

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

Alice Mouton[‡], Anissa El Mojahid[‡], Nedko Nedyalkov[§], Johan Michaux[‡]

[‡] Conservation genetic lab/INBIOS, University of Liege, Liege, Belgium

[§] National Museum of Natural History, Bulgarian Academy of Sciences, Sofia, Bulgaria

Corresponding author: Alice Mouton (alicemoutonresearch@gmail.com)

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

Presenting author

Alice Mouton

Presented at

Oral presentation at the 11th International Dormouse Conference 2022

Conflicts of interest