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Deep Divergences within *Liolaemus nigroviridis* (Squamata, Liolaemidae) Lineages Associated with Sky Islands in Central Chile

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Abstract

Evolution of montane species may be strongly influenced by climate oscillations, particularly species distributed in isolated high-elevation areas (sky islands). Chilean topography is exemplified by montane environments including the Andes and Coastal Mountains. To test hypotheses related to genetic divergence associated with sky islands, we explored population genetics and phylogenetic signatures in the montane lizard *Liolaemus nigroviridis* Müller and Hellmich 1932. We sequenced the mitochondrial cytochrome *b* for samples collected from six montane areas in central Chile. We found high genetic divergence among populations, congruent with well-supported clades from phylogeny reconstructions. The most recent common ancestor of all samples of *L. nigroviridis* was dated around the limit of Pliocene-Pleistocene (2.7 Mya), congruent with early vicariance of Andean and coastal populations. Deep lineage divergences suggest that allopatric populations accumulated high nucleotide differences and maintained long periods without gene exchange. We discuss potential taxonomic revisions considering relative genetic divergence.

Key words: Phylogeography, montane species, Sauria, cytochrome *b*, subspecies, candidate species

Introduction

Montane regions are strongly influenced by climatic changes associated with Pleistocene glacial cycles and constitute excellent systems for investigations of species distributions and divergence. Ecological changes in montane environments during climatic oscillations may result in isolation of populations. For example, if habitats shift in elevation, populations may become fragmented, with individuals unable to disperse across new (i.e. valleys) barriers (Guralnick 2007; Hewitt 2000; Hewitt 2004; Kozak & Wiens 2006). These processes may be particularly relevant for species inhabiting sky islands (high elevations patches of habitat that differ markedly from those in the intervening valleys) (Brown 1971; Knowles 2000; Shepard & Burbrink 2008). Population genetic processes such as genetic drift can generate high levels of interpopulation genetic divergence depending on the duration of isolation events. Montane environments are an essential component of the Chilean topography, including the Andes (elevations up to 5,000 m.) and the coastal mountains that parallel the Andes (up to 2,000 m.). The intervening valley, which is also heavily impacted by human activities, separates both montane regions by distinct low-elevation habitats.

The lizard genus *Liolaemus* Wiegmann 1834 (Liolaemidae) is widely distributed in southern South America, ranging from arid Patagonian to high-altitude Andean environments, including valley and coastal ranges (Cei 1986; Pincheira-Donoso *et al.* 2008). An adaptive radiation within *Liolaemus* has produced extensive genetic and morphological variation, resulting in a taxonomically complex and species-rich genus (Abdala *et al.* 2012; Fontanella *et al.* 2012; Lobo *et al.* 2010; Morando *et al.* 2008; Pincheira-Donoso 2011; Torres-Pérez *et al.* 2009). These features characterize *Liolaemus* as one of the most studied vertebrate taxa in southern South America across multiple spatial and temporal scales. In Chile, *Liolaemus* inhabits most environments from the arid desert in the north to cold and wet Patagonia in the south, and both coastal and Andean mountain environments from 0–4500 m

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