

Title: Using Phylogeography to promote dormouse conservation: the case of *Muscardinus avellanarius* (Rodentia, Gliridae), *Peckiana*, 2012

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Country: Europe

Background to study

Understanding historical processes that shape the current distribution of species (Phylogeography) is an important tool for conservation. It can help to identify long-term isolated population that might have distinct gene pools and local adaptations. The common dormouse is a conservation priority and information on the phylogeographic structure of the species could provide valuable information that could aid in its future conservation.

Method

- 120 tissue samples from common dormice were collected from countries across their European range. DNA was extracted from each sample which had been preserved in 96% ethanol.
- DNA was then amplified within a laboratory to determine structural patterns in the cyt b region of the mitochondrial DNA gene which is maternally inherited as an intact structure. The random mutations that occur within the gene allow patterns in variation to be assigned to different regions across the species range. Patterns of genetic variation were used to construct phylogenetic trees to show genetic structuring of dormice across Europe.

Key results

- Two distinct genetic clusters (lineages) were identified also known as genetic lineages.
- Lineage 1 included 2 sublineages; individuals from Western Europe (Belgium, Switzerland and France) and individuals from Italy.
- Lineage 2 included three sublineages; individuals from Central North Europe (Lithuania, Germany, Czech Republic & Slovakia), individuals from the Balkan Peninsular (Slovenia, Serbia and Macedonia) and individuals from Turkey.
- A high level of genetic divergence was observed among all lineages and sublineages suggesting a low dispersal of the common dormouse population across Europe.
- High levels of genetic diversity were observed in the Balkan Peninsular and Italian lineages suggesting these regions were refugia during the Quaternary glaciations. High levels of endemism in these regions suggest these populations did not contribute to postglacial recolonisation of Central Northern Europe.
- Lineages 1 and 2 were estimated to have separated 10 Mya whereas the divergence between sublineages was estimated at around 3.3 Mya. Both divergence periods correlate to climatic and faunal changes in Europe and follow similar divergence patterns observed in other mammals.

Key messages to landowners and managers derived from these results

- Five sublineages of dormice (West European, Italian, Turkish, Central North European, and Balkans) are currently identified and should be regarded as independent conservation units. Translocation of individuals from different lineages is not recommended as this could threaten their genetic integrity and ability to cope with different environmental conditions.
- Habitat enhancements to improve connectivity of populations need to consider whether populations were historically connected. The effects of connecting different lineages are currently undetermined but not recommended without knowledge of its effects on the fitness of out crossed individuals.

Key words/phrases

Common dormouse; *Muscardinus avellanarius*; phylogeographic structure; mitochondrial DNA; conservation management units