

INTEGRATIVE TAXONOMY, SYSTEMATICS AND HYDROGRAPHIC HISTORY OF THE GENUS TELMATOBIUS (ANURA: TELMATOBIIDAE): DISENTANGLING THEIR HIDDEN BIODIVERSITY AND DIVERSIFICATION HISTORY.

Abstract. The Altiplano provides a natural laboratory to study the mechanisms and processes of speciation in different taxa, allowing us to understand the speciation process from a comparative perspective. The genus *Telmatobius* includes species endemic to the Altiplano and high altitude inter-Andean systems distributed in the Andes of Ecuador, Peru, Bolivia, Argentina and Chile. The species of this group inhabit lotic and lentic environments in springs, small lakes and high Andean wetlands, covering an altitudinal range which extends from 2,600 to 4,600 m above sea level. In the present proposal we will examine the phylogenetic and phylogeographic history of species of the genus *Telmatobius* Wiegmann, 1835 from Chile, Bolivia, Argentina and Peru, focusing on 1) the taxonomic delimitation of species and 2) the mechanisms and processes that stimulated their divergence. Taxonomic delimitations within *Telmatobius*, based on classical taxonomic characters (i.e. external morphology, osteology, chromosomes), have long been a puzzle. The high degree of morphological similarity found in these amphibians makes the identification of the species difficult. De la Riva (2005) mentioned that “intra- and inter-populational variation and the lack of clear diagnostic characters confounds taxonomists working with living *Telmatobius*”. Molecular techniques (mitochondrial DNA) have been applied as an alternative and valuable tool for *Telmatobius* species identification and as a method for estimating species diversity, but recent molecular phylogenetic analyses that included species of Bolivia and Chile showed that it was not possible to recover the monophyly of the majority of nominal species, which is in disagreement with other studies performed in co-distributed taxa. In order to uncover cryptic diversity in *Telmatobius*, this study proposes to apply to this group an integrative approach that combines multiple types of characters (i.e. morphological, osteological, chromosomal, molecular markers); thus defining lineages and delimiting species. We will perform a four-step formalized strategy of integrative taxonomy for species delimitation in *Telmatobius* (Puillandre et al., 2012): (1) Optimize taxon coverage. Covering a wide distribution range of the genus in the southern cone of South America and particular habitats of species will increase the probability of sampling closely related species; (2) Construct Primary Species Hypotheses (PSHs). PSHs will be constructed based on a DNA barcode approach (Cyt b). To determine PSHs we will use methods of phylogenetic reconstruction including parsimony, likelihood, Bayesian analyses and genetic distances, together with coalescent methods; (3) Visualization of PSHs using Klee diagrams. This method works over genomic data sets based on an indicator vector that allows classifying a taxonomic group through an accurate quantitative display of correlation affinities within and among genetic groups; (4) Consolidation of PSHs into secondary species hypotheses (SSHs). For *Telmatobius*, SSHs will be determined incorporating additional data sources such as osteological traits, cytogenetic analysis, phylogeographic analysis, other molecular markers (i.e. nuclear genes) and habitat attributes (e.g. altitude). This strategy of integrative approach, which begins with molecular characters, is particularly applicable for complex groups such as *Telmatobius*, where most species are difficult to recognize and for which the quality of morphological characters as proxies for determining species boundaries is doubtful. In the Andean Altiplano, the distribution patterns of codistributed taxa (fish of the genus *Orestias*, snails of genus *Biomphalaria* and *Heleobia*) suggest that the scenario of evolutionary divergence and eventual speciation in *Telmatobius* may involve a mixture of processes which would make it difficult to elucidate the evolutionary forces that have produced the divergence in this group. In order to contribute to resolve the importance of these mechanisms, this proposal aims to use phylogenetic hypotheses, diversification rates and

estimation of divergence times; with this information we will model the tempo and mode in the evolution of the genus *Telmatobius* in the Altiplano. These data, analyzed together with the distribution of the species in the area, will allow the generation of a biogeographic model to explain the presence of these species in the region. All this historical information (a robust phylogeny and divergence times) may be extremely relevant to provide an essential framework for enlightened decisions in conservation biology. This is particularly critical in the case of species of *Telmatobius*, where most species have in endangered status.

