



***Dendropsophus minutus* (Anura: Hylidae) of the Guiana Shield: using DNA barcodes to assess identity and diversity**

MONTY A. HAWKINS¹, JACK W. SITES JR.¹, BRICE P. NOONAN²

¹Department of Integrative Biology, Brigham Young University, Provo, UT 84602, USA

²Department of Biology, Duke University, Durham, NC 27708, USA. E-mail: bnoonan@bioguiana.org

Abstract

Herein we discuss the geographic structure of genetic variation of the widely distributed lesser treefrog (*Dendropsophus minutus*) from the Guianas in a preliminary examination of the status of Guianan populations referred to this taxon. Current sampling is insufficient to determine the status of all lineages of this complex within South America, but our results do indicate the presence of cryptic species within this relatively small portion of the ‘species’ range. Our findings reveal a geographic discontinuity of genetic structure within this region that appears to be correlated with elevation. We also present evidence that supports previous assertions that the conventional DNA barcode locus (COI) is not suitable for amphibians.

Key words: *Dendropsophus minutus*, DNA barcoding, Guiana Shield

Resumen

Se discute la estructura geográfica de la variación genética en la ranita trepadora (*Dendropsophus minutus*), ampliamente distribuida en Sudamérica. Las muestras analizadas provienen de las Guayanas en una evaluación preliminar del estatus de las poblaciones incluidas en este taxon. El muestreo actual no es suficiente para determinar el estatus de todos los linajes de este complejo de América del Sur, sin embargo nuestros resultados indican la presencia de especies crípticas dentro de esta porción relativamente pequeña del intervalo de distribución de esta ‘especie’. Nuestros resultados revelan una discontinuidad geográfica de la estructura genética dentro de esta región que parece estar correlacionada con la altitud. También mostramos evidencia que apoya las observaciones previas de que el locus COI, convencionalmente usado en DNA barcoding, no es adecuado para ser utilizado en anfibios.

Introduction

In 1979 John Lynch observed that fewer than 5% of known Neotropical forest amphibian species were “widely distributed”. He predicted that within a decades time, intensive study of taxonomy and distributions would reveal that there are very few species whose distributions are truly so extensive. While it took slightly more time than Lynch had anticipated, his theory has largely been supported by intensive phylogeographic analyses of many of these widespread ‘species’ (Camargo *et al.* 2006; Fouquet *et al.* 2007; Heyer *et al.* 1996). It appears that the single largest obstacle currently preventing the continued study of these ‘species’ is the lack of a comprehensive sample of molecular material that will permit the analysis of geographic structure of genetic variation. For many of these widespread ‘species’, the lack of differentiable, diagnostic phenotypes as well as trained taxonomists able to interpret these characters has left the task incomplete. DNA barcoding provides a means whereby today’s taxonomists can streamline the sorting process and focus their attention on populations/lineages that merit consideration for further examination as potential species.