

# Population genomics of the Forest Dormouse (*Dryomys nitedula*) in Bulgaria

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## Abstract

The Forest Dormouse (*Dryomys nitedula*) is one of the most widespread species of the Gliridae family, occurring in the Eastern Mediterranean, Central Asia, Caucasus and the Arabian plateau. The populations are mostly threatened by the destruction of their forest habitats. Despite being considered as Least Concern by the International Union for Conservation of Nature (IUCN), the general population trend is unknown and the species is listed in Annex IV of the Habitat Directive in Europe and Annex III of the Bern Convention. Our goal was to determine its population structure in Bulgaria, where the species is well studied. We generated reduced representation genomic libraries using the 3RAD method on 62 samples collected from April 2020 to June 2021 from several study sites. Preliminary results based on cluster analyses suggest the presence of several geographically well-structured populations. With this study, we hope to gain new insights into the population genetics and trends of this overlooked species.

## Keywords

forest, population genetics, Gliridae, 3RAD

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