Speciation across mountains: Phylogenomics, species delimitation and taxonomy of the Liolaemus leopardinus clade (Squamata, Liolaemidae)

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Organisms rapidly diversifying across unstable environments such as mountain tops provide substantial challenges for resolving evolutionary histories and delimiting species. The Liolaemus leopardinus clade is a group of five species of lizards adapted to high altitudes in central Chile, with most species found in the Andes, but one species, L. frassinettii is found in the independent Costa Cordillera. Despite their allopatric distributions, they display shallow mitochondrial divergences, making phylogenetics and species delimitation of this clade hard to resolve. We use an integrative approach to delimit species by considering morphological data (linear and landmark-based), mitochondrial DNA (mtDNA), and nuclear DNA (Sequences and SNPs collected with ddRADseq). We find strong conflicting signals between phylogenetic analyses of the nuclear and mtDNA data. While mtDNA places L. frassinettii as sister to the rest of the clade, the SNPs support a south to north order of divergences, with southernmost species (new taxon described here) as sister to the rest of the clade. Moreover, species delimitation using mtDNA only supports two species (one in the Costa and one in the Andes), whereas combined analyses using the nuclear data and morphology support multiple Andean taxa, including a new one we describe here. Based on these results, population structure analyses and our knowledge of the geological and climatic history of the Andes, we argue that this mito-nuclear discordance is explained by past introgression among the Andean taxa, likely during glacial periods that forced these lizards to lower altitudes where they would

hybridize. The complete isolation between the Costa and Andes cordilleras has prevented any further contact between taxa on either mountain chain. Our study highlights the importance of using multiple lines of evidence to resolve evolutionary histories, and the potential misleading results from relying solely on mtDNA.