



Morphological diversity and phylogenetic relationships within a South-American clade of iguanian lizards (Liolaemidae: *Phymaturus*)

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Abstract

With 36 species and at least nine potentially independent lineages (not formally described yet) occurring mostly in the Andes and adjacent Patagonia and Puna plateau areas, *Phymaturus* lizards represent one of the most endemic vertebrate groups of the arid southwestern region of South America. Phylogenetic relationships among species of *Phymaturus* are inferred using mainly a morphological data set of 206 characters. Also available sequences of mitochondrial DNA for seven terminals were added for a total evidence analysis. Most information is included in the discrete characters block; most characters involve color pattern, osteology and squamation. Continuous characters were taken from body proportions, squamation and skeletons. Among morphological data, binary polymorphic characters were analyzed applying the scaled coding criteria. Continuous characters were entered in the analysis using standardized ranges, a method that allows a simple optimization to estimate distances/costs avoiding the arbitrary coding as discrete characters. For our parsimony analyses we chose the implied weights method, which underweights homoplastic characters. Several runs were made analyzing all the information combined and also separating morphological from molecular datasets. Binary polymorphisms were also analyzed as missing data. All characters affected by sexual dimorphism were analyzed separating the sexes; female information was more congruent with the total evidence analysis. Characters involving continuous and polymorphic information are relevant for searching and building phylogenetic hypotheses in *Phymaturus*. There exists significant congruence between the molecular information analyzed in this study and previous published analyses. Within both main clades of *Phymaturus*, northern subgroups are those more recently originated during the genus diversification. Species belonging to the puna subclade of the *palluma* group are arranged in two natural groups, one distributed in the north (Catamarca and La Rioja provinces), and the other in the south, La Rioja and San Juan provinces. Within the *patagonicus* group, the majority of the species are arranged in a south-central Chubut clade, eastern-central Chubut clade, central Rio Negro clade and a Payunia clade.

Key words: *Phymaturus*, morphology, phylogeny

Resumen

Con 36 especies y otras 9 poblaciones, potenciales linajes independientes (no descriptas formalmente aún) y viviendo en su mayoría en los Andes y en áreas de las mesetas patagónicas y de la Puna, las lagartijas del género *Phymaturus* representan uno de los grupos de vertebrados más endémicos de la región árida del sudoeste de Sudamérica. Las relaciones filogenéticas entre especies de *Phymaturus* son inferidas utilizando principalmente un conjunto de datos morfológicos basados en 206 caracteres. También secuencias de ADN mitocondrial disponibles para 7 terminales fueron sumadas para un análisis de evidencia total. La mayor parte de la información fue incluida en el bloque de caracteres discretos; la mayoría de los caracteres involucran patrón de coloración, esqueletos y lepidosis. Los caracteres continuos fueron tomados de proporciones corporales, lepidosis y esqueletos. Entre los datos morfológicos, los caracteres binarios polimórficos fueron analizados aplicando el criterio de codificación de “escalados”. Los caracteres continuos fueron ingresados en el análisis utilizando rangos estandarizados, un método que permite la simple optimización para estimar distancia/costos evitando la codificación arbitraria como caracteres discretos. Para nuestro análisis de parsimonia elegimos el método de pesos implícitos el cual le brinda menos peso a los caracteres homoplásticos. Varias pruebas se hicieron analizando toda la información combinada y también separando los conjuntos de datos morfológicos y moleculares. Los caracteres binarios