

Rapid Communication

Morphology and molecular data reveal invasion of cryptic golden tegus (*Tupinambis cryptus* Murphy et al., 2016) in FloridaR. Alexander Pyron¹, Robert N. Reed², Timothy J. Colston¹ and Michael R. Rochford^{3,*}¹The George Washington University, Department of Biological Sciences, Bell Hall 302, 2029 G Street NW, Washington, DC 20052, USA²U.S. Geological Survey, Fort Collins Science Center, 2150 Centre Ave, Bldg B, Fort Collins, CO 80526, USA³University of Florida, Fort Lauderdale Research and Education Center, 3205 College Avenue, Davie, Florida 33314, USAAuthor e-mails: rapyron@colubroid.org (RAP), reedr@usgs.gov (RNR), tim@maddreptiles.com (TJC), miker@ufl.edu (MRR)

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Received: 19 October 2018**Accepted:** 23 February 2019**Published:** 15 April 2019**Handling editor:** Stelios Katsanevakis**Copyright:** © Pyron et al.This is an open access article distributed under terms of the Creative Commons Attribution License ([Attribution 4.0 International - CC BY 4.0](https://creativecommons.org/licenses/by/4.0/)).**OPEN ACCESS****Abstract**

Golden tegus (*Tupinambis teguixin sensu lato*) are native to South America but have established a reproducing population in Miami-Dade County, Florida. Recent work divided the golden tegu into four distinct species, leaving the specific identity of golden tegus in Florida unknown. We used morphometric and mitochondrial data to determine the species identity and likely area of geographic origin for a specimen of golden tegu collected in Miami-Dade County. Our results confirm that cryptic golden tegus (*Tupinambis cryptus*) are at least one of the species established in Florida. Their geographic origin is likely mainland Guyana or Venezuela. The presence of *T. teguixin* in Florida remains possible, based on other specimens of ambiguous scalation. Further study is needed to determine the identity and origin of these populations.

Key words: cryptic species, invasive species, biological invasions, pet trade, species identification, tegu lizards

Introduction

Murphy et al. (2016) revised the *Tupinambis teguixin* group, recognizing four species from South America. Krysko et al. (2016) and Edwards et al. (2017) provided evidence for establishment of *Tupinambis teguixin sensu lato* in Miami-Dade County, Florida, USA, but did not determine species identity as described by Murphy et al. (2016). These lizards are common in the pet and skin trades, and all tegus in the genera *Tupinambis* and *Salvator* are listed as CITES Appendix II species. They are also of concern as invasive species, and both *T. teguixin (sensu lato)* and *S. merianae* have established invasive populations on islands off of South America and in Florida (Fitzgerald et al. 2005; Bovendorp et al. 2008; Klug et al. 2015). These species are relatively easy to identify and localize to their geographic area of origin based on external morphological characters and molecular sequence data.

Table 1. Size and scale-count data for other Florida specimens of *Tupinambis*. Size (SVL) is given in mm.

Specimen	SVL	Ciliaries	Supraoculars	# in contact
174003	240	9	5	2
2595	215	9	5	2
174005	215	9	5	2
169211	200	9	5	2
152989	355	10	6	3
174730	–	10	5	3

Materials and methods

We received a tegu trapped on 1 December 2016 by a private trapper near the junction of SW 187th Ave and SW 276 St, Florida City, Miami-Dade County, Florida, USA and deposited the specimen at NMNH (USNM 590031 [specimen]; UF-Herpetology 179332 [photo voucher]). We recorded key morphometric data including sex, snout-vent length (SVL), number of supraocular scales, number of ciliaries in contact with fifth supraocular scale, number of vertebral scale rows, and number of midbody scale rows. We extracted genomic DNA using Qiagen DNEasy kits under the standard protocol and sequenced the SqCL markers (Singhal et al. 2017) on the Illumina platform using the commercial facility at Arbor Biosciences, Inc. (Ann Arbor) as part of a genomic sequencing run for the VertLife project (SRA accession SAMN09221389). Using the standard plugins in Geneious (Biomatters Ltd.), we mapped the raw Illumina reads to the reference dataset from Murphy et al. (2016) to reconstruct the 12S gene. We then added this to the alignment and used the Neighbor-Joining method in Geneious to construct a basic phylogeny.

We also re-analyzed the morphological dataset from Murphy et al. 2016 with the inclusion of data from our new specimen. We obtained cephalic scale-counts for several other *Tupinambis* specimens preserved at the Florida Museum of Natural History (Table 1) in an attempt to ascertain the identity of other potential tegu populations in Florida.

Results and discussion

The new specimen is an adult male (indicated by the everted hemipenes; Figure 1A, B), 305 mm SVL, 984 g body mass, with five supraoculars, three ciliaries in contact with the fifth supraocular, 105–107 vertebral rows and 104–105 midbody rows (Figure 1A–C). This identifies it as *Tupinambis cryptus* (cryptic golden tegu), falling within the published adult male size-range of 216–391 mm SVL (Murphy et al. 2016; Figure 2). Similarly, clustering analysis of the 12S data indicate affinity with *T. cryptus* from the Guyana Shield (Figure 3).

This species is primarily distributed in Guyana, Venezuela, and Trinidad and Tobago (Murphy et al. 2016). However, the transverse golden bands on the dorsum are indistinct and mottled with age, suggesting this specimen

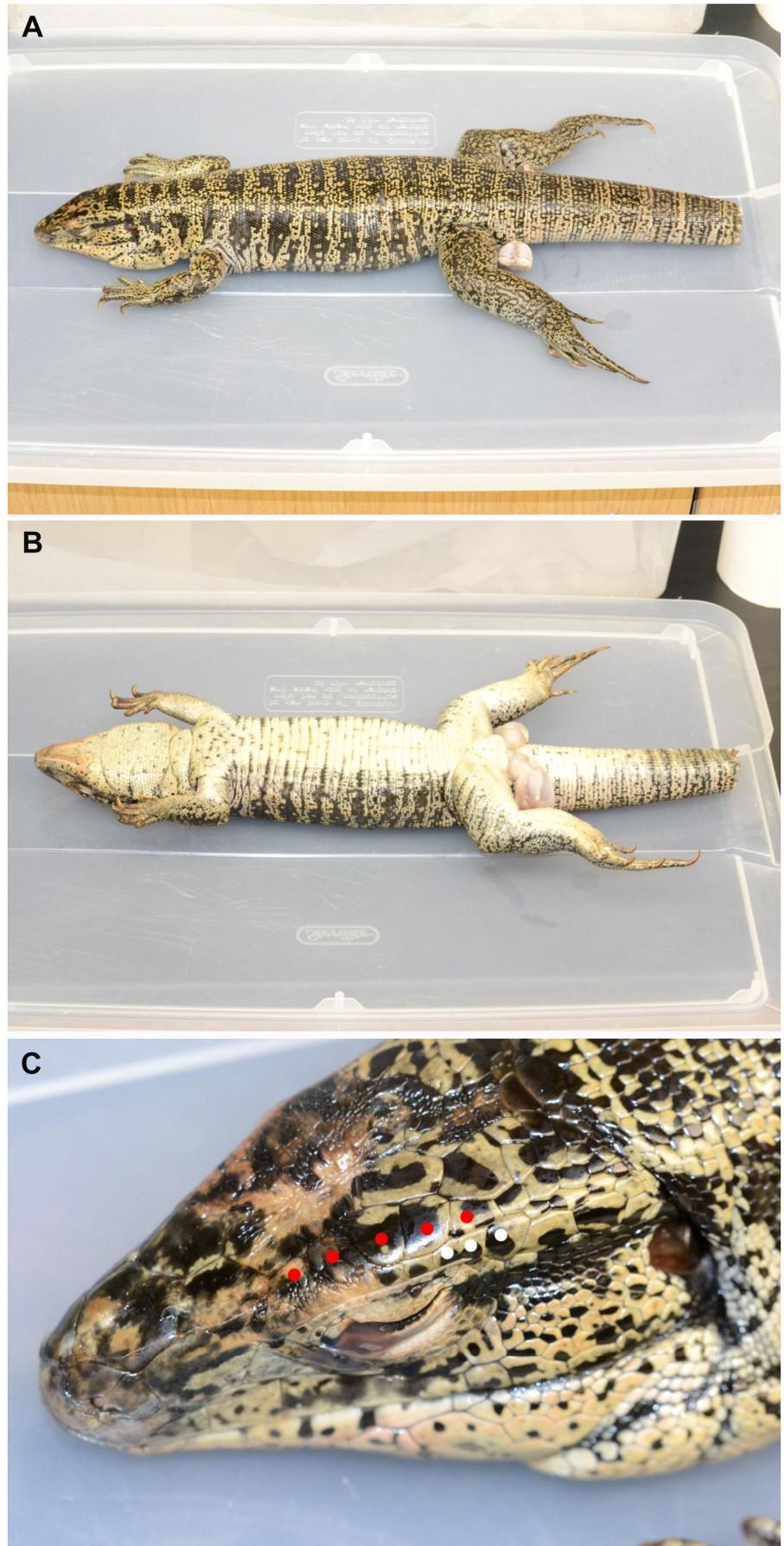


Figure 1. Photographs in preservative of USNM 590031, showing dorsal (A) and ventral (B) color pattern, and (C) supraoculars (red) and ciliaries (white). Photos by TJC.

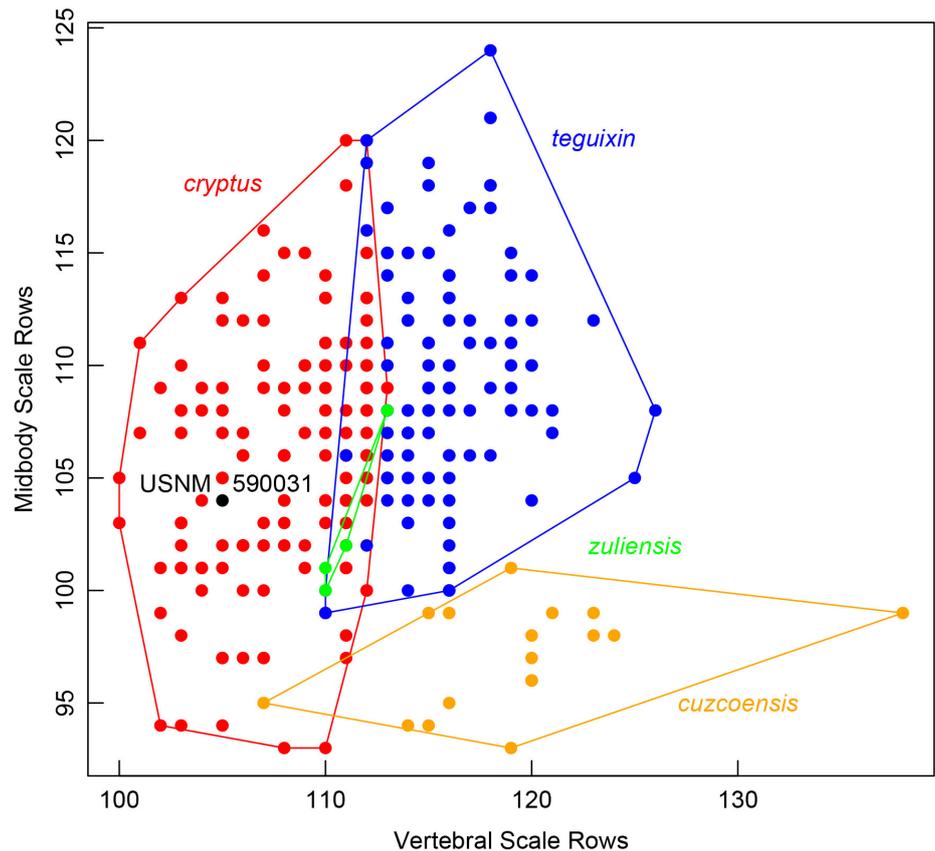


Figure 2. Re-analysis of Figure 9 from Murphy et al. (2016), illustrating the location of USNM 590031 (UF-Herpetology 179332) in the morphometric analysis, clustered with *Tupinambis cryptus*. Excludes AMNH140938, an apparent outlier which may have been miscounted.

did not originate from Trinidad and Tobago, where distinct bands are retained into adulthood. Thus, these data suggest a mainland origin in Guyana or Venezuela. From 2000 to 2018, 17,820 live specimens of *Tupinambis* were exported from Guyana to the United States, representing 30% of all *Tupinambis* imports to the U.S. during this period (total = 58,832; exporter-reported values; <https://trade.cites.org/> accessed 30 July 2018). This number is second only to Colombia for the same period (39,739), and no *Tupinambis* exports were reported from Venezuela. Thus, we conclude that Guyana is the most likely origin.

The data from the other Florida specimens held in FLMNH are not dispositive but suggest the presence of both *Tupinambis cryptus* and *T. teguixin* (Table 1). Two specimens are referable to *T. cryptus* based on size (152989) and the contact of three ciliaries with the final supraocular (152989 and 174730). The largest *T. teguixin* examined by Murphy et al. was 279 mm SVL, while 152989 is 355 mm. In contrast, four specimens (2595, 169211, 174003, and 174005) are smaller (200–240 mm SVL) and have only two ciliaries in contact with the fifth and final supraocular, characters associated with *T. teguixin*. Additional data from vertebral and midbody scale rows and DNA sequence are needed for certainty. If there are indeed populations of *T. teguixin* established in Florida, their geographic origin is presently unclear.

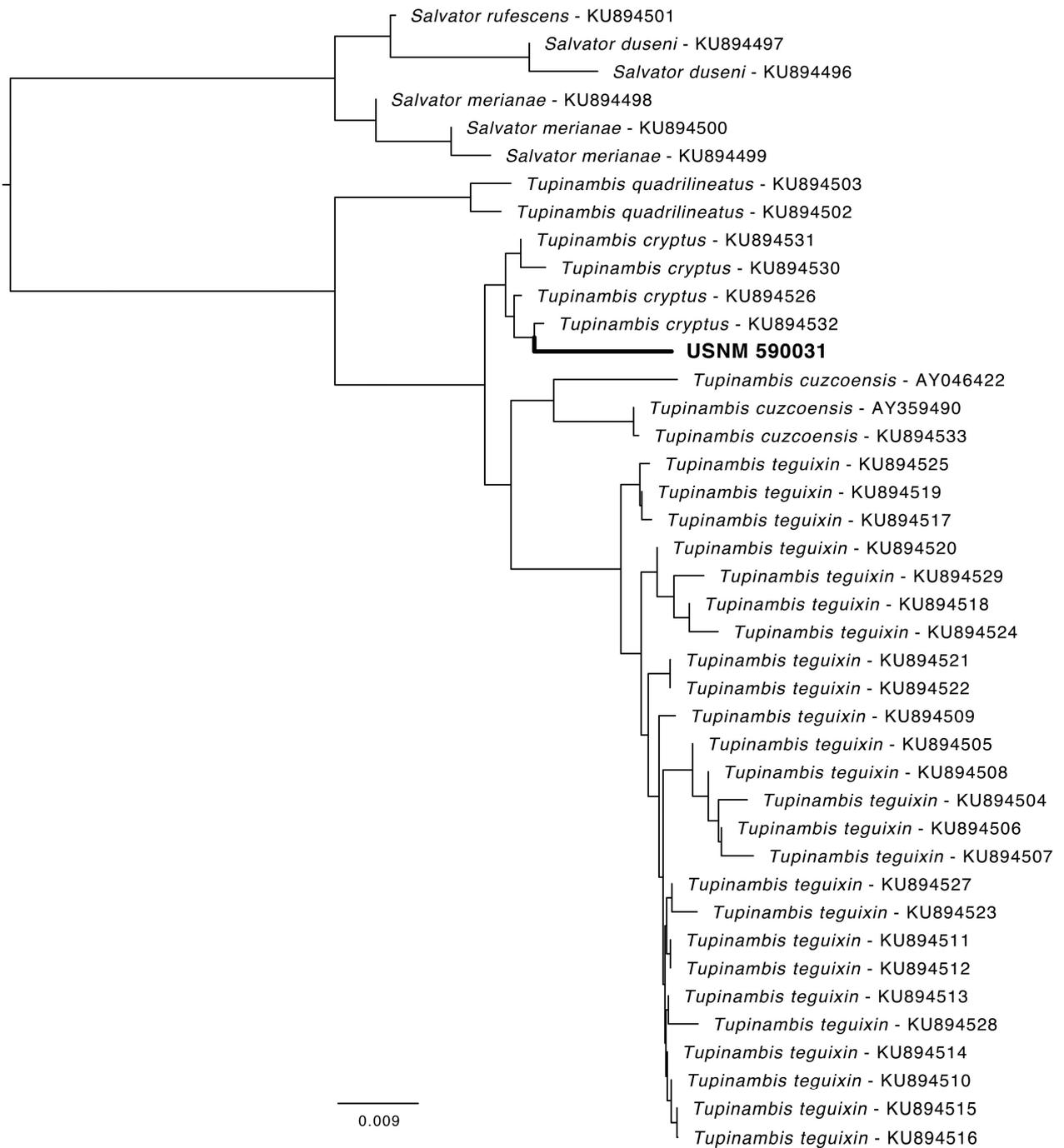


Figure 3. Neighbor-joining phylogenetic tree of 12S data analyzed by Murphy et al. (2016). The specimen USNM 590031 clusters with other *Tupinambis cryptus* samples from Guyana, Venezuela, and Trinidad and Tobago (blue). Terminal names are GenBank accession numbers (see Murphy et al. 2016; Table S1).

The *Tupinambis teguixin* complex is the second tegu group in Florida known to have established a reproducing population. A population of Argentine black and white tegu (*Salvator merianae*) is syntopic with *T. cryptus/teguixin* in Miami-Dade County. However, *S. merianae* are more commonly encountered and more widespread than *T. cryptus/teguixin*. Identifying the Florida population of golden tegus as *T. cryptus* and potentially *T. teguixin* may help refine recent predictions (e.g., Jarnevich et

al. 2018) of which areas in the U.S. and elsewhere may be suitable for population establishment by these potentially invasive large-bodied lizards. Removal of these invasive species is underway due to their ability to inflict harm on native wildlife. Baited traps and drift fences effectively capture all tegu species.

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