Russian Journal of Herpetology Vol. 22, No. 3, 2015, pp. 219 – 223

NEW RECORD OF THE SMALL-SPOTTED LIZARD, *Mesalina guttulata* (LICHTENSTEIN, 1823) FROM DONGONAB BAY, RED SEA

Sumaia Mohamed Ahmed Abukashawa[1] and Mukhtar Mohamed Mahmoud[1]

Submitted March 24, 2014.

The Small Spotted-Lizard *Mesalina guttulata* is recorded for the first time from Um Elsheikh island at Dongonab Bay in the Red Sea State, Sudan.

Keywords: Lacertidae; new record; distribution; Red Sea; Sudan.

INTRODUCTION

The Small Spotted-Lizard *Mesalina guttulata* belongs to the family Lacertidae. Lichtenstein (1823) was the first to describe the species occurrence in Sudan without mentioning a specific area, while Arnold (1986) described its range including northern and western Saudi Arabia, North Africa, Iraq, Jordan, Yemen and Palestine. There is no published record of the small spotted-lizard *Mesalina guttulata* from the Sudanese Red Sea Coast.

Dungonab Bay lies about 176 km north of Port Sudan on the Sudan Red Sea Coast, at latitude 20°56′ N and longitude 37°05′ E and 37°15′ E. The total area of the bay is 284.5 km^2, and extends from north to south about 31 km. The maximum breadth of the bay is (14.5 km) and the minimum breadth is only (3.2 km) wide. Dungonab bay contains many sandstone islands the foundation of which is the coral rock (Crossland, 1911; Nasr, 1982; Elamin and Elamin, 2014). These islands are small and numerous at the southern end of Dungonab Bay with halophytic vegetation.

MATERIAL AND METHODS

Sample Collection and Morphological Analysis

Field herpetofaunal survey was carried out on May 2013 in islands of Dongonab Bay at the Sudanese Red Sea coast (Fig. 1). The survey included inshore islands of Um Elsheikh located at 21°04′55.05″ N 37°08′54.85″ E as shown in Fig. 2. The habitat of Um Elsheikh Island with its characteristic haplophytes was photographed (Fig. 3).

Lizard specimens were collected by hand, photographed and brought back to the laboratory. Lizards were measured using a vernier to the nearest 0.1 mm. The samples were marked with date, location and deposited in the herpetological archive collection of the Sudan Natural History Museum, University of Khartoum. The specimens were identified according to the reviews of Sharif

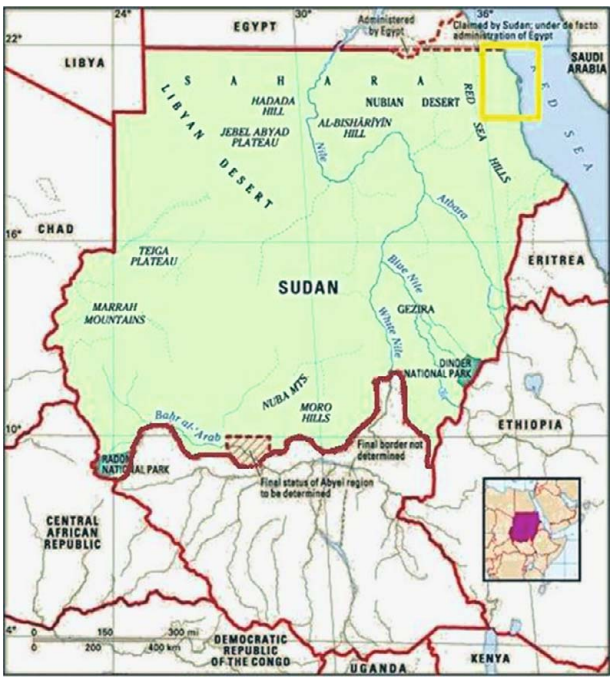

Fig. 1. Map of Sudan illustrating the position of the study area at the Sudanese Red Sea coast (yellow square).

[1] Zoology of Department, Faculty of Science, University of Khartoum, P. O. Box 321 Khartoum, 11115, Sudan;
e-mail: abukashawa@uofk.edu, mukhtar.m.hassan87@gmail.com

Fig. 2. Photo of Um Elsheikh Island where the specimens of *Mesalina guttulata* were collected.

Baha Eldin (2006). Terminology of morphological characters follows Rösler et al. (2008) and Luu et al. (2013). Abbreviations are as follows: TL (total length): from tip of snout to anterior margin of cloaca; TaL (Tail length): from posterior margin of cloaca to the tip of the tail.

Molecular Analysis

The total genomic DNA was extracted from the tail tip tissues of three adult specimens using potassium acetate protocol (Dellaporta et al., 1993). The extracted DNA was used for PCR amplification of portion of the mitochondrial the cytochrome b (cyt-b) gene using the oligonucleotide primers R: 5′AAACTGCAGCCCCTC-AGAATGATATTTGTCCTCA-3′ (forward); F: 5′AAAA-AGCTTCCATCCAACATCTCAGCATGATGAAA-3′ (reverse) described by Kocher et al. (1989). Reactions were carried out in a G-STORM system 482 Thermal Cycler in a volume of 25 µl containing 2 µl of template DNA, 1 µl of each forward and reverse primers (10 pmole/µl), 1 µl of each dNTP (250 µM), 1 µl $MgCl_2$ (2.5 mM), 1 µl of 1x PCR buffer, µl of Taq DNA Polymerase (1 U) and 15 µl of distilled water. Amplification conditions were as follows: denaturation at 94°C for 3 min followed by cycling of 1 min at 94°C, annealing for 1 min at 53°C, and extension for 1 min at 72°C. Thirty-five amplification cycles were performed followed by a final extension of 10 min at 72°C.

The PCR products were purified and then sequenced (BGI-Hong Kong Co., Ltd). Sequencing was performed using the (cyt-b) oligonucleotide primers. Sequences were analyzed using BioEdit, MEGA 5.05 and CLC work bench.

A total of 3 *Mesalina guttulata* sequences were used in the phylogenetic analyses including one sequence from Um Elsheikh Island (this study) and two sequences from Mesharef Island, Sudan (Mukhtar and Abukashawa, 2014, unpublished). The comparison included six additional sequences of *M. guttulata* from six different geographical locations (Egypt, Jordan, Libya, Morocco,

Fig. 3. Habitat of *Mesalina guttulata* at the Island of Um Elsheikh, Dongonab Bay, Sudan (21°04’55.05″ N 37°08′54.85″ E).

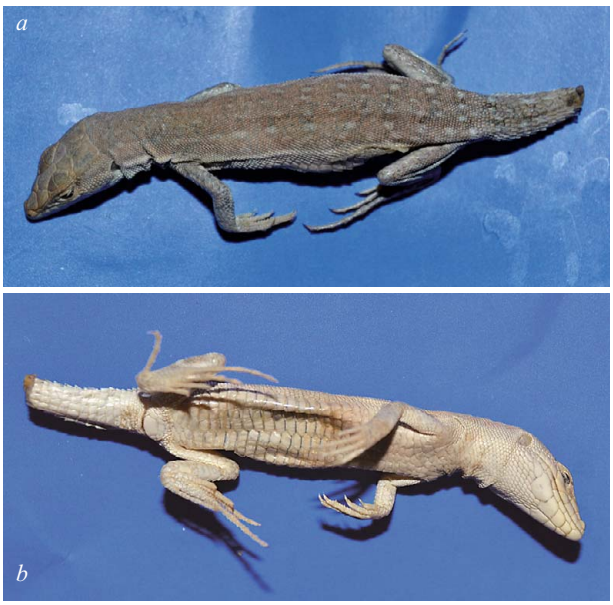

Fig. 4. Photo of *Mesalina guttulata* from this study: *a*, dorsal view; *b*, ventral view.

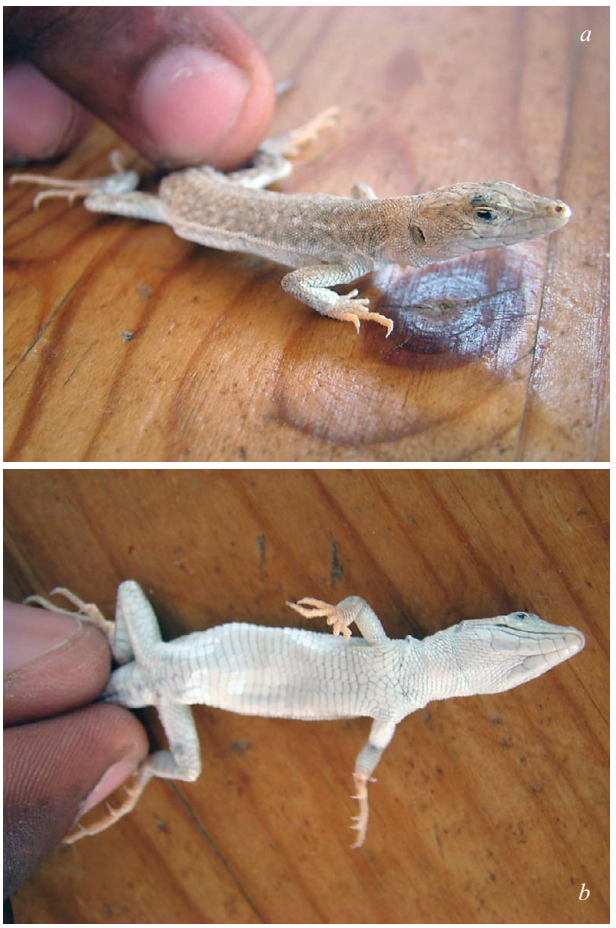

Fig. 5. *Mesalina guttulata*, live specimen brought to the lab for identification and documentation: *a*, dorsal view; *b*, ventral view.

Tunisia, and Yemen) and one *M. brevirostris* sequence (Syria) that were extracted from GenBank (Table 1).

Phylogenetic Analysis

The evolutionary history was inferred using the Neighbor-Joining method and a phylogenetic tree was constructed for the ten nucleotide sequences. Evolutionary analysis was conducted using MEGA5 (Thompson et al., 1994; Tamura et al., 2007) and the evolutionary distances were computed using the Kimura 2-parameter method. Codon positions included were $1^{st} + 2^{nd} + 3^{rd} +$ noncoding and all positions containing gaps and missing data were eliminated. There were a total of 305 positions in the final dataset. The percentage of replicate trees in which the associated ten taxa clustered together in the bootstrap test (1000 replicates) was shown next to the branches. The optimal tree with the sum of branch length = 0.46211403 was drawn to scale with branch

TABLE 1. List of Samples of *M. guttulata* Including Geographical Origin and GeneBank Accession Numbers, Including Sequences of *Mesalina* Species Taken from GeneBank for the Taxon-Wide Phylogeny

Species	Locality	GeneBank	Source
M. guttulata	Yemen	JN828648	Jiři Šmid and D. Frynta, 2013
M. guttulata	Tunisia	EF555268	Kapli et al., 2008
M. guttulata	Morocco	EF555255	Kapli et al., 2008
M. guttulata	Libya	EF555254	Kapli et al., 2008
M. guttulata	Jordon	EF555279	Kapli et al., 2008
M. guttulata	Egypt	AY217815	Whiting et al., 2003
M. brevirostris	Syria	EF555266	Kapli et al., 2008
M. guttulata	Um Elseikh Island, Sudan	—	This study
M. guttulata	Mesharef Island, Sudan	—	This study
M. guttulata	Mesharef Island, Sudan	—	This study

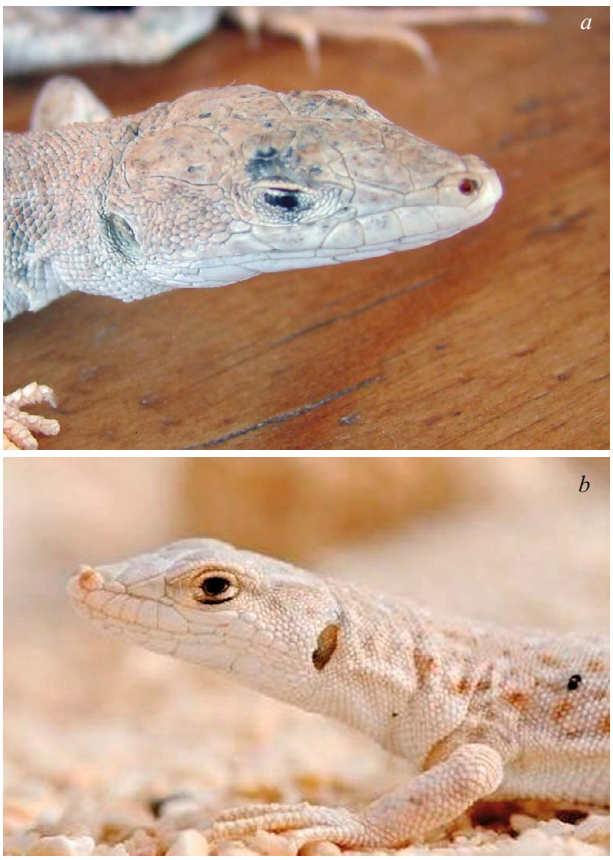

Fig. 6. Small-spotted lizard *Mesalina guttulata* from this study (details of head) (*a*) and short-snouted lizard *Mesalina* brevirostris from Baha El Din (2006) (details of head) (*b*).

lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree.

RESULTS

The three adult male specimens examined were identified as *Mesalina guttulata* (Fig. 4). Specimens were found on the 21 of May 2013 morning before sunrise camouflaged under the shrubs of halophytes as the first record of the species in the Red Sea State (Fig. 5). From the morphological features, *Mesalina guttulata* can be described as a small, slim lizard with a long, narrow snout and a light brown-gray body. As its common name suggests, the upper parts of this species are covered in conspicuous light and dark spots, which sometimes form a lined pattern. The under parts of the small-spotted lizard are whitish. The body length (TL) was 78.3 mm; the tail length (TaL) was 31.8 mm (Fig. 6).

The phylogenetic tree based on the cyt-b gene sequences (Fig. 7) confirms that the collected specimens belong to *Mesalina guttulata*. The species of *Mesalina*

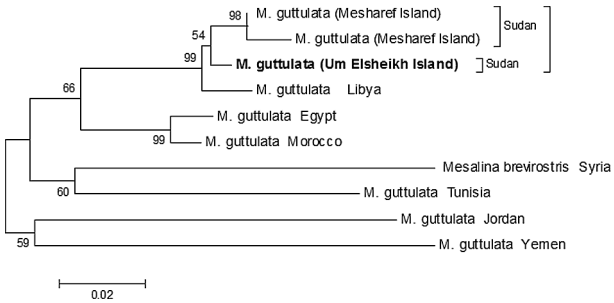

Fig. 7. Neighborhood-joining dendogram showing relationships among *M. guttulata* based on cytochrome b sequences. Numbers on branches are bootstrap values over 1000 replicates.

guttulata from both Donganab Bay islands clustered with *M. guttulata* recorded by Kapli et al. (2008) from Libya.

DISCUSSION AND CONCLUSIONS

This novel record on the species highlights not only the need for more research on this taxonomic group but also the need for research on the herpetofauna of Dongonab Bay as it adds more to the biodiversity of this area which is declared as an (MPA) Marine Protected Area. Accordingly, only with improved knowledge can we hope to implement effective management strategies for the biodiversity conservation in Dongonab Bay biome.

Acknowledgments. We would like to thank Fereeda Hamdan and Esra Elfaki for their assistance in the field surveys. This work is funded by University of Khartoum.

REFERENCES

Arnold E. N. (1986), "A key and annotated checklist to the lizards and amphisbaenians of Arabia," in: *Fauna of Saudi Arabia*, Vol. 8, pp. 385 – 435.

Baha El Din S. M. (2006), *A Guide to the Reptiles and Amphibians of Egypt*, *The Am. Univ. in Cairo Press*, Cairo – New York.

Crossland C. (1911), "Reports on the marine biology of the Sudanese red Sea. A physical description of khor Dungonab," *J. Linn. Soc. Zool.*, **31**, 265 – 286.

Dellaporta S. L., Wood J., and Hicks J. B. (1983), "A plant mini preparation, version II," *Plant Mol. Biol. Rep.*, **1**, 19 – 20.

Elamin M. E. and Elamin S. (2014), "Biometric relationships of the mother of pearl oyster (*Pinctata margaritifera* var. *erythraensis*) from Dongonab Bay, Red Sea," *Int. J. Sci. Env. Technol.*, **3**(3), 1193 – 1204.

Kapli P., Lymberakis P., Poulakakis N., Mantziou G., Parmakelis A., and Mylonas M. (2008), "Molecular phylogeny of three *Mesalina* (Reptilia: Lacertidae) species

(*M. guttulata*, *M. brevirostris*, and *M. bahaeldini*) from North Africa and the Middle East: Another case of paraphyly?" *Mol. Phylogen. Evol.*, **49**, 102 – 110.

Kocher T. D., Thomas W. K., Meyer A., Edwards S. V., Paabo S., Villablanca F. X. and Wilson A. C. (1989), "Dynamics of mitochondrial DNA evolution in animals: amplification and sequencing with conserved primers," *Proc. Natl. Acad. Sci. USA*, **86**, 6196 – 6200.

Lichtenstein M. H. C. (1823), *Verzeichniss der Doubletten des zoologischen Museums der Königl. Universität zu Berlin nebst Beschreibung vieler bisher unbekannter Arten von Säugethieren, Vögeln, Amphibien und Fischen*, Königl. Preuss. Akad. Wiss. T. Trautwein, Berlin, Vol. X, pp. 97 – 107.

Luu V. Q., Nguyen T. Q., Calame T., Hoang T. T., Southichack S., Bonkowski M., and Ziegler T. (2013), "New country records of reptiles from Laos," *Biodivers. Data J.*, **1**, e1015; doi:10.3897/BDJ.1.e1015.

Nasr D. H. (1982), "Observation on the mortality of the mother of pearl oyster (*Pinctata margaritifera*) in Dongonab Bay, Red Sea," *Aquaculture*, **28**, 271 – 281.

Rösler H., Vu T. N., Nguyen T. Q., Ngo T. V., and Ziegler T. (2008), "A new *Cyrtodactylus* (Squamata: Gekkonidae) from Central Vietnam," *Hamadryad*, **33**(1), 48 – 63.

Šmid J. and Frynta D. (2012), "Genetic variability of *Mesalina watsonana* (Reptilia: Lacertidae) on the Iranian plateau and its phylogenetic and biogeographic affinities as inferred from mtDNA sequences," *Acta Herpetol.*, **7**(1), 139 – 153.

Tamura K., Dudley J., Nei M., and Kumar S. (2007), "MEGA4: Molecular Evolutionary Genetics Analysis (MEGA) software version 4.0.," *Mol. Biol. Evol.*, **24**, 1596 – 1599.

Thompson J. D., Higgins D. G., and Gibson T. J. (1994), "CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice," *Nucl. Acids Res.*, **22**, 4673 – 4680.

Whiting A. S., Bauer A. M., and Sites J. W. (2003), "Phylogenetic relationships and limb loss in sub-Saharan African scincine lizards (Squamata: Scincidae)," *Mol. Phylogen. Evol.*, **29**, 582 – 598.