Journal of Species Research 14(2):213-223, 2025
https://doi.org/10.12651/JSR.2025.14.2.213

Open Access

A new species of the genus *Synanthedon* Hübner, 1819 (Lepidoptera: Sesiidae) from Korea

Woo Jin Kim[1,2], Sung-Soo Kim[3], Seung Hyun Lee[4], Jeong Sun Park[4,5], Sei-Woong Choi[6] and Iksoo Kim[4,*]

[1]*Department of Forest-Bio, Jeollanam-do Forest Research Institute, Naju-si 58213, Republic of Korea*
[2]*Department of Plant Protection and Quarantine, Chonnam National University, Gwangju 61186, Republic of Korea*
[3]*Institute for East Asian Environment and Biology, Seoul 05841, Republic of Korea*
[4]*Department of Applied Biology, Chonnam National University, Gwangju 61186, Republic of Korea*
[5]*Department of Agricultural Biology, National Academy of Agricultural Science, Rural Development Administration, Wanju 55365, Republic of Korea*
[6]*Department of Environmental Education, Mokpo National University, Muan 58554, Republic of Korea*

**Correspondent: ikkim81@chonnam.ac.kr*

Synanthedon namdoelegans sp. nov., a new clearwing moth, is described from southern South Korea. It is closely related to *Synanthedon soffneri* Špatenka, 1983, *Synanthedon bastak* Gorbunov & Koshkin, 2023, and *Synanthedon velox* Fixsen, 1887, but can be distinguished by differences in the forewing's black band, the hindwing's discoidal vein spot, and male genitalia. The female and larval stages are unknown. DNA barcode sequences show minimal variation (0.46%) within *S. namdoelegans*, with divergence from other *Synanthedon* species ranging from 1.98% to 12.46%. Phylogenetic analysis shows separation of *S. namdoelegans* from its closest relatives, *Synanthedon fulvipes* Harris, 1839 and *Synanthedon culiciformis* Linnaeus, 1758. These differences provide clear morphological and molecular separation from other *Synanthedon* species.

Keywords: clearwing moths, Lepidoptera, new species, South Korea, *Synanthedon namdoelegans*, Synanthedonini, taxonomy

All content in the Journal of Species Research (JSR), published by the National Institute of Biological Resources (NIBR), is Open Access, meaning it is freely accessible online to everyone without fees or the need for authors' permission. Open Access articles are automatically archived in the Korea Institute of Science and Technology Information (KISTI)'s Open Access repository, AccessON. All JSR content is published and distributed under the terms of the Creative Commons Attribution-NonCommercial-NoDerivatives 4.0 International License (CC BY-NC-ND 4.0). This license permits non-commercial use, distribution, and reproduction in any medium, provided the original author and source are properly credited. However, no modifications or derivative works are allowed.

Introduction

The genus *Synanthedon* Hübner, 1819 [1816] (Lepidoptera: Sesiidae) was designated with the type species *Sphinx oestriformis* Rottemburg, 1775 (a junior synonym of *Sphinx vespiformis* Linnaeus, 1761) and comprises 234 species and nine subspecies worldwide (Pühringer and Kallies, 2024). Sixteen and eight species of the genus *Synanthedon* are known from the Russian Far East and Korea (Arita *et al*., 2004; Gorbunov and Koshkin, 2023). The species of the genus are distinguished by a well-developed proboscis, transparent forewing, and nearly identical venation of fore- and hindwings (Gorbunov and Koshkin, 2023). Since this genus is species-rich within the family, question regarding its monophyly has been raised (Kallies, 2020) and the genus was divided into several taxa (Gorbunov and Arita, 1999; 2000; 2005; McKern and Szalanski, 2008; McKern *et al*., 2008; Taft *et al*., 2016; Lait and Hebert, 2018; Cognato *et al*., 2023; Kim *et al*., 2024).

In 2023 and 2024, field surveys were conducted to investigate *Synanthedon bicingulata* (Staudinger, 1887), a species known to cause a significant damage to urban trees, particularly cherry trees in city forests and parks (Lee *et al*., 2004; Korea Forest Service, 2023). During these surveys, adult male specimens of *Synanthedon* were

©2025 National Institute of Biological Resources.
This article was authored by [Woo Jin Kim, Sung-Soo Kim, Seung Hyun Lee, Jeong Sun Park, Sei-Woong Choi and Iksoo Kim] and is published by the National Institute of Biological Resources under the terms of the Creative Commons Attribution-NonCommercial-NoDerivatives 4.0 International License (CC BY-NC-ND 4.0). Non-commercial use, distribution, and reproduction in any medium are permitted, provided the original authors are properly credited and the work is not modified in any way.

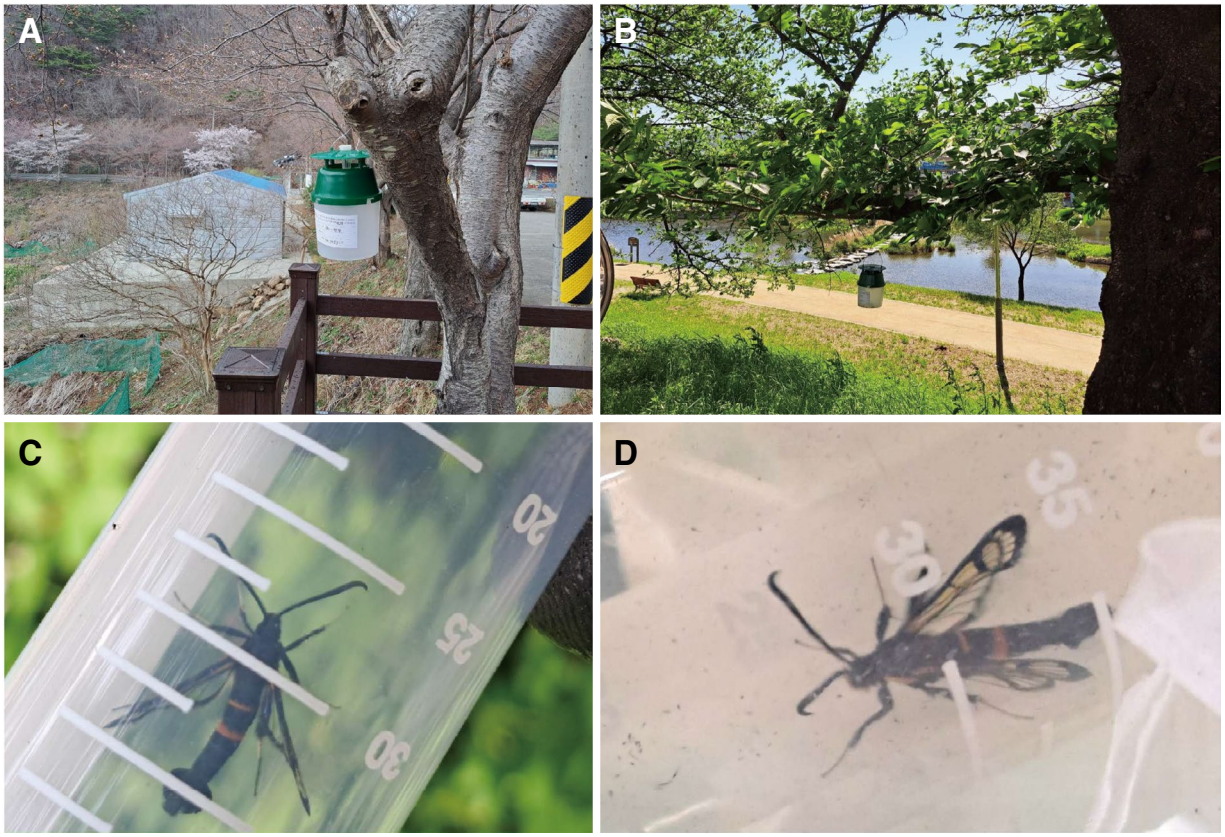

Fig. 1. *Synanthedon namdoelegans* collected in pheromone trap. (A) A pheromone trap installed on cherry tree *Prunus* × *yedoensis*. (B) A riverside, where a pheromone trap was installed. (C) and (D) An adult male transferred to a conical tube.

collected using sex pheromone traps, a method commonly employed in lepidopteran pest surveys. While their overall characteristics were similar to those of *S. velox* Fixsen, 1887 as redefined by Lee *et al.* (2011), notable morphological differences were detected. In this study, *Synanthedon namdoelegans* sp. nov. is described as new. All available information is presented, including the collection locations, and illustration of male and its genitalia. DNA barcodes are provided for precise identification.

Materials and Methods

Specimen collection and morphological analysis

Six males of *S. namdoelegans* were collected from April 2023 to May 2024 using funnel traps (170 × 250 mm) installed with the pheromone lure specific to *S. bicingulata* (Green Agrotech, Gyeongsan, South Korea). Traps were installed on the branches of the cherry tree, *Prunus* × *yedoensis*, and neighboring trees at a height of 1.2 to 1.5 meters above the ground (Fig. 1). Three non-*S. bicingulata* from Suncheon (34°58′44.4″N, 127°23′06.7″E) (MNU14991, CNU17888, and CNU17889), two from Naju (35°02′10.7″N, 126°42′22.7″E) (MNU14989 and MNU14990), and one from Jangseong (35°18′17.6″N, 126°46′40.1″E) (CNU17891) in Jeollanamdo Province, South Korea, were collected in the *S. bicingulata* traps. For adult morphological examination, one specimen of *S. namdoelegans*, which was collected from Naju (MNU14990) was used. Type specimens were deposited at Mokpo National University, Muan, Korea under the voucher specimen numbers MNU14989 and MNU14990 from Naju and MNU14991 from Suncheon. Adult images of *S. namdoelegans* (MNU14990) were taken with a Canon EOS 70D camera and a 100 mm-macro lens. For male genitalia examination, the abdomen of MNU14990, one of the individuals collected from Naju, was boiled in 10% KOH solution for approximately 20 min, removed scales and tissues, were stained with Chlorazol black, and mounted on slides in Euparal solution (Miller, 1996).

Molecular experiment

To ensure an accurate species identification, we sequenced the *COI* (DNA barcoding region) and *ND1* fragments in the mitochondrial genome and compared the genetic divergence of currant samples to those of

Synanthedon species that are publicly available. DNA sequencing was performed for four specimens, two from Suncheon, one from Naju, and one from Jangseong. The leftover tissues and DNA were deposited at Chonnam National University, Gwangju, Korea under the sample numbers CNU17888 and CNU17889 for Suncheon samples, CNU17890 for Naju sample, and CNU17891 for Jangseong sample. The specimen, MNU14990, which was used for the examination of morphological features, was also used for DNA sequencing analysis (CNU17890). Total DNA was extracted from the hind legs using the Wizard™ Genomic DNA Purification Kit (Promega, WI, USA).

The DNA barcode region is part of *COI* gene (658 bp), while *ND1* fragment (585 bp) contains a portion of the 3′ end of the *16S rRNA* gene, whole $tRNA^{Leu}$ and a portion of the 5′ end of the *ND1* gene. Primers for DNA barcode region were adapted from Hebert *et al*. (2004): LepF1 (forward primer), 5′-ATTCAACCAATCATAAAGATATTGG-3′ and LepR1 (reverse primer), 5′-TAAACTTCTGGATGTCCAAAAAATCA-3′. Primers for *ND1* fragment were adapted from Weller *et al*. (1994): forward primer, 5′-TAGAATTAGAAGATCAACCAGC-3′ and reverse primer, 5′-ACATGATCTGAGTTCAAACCGG-3′.

PCR was conducted under the following conditions using the AccuPower® PCR PreMix (Bioneer, Daejeon, South Korea): an initial denaturation step at 94°C for 5 min, 35-cycle amplification (94°C for 1 min, 48−56°C for 1 min, and 72°C for 1 min), and the final extension step continued for 7 min at 72°C. Electrophoresis was conducted to confirm successful DNA amplification using 0.5× TAE buffer on 1% agarose gel. The PCR products were purified using a PCR Purification Kit (Qiagen, Hilden, Germany). DNA sequencing for both strands was conducted using the ABI PRISM BigDye Terminator ver. 3.1 Cycle Sequencing Kit with an ABI 3100 Genetic Analyzer (PE Applied Biosystems, CA, USA).

Sequence analysis

The boundary of each directional sequence was delimitated using the SeqMan software from the DNASTAR package (SeqMan NGen®, ver. 13.0, DNASTAR, WI, USA), and both directional sequences of each individual were aligned using MAFFT ver. 7 (Katoh *et al*., 2002) to have a complete individual sequence. A search of available public sequence databases, such as GenBank, through BLAST search (https://blast.ncbi.nlm.nih.gov/Blast.cgi) and the BOLD system (https://v4.boldsystems.org/) was conducted to obtain the sequences belonging to the genus of *Synanthedon*. Forty-five DNA barcode sequences and six *ND1* fragment sequences were obtained from GenBank, but one sequence for DNA barcode sequence was obtained from BOLD system (*S. velox*, unpublished, BOLD system acc. no. AEZ9646). Sequence divergence was analyzed by unrooted pairwise comparison using PAUP ver. 4.0b (Swofford, 2002).

Phylogenetic analysis

Phylogenetic analysis was conducted with DNA barcoding sequences, consisted of 46 downloaded and four current data with the addition of two congeneric species (*Sophona snellingi* and *S. greenfield* (unpublished; GenBank acc. no. HQ564703 and HQ564718) as outgroups. The GTR + GAMMA + I model was selected using PartitionFinder 2 with the greedy algorithm (Lanfear *et al*., 2017), which is integrated into PhyloSuite, ver. 1.2.3 (Xiang *et al*., 2023) and applied to IQ-TREE (Nguyen *et al*., 2015). Branch supports were assessed using 1,000 replicates of Ultrafast Bootstrap (UFBoot) (Minh *et al*., 2013) and the Shimodaira-Hasegawa approximate likelihood ratio test (SH-aLRT) (Guindon *et al*., 2010). The phylogenetic tree was visualized using FigTree ver. 1.42 (http://tree.bio.ed.ac.uk/software/figtree/accessed 25 October 2024).

Results and Discussion

Systematics

Taxonomy account

Synanthedon Hübner, [1819]

Synanthedon Hübner, [1819], Verz. bek. Schmett. (9): 129. TS. *Sphinx oestriformis* Rottemburg, 1775 (= *Synanthedon vespiformis* (Linnaeus, 1761)).

Korean name: Nam-do-meot-jaeng-i-yu-ri-na-bang

Synanthedon namdoelegans Kim, Kim and Choi sp. nov.
urn:lsid:zoobank.org:pub:C425E3CC-2FB4-4CFE-8B1F-5121298651E6

Type material. Holotype. ♂ [MNU14991]. Suncheon, Jeollanamdo Province, 30. IV. 2024, Kim, Woo Jin leg. **Paratypes.** Suncheon, Jeollanamdo Province, 2♂ [CNU 17888, CNU17889], 26. IV. 2023, Kim, Woo Jin leg.; Naju, Jeollanamdo Province, 1♂ [MNU14989], 1. V. 2023; 1♂ [MNU14990], 30. IV. 2024, Kim, Woo Jin leg.; 1♂ [CNU 17891], Jangseong, Jeollanamdo Province, 1. V. 2024, Kim, Woo Jin leg.

Diagnosis. Superficially, this new species resembles *S. soffneri* Špatenka, 1983, and *S. bastak* Gorbunov & Koshkin, 2023. However, it can be distinguished by subtle differences in the thickness and shape of the black band along the forewing's outer margin and the spot on the discal vein of the hindwing. Additionally, while the male genitalia are similar to those of *S. velox*, the shapes

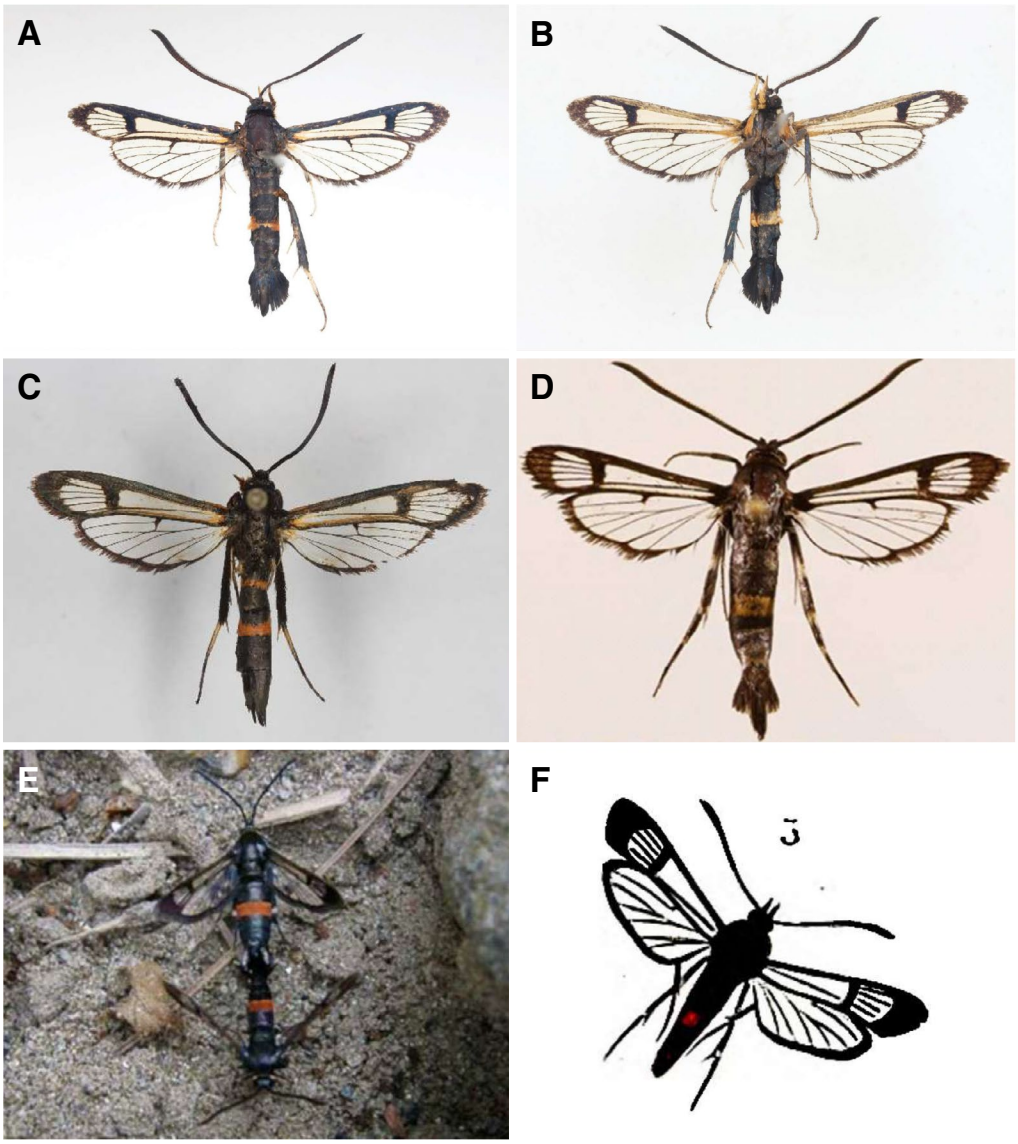

Fig. 2. *Synanthedon namdoelegans* collected in this study, along with available public data of *S. velox*. (A) and (B) The dorsal and ventral image of *S. namdoelegans* adult male, respectively (voucher specimen no. MNU14990). Photographed by one of the authors, Sung-Soo Kim. (C) The dorsal image of the proposed *S. velox* adult female collected from South Korea and registered in the BOLD system. Photographed by Sesiidae Research Group. (D) The dorsal image of *S. velox* adult male collected from South Korea and reported in Lee *et al.* (2011). (E) Copulation of *S. velox* on the ground, reported in Lee *et al.* (2011). (F) A schematic illustration of *S. velox* adult reported in Fixsen (1887).

of the crista sacculi and saccus differ.

Description. Holotype (Fig. 2A and 2B). Alar expanse 26 mm; body length 14.5 mm; forewing 11.5 mm; antenna about 9 mm. **Head**: Antennae black with a blue sheen, scapus covered in black scales; frons black, narrowly covered with white scales between frons and the compound eyes; vertex dark brown to black. Labial palpus dorsally dark brown, ventrally covered with pale orange scales, with some black scales on the sides; pericephalic scales black.

Thorax: Dorsally, laterally, and ventrally all black; patagia black; tegula and thoracic dorsum devoid of scales, laterally clearly marked with nearly triangular yellow scales, accompanied by a band of long pale yellow hairs anteriorly. Fore-, mid-, and hind-tarsi with yellow and black scales, otherwise all black, except for a few yellow scales on the ventral surface of the distal third of each femur; spurs black at the base but mostly yellow. Forewing glossy bluish with transparency; costal margin black, with a few indistinct yellow scales near the base; hind margin black, with a yellowish tinge at the basal third; discal spot black, almost as wide as the costal margin, with a

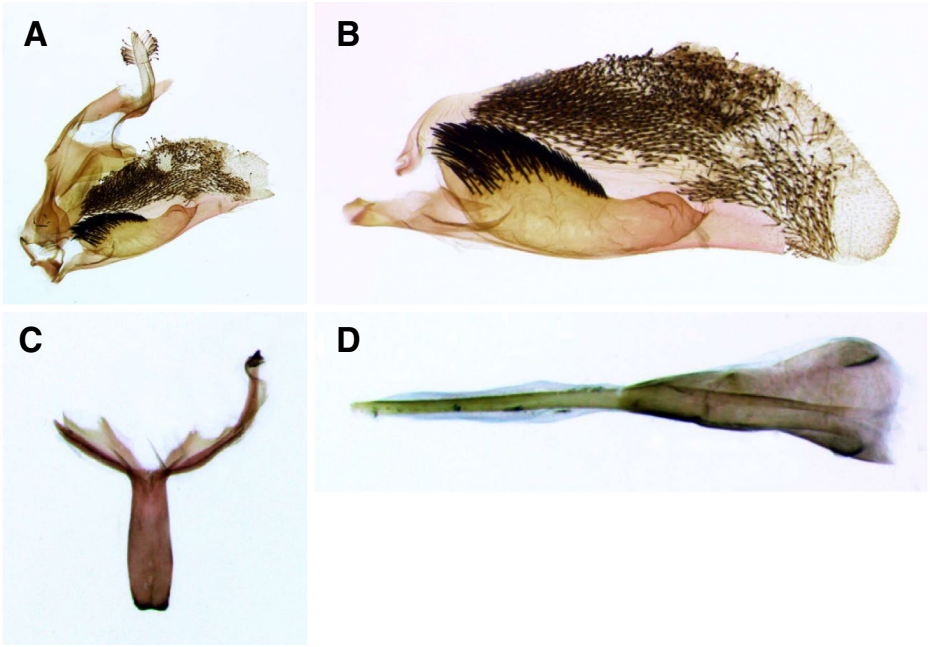

Fig. 3. Male genitalia of *Synanthedon namdoelegans*. (A) Tegumen-uncus complex. (B) Valva. (C) Saccus. (D) Aedeagus.

few yellow scales distally; veins black; outer margin dark brown; hind margin of the discoidal cell more strongly yellowish than other veins, turning yellow toward the base; cilia blackish-brown. Hindwing glossy bluish with transparency; discal spot narrow, tapering distally; veins and outer margin dark brown; cilia black, becoming longer with a few yellow hairs toward the underside. Underside of wings similar to upperside but with more abundant yellow scales at the base. Abdomen: Black with a bright blue sheen; tergite 1 yellow on the posterior third; tergites 3 and 5 each with a broad yellow stripe posteriorly; sternites black, except for sternite 5, which is orange with scattered black scales; anal tuft black with a bright blue sheen.

Male genitalia (Fig. 3): Tegumen-uncus complex not very wide; scopula androconialis less developed, measuring less than half of the tegumen-uncus complex; crista gnathi medialis short; crista gnathi lateralis slightly narrower than crista gnathi medialis; valva elongated and trapeziform-oval; crista sacculi high and pocket-shaped, not separated from the sensory field of setae proximally; saccus slightly thick, with a somewhat bifurcate basally, and slightly shorter than the vinculum. Aedeagus narrow, one-third the width of the valva; vesica without a cornutus.

Distribution. Korea (Jeollanamdo Province (Suncheon-si, Naju-si, and Jangseong-gun)].

Remarks. Most of the specimens suffered damage to their wings and bodies as a result of being trapped by the pheromone lures.

Etymology. The meaning of the name of this new species is derived from the combination of the collection site, southern part of Korea, Jeollanamdo Province, and its fine clear wings, "elegant".

Molecular data. The barcode of *Synanthedon namdoelegans* sp. nov.

Molecular analysis

DNA barcode sequences of *S. namdoelegans* specimens were either identical or had a maximum difference of only 0.46% (3 bp) (Table 1). Comparison of *S. namdoelegans* sequences to those of other *Synanthedon* species showed the sequence divergence ranging from 0.3% (2 bp; *S. velox*, unpublished, BOLD system acc. no. AEZ9646) to 12.46% (82 bp; *S. refulgens*, Lait and Hebert, 2018, MH592815). Thus, the BOLD system-registered *S. velox* sequence is well within the divergence range of *S. namdoelegans* sequences. However, after excluding *S. velox*, the minimum sequence divergence increased to 1.98% (13 bp; *Synanthedon fulvipes* Harris, 1839, unpublished, JF848560) (Table 1). Therefore, our divergence estimates strongly indicate that the proposed *S. velox* registered in BOLD system is highly likely to be *S. namdoelegans*, given that no other *S. velox* sequence is available.

For comparison of the *ND1* fragment, four sequence sequences of *S. namdoelegans* and six individual sequences in three *Synanthedon* species registered in public data were used. *S. namdoelegans* sequences were either identical or had maximum difference of only 0.52% (3 bp), while comparison of *S. namdoelegans* to other species

Table 1. Pairwise comparisons among barcode sequences of *Synanthedon* species (658 bp) obtained from current study and public data.

No.	Species	Accssion no.	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
1	*S. namdoelegans*	This study	–	0	0	0.46	0.30	7.90	7.90	9.42	10.18	10.03	7.30	8.83	9.27	8.82	9.27	2.13	7.60	10.33	8.82	9.42
2	*S. namdoelegans*	This study	0	–	0	0.46	0.30	7.90	7.90	9.42	10.18	10.03	7.30	8.83	9.27	8.82	9.27	2.13	7.60	10.33	8.82	9.42
3	*S. namdoelegans*	This study	0	0	–	0.46	0.30	7.90	7.90	9.42	10.18	10.03	7.30	8.83	9.27	8.82	9.27	2.13	7.60	10.33	8.82	9.42
4	*S. namdoelegans*	This study	3	3	3	–	0.76	8.06	8.21	9.27	10.03	9.88	7.60	8.98	9.57	8.97	9.27	1.98	7.60	10.33	9.27	9.27
5	*S. velox*	AEZ9646	2	2	2	5	–	7.90	8.21	9.42	10.18	10.03	7.30	9.13	9.27	8.82	9.27	2.13	7.90	10.03	8.82	9.42
6	*S. soffneri*	KT782535	52	52	52	53	52	–	10.49	11.09	11.09	10.94	10.18	10.35	11.55	11.09	12.01	7.90	10.33	11.40	10.18	10.64
7	*S. formicaeformis*	HM873903	52	52	52	54	54	69	–	10.94	11.85	11.40	9.73	11.42	10.49	10.79	10.79	8.66	8.21	11.09	9.57	9.27
8	*S. scoliaeformis*	HM873899	62	62	62	61	62	73	72	–	11.40	11.55	10.33	10.96	12.01	10.94	10.79	9.42	8.97	11.55	11.25	11.70
9	*S. cruciate*	GU731637	67	67	67	66	67	73	78	75	–	0.46	11.40	6.09	12.01	12.61	12.92	9.57	9.27	13.98	12.61	12.61
10	*S. loranthi*	GU731629	66	66	66	65	66	72	75	76	3	–	11.25	5.94	11.85	12.46	12.77	9.42	9.12	13.83	12.61	12.46
11	*S. polaris*	MZ610629	48	48	48	50	48	67	64	68	75	74	–	10.81	10.64	10.94	10.79	8.36	8.66	11.85	9.42	11.85
12	*S. tipuliformis*	MZ609921	58	58	58	59	60	68	75	72	40	39	71	–	12.18	11.72	12.48	8.98	9.59	12.18	11.72	10.96
13	*S. vespiformis*	OU906976	61	61	61	63	61	76	69	79	79	78	70	80	–	11.55	11.25	8.97	9.12	12.01	10.79	13.22
14	*S. novaroensis*	GU661886	58	58	58	59	58	73	71	72	83	82	72	77	76	–	4.56	8.36	9.27	12.16	10.03	12.16
15	*S. pini*	JN279256	61	61	61	61	61	79	71	71	85	84	71	82	74	30	–	8.97	8.97	11.85	10.49	12.16
16	*S. fulvipes*	JF848560	14	14	14	13	14	52	57	62	63	62	55	59	59	55	59	–	7.60	9.88	9.12	9.42
17	*S. acerrubri*	JF848555	50	50	50	50	52	68	54	59	61	60	57	63	60	61	59	50	–	10.94	8.66	10.64
18	*S. scitula*	HQ977589	68	68	68	68	66	75	73	76	92	91	78	80	79	80	78	65	72	–	11.25	12.77
19	*S. sapygaeformis*	HQ977588	58	58	58	61	58	67	63	74	83	83	62	77	71	66	69	60	57	74	–	11.85
20	*S. rubrofascia*	HQ977587	62	62	62	61	62	70	61	77	83	82	78	72	87	80	80	62	70	84	78	–
21	*S. kathyae*	HQ977584	58	58	58	57	57	72	65	61	73	72	56	75	64	63	58	57	54	68	63	77
22	*S. exitiosa*	HQ977582	49	49	49	51	49	67	60	60	69	68	65	66	65	59	60	52	46	69	63	71
23	*S. decipiens*	HQ977579	57	57	57	59	57	74	58	74	72	72	67	76	72	75	72	54	55	79	55	70
24	*S. acerni*	HQ977575	53	53	53	53	53	63	59	67	66	65	62	68	72	61	58	56	50	66	69	73
25	*S. albicornis*	HQ977574	65	65	65	67	63	79	67	79	78	77	70	83	74	82	79	63	68	78	68	78
26	*S. rhododendri*	HQ957068	64	64	64	65	64	71	74	71	74	73	70	76	77	69	65	65	61	81	70	77
27	*S. mellinipennis*	HM902931	72	72	72	73	72	73	77	84	88	88	74	85	78	78	81	73	71	89	70	77
28	*S. bibionipennis*	HM902929	75	75	75	76	75	74	74	74	80	80	78	77	79	77	81	75	63	83	74	82
29	*S. saxifragae*	HM902927	50	50	50	52	50	62	61	75	75	72	58	68	66	68	67	49	56	72	63	70
30	*S. bolteri*	HM902924	55	55	55	57	57	67	29	69	72	69	64	67	65	67	65	55	52	68	65	62
31	*S. fatifera*	HQ564768	58	58	58	60	56	71	58	59	68	65	63	62	62	65	58	56	47	64	60	72
32	*S. polygoni*	GU685617	71	71	71	70	73	77	74	80	78	78	77	78	90	70	75	72	64	77	75	81
33	*S. flaviventris*	JF854645	71	71	71	70	73	77	74	80	78	78	77	78	90	70	75	72	64	77	75	81
34	*S. spheciformis*	JF854620	67	67	67	67	65	71	75	69	73	74	66	70	77	79	79	71	72	80	90	94
35	*S. mesiaeformis*	JF853916	54	54	54	53	52	67	65	51	74	73	66	74	66	65	69	49	56	76	70	69
36	*S. culiciformis*	HM871045	31	31	31	32	31	61	57	74	72	71	62	68	62	64	62	29	57	67	64	68
37	*S. alleri*	MH592905	53	53	53	52	54	71	64	61	72	71	58	72	64	62	57	50	54	65	63	75
38	*S. pictipes*	MH592903	49	49	49	48	49	63	64	50	63	62	61	65	72	53	46	49	48	76	63	64
39	*S. myopaeformis*	MH592898	64	64	64	65	64	74	75	67	78	77	72	76	73	70	61	63	62	74	62	79
40	*S. sequoiae*	MH592890	59	59	59	59	59	67	66	71	74	73	73	73	72	48	38	56	53	77	61	76
41	*S. sigmoidea*	MH592865	48	48	48	51	46	61	62	70	68	67	42	68	67	68	67	51	58	75	60	62
42	*S. rileyana*	MH592838	72	72	72	71	72	94	89	84	88	87	89	88	87	86	85	76	86	92	94	102
43	*S. canadensis*	MH592819	55	55	55	54	57	70	62	65	86	85	72	74	71	72	73	56	60	74	64	65
44	*S. refulgens*	MH592815	82	82	82	81	84	84	85	80	95	95	79	92	79	87	85	77	74	97	80	94
45	*S. geliformis*	MH592790	67	67	67	69	69	72	68	74	83	84	81	84	79	81	77	67	65	40	80	87
46	*S. arkansasensis*	MH592782	79	79	79	80	79	91	84	79	84	82	87	85	85	88	94	76	80	91	78	89
47	*S. arctica*	GU097106	59	59	59	57	57	71	70	71	72	71	44	76	72	74	71	57	63	86	73	73
48	*S. andrenaeformis*	GU706630	53	53	53	54	53	58	64	69	69	68	67	70	67	64	67	56	54	74	64	72
49	*S. cephiformis*	KX040880	68	68	68	69	68	79	84	84	48	48	80	49	88	81	85	70	77	88	83	84
50	*S. stomoxiformis*	AJ864355	66	66	66	69	66	68	77	71	77	74	71	69	73	75	80	69	68	87	81	78

Table 1. Continued.

No.	Species	Accession no.	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
1	*S. namdoelegans*	This study	8.82	7.45	8.66	8.06	9.88	9.73	10.94	11.40	7.60	8.36	8.82	10.79	10.79	10.18	8.21	4.71	8.06	7.45	9.73	8.97
2	*S. namdoelegans*	This study	8.82	7.45	8.66	8.06	9.88	9.73	10.94	11.40	7.60	8.36	8.82	10.79	10.79	10.18	8.21	4.71	8.06	7.45	9.73	8.97
3	*S. namdoelegans*	This study	8.82	7.45	8.66	8.06	9.88	9.73	10.94	11.40	7.60	8.36	8.82	10.79	10.79	10.18	8.21	4.71	8.06	7.45	9.73	8.97
4	*S. namdoelegans*	This study	8.66	7.75	8.97	8.06	10.18	9.88	11.09	11.55	7.90	8.66	9.12	10.64	10.64	10.18	8.06	4.86	7.90	7.30	9.88	8.97
5	*S. velox*	AEZ9646	8.66	7.45	8.66	8.06	9.57	9.73	10.94	11.40	7.60	8.66	8.51	11.09	11.09	9.88	7.90	4.71	8.21	7.45	9.73	8.97
6	*S. soffneri*	KT782535	10.94	10.18	11.25	9.57	12.01	10.79	11.09	11.25	9.42	10.18	10.79	11.70	11.70	10.79	10.18	9.27	10.79	9.57	11.25	10.18
7	*S. formicaeformis*	HM873903	9.88	9.12	8.82	8.97	10.18	11.25	11.70	11.25	9.27	4.41	8.82	11.25	11.25	11.40	9.88	8.66	9.73	9.73	11.40	10.03
8	*S. scoliaeformis*	HM873899	9.27	9.12	11.25	10.18	12.01	10.79	12.77	11.25	11.40	10.49	8.97	12.16	12.16	10.49	7.75	11.25	9.27	7.60	10.18	10.79
9	*S. cruciate*	GU731637	11.09	10.49	10.94	10.03	11.85	11.25	13.37	12.16	11.40	10.94	10.33	11.85	11.85	11.09	11.25	10.94	10.94	9.57	11.85	11.25
10	*S. loranthi*	GU731629	10.94	10.33	10.94	9.88	11.70	11.09	13.37	12.16	10.94	10.49	9.88	11.85	11.85	11.25	11.09	10.79	10.79	9.42	11.70	11.09
11	*S. polaris*	MZ610629	8.51	9.88	10.18	9.42	10.64	10.64	11.25	11.85	8.82	9.73	9.57	11.70	11.70	10.03	10.03	9.42	8.82	9.27	10.94	11.09
12	*S. tipuliformis*	MZ609921	11.42	10.05	11.57	10.35	12.63	11.57	12.94	11.72	10.35	10.20	9.44	11.87	11.87	10.65	11.26	10.35	10.96	9.89	11.57	11.11
13	*S. vespiformis*	OU906976	9.73	9.88	10.94	10.94	11.25	11.70	11.85	12.01	10.03	9.88	9.42	13.68	13.68	11.70	10.03	9.42	9.73	10.94	11.09	10.94
14	*S. novaroensis*	GU661886	9.57	8.97	11.40	9.27	12.46	10.49	11.85	11.70	10.33	10.18	9.88	10.64	10.64	12.01	9.88	9.73	9.42	8.06	10.64	7.30
15	*S. pini*	JN279256	8.82	9.12	10.94	8.82	12.01	9.88	12.31	12.31	10.18	9.88	8.82	11.40	11.40	12.01	10.49	9.42	8.66	6.99	9.27	5.78
16	*S. fulvipes*	JF848560	8.66	7.90	8.21	8.51	9.57	9.88	11.09	11.40	7.45	8.36	8.51	10.94	10.94	10.79	7.45	4.41	7.60	7.45	9.57	8.51
17	*S. acerrubri*	JF848555	8.21	6.99	8.36	7.60	10.33	9.27	10.79	9.57	8.51	7.90	7.14	9.73	9.73	10.94	8.51	8.66	8.21	7.30	9.42	8.06
18	*S. scitula*	HQ977589	10.33	10.49	12.01	10.03	11.85	12.31	13.53	12.61	10.94	10.33	9.73	11.70	11.70	12.16	11.55	10.18	9.88	11.55	11.25	11.70
19	*S. sapygaeformis*	HQ977588	9.57	9.57	8.36	10.49	10.33	10.64	10.64	11.25	9.57	9.88	9.12	11.40	11.40	13.68	10.64	9.73	9.57	9.57	9.42	9.27
20	*S. rubrofascia*	HQ977587	11.70	10.79	10.64	11.09	11.85	11.70	11.70	12.46	10.64	9.42	10.94	12.31	12.31	14.29	10.49	10.33	11.40	9.73	12.01	11.55
21	*S. kathyae*	HQ977584	–	8.82	10.03	8.36	10.49	9.88	11.09	10.79	8.97	9.12	8.97	10.49	10.49	10.18	9.42	8.82	1.82	8.06	8.82	8.51
22	*S. exitiosa*	HQ977582	58	–	10.33	9.73	9.88	8.82	11.40	9.73	8.51	8.51	8.06	9.88	9.88	11.09	6.99	8.06	8.97	6.84	8.82	8.66
23	*S. decipiens*	HQ977579	66	68	–	10.49	10.03	10.79	11.55	11.25	8.36	8.97	10.03	11.70	11.70	12.46	10.33	8.51	9.57	9.42	10.33	9.42
24	*S. acerni*	HQ977575	55	64	69	–	9.27	10.33	10.79	10.18	9.73	8.66	7.90	10.03	10.03	10.49	10.33	8.51	7.60	8.82	9.73	8.82
25	*S. albicornis*	HQ977574	69	65	66	61	–	12.16	11.85	12.46	9.27	9.27	9.42	12.61	12.61	10.49	10.94	10.49	10.49	9.88	11.09	10.18
26	*S. rhododendri*	HQ957068	65	58	71	68	80	–	12.77	10.64	10.79	11.25	10.49	11.40	11.40	11.70	10.33	9.42	10.49	8.66	10.94	9.73
27	*S. mellinipennis*	HM902931	73	75	76	71	78	84	–	9.73	11.09	11.40	10.79	9.88	9.88	13.83	11.70	11.70	10.79	11.09	12.46	12.01
28	*S. bibionipennis*	HM902929	71	64	74	67	82	70	64	–	10.18	10.33	9.57	9.27	9.27	12.16	9.88	11.55	11.70	9.42	11.25	11.09
29	*S. saxifragae*	HM902927	59	56	55	64	61	71	73	67	–	8.36	8.97	11.55	11.55	10.94	8.51	9.12	9.12	8.36	10.03	9.73
30	*S. bolteri*	HM902924	60	56	59	57	61	74	75	68	55	–	7.75	10.94	10.94	10.79	10.49	8.36	8.97	8.66	10.79	9.88
31	*S. fatifera*	HQ564768	59	53	66	52	62	69	71	63	59	51	–	10.94	10.94	10.18	8.97	9.73	8.51	8.21	8.06	9.27
32	*S. polygoni*	GU685617	69	65	77	66	83	75	65	61	76	72	72	–	0	12.61	10.79	11.40	10.03	9.73	11.55	11.09
33	*S. flaviventris*	JF854645	69	65	77	66	83	75	65	61	76	72	72	0	–	12.61	10.79	11.40	10.03	9.73	11.55	11.09
34	*S. spheciformis*	JF854620	67	73	82	69	69	77	91	80	72	71	67	83	83	–	11.40	11.40	10.64	10.33	12.01	12.16
35	*S. mesiaeformis*	JF853916	62	46	68	68	72	68	77	65	56	69	59	71	71	75	–	9.12	9.73	7.45	10.33	9.57
36	*S. culiciformis*	HM871045	58	53	56	56	69	62	77	76	60	55	64	75	75	75	60	–	8.66	8.82	9.88	8.36
37	*S. alleri*	MH592905	12	59	63	50	69	69	71	77	60	59	56	66	66	70	64	57	–	8.51	8.82	8.66
38	*S. pictipes*	MH592903	53	45	62	58	65	57	73	62	55	57	54	64	64	68	49	58	56	–	9.73	7.60
39	*S. myopaeformis*	MH592898	58	58	68	64	73	72	82	74	66	71	53	76	76	79	68	65	58	64	–	10.03
40	*S. sequoiae*	MH592890	56	57	62	58	67	64	79	73	64	65	61	73	73	80	63	55	57	50	66	–
41	*S. sigmoidea*	MH592865	58	54	62	62	66	69	70	69	50	50	57	76	76	67	58	55	62	52	67	69
42	*S. rileyana*	MH592838	79	81	87	75	91	86	94	99	74	86	88	91	91	95	77	82	74	77	86	82
43	*S. canadensis*	MH592819	67	61	69	66	76	64	78	71	60	65	63	75	75	89	66	61	65	62	67	71
44	*S. refulgens*	MH592815	79	82	82	86	93	82	91	85	81	87	89	88	88	94	79	83	81	81	89	84
45	*S. geliformis*	MH592790	74	71	72	68	81	79	85	75	70	67	67	77	77	75	74	67	75	75	82	74
46	*S. arkansasensis*	MH592782	74	76	81	91	83	79	86	87	75	75	72	93	93	89	84	85	79	74	81	93
47	*S. arctica*	GU097106	64	64	75	67	69	77	82	83	59	62	65	83	83	69	68	67	70	59	69	77
48	*S. andrenaeformis*	GU706630	62	60	62	58	72	60	78	67	58	65	53	76	76	78	68	57	61	58	62	62
49	*S. cephiformis*	KX040880	78	73	71	80	91	75	94	82	75	82	78	80	80	87	77	73	79	67	72	75
50	*S. stomoxiformis*	AJ864355	67	63	72	74	72	73	79	78	69	66	66	83	83	68	70	71	72	65	85	77

Table 1. Continued.

No.	Species	Accession no.	41	42	43	44	45	46	47	48	49	50
1	*S. namdoelegans*	This study	7.30	10.94	8.36	12.46	10.18	12.01	8.97	8.06	10.33	10.03
2	*S. namdoelegans*	This study	7.30	10.94	8.36	12.46	10.18	12.01	8.97	8.06	10.33	10.03
3	*S. namdoelegans*	This study	7.30	10.94	8.36	12.46	10.18	12.01	8.97	8.06	10.33	10.03
4	*S. namdoelegans*	This study	7.75	10.79	8.21	12.31	10.49	12.16	8.66	8.21	10.49	10.49
5	*S. velox*	AEZ9646	6.99	10.94	8.66	12.77	10.49	12.01	8.66	8.06	10.33	10.03
6	*S. soffneri*	KT782535	9.27	14.29	10.64	12.77	10.94	13.83	10.79	8.82	12.01	10.33
7	*S. formicaeformis*	HM873903	9.42	13.53	9.42	12.92	10.33	12.77	10.64	9.73	12.77	11.70
8	*S. scoliaeformis*	HM873899	10.64	12.77	9.88	12.16	11.25	12.01	10.79	10.49	12.77	10.79
9	*S. cruciate*	GU731637	10.33	13.37	13.07	14.44	12.61	12.77	10.94	10.49	7.30	11.70
10	*S. loranthi*	GU731629	10.18	13.22	12.92	14.44	12.77	12.46	10.79	10.33	7.30	11.25
11	*S. polaris*	MZ610629	6.38	13.53	10.94	12.01	12.31	13.22	6.69	10.18	12.16	10.79
12	*S. tipuliformis*	MZ609921	10.35	13.39	11.26	14.00	12.79	12.94	11.57	10.65	7.46	10.50
13	*S. vespiformis*	OU906976	10.18	13.22	10.79	12.01	12.01	12.92	10.94	10.18	13.37	11.09
14	*S. novaroensis*	GU661886	10.33	13.07	10.94	13.22	12.31	13.37	11.25	9.73	12.31	11.40
15	*S. pini*	JN279256	10.18	12.92	11.09	12.92	11.70	14.29	10.79	10.18	12.92	12.16
16	*S. fulvipes*	JF848560	7.75	11.55	8.51	11.70	10.18	11.55	8.66	8.51	10.64	10.49
17	*S. acerrubri*	JF848555	8.82	13.07	9.12	11.25	9.88	12.16	9.57	8.21	11.70	10.33
18	*S. scitula*	HQ977589	11.40	13.98	11.25	14.74	6.08	13.83	13.07	11.25	13.37	13.22
19	*S. sapygaeformis*	HQ977588	9.12	14.29	9.73	12.16	12.16	11.85	11.09	9.73	12.61	12.31
20	*S. rubrofascia*	HQ977587	9.42	15.50	9.88	14.29	13.22	13.53	11.09	10.94	12.77	11.85
21	*S. kathyae*	HQ977584	8.82	12.01	10.18	12.01	11.25	11.25	9.73	9.42	11.85	10.18
22	*S. exitiosa*	HQ977582	8.21	12.31	9.27	12.46	10.79	11.55	9.73	9.12	11.09	9.57
23	*S. decipiens*	HQ977579	9.42	13.22	10.49	12.46	10.94	12.31	11.40	9.42	10.79	10.94
24	*S. acerni*	HQ977575	9.42	11.40	10.03	13.07	10.33	13.83	10.18	8.82	12.16	11.25
25	*S. albicornis*	HQ977574	10.03	13.83	11.55	14.13	12.31	12.61	10.49	10.94	13.83	10.94
26	*S. rhododendri*	HQ957068	10.49	13.07	9.73	12.46	12.01	12.01	11.70	9.12	11.40	11.09
27	*S. mellinipennis*	HM902931	10.64	14.29	11.85	13.83	12.92	13.07	12.46	11.85	14.29	12.01
28	*S. bibionipennis*	HM902929	10.49	15.05	10.79	12.92	11.40	13.22	12.61	10.18	12.46	11.85
29	*S. saxifragae*	HM902927	7.60	11.25	9.12	12.31	10.64	11.40	8.97	8.82	11.40	10.49
30	*S. bolteri*	HM902924	7.60	13.07	9.88	13.22	10.18	11.40	9.42	9.88	12.46	10.03
31	*S. fatifera*	HQ564768	8.66	13.37	9.57	13.53	10.18	10.94	9.88	8.06	11.85	10.03
32	*S. polygoni*	GU685617	11.55	13.83	11.40	13.37	11.70	14.13	12.61	11.55	12.16	12.61
33	*S. flaviventris*	JF854645	11.55	13.83	11.40	13.37	11.70	14.13	12.61	11.55	12.16	12.61
34	*S. spheciformis*	JF854620	10.18	14.44	13.53	14.29	11.40	13.53	10.49	11.85	13.22	10.33
35	*S. mesiaeformis*	JF853916	8.82	11.70	10.03	12.01	11.25	12.77	10.33	10.33	11.70	10.64
36	*S. culiciformis*	HM871045	8.36	12.46	9.27	12.61	10.18	12.92	10.18	8.66	11.09	10.79
37	*S. alleri*	MH592905	9.42	11.25	9.88	12.31	11.40	12.01	10.64	9.27	12.01	10.94
38	*S. pictipes*	MH592903	7.90	11.70	9.42	12.31	11.40	11.25	8.97	8.82	10.18	9.88
39	*S. myopaeformis*	MH592898	10.18	13.07	10.18	13.53	12.46	12.31	10.49	9.42	10.94	12.92
40	*S. sequoiae*	MH592890	10.49	12.46	10.79	12.77	11.25	14.13	11.70	9.42	11.40	11.70
41	*S. sigmoidea*	MH592865	–	13.98	10.64	12.01	11.09	11.25	4.26	8.66	10.79	8.21
42	*S. rileyana*	MH592838	92	–	13.83	15.65	14.29	15.05	13.98	13.83	13.83	14.89
43	*S. canadensis*	MH592819	70	91	–	12.31	10.79	12.92	12.01	9.88	12.31	11.09
44	*S. refulgens*	MH592815	79	103	81	–	13.53	15.65	12.77	12.77	13.83	13.83
45	*S. geliformis*	MH592790	73	94	71	89	–	14.29	12.31	10.49	13.68	12.61
46	*S. arkansasensis*	MH592782	74	99	85	103	94	–	12.01	12.46	14.89	12.92
47	*S. arctica*	GU097106	28	92	79	84	81	79	–	10.18	12.61	10.79
48	*S. andrenaeformis*	GU706630	57	91	65	84	69	82	67	–	11.25	10.49
49	*S. cephiformis*	KX040880	71	91	81	91	90	98	83	74	–	12.31
50	*S. stomoxiformis*	AJ864355	54	98	73	91	83	85	71	69	81	–

The numbers above the diagonal are the mean distance values; the numbers below the diagonal are the absolute distance values.

Table 2. Pairwise comparisons among ND1 sequences of *Synanthedon* species (585 bp) obtained from current study and public data.

No.	Species	Genbank no.	1	2	3	4	5	6	7	8	9	10
1	*S. namdoelegans*	This study	–	0.17	0.17	0.35	2.79	3.14	2.96	2.79	2.97	11.01
2	*S. namdoelegans*	This study	1	–	0.00	0.52	2.61	2.96	2.79	2.62	2.79	10.84
3	*S. namdoelegans*	This study	1	0	–	0.52	2.61	2.96	2.79	2.62	2.79	10.84
4	*S. namdoelegans*	This study	2	3	3	–	2.79	3.48	2.96	3.14	3.31	11.34
5	*S. culiciformis*	AY304162	16	15	15	16	–	1.04	0.17	1.22	1.05	9.97
6	*S. culiciformis*	AY304163	18	17	17	20	6	–	1.22	0.87	0.70	10.14
7	*S. culiciformis*	AY304166	17	16	16	17	1	7	–	1.39	1.22	10.12
8	*S. pamphyla*	AY304164	16	15	15	18	7	5	8	–	0.17	9.79
9	*S. pamphyla*	AY304165	17	16	16	19	6	4	7	1	–	9.62
10	*S. spheciformis*	AY304167	63	62	62	65	57	58	58	56	55	–

The numbers above the diagonal are the mean distance values; the numbers below the diagonal are the absolute distance values.

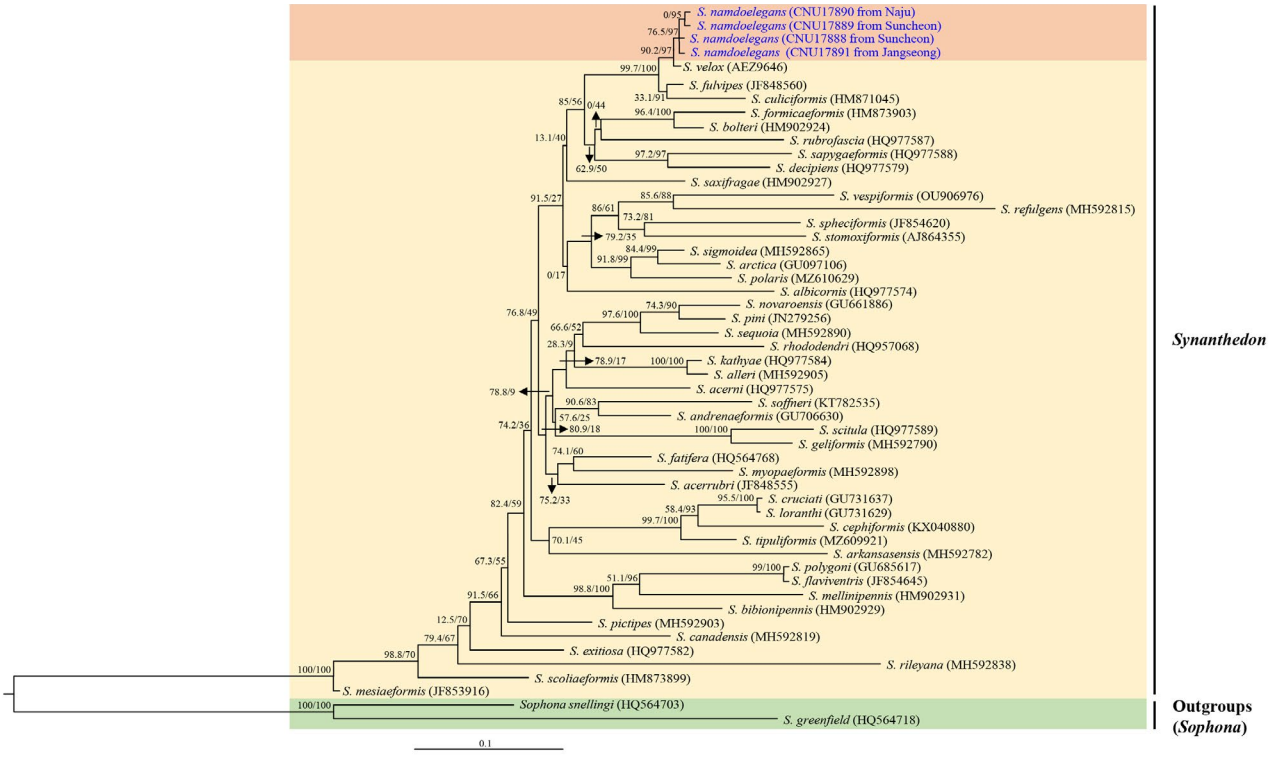

Fig. 4. Maximum-likelihood tree for 50 DNA barcode sequences of *Synanthedon* genus, including *Synanthdon namdoelegans*. The numbers at each node specifies SH-aLRT/UFBoot values. The scale bar indicates the number of substitutions per site. *Sophona snellingi* (HQ564703, unpublished), and *Sophona greenfield*, (HQ564718, unpublished) were used as outgroups. *S. namdoelegans* sequenced in this study are provided for the specimen number and collected locality within parenthesis. GenBank or BOLD system accession numbers for public data are provided in parentheses after the scientific names.

revealed the sequence divergence ranging from 2.61% (15 bp) to 11.34% (65 bp), indicating a distinct difference of *S. namdoelegans* to other species (Table 2).

Phylogenetic analysis showed that the current four samples of *S. namdoelegans* formed a well-supported inclusive group with higher nodal supports (SH-aLRT = 76.5, UFBoot = 97), but *S. namdoelegans* and the proposed *S. velox* formed the sister group with the higher nodal supports (SH-aLRT = 90.2, UFBoot = 97) (Fig. 4). As mentioned in pairwise comparison of barcode region, however, the proposed *S. velox* may have been misidentified as *S. velox*, instead of *S. namdoelegans*. Excluding the

proposed *S. velox* sequence, *S. namdoelegans* formed the sister group with *S. fulvipes* and *S. culiciformis* Linnaeus, 1758 (Mutanen *et al*., 2016, HM871045) with the higher nodal supports (SH-aLRT = 99.7, UFBoot = 100) (Fig. 4).

Our morphological and molecular analysis indicate that *S. namdoelegans* is a previously unknown species in *Synanthedon*. Its morphological features resemble those of *S. velox* (Lee *et al*., 2011), but a substantial difference was detected. The male genitalia are superficially similar to *S. velox* (Lee *et al*., 2011), but the shapes of the crista sacculi and saccus are different.

In the BOLD system, however, one dorsal image of an adult, which is designated as *S. velox* collected from South Korea (without further detailed information) is uploaded (Fig. 2C), along with the DNA barcode sequence (acc. no. AEZ9646; Table 1 and Fig. 4). The proposed *S. velox* has yellow stripes that are located in the 3rd and 5th tergites separately, rather than broadly at 4th and 5th tergites (Fig. 2C), indicating that the proposed *S. velox* is more similar to *S. namdoelegans* (Fig. 2A and 2B), rather than *S. velox* (Fig. 2D, 2E, and 2F). Moreover, *S. velox* adults are known to emerge and captured from July in South Korea (Lee *et al*., 2011), but the proposed *S. velox* is recorded for the collection date at May 10 in South Korea. Similarly, we collected *S. namdoelegans* adults from April to May in South Korea. Therefore, we believe that the proposed *S. velox* is more likely to be current *S. namdoelegans*, rather than *S. velox*. Considering all these factors, we conclude that *S. namdoelegans* is a distinct species within the genus of *Synanthedon*.

Conflicts of Interest

The author of this paper have no affiliation with any interests and is solely responsible for the paper.

Acknowledgements

This work 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 (NIBR202402202).

References

Arita, Y., Y.S. Bae, C.M. Lee and M. Ikeda. 2004. Sesiidae (Lepidoptera) of Korea. The Lepidopterological Society of Japan 55(1):1-12.

Cognato, A.I., W. Taft, R.K. Osborn and D. Rubinoff. 2023. Multi-gene phylogeny of North American clear-winged moths (Lepidoptera: Sesiidae): a foundation for future evolutionary study of a speciose mimicry complex. Cladistics 39(1):1-17.

Fixsen, C. 1887. Lepidoptera aus Korea. In: N.M. Romanoff (ed.), Mémoires sur les Lépidoptères, Hachette BNF Press, Maurepas. pp. 356.

Gorbunov, O.G. and E.S. Koshkin. 2023. A new species of the genus *Synanthedon* Hübner, 1819 (Lepidoptera: Sesiidae) from the Russian Far East. Far Eastern Entomologist 20(473):20-28.

Gorbunov, O.G. and Y. Arita. 1999. New taxa of the clearwing moths (Lepidoptera, Sesiidae) from Nepal. Tinea 16(2):106-143.

Gorbunov, O.G. and Y. Arita. 2000. *Ravitria* nom. nov. for *Vitraria* Gorbunov & Arita, 1999 (Lepidoptera, Sesiidae). Tinea 16(4):231.

Gorbunov, O.G. and Y. Arita. 2005. A new genus and two new species of Synanthedonini (Lepidoptera, Sesiidae) from the Oriental Region. Tinea 18(Supplement 3):86-95.

Guindon, S., J.F. Dufayard, V. Lefort, M. Anisimova, W. Hordijk and O. Gascuel. 2010. New algorithms and methods to estimate maximum-likelihood phylogenies: assessing the performance of PhyML 3.0. Systematic Biology 59(3):307-321.

Hebert, P.D.N., E.H. Penton, J.M. Burns, D.H. Janzen and W. Hallwachs. 2004. Ten species in one: DNA barcoding reveals cryptic species in the neotropical skipper butterfly *Astraptes fulgerator*. Proceedings of the National Academy of Sciences 101(41):14812-14817.

Kallies, A. 2020. The clearwing moths (Lepidoptera, Sesiidae) of Australia, New Guinea and the Pacific Islands. Zootaxa 4833(1):1-64.

Katoh, K., K. Misawa, K.I. Kuma and T. Miyata. 2002. MAFFT: a novel method for rapid multiple sequence alignment based on fast Fourier transform. Nucleic Acids Research 30(14):3059-3066.

Kim, W.J., S.H. Lee, J.S. Park and I. Kim. 2024. Complete mitochondrial genome of the clearwing moth *Synanthedon bicingulata* (Lepidoptera: Sesiidae). Mitochondrial DNA Part B-Resources 9(1):1528-1532.

Korea Forest Service. 2023. Street trees planting and maintenance business performance in 2022 [Internet]. Korea Forest Service, Daejeon, Accessed 11 Feb 2025, https://www.forest.go.kr/sn3hcv_skin/doc.html?fn=CMS_2024032210421231 23981&rs=/kfsweb/sn3hcv_result/

Lait, L.A. and P.D. Hebert. 2018. A survey of molecular diversity and population genetic structure in North American clearwing moths (Lepidoptera: Sesiidae) using cytochrome c oxidase I. PLoS One 13(8):e0202281.

Lanfear, R., P.B. Frandsen, A.M. Wright, T. Senfeld and B. Calcott. 2017. PartitionFinder 2: new methods for selecting partitioned models of evolution for molecular and morphological phylogenetic analyses. Molecular Biology and Evolution 34(3):772-773.

Lee, C.M., Y. Arita and Y.S. Bae. 2011. Redescription of *Syn-*

anthedon velox (Fixsen) and a new record of *Bembecia pavicevici* Tošševski (Lepidoptera: Sesiidae) from Korea. Korean Journal of Applied Entomology 50(3):221-225.

Lee C.M., Y.S. Bae and Y. Arita. 2004. Morphological description of *Synanthedon bicingulata* (Staudinger, 1887) in life stages (Lepidoptera, Sesiidae). Journal of Asia-Pacific Entomology 7(2):177-185.

McKern, J.A. and A.L. Szalanski. 2008. Genetic variation of the lesser peach tree borer, *Synanthedon pictipes* (Lepidoptera: Sesiidae) in Arkansas. Journal of Agricultural and Urban Entomology 25(1):25-35.

McKern, J.A., A.L. Szalanski, D.T. Johnson and A.P. Dowling. 2008. Molecular phylogeny of Sesiidae (Lepidoptera) inferred from mitochondrial DNA sequences. Journal of Agricultural and Urban Entomology 25(3):165-177.

Miller, J.S. 1996. Phylogeny of the neotropical moth tribe Josiini (Notodontidae: Dioptinae): a hidden case of müllerian mimicry. Zoological Journal of the Linnean Society 118(1):1-45.

Minh, B.Q., M.A.T. Nguyen and A. von Haeseler. 2013. Ultrafast approximation for phylogenetic bootstrap. Molecular Biology and Evolution 30(5):1188-1195.

Mutanen, M., S.M. Kivelä, R.A. Vos, C. Doorenweerd, S. Ratnasingham, A. Hausmann, P. Huemer, V. Dincă, E.J. van Nieukerken, C. Lopez-Vaamonde, R. Vila, L. Aarvik, T. Decaëns, K.A. Efetov, P.D.N. Hebert, A. Johnsen, O. Karsholt, M. Pentinsaari, R. Rougerie, A. Segerer, G. Tarmann, R. Zahiri and H.C.J. Godfray. 2016. Species-level para-and polyphyly in DNA barcode gene trees: strong operational bias in European Lepidoptera. Systematic Biology 65(6):1024-1040.

Nguyen, L.T., H.A. Schmidt, A. von Haeseler and B.Q. Minh. 2015. IQ-TREE: a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. Molecular Biology and Evolution 32(1):268-274.

Pühringer, F. and A. Kallies. 2024. Checklist of the Sesiidae of the world (Lepidoptera: Ditrysia) [Available from: https://www.sesiidae.net/, accessed 3 December 2024].

Swofford, D.L. 2002. PAUP*, phylogenetic analysis using parsimony (*and other method) ver. 4. 10. Sinauer Associates, Sunderland, MA, USA.

Taft, W.H., A.I. Cognato and P.A. Opler. 2016. Phylogenetic analysis supports the recognition of *Albuna beutenmulleri* Skinner as a species distinct from *A. pyramidalis* Walker (Lepidoptera: Sesiidae). The Journal of the Lepidopterists' Society 70(3):211-217.

Weller, S.J., D.P. Pashley, J.A. Martin and J.L. Constable. 1994. Phylogeny of noctuoid moths and the utility of combining independent nuclear and mitochondrial genes. Systematic Biology 43(2):194-211.

Xiang, C.-Y., F. Gao, I. Jakovlić, H.-P. Lei, Y. Hu, H. Zhang, H. Zou, G.T. Wang and D. Zhang. 2023. Using PhyloSuite for molecular phylogeny and tree-based analyses. iMeta 2(1):e87.

Submitted: December 9, 2024
Revised: February 17, 2025
Accepted: March 4, 2025