

# Birth of a hotspot of intraspecific genetic diversity: notes from the underground

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## Abstract

Hotspots of intraspecific diversity have been observed in most species, often within areas of putative Pleistocene refugia. They have thus mostly been viewed as the outcome of prolonged stability of large populations within the refugia. However, recent evidence has suggested that several other microevolutionary processes could also be involved in their formation. Here, we investigate the contribution of these processes to current range-wide patterns of genetic diversity in the Italian endemic mole *Talpa romana*, using both nuclear (30 allozyme loci) and mitochondrial markers (cytochrome *b* sequences). Southern populations of this species showed an allozyme variation that is amongst the highest observed in small mammals (most populations had an expected heterozygosity of 0.10 or above), which was particularly unexpected for a subterranean species. Population genetic, phylogeographic and historical demographic analyses indicated that *T. romana* populations repeatedly underwent allopatric differentiations followed by secondary admixture within the refugial range in southern Italy. A prolonged demographic stability was reliably inferred from the mitochondrial DNA data only for a population group located north and east of the Calabrian peninsula, showing comparatively lower levels of allozyme variability, and lacking evidence of secondary admixture with other groups. Thus, our results point to the admixture between differentiated lineages as the main cause of the higher levels of diversity of refugial populations. When compared with the Pleistocene evolutionary history recently inferred for species from both the same and other geographic regions, these results suggest the need for a reappraisal of the role of gene exchange in the formation of intraspecific hotspots of genetic diversity.

*Keywords:* gene flow, genetic diversity, hotspots, multiple refugia, *Talpa romana*

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## Introduction

The patterns of geographic distribution of genetic diversity have been studied and compared in countless species (for extensive reviews, see Hamrick & Godt 1989; Avise 2000; Hewitt 2004a, b). It has been shown that usually genetic diversity is unevenly distributed among species populations, allowing us to define areas of so-called hotspots and 'cold spots' of diversity, and that these areas are often coincident among many species (Hewitt 1996, 2000). Quaternary climatic oscillations

would have played a major role in the formation of such range-wide patterns of genetic diversity, particularly in temperate areas (reviews in Hewitt 1996, 2000, 2004a, b; Hewitt & Ibrahim 2001). Indeed, species distributions underwent cycles of contraction—and eventually fragmentation—followed by expansion, dependent on oscillations of climate and climate-linked landscape features. The long-term persistence of favourable environmental conditions, within the so-called refugia, would have allowed the maintenance of stable and genetically variable populations in these areas. By contrast, the (re-)colonization of previously unsuitable habitats would have occurred through serial population bottlenecks at the expanding front, leading to progressive

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