ASED http://e-ASED.org
Animal Systematics, Evolution and Diversity

Anim. Syst. Evol. Divers. Vol. 37, No. 3: 229-234, July 2021
https://doi.org/10.5635/ASED.2021.37.3.007

Short communication

First Record of *Scolelepis* (*Scolelepis*) *daphoinos* (Annelida: Polychaeta: Spionidae) in South Korea

Geon Hyeok Lee, Gi-Sik Min*

Department of Biological Sciences, Inha University, Incheon 22212, Korea

ABSTRACT

Scolelepis (*Scolelepis*) *daphoinos* is newly reported in Korean fauna. This species can be distinguished from its congeners by the following characteristics: the presence of reddish pigment patches on the posterior part of the prostomium, notopodial postchaetal lamellae that are partially fused to the branchiae, and the presence of only the bidentate hooded hooks. The morphological diagnosis and photographs of *S.* (*S.*) *daphoinos* are provided. The partial mitochondrial cytochrome *c* oxidase subunit I (COI), 16S ribosomal DNA (16S rDNA), and the nuclear 18S ribosomal DNA (18S rDNA) sequences from Korean specimens of *S.* (*S.*) *daphoinos* were determined. Species identification was supported by a comparison of DNA barcode sequences of COI and 16S rDNA with morphological examination from the specimens of type locality, China.

Keywords: *Scolelepis* (*Scolelepis*) *daphoinos*, COI, 16S rDNA, 18S rDNA, Korea

INTRODUCTION

The genus *Scolelepis* Blainville, 1828 is one of the largest groups of spionid polychaetes commonly found on soft bottoms in intertidal to deep-sea waters (Sikorski and Pavlova, 2015). Members of this genus are taxonomically defined by a distally pointed prostomium, the presence of branchiae from chaetiger 2 that are fused to the notopodial postchaetal lamellae, an absence of ciliated grooves on palps, and a cushion-like pygidium without cirri (Surugiu, 2016). In the Far East, *Scolelepis* (*Scolelepis*) *daphoinos* Zhou, Ji and Li, 2009 (type locality, China), commonly found on the sandy beaches of Yellow Sea, had been long confused as *S.* (*S.*) *squamata* (O.F. Muller, 1806) because of their morphological similarity in Chinese waters (Zhou et al., 2009). Zhou et al. (2009) had identified that morphological differences existed between these two *Scolelepis* species in the dentitions of hooded hooks and presence of pigmentations in the anterior chaetigers. But a molecular comparison between two species has never been conducted. In Korean waters, only four *Scolelepis* species, *Scolelepis* (*Parascolelepis*) *papillosa* (Okuda, 1937), *S.* (*P.*) *yamaguchii* (Imajima, 1959), *S.* (*S.*) *kudenovi* Hartmann-Schröder, 1981, and *S.* (*S.*) *sagittaria* Imajima, 1992 have been reported (Okuda, 1937; Paik, 1982, 1989; Choi and Yoon, 2016; Lee et al., 2018).

The sequences of mitochondrial cytochrome *c* oxidase subunit I (*COI*), 16S ribosomal DNA (16S rDNA), and the nuclear 18S ribosomal DNA (18S rDNA) have been used as DNA barcode markers for the molecular identification of spionid polychaetes (Radashevsky and Pankova, 2013; Sato-Okoshi and Abe, 2013). Despite the high species diversity of *Scolelepis*, its DNA barcode data is very poor.

In this paper, adult *S.* (*S.*) *daphoinos* collected from the sandy beaches is reported for the first time in South Korea. Three DNA barcode gene regions from Korean specimens of *S.* (*S.*) *daphoinos* were determined with their morphological diagnosis and photographs.

RESULTS AND DISCUSSION

The adult specimens were collected from intertidal sandy beaches using 500 μm mesh sieves. The morphological observation was carried out in live specimens anesthetized in 10% magnesium chloride solution under a stereomicroscope (SZX12; Olympus, Japan) and optical microscope (DM2500; Leica, Germany). The photographs were taken using a digital camera (Tucsen Dhyana 400DC; Fuzhou, Fujian, China) with

*To whom correspondence should be addressed
Tel: 82-32-860-7692, Fax: 82-32-874-6737
E-mail: mingisik@inha.ac.kr

eISSN 2234-8190

Table 1. Pairwise genetic distances of COI sequences (600 bp) between *Scolelepis* (*Scolelepis*) *daphoinos* Zhou, Ji and Li, 2009 and *S.* (*S.*) *squamata* (O.F. Muller, 1806)

No.	Species	Location	Voucher No.	GenBank accession No.	1	2	3	4	5	6	7	8	Data source
1	*S.* (*S.*) *daphoinos*	Mapo-ri	NIBRIV0000879441	MW509617									Present study
2		Mapo-ri	NIBRIV0000880684	MW509618	0.000								Present study
3		Mapo-ri	NIBRIV0000880685	MW509619	0.003	0.003							Present study
4		Hanun-ri	NIBRIV0000880686	MW509620	0.005	0.005	0.008						Present study
5		Hanun-ri	NIBRIV0000880687	MW509621	0.005	0.005	0.008	0.010					Present study
6		Hanun-ri	NIBRIV0000880688	MW509622	0.000	0.000	0.003	0.005	0.005				Present study
7		Seo-myeon	NIBRIV0000880689	MW509623	0.005	0.005	0.008	0.010	0.003	0.005			Present study
8		Yangkou, China	N6	GU362687	0.008	0.008	0.012	0.013	0.007	0.008	0.007		Zhou et al. (2010)
9	*S.* (*S.*) *squamata*	Canada	BIOUG＜CAN＞:BAMPOL0179	HM473680	0.264	0.264	0.269	0.264	0.261	0.264	0.264	0.266	Carr et al. (2011)

COI, cytochrome *c* oxidase subunit I.

Table 2. Pairwise genetic distances of 16S rDNA sequences (401 bp) between *Scolelepis* (*Scolelepis*) *daphoinos* Zhou, Ji and Li, 2009 and *S.* (*S.*) *eltaninae* Blake, 1983

No.	Species	Location	Voucher No.	GenBank accession No.	1	2	3	4	5	6	7	8	Data source
1	*S.* (*S.*) *daphoinos*	Mapo-ri	NIBRIV0000879441	MW494645									Present study
2		Mapo-ri	NIBRIV0000880684	MW494646	0.000								Present study
3		Mapo-ri	NIBRIV0000880685	MW494647	0.003	0.003							Present study
4		Hanun-ri	NIBRIV0000880686	MW494648	0.005	0.005	0.008						Present study
5		Hanun-ri	NIBRIV0000880687	MW494649	0.000	0.000	0.003	0.005					Present study
6		Hanun-ri	NIBRIV0000880688	MW494650	0.003	0.003	0.005	0.008	0.003				Present study
7		Seo-myeon	NIBRIV0000880689	MW494651	0.005	0.005	0.008	0.010	0.005	0.008			Present study
8		Yangkou, China	N6	GU362676	0.000	0.000	0.003	0.005	0.000	0.003	0.005		Zhou et al. (2010)
9	*S.* (*S.*) *eltaninae*	Antarctic	Polychaeta1B8_St95	KF713470	0.157	0.157	0.157	0.160	0.157	0.160	0.157	0.157	Gallego et al. (2014)

16S rDNA, 16S ribosomal DNA.

Table 3. Pairwise genetic distances 18S rDNA sequences from four *Scolelepis* (*Scolelepis*) species (1,232 bp)

No.	Species	GenBank accession No. (Voucher No.)	1	2	3	Data source
1	*S.* (*S.*) *daphoinos*	MW494652 (NIBRIV0000879441)				Present study
2	*S.* (*S.*) *laonicola*	EF569206	0.006			Vortsepneva et al. (2008)
3	*S.* (*S.*) *bonnieri*	EU084878	0.007	0.007		Vortsepneva et al. (2008)
4	*S.* (*S.*) *squamata*	AF448164	0.008	0.008	0.002	Bleidorn et al. (2003)

18S rDNA, nuclear 18S ribosomal DNA.

a capture program (Tucsen Mosaic version 15). The specimens were subsequently fixed in 4% formaldehyde solution for morphological and in 95% ethanol for molecular studies. All voucher specimens were deposited at the National Institute of Biological Resources.

Genomic DNA was extracted from palps of seven Korean *S.* (*S.*) *daphoinos* specimens using a DNeasy Blood & Tissue Kit (Qiagen, Hilden, Germany). PCR amplification was performed with primers for regions of the following three genes: LCO1490 and HCO709 for COI (Blank et al., 2008), 16Sar and 16Sbr for 16S rDNA (Kessing et al., 1989), and 18E and 18B for 18S rDNA (Mincks et al., 2009). The newly determined sequences of *S.* (*S.*) *daphoinos* were registered in the GenBank (accession Nos. MW509617–23 for COI [up to 669 bp], MW494645–51 for 16S rDNA [up to 524 bp], and MW494652 for 18S rDNA [up to 1,763 bp]). The sequences of *S.* (*S.*) *daphoinos* were aligned with other *Scolelepis* species using Geneious v.8.1.9 (Biomatters, Auckland, New Zealand). To confirm the barcode gap, the pairwise genetic distances (p-distances) were calculated by MEGA X software (Kumar et al., 2018) among *S.* (*S.*) *daphoinos* and its congeners, *S.* (*S.*) *bonnieri* (Mesnil, 1896), *S.* (*S.*) *eltaninae* Blake, 1983, *S.* (*S.*) *laonicola* (Tzetlin, 1985), and *S.* (*S.*) *squamata*, retrieved from GenBank (Bleidorn et al., 2003; Vortsepneva et al., 2008; Carr et al., 2011; Gallego et al., 2014) (Tables 1–3).

Order Spionida *sensu* Rouse and Fauchald, 1997
Family Spionidae Grube, 1850
Genus *Scolelepis* Blainville, 1828

[1]**Scolelepis* (*Scolelepis*) *daphoinos* Zhou, Ji and Li, 2009 (Fig. 1)

Scolelepis (*Scolelepis*) *squamata*: Yang and Sun, 1988: 216, fig. 97E–G.

Scolelepis (*Scolelepis*) *daphoinos* Zhou, Ji and Li, 2009: 39, fig. 1.

Material examined. Korea: 54 inds., Jeollabuk-do: Buan-gun, Byeonsan-myeon, Mapo-ri, 35°39′16.4″N, 126°29′26.0″E, 19 Sep 2020, sandy beach (NIBRIV0000879441, NIBRIV0000880684–5); 26 inds., Buan-gun, Byeonsan-myeon, Daehang-ri, 35°40′44.2″N, 126°31′29.7″E, 21 Sep 2020, sandy beach; 8 inds., Buan-gun, Byeonsan-myeon, Mapo-ri, 35°39′16.4″N, 126°29′26.0″E, 21 Sep 2020, sandy beach; 5 inds., Jeollanam-do: Sinan-gun, Jaeun-myeon, Hanun-ri, 34°55′12.0″N, 126°03′26.2″E, 2 Oct 2020, sandy beach (NIBRIV0000880686–8), 19 inds., 4 Oct 2020, sandy beach, 11 inds., 5 Oct 2020, sandy beach; 5 inds., Chungcheongnam-do: Seocheon-gun, Seo-myeon, 36°09′41.2″N, 126°31′11.1″E, 19 Oct 2020, sandy beach (NIBRIV0000880689); 5 inds., Boryeong-si, Ungcheon-eup, Gwandang-ri, 36°14′26.1″N, 126°31′49.1″E, 20 Sep 2020, sandy beach. All specimens were collected at the adult stage.

Diagnosis. Prostomium elongated, anteriorly pointed. Two pairs of black eyes arranged in a transverse row. Occipital tentacle absent. Caruncle extending posteriorly to chaetiger 1. Peristomium separated from chaetiger 1, forming lateral wings. Reddish to orange-brownish patches present in posterior part of prostomium and dorsal side of anteriormost chaetigers. Transversal ciliated bands present throughout body and as dorsal crests in posteriormost chaetigers (Fig. 1A–E). Palps reaching back to chaetigers 5–12 (Fig. 1C). Chaetiger 1 well developed with notochaetae. Branchiae present from chaetiger 2, continuing to posterior end of body. Notopodial postchaetal lamellae almost fused with branchiae, becoming free from branchiae distally (Fig. 1A–E). Neuropodial postchaetal lamellae oval, becoming low and rounded from about chaetiger 30, divided into two lobes from chaetigers 25–35. Bidentate hooded hooks present from chaetigers 25–40 in neuropodia (Fig. 1F), chaetigers 48–60 in notopodia. Ventral sabre chaetae absent. Pygidium cushion-like, without lateral anal cirri, anus opening dorsally.

Remarks. The Korean specimens of *S.* (*S.*) *daphoinos* agree well with the original description based on the following combination of characteristics: (1) the presence of reddish pigment patches on the posterior part of the prostomium and pigmentations on the dorsal side of the anteriormost chaetigers, (2) the notopodial postchaetal lamellae partially fused to branchiae, and (3) the presence of bidentate hooded hooks only (see Zhou et al., 2009). There are several intra-specific variations between Chinese and Korean specimens of *S.* (*S.*) *daphoinos*: palps usually extending posteriorly to chaetiger 3 in Chinese vs. chaetigers 5–12 in Korean specimens, eyes far from the caruncle in Chinese (illustrated in the original description) vs. very close to caruncle in Korean specimens, and neuropodial hooded hooks present from chaetiger 32 in Chinese vs. chaetiger 25 in Korean specimens. In Korean waters, *S.* (*S.*) *daphoinos* is similar to *S.* (*S.*) *kudenovi sensu* Choi and Yoon, 2016 in having the bidentate hooded hooks only and the caruncle attached to dorsum, but differs by the presence of distinct pigmentations in anteriormost body instead of indistinct in formalin fixed materials (Choi and Yoon, 2016).

The pairwise genetic distances among Chinese and Korean specimens were 0.7–1.3% in COI and 0.0–0.05% in 16S rDNA, whereas inter-specific genetic distances among *S.*

Korean name: [1]*붉은넓적얼굴갯지렁이

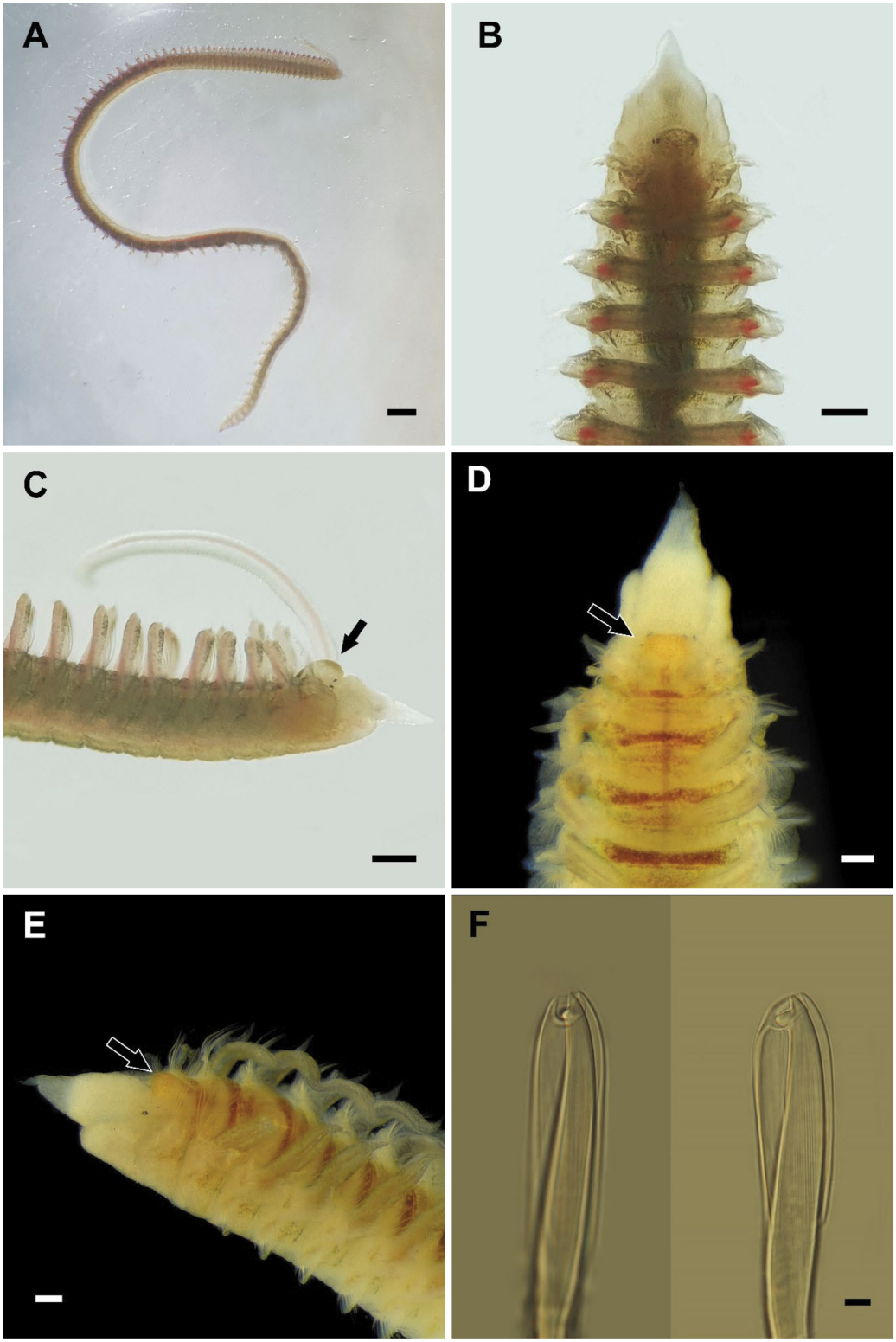

Fig. 1. *Scolelepis* (*Scolelepis*) *daphoinos* Zhou, Ji and Li, 2009. A–C, Alive specimen in seawater (NIBRIV0000879441): A, Whole body; B, Dorsal view of the anterior end; C, Lateral view of the anterior end; D–F, Formalin fixed specimen: D, Dorsal view of the anterior end; E, Lateral view of the anterior end; F, Front (left) and lateral (right) views of the bidentate neuropodial hooded hooks from the posterior chaetiger. Arrows indicating reddish pigment patches on posterior part of prostomium. Scale bars: A = 1.0 mm, B, C = 0.2 mm, D, E = 0.1 mm, F = 10.0 μm.

(*S*.) *daphoinos* and its congeners were 26.1–26.9% in COI and 15.7–16.0% in 16S rDNA (Tables 1, 2). No intra-specific variation was detected among Korean specimens in 18S rDNA. On the contrary, the inter-specific genetic distances between *S*. (*S*.) *daphoinos* and other *Scolelepis* species available in GenBank was 0.6–0.8% in 18S rDNA (Tables 1–3).

Distribution. China (type locality), Korea.

ORCID

Geon Hyeok Lee: https://orcid.org/0000-0001-7517-3086
Gi-Sik Min: https://orcid.org/0000-0003-2739-3978

CONFLICTS OF INTEREST

Gi-Sik Min, a contributing editor of the Animal Systematics, Evolution and Diversity, was not involved in the editorial evaluation or decision to publish this article. The remaining author has declared no conflicts of interest.

ACKNOWLEDGMENTS

This study was supported by the research funds from the National Institute of Biological Resources (NIBR), funded by the Ministry of Environment (MOE) of the Republic of Korea (NIBR 202002204).

REFERENCES

Blank M, Laine A, Jürss K, Bastrop R, 2008. Molecular identification key based on PCR/RFLP for three polychaete sibling species of the genus *Marenzelleria*, and the species' current distribution in the Baltic Sea. Helgoland Marine Research, 62:129-141. https://doi.org/10.1007/s10152-007-0081-8

Bleidorn C, Vogt L, Bartolomaeus T, 2003. A contribution to sedentary polychaete phylogeny using 18S rRNA sequence data. Journal of Zoological Systematics and Evolutionary Research, 41:186-195. https://doi.org/10.1046/j.1439-0469.2003.00212.x

Carr CM, Hardy SM, Brown TM, Macdonald TA, Hebert PDN, 2011. A tri-oceanic perspective: DNA barcoding reveals geographic structure and cryptic diversity in Canadian polychaetes. PLoS ONE, 6:e22232. https://doi.org/10.1371/journal.pone.0022232

Choi HK, Yoon SM, 2016. *Scolelepis* (*Scolelepis*) *kudenovi* (Polychaeta: Spionidae) new to Korea. Journal of Species Research, 5:355-358. https://doi.org/10.12651/JSR.2016.5.3.355

Gallego R, Lavery S, Sewell MA, 2014. The meroplankton community of the oceanic Ross Sea during late summer. Antarctic Science, 26:345-360. https://doi.org/10.1017/S0954102013000795

Kessing B, Croom H, Martin A, McIntosh C, Owen McMillian W, Palumbi S, 1989. The simple fool's guide to PCR. Department of Zoology, University of Hawaii, Honolulu, HI, pp. 1-47.

Kumar S, Stecher G, Li M, Knyaz C, Tamura K, 2018. MEGA X: Molecular evolutionary genetics analysis across computing platforms. Molecular Biology and Evolution, 35:1547-1549. https://doi.org/10.1093/molbev/msy096

Lee GH, Choi HK, Yoon SM, 2018. Two new records of spionid polychaetes (Polychaeta: Spionidae) in Korean fauna. Animal Systematics, Evolution and Diversity, 34:152-158. https://doi.org/10.5635/ASED.2018.34.3.152

Mincks SL, Dyal PL, Paterson GLJ, Smith CR, Glover AG, 2009. A new species of *Aurospio* (Polychaeta, Spionidae) from the Antarctic shelf, with analysis of its ecology, reproductive biology and evolutionary history. Marine Ecology, 30:181-197. https://doi.org/10.1111/j.1439-0485.2008.00265.x

Okuda S, 1937. Spioniform polychaetes from Japan. Journal of the Faculty of Science Hokkaido Imperial University Series 6. Zoology, 5:217-254. http://hdl.handle.net/2115/27002

Paik EI, 1982. Taxonomic studies on polychaetous annelids in Korea. Research Bulletin of the Hyosung Women's University, 24:745-913.

Paik EI, 1989. Illustrated encyclopedia of fauna and flora of Korea. Vol. 31. Ministry of Education Press, Seoul, pp. 452-468.

Radashevsky VI, Pankova VV, 2013. Shell-boring versus tube-dwelling: is the mode of life fixed or flexible? Two cases in spionid polychaetes (Annelida, Spionidae). Marine Biology, 160:1619-1624. https://doi.org/10.1007/s00227-013-2214-8

Sato-Okoshi W, Abe H, 2013. Morphology and molecular analysis of the 18S rRNA gene of oyster shell borers, *Polydora* species (Polychaeta: Spionidae), from Japan and Australia. Journal of the Marine Biological Association of the United Kingdom, 93:1279-1286. https://doi.org/10.1017/S002531541200152X

Sikorski AV, Pavlova LV, 2015. New species of *Scolelepis* (Polychaeta, Spionidae) from the Norwegian coast and Barents Sea with a brief review of the genus. Fauna Norvegica, 35:9-19. https://doi.org/10.5324/fn.v35i0.1666

Surugiu V, 2016. On the taxonomic status of the European *Scolelepis* (*Scolelepis*) *squamata* (Polychaeta: Spionidae), with description of a new species from southern Europe. Zootaxa, 4161:151-176. https://doi.org/10.11646/zootaxa.4161.2.1

Vortsepneva E, Tzetlin A, Purschke G, Mugue N, Hass-Cordes E, Zhadan A, 2008. The parasitic polychaete known as *Asetocalamyzas laonicola* (Calamyzidae) is in fact the dwarf male of the spionid *Scolelepis laonicola* (comb. nov.).

Invertebrate Biology, 127:403-416. https://doi.org/10.1111/j.1744-7410.2008.00137.x

Yang DJ, Sun RP, 1988. Polychaetous annelids commonly seen from the Chinese waters. China Agriculture Press, Beijing, pp. 1-352.

Zhou H, Zhang Z, Chen H, Sun R, Wang H, Guo L, Pan H, 2010. Integrating a DNA barcoding project with an ecological survey: a case study on temperate intertidal polychaete communities in Qingdao, China. Chinese Journal of Oceanology and Limnology, 28:899-910. https://doi.org/10.1007/s00343-010-9131-1

Zhou J, Ji W, Li X, 2009. A new species of *Scolelepis* (Polychaeta: Spionidae) from sandy beaches in China, with a review of Chinese *Scolelepis* species. Zootaxa, 2236:37-49. https://doi.org/10.11646/zootaxa.2236.1.3

Received February 9, 2021
Revised June 24, 2021
Accepted July 1, 2021