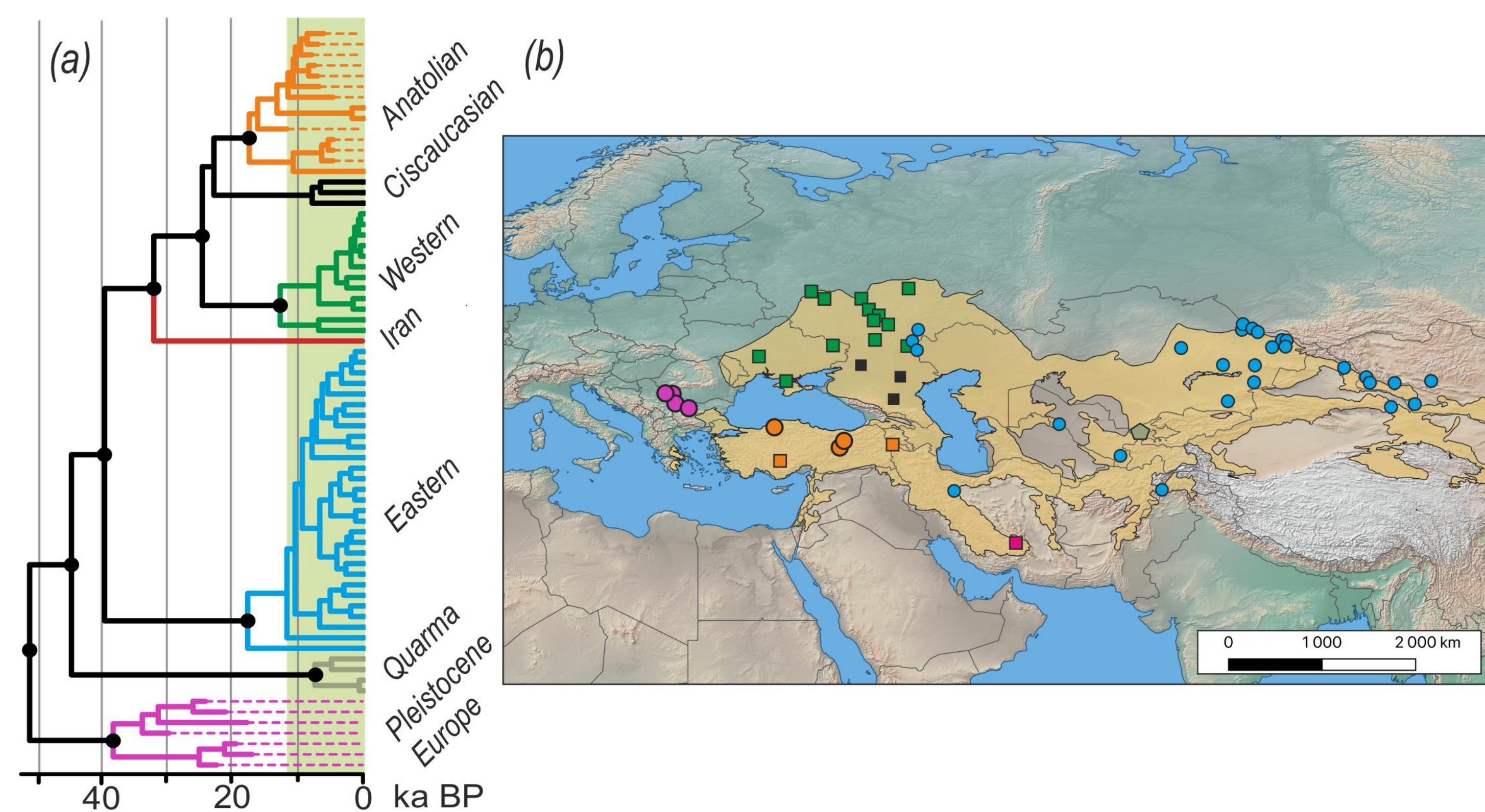


Fig. 3 Calibrated mitochondrial phylogeny of dwarf grey hamsters (*N. migratorius*) reconstructed in BEAST 1.10.5 (a) and map of sampling sites (b). Black dots at nodes indicate ultrafast bootstrap support >0.95.

Conclusions

- Ancient mitochondrial DNA analysis has clearly shown that **both hairy-footed and grey dwarf hamsters were present in Late Pleistocene Europe**: the hairy-footed hamster (*Cricetiscus sungorus*) in Central and Western Europe and the grey dwarf hamster (*Nothocricetulus migratorius*) in the Balkans with is consistent with their ecological characteristics.
- The topology of the mitochondrial phylogenies of both hamster species suggests **repeated population expansions** rather than long-term population continuity as observed in narrow-headed voles.
- Despite inhabiting similar ecological niches, **species respond in specific ways** to past climate change.

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