Journal of Species Research 5(2):220-222, 2016

A new record of *Lyssa zampa* (Butler) from Korea

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An Uraniidae moth, *Lyssa zampa* (Butler, 1869) is newly discovered from southern Korea. One male specimen was collected at a valley of south aspect of Mt. Hallasan, Jejudo in July, 2014. This species is briefly described and illustrated here. DNA barcoding sequence (Genbank KU160388) for the species was provided for species identification.

Keywords: Jejudo, Korea, *Lyssa*, Uraniidae

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DOI:10.12651/JSR.2016.5.2.220

Introduction

An Uraniinae moth, a subfamily of Uradniidae is of large sized moth with slender body and deep triangular forewings and tailed or angled hindwings. They are characterized by having the sexual dimorphism in the position of the tympanal organ (the ventral base of the abdomen in female and the lateral tergites between 2nd and 3rd abdomen in male) and the forewing venation that shows the lacking areole, having R3+R4 as the terminal bifurcation of the Rs system, with R5 well separate from this system, sharing a common stalk or more rarely being connate with M1 (Holloway, 1998). The Uraniidae is comprised four subfamilies: Auzeinae, Epipleminae, Microniinae and Uraniinae (Minet and Scoble, 1999). In Korea, one species of Microniinae and 11 species of Epipleminae are known. However, no species of the subfamily Uraniinae was known.

The genus *Lyssa* Hübner, one of the largest uraniids is mainly nocturnal and widely distributed in Indo-Australian tropics (Holloway, 1998). Both fore- and hindwings are striking with straight, narrow white bands on brownish gray background color of wings and the hindwings tailed at M1 as well as M3, with vein CuA1 strongly incorporated in M3 and tails are tipped with white (Holloway, 1998). Recently one of us has found a male specimen at a valley of southern aspect of Mt. Hallasan, Jejudo. Thus we report the occurrence of this species, *Lyssa zampa* for the first time in Korea.

DNA extraction, PCR, and sequencing

Total DNA was extracted from one leg using the Wizard Genomic DNA Purification kit, according to the manufacturer's instructions (Promega, Madison, WI, USA). DNA barcoding region was amplified using the primer pair adapted from Hajibabaei *et al*. (2006). Detailed PCR and sequencing methods were carried out following the methods described by Kim *et al*. (2015).

A search of available public sequence databases, such



Fig. 1. Adult of *Lyssa zampa* from Jejudo, Korea.

			30			60
***Lyssa zampa* (South Korea)**	AACATTATAT	TTTATTTTTG	CGATTTGAGC	AGGAATAGTA	GGAACCTCTT	TAAGCTTACT
***Lyssa macleayi* (Australia)**	C	....	GA........	....	.....T....	....TC..T.
			90			120
***Lyssa zampa* (South Korea)**	AATTCGAGCT	GAATTAGGTA	ACCCAGGATC	CTTAATTGGA	GATGATCAAA	TTTATAATAC
***Lyssa macleayi* (Australia)**	....	....	.T........	T.........	.....C....	....
			150			180
***Lyssa zampa* (South Korea)**	TATTGTCACA	GCTCATGCTT	TCATTATAAT	TTTTTTTATA	GTAATACCTA	TTATAATTGG
***Lyssa macleayi* (Australia)**	......T...	....	....	....	....	....
			210			240
***Lyssa zampa* (South Korea)**	AGGATTTGGA	AATTGATTAG	TACCTTTAAT	ATTAGGAGCA	CCTGATATAG	CATTTCCTCG
***Lyssa macleayi* (Australia)**	....	....	....A.....	....	....	.T..C..C..
			270			300
***Lyssa zampa* (South Korea)**	AATAAATAAT	ATAAGATTTT	GATTACTACC	TCCATCATTA	TCTTTATTAA	TTTCAAGAAG
***Lyssa macleayi* (Australia)**	....	....	.....T....	....	...C......	....
			330			360
***Lyssa zampa* (South Korea)**	AATTGTAGAA	AATGGAGCAG	GAACAGGATG	AACAGTTTAT	CCCCCACTTT	CATCTAATAT
***Lyssa macleayi* (Australia)**	....	....	....	C	....	....
			390			420
***Lyssa zampa* (South Korea)**	TGCCCATGGA	GGAAGTTCTG	TAGATTTAGC	TATTTTCTCT	CTTCATTTAG	CTGGAATTTC
***Lyssa macleayi* (Australia)**	...T......	........A.	....	......T..C	....	....
			450			480
***Lyssa zampa* (South Korea)**	TTCAATTTTA	GGTGCTATTA	ATTTTATTAC	AACAATTATT	AATATACGAT	TAAATAATAT
***Lyssa macleayi* (Australia)**	....	....	....	....	....	....
			510			540
***Lyssa zampa* (South Korea)**	ATCTTTCGAT	CAAATACCTT	TATTTGTATG	AGCTGTAGGA	ATTACAGCAT	TTTTATTATT
***Lyssa macleayi* (Australia)**	......T...	CC	....	....	....	....
			570			600
***Lyssa zampa* (South Korea)**	ATTATCTTTA	CCAGTTTTAG	CCGGTGCTAT	TACTATATTA	TTAACTGACC	GAAACTTAAA
***Lyssa macleayi* (Australia)**	....	....	T.........	....	........T.	....T.....
			630			658
***Lyssa zampa* (South Korea)**	TACATCATTT	TTTGATCCTG	CTGGAGGAGG	TGATCCTATT	TTATATCAAC	ATTTATTT
***Lyssa macleayi* (Australia)**	....	........A.	....	....	....	..C.....

Fig. 2. Sequence alignment of DNA barcoding region from *Lyssa zampa* and *L. macleayi* (HQ923156, Hebert *et al*., 2013). Nucleotide sequence divergence was 4.56% between them. Consensus sequences are dotted, whereas different sequences are presented.

as GenBank, through a Blast search (http://blast.ncbi.nlm.nih.gov/Blast.cgi) and the BOLD system (http://boldsystems.org; Ratnasingham and Hebert, 2007) allowed us to find one barcode sequence from congeneric species, *Lyssa macleayi*, originated from Australia (Hebert *et al*., 2013). This sequence was aligned with that of current *L. zampa* to refer the sequence divergence between them.

Taxonomic Account

Lyssa Hübner, 1823, Verz. bek. Schmett.: 289.

Type species: *Nyctelemon patroclus* Linnaeus, 1758.

***Lyssa zampa* (Butler, 1869) (큰남방제비나방 (신칭))**

Nyctalemon zampa Butler, 1869, Ent. Monthly Mag. 5: 273. Type locality: Assam: Silhet.

Nyctalemon crameri Boisduval, 1874, Revue mag. Zool. (3), 2: 441. Type locality: India.

Nyctalemon najabula Moore, 1877, Proc. zool. Soc. Lond., 1877: 629. Type locality: Port Blair, S. Andaman.

Nyctalemon docile Butler, 1877, Trans. Linn. Soc. Lond. (2) 1: 562. Type locality: Malacca.

Nyctalemon dilutus Röber, 1927, Int. ent. Z., 20: 429. Type locality: Tombugu, E. Celebes (Sulawesi).

Lyssa zampa: Holloway, 1998, Malayan Nature J. 52: 76.

Diagnosis. Wingspan 94 mm. This large brownish winged species can be easily distinguished by the filiform antennae, the well projected whitish labial palpi, the slender brownish frons, the whitish body, the brownish fore- and hindwings with a whitish straight medial line and one medial short and one distal long tail on hindwing. The male genitalia can be distinguished by the

long slender uncus with hairs on ventral margin, a pair of short and hairy transtilla, a large hairy valva and the medially bent aedeagus with one pair of large spinular coremata bundles.

Material examined. 1 male, 17.VII.2014. JJ: Seoguipo, Donnaeko valley. Heon-Cheon Jeong leg.

Barcode sequence. Barcode sequence of *L. zampa* was 658 bp as typical and no atypical sequence such as sudden stop codon was found when translated. The sequence was deposited in the GenBank with the accession number KU160388. Sequence alignment of *L. zampa* to available congeneric species, *L. macleayi*, originated from Australia (Hebert *et al*., 2013) has shown the sequence divergence of 4.56%.

Biology. The larvae feed on *Endospermum peltatum* and other members of the Euphorbiaceae (Holloway, 1998).

Distribution. Korea (newly recorded), Himalaya to southern China, Thailand, Andamans, Philippines, Sulawesi, Japan.

Acknowledgements

This study was supported by a grant from the National Institute of Biological Resources (NIBR), funded by the Ministry of Environment (MOE) of the Republic of Korea (NIBR201501203).

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Submitted: November 18, 2015
Revised: May 10, 2016
Accepted: June 15, 2016