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Article



Taxonomic identity of the patagonian frog *Atelognathus jeinimenensis* (Anura: Neobatrachia) as revealed by molecular and morphometric evidence

HELEN DÍAZ-PÁEZ^{1,4}, MARCELA A. VIDAL², JUAN C. ORTIZ^{3,4},

CARMEN A. ÚBEDA⁵ & NÉSTOR G. BASSO⁶

¹Departamento de Ciencias Básicas, Campus Los Ángeles, Universidad de Concepción. Casilla 341, Los Ángeles, Chile ²Laboratorio de Genómica y Biodiversidad, Departamento de Ciencias Básicas, Facultad de Ciencias, Universidad del Bío-Bío. Casilla 447, Chillán, Chile

³Departamento de Zoología, Universidad de Concepción. Casilla 160-C. Concepción, Chile

⁴Centro de Investigación en Ecosistemas de la Patagonia (CIEP)

⁵Departamento de Zoología, Centro Regional Bariloche, Universidad Nacional del Comahue, Quintral 1250, R 8400 FRF - Bariloche, Argentina

⁶Centro Nacional Patagónico (CENPAT-CONICET). Bvd. Brown 2915, U9120ACF Puerto Madryn, Chubut, Argentina ¹Corresponding author. E-mail: hediaz@udec.cl

Abstract

The frog genus *Atelognathus* is currently represented by nine species distributed in Argentinean and Chilean Patagonia. It is mainly distributed in Argentina, and there are only three species in Chile (*A. ceii, A. grandisonae* and *A. jeinimenensis*). Regarding the morphological relationships among *Atelognathus* species, Meriggio *et al.* (2004) suggest that *A. jeinimenensis* is more related to *A. salai* than other species. *A. salai* was described from Laguna Los Gendarmes (Argentina), 90 km air line from the type locality of *A. jeinimenensis*. This paper presents a morphological analysis and a study of population genetics using mtDNA nucleotide data from Argentinean and Chilean localities to assess the genetic distance between *A. salai* and *A. jenimenensis*. We obtained 477 bp-long *d-loop* sequences from 51 *Atelognathus* species, in addition to which a simple geographic pattern of genetic diversity suggests a single species of *Atelognathus*. Also, the populations from Chile (Cerro Castillo, RN Lago Jeinimeni and Chile Chico) and Argentina (Laguna de Los Gendarmes) have low levels of genetic divergence that may be consistent with glaciations during the Late Pleistocene. We propose *Atelognathus jeinimenensis* as a junior synonym of *A. salai* and that the Chilean populations should be assigned to *A. salai*.

Key words: d-loop, haplotypes network, mtDNA, population genetics, taxonomic, morfology, Anura, *Atelognathus salai*, *Atelognathus jeinimenensis*

Introduction

The frog genus *Atelognathus* Lynch, 1978 is currently represented by nine species with distribution in the Argentinean and Chilean Patagonia, between 38° 40' and 49° S (Basso 1998). According to Lynch (1978), the genus *Atelognathus* is diagnosed primarily by the presence of a large, exposed frontoparietal fontanelle, short palatine bones, large nasals, and the absence of quadratojugals, columella, tympanic annuli, and cavity tympani. According to paleoenvironmental data, the genus would have had a wide ancestral Patagonian distribution, which could have been fragmented as a result of paleoclimatic changes in the area (Lynch 1978; Cei 1984; Cei & Roig 1968). Patagonia was affected by repeated glaciations during Plio-Pleistocene times, which shaped it into its present physical and biological configuration (Villagrán *et al.* 1986; Denton *et al.* 1999; Moreno & León 2003). During the Last Glacial Maximum (LGM) (~26,000–17,500 cal yr BP [calendar years before present]), piedmont glacier lobes covered vast areas on both sides of the Andes range. Palynological studies suggest millennial-scale changes in temperature and hydrological balance during the LGM, with mean summer temperatures during the coldest stadials around 6–8°C lower than present (Heusser *et al.* 1999; Moreno *et al.* 1999; Lamy *et al.* 2007).