

Population genetic structure and diversity of the Apennine endemic stream frog, *Rana italica* – insights on the Pleistocene evolutionary history of the Italian peninsular biota

DANIELE CANESTRELLI, ROBERTA CIMMARUTA and GIUSEPPE NASCETTI

Dipartimento di Ecologia e Sviluppo Economico Sostenibile, Università della Tuscia, Largo dell'Università s.n.c., 01100 Viterbo, Italy

Abstract

For most species in the Western Palearctic region, southern Mediterranean peninsulas have been identified as major Quaternary refugia and hotspots of intraspecific diversity, and thus, as areas of particular relevance for the conservation of the evolutionary potential. We analysed the patterns of geographical variation among 26 populations of the Italian stream frog, using both nuclear (allozymes) and mitochondrial (partial cytochrome *b* sequences) markers. Phylogenetic, phylogeographical and population genetic analyses suggested that the species survived the last glacial–interglacial cycles in two distinct refugia, one restricted to the tip of the Calabrian peninsula, at the extreme south of the species' range, the other spanning from central Calabria to central Apennines and showing evidences for further population subdivision therein. Historical demographic tests suggested a significant population expansion from the latter, which most likely began around the last pleniglacial. This expansion would have led to the rapid colonization of the northern Apennines to the north, and to a secondary contact and population admixture with the population from the southern refugium in southern central Calabria. A comparison of the evolutionary history inferred for the Italian stream frog with the data emerging for other codistributed species suggests: (i) the generality of a multiple-refugia scenario for the Italian peninsula, (ii) the possible occurrence of at least one suture zone in southern Italy, and (iii) that for most species, this Pleistocene refugium is not only a hotspot, but also a melting pot of intraspecific genetic diversity. Finally, the conservation implications of these results are also briefly highlighted.

Keywords: allozymes, Italian peninsula, mtDNA, multiple refugia, phylogeography, *Rana italica*

Received 3 April 2008; revision received 4 June 2008; accepted 9 June 2008

Introduction

The contribution of Pleistocene climatic oscillations to the patterns of species distribution, population genetic structure and their variations through space and time has been investigated in a large amount of taxa (recent reviews in Hewitt 2004a, b; Schmitt 2007). The identification of putative refugial ranges, as well as routes and processes involved in postglacial range expansions, has been the main focus to date. Recently, however, more attention is also being paid to evolutionary processes within putative

refugial ranges (e.g. Comes 2004; Weiss & Ferrand 2006). These areas are often — albeit not exclusively — located in the low-latitude portion of the present-day species ranges (Hampe & Petit 2005) and typically harbour a large fraction of intraspecific diversity (Hewitt 1996). Due to their relevance as long-term stores of species' genetic diversity and their role in diversification processes, they are now regarded as disproportionately important for the conservation of the evolutionary potential of the species, and for the evolution and survival of biota (Hampe & Petit 2005; Weiss & Ferrand 2006).

In the Western Palearctic region, important glacial refugia have been identified within the southern Mediterranean peninsulas of Iberia, Italy and the Balkans. Besides being

Correspondence: Daniele Canestrelli, Tel. +39-0761-357758; Fax: +39 0761 357751; E-mail: canestrelli@unitus.it