



## DNA barcoding assessment of genetic variation in two widespread skinks from Madagascar, *Trachylepis elegans* and *T. gravenhorstii* (Squamata: Scincidae)

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### Abstract

*Trachylepis elegans* and *T. gravenhorstii* are two of the most widespread reptiles in Madagascar, inhabiting a wide variety of habitats. Previous studies have indicated a considerable mitochondrial DNA (mtDNA) variation within these species, but the geographic distribution of the major haplotype lineages is poorly known. Herein we analyse the phylogeography of these lizards based on 107 sequences of the mitochondrial cytochrome oxidase subunit I gene, 101 of which newly determined. As in previous mtDNA assessments, *T. elegans* and *T. gravenhorstii* were not reciprocally monophyletic, although recent analyses including nuclear markers indicated their probable monophyly, respectively. The main lineages within *T. gravenhorstii* were found in strict allopatry and could be divided into a subclade of roughly northern and eastern distribution (lineages 1 and 2) and a subclade of roughly southern and western distribution (lineages 3, 4a, 4b, and 5, plus *T. elegans*). Our data serve to identify more precisely the probable contact zones among *T. gravenhorstii* lineages. The two main mtDNA clades (represented by lineages 2 and 3, respectively) can be expected to come into close contact in the area of the upper Mangoro river and Alaotra Lake, and (lineages 2 and 4a) in the Southern Central East between Mananjary and Ranomafana. Future studies intensively sampling these contact zones have the potential to assess hybridization and admixture among these lineages, and to test whether they are deep conspecific lineages of *T. gravenhorstii* as currently understood, or might represent distinct species.

**Key words:** Squamata, Scincidae, Lygosominae, *Trachylepis*, Madagascar, cytochrome oxidase subunit I, biogeography

### Introduction

The “*Mabuya* clade” represents a species rich pantropical radiation of mostly medium sized lizards of the family Scincidae, characterized by a highly conserved morphology combined with a relatively convoluted taxonomic history. Phylogenetic studies published during the last decade led to splitting the former genus *Mabuya* sensu lato into four geographically distinct monophyletic genera, i.e., *Eutropis* in Asia, *Trachylepis* mainly in Africa and Madagascar, *Mabuya* sensu stricto in the Neotropics and *Chioninia* in the Cape Verde archipelago (Mausfeld *et al.* 2002, Carranza & Arnold 2003), and a phylogenetic meta-analysis of squamates revealed two additional genera (*Dasia* in Asia and *Eumecia* in Southern Africa) nested within the “*Mabuya* clade” (Pyron *et al.* 2013).

Recent molecular studies focusing on these different genera have shown that most of the taxa alleged to be common species with wide geographic distributions were actually constituted by complexes of several cryptic or pseudo-cryptic species with relatively restricted allopatric distributions (Datta-Roy *et al.* 2012; Hedges & Conn 2012; Miralles *et al.* 2009, 2011, Miralles & Carranza 2010; Sindaco *et al.* 2012). These observations led us to investigate herein the molecular differentiation within two Madagascar-endemic species of *Trachylepis* that are among the most widespread and common Malagasy reptiles, namely, *T. elegans* (Peters) and *T. gravenhorstii* (Duméril & Bibron).

## Acknowledgments

We are grateful to numerous friends, colleagues and students who contributed to collecting samples used in this study, in particular to Sebastian Gehring, Fanomezana Ratsoavina, and David R. Vieites. This work was carried out in the framework of institutional collaborations with the Université d'Antananarivo, Département de Biologie Animale. We are grateful to the Malagasy authorities for research and export permits. Financial support was granted by the Volkswagen Foundation to MV. The European Social Fund (ESF) and the Human Potential Operational Programme (POPH) supported this study through the doctoral grant of AL (SFRH/BD/47438/2008) from “Fundação para a Ciência e Tecnologia” (FCT).

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