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# A new species of short-fingered geckos *Stenodactylus* (Squamata, Geckonidae) from South Iran with taxonomic notes on validity of the genus *Trigonodactylus* Hass, 1957

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## Abstract

In the present study we provide evidence for the validity of the genus *Trigonodactylus* Hass, 1957, improve the diagnosis for this genus and describe a new species that belongs to it—*Trigonodactylus persicus* **sp. nov.**, from the sand dunes in Khuzestan Province, southwestern Iran. The new species is closely related to *Trigonodactylus* [*Stenodactylus*] *arabicus sensu* Hass, and can be distinguished by the following morphological characteristics: small size, maximum SVL 34 mm; SVL/TailL—approximately 1:1; ventral scales roundish, weakly keeled, 54-61 longitudinal rows at midbody and 190-25 along midbody. No enlarged postmentals. Fingers and toes slightly flattened dorso-ventrally. Lateral edge of digits fringed by series of projecting triangular scales. No web between digits. No preanal and femoral pores. Dorsal color pattern formed by thin, dark, irregular vermicular patches and spots. Sometimes these dark dorsal patterns blend with each other and form transverse bands. There is a narrow, dark, longitudinal line between forelimbs and hindlimbs on lateral sides. Dark, well developed  $\Lambda$ -shaped marking on snout, which continues behind orbit on tympanum region, approaches the upper ear opening and ends on the pectoral arch. Labial scales white, in some cases with grey-brown dots. Dorsal surfaces of limbs and digits with irregular dark bands. Dorsal surface of tail with 8–10 wide, dark brown bands with irregular margins, same size as alternating light bands. Ventral surface of body and limbs white, tail with dark spots that become more distinct posteriorly.

Key words: systematics, taxonomy, Reptilia, Middle East, zoogeography, new species, COI, DNA-barcoding

## Introduction

To date, the genus *Stenodactylus* Fitzinger comprises from 11 to 14 species: *S. affinis* (Murray), *S. arabicus* (Haas), *S. doriae* (Blanford), *S. grandiceps* Haas, *S. khobarensis* (Haas), *S. leptocosymbotes* Leviton and Anderson, *S. mauritanicus* Guichenot, *S. petrii* Anderson, *S. pulcher* Anderson, *S. sharqiyahensis* Metallinou & Carranza, *S. slevini* Hass, *S. stenurus* Werner, *S. sthenodactylus* (Lichtenstein), and *S. yemenensis* Arnold—distributed in North Africa, the Arabian Peninsula and the Middle East. Recent molecular studies (Fujita & Papenfuss 2011) support revalidation of the genus *Pseudoceramodactylus* Haas, with a single representative *P. khobarensis*. This species is common in the eastern part of the Arabian Peninsula and in southern Iran (i.e., on the both sides of the Persian Gulf). Another team of researchers (Metallinou *et al.* 2012) carried out an extensive study on the molecular phylogeny of this group and clearly-confirmed the monophyly of *Pseudoceramodactylus*. This study revealed significant isolation of the *S. arabicus* group *sensu lato* from other *Stenodactylus* and demonstrated deep divergence between the different populations of this group. Later one of these populations from Oman was described as a new species *S. sharqiyahensis* (Metallinou & Carranza 2013).

Haas (1957) proposed the genus *Trigonodactylus* for the cf. *arabicus* group and we believe that *Trigonodactylus* is a valid genus and some of the evidence in support of our point is presented below. In addition, a new species that belong to this genus is described herein. However, the diagnosis of the genus *Trigonodactylus sensu* Hass requires clarification, since not all of the representatives of the group in the modern sense have webbing between the fingers. An extended and revised diagnosis of this genus is presented below.

## Material and methods

Fieldwork was conducted in the Iranian province of Khuzestan, 100 km northwest of Ahvaz city. Specimens were anaesthetized, fixed using ethanol and subsequently deposited in the collections of Zoological Museum of Moscow State University (ZMMU), Zoological Institute of the Russian Academy of Sciences, St. Petersburg (ZISP) and Department of Biodiversity, Institute of Environmental Science, International Center for Science, High Technology & Environmental Science, Kerman, Iran (ICSTZ). The global distribution of the genus *Trigonodactylus* is presented on the map (Fig.1).



**FIGURE 1.** Distribution of the genus *Trigonodactylus*: circle—*Trigonodactylus persicus* **sp. nov.**, squares—*T. arabicus*, diamonds—*T. sharqiyahensis*, triangles—*T. pulcher*; red colour denotes type localities of abovementioned species; blue colour—records from previously published data; green colour—our findings.

**Morphology.** A total of 36 specimens that belong to the three recognized species of *Trigonodactylus* were examined for morphological descriptions and comparisons. Thirty morphological features, including 16 morphometric characteristics (all measures were taken rounded to the nearest 0.1 mm using digital calipers) and 14 scalation characters (chosen based on Anderson 1999; Arnold 1980; Nazarov *et al.*, 2012; Szczerbak & Golubev 1986) were studied. In addition, 88 exemplars of *Stenodactylus* and 16 exemplars of the genus *Pseudoceramodactylus* were examined (Appendix 1).

**Measurements.** Measurements used in the study are the following: snout-vent length (SVL, from tip of snout to vent); tail length (TailL, from vent to tip of tail); head length (HeadL, distance between retroarticular process of jaw and snout-tip); head width (HeadW, maximum width of head); head height (HeadH, maximum height of head, from occiput to underside of jaws); orbital diameter (OrbD, greatest diameter of orbit); snout to eye distance (SnEye, distance between anteriormost point of eye and tip of snout); ear length (EarL, longest dimension of ear); trunk length (TrunkL, distance from axilla to groin measured from posterior edge of forelimb insertion to anterior edge of hindlimb insertion); shoulder length (LS, measured on ventral surface from base of shoulder to posterior margin of elbow while forelimb bent by 90° at elbow); forearm length (ForeaL, measured on dorsal surface while forelimb bent by 90° at elbow from posterior margin of elbow to inflection of bent wrist); femur length (FemurL, measured on ventral surface from base of femur to knee while hindlimb bent by 90°); crus length (Crus L, or tibia length, on ventral surface from posterior surface of knee to base of heel while hindlimb bent by 90°); length of finger IV (LF4, length of free distal phalanx of forth finger, without claw); length of toe IV (LT4, length of free distal phalanx of forth finger, without claw); length of toe IV (LT4, length of free distal phalanx of forth finger); eye to ear distance (EyeEar, distance from anterior edge of ear opening to posterior corner of eye); maximal length of rostral plate (RW), maximal height of rostral plate (RH), maximal length of mental plate (MW), maximal height of mental plate (MH).

Meristic counts were: number of scales across middle of body (V); number of scales around midbody including ventral and dorsal scales (SAB); number of scales along midbody from mental shield to anterior edge of cloaca (SLB); number of supralabials (SL); number of infralabials (IL); number of subdigital lamellae under fourth finger (LF 4); number of subdigital lamellae under fourth toe (FT 4); number of triangular fringed scales on both sides (left and right) of fourth finger (right side FFr 4, left side FFl 4) and fourth toe (right side TFr 4, left side TFl4); number of postcloacal spurs on basis of tail on both sides (Spurs); number of scales along middle of head, between occipital sinus and supranasals (SLH); scales across head, between top of ear openings (SAH).

The cranial skeletons of the eight representatives of *Stenodactylus*, *Trigonodactylus* and *Pseudoceramodactylus*: *affinis*, *doriae*, *grandiceps*, *leptocosymbotes*, *petrii*, *persicus* **sp. nov.**, *sthenodactylus* and *khoborensis* were compared. The shape and ratios of the measurements of the skulls and separate cranial bones were analyzed. This enabled us to find some additional diagnostic characteristics for this group.

**Molecular comparisons.** For the molecular sturdy, we analyzed 25 specimens that belong to nine species of *Stenodactylus*, *Trigonodactylus* and *Pseudoceramodactylus* from the Middle East, Arabia and Iran. (Table 1). In phylogenetic reconstructions the sequence of *Tropiocolotes algericus* from Morocco was used as an outgroup.

**DNA extraction, PCR, and sequencing.** Total genomic DNA was extracted from ethanol-preserved muscle or liver tissues using standard phenol-chloroform extraction procedures (Hillis et al. 1996), followed by isopropanol precipitation. A fragment of Cytochrome oxidase I (COI) gene with the maximal length of 655 b. p. was amplified. Cytochrome oxidase I (COI) gene is a mitochondrial marker, it is widely used for barcoding of invertebrates (Hebert & Gregory 2005; Smith et al. 2008) and it has proved to be useful for species identification in reptiles (Solovyeva et al. 2011; Nazarov et al. 2012; Nagy et al. 2012; Hartmann et al. 2013). The following primers VF1-d (5'-TTC TCA ACC AAC CAC AAR GAY ATY GG-3'), VR1-d (5'-TAG ACT TCT GGG TGG CCR AAR AAY CA-3') (Ivanova et al. 2006), RepCOI-F (5'-TNT TMT CAA CNA ACC ACA AAG A-3') and RepCOI-R (5'-ACT TCT GGR TGK CCA AAR AAT CA-3') (Nagy et al. 2012) were used for both PCR and sequencing. The obtained fragments were sequenced in both directions for each sample, and a consensus sequence was generated. PCRs were performed in 25 µl reactions using ca. 50 ng of genomic DNA, 10 pmol of each primer, 15 nmol of each dNTP, 50 nmol of additional MgCl., Taq PCR buffer (10 mM Tris-HCl, pH 8.3, 50 mM KCl, 1.1 mM MgCl, and 0.01% gelatine) and 1 U of Taq DNA polymerase. The PCR conditions were as follows: initial denaturation step at 95° C for 3 min; 5 cycles at 95° C for 30 s; annealing at 45° C for 1 min; extension at 72° C for 2 min; 35 cycles at 95° C for 30 s; annealing at 48~51° C for 1 min; extension at 72° C for 2 min; final extension of 5 min at 72° C; storage at 4° C. PCR products were loaded onto 1% agarose gels stained with GelStar gel stain (Cambrex) and visualized in a dark reader transilluminator (Clare Chemical). If results were satisfactory, the

Species	Collection number	N	ы	a.s.l.	Locality	GenBank AN
S. affinis	ZMMU R-14763-1-2	32°47'	46°56'	358	Iran, Ilam prov, 20 km N of Dehloran.	MH287439-MH287440
S. doriae	ZMMU R-14761-1-3	27°24'	56°57'	77	Iran, Khuzestan prov, 100 km NW form Ahvaz, sand-drifts between Alvan and Bostan.	MH287434-MH287436
S. cf. doriae	ZMMU R-13898-1-2	25° 27'	58° 45'	308	Oman, Ash Sharqiyah province, Wahiba sand dunes, near Bidiyah.	MH287437-MH287438
S. leptocosymbotes	ZMMU RAN- 2431– 2433	18° 53'	56° 58'	42	Oman, Al Wusta Governorate, 50 km W from Al Jawarah, send dunes near coast.	MH287445-MH287447
S. grandiceps	ZMMU RAN- 2556 – 2559	31° 44'	36° 50'		Jordan, Zarga prov, 10 km S from Azraq city.	MH287441-MH287444
S. stenodactylus	ZMMU RAN-190	27° 13'	37° 50'	30	Egypt, Red Sea Governorate, near Hurghada.	MH287457
T. sharqiyahensis	ZMMU R-14667-1-2	22° 27'	58° 45'	308	Oman, Ash Sharqiyah province, Wahiba sand dunes, near Bidiyah.	MH287454-MH287455
T. persicus sp.nov.	ZMMU R-14669; ZISP 29581; 29582	27°24'	56°57'	77	Iran, Khuzestan prov, 100 km NW of Ahvaz, sand-drifts between Alvan and Bostan.	MH287448-MH287450
T. arabicus	ZMMU R-14666-1-3	19°35'	54° 52'	113	Oman, Dhofar Governorate, near Mughshin, send dunes.	MH287451-MH287453
Tropiocolotes algericus	ZMMU RAN 1664				Morocco	MH287456

Table 1. List of specimens examined in the phylogenetic part of this study. AN - GenBank accession number.

products were purified using 2  $\mu$ l of a 1:4 diluted ExoSapIt solution (Amersham) per 5  $\mu$ l of PCR product prior to cycle sequencing. A 10  $\mu$ l sequencing reaction included 2  $\mu$ L of template, 2.5  $\mu$ l of sequencing buffer, 0.8  $\mu$ l of 10 pmol primers, 0.4  $\mu$ l of BigDye Terminator version 3.1 Sequencing Standard (Applied Biosystems) and 4.2  $\mu$ l of water. The sequence reaction was as follows: 35 cycles at 96° C for 10 s, 10 s at 50° C and 4 min at 60° C. Cycle sequencing products were purified using ethanol precipitation. Sequence data collection and visualization were performed on an ABI 3730xl automated sequencer (Applied Biosystems). Sequences obtained were deposited in GenBank under accession numbers MH287434–MH287457.

Phylogenetic analysis. Final alignment used for phylogenetic analysis contained 654 bp of COI gene for 25 specimens of six Stenodactylus species, three Trigonodactylus species and a sequence for Tropiocolotes algericus as an outgroup (Table 1). Sequences were aligned visually using BioEdit Sequence Alignment Editor 5.0.9 (Hall 1999). Phylogenetic analyses were conducted using PAUP version 4.0b4a (Swofford 1998), MEGA6 (Tamura et al. 2013), Treefinder (Jobb et al. 2004) and MrBayes 3.1.2 (Huelsenbeck & Ronquist 2001; Ronquist & Huelsenbeck 2003) software. Uncorrected genetic distances (p-distance values) between sequences were calculated using MEGA6. Optimal Neighbor-Joining (NJ) trees were constructed using MEGA6 based on the evolutionary distances obtained using the Maximum Composite Likelihood method (Tamura et al. 2004) with transitions, transversions and all three codon-positions included into the analysis. MODELTEST v.3.06 (Posada & Crandall 1998) was used to estimate the optimal evolutionary models to be used for the analysis of the data set. The preferred model (GTR + I + G) was suggested by the Akaike information criterion (AIC). The MP analyses were conducted using the PAUP version 4.0b4a (Swofford 1998) software. Heuristic search and the closest step-wise sequence addition algorithm were used. Most-parsimonious trees were generated using 100 random-addition sequences and the tree-bisection-reconnection (TBR) algorithm for branch swapping. For the maximum parsimony (MP) analysis ten random-addition replicates were performed. The ML analyses were conducted using Treefinder (Jobb et al. 2004). Transitions and transversions were equally weighted, and gaps were treated as missing data. Confidence in tree topology was tested using MrBayes 3.1.2 (Huelsenbeck & Ronquist 2001) by non-parametric bootstrap analysis (Felsenstein 1985) with 1000 replicates performed, and by posterior probability (PP) for Bayesian inference (BA). Branches with bootstrap values of 85% or greater and posterior probability values over 0.95 were regarded as sufficiently resolved (Huelsenbeck & Hillis 1993).

#### Results

Sequence and statistics. The COI mtDNA fragment used in the study consisted of 654 sites, of which 399 sites were found to be conserved, 252 were variable, and 235 were recovered as potentially parsimony-informative. The transition-transversion bias was estimated to be 6.94 (all data given for ingroups only). Substitution pattern and rates were estimated using the Kimura (1980) 2-parameter model (+G+I). The nucleotide frequencies were as follows: 26.23% (A), 26.15% (T), 16.75% (C), and 30.87% (G).

**Sequence divergence.** Uncorrected genetic distances (*p*-distances) within and between studied species of *Stenodactylus sensu lato* are presented in Table 2.

Our analysis revealed that intraspecific variation of the COI-gene within the studied *Stenodactylus* populations is quite low. The maximum value of within-group *p*-distance found was between the populations of *S. affinis* and was equal to 1.27%. Intraspecific variation within the populations of other *Stenodactylus* species was minimal (less than 0.30% of substitutions) or was equal to zero (Table 2). The only exception is the population of *Trigonodactylus* from the sand dunes near Mughshin: the three samples from this locality belong to two mtDNA lineages with *p*-distance of 2.06% between them.

The interspecific differentiation between the sequences of the COI gene fragment of species assessed in this research proved to be quite high. The minimum uncorrected genetic *p*-distance between presently recognized species found was between *S. grandiceps* and *S. doriae* from the Wahba sand dunes, Oman (p = 12.34%). The maximum distance (p = 21.16%) found was between *Trigonodactylus arabicus* and *Stenodactylus affinis* (Table 2). In general, the distances between the species assigned to the clades of *Stenodactylus sensu stricto* and the *Trigonodactylus arabicus* complex are greater (p = 17.30-21.16%) than the distances between those within the clades (p = 9.07-20.25%). The maximum genetic distance between the outgroup and ingroup species was observed between *Tropiocolotes algericus* and *S. sthenodactylus* (p = 25.23%), and the minimum between *T. algericus* and

*Trigonodactylus arabicus* (p = 19.96%). Thus, the values of genetic distances in ingroup and outgroup comparisons slightly overlap.

We revealed deep divergence within the two species complexes of *Stenodactylus* sensu lato, in which the genetic distances for the COI gene between the isolated populations are much higher than for intraspecific comparisons of gekkonids (Nazarov *et al.*, 2012). For instance, the genetic distance between the populations of the *S. doriae* species complex from Oman and western Iran is estimated to be as high as p = 9.07%. Another case of deep divergence was revealed within the *T. arabicus* species complex—the population from Wahiba sands in eastern Oman is the most divergent (p = 11.92-12.70%). Significant differentiation was also found between typical *T. arabicus* from Oman and the population from Khuzestan province in western Iran, identified as *T. cf. arabicus* (p = 9.74%).

species studied (below the diagonal row), mean <i>p</i> -distances within group (diagonal row) and calculation errors (above the diagonal row).	TABLE 2. Uncorrected p-distances (percentages) between COI sequences for Stenodactylus and Trigonodactylus
	species studied (below the diagonal row), mean <i>p</i> -distances within group (diagonal row) and calculation errors (above the diagonal row).

	Species	1	2	3	4	5	6	7	8	9	10
1	S. doriae (Iran)	0.24	1.20	1.34	1.54	1.46	1.68	1.83	1.75	1.75	1.82
2	S. cf. doriae (Oman)	9.07	0.00	1.31	1.56	1.45	1.69	1.71	1.60	1.72	1.86
3	S. leptocosymbotes	11.92	12.52	0.24	1.60	1.41	1.68	1.74	1.61	1.79	1.91
4	S. affinis	15.59	15.44	17.02	1.27	1.43	1.81	1.89	1.73	1.82	2.05
5	S. grandiceps	12.58	12.34	13.97	12.83	0.09	1.64	1.83	1.57	1.75	1.84
6	S. sthenodactylus	17.60	18.15	19.06	20.25	16.88	-	1.90	1.77	1.83	1.92
7	T. sharqiyahensis	17.30	17.79	18.87	21.98	19.96	19.42	0.00	1.48	1.25	1.81
8	T. persicus sp. nov.	18.39	18.57	19.18	20.38	19.30	19.30	12.70	0.24	1.24	1.66
9	T. arabicus	20.02	19.36	21.05	21.16	20.63	20.81	11.92	9.74	2.06	1.80
10	Tropiocolotes algericus	22.26	21.96	22.26	23.89	23.05	25.23	20.51	20.21	19.96	-

**Phylogenetic relationships.** The phylogenetic analysis of the mtDNA molecular markers in this study is used to augment the diagnostics of cryptic biodiversity within the taxonomically complicated genus *Stenodactylus*, since the estimation of the taxonomic rank of certain lineages using only morphological data is often problematic. However, phylogenetic analysis of the COI gene fragment in this study yielded a well-resolved tree with significant node support values. Phylogenetic relationships of the genus *Stenodactylus* have recently been assessed in a number of studies (Fujita & Papenfuss 2011; Metallinou *et al.* 2012). Our results are concordant with the phylogeny reported in these studies. These phylogenetic patterns are presented in Figure 2 and are briefly discussed below.

Our results support the basal split of the genus *Stenodactylus sensu lato* into two monophyletic groups: the clade that unites members of the *arabicus* species complex (*Trigonodactylus*), and the clade that unites all other species used in the analysis (*Stenodactylus sensu stricto*).

The *Trigonodactylus* clade includes three lineages. The most basal position is occupied by *Trigonodactylus* (*Stenodactylus*) *sharqiyahensis* Metallinou & Carranza, 2013 from Wahiba sand dunes, eastern Oman, which is sister to two species of the *Trigonodactylus arabicus* species complex.

Our study reveals high genetic divergence between the population of *Trigonodactylus* cf. *arabicus* from Mughshin sand dunes, Oman, which corresponds to the nominal form of *Trigonodactylus arabicus sensu* Hass, and the population from Khuzestan Province, western Iran, which was not included in previous studies. The Iranian form is described herein as a new species, *Trigonodactylus persicus* **sp. nov**.

The *Stenodactylus sensu stricto* clade consists of two subclades: one includes the Afro-Saharan species (*S. sthenodactylus* in our analysis), and the other comprises mostly Middle Eastern species of *Stenodactylus*.

The Middle Eastern *Stenodactylus* clade comprises two subclades; one includes the reciprocally monophyletic *S. grandiceps* from Jordan and *S. affinis* from Iran, and the other clade includes *S. leptocosymbotes* from Oman and the *S. doriae* species complex.

Stenodactylus doriae comprises two highly divergent (p = 9.07%) clades, one from western Iran, and the other

represented in our analysis by a population from the the Wahiba sand dunes, Oman. Monophyly of *S. doriae sensu lato* is poorly supported and the clade *S. leptocosymbotes—S.* cf. *doriae* from Oman—*S. doriae* from Iran is practically unresolved.

Based on all presented data, we herein propose a revised diagnosis for Trigonodactylus.



**FIGURE 2.** ML-tree of studied *Stenodactylus* and *Trigonodactylus* species based on the analyses of 602 bp COI mtDNA gene fragment. Node colour indicates support values: black for well-supported and sufficiently supported nodes, grey for moderately or poorly supported nodes. Node support values are shown above or below tree nodes for ML BS/MP BS/BI PP analyses respectively.

## Type species: Trigonodactylus arabicus Hass, 1957

**Diagnosis**: Ground-dwelling, psammophilous, small-sized geckos (SVL less than 40 mm *versus* SVL more than 40 mm in *Stenodactylus* and *Pseudoceramodactylus*). Habitus very slender. Head and body strongly flattened (as compared with massive head and round body in *Stenodactylus* and *Pseudoceramodactylus*). Head elongated and relatively narrow as opposed to large, well-defined head in *Stenodactylus* and *Pseudoceramodactylus*. Edges of fingers and toes with large elongated triangular scales that form a fringed edge. Claws thin and long, significantly compressed. Minute, imbricate, triangular scales cover undersides of fingers; only a few transversely widened scales at their tips (usually three). Upper surface of hands covered with keeled, imbricate, rather elongated scales. Toes elongated, slender, with strongly compressed long claws; margins of toes fringed; web between fingers present in some species. Dorsal scales flat, juxtaposed with each other, slightly keeled, elliptic. Ventral scales slightly keeled. Contracted pupil forms a vertical slit. No precloacal or femoral pores (present in some *Stenodactylus*). Moderate hemipenial swellings; two-three precloacal spurs on each side at basis of tail. Tail round in cross-section, tapering uniformly; length equal to that of body.

Prefrontal relatively small with rounded distal surface; no prefrontal projection; postorbitofrontal relatively small with rounded distal edge; nasal relatively small, of same size as premaxillary (*versus* relatively larger prefrontal often with apical growth, relatively larger posterior frontal with elongated distal edge, which are typical for representatives of *Stenodactylus* and *Pseudoceramodactylus*. Locomotion of this group of geckos is very distinctive. *Trigonodactylus* move pressing their body to the surface of the substrate, where *Stenodactylus* keep their body raised high above the surface.

#### Trigonodactylus persicus sp. nov.

(Fig. 3; 4c; 5a.)

**Holotype:** Adult male ZMMU R-14668: Iran, Khuzestan province, 100 km northwest of Ahvaz, 27°24' N 56°57' E; altitude 77 m a. s. l., June 22, 2011, coll. Daniel A. Melnikov, Roman A. Nazarov and Khosrow Rajabizadeh (Fig. 3a).

**Paratypes:** ZMMU R-14669, R-15160, R-15161, R-15162; ZISP-29581, 29582, 29583; ICSTZ-M6H1293, M6H1294, M6H1295; with the same data as a holotype. Measurements of holotype and type series are presented in Table 3.

**Diagnosis:** Small sized geckos, maximum SVL 34 mm; SVL/TailL approximately 1:1. Dorsal surface covered with small homogenous granular scales. Ventral scales rounded, weakly keeled (Fig. 3b), 54–61 longitudinal rows at midbody (V), 190–225 scales along midbody (SLB), 88–97 scales around midbody (SAB). Nostrils surrounded by convex scales. No enlarged postmentals. Fingers and toes weakly flattened dorsoventrally, lateral edge of digits fringed by series of projecting triangular scales. No web between digits. Usually, three median lamellae present only on distal part of digits (Fig. 3c); no precloacal or femoral pores.

Main dorsal background color is cream with beige shade. Dark ^- shaped stripe on dorsal surface of rostral part of snout, which passes through eye above ear opening and continues on side of body. Labials white, in some cases, with grey-brown dots. Patterns on dorsum formed by dark thin irregular vermicular patches, spots, and lines. Sometimes these dark dorsal patterns blend with each other and form transverse bands. There is a dark longitudinal narrow stripe between forelimbs and hindlimbs on sides of body. Dorsal surfaces of limbs and digits with irregular dark bands. Dorsal surface of tail with 8–10 dark-brown wide bands with irregular margins, same size as light bands with which they alternate. Ventral surface of body and limbs white. Ventral surface of tail with dark spots that become more distinct posteriorly.

**Description of Holotype:** Adult male, small-sized (SVL 28.7 mm, TailL 29.0 mm), HeadL 8.2 mm, HeadW 4.8 mm, HeadH 3.2 mm, SnEye 2.8 mm, OrbD 1.8 mm, EarL 0.8 mm, EyeEar 2.0 mm. Proportions as follows: SVL/ HeadL 3.5, HeadL/ HeadW 1.7, HeadL/ HeadH 2.56, SnEye/ EyeEar 1.4, HeadL/ OrbD 4.5.

Rostral width greater than height (RW 1.1 mm, RH 0.5 mm, RW/ RH 2.2) with a median groove which divides rostral at two thirds of its length; supralabials 13/13; small scales between orbit and tenth supralabial 2/1; infralabials 10/10; nares surrounded anteriorly by rostral, laterally by first supralabial, posteriorly by supranasal and two nasals; supranasals not enlarged—same size as nasals, rostral about 7–8 times larger than supranasal; supranasals separated from each other by 3 intersupranasals (three times smaller than supranasals); snout scales that lie medially large, granular, scales that lie laterally flattened, about 1.5–2 times smaller than medial ones; head scales large, granular, same size as median snout scales; mental rectangular with undulating posterior edge, slightly wider than rostral (MW 1.3mm; MH 0.9 mm, MW/ MH 1.4) (Fig. 4m); no enlarged postmentals; dorsal scales granular, same size as ventral scales; no enlarged dorsal tubercles; ventral scales weakly keeled, 61 longitudinal rows at midbody; lateral folds not developed; dorsal surfaces of forelimbs and hindlimbs covered with weakly keeled granular scales; fingers and toes without webbing, median lamellae present only on distal surface of digits, four under fourth finger, two under fourth toe; no enlarged precloacal and femoral scales and pores; three pairs of enlarged postcloacal spurs; tail without whorls or segments, dorsally covered with flattened and rounded weakly keeled scales; subcaudals without enlarged plate row, flat, weakly keeled, imbricate, same size as dorsal scales on tail.

**Coloration:** Main background color of body cream with beige shade. Dark ^- shaped band located on dorsal surface of rostral part of head, which passes through eye and above ear opening. Horseshoe-shaped thin dark line, few roundish dark brown patches at occipital region; dark brown transverse stripe on frontal between anterior margins of eyes. Labials white, with grey-brown dots. Dorsum patterns formed by dark thin irregular vermicular patches spots and lines. There is a dark, narrow, longitudinal line between forelimbs and hindlimbs on sides of body. Dorsal surfaces of limbs and digits with irregular dark bands. Dorsal surface of tail with nine dark brown wide bands with irregular margins, same size as the light bands with which they alternate (Fig. 5a). Ventral surface of body and limbs white. Ventral surface of tail with dark spots that become more distinct posteriorly.

**Variation of paratypes:** Table 3 shows variation of type specimens. Dorsal surface pattern is somewhat variable. Sexual dimorphism weakly developed, males smaller than females (SVL max 31 mm *versus* 34 mm) and males have better developed postcloacal spurs.

	Holotype		Paratypes								
	ZMMU R-14668	ZMMU R-14669	ZMMU R-15160	ZMMU R-15161	ZMMU R-15162	ZISP 29582	ZISP 29583	ZISP 29581	M6H 1295	M6H 1296	M6H1294
Sex	ш	f	f	f	в	ш	ш	f	f	н	f
SVL	28.7	29.8	34.0	33.5	31.2	31	27.4	30.0	32.1	30.4	28.3
TailL	29	18*	27*	21.5*	30.3	*	29.4	30.8	32	25*	29
Head L	8.2	8.6	9.7	9.6	9.3	9.7	8.0	8.8	9.0	9.0	8.5
Head W	4.8	5.2	5.8	5.7	5.8	5.3	4.8	5.0	5.4	5.1	4.5
Head H	3.2	2.8	3.2	3.6	3.5	3.2	3.4	3.0	3.2	3.3	2.9
SnEye	2.8	3.3	3.7	3.6	3.0	3.4	3.2	3.3	3.2	3.3	3.0
OrbD	1.8	2.1	2.2	2.3	2.3	2.3	2.0	2.0	1.9	2.0	2.0
EarL	0.8	0.7	0.8	0.8	0.7	0.8	0.8	08	0.7	0.8	0.6
EyeEar	2.0	2.0	2.5	2.6	2.6	2.2	2.0	2.1	2.4	2.1	2.0
TrunkL	12.3	14	16.7	16.1	14.5	14.7	13.0	13.1	15.3	14.8	14.0
LS	4.5	5.0	5.2	5.8	5.0	5.1	5.2	4.8	5.3	5.5	5.0
ForeaL	3.8	4.2	4.2	4.7	4.3	4.5	4.3	3.9	4.2	4.5	4.0
FemurL	6.0	5.7	7.0	7.0	6.1	6.2	6.0	6.5	6.5	6.3	5.8
Crus L	4.7	5.1	5.7	5.9	4.9	5.2	5.3	5.6	5.5	5.2	4.7
LD4A	1.7	2.0	3.0	2.6	2.2	2.6	2.7	2.4	3.0	2.8	2.6
LD4P	3.2	4.0	4.0	3.8	3.8	4.0	4.0	3.6	4.5	4.1	3.9
V (SAB)	61(96)	58(95)	60(96)	58(92)	53(90)	59(97)	54(89)	57(96)	59(96)	57(88)	60(95)
SLB	210	225	209	223	206	208	192	190	200	198	214
FFI 4/FFr 4/LF 4	16/13/3	18/12/3	16/13/2	18/13/4	17/12/1	15/12/3	15/12/3	16/12/3	17/13/3	16/12/2	16/13/3
TFl 4/TFr 4/LT 4	22/19/4	26/17/3	23/17/4	27/19/3	26/18/2	24/18/3	28/18/4	29/19/3	26/20/2	25/16/3	24/18/4
SL	13	12	12	13	12	11	11	13	12	11	13
IL	10	11	10	10	11	6	10	11	11	10	11
Spurs(l/r)	2/2	2/2	2/2	2/2	2/2	3/2	3/3	2/2	2/2	3/2	3/2
SLH	42	46	41	47	40	47	44	43	47	48	48
SAH	42	40	39	41	32	38	36	35	38	40	40

**Comparisons:** *Trigonodactylus persicus* **sp. nov.** is closely related to *T. arabicus* Hass,1957 and can be distinguished by the shape of forelimbs and hindlimbs. The new species does not have any webbing between the fingers and toes, but *T. arabicus* has well-developed webs (Fig.6a). Moreover, *T. arabicus* has very large eyes: Its HeadL/OrbD ratio is 3.65, while this value for the new species is 4.35. The shape of the mental can be used as an additional character distinguish the new species from *T. arabicus*. *Trigonodactylus persicus* **sp. nov.** has a relatively wider and deeper mental plate than *T. arabicus* (Fig.4).



**FIGURE 3.** Holotype of *Trigonodactylus persicus* sp. nov.: (*a*) specimen *in situ*; (*b*) ventral view sowing roundish and keeled ventral scales; (*c*) thenar surface of fingers showing fringes and few median lamellae on distal edge of digits.



**FIGURE 4.** Dorsal (upper row), lateral (median row) and mental (lower row) views of heads of all members of the genus *Trigonodactylus: T. arabicus* holotype CAS 84321 (a; f; k); *T. arabicus* ZMMU R-14666-1 (b; e; l); *Trigonodactylus persicus* **sp. nov.** ZMMUR-14669 (c; h; m); *T. sharqiyahensis* ZMMU R-14667-1 (d; i; n); *T. pulcher* holotype BMNH 1946.8.23.38. (e; j; o).

*Trigonodactylus persicus* **sp. nov.** differs from the recently described *Trigonodactylus* [*Stenodactylus*] *sharqiyahensis* by the form of the digits. The new species has more elongated, thinner fingers, and there is no webbing between them. The dorsal patterns specific for *T. sharqiyahensis*, which comprise longitudinal dark bands, can also be used to distinguish this species from *T. persicus* **sp. nov.** (dorsal patterns consist of small separate irregular spots and dots). The posterior edge of the mental plate in the new species is undulating, whereas in *T. sharqiyahensis* it has a roundish posterior edge (Fig. 4).

Discriminant analysis of 16 morphometric measurements of the three species of the genus *Trigonodactylus* has shown that the major contributing factors to the diversification of these species are the diameter of the eye (OrbD) and the length of the fourth finger and toe (LD4A, LD4P). A separate comparison of males and females has shown that morphometric differences between females of these species are deeper than in males (Fig.7).

The new species is significantly smaller in size, shape and proportions of the body and the head compared to all *Stenodactylus s. s.* except one species, *S. pulcher* (Fig. 8), which has approximately the same size as *Trigonodactylus persicus* **sp. nov**. The following characteristics enable us to distinguish *S. pulcher* from the new species: gular and ventral scales smooth, granular, without keels (*versus* keeled oval gular and ventral scales in the new species); relatively smaller eyes: HeadL/OrbD is 4.94 (4.35 in the new species); elongated fingers: SVL/LD4A 14.4 (*versus* 16.9 in the new species). Detailed diagnostic characteristics of the two genera (*Trigonodactylus* and *Stenodactylus*) are presented below.



**FIGURE 5.** Members of the genus *Trigonodactylus in situ*: a—*Trigonodactylus persicus* sp. nov.; b—*T. sharqiyahensis* (Metallinou & Carranza, 2013); c—*T. arabicus* Hass, 1957.



**FIGURE 6.** Thenar views of fore- (upper row) and hindlimbs (lower row) of the genus *Trigonodactylus* representatives: (a; b)—*T. arabicus* with well-developed webbing between fingers and toes; (c; d)—*Trigonodactylus persicus* **sp. nov.** and (e; f)—*T. sharqiyahensis* without webbing on fingers and toes.

Etymology: The new species was named after the geographic region, where it was found, Persia.

**Natural history:** *Trigonodactylus persicus* **sp. nov.** usually inhabits slopes of sand dunes, where they burrow under the bushes of desert grass. These nocturnal lizards were found just after the sunset and could be seen during the entire night. Their activity decreased after midnight. The following sympatric reptile species were found in the same biotope: *Stenodactylus doriae* (Blanford), *Scincus mitranus* Anderson, *Acanthodactylus schmidti* Haas, *Eryx jayakari* Boulenger, *Phrynocephalus ahvazicus* Melnikov *et al.*, *Cerastes gasperettii* Leviton & Anderson, *Bunopus tuberculatus* Blanford, and *Trapelus persicus* (Blanford).

**Distribution:** The new species are known only from the type locality (Fig.1): Iran, Khuzestan Province, 80 km northwest of Ahvaz, 31°44' N, 48°06' E, 30 m a. s. l.

#### Discussion

**Differentiation within** *Stenodactylus.* In this study we used phylogenetic analysis of the COI *mt*DNA gene fragment for barcoding and evaluation of potential cryptic diversity within the Saharo-Arabian gecko genus *Stenodactylus.* The phylogenetic data in this study does not bring new insights on *Stenodactylus* phylogenetic relationships, which were resolved by Metallinou *et al.* (2012). However, it provides additional information on genetic variation within "*arabicus*" and "*doriae*" species complexes, which allows us to discuss the taxonomic status of certain populations, in particular, from Iran and Oman, which was not covered in previous studies.

Both phylogenetic studies on the subject published to date (Fujita & Papenfuss 2011; Metallinou *et al.* 2012) agree on deep divergence between the *arabicus* group from Arabia and the other species of *Stenodactylus*. Metallinou *et al.* (2012) estimated the divergence within *S. arabicus* clade (which, according to their data, also

includes *S. pulcher* from Yemen) to be 29.5 mya, whereas the basal differentiation of the rest of *Stenodactylus* occurred much later, around 21.8 mya. Data from this study supports this topology. Taking into account significant morphological differences between the *arabicus* group and the other *Stenodactylus* species, we consider that the genus *Trigonodactylus*, originally proposed by Haas (1957) in his description of *Trigonodactylus arabicus*, should be resurrected. Morphological differences of *Trigonodactylus* from *Stenodactylus sensu stricto* are considerable and are discussed below.



**FIGURE 7.** Results of discriminant analysis of *T. arabicus* (diamonds), *Trigonodactylus persicus* **sp. nov.** (circles), and *T. sharqiyahensis* (squares) based on 16 morphometric characters (SVL, TailL, HeadL, HeadW, HeadH, SynEye, OrbD, EarL, EyeEar, TrunkL, LS, ForeaL, FemurL, CrusL, LD4A, LD4P) (a—males; b—females; c—both sexes analyzed together).



**FIGURE 8.** Holotype of *Stenodactylus pulcher* Anderson BMNH 1946.8.23.38 in dorsal, ventral and lateral aspects (photo by Patrick Campbell and Stephen Mahony; courtesy of BMNH).

Our sampling of *Stenodactylus sensu stricto* species is limited compared to that of Metallinou *et al.* (2012); according to their data, this genus includes *S. affinis*, *S. doriae*, *S. grandiceps*, *S. leptocosymbotes*, *S. mauritanicus*, *S. petrii*, *S. slevini*, *S. sthenodactylus*, *S. yemenensis*, and, possibly, *S. stenurus*. The genus *Trigonodactylus* includes the type species, *Trigonodactylus arabicus*, the species described herein, *Trigonodactylus persicus* **sp. nov.**, *Trigonodactylus sharqiyahensis*, and possibly *Trigonodctylus pulcher*. Unfortunately, we do not have material of *T. pulcher* for morphological sturdy except images of the holotype (BMNH 1946.8.23.38), which were kindly provided us by Patrick Campbell and Stephen Mahony.



**FIGURE 9.** Dorsal view of skulls of representatives of the genera *Stenodactylus*, *Pseudoceramodactylus* and *Trigonodactylus*; (A–H)—photos; (a–h)—schematic drawing showing the shape of skull roof. (A, a)—S. affinis; (B, b)—S. doriae; (C, c)—S. grandiceps; (D, d)—S. leptocosymbotes; (E, e)—S. petrii; (F, f)—S. sthenodactylus; (G, g)—P. khobarensis; (H, h)—Trigonodactylus persicus **sp.nov.** Colours denote the following bones: frontal—light grey; parietal—dark grey; postorbitofrontal—yellow; prefrontal—orange; nasal—brown; intermaxillary—grey.



**FIGURE 10.** Frontal (left column), lateral (median column), and ventral (right column) skull projections of the members of the genera *Stenodactylus*, *Pseudoceramodactylus* and *Trigonodactylus*: a—S. *affinis*; b—S. *doriae*; c—S. *grandiceps*; d—S. *leptocosymbotes*; e—S. *petrii*; f—S. *sthenodactylus*; g—P. *khobarensis*; h—*Trigonodactylus persicus* **sp. nov.** Colours denote the following bones: maxillary—yellow; prefrontal—orange; nasal—light green; permaxillary—blue; pterygoid—pink; palatine—green.

Both previous studies had limited sampling of the *T. arabicus* species complex, which included populations from Oman (Fujita & Papenfuss 2011) or Qatar, the United Arab Emirates and Kuwait (Metallinou *et al.* 2012), but did not include the Iranian part of the range in Khuzestan Province.

Fujita and Papenfuss (2011) were the first to show the deep genetic divergence between the Wahiba population of T. arabicus and populations from western Oman, which are referred to as nominal T. arabicus. These results were later supported by Metallinou et al. (2012), who demonstrated deep divergence between the Wahiba population from Oman and T. arabicus from Oman, Kuwait, and the United Arab Emirates, which shows much less variation along its range. Metallinou et al. (2012) referred to the Wahiba population as "S. cf. arabicus" and realized the possibility of existence of cryptic species within the species group. In this study, the population from Khuzestan, western Iran, was included in the analysis. Our study shows that the T. arabicus species complex comprises at least three species, distinct both morphologically and genetically. One of them is described as the new species Trigonodactylus persicus sp. nov. The sandy area, where the new species was discovered is isolated from the habitat of T. arabicus by the Euphrates, Tigris and Korun rivers. In contrast, there is no clear geographic barrier between the population of T. sharqiyahensis and T. arabicus. The clade of T. arabicus and T. persicus sp. nov. collectively have a sister relationship with T. sharqiyahensis. Similar phylogenetic relationships were discovered between toad-headed agamas of the Phrynocephalus arabicus complex (Melnikov et al. 2015). Phrynocephalus ahvazicus Melnikov et al., 2014 from the same Ahvaz sands is closely related to P. arabicus sensu stricto from central Arabia, and P. sakoi from the Sharqiyah sands in Oman forms a clade that has sister relationship to these species.

The divergence found within the population of *T. arabicus* sensu stricto likely has no taxonomic value but might indicate a complicated phylogeographic history of the species. Further study of the genetic and morphological variation of the *T. arabicus* species complex is needed, since it might lead to discovery of new and yet to be reported lineages.

Metallinou *et al.* (2012) studied samples of the *S. doriae* complex from Kuwait, Yemen, Israel, Jordan, the United Arab Emirates, and Oman and demonstrated comparatively low substructuring within the species' range. Fujita and Papenfuss (2011), however, included *S. doriae* population from Khuzestan Province, western Iran, in their analysis and demonstrated deep divergence between the Khuzestan population and *S. doriae* from Oman. Data from the present study confirms their results and shows that *S. doriae* from Khuzestan and Oman (in our study, Wahiba sand dunes) might belong to distinct species. However, the taxonomic history of *S. doriae* is complicated: this species was described by Blanford from "Bandar Abbas, Persia", i.e., from the environs of the Iranian port located just across the Strait of Hormuz that separates Iran from the territory of Oman (referred to herein as *S. cf. doriae*). Without the materials from the type locality of *S. doriae* or the careful morphological examination of Blanford's types, it is impossible to evaluate the taxonomic status of the Khuzestan population of *S. doriae* complex, which we herein refer to as *S. doriae*.

**Morphology.** Comparison of the cranial skeleton of the six members of the genus *Stenodactylus*, three members of the genus *Trigonodactylus* and one species of the genus *Pseudoceramodactylus* allowed us to identify a number of diagnostic characters for these groups.

All studied representatives of the genus *Stenodactylus* have the following characteristics: Prefrontale—relatively large with outgrowth or extension at the frontal part of the orbit (prefrontal projection) that makes the front edge of eye socket wider. This projection is most well developed in *S. leptocosymbotes*, while in *S. sthenodactylus* the prefrontal is almost smooth, but its size is relatively large (Fig. 9f). In *S. cf. doriae* serrated spines in the apical part of the prefrontal are well developed (fig. 10b). Posteriofrontal (*sensu* Daza & Bauer 2010)—relatively large, almost triangular with an extended distal part.

Stenodactylus leptocosymbotes demonstrates a unique morphology of the cranial skeleton compared to the other representatives of the genus (Fig. 9d; 10d.): elongated and narrow rostrum, long and relatively narrow nasals, and relatively short parietal, unlike the other *Stenodactylus* species. The ratio of skull section changes its overall kinetic movement pattern—it can be compared with forceps (i.e., these geckos are possibly adapted to relatively small and solid food objects—the maximum force is applied to the object at the tip of the jaws). The other structures of the skull in *Stenodactylus sensu stricto* are rather conservative and members of this genus have broader and shorter skulls (crushing type).

*Trigonodactylus* representatives, in contrast, are characterized by relatively small prefrontal and postorbitofrontal bones and a shortened nasal (Fig. 6g). Skull proportions in *Trigonodactylus* are different from

*Stenodactylus*; the skull is relatively elongated and narrow in *Trigonodactylus*. Length to width ratio in *Trigonodactylus persicus* **sp. nov**. is 1.71 (n =14); in *T. sharqiyahensis* 1.64 (n=8); in *T. arabicus* 1.69 (n=17). Alternatively, this ratio in *Stenodactylus sthenodactylus* is 1.44 (n=8); in *S. doriae* 1.3 (n=10); in *S. petrii* 1.3 (n=8); in *S. leptocosymbotes* 1.27 (n=9); in *S. affinis* 1.3 (n=3); in *S. grandiceps* 1.28 (n=4).

Skull construction of *Pseudoceramodactylus khobarensis* is similar to that of *S. leptocosymbotes*; the skull is relatively elongated with a narrow rostral part (Fig. 9 and 10). The parietal part of the skull, on the other hand, is relatively large, as in the members of genus *Stenodactylus sensu stricto*.

In general, we can conclude that the range of variability between the forms and features of the skull kinetic within the group *Stenodactylus sensu stricto* is the same as the range of variability between *Stenodactylus*, *Pseudoceramodactylus* and *Trigonodactylus*. This aspect, of course, requires additional study; however, at first glance, we are under the impression that the design of the skull is adaptive and very plastic, and it is able to change relatively fast within the same group. It is worthy of note that appearance or reduction of the webbing between the fingers and toes (an important characteristic in lizard taxonomy), occurred within species of the genus *Trigonodactylus*, which diversified relatively recently.

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## APPENDIX 1. List of the examined specimens.

- *Trigonodactylus arabicus* (n=30): CAS 84321 (holotype), Saudi Arabia, Abqaiq; CAS 84318, 84323 (paratypes) Saudi Arabia, Abqaiq; CAS 228532–228533, 228746–228747 United Arab Emirates, Dubai, Jebel Ali, 7.8 km S by Port and Free Zone Exit Rd, then 1.1 km NW by dirt Rd; CAS 250879–250881 United Arab Emirates, Fujairah 4.77 km N (by air) of Manama; ZMMU R-14666-1–20, Oman, Dhofar Governorate, near Mughshin, sand dunes.
- *Trigonodactylus sharqiyahensis* (n=19): CAS 225394–225397 Oman, Wahiba sands, Hwy 23. 7 km NW (by rd) of Al Mintirib, Bidiyah; CAS 250936–250939 Oman, Ash Sarqiyah North Gov. HWY 23. 35 km (by rd) of Ibra, Wahiba sand dunes; CAS 251010–251011 Oman, Ash Sarqiyah North Gov. 21 km (by rd) of Al Ashkhara. ZMMU R-14667-1–9, Oman, Ash Sarqiyah, near Bidiyah, Wahiba sand dunes.
- *Pseudoceramodactylus khobarensis* (n=16): CAS 84458 (holotype). Saudi Arabia, Al Khabar; ZMMU R-14248-1–15, Oman, Al–Vusta prov., near Filim.
- *Stenodactylus affinis* (n=3): ZMMU R-14763-1–3, Iran, Ilam prov., 20 km NW of Dehloran.
- Stenodactylus doriae (n=49): ZMMU R-13199-1–10, R-14252-1–6, R-14760-1–3, R-14761-1–10, Iran, Khuzestan prov., 100 km NW of Ahvaz, sand-drifts between Alvan and Bostan; ZMMU R-13471, R-13474, United Arab Emirates, Wadi Malriha; ZMMU R-14762-1–2, UAE; ZMMU R-13900-1–3, R-14201-1–10, Oman, Dhofar Governorate, near Mughshin, sand dunes; ZMMU R 13898-1–3, Oman, Ash Sarqiyah, near Bidiyah, Wahiba sand dunes.
- Stenodactylus grandiceps (n=4): ZMMU RAN-2556–2559, Jordan, Zarga Prov, 10 km S of Azraq city.

*Stenodactylus leptocosymbotes* (n=14): CAS 97841 (holotype), Trucial States, Abu Dhabi, half way between Dubai and Abu Dhabi; CAS 102366 (paratype), Saudi Arabia, 35 km N and 60 km W of Al Lith, near Bir Khadrah; ZMMU R-14240-1–7, Oman, Dhofar Governorate, 40 km E of Thamrait; ZMMU R-14203, Oman, Al–Vusta Prov., 40 km N of Duqum; ZMMU R-14200-1–4. Oman, Al–Vusta Prov., Nizma–Hayma Rd.

Stenodactylus mauritanicus (n=2): ZMMU R-15414-1-2, Morocco, 35 km SW of Assa.

*Stenodactylus petrii* (n=4): ZMMU R-12648-1-4, Egypt;

Stenodactylus slevini (n=2): CAS 84592 (holotype), Saudi Arabia, Dhahran; CAS 84540 (paratype), Saudi Arabia, Dhahran.

*Stenodactylus sthenodactylus* (n=9): ZMMU R-10020-1–7, Egypt, Aswan, Nili Island; ZMMU R-10065, Egypt; ZMMU RAN-190, Egypt, Hurghada.

*Stenodactylus yemenensis* (n=1): CAS 144212 (paratype), Saudi Arabia, near Sugayg.