



Endemic species may have complex histories: within-refugium phylogeography of an endangered Iberian vole

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Abstract

Glacial refugia protected and promoted biodiversity during the Pleistocene, not only at a broader scale, but also for many endemics that contracted and expanded their ranges within refugial areas. Understanding the evolutionary history of refugial endemics is especially important in the case of endangered species to recognize the origins of their genetic structure and thus produce better informed conservation practices. The Iberian Peninsula is an important European glacial refugium, rich in endemics of conservation concern, including small mammals, such as the Cabrera vole (*Microtus cabrerae*). This near-threatened rodent is characterized by an unusual suite of genetic, life history and ecological traits, being restricted to isolated geographic nuclei in fast-disappearing Mediterranean subhumid herbaceous habitats. To reconstruct the evolutionary history of the Cabrera vole, we studied sequence variation at mitochondrial, autosomal and sex-linked loci, using invasive and noninvasive samples. Despite low overall mitochondrial and nuclear nucleotide diversities, we observed two main well-supported mitochondrial lineages, *west* and *east*. Phylogeographic modelling in the context of the Cabrera vole's detailed fossil record supports a demographic scenario of isolation of two populations during the Last Glacial Maximum from a single focus in the southern part of the Iberian Peninsula. In addition, our data suggest subsequent divergence within the east, and secondary contact and introgression of the expanding western population, during the late Holocene. This work emphasizes that refugial endemics may have a phylogeographic history as rich as that of more widespread species, and conservation of such endemics includes the preservation of that genetic legacy.

Keywords: conservation genetics, glacial refugia, *Microtus cabrerae*, multilocus phylogeography, noninvasive sampling

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Introduction

Much of phylogeographic reconstruction has involved tracking the colonization of widespread temperate