Forest Dormouse, *Dryomys nitedula*, populations in southern Italy (Calabria region) belong to a deeply divergent evolutionary lineage

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Introduction

Within the Italian peninsula, the Forest Dormouse (*Dryomys nitedula*) populations are restricted to forested mountain areas of two largely disconnected regions: eastern Alps and southern Italy (Aspromonte, Sila, and Pollino mountain massifs). The two populations have so far been described as distinct subspecies (*D. n. intermedius* and *D. n. aspromontis*, respectively) based on morphological characters, but a thorough evaluation of their genetic divergence is still lacking. Here, we investigate the pattern of genetic differentiation between *D. n. aspromontis* and its geographically closest relative *D. n. intermedius*, in order to fill this gap of knowledge and to promote informed conservation efforts for the Forest Dormouse populations in the Calabria Region.

Methods

A total of 15 samples of *D. nitedula* were analysed, 8 from southern Italy (*D. n. aspromontis*) and 7 from the north-eastern Alps. Patterns of genetic diversity were analysed at the level of sequence variation of one mitochondrial (CYTB) and three nuclear gene fragments (GHR; IRBP; RAG1). Phylogenetic analyses were carried out using Bayesian inference methods.

Results and Discussion

*D. n. aspromontis* and *D. n. intermedius* were found to be reciprocally monophyletic (no shared haplotypes were found), with all the genetic markers analysed. Genetic divergence between *D. n. aspromontis* and *D. n. intermedius* estimated at the mitochondrial CYTB gene was conspicuous (HKY: 0.044) when compared to values previously observed among many sister species of rodents. The reciprocal monophony, deep genetic divergence, and morphological differences, among *D. n. aspromontis* and *D. n. intermedius* clearly indicate that *D. n. aspromontis* belong to a distinct evolutionary significant unit (ESU), whose taxonomic rank might need re-evaluation. Furthermore, this ESU is geographically restricted, and strongly fragmented into separate populations inhabiting distinct mountain massifs (Aspromonte, Sila, Pollino), thus warranting conservation concern. Further studies are in progress to go deeper inside the population’s genetic structure, to investigate its demographic structure, and to identify appropriate conservation efforts for this endemic lineage.

References

7. Bisconti et al., 2017. – 47.
8. Bisconti et al., 2017. – 47.

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