

First national record of *Tarentola parvicarinata* (Squamata Phyllodactylidae) from Côte d'Ivoire

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ABSTRACT

We reported the first record of *Tarentola parvicarinata* Joger, 1980 (Squamata Phyllodactylidae) from Mondoukou, Grand-Bassam, Côte d'Ivoire based on photographic and genetic evidence. A breeding population was observed near human settlement in the area. Morphologically, the specimens were consistent with the original descriptions of *T. parvicarinata* from Mali. Genetic analysis based on mitochondrial cytochrome oxidase subunit 1 (COI) gene fragment revealed low genetic divergence between the Côte d'Ivoire and Mali populations. Phylogenetically, the samples clustered with the sequence of *T. parvicarinata* from Mali and Mauritania. We also provided additional data on its natural history in Côte d'Ivoire. Future in-depth studies and broader scale sampling in the country are needed to investigate its distribution, ecology and genetic diversity.

KEY WORDS

Ivory Coast; herpetology; gecko; molecular analysis; West Africa.

Received 06.06.2025; accepted 18.07.2025; published online 16.08.2025

INTRODUCTION

The phyllodactylid genus *Tarentola* Gray, 1825 (Squamata Phyllodactylidae), is widely distributed across the West Indies, mainland Africa, Macaronesia and the Mediterranean region (Joger, 1984a; Schleich, 1984; Sprackland & Swinney, 1998). Currently, the genus comprised of 33 recognised species (Uetz et al., 2025). They occur in a wide range of habitats and can be found in desert, subtropical, tropical, and Mediterranean climates. Most species are primarily nocturnal and tend to climb and occupy rocky surfaces, trees and man-made structures (Schleich et al., 1996; Trape et al., 2012). To date, only a single species, namely *Tarentola ephippiata* O'Shaughnessy, 1875, has been recorded in Côte d'Ivoire (Rödel et al., 1997; Trape et al., 2012).

The White-Spotted Wall Gecko, *Tarentola parvicarinata* Joger, 1980 is a robust-bodied gecko oc-

curring in West Africa and Northwestern Africa. Populations have been documented in Mali, Niger, Sierra Leone, Guinea, Mauritania, Western Sahara, Gambia, Senegal and Burkina Faso (Böhme et al., 1996; Böhme et al., 2011; Trape et al., 2012; Uetz et al., 2025). The species may also occur in Morocco as population have been found close to the Moroccan borders (Geniez et al., 2004; del Mármol et al., 2019).

During recent field surveys conducted in southeastern Côte d'Ivoire, we observed some large-sized and robust gekkotan lizard inhabit around human settlements, which appeared morphologically different from any of the Gekkota known in the country. The individuals can be readily assigned to the genus *Tarentola* based on their size, heavily tuberculated lepidosis, and toe characteristics (Schleich et al., 1996). Compared to other gekkotan lizards, it possesses claws only on the III

and IV digits (Sprackland & Swinney, 1998; Khan-noon et al., 2015). In addition, it is distinguished from country-recorded congener *Tarentola ehippiata*, by the presence of white speckles on dorsal tubercles, and the absence of multiple large whitish dorsal patterns and ladder-like arrangements of reddish-brown crescents (Grandison, 1961; Trape et al., 2012). Detailed morphological examinations and molecular analysis indicated that these specimens should be categorised as *Tarentola parvicarinata*. Herein we report here as a new country record for Côte d'Ivoire.

MATERIAL AND METHODS

Study area

Field surveys were conducted from December 2024 to January 2025 in Mondoukou, Grand-Bassam, Sud-Comoé region, southeastern Côte d'Ivoire

(Fig. 1). The area is a coastal village adjacent to the Ebrié lagoon which is dominated by Arecaceae plantations (Fig. 2).

Sampling, DNA extraction and sequencing

In order to ascertain the identity of the population, two individuals were caught for morphological examination and photography records following the guidelines approved by the American Society of Ichthyologists and Herpetologists for animal care (Beaupre et al., 2004). The tips of their tails were preserved separately in 95% ethanol prior to further molecular analysis. All sampling individuals were released at the locality immediately. The photographic vouchers have been deposited in the collection of the Natural History Museum of Crete (voucher numbers: NHMC80.3.86.163, NHMC80.3.86.164, NHMC80.3.86.165). Genomic DNA was extracted from the tissue using a Qiagen DNeasy Blood & Tissue Kit (QIAGEN, Germany

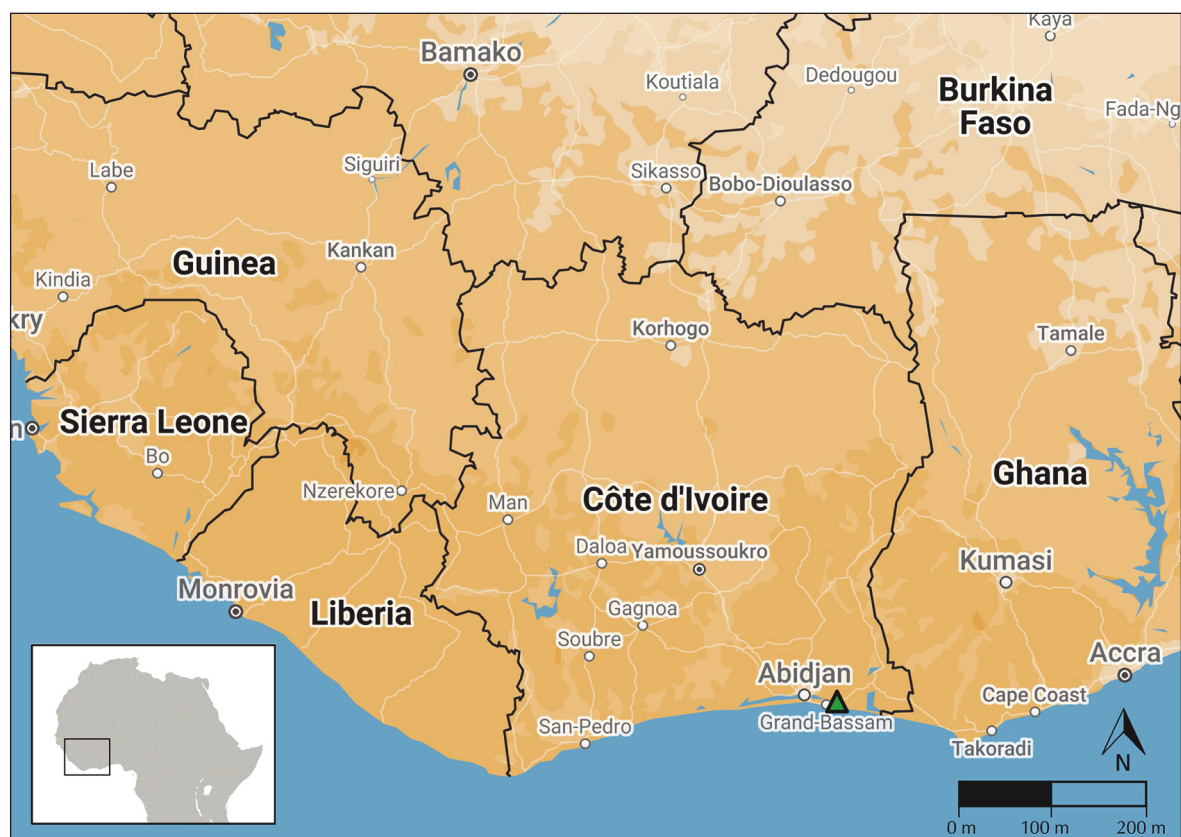


Figure 1. Map showing known distribution of species *Tarentola parvicarinata* in Côte d'Ivoire. Locality. Mondoukou, Grand-Bassam, Sud-Comoé region (Triangle).

Qiagen). The mitochondrial gene cytochrome c oxidase 1 (COI) fragment was amplified using degenerate primers RepCOI-F (primer forward, 5'-TNTTMTCAACNAACCACAAAGA-3') and RepCOI-R (primer reverse, 5' ACTTCTG-GRTGKCCAAARAATCA-3') following Velo-Antón et al. (2022). A touchdown PCR was performed with the following conditions: initial denaturation at 95 °C for 10 min, followed by an initial phase of 9 cycles of 40 s of denaturation at 95 °C, 30 s of annealing at 52 °C with a decrease in the annealing temperature by 0.5 °C per cycle until 48 °C, and extension at 72 °C for 45 s, and then followed by a second phase with 31 cycles of 40 s of denaturation at 95 °C, 30 s of annealing at 48 °C, and elongation during 45 s at 72 °C, and a final extension cycle of 10 min at 72 °C. Quality of PCR products were checked by visual examination in electrophoresis using 2% agarose gel. PCR products were purified with spin columns and then sequenced with forward primers using BigDyeTerminator Cycle Se-

quencing Kit as per the guidelines on an ABI Prism3730 automated DNA sequencer. The sequences were deposited at GenBank (accession number PW765466 and PW765467).

Phylogenetic analyses

Sequences obtained were edited in Geneious Prime 2022.0.1 software (Kearse et al., 2012) and compared with GenBank sequences for species identification using BLAST. Additional sequences of *T. parvicarinata* and other species of genus *Tarentola* available from GenBank were included in further phylogenetic analyses, and *Ptyodactylus rivapadiali* Trape, 2017 was selected as out-group (Velo-Antón et al., 2022). Bayesian inference (BI) was performed using Geneious Prime 2025.1 software developed by Kearse et al. (2012) and Mr-Bayes 3.2.6 software by Ronquist et al. (2012) with the HKY+G+I model recommended by the Akaike Information Criterion as implemented in jModel-



Figure 2. Habitat of *Tarentola parvicarinata* population in Mondoukou, Grand-Bassam, Côte d'Ivoire. Photo by Junior Kouadio Yao.

Test 2.1.2 by Darriba et al. (2012). Pairwise divergences (uncorrected p -distance) between species on COI dataset were calculated using Geneious Prime 2025.1 software.

RESULTS

Tarentola parvicarinata Joger, 1980

MATERIAL EXAMINED. CÔTE D'IVOIRE • 2 spm; Mondoukou, Grand-Bassam, Sud-Comoé region; 5°11'14.5"N, 3°41'05.8"W; datum WGS84; 3 m elevation); 30 December 2024; W.H.Y. Yeung & H.A. Koné; NHMC80.3.86.163 • AHCI22511 (Fig. 4), NHMC80.3.86.164 • AHCI22512 (Fig. 3), NHMC80.3.86.165 • AHCI22513 (Fig. 3).

MORPHOLOGICAL IDENTIFICATION. The individuals (NHMC80.3.86.163–65) can be assigned to the genus *Tarentola* by toe characteristics compared to other gekkotan lizards, which the claws on digits III and IV of both the manus and pes are retained, with digits I, II, and V strongly reduced, or lacking them entirely (Trape et al., 2012; Khannoon et al., 2015). Adult individuals are robust and large-sized (SVL 95 mm; Total Length 181 mm; Fig. 4). Visible tubercles were present throughout dorsal scales (Fig. 3). The presence of white speckles on the dorsal tubercles is clearly seen, which fully matches the morphological diagnosis of *T. parvicarinata* (Joger, 1984a; Trape et al., 2012). These characteristics clearly distinguish *T. parvicarinata* from all the other gecko species known in Côte d'Ivoire.

And this morphological identification agrees with the genetic identification result below.

GENETIC ANALYSIS. We successfully amplified 624 base pairs of COI sequences. The nucleotide BLAST (BLASTN) search showed the sequences generated share 99.2% sequence identity with confirmed *T. parvicarinata* sequences from Bindougou, Kayes region, Mali (GenBank accession no. ON943891). Bayesian inference (BI) phylogenetic tree is constructed based on DNA sequences of the mitochondrial COI gene (Fig. 4). The two samples from Côte d'Ivoire formed a clade with the two *T. parvicarinata* sequences from Mali (GenBank accession no. ON943891, ON943890) with high support levels (0.99 for BI values) in the phylogenetic analysis. Together this clade was grouped with other *T. parvicarinata* sequences analysed from Mauritania with high levels of nodal support (0.99 for BI values). The genetic distance (uncorrected p -distance) between the Grand-Bassam samples, and sequences from Mali and Mauritania ranged from 0.8 to 11.4%. *Tarentola parvicarinata* was found to be the sister taxon of *T. annularis* with high levels of nodal support (0.99 for BI values).

NATURAL HISTORY. A breeding population consists of eleven adult and subadult individuals, and four juveniles were observed near human settlements in Mondoukou area. Adults and subadults were primarily found on vertical plaster walls, actively preying on insects attracted by artificial light sources. They were alerted and quickly escaped into crevices when the spotlight pointing towards. While



Figure 3. *Tarentola parvicarinata* in situ from Mondoukou, Grand-Bassam, Côte d'Ivoire: (left) juvenile, NHMC80.3.86.164; (right) adult, NHMC80.3.86.165.

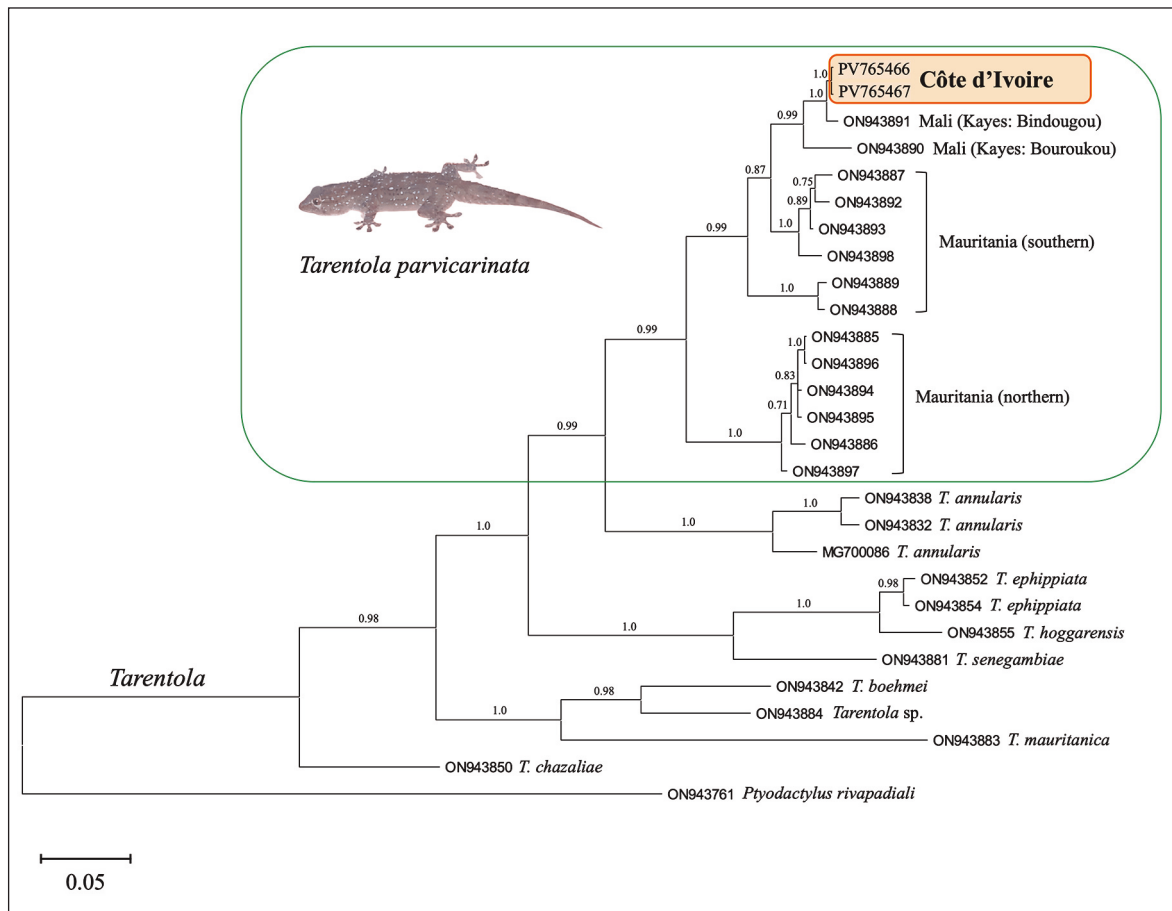


Figure 4. Bayesian inference (BI) tree derived from partial sequences of the combined fragments of COI genes. Numbers above branches are Bayesian posterior probabilities (>0.7 retained).

the juveniles were found on the trunks of Arecaceae trees. The population was found to be sympatric with *Hemidactylus mabouia* (Moreau de Jonnès, 1818) and *Agama picticauda* Peters, 1877 in the area. They are strictly nocturnal which no individuals were detected during repeated diurnal survey on 31 December 2024.

DISCUSSION

The species represent a new country record for Côte d'Ivoire. Considering their large-size, and their occurrence adjacent to human settlement, the fact that this species was overlooked in prior studies is unusual. One possible explanation is its sympatric occurrence with *Hemidactylus* geckos in the region, which may have led to species misidentification

and consequently overlooked. Additionally, previous studies conducted in the country may have been focused on protected areas and national parks areas, where the species appeared to be absent (Rödel et al., 1997). As with the findings of Kopetsch & Böhme (2017) on *H. pseudomuriceus* Henie et Böhme, 2003 in West and Central Africa, revisiting deposited gekkotan specimen collections may uncover additional records in the country.

Yet, accidental human-facilitated introductions could be a possible reason explaining the recent appearance of this species in Côte d'Ivoire. Previous studies have considered populations of *T. parvicarinata* in Burkina Faso and Senegal are, in fact, introduced (Joger, 1980; Joger, 1984b; Böhme et al., 1996). Species of the genus *Tarentola* have been consistently documented as introduced species in various countries (Jamison et al., 2017; Rosenfeld

et al., 2020). Their congener, *T. mauritanica* (Linnaeus, 1758), is also known to be a remarkable global colonizer (Medina et al., 2019; Rato et al., 2023). Our Bayesian phylogenetic analysis shows that samples from Côte d'Ivoire cluster closely with a sample from Bindougou, Kayes region, Mali. And then subsequently form a clade with another sample from Bouroukou, Kayes region, Mali. This pattern is somewhat unexpected, as the geographic distance between these localities would typically suggest greater genetic divergence. Considering the extremely low genetic divergence observed between our samples and Mali samples, combined with the locality where we recorded the individuals, it is not surprised that the species may have been introduced into Côte d'Ivoire from Mali. A broader-scale sampling of *T. parvicarinata* in the country is awaited to assess the distribution, and genetic diversity across populations, thus confirming the species' nativeness in the country.

To date, the distribution, taxonomic status and ecology of *T. parvicarinata* is still poorly known. Only a handful of studies on the species have been carried out, and all molecular sequences available on Genbank were restricted to the West Sahara-Sahel region (Velo-Antón et al., 2022). The distribution of *T. parvicarinata* in Sierra Leone remains controversial as the occurrence awaits further confirmation. Trape et al. (2012) excluded the species distribution in the country, and described the country's population from the Loma Mountains as a distinct species, namely *T. pastoria* Trape, Baldé et Ineich, 2012. However, a recent study conducted in the Bombali district reported the widespread presence of *T. parvicarinata* in urban areas (Peña-Fernández et al., 2024). Given that the herpetological exploration in West Africa is still insufficient, future studies on their distribution and population status across West Africa is imperative in order to assess their status in the region.

ACKNOWLEDGMENTS

We are thankful to Helen K.H. Cheung, Julien Kouamé, Junior Kouadio Yao, and César Koffi Yebouet for their invaluable assistance during the survey. Jean-Charles Amichia, Alou Fofana, Moussa Karamoko, and Yenatama Koné are kindly acknowledged for their hospitality and lo-

gistics supports. We acknowledge the Université Péléforo Gon Coulibaly for supporting the study. We are grateful to the editors and reviewers, for their helpful comments and reviews on our manuscript.

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