First use of molecular evidence to match sexes in the Monstrilloida (Crustacea: Copepoda), and taxonomic implications of the newly recognized and described, partly *Maemonstrilla*-like females of *Monstrillopsis longilobata* Lee, Kim & Chang, 2016 (#26448)

First submission

Editor guidance

Please submit by 19 Apr 2018 for the benefit of the authors (and your \$200 publishing discount).



Structure and Criteria

Please read the 'Structure and Criteria' page for general guidance.



Custom checks

Make sure you include the custom checks shown below, in your review.



Raw data check

Review the raw data. Download from the materials page.



Image check

Check that figures and images have not been inappropriately manipulated.

Privacy reminder: If uploading an annotated PDF, remove identifiable information to remain anonymous.

Files

Download and review all files from the <u>materials page</u>.

○ Custom checks

14 Figure file(s)

4 Table file(s)

DNA data checks

- Have you checked the authors <u>data deposition statement?</u>
- Can you access the deposited data?
- Has the data been deposited correctly?
- Is the deposition information noted in the manuscript?

Structure your review

The review form is divided into 5 sections.

Please consider these when composing your review:

- 1. BASIC REPORTING
- 2. EXPERIMENTAL DESIGN
- 3. VALIDITY OF THE FINDINGS
- 4. General comments
- 5. Confidential notes to the editor
- You can also annotate this PDF and upload it as part of your review

When ready submit online.

Editorial Criteria

Use these criteria points to structure your review. The full detailed editorial criteria is on your guidance page.

BASIC REPORTING

- Clear, unambiguous, professional English language used throughout.
- Intro & background to show context.
 Literature well referenced & relevant.
- Structure conforms to <u>PeerJ standards</u>, discipline norm, or improved for clarity.
- Figures are relevant, high quality, well labelled & described.
- Raw data supplied (see <u>PeerJ policy</u>).

EXPERIMENTAL DESIGN

- Original primary research within Scope of the journal.
- Research question well defined, relevant & meaningful. It is stated how the research fills an identified knowledge gap.
- Rigorous investigation performed to a high technical & ethical standard.
- Methods described with sufficient detail & information to replicate.

VALIDITY OF THE FINDINGS

- Impact and novelty not assessed.
 Negative/inconclusive results accepted.
 Meaningful replication encouraged where rationale & benefit to literature is clearly stated.
- Data is robust, statistically sound, & controlled.
- Conclusions are well stated, linked to original research question & limited to supporting results.
- Speculation is welcome, but should be identified as such.

Standout reviewing tips



The best reviewers use these techniques

	p

Support criticisms with evidence from the text or from other sources

Give specific suggestions on how to improve the manuscript

Comment on language and grammar issues

Organize by importance of the issues, and number your points

Please provide constructive criticism, and avoid personal opinions

Comment on strengths (as well as weaknesses) of the manuscript

Example

Smith et al (J of Methodology, 2005, V3, pp 123) have shown that the analysis you use in Lines 241-250 is not the most appropriate for this situation. Please explain why you used this method.

Your introduction needs more detail. I suggest that you improve the description at lines 57-86 to provide more justification for your study (specifically, you should expand upon the knowledge gap being filled).

The English language should be improved to ensure that an international audience can clearly understand your text. Some examples where the language could be improved include lines 23, 77, 121, 128 - the current phrasing makes comprehension difficult.

- 1. Your most important issue
- 2. The next most important item
- 3. ...
- 4. The least important points

I thank you for providing the raw data, however your supplemental files need more descriptive metadata identifiers to be useful to future readers. Although your results are compelling, the data analysis should be improved in the following ways: AA, BB, CC

I commend the authors for their extensive data set, compiled over many years of detailed fieldwork. In addition, the manuscript is clearly written in professional, unambiguous language. If there is a weakness, it is in the statistical analysis (as I have noted above) which should be improved upon before Acceptance.



First use of molecular evidence to match sexes in the Monstrilloida (Crustacea: Copepoda), and taxonomic implications of the newly recognized and described, partly *Maemonstrilla*-like females of *Monstrillopsis longilobata* Lee, Kim & Chang, 2016

Donggu Jeon 1 , Donghyun Lim 2 , Wonchoel Lee $^{\text{Corresp.}}$ 1 , Ho Young Soh $^{\text{Corresp.}}$ 3

Corresponding Authors: Wonchoel Lee, Ho Young Soh Email address: wlee@hanyang.ac.kr, hysoh@chonnam.ac.kr

Two forms of monstrilloid copepod, one represented by males, the other by females, were dominant among the monstrilloids collected while sampling zooplankton with a light trap in southern coastal waters of Korea. Morphological examination revealed that the males are conspecific with the previously reported and rather specialized Korean species Monstrillopsis longilobata Lee, Kim & Chang, 2016, hitherto known only from males that have extremely long genital lappets. The females also show several diagnostic features of Monstrillopsis, such as prominent eyes, bilobed fifth legs with the inner lobe unarmed and reduced, and four urosomal somites. In addition, though, these females are extraordinary among all Monstrilloida in that their ovigerous spines are directed ventrally, not posteriorly as in most species or anteriorly as in those assigned to Maemonstrilla. Genetic divergence analyses based on partial mtCOI, complete ITS1-5.8S-ITS2, and partial 28S rRNA revealed little or no genetic divergence between the present males and females, thus demonstrating that they are mutually conspecific. The present report 1) provides the first morphological description of female Monstrillopsis longilobata with the proposal of a revised nomenclature for antennular setal armament; 2) presents the molecular evidence for conspecificity of the males and females; and 3) lists several morphological characteristics that are sexually dimorphic in this species, and thus likely also in other monstrilloids. Matters bearing on the validity of the genera Haemocera, Monstrillopsis, and Maemonstrilla are discussed.

¹ Department of Life Science, College of Natural Sciences, Hanyang University, 222 Wangsimni-ro, Seongdong-gu, Seoul 04763, South Korea

² Jeju Branch Office, Korea Fisheries Resources Agency (FIRA), 23, Ongpo 7-gil, Hallim-eup, Jeju-si, Jeju-do 63012, South Korea

Faculty of Marine Technology, College of Fisheries and Ocean Science, Chonnam National University, 50 Daehak-ro, Yeosu-si, Jeollanam-do 59626, South Korea



First use of molecular evidence to match sexes in the Monstrilloida (Crustacea: Copepoda), and taxonomic implications of the newly recognized and described, partly *Maemonstrilla*-like 2 females of *Monstrillopsis longilobata* Lee, Kim & Chang, 2016 3 4 Donggu Jeon¹, Donghyun Lim², Wonchoel Lee¹ and Ho Young Soh³ 5 6 ¹ Department of Life Science, College of Natural Sciences, Hanyang University, 222 7 Wangsimni-ro, Seongdong-gu, Seoul 04763, South Korea 8 ² Jeju Branch Office, Korea Fisheries Resources Agency (FIRA), 23, Ongpo 7-gil, Hallim-eup, 9 Jeju-si, Jeju-do 63012, South Korea 10 ³ Faculty of Marine Technology, College of Fisheries and Ocean Science, Chonnam National 11 12 University, 50 Daehak-ro, Yeosu-si, Jeollanam-do 59626, South Korea 13 14 Co-corresponding authors: Wonchoel Lee¹ 15 Ho Young Soh³ 16 17

Email addresses: Wonchoel Lee, wlee@hanyang.ac.kr; Ho Young Soh, hysoh@chonnam.ac.kr





20

21

22

23

24

25

26

27

28

29

30

31

32

33

34

35

36

37

ABSTRACT



Two forms of monstrilloid copepod, one represented by males, the other by females, were dominant among the monstrilloids collected while sampling zooplankton with a light trap in southern coastal waters of Korea. Morphological examination revealed that the males are conspecific with the previously reported and rather specialized Korean species *Monstrillopsis* longilobata Lee, Kim & Chang, 2016, hitherto known only from males that have extremely long genital lappets. The females also show several diagnostic features of *Monstrillopsis*, such as prominent eyes, bilobed fifth legs with the inner lobe unarmed and reduced, and four urosomal somites. In addition, though, these females are extraordinary among all Monstrilloida in that their ovigerous spines are directed ventrally, not posteriorly as in most species or anteriorly as in those assigned to Maemonstrilla. Genetic divergence analyses based on partial mtCOI, complete ITS1-5.8S-ITS2, and partial 28S rRNA revealed little or no genetic divergence between the present males and females, thus demonstrating that they are mutually conspecific. The present report 1) provides the first morphological description of female *Monstrillopsis longilobata* with the proposal of a revised nomenclature for antennular setal armament; 2) presents the molecular evidence for conspecificity of the males and females; and 3) lists several morphological characteristics that are sexually dimorphic in this species, and thus likely also in other monstrilloids. Matters bearing on the validity of the genera *Haemocera*, *Monstrillopsis*, and Maemonstrilla are discussed.

38

39

40



Key Words: COI primer, Korea, mitochondrial and nuclear genes, nomenclature for antennular setation, sexual dimorphism, taxonomy.

41



64

INTRODUCTION

The order Monstrilloida Sars, 1901 is distinctive among copepods both morphologically and 43 44 ecologically. Monstrilloids have a protelean life history that includes an endoparasitic juvenile phase and a planktonic adult phase. The early infectious nauplii are free-living but soon infect 45 several kinds of marine invertebrates such as polychaete worms, gastropod and bivalve molluscs, 46 47 and sponges (Boxshall & Halsey, 2004; Huys et al., 2007; Suárez-Morales et al., 2014). Details of the endoparasitic stages are still unclear, but they probably undergo several copepodite instar 48 49 molts during the process of development (Malaquin, 1901; Raibaut, 1985; Suárez-Morales et al., 2014). The free-swimming adults are non-feeding, with no oral appendages or second antennae, 50 and seem to be only reproductive forms. These reductions have the ffect of making most 51 monstrilloid species morphologically similar and, together with the paucity of knowledge about 52 their biology, frequently cause problems in species differentiation and identification. 53 According to Suárez-Morales (2011), about 120 species were then known in the family 54 55 Monstrillidae Dana, 1849. Only 21 of them (18% of the total) had been reported from both sexes 56 whereas 95 species (82%) were known only from a single sex. Currently about 160 species have been recognized on the strength of a large body of new taxonomic work, especially studies like 57 58 those of Suárez-Morales, Bello-Smith & Palma (2006), Grygier & Ohtsuka (2008), and Suárez-Morales & McKinnon (2014, 2016). These copepods are currently classified into six supposedly 59 60 valid genera: Monstrilla Dana, 1849, Cymbasoma Thompson, 1888, Monstrillopsis Sars, 1921, 61 Maemonstrilla Grygier & Ohtsuka, 2008, Australomonstrillopsis Suárez-Morales & McKinnon, 62 2014, and Caromiobenella Jeon, Lee & Soh, 2018. 63 Despite recent taxonomic advancements, the species newly reported during the years

2011 to 2017 were still mostly each based on a single sex. Of the 39 newly described species in



66

67

68

69

70

71

72

73

74

75

76

77

78

79

80

81

82

83

84

85

86

87

four genera reported during that period, only four are known from both sexes (Razouls et al., 2005-2017; Walter & Boxshall, 2017). In the extreme case of *Maemonstrilla*, all 11 species are known only from females. To shed more light on monstrilloid taxonomy, the confirmation of sexual counterparts and the provision of new morphological criteria for genus and species recognition are still needed. Matching the two sexes seems not to be an easy task. One main obstacle is the high degree of sexual dimorphism (Suárez-Morales, 2007; Suárez-Morales, Ramírez & Derisio, 2008), which makes some of the traditional and conventional methods, especially those dependent on morphological characters, unreliable. Methods based on cooccurrence of both sexes and their utilization of a common host may also fail to guarantee perfect pairing (Grygier & Ohtsuka, 2008; Suárez-Morales, 2011; also see Discussion). The use of molecular markers is likely to be far the most effective and definitive method for matching male monstrilloids to their corresponding females. With the great advances in molecular technology over the past several decades, much nucleotide sequence data has become available and also been practically applied to various purposes such as DNA-based taxonomy and DNA barcoding (Vogler & Monaghan, 2007). DNA-based taxonomy, which typically involves species circumscription and delineation, has been widely used in various taxa, and many gene markers have been developed and applied accordingly (Vogler & Monaghan, 2007; Bucklin, Steinke & Blanco-Bercial, 2011). The application of molecular tools to monstrilloid research has been rare, and only 63 sequence search results based on the keyword "Monstrilloida" could be obtained from GenBank (accessed on 24 July 2017). A few previous studies such as Huys et al. (2007) and Baek et al. (2016) have utilized genetic information obtained from monstrilloids, but only at the level of the order; genus and species relations remain uncertain.



89

90

91

92

93

94

95

96

97

98

99

100

101

102

103

104

In this new study, we demonstrate the conspecificity of individuals by using both morphological and molecular evidence. The two sexes of *Monstrillopsis longilobata* Lee, Kim & Chang, 2016 show extreme sexual dimorphism in their main features, but microcharacters such as pore patterns display potential homologies. To confirm the validity of such morphological matching of the sexes, sequences of three gene markers, viz., the region coding for partial mitochondrial cytochrome c oxidase subunit I (mtCOI), the nuclear multigene region consisting of partial 18S ribosomal RNA (rRNA)-Internal Transcribed Spacer 1 (ITS1)-5.8S rRNA-ITS2partial 28S rRNA (called ITS1-5.8S-ITS2 hereinafter), and an additional region of partial 28S rRNA were used for analyses of genetic divergence. Mitochondrial DNA sequences, known to characterize a fast-evolving gene (Blanco-Bercial, Bradford-Grieve & Bucklin, 2011; Willett, 2012), are the most frequently used sequences for genetic and phylogenetic investigations. In contrast, nuclear genes with a relatively small number of genetic mutations have generally been judged inadequate for species delimitation. Machida & Tsuda (2010), however, noted various errors that might arise from analyses based only on mitochondrial genes, problems that could be caused by the existence of nuclear mitochondrial pseudogenes, the occurrence of mitochondrial introgression, and the pattern of decent via maternal inheritance. We therefore consider it worthwhile to include the results from nuclear gene sequences, for the sake of any support they may provide for the current results based on mitochondrial genes.

106

107

108

105

MATERIALS AND METHODS

- Sample collection and treatment for morphological analyses
- A hand-made light trap was used, consisting of a 400 mm long PVC pipe with a mouth diameter
- of 100 mm. A conical funnel was attached within one end, and the other end was completely

112

113

114

115

116

117

118

119

120

121

122

123

124

125

126

127

128

129

130

131

132

133

closed with a cap equipped a light-emitting diode (LED) flashlight of 110 lumens (Kovea, Incheon, Korea) as a light source. After use, the trap's contents were filtered through a sieve of 63 µm mesh and the retained material, including copepods, was immediately washed several times with 99.5% ethanol, which was replaced with newly prepared 99.5% ethanol upon arrival at the laboratory. All samples were stored in a refrigerator at 4°C and monstrilloids were sorted out later under a SMZ645 stereomicroscope (Nikon, Tokyo, Japan). Specimens of *Monstrillopsis longilobata* were first examined as whole mounts on depression slides using 0.25–0.50% sodium phosphate tribasic dodecahydrate (Na₃PO₄·12H₂O) (Daejung, Siheung, Korea) solution as the slide mountant (Van Cleave & Ross, 1947; Huys & Boxshall, 1991) in order to restore their original shape. Drawings were made using an Eclipse 80i compound microscope (Nikon) with differential interference contrast optics and a drawing tube. After the observation of habitus, a specimen of each sex (NIBRIV0000812791 for the male, and NIBRIV0000812792 for the female) was dissected and each part was mounted on a slide glass with lactophenol for further microscopic observation. All measurements were done using an AxioVision LE64 software (AxioVs40x64v 4.9.1.0; Carl Zeiss, Oberkochen, Germany). For scanning electron microscopy (SEM), adult specimens were dehydrated with absolute ethanol for 15 min. The usual procedure of using a graded ethanol series was skipped since the specimens had been preserved initially in 99.5% ethanol. Sample drying was done using hexamethyldisilazane, HMDS, (CH₃)₃SiNHSi(CH₃)₃ (Samchun, Pyeongtaek, Korea) (Braet, De Zanger & Wisse, 1997; Shively & Miller, 2009). Each specimen dehydrated in ethanol was immersed in 1–2 ml HMDS in a 24-well plate, and the plate was placed in a fume hood until the HMDS had totally evaporated. Dried samples were mounted on aluminum SEM stubs and observations were carried out with an S-3000N scanning electron microscope (Hitachi,

Tokyo, Japan) operating at an accelerating voltage of 20.0 kV.

135

136

137

138

139

140

141

142

143

144

145

146

147

148

149

150

151

152

153

154

155

156

134

Description of morphological characters

Total body length was measured from the anteriormost part of the cephalothorax to the posterior margin of the anal somite. The length of the caudal rami was measured from the inner proximal articulation of a ramus to its most distal point, and width of the rami was measured perpendicular to the length at the level of the insertion of the outermost caudal seta. The terminology for body segmentation used by Grygier & Ohtsuka (2008) was adopted herein.

To describe the antennular setation patterns, the terms and definitions proposed by Grygier & Ohtsuka (1995) and Huys et al. (2007) were mainly used. Distally, however, we found it necessary to propose and define some new descriptive terms in order to help standardize the different terminologies of the two earlier systems. Our schematic diagram of monstandial antennular setation is mainly based on eight species of Korean monstrilloids (Fig. 1, Table S1). The highly branched setae "b₁₋₃" and the slightly branched seta "b₅" of Grygier & Ohtsuka (1995), which correspond to four of the 3-dimensionally branched setae "A–E" of Huys et al. (2007), are here relabeled with upper-case letters, the most dorsal seta as "A", the two adjacent outer lateral setae as "B" and "C", and the most distal seta as "D". These elements are unbranched in some monstrilloid species, but are still distinguishable by their greater length and thickness from the simple setae "b₄" and "b₆" of Grygier & Ohtsuka (1995), which correspond to the unmodified setal elements "3" and "4" of Huys et al. (2007). These simple setae are labeled herein with lower-case letters, as proximal "a" and distal "b". The apical spines "6_{1,2}" and inner lateral spine "5" of Grygier & Ohtsuka, (1995), which correspond to the unmodified apical spiniform elements "1" and "2" and one inner lateral element "5" of Huys et al., (2007), are



labeled herein as "5_{1–3}". The apical aesthetasc, called "6aes" by Grygier & Ohtsuka (1995), is here relabeled as "5aes". Three long, biserially plumose, strap-like setae called "Vd, Vm and Vv" by Grygier & Ohtsuka (1995) on account of their dorsal, medial, and ventral positions, respectively, are all present in females, but in most males the former two elements are absent and only "Vv" remains, corresponding to setal element "6" of Huys *et al.* (2007). The more proximal inner minute spiniform element "7" of Huys *et al.* (2007) is relabeled as "5a" herein. The names of the setal elements on the first to fourth antennular segments generally follow Grygier & Ohtsuka (1995) with the addition of "4a" for a minute spiniform element that has not been mentioned in previous studies. The letter "a" used in the names of the elements "4a" and "5a" means "accessory", since their consistency of appearance in both males and females and/or in other earlier studied monstrilloids is doubtful.

<Figure 1>

Preparation for molecular analysis

Genomic DNA extraction using Chelex® 100 chelating resin (molecular biology grade, 200–400 mesh, sodium form; Bio-Rad, Hercules, CA, USA) was done mainly as in earlier studies (Estoup *et al.*, 1996; Casquet, Thebaud & Gillespie, 2012), but with the final volume reduced to 100–150 μl in order to increase the DNA concentration.

Two partial gene sequences, those of mtCOI and 28S rRNA, and the complete gene sequence of ITS1–5.8S–ITS2 were amplified using AccuPower® HotStart PCR PreMix kit (Bioneer, Daejeon, Korea) and thermal cycling was performed using Matercycler® (Eppendorf, Hamburg, Germany). 20 µl of total reaction volume per reaction tube was prepared by adding 2



 μ l of DNA template and 1 μ l each of forward and reverse primers to 16 μ l of distilled water. The primers and the thermal cycling profile for each gene amplification are given in Table 1.

183 < *Table 1*>

Amplification of the mtCOI gene by Polymerase Chain Reaction (PCR) was initially attempted using the so-called "universal primers" LCO1490 and HCO2198 (Folmer *et al.*, 1994), but the amplification success rate was generally low. Jeon, Lee & Soh (2018) were able to determine 24 mtCOI gene sequences from 41 monstrilloid individuals, a success rate of just 58.5%. The rate was especially low for *Caromiobenella castorea* Jeon, Lee & Soh, 2018 (2 of 5 individuals; 40%), *Monstrilla grandis* Giesbrecht, 1891 (0 of 9; 0%), and *Monstrillopsis longilobata* (2 of 6; 33%), although the other six studied species had much higher success rates (Jeon, Lee & Soh, 2018: S1 Table). For successful PCR in the present study, the internal forward primer XcoiF was newly designed on the basis of the alignment of previously submitted monstrilloid mtCOI gene sequences (Table S2, Fig. S1). Further amplification using the new forward primer and HCO2198 worked properly and resulted in, as expected, a little shorter sequence length in gel electrophoresis, whereas PCR using the universal primers consistently failed (Fig. S2).

The PCR products were run on a 1% Tris acetate-EDTA (TAE) agarose gel for 20 min at a voltage of 100 V with a 100 base pair (bp) DNA ladder (Bioneer). The PCR products with positive results were sent to Macrogen (Seoul, Korea) for purification and DNA sequencing.

Sequencing reactions were performed in a DNA Engine Tetrad 2 Peltier Thermal Cycler (Bio-Rad) using the ABI BigDye® Terminator v3.1 Cycle Sequencing Kit (Applied Biosystems,



204

205

206

207

208

209

210

211

212

213

214

215

216

217

218

219

220

221

222

223

224

225

Foster City, CA, USA) following the protocols supplied by the manufacturer. Single-pass sequencing was performed on each template using the corresponding primer. The fluorescentlabeled fragments were purified by the method that Applied Biosystems recommends as it removes the unincorporated terminators and dNTPs. For electrophoresis, the samples were injected into an ABI 3730xl DNA Analyzer (Applied Biosystems). The sequencing chromatograms were read using FinchTV ver 1.4.0 software. Inspected sequences were taken to MEGA7 (ver 7.0.21) and then the both forward and reverse primer sites were excluded. The forward and reverse strands were aligned by ClustalW embedded in MEGA7. Multigene sequences consisting of complete ITS1-5.8S-ITS2 with partial 18S rRNA at the 5'-end and partial 28S rRNA at the 3'-end were compared as a whole, without specific gene region delimitation, since pin-pointing of each gene position by transcript analysis was not attempted. The 5.8S rRNA gene regions in the multigene sequences were, however, estimated by comparing with other complete 5.8S rRNA sequences of copepods from GenBank: Tigriopus californicus (Baker, 1912) (AY599492), T. japonicus Mori, 1938 (EU057580), Cletocamptus deitersi (Richard, 1897) (AF315025), Ergasilus parasiluri (Yamaguti, 1936) (AY297732), Oithona similis Claus, 1866 (KF153700), Cyclops kolensis Lilljeborg, 1901 (KF153689), and Diacyclops bicuspidatus (Claus, 1857) (KF153697). Doing so eventually allowed the separation of three gene regions: partial 18S rRNA-complete ITS1, 5.8S rRNA, and complete ITS2-partial 28S rRNA. Nucleotide sequences from three gene regions were newly obtained from six specimens to demonstrate conspecificity between the females and males. Previously submitted nucleotide sequences of Monstrillopsis longilobata for the mtCOI and 28S rRNA genes were also retrieved from GenBank and included in the analysis. In all, eight sequences of mtCOI, nine of ITS1-





226	5.8S-ITS2, and 11 of 28S rRNA were obtained. All gene sequences used for the molecular
227	analysis are listed on Table 2 with accession numbers.
228	
229	<table 2=""></table>
230	
231	Genus-name abbreviations
232	Because two of the generic names that appear frequently in this paper, Monstrillopsis and
233	Maemonstrilla, both start with the same letter "M", two-letter abbreviations are used throughout
234	to refer to them unambiguously, Mn. for Monstrillopsis and Ma. for Maemonstrilla. Another
235	generic name, Monstrilla, which also starts with "M", but it appears only once in the Discussion
236	and is never abbreviated.
237	
238	SYSTEMATICS
239	Order Monstrilloida Sars, 1901
240	Family Monstrillidae Dana, 1849
241	Genus Monstrillopsis Sars, 1921
242	Monstrillopsis longilobata Lee, Kim & Chang, 2016
243	(Figs. 2–12)
244	
245	Sampling locality. Soho-dong (34°44'50.82"N, 127°39'30.14"E), Yeosu-si, Jeollanam-
246	do, Korea. (English equivalents of political divisions in Korea: dong = village; si = city; do =
247	province)
248	



Material examined. Specimens were collected by using a light trap from 18:31 to 22:59 h at the sampling locality on 21 April 2016. The depth there was about 3 m, and the water temperature cooled from 16.9°C to 16.1°C while the trap was deployed. The female and male specimens used for drawings and measurements are deposited in the National Institute of Biological Resources (NIBR), Incheon, Korea with the following accession numbers: female dissected and mounted on eight slides in lactophenol (NIBRIV0000812792); six intact females in 99.5% ethanol vial (NIBRIV0000812794); sub-mature female in 99.5% ethanol vial (NIBRIV0000812795); male dissected and mounted on eight slides in lactophenol (NIBRIV0000812791); and six intact males in 99.5% ethanol vial (NIBRIV0000812793). Three additional specimens for each sex were used for SEM and deposited in the Laboratory of Zooplankton Diversity, Chonnam National Expressity, Korea. Six additional specimens (three females and three males) were sacrificed for molecular analysis.



Diagnosis (Female). Total body length 1.48–1.75 mm (mean 1.64; N = 6). Length ratio of cephalothorax, metasome, and urosome 47.9 (range 45.9–49.6): 30.5 (28.1–33.5): 21.6 (19.8–24.6) in lateral view. Metasomal somites brown or dark red except for semi-transparent, bulbous cephalothorax (latter often green due to internal egg mass). Urosomal somites more lightly pigmented than metasomal somites. Anterior dorsum of cephalothorax with narrow band of transverse striations. Two ventral pores between antennular bases. Two prominent scars situated posterior to antennular bases, followed by pair of pores. Faint, incompletely closed reticulation present on part of cephalothorax. Oral papilla moderately developed, located about 21.4% (17.6–24.3%) of way along ventral side of cephalothorax. Two lateral eyes and one ventral eye well-developed and pigmented. Lateral eyes generally bean-shaped in dorsal view,



273

274

275

276

277

278

279

280

281

282

283

284

285

286

287

288

289

0.14 mm long, 0.08 mm wide. Ventral eye round, 0.14 mm in diameter. Antennules 2segmented; second segment formed by incomplete fusion of four subsidiary segments. Antennules 17.3% (16.2–18.7%) as long as total body length. Length ratio of first and second antennular segments 26.8 (25.3–28.6): 73.2 (71.4–74.7). Intercoxal sclerites of leg pairs 2–4 wide and low whereas these of leg pair 1 relatively narrow and high, resulting in widely separated legs 2–4, closely located legs 1 (Fig. 2A, D). Ratio of distal width to height of intercoxal sclerites increasing to posterior pairs. Legs of pair 5 also widely separated, bilobed with exopodal lobe carrying three terminal setae, endopodal lobe unarmed, reduced. Urosomal somites with conspicuous longitudinal striations. Genital somite almost completely fused with succeeding somite, forming genital compound somite with prominent dorsal suture; anteroventral part bearing pair of ventrally directed ovigerous spines (Fig. 2B, C) 23.0% (21.0– 25.3%) as long as total body length. Egg masses carried by ovigerous spines laterally compressed, oval in lateral view, reaching posterior face of first swimming legs (Fig. 2C). Caudal rami subtriangular in dorsal view, each bearing four caudal setae: outer lateral seta arising from midlength of outer margin, two terminal setae, and one remarkably short ventral seta. Inner terminal seta longest, lateral and outer terminal setae subequal in length. Ventral seta reaching only slightly beyond caudal ramus bearing it and hard to distinguish under low magnification.

290 < Figure 2>

291

292

293

294



Diagnosis (Male). Total body length 1.12–1.28 mm (mean 1.21; N = 7). Length ratio of cephalothorax, metasome, and urosome 45.3 (range 44.5–46.8) : 35.2 (32.8–37.0) : 19.5 (17.1–20.7) in lateral view. Whole body light brown. Cephalothorax generally cylindrical, slightly





296

297

298

299

300

301

302

303

304

305

306

307

308

309

310

311

312

313

constricted from midlength to anterior part of incorporated first pediger. Dorsal transverse striations situated halfway back from anterior end of cephalothorax, reaching to dorsolateral half. Two pores between antennular bases. Two prominent scars situated posterior to antennular bases. followed by pair of pores. Ventral surface from scars to oral papilla transversally striated. Ventral half of cephalothorax bearing narrow, faint band of striations. Oral papilla located anteriorly on ventral surface of cephalothorax, 29.3% (28.1–30.9%) of way back from anterior end. Two lateral eyes and one ventral eye well-developed and pigmented. Lateral eyes generally bean-shaped in dorsal view, 0.11 mm long. Ventral eye round, 0.11 mm in diameter, slightly larger than lateral eyes. Antennules 5-segmented with segments 2 and 3 partly fused. Minute spiniform elements 4a and 5a present on antennular segments 4 and 5, respectively. Fifth antennular segment modified with inner hyaline bump and elongated apical spine 5₂. Antennules 40.0% (38.3–42.9%) as long as body length. Length ratio of antennular segments from proximal to distal 13.9 (12.4–14.8): 20.1 (19.6–21.0): 9.0 (8.1–9.8): 22.4 (21.7–23.2): 34.6 (33.6–35.3). Intercoxal sclerites of leg pairs 1–4 narrow and long, rectangular. Leg pair 5 absent. Fourth free pedigerous somite with longitudinal striations on lateral side. Genital somite bearing robust genital shaft 0.06 mm long and two extremely elongated genital lappets these 0.15 mm long, approximately reaching or slightly exceeding posterior margin of anal somite. Caudal rami subtriangular in dorsal view with 4 well-developed caudal setae: one outer lateral, two dorsoapical, one ventral.

314

315

316

317

Description of female, NIBRIV0000812792. Total body length 1.60 mm in dorsal view, 1.68 mm in lateral view. Body consisting of eight somites: cephalothorax incorporating first pedigerous somite, free somites 1–4, genital compound somite, penultimate somite, and anal



318	somite. Length ratio of somites as percentage of total body length
319	45.9:11.6:11.0:10.6:5.2:9.1:2.4:4.3 in dorsal view, 45.9:11.9:11.3:10.3:5.0:9.3:2.4:3.9 in lateral
320	view. Cephalothorax bulbous (Figs. 3A, B, 4A), 0.73 mm long in dorsal view, 0.77 mm in lateral
321	view. Cephalothorax significantly broadening to greatest width of 0.05 mm at 45.0% of its
322	length. At narrowest point, 81.1% of way back, width of waist 0.34 mm. Width of incorporated
323	pediger 0.37 mm at 92.3% length of cephalothorax. Length of metasome including first to third
324	free pediger 0.53 mm in dorsal view, 0.56 mm in lateral view. Length of urosome from first
325	urosomal somite to tip of anal somite 0.33 mm in dorsal view, 0.35 mm in lateral view.
326	Forehead round with two hair-like sensilla on anterior dorsal surface. Anterior fourth of
327	cephalothorax with several pores and striations on dorsal surface (Figs. 3A, 6A). At least four
328	anterior pores recognized, aligned in semi-circle; other pores located slightly behind them. Band
329	of transverse striations present starting behind of posterior pore group, not extending onto lateral
330	side (Fig. 3B). Moderately developed oral papilla located ventrally at 17.6% length of
331	cephalothorax, protruding 0.03 mm from ventral surface (Figs. 3B, 4A, 6B). Ventral region
332	halfway from antennular bases to oral papilla with pair of prominent scars followed by transverse
333	striations (Fig. 4A). Ventral pores including anterior pair with subcuticular ducts situated
334	between antennular bases (Fig. 6B) and second pair located closer to midline slightly behind
335	scars (Fig. 6B). Another pair of ventrolateral pores also present.
336	Two lateral eyes and one ventral eye within anterior quarter of cephalothorax, all well-
337	developed, pigmented (Fig. 3B). Lateral eyes round in any direction of view, 147 μm in
338	diameter, situated close together in dorsal view. Ventral eye oval in lateral view, round in dorsal
339	view, 155 μm in diameter, thus slightly bigger than lateral eyes.
340	Antennules (Fig. 4B, C) 2-segmented, not geniculate, directed straight forwards, 0.31



mm long, equaling 40.7% of cephalothorax length, 18.7% of total body length. Length ratio of two segments 27.1:72.9; distal segment evidently formed by incomplete separation of four segments, hereinafter referred to as putative segments 2 to 5. First segment armed with spine 1 on inner terminal corner. Putative segment 2 armed with five spines (2d_{1, 2}, 2v₁₋₃) and long, strap-like, biserially plumose dorsal seta (IId); ventral spines of 2v series generally longer than dorsal spines of 2d series, 2v₃ longest. Putative segment 3 armed with medial spine 3 and IIId and IIIv setae. Putative segment 4 armed with five spines (4d_{1, 2}, 4v₁₋₃), setae IVd and IVv, and ventral aesthetase (4aes), with 4aes reaching distal margin of antennule. Distal part of antennule (putative segment 5) armed with 13 setal elements: long, strap-like setae Vm, Vd, and Vv, three unmodified spines 5₁₋₃, dichotomously branched setae A–D, simple setae a and b, and apical aesthetase (5aes). Minute setal elements 4a and 5a not observed.

Incorporated first pedigerous somite and first three free pedigers each bearing pair of swimming legs (Figs. 5A–D, 12E). Protopod consisting of large coxa and small basis separated by diagonal articulation on posterior face and slight indentation on outer margin of anterior face. Seta present on outer margin of each basis, this seta being thin, smooth, and short in legs 1, 2, and 4, reaching approximately to midlength of first exopodal segment, but biserially plumose and much longer in leg 3, reaching to end of exopod (Fig. 5C). Tri-articulate exopod and endopod situated on distal margin of each basis, with endopod always inserted more anteriorly than exopod and shorter than latter, reaching to midlength of third exopodal segment. Setation patterns of swimming legs almost all alike: endopodal segments 1 and 2 each armed with one inner seta, third endopodal segment bearing one outer, two distal, and two inner setae; all endopodal setae biserially plumose, well-developed, subequal in length. Exopodal segment 1 armed with short, robust spine on outer distal corner and short, thin inner seta reaching to about



365

366

367

368

369

370

371

372

373

374

375

376

377

378

379

380

381

382

383

384

385

386

midlength of third endopodal segment. Second exopodal segment bearing well-developed inner seta, outer margin lacking setal elements. Third exopodal segment bearing short, robust spine on outer distal corner plus two terminal and two inner setae on leg 1, two terminal and three inner setae on legs 2–4. Most setae on exopodal segments 2 and 3 biserially plumose, subequal in length, and as long as in endopods, but outermost seta on third exopodal segment serrate along outer margin, uniserially plumose along inner margin. Anterior faces of all third endopodal and exopodal segments with pore. Endopodal segments 1 and 2 fringed along outer margins, exopodal segment 2 also so fringed, but hard to observe by light microscopy. Leg pairs 1–4 all joined by transversally wide trapezoidal sclerites, distal margin (presumably important to secure enough space for subthoracic egg brooding) of which respectively 1.8, 2.5, 3.3, and 4.0 times longer than height. Height of each respectively 82, 62, 51, and 44 µm. Leg 5 twice as long as wide, members of pair separated at base and widely diverging (Figs. 4F, 6E). Unsegmented protopod dividing into two rami at distal one-third of length. Outer lobe armed with three setae, two of them apical, one at outer distal corner; two outer setae subequal in length, innermost seta thinner and short, all biserially plumose. Inner lobe smooth, unarmed. Incorporated first pedigerous somite and first three free pedigerous somites with several pairs of pit-setae (sensu Grygier & Ohtouka, 1995) mainly on dorsal and lateral surfaces (Figs. 3A, B, 7A-D): five pairs (nos. 1-5) on incorporated pediger; three pairs (nos. 6-8) on first free pediger; four pairs (nos. 9–12) on second free pediger; and two pairs (nos. 13, 14) on third free pediger. Pit-setae thin, long. No pit-setae present more posteriorly, but first urosomal somite displaying three simple pores (i, ii) on anterior dorsal margin (Fig. 7E).

First urosomal somite mainly its posterior half and anterior part of anal somite strongly

wrinkled longitudinally (Figs. 3B, 4D, 6C, D). Anterodorsal part of latter unwrinkled, but strong,

 \bigcirc

 \bigcirc



transverse dorsal	suture p	resent at m	idlength o	of somite.	Longitudinal	wrinkling	present	behind
suture and contin	uing ont	to anterior 1	part of ana	al somite.				

Genital compound somite with swollen anteroventral and posteroventral margins and pair of ovigerous spines arising from anterior ventral surface. These spines directed ventrally perpendicular to body axis, separate basally with distal third thinner than rest, and subequal in length, equal to 25.3% of total body length and 1.2 times longer than urosome (Figs. 4D, 6D).

Pair of caudal rami diverging from posterior part of anal somite. Each ramus 0.11 mm long, 0.06 mm wide, and bearing four caudal setae (Figs. 3A, 4E): one outer lateral, two terminal, one inner ventral, this last seta being remarkably short (Figs. 4E, 7F).

Variation. Specimen (NIBRIV0000812795), carrying unlaid eggs within cephalothorax, with relatively short, corrugated ovigerous spines, seemingly not fully outstretched, only 11.2% of total body length, but still directed ventrally.

401 <*Figure 3–7>*

Description of male, NIBRIV0000812791. Total body length 1.17 mm in dorsal view, 1.23 mm in lateral view. Body consisting of nine somites: cephalothorax incorporating first pedigerous somite, free somites 1–4, genital somite, post-genital somite, penultimate somite, and anal somite. Last two body somites partly fused, and dorsal articulation represented only by fine suture. Length ratio of somites as percentage of total body length 45.3:11.8:10.6:10.3:4.5:4.9:3.9:3.4:5.4 in dorsal view; 45.3:13.9:11.7:9.6:3.9:4.3:3.4:2.7:5.2 in lateral view.



411

412

413

414

415

416

417

418

419

420

421

422

423

424

425

426

427

428

429

430

431

432

Cephalothorax cylindrical (Figs. 8A, B, 11A), 0.53 mm long in dorsal view, 0.56 mm in lateral view. Greatest width 0.21 mm at half length. At narrowest point, width of waist 0.17 mm. Width of incorporated first pediger 0.21 mm. Metasome 0.38 mm long in dorsal view, 0.43 mm in lateral view. Urosome 0.26 mm long in dorsal view, 0.24 mm in lateral view. Forehead round with two thin sensilla on anterior dorsal surface. Anterior fifth of cephalothorax with several (at least 10) pores (Figs. 8A, 11B–D): four anterior and six posterior pores, both sets aligned in semi-circle. Dorsal transverse striations at midlength of cephalothorax (Figs. 8A, 11A), reaching to dorsolateral half, forming band-like structure in low magnification (Fig. 8B). Pair of pores with subcuticular ducts situated between antennular bases (Figs. 9A, 11E). Prominent pair of scars situated behind antennular bases (Figs. 9A, 11E). Another pair of pores located slightly behind scars, closer to midline (Fig. 11E). Small oral papilla situated 28.4% of way along ventral side of cephalothorax (Figs. 8B, 9A, 11E). Ventral striations between scars and oral papilla, reaching to ventrolateral half. More ventral striations found at midlength of cephalothorax, these much narrower than dorsal striations (Figs. 9A, 11E). Two lateral eyes and one ventral eye in anterior one-fifth of cephalothorax, all welldeveloped, pigmented (Figs. 8B, 9A). Lateral eyes round in lateral view, oval in dorsal view, 110 μm in diameter, situated close together. Ventral eye oval in lateral view, round in ventral, 117 um in diameter, thus slightly bigger than lateral eyes. Antennules (Fig. 9B) 5-segmented, pointing straight forward, geniculate between fourth and fifth segments, 0.53 mm long, equaling 94.6% of cephalothorax length and 42.9% of total body length. Length ratio of antennular segments from proximal to distal 14.2:19.6:9.7:21.9:34.6. Second and third segments partly fused in dorsal view, clearly separated in lateral and ventral views. Distal antennular segment with crescent-like hyaline bump on inner





434

435

436

437

438

439

440

441

442

443

444

445

446

447

448

449

450

451

452

453

454

455

side at midlength. First antennular segment armed with spine 1 on inner terminal corner. Second segment armed with five spines of subequal length $(2d_{1,2}, 2v_{1-3})$ and long, biserially plumose strap-like seta (IId). Third segment armed with spine 3 and plumose IIId and IIIv setae. Fourth segment armed with six spines $(4d_{1,2}, 4v_{1-3}, 4a)$, seta IVv, and relatively long ventral aesthetasc (4aes); all spiniform elements except 4a biserrate along outer margin. Fifth segment armed with 12 setal elements: spines 5_{1-3} , short distal aesthetasc 5aes, dichotomously branched setae A–D, simple and relatively short setae a and b, ventrally located biplumose strap-like seta Vv, and minute spine 5a. Two spines located apically, 51 short, 52 long and robust; 53 located at midlength of fifth segment and moderately developed. Setal elements Vm and Vd absent. Incorporated first pedigerous somite and three succeeding free pedigers each bearing pair of swimming legs almost identical to those in females (Figs. 10A–D, 12D). Intercoxal sclerites rectangular, 1.5 times longer than wide, all of almost same width. Leg 5 absent. These four somites also displaying several pairs of pit-setae mainly on dorsal and lateral surfaces (Figs. 8A, B, 12A): five pairs (nos. 1–5) on incorporated pediger, with outermost two pit-setae on each side situated close together; three pairs (nos. 6–8) on first free pediger; four pairs (nos. 9–12) on second free pediger; two pairs (nos. 13, 14) on third free pediger. First urosomal somite bearing three simple pores at anterior dorsal margin (Fig. 12B). First urosomal somite with longitudinal striations mainly on lateral side (Figs. 8B, 11F). More posterior somites without striations. Genital somite bearing well developed genital apparatus consisting of robust, 0.07 mm long basal shaft arising from ventral side of somite and two long genital lappets arising from distal corners of shaft (Figs. 9C, D, 11F, G). Lappets 0.15 mm long, extending beyond end of anal somite, each lappet partly rugose with at least three small, sawtooth-like protuberances at its posterior base (Fig. 9D).



Pair of caudal rami diverging from distal margin of anal somite, 0.08 mm long, 0.05 mm wide, club-shaped with posterior part slightly bulging (Figs. 9C, E, 11G, 12C). Each ramus bearing four well-developed caudal setae: one outer lateral, two terminal, one ventral; all setae subequal in length, biserially plumose.

461 <*Figure 8–12>*

Remarks. The present female specimens have the diagnostic genus-level characters mentioned by Sars (1921): an anteriorly located oral papilla, fully developed eyes, bilobed fifth legs with the outer lobe armed with three setae, a 4-segmented urosome including a genital compound somite, and four setae on each caudal ramus. Some of these features are alsomentioned in connection with *Monstrillopsis* in the keys provided by Davis (1949), Isaac (1975), and Boxshall & Haley (2004). The most recent generic diagnosis by Suárez-Morales, Bello-Smith & Palma (2006) applied stricter morphological criterion with respect to the number of caudal setae, and it eventually excluded the species with other than four caudal setae from the genus.

Five species of *Monstrillopsis* known from females have been recognized as valid: *Monstrillopsis dubia* (Scott, 1904), *Mn. dubioides* Suárez-Morales, 2004 (see Suárez-Morales & Ivanenko, 2004), *Mn. ferrarii* Suárez-Morales & Ivanenko, 2004, *Mn. chilensis* Suárez-Morales, Bello-Smith & Palma, 2006, and *Mn. igniterra* Suárez-Morales, Ramirez & Derisio, 2008. The cephalothorax of female *Mn. longilobata* is distinctly bulbous at its midlength, different from the rather elongate, cylindrical ones of its congeners (cf. Scott, 1904; Sars, 1921; Suárez-Morales & Ivanenko, 2004; Suárez-Morales, Bello-Smith & Palma, 2006; Suárez-Morales, Ramírez &



excluded from consideration by their size—3.3 mm for Mn. dubia and 3.8 mm for Mn. dubioides 480 (Scott, 1904; Suárez-Morales & Ivanenko, 2004)—which far exceeds the mean size of the 481 current female specimens (1.64 mm). 482 Additional differences mainly concern the relative proportions of the body segments. 483 484 Mn. dubia and Mn. dubioides have a relatively short genital compound somite, respectively 4% and 4.7% of the body length (Scott, 1904; Suárez-Morales & Ivanenko, 2004), in contrast to 485 9.3% in Mn. longilobata. Conversely, the cephalothorax is relatively much longer in the two 486 former species than in the Korean females, comprising over 60% of the body length in the 487 former, but on average 47.9%, and always less than 50%, in Mn. longilobata. Two other 488 congeners, Mn. ferrarii (61.3%) and Mn. igniterra (61.3%), can be also distinguished from the 489 current females the same way (cf. Suárez-Morales & Ivanenko, 2004; Suárez-Morales, Ramírez 490 & Derisio, 2008). The size of the genital compound somite in both species (respectively 8% and 491 492 8.3% of the body length) is similar to, but still slightly shorter than that of Mn. longilobata (9.3%).493 In terms of body proportions, *Monstrillopsis chilensis* is the closest species to *Mn*. 494 495 longilobata with its cephalothorax constituting 52.3%, and the genital compound somite 9.6%, of the body length (Suárez-Morales, Bello-Smith & Palma, 2006). The total body length (1.76 mm 496 497 in the holotype of Mn. chilensis vs. a mean length of 1.64 mm among six females of Mn. 498 longilobata) and the relative length of the antennules (17.7% and 17.3% of the body length, respectively) are also similar, but other details distinguish the two species. In Mn. longilobata the 499 500 inner seta on the first exopodal segment of legs 1–4 is shorter than the respective endopod, 501 reaching to about midlength of the third endopodal segment, whereas in Mn. chilensis these setae

Derisio, 2008). Among the known females, Mn. dubia and Mn. dubioides can be instantly



overreach the endopods and reach to about the end of the bearing exopod. Furthermore, the innermost caudal seta of *Mn. chilensis* is the shortest, just one-fifth as long as the longest middle seta (Suárez-Morales, Bello-Smith & Palma, 2006), whereas the ventral caudal seta is the shortest in *Mn. longilobata*, arising from a small, swollen base and only slightly exceeding the distal end of the caudal ramus. *Mn. longilobata* is also distinguished from *Mn. chilensis* by the presence of a ventral swelling on the posterior margin of the genital compound somite.

The most striking morphological feature of *Monstrillopsis longilobata* is the pair of ventrally protruding ovigerous spines, which distinguish the present females from any other known female *Monstrillopsis*. The pair of ovigerous spines carries laterally compressed egg masses, which are brooded subthoracically in much the same way as those of *Maemonstrilla* species (see Grygier & Ohtsuka, 2008), but with the anterior margin of the egg mass reaching less far forward and not impinging on the first leg pair. Similar morphological modification of the intercoxal sclerites of legs 2–4, but not that of the first pair of legs, facilitates subthoracic egg brooding inasmuch as the intercoxal sclerites of legs 2–4 are wider than long, thus widely separating the members of each pair, as well as the fifth pair.

The present male specimens obtained from the same samples as the females agree well with the original description of male *Monstrillopsis longilobata* collected from the eastern coastal waters of Korea, including the possession of extremely long genital lappets. The main difference between the original type series and the current specimens is in the body size: mean 1.26 mm (sum of lengths of body and caudal rami) for the present specimens vs. 1.74 mm for the holotype. In size, the current males resemble *Mn. sarsi* Isaac, 1974 (see Isaac, 1974a) at 1.2 mm, but other morphological details more closely resemble those of *Mn. longilobata* than those of the latter species. In the original report of Lee, Kim & Chang (2016), *Mn. longilobata* was



526

527

528

529

530

531

532

533

534

535

536

537

538

539

540

541

542

543

544

545

546

differentiated from *Mn. sarsi* by the presence of conspicuous transverse striation on the cephalothorax, a more posteriorly located oral papilla, and very long genital lappets. In addition, the level of modification of the distal antennular "segment" differed. *Mn. sarsi* alone was depicted with the distal part of the antennular segment elongate and rather slender; *Mn. longilobata* had no such prominent distal elongation.

SEM provided additional detailed information concerning the pore and pit-seta patterns of the present specimens. The anterior dorsum of the cephalothorax indeed bears two groups of pores as Lee, Kim & Chang (2016) described, but the anterior pores are aligned in a semi-circle as wide as the array of posterior pores, not only aggregated as those authors stated. Five pairs of pit-setae are symmetrically situated both laterally and dorsally on the part of the cephalothorax corresponding to the first pedigerous somite, and the most lateral pit-setae (no. 5) and adjacent dorsolateral pit-setae (no. 4) are close to each other. Only one of these pores was depicted in the original description. In general, the number and the location of pores in the examined males coincided well with those of the present females. Both sexes also showed the same kind of ventral band structure consisting of fine transverse striations behind the oral papilla. These striations are finer than the dorsal ones as Lee, Kim & Chang (2016) also noted. The penultimate and anal somites are separated in males by a fine seam on the dorsal surface without prominent arthrodial membrane between them, while the articulation on the ventral side is well defined (Fig. 11H). This feature is also homologous with the previous males reported by Lee, Kim & Chang (2016).

Lee, Kim & Chang (2016) reported the occurrence of males of *Monstrillopsis* longilobata in southern coastal waters of Korea at Geumo Island, Yeosu, which is close to the



current research site at Soho-dong, Yeosu. Morphological similarities and commonality of distribution tend to confirm the conspecificity of the present males with *Mn. longilobata*.



MOLECULAR ANALYSIS

The gene sequences were aligned for a length of 523 bp for mtCOI, 794 bp for ITS1–5.8S–ITS2, and 688 bp for 28S rRNA, and the average GC content for each was 30.0%, 44.0%, and 49.0%, respectively. Mean genetic divergence for each group was calculated under the Kimura two-parameter model (K2P) by generating 3,000 bootstrapping replicates. The mean divergence of mtCOI was 0.18% (0.00–0.58%). The mtCOI sequences were, then, translated into amino acid sequences on the basis of an invertebrate mitochondrial genetic code. The amino acid sequences, comprising 174 amino acids (translation starting from the second base), were all identical, without any unexpected internal stop codons. There was 0.15% (0.00–0.38%) mean genetic divergence among the ITS1–5.8S–ITS2 sequences from nine individuals, but no genetic divergence at all (0.00%) among the 28S rRNA gene sequences from 11 specimens.

DISCUSSION

Systematics of the genus Monstrillopsis

About 20 species of *Monstrillopsis* have been described globally (Razouls et al., 2005-2017).



Both sexes of *Monstrilla reticulata* Davis, 1949 were once assigned to *Monstrillopsis* by Isaac

(1975), but a later study by Suárez-Morales, Bello-Smith & Palma (2006) returned the females to

Monstrilla by virtue of the presence of five caudal setae and a seta on the inner lobe of the fifth

leg. The males, currently seen as a different species from the females, remained in *Monstrillopsis*

on account of the four caudal setae, modification on the last antennular segment, and the



570	complete absence of the fifth legs (Suárez-Morales, Bello-Smith & Palma, 2006). Another two
571	species, Mn. angustipes Isaac, 1975 (n. nud.) and Mn. ciqroi Suárez-Morales, 1993, which have
572	been known only from females, were also excluded from Monstrillopsis due to some
573	morphological discrepancies with respect to their current generic diagnosis of Suárez-Morales,
574	Bello-Smith & Palma (2006). Conversely, <i>Haemocera filogranarum</i> Malaquin, 1901 (= <i>Mn</i> .
575	filogranarum sensu Suárez-Morales, Bello-Smith & Palma, 2006) has been reallocated to
576	Monstrillopsis, and Mn. zernowi Dolgopol'skaya, 1948 is tentatively assigned to this genus even
577	though it exhibits an unusual number of caudal setae: six on each caudal ramus in the female,
578	five in the male. An unusual number of caudal setae has been also reported from two other
579	supposedly congeneric males, Mn. cahuitae Suárez-Morales & Carrillo, 2013 (see Suárez-
580	Morales, Carrillo & Morales-Ramírez, 2013) with six caudal setae, and Mn. nanus Suárez-
581	Morales & McKinnon, 2014 with five. If the recent generic diagnosis of <i>Monstrillopsis</i> is strictly
582	applied, only 13 species can be recognized as valid: Mn. dubia, the male of Mn. reticulata, Mn.
583	sarsi, Mn. fosshageni Suárez-Morales & Dias, 2001 (number of caudal setae unknown), Mn.
584	dubioides, Mn. ferrarii, Mn. chilensis, Mn. igniterra, Mn. chathamensis Suárez-Morales &
585	Morales-Ramírez, 2009, Mn. boonwurrungorum Suárez-Morales & McKinnon, 2014, Mn.
586	hastata Suárez-Morales & McKinnon, 2014, Mn. longilobata, and Mn. coreensis. Among these
587	species, three (Mn. dubia, Mn. dubioides, and Mn. chilensis) are known from both sexes, two
588	(Mn. ferrarii and Mn. igniterra) only from females, and the other eight species only from males.
589	Another enigmatic species, Monstrillopsis latipes, was introduced in the unpublished
590	doctoral thesis of Isaac (1974b). No later publication or further use of the name followed, and
591	this specific name remains a <i>nomen nudum</i> . Suárez-Morales, Bello-Smith & Palma (2006)
592	brought attention to the unusual ovigerous spines of Mn. latipes that are "anteriorly directed" and



proposed a possible relation with the at that time still undescribed genus *Maemonstrilla*, the females of which are characterized by anteriorly pointing ovigerous spines. Grygier & Ohtsuka (2008), however, declined to assign this species to *Maemonstrilla* because the ovigerous spines were described and illustrated by Isaac (1974b) as being directed ventrally, nearly perpendicular to the body axis, not anteriorly, and on account of the lack of information about the intercoxal sclerites and other diagnostic features of the limbs. The ovigerous spines of the present Korean female specimens are also directed ventrally; in some specimens they are inclined slightly anteriorly, but much less so than in *Maemonstrilla*.

The bilobed fifth legs support the possible assignment of *Monstrillopsis latipes* to *Monstrillopsis*, but the number of caudal setae does not. It has been reported to have three caudal setae (Isaac, 1974b; see also Suárez-Morales, Bello-Smith & Palma, 2006), but the actual number may be more. Among the four caudal setae of female *Mn. longilobata*, the inner ventral one is very short and thus often hardly recognizable by low magnification light microscopy. Such a seta may well have been overlooked in *Mn. latipes*, but if not, assignment of this species to *Monstrillopsis* may be unsupportable under the current generic diagnosis. Reexamination of the specimen, currently housed in the Natural History Museum, London (unregistered material, labeled Monstrilloida, Jersey. J. Sinel; as stated in Isaac, 1974b), is a priority for further research.

Several criteria for matching the sexes of monstrilloid species have been used and/or proposed (Gallien, 1934; Grygier & Ohtsuka, 2008; Suárez-Morales, 2011; Lee, Kim & Chang, 2016): co-occurrence of both sexes in a plankton sample or in serial collections conducted over a limited time span at a particular location; the recovery of one form each of both sexes from a single host



species; and the sharing of distinctive morphological characters in both sexes. However, each method still carries a high risk of mispairing.

Co-occurrence is the most frequently used matching method, but it is hard to apply with any confidence to samples from places known for high monstrilloid species richness and abundance, such as coral reefs (Sale, McWilliam & Anderson, 1976; Suárez-Morales, 2001; Grygier & Ohtsuka, 2008). The reliability of host specificity is constrained by the lack of much ecological research on host utilization by these copepods. There is currently no guarantee of one-to-one host-parasite specificity in monstrilloids. For all we know, congeneric species with a similar morphological structure may share the same host during the endoparasitic phase of their development.

The male specimens of *Monstrillopsis longilobata* obtained together with the current females display all the typical features of *Monstrillopsi* ome of the major morphological features involved are sexually dimorphic, however: the general shape of the cephalothorax (bulbous in females vs. rather slender and cylindrical in males), the shape of the intercoxal sclerites (wider than long and trapezoidal in females vs. longer than wide and rectangular in males), the detailed morphology of the caudal setae (inner ventral seta short in females), and the presence of sex-specific characters such as the modified distal antennular segment in males, the fifth legs in females, and the totally different genitalia in both sexes. Grygier & Ohtsuka (2008) proposed several species-specific characters of females of *Maemonstrilla*, for examples, the ornamented coxal lobes of *Ma. polka* Grygier & Ohtsuka, 2008 and *Ma. spinicoxa* Grygier & Ohtsuka, 2008 and the dorsal spiniform scales of *Ma. turgida* (Scott, 1909), that might serve as morphological markers if they are also present in the unknown males of these species (see Grygier & Ohtsuka, 2008); However, among the larger males in their samples they found none



that exhibited such features. Our present observation of *Mn. longilobata* demonstrated little evidence of morphological similarity between both sexes, and we conclude that matching the sexes by using, or at least solely relying on morphological characters will likely lead to error. Minor features hold some promise. In *Mn. longilobata*, the pore patterns (e.g., the general alignment of the integumental organs on the anterior ventral surface of the cephalothorax, the closely adjacent pit-setae 4 and 5 on the dorsolateral side of the incorporated first pediger, and the odd number (three) anterior dorsal pores on the first urosomal somite) and striations (e.g., those between the antennular bases and the oral papilla, and also the dorsal band, agree in both sexes); Lee, Kim & Chang (2016) even predicted that this would be so for the striations. The practical use of such characters to demonstrate conspecificity is, however, restricted by imperfect observations made by light microscopy and the lack of relevant data from earlier studies.

Under these circumstances, the use of molecular techniques is likely to be one of the most efficient and reliable methods for pairing males and females. The molecular analyses presented here support the conspecificity of both sexes of *Monstrillopsis longilobata* by revealing little or no genetic divergence between them. Hebert, Ratnasingham & de Waard (2003) concluded that mtCOI usually shows about 10% sequence divergence between congeneric species, but that there is a higher, 15.4%, mean divergence in crustaceans. Lefébure *et al.* (2006) similarly proposed a 0.16 substitution rate per site in the mtCOI sequence as the molecular threshold for species delimitation. Both of the above-mentioned species-delimitation values are much higher than the current mtCOI divergence (mean 0.18%) between male and female *Mn. longilobata*. Baek *et al.* (2016) showed a mean of mtCOI divergence of 2.42% within individual species of copepods, and in particular 1.93% within a species of monstrilloid.



662

663

664

665

666

667

668

669

670

671

672

673

674

675

676

677

678

679

680

681

682

683

In eukaryotes, ribosomal RNA genes are one of the most conserved classes of genes, but they still differ between species (Eickbush & Eickbush, 2007; Rebouças et al., 2013; Zagoskin et al., 2014). In this respect, the 5.8S rRNA gene regions within the present ITS1-5.8S-ITS2 sequences should be also expected to show no difference among individuals of *Monstrillopsis* longilobata. No transcript analysis for strictly distinguishing and determining any particular gene region was carried out, but we were nonetheless able to estimate the 5.8S rRNA region by aligning and comparing the present gene sequences with the other complete 5.8S rRNA gene sequences registered in GenBank. The comparisons involved at least 155 bp of the 5.8S rRNA region from the present sequences, and the 5.8S rRNA sequences in this position are all homologous in the present six sequenced male and female specimens of Mn. longilobata. By setting the 5.8S rRNA region as standard, we were also able to distinguish the 18S–ITS1 region (302 bp) and ITS2–28S region (337 bp) because the 5.8S rRNA gene is located between those two regions. The estimated divergences of the 18S-ITS1 and ITS2-28S regions were 0.13% and 0.23% respectively. These values are probably underestimated because each region contains a small portion of conserved ribosomal RNAs (i.e., partial 18S and 28S rRNAs). Precise positioning of the genes would allow more accurate divergence information to be gathered, but our rough estimates at least show that the 5.8S rRNA is highly conserved between the sexes, a fact that supports the conspecificity of the current males and females. Machida & Tsuda (2010) reported a mean genetic p-distance of less than 0.002 based on "ITS region" within *Neocalanus* species, but higher values between species: 0.004 for N. cristatus (Kröyer, 1845) vs. N. flemigeri Miller, 1988, and 0.007 for N. cristatus vs. N. plumchrus (Marukawa, 1921). As they defined it, their "ITS region" was equivalent to the present study's ITS1-5.8S-ITS2-28S complex, so the values derived from their "ITS region"





can only be compared with the mean genetic divergence of 0.15% (i.e., 0.0015) derived from the present complete sequence data. This is close to Machida & Tsuda's (2010) within-species value, and distinctly lower than their between-species values. Krajíček *et al.* (2016) calculated the mean intra- and inter-genetic divergences of ITS1 sequences from 13 European species of *Cyclops*. Similarly to the previous study, the mean within-species genetic divergence was 0.26% (calculated based on their Table S8), and the between-species divergence ranged from 3.7% to 20.7%. The purported ITS1 region (i.e., 18S–ITS1) of the present *Monstrillopsis* species showed a mean genetic divergence of 0.13%, which is much lower than the above-cited between-species values.

Individual consideration of the three gene regions that comprise ITS1–5.8S–ITS2 shows that the genetic differences mainly occurred in the "relatively variable" ITS1 and ITS2 regions but not in the "conserved" 5.8S rRNA region. Similarly, sequences of another form of ribosomal RNA, partial 28S rRNA, from 11 individuals of *Monstrillopsis longilobata* were all identical. In Jeon, Lee & Soh's (2018) study of 28S rRNA in 11 species of monstrilloids, the sequences within each species group were essentially identical, but they differed between the each species group (21.73% mean divergence). In general, the divergences we found for *Mn. longilobata* from these three different gene regions were consistently lower than other reported species-delimitation thresholds or divergence ranges for copepods. This further confirms the conspecificity of the present males and females.

Comparison between females of Monstrillopsis longilobata and Maemonstrilla species

The present females of Monstrillopsis longilobata exhibit an unexpected mixture of
morphological characters of the two genera Monstrillopsis as defined by Sars (1921) and Suárez-



Morales, Bello-Smith & Palma (2006) and *Maemonstrilla* as defined by Grygier & Ohtsuka (2008). *Monstrillopsis*-like features include a moderately developed oral papilla, an inner seta on the first exopodal and endopodal segments of legs 1–4, four caudal setae, and the general shape of the bilobed fifth legs, with the outer lobe bearing three setae and the inner lobe reduced and unarmed; *Maemonstrilla*-like features include the rather bulbous cephalothorax and the low and wide intercoxal sclerites of legs 2–4 (present on legs 1–4 in females of *Maemonstrilla*) that appears to be related to subthoracic egg brooding as discussed above. Some characters of *Mn. longilobata* are literally intermediate, notably the ventrally directed ovigerous spines (not posteriorly directed as in all other female *Monstrillopsis*, nor anteriorly directed as in female *Maemonstrilla*) and the presence on the cephalothorax of relatively prominent transverse striations (as in *Monstrillopsis*) combined with faint, incompletely closed reticulations that are reminiscent of, but much weaker than the general pattern in *Maemonstrilla*.

A phylogenetic systematic evaluation of the relationship between *Monstrillopsis* and *Maemonstrilla* is rendered more complex by the present females. *Maemonstrilla* is one of the most clearly defined monstrilloid genera or species-groups and is characterized by unique and complex set of characters. Most of the members (mainly those of the *Maemonstrilla hyottoko* species group) can be distinguished from the current female *Monstrillopsis longilobata* by their fifth legs which are long, slender, and rod-shaped with two apical setae, and by the absence of inner setae on the first exopodal and endopodal segments. The *Maemonstrilla turgida* species group (i.e., *Ma. turgida* and *Ma. crenulata* Suárez-Morales & McKinnon, 2014) is not quite so distinct. Like the present females, these two species have bilobed fifth legs and an inner seta on the first exopodal and endopodal segments. There are, however, still some differences from *Mn. longilobata*: the inner lobe of the fifth leg is armed with a single seta, and the inner setae on the



730

scales in Ma. turgida (cf. Grygier & Ohtsuka, 2008: fig. 26B, C) and Ma. crenulata (cf. Suárez-731 Morales & McKinnon, 2014: fig. 21A) was detected using SEM in Mn. longilobata. 732 The number of caudal setae of *Monstrillopsis longilobata* is also different from that of 733 Maemonstrilla. In the different monstrilloid genera, variation in the number of caudal setae is 734 735 quite frequent: five or six in different species of Monstrilla, Maemonstrilla, and Caromiobenella; three or four in different species or sexes of Cymbasoma; and five in Australomonstrillopsis (i.e., 736 A. crassicaudata Suárez-Morales & McKinnon, 2014; monotypic) (Huys & Boxshall, 1991; 737 738 Grygier & Ohtsuka, 2008; Suárez-Morales, 2011; Suárez-Morales & McKinnon, 2014; Jeon, Lee & Soh, 2018). Monstrillopsis displays the widest known range of caudal seta number among the 739 monstrilloid genera, with four to six caudal setae in different species. The majority have four, 740 and this has been regarded as one of the generic characters of *Monstrillopsis* (sensu Suárez-741 Morales, Bello-Smith & Palma, 2006), but some species have more: Mn. zernowi (six in female, 742 743 five in male), Mn. cahuitae (six in male; female unknown), and Mn. nanus (five in male; female unknown). The current study also raises the question of the true phylogenetic relationship 744 between Monstrillopsis and Maemonstrilla, especially the Maemonstrilla turgida species group, 745 746 as well as the validity of the latter genus. The set of extraordinary features of the female of Mn. longilobata presents overlaps with both generic diagnoses. It is, however, impossible to come to 747 748 any conclusion because: 1) no phylogenetic analysis has yet demonstrated whether any 749 morphological characters or character combinations support the monophyly of *Monstrillopsis* or Maemonstrilla; 2) the unknown males of Maemonstrilla may provide crucial evidence for one 750 751 classification or another; 3) There are insufficient molecular data to address phylogenetic 752 considerations within the Monstrilloida; 4) the current female Mn. longilobata itself is

first endopodal segment of legs 1–4 are weakly developed. Furthermore, no dorsal spiniform





/53	disqualified to represent <i>Monstrillopsis</i> in this connection on account of its unusual
754	morphological character set; and 5) a nomenclatural problem is presented by the possible
755	synonymy of <i>Monstrillopsis</i> and <i>Haemocera</i> , the latter having priority (see Jeon, Lee & Soh,
756	2018).
757	
758	Considerations on subthoracic egg brooding in the current females
759	The present females form and carry the egg masses in a manner typical for monstrilloids. They
760	attach the eggs along the ovigerous spines using a mucous substance without forming egg sacs
761	(Malaquin, 1901; Huys & Boxshall, 1991). The general shape of the egg mass is especially
762	similar to egg masses borne by females of Maemonstrilla (Grygier & Ohtsuka, 2008).
763	Subthoracic egg brooding is responsible for this, but one of the most prominent differences
764	between Monstrillopsis longilobata and Maemonstrilla species concerns the anterior extent of
765	the egg mass. In Maemonstrilla, the anterior parts of the large egg masses reach as far forward as
766	the level of the ventral oral papilla on the cephalothorax (see Grygier & Ohtsuka, 2008: fig. 13;
767	Suárez-Morales & McKinnon, 2014: fig. 17). Grygier & Ohtsuka (2008) explained other
768	morphological modifications and adaptions, including the modified intercoxal sclerites of legs 1-
769	4 in Maemonstrilla, for achieving the complete form of subthoracic egg brooding. This
770	explanation is generally applicable to the current females as well, except that the intercoxal
771	sclerite of the first leg pair is relatively narrower and higher than those of leg pairs 2–4. The egg
772	mass, therefore, reaches to just behind the first leg pair, but cannot pass it over forwardly. The
773	ventrally directed ovigerous spines are probably a subsequent adaptation for preventing the
774	physical interruptions between the first leg pair and the egg mass during swimming.



There is also a subtle difference from usual in the shape of the egg mass; in both *Monstrillopsis longilobata* and *Maemonstrilla okame* (cf. Grygier & Ohtsuka, 2008: 502) it is laterally compressed with flattened lateral sides. The current females are distinguished from the other species of *Maemonstrilla*, except for those of the *Maemonstrilla turgida* species group, by the presence of an inner setae on the first exopodal and endopodal segments. It has been suggested that the absence of the inner setae in other *Maemonstrilla* species provides room for bearing eggs beneath the thoracic segments (Grygier & Ohtsuka, 2008: 502), but in *Ma. turgida* et al. and in *Mn. longilobata*, their presence might be useful in arranging the eggs and forming the egg mass into the specific shape noted above. Although actual observation in life remains to be done, the inner setae on the first endopodal segments of legs 1–4 may perhaps be involved in evenly distributing the eggs along the ovigerous spines, so as to prevent large parts of the egg mass from falling off and/or minimizing risk from the loss of large egg part at once.

CONCLUSION

The present study describing females of *Monstrillopsis longilobata* has led to the following conclusions: 1) The present females of *M. longilobata* are distinct from any other known congeners of *Monstrillopsis* in many morphological aspects, especially with the unusually directed ovigerous spines; latter characteristic is also unfamiliar to the genus *Monstrillopsis*. 2) The presence of severe sexual dimorphism between the females and males of *M. longilobata* implies that many other monstrilloid species reported from a single sex could possibly have such morphological differences, thus solely relying on the morphological features could be erroneous for a perfect sexual matching. 3) The minor features such as pore patterns and integumental ornamentation, which of those have not been previously inspected enough for species identification, are more informative than we ever thought, and thus more attention to the these features are needed. 4) To



799

800

801

802

803

804

805

806

807

808

809

810

prevent further confusion caused by the current usage of two different antennular setal nomenclatures by each sex, those two sets of terms were revised and unified with newly defined terms; the present proposal for the antennular nomenclature well explains the general setal patterns of eight different species of Korean monstrilloid copepods. 5) The application of molecular tools is one of the promising methods for compensating the defects caused by insufficient morphological characteristics; newly designed forward primer XcoiF resulted in a little shorter mtCOI sequence product than the case using the "universal primers", but those sequences are still long enough to confirm a conspecificity of *M. longilobata*. 6) The present females of *M. longilobata* exhibit mixed characteristics of *Monstrillopsis* and *Maemonstrilla*, whereas the males are in typical fashion of *Monstrillopsis*. With the current limited information available, it is insufficient to evaluate the true relationship of two genera, thus more species descriptions and following molecular analyses still remain to be done.

811

812

813

ACKNOWLEDGEMENTS

- We are grateful to Dr. Mark J. Grygier (Center of Excellence for the Oceans, National Taiwan
- Ocean University, Taiwan) for providing valuable, inspiring comments, and kind English
- rewording for overall quality improvements of the manuscript.

816

817

REFERENCES

- 818 Baek SY, Jang KH, Choi EH, Ryu SH, Kim SK, Lee JH, Lim YJ, Jun J, Kwak M, Lee Y-S,
- Hwang J-S, Venmathi Maran BA, Chang CY, Kim I-H, Hwang UW. 2016. DNA
- barcoding of metazoan zooplankton copepods from South Korea. *PLoS ONE* 11:
- e0157307 DOI: 10.1371/journal.pone.0157307.



822	Blanco-Bercial L, Bradford-Grieve J, Bucklin A. 2011. Molecular phylogeny of the Calanoida	
823	(Crustacea: Copepoda). Molecular Phylogenetics and Evolution 59: 103–113 DOI:	
824	10.1016/j.ympev.2011.01.008.	
825	Boxshall GA, Halsey SH. 2004. An introduction to copepod diversity. The Ray Society, London.	
826	Braet F, De Zanger R, Wisse E. 1997. Drying cells for SEM, AFM and TEM by	
827	hexamethyldisilazane: a study on hepatic endothelial cells. Journal of Microscopy 186:	
828	84–87 DOI: 10.1046/j.1365-2818.1997.1940755.x.	
829	Bucklin A, Steinke D, Blanco-Bercial L. 2011. DNA barcoding of marine Metazoa. Annual	
830	Review of Marine Science 3: 471–508 DOI: 10.1146/annurev-marine-120308-080950.	
831	Casquet J, Thebaud C, Gillespie RG. 2012. Chelex without boiling, a rapid and easy technique to	
832	obtain stable amplifiable DNA from small amounts of ethanol-stored spiders. Molecular	
	Ecology Resources 12: 136–141 DOI: 10.1111/j.1755-0998.2011.03073.x.	
833	Leology Resources 12. 130 141 DOI: 10.1111/J.1/35-07/0.2011.030/3.x.	
833	Chang, CY. 2012. First record of monstrilloid copepods in Korea: description of a new species of	
834	Chang, CY. 2012. First record of monstrilloid copepods in Korea: description of a new species of	(
834 835	Chang, CY. 2012. First record of monstrilloid copepods in Korea: description of a new species of the genus <i>Cymbasoma</i> (Monstrilloida, Monstrillidae). <i>Animal Systematics, Evolution and</i>	
834 835 836	Chang, CY. 2012. First record of monstrilloid copepods in Korea: description of a new species of the genus <i>Cymbasoma</i> (Monstrilloida, Monstrillidae). <i>Animal Systematics, Evolution and Diversity</i> 28: 126–132 DOI: 10.5635/ASED.2012.28.2.126.	
834 835 836 837	Chang, CY. 2012. First record of monstrilloid copepods in Korea: description of a new species of the genus <i>Cymbasoma</i> (Monstrilloida, Monstrillidae). <i>Animal Systematics, Evolution and Diversity</i> 28: 126–132 DOI: 10.5635/ASED.2012.28.2.126. Chang CY. 2014. Two new records of monstrilloid copepods (Crustacea) from Korea. <i>Animal</i>	
834 835 836 837 838	Chang, CY. 2012. First record of monstrilloid copepods in Korea: description of a new species of the genus <i>Cymbasoma</i> (Monstrilloida, Monstrillidae). <i>Animal Systematics, Evolution and Diversity</i> 28: 126–132 DOI: 10.5635/ASED.2012.28.2.126. Chang CY. 2014. Two new records of monstrilloid copepods (Crustacea) from Korea. <i>Animal Systematics, Evolution and Diversity</i> 30: 206–214 DOI: 10.5635/ASED.2014.30.3.206.	
834 835 836 837 838 839	Chang, CY. 2012. First record of monstrilloid copepods in Korea: description of a new species of the genus <i>Cymbasoma</i> (Monstrilloida, Monstrillidae). <i>Animal Systematics, Evolution and Diversity</i> 28: 126–132 DOI: 10.5635/ASED.2012.28.2.126. Chang CY. 2014. Two new records of monstrilloid copepods (Crustacea) from Korea. <i>Animal Systematics, Evolution and Diversity</i> 30: 206–214 DOI: 10.5635/ASED.2014.30.3.206. Eickbush TH, Eickbush DG. 2007. Finely orchestrated movements: evolution of the ribosomal	
834 835 836 837 838 839 840	Chang, CY. 2012. First record of monstrilloid copepods in Korea: description of a new species of the genus <i>Cymbasoma</i> (Monstrilloida, Monstrillidae). <i>Animal Systematics, Evolution and Diversity</i> 28: 126–132 DOI: 10.5635/ASED.2012.28.2.126. Chang CY. 2014. Two new records of monstrilloid copepods (Crustacea) from Korea. <i>Animal Systematics, Evolution and Diversity</i> 30: 206–214 DOI: 10.5635/ASED.2014.30.3.206. Eickbush TH, Eickbush DG. 2007. Finely orchestrated movements: evolution of the ribosomal RNA genes. <i>Genetics</i> 175: 477–485 DOI: 10.1534/genetics.107.071399.	
834 835 836 837 838 839 840 841	Chang, CY. 2012. First record of monstrilloid copepods in Korea: description of a new species of the genus <i>Cymbasoma</i> (Monstrilloida, Monstrillidae). <i>Animal Systematics, Evolution and Diversity</i> 28: 126–132 DOI: 10.5635/ASED.2012.28.2.126. Chang CY. 2014. Two new records of monstrilloid copepods (Crustacea) from Korea. <i>Animal Systematics, Evolution and Diversity</i> 30: 206–214 DOI: 10.5635/ASED.2014.30.3.206. Eickbush TH, Eickbush DG. 2007. Finely orchestrated movements: evolution of the ribosomal RNA genes. <i>Genetics</i> 175: 477–485 DOI: 10.1534/genetics.107.071399. Estoup A, Largiadèr CR, Perrot E, Chourrout D. 1996. Rapid one-tube DNA extraction for	



845	mitochondrial cytochrome c oxidase subunit I from diverse metazoan invertebrates.
846	Molecular Marine Biology and Biotechnology 3: 294–299.
847	Gallien L. 1934. Description du mâle de <i>Monstrilla helgolandica</i> Claus. Synonymie de
848	Monstrilla serricornis G. O. Sars et de Monstrilla helgolandica Claus. Bulletin de la
849	Societe zoologique de France 59: 377–382.
850	Grygier MJ, Ohtsuka S. 1995. SEM observation of the nauplius of <i>Monstrilla hamatapex</i> , new
851	species, from Japan and an example of upgraded descriptive standards for monstrilloid
852	copepods. Journal of Crustacean Biology 15: 703-719 DOI: 10.1163/193724095X00118.
853	Grygier MJ, Ohtsuka S. 2008. A new genus of monstrilloid copepods (Crustacea) with anteriorly
854	pointing ovigerous spines and related adaptations for subthoracic brooding. Zoological
855	Journal of the Linnean Society (London) 152: 459–506 DOI: 10.1111/j.1096-
856	3642.2007.00381.x.
857	Hebert PDN, Ratnasingham S, deWaard JR. 2003. Barcoding animal life: cytochrome c oxidase
858	subunit 1 divergences among closely related species. Proceedings of the Royal Society of
859	London, Series B: Biological Sciences 270: S96–S99 DOI: 10.1098/rsbl.2003.0025.
860	Huys R, Boxshall GA. 1991. Copepod evolution. The Ray Society, London.
861	Huys R, Llewellyn-Hughes J, Conroy-Dalton S, Olson PD, Spinks JN, Johnston DA. 2007.
862	Extraordinary host switching in siphonostomatoid copepods and the demise of the
863	Monstrilloida: Integrating molecular data, ontogeny and antennulary morphology.
864	Molecular Phylogenetics and Evolution 43: 368–378 DOI:
865	10.1016/j.ympev.2007.02.004.
866	Isaac MJ. 1974a. Copepoda Monstrilloida from south-west Britain including six new species.
867	Journal of the Marine Biological Association of the United Kingdom 54: 127–140 DOI:



868	10.1017/S0025315400022116.
869	Isaac MJ. 1974b. Studies on planktonic arthropods. D. Phil. Thesis, University of Wales,
870	Swansea, UK.
871	Isaac MJ. 1975. Copepoda, Sub-order: Monstrilloida. Fiches d'Identification du Zooplancton
872	144/145: 1–10.
873	Jeon D, Lee W, Soh HY. 2018. A new genus and two new species of monstrilloid copepods
874	(Copepoda: Monstrillidae): integrating morphological, molecular phylogenetic and
875	ecological evidence. Journal of Crustacean Biology 38: 45-65 DOI:
876	10.1093/jcbiol/rux095.
877	Krajíček M, Fott J, Miracle MR, Ventura M, Sommaruga R, Kirschner P, Černý M. 2016. The
878	genus Cyclops (Copepoda, Cyclopoida) in Europe. Zoologica Scripta 45: 671-682 DOI:
879	10.1111/zsc.12183.
880	Lee J, Chang CY. 2016. A new species of <i>Monstrilla</i> Dana, 1849 (Copepoda: Monstrilloida:)
881	Monstrillidae) from Korea, including a key to species from the north-west Pacific.
882	Zootaxa 4174: 396–409 DOI: 10.11646/zootaxa.4174.1.24.
883	Lee J, Kim D, Chang CY. 2016. Two new species of the genus Monstrillopsis Sars, 1921
884	(Copepoda: Monstrilloida: Monstrillidae) from South Korea. Zootaxa 4174: 410-423
885	DOI: 10.11646/zootaxa.4174.1.25.
886	Lefébure T, Douady CJ, Gouy M, Gibert J. 2006. Relationship between morphological taxonomy
887	and molecular divergence within Crustacea: Proposal of a molecular threshold to help
888	species delimination. Molecular Phylogenetics and Evolution 40: 435-447 DOI:
889	10.1016/j.ympev.2006.03.014.
890	Machida RJ, Tsuda A. 2010. Dissimilarity of species and forms of planktonic Neocalanus



891	copepods using mitochondrial COI, 12S, nuclear ITS, and 28S gene sequences. PLoS
892	ONE 5: e10278 DOI: 10.1371/journal.pone.0010278.
893	Malaquin A. 1901. Le parasitisme évolutif des Monstrillides (Crustacés Copépodes). Archives de
894	Zoologie Expérimentale et Générale 9: 81–232.
895	Ortman BD. 2008. DNA barcoding the Medusozoa and Ctenophora. D. Phil. Thesis, University
896	of Connecticut, Storrs, CT, USA.
897	Raibaut A. 1985. Les cycles évolutifs des Copépodes parasites et les modalités de l'infestation.
898	Anneé Biologique 24: 233–274.
899	Razouls C, de Bovée F, Kouwenberg J, Desreumaux N. 2005-2017. Diversity and geographic
900	distribution of marine planktonic copepods. Available at http://copepodes.obs-
901	banyuls.fr/en.
902	Rebouças EL, Costa JJN, Passos MJ, Passos JRS, Van Den Hurk R, Silva JRV. 2013. Real time
903	PCR and importance of housekeepings genes for normalization and quantification of
904	mRNA expression in different tissues. Brazilian Archives of Biology and Technology 56:
905	143–154 DOI: 10.1590/S1516-89132013000100019.
906	Sale PF, McWilliam PS, Anderson DT. 1976. Composition of the near-reef zooplankton at
907	Heron Reef, Great Barrier Reef. Marine Biology 34: 59-66 DOI: 10.1007/BF00390788.
908	Sars GO. 1921. An account of the Crustacea of Norway with short descriptions and figures of all
909	the species. Vol. III. Copepoda Monstrilloida & Notodelphyoida. The Bergen Museum,
910	Bergen.
911	Scott T. 1904. IVNotes on some rare and interesting marine Crustacea. Twenty-second Annual
912	Report of the Fishery Board for Scotland Part III: 242–260, Pls. 13–15.
913	Shively S, Miller WR. 2009. The use of HMDS (hexamethyldisilazane) to replace Critical Point



	Drying (CPD) in the preparation of tardigrades for SEM (Scanning Electron Microscope)
915	imaging. Transactions of the Kansas Academy of Science 112: 198-200.
916	Suárez-Morales E. 2001. An aggregation of monstrilloid copepods in a western Caribbean reef
917	area: ecological and conceptual implications. Crustaceana 74: 689-696.
918	Suárez-Morales E. 2007. Historical record and supplementary description of Cymbasoma
919	bullatum (A. Scott) (Copepoda: Monstrilloida) from the "Albatross" cruise in the
920	Philippines. Zootaxa 1662: 25–33.
921	Suárez-Morales E. 2011. Diversity of the Monstrilloida (Crustacea: Copepoda). <i>PLoS ONE</i> 6:
922	e22915 DOI: 10.1371/journal.pone.0022915.
923	(Suárez-Morales E, Dias C. 2000. Two new species of <i>Monstrilla</i> (Copepoda: Monstrilloida)
924	from Brazil. Journal of the Marine Biological Association of the United Kingdom 80:
925	(1031–1039.)
026	
926	Suárez-Morales E, Ivanenko VN. 2004. Two new species of <i>Monstrillopsis</i> Sars (Crustacea:
926	Suárez-Morales E, Ivanenko VN. 2004. Two new species of <i>Monstrillopsis</i> Sars (Crustacea: Copepoda: Monstrilloida) from the White Sea and Norway, with comments on <i>M. dubia</i>
927	Copepoda: Monstrilloida) from the White Sea and Norway, with comments on <i>M. dubia</i>
927 928	Copepoda: Monstrilloida) from the White Sea and Norway, with comments on <i>M. dubia</i> Scott. <i>Arctic</i> 57: 37–46.
927 928 929	Copepoda: Monstrilloida) from the White Sea and Norway, with comments on <i>M. dubia</i> Scott. <i>Arctic</i> 57: 37–46. Suárez-Morales E, McKinnon AD. 2014. The Australian Monstrilloida (Crustacea: Copepoda) I.
927928929930	Copepoda: Monstrilloida) from the White Sea and Norway, with comments on <i>M. dubia</i> Scott. <i>Arctic</i> 57: 37–46. Suárez-Morales E, McKinnon AD. 2014. The Australian Monstrilloida (Crustacea: Copepoda) I. <i>Monstrillopsis</i> Sars, <i>Maemonstrilla</i> Grygier & Ohtsuka, and <i>Australomonstrillopsis</i> gen.
927928929930931	Copepoda: Monstrilloida) from the White Sea and Norway, with comments on <i>M. dubia</i> Scott. <i>Arctic</i> 57: 37–46. Suárez-Morales E, McKinnon AD. 2014. The Australian Monstrilloida (Crustacea: Copepoda) I. <i>Monstrillopsis</i> Sars, <i>Maemonstrilla</i> Grygier & Ohtsuka, and <i>Australomonstrillopsis</i> gen. nov. <i>Zootaxa</i> 3779: 301–340 DOI: 10.11646/zootaxa.3779.3.1.
927928929930931932	Copepoda: Monstrilloida) from the White Sea and Norway, with comments on <i>M. dubia</i> Scott. <i>Arctic</i> 57: 37–46. Suárez-Morales E, McKinnon AD. 2014. The Australian Monstrilloida (Crustacea: Copepoda) I. <i>Monstrillopsis</i> Sars, <i>Maemonstrilla</i> Grygier & Ohtsuka, and <i>Australomonstrillopsis</i> gen. nov. <i>Zootaxa</i> 3779: 301–340 DOI: 10.11646/zootaxa.3779.3.1. Suárez-Morales E, McKinnon AD. 2016. The Australian Monstrilloida (Crustacea: Copepoda) II.
927928929930931932933	Copepoda: Monstrilloida) from the White Sea and Norway, with comments on <i>M. dubia</i> Scott. <i>Arctic</i> 57: 37–46. Suárez-Morales E, McKinnon AD. 2014. The Australian Monstrilloida (Crustacea: Copepoda) I. <i>Monstrillopsis</i> Sars, <i>Maemonstrilla</i> Grygier & Ohtsuka, and <i>Australomonstrillopsis</i> gen. nov. <i>Zootaxa</i> 3779: 301–340 DOI: 10.11646/zootaxa.3779.3.1. Suárez-Morales E, McKinnon AD. 2016. The Australian Monstrilloida (Crustacea: Copepoda) II. <i>Cymbasoma</i> Thompson, 1888. <i>Zootaxa</i> 4102: 1–129 DOI: 10.11646/zootaxa.4102.1.1.



937	Suárez-Morales E, Carrillo A, Morales-Ramírez A. 2013. Report on some monstrilloids
938	(Crustacea: Copepoda) from a reef area off the Caribbean coast of Costa Rica, Central
939	America with description of two new species. Journal of Natural History 47: 619-638
940	DOI: 10.1080/00222933.2012.742933.
941	Suárez-Morales E, Harris LH, Ferrari FD, Gasca R. 2014. Late postnaupliar development of
942	Monstrilla sp. (Copepoda: Monstrilloida), a protelean endoparasite of benthic
943	polychaetes. Invertebrate Reproduction & Development 58: 60–73 DOI:
944	10.1080/07924259.2013.816787.
945	Suárez-Morales E, Ramírez FC, Derisio C. 2008. Monstrilloida (Crustacea: Copepoda) from the
946	Beagle Channel, South America. Contributions to Zoology 77: 217–226.
947	Van Cleave HJ, Ross JA. 1947. A method for reclaiming dried zoological specimens. Science
948	105: 318.
949	Vogler AP, Monaghan MT. 2007. Recent advances in DNA taxonomy. Journal of Zoological
950	Systematics and Evolutionary Research 45: 1–10 DOI: 10.1111/j.1439-
951	0469.2006.00384.x.
952	Walter TC, Boxshall GA. 2017. World of Copepods database. Available at
953	http://www.marinespecies.org/copepoda.
954	White TJ, Bruns T, Lee S, Taylor J. 1990. Amplification and direct sequencing of fungal
955	ribosomal RNA genes for phylogenetics. In: PCR protocols. London: Academic Press,
956	315–322.
957	Willett CS. 2012. Quantifying the elevation of mitochondrial DNA evolutionary substitution
958	rates over nuclear rates in the internal copepod Tigriopus californicus. Journal of
959	Molecular Evolution 74: 310–318 DOI: 10.1007/s00239-012-9508-1.

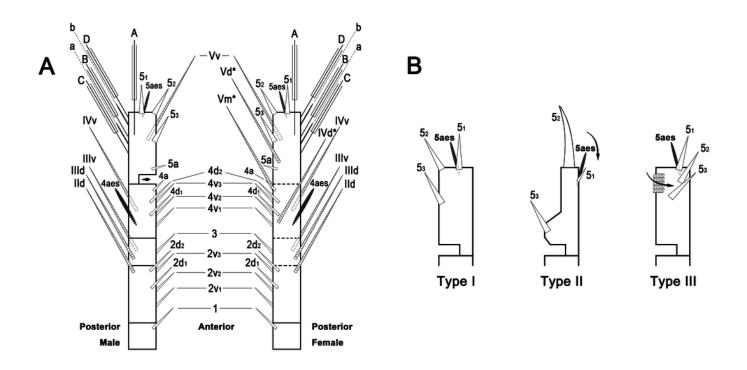




960	Zagoskin MV, Lazareva VI, Grishanin AK, Mukha DV. 2014. Phylogenetic information content
961	of Copepoda ribosomal DNA repeat units: ITS1 and ITS2 impact. BioMed Research
962	International 2014: Article ID 926342, 15 pages DOI: 10.1155/2014/926342.

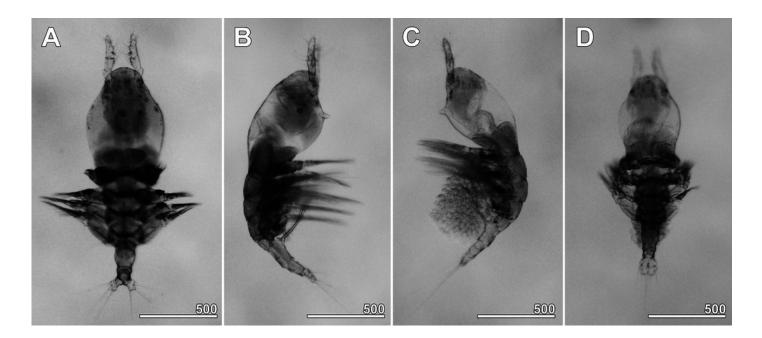
Schematic diagram of basic setal armature of adult monstrilloids.

(A) Updated nomenclatural terms for setal elements of males (left) and females (right), with geniculation indicated by arrow. With respect to the anatomical axes of the antennules, the terms "anterior" and "posterior" pertain to the ancestral, fundamental condition, following Huys et al. (2007). **(B)** Recommended convention for labeling setal elements on various types of distal antennular segment in male monstrilloids, with apical aesthetasc 5aes serving as reference marker and potential translocation patterns of spiniform elements 5_{1-3} shown by arrows—not to be constructed as an evolutionary hypothesis of character transformation.



Monstrillopsis longilobata Lee, Kim & Chang, 2016, microphotographs of females.

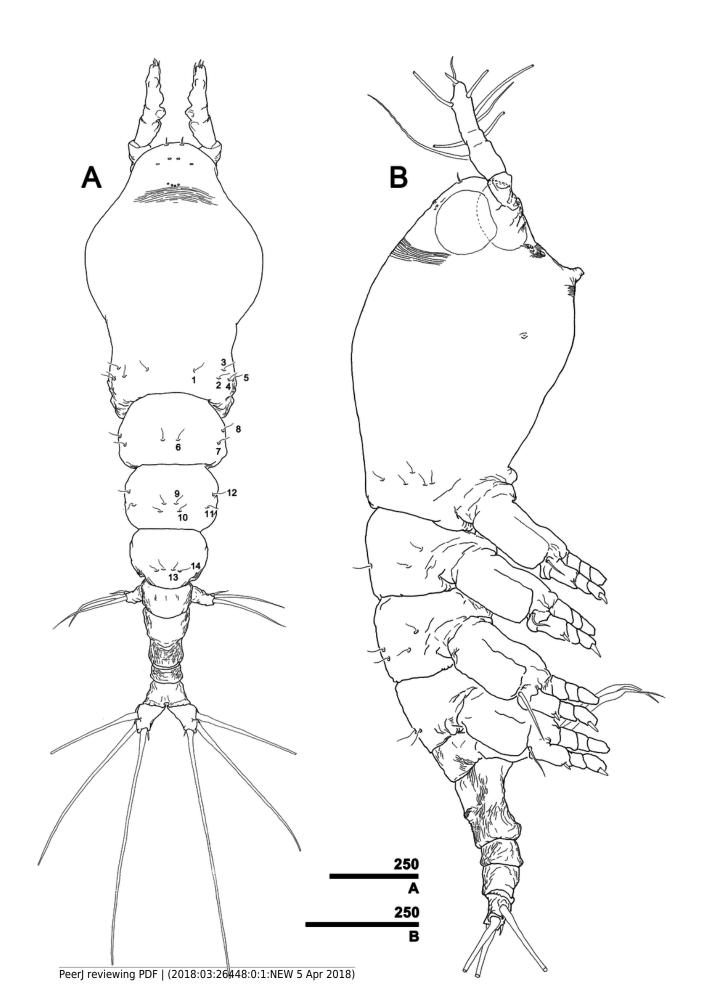
(A) Habitus showing widely spread legs 2–4, dorsal. (B) Habitus showing ventrally projecting ovigerous spines without eggs, lateral. (C) Habitus showing egg mass attached to ovigerous spines, lateral. (D) Habitus with subthoracic brooding, dorsal. Scale bars in µm.





Monstrillopsis longilobata Lee, Kim & Chang, 2016, female.

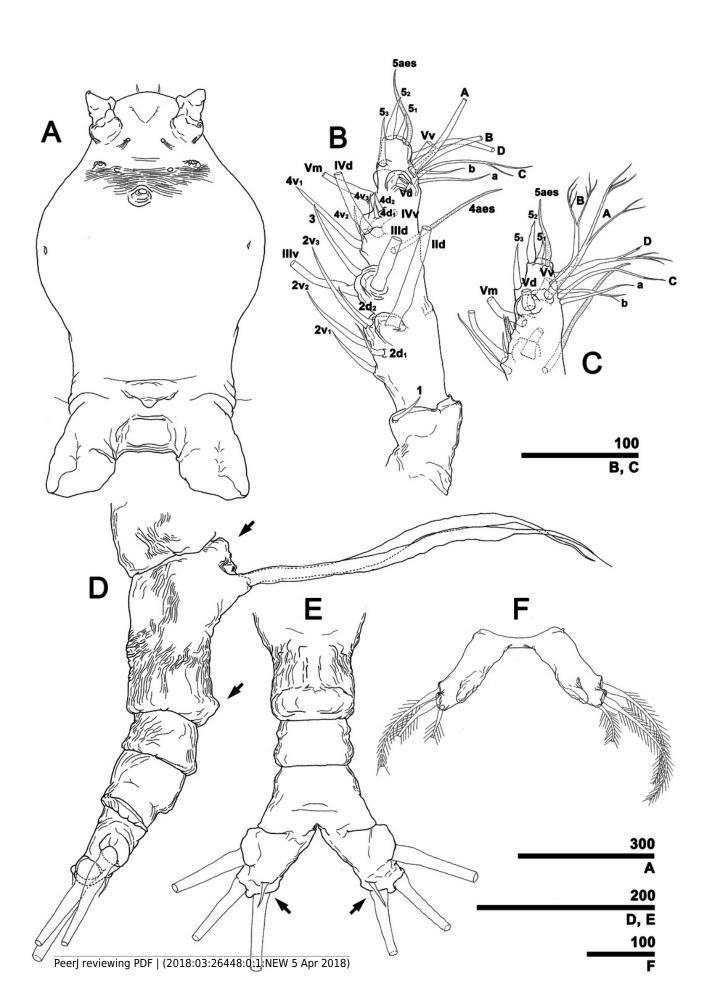
(A) Habitus, dorsal, with right pit-setae 1-14 of right side indicated (cf. Fig. 7A-D). (B) Habitus, lateral. Scale bars in μm .





Monstrillopsis longilobata Lee, Kim & Chang, 2016, female.

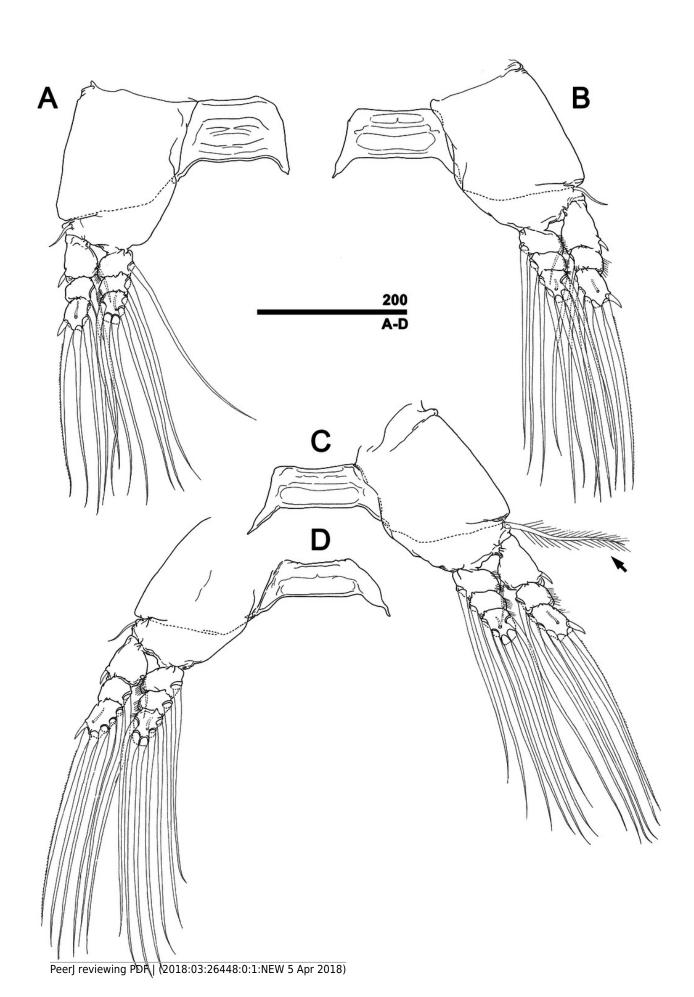
- (A) Cephalothorax, ventral. (B) Antennule, right, dorsal, setal elements labeled as in Fig 1A.
- (C) Detailed of tip of antennule (putative segment 5), right, dorsal, setal elements labeled as in Fig 1A. (D) Urosome, lateral, showing antero- and posteroventral protuberances of genital compound somite (arrows) and ovigerous spines. (E) Urosome, ventral, showing caudal rami with short ventral setae (arrows) (cf. Fig. 7A). (F) Fifth legs, anterior. Scale bars in µm.





Monstrillopsis longilobata Lee, Kim & Chang, 2016, female, swimming legs with intercoxal sclerites.

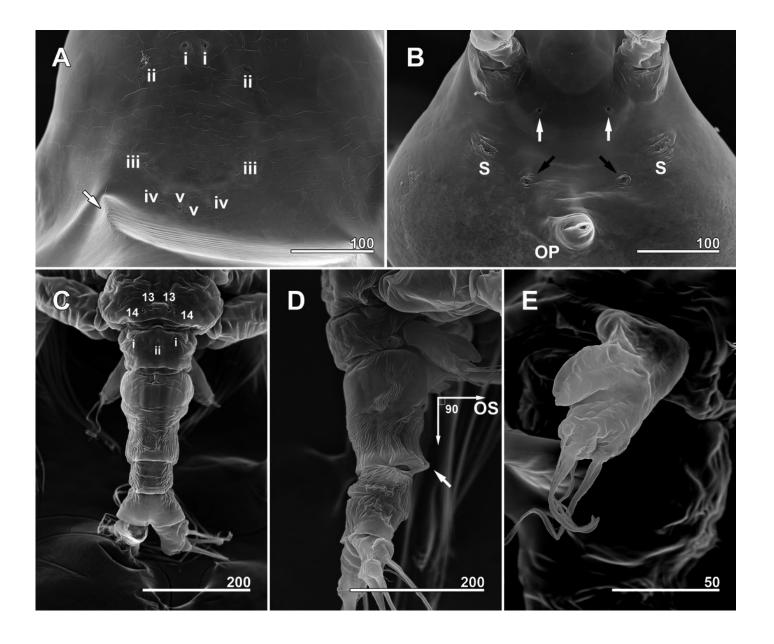
(A) Leg 1, right, anterior. (B) Leg 2, left, anterior. (C) Leg 3 with well-developed basal seta (arrow), left, anterior. (D) Leg 4, right, anterior. Scale bar in μm.





Monstrillopsis longilobata Lee, Kim & Chang, 2016, female, SEM.

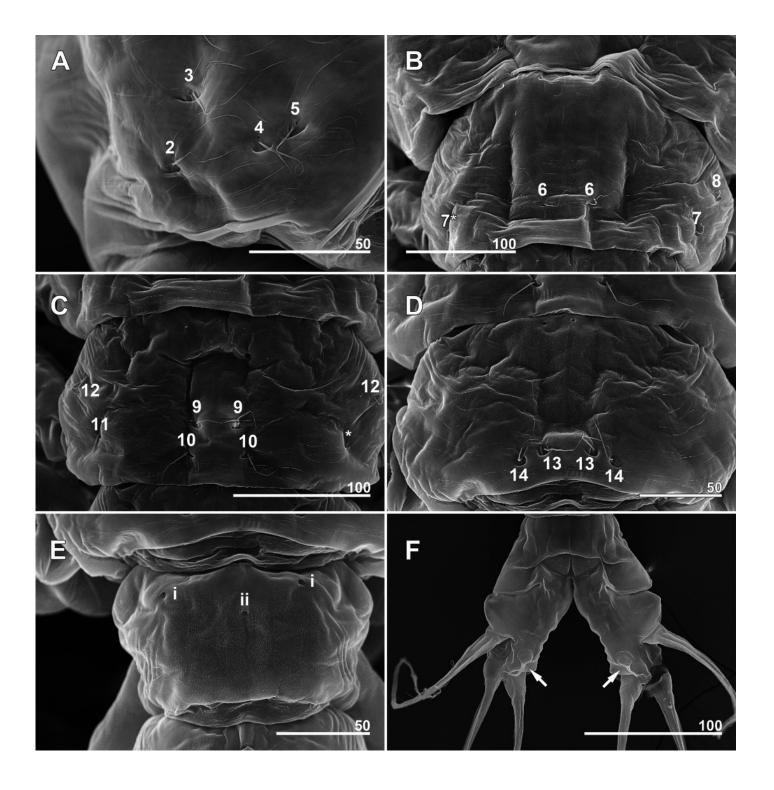
(A) Anterior dorsum of cephalothorax showing simple pores (i–v) and band of striations (arrow). (B) Anterior ventral surface of cephalothorax showing scars (S), oral papilla (OP), and pores (arrows). (C) Urosome, dorsal, showing wrinkling on genital compound somite and postgenital somite, pit-setae (13, 14), and simple pores (i, ii). (D) Urosome, lateral, with ventrally projecting ovigerous spines (OS) and posteroventral bulge of genital compound somite (arrow). (E) Fifth leg, left. Scale bars in µm.





Monstrillopsis longilobata Lee, Kim & Chang, 2016, female, arrangement of pit-setae (1–14) and urosomal pores (i, ii), SEM.

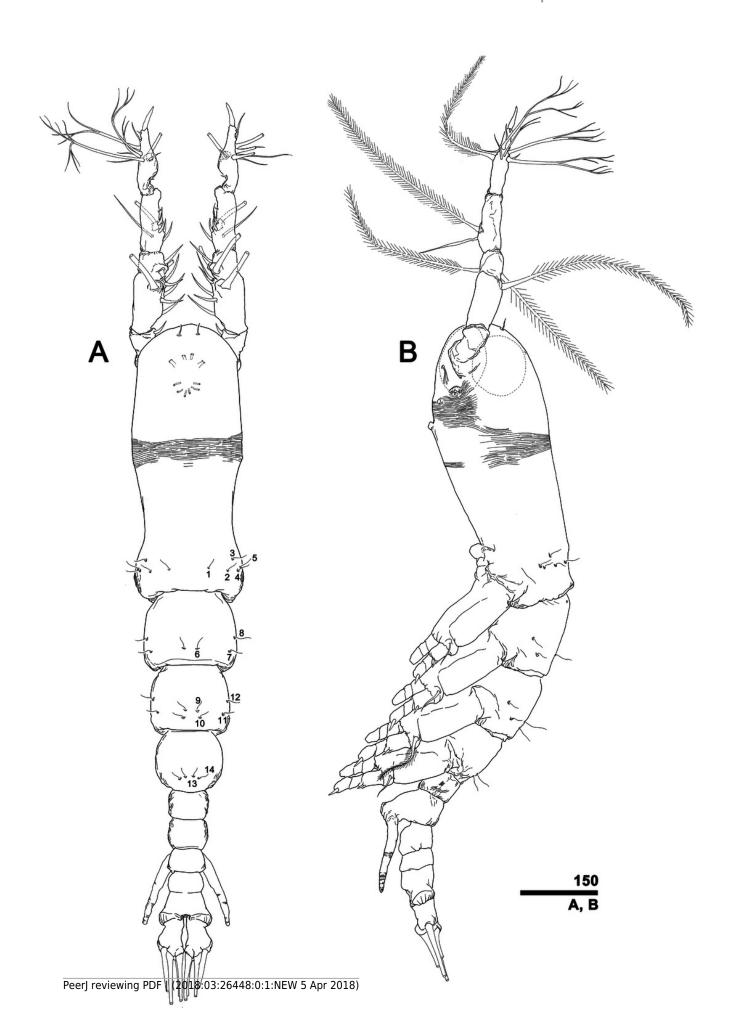
(A) Incorporated first pediger, right side, dorsolateral, showing closely spaced pit-setae 4 and 5. (B) First free pediger, dorsal, left element 7* somewhat ambiguous while right side clearly displaying three pit-setae. (C) Second free pediger, dorsal, presumed site of unseen element 11 on right side marked with asterisk (*). (D) Third free pediger, dorsal. (E) First urosomal somite, dorsal, showing odd number (3) simple pores (i, ii). (F) Caudal rami with extremely short ventral setae (arrows), ventral. Scale bars in µm.





Monstrillopsis longilobata Lee, Kim & Chang, 2016, male.

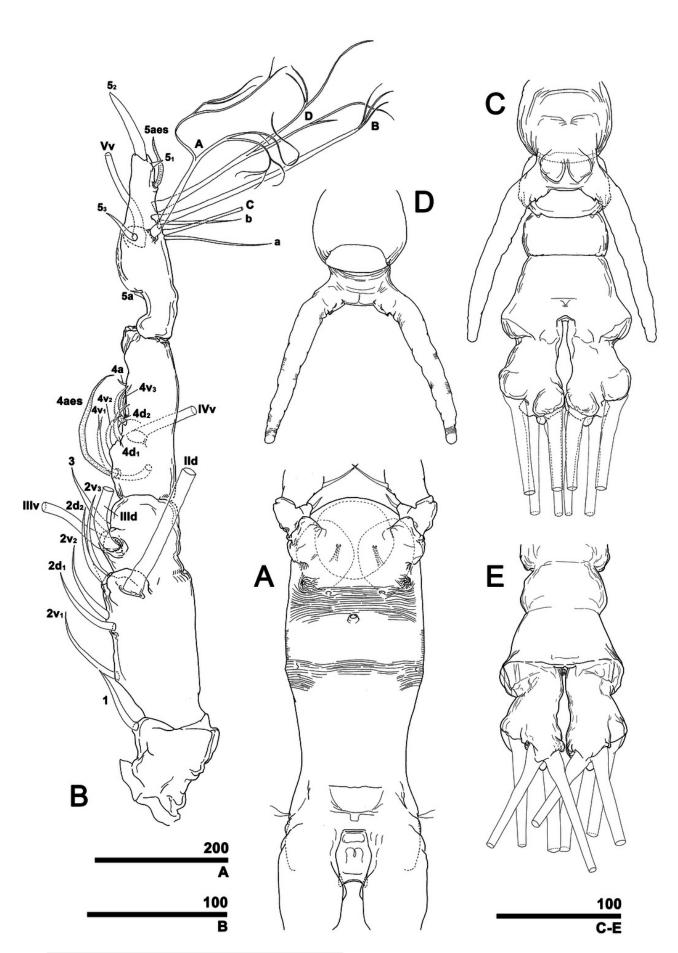
(A) Habitus, dorsal, with right pit-setae 1–14 of right side indicated. (B) Habitus, lateral. Scale bar in μm .





Monstrillopsis longilobata Lee, Kim & Chang, 2016, male.

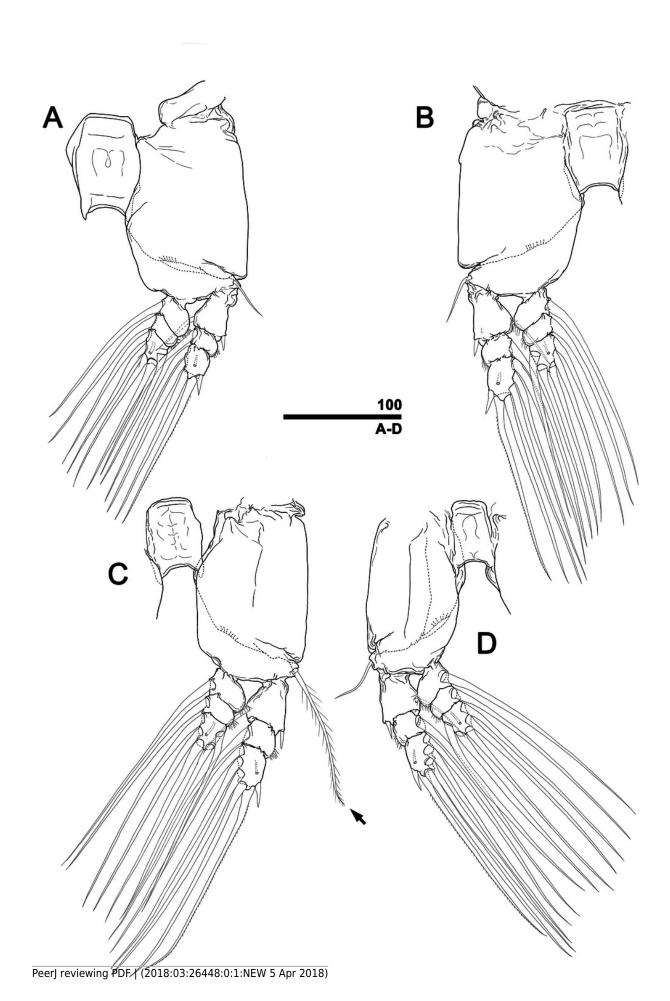
(A) Cephalothorax, ventral. (B) Right antennule, dorsal, with setal elements labeled as in Fig. 1A. (C) Urosome, ventral (cf. Fig. 11G). (D) Genital apparatus, dorsal. (E) Posterior part of urosome, dorsal (cf. Fig. 12C). Scale bars in μm.





Monstrillopsis longilobata Lee, Kim & Chang, 2016, male, swimming legs with intercoxal sclerites.

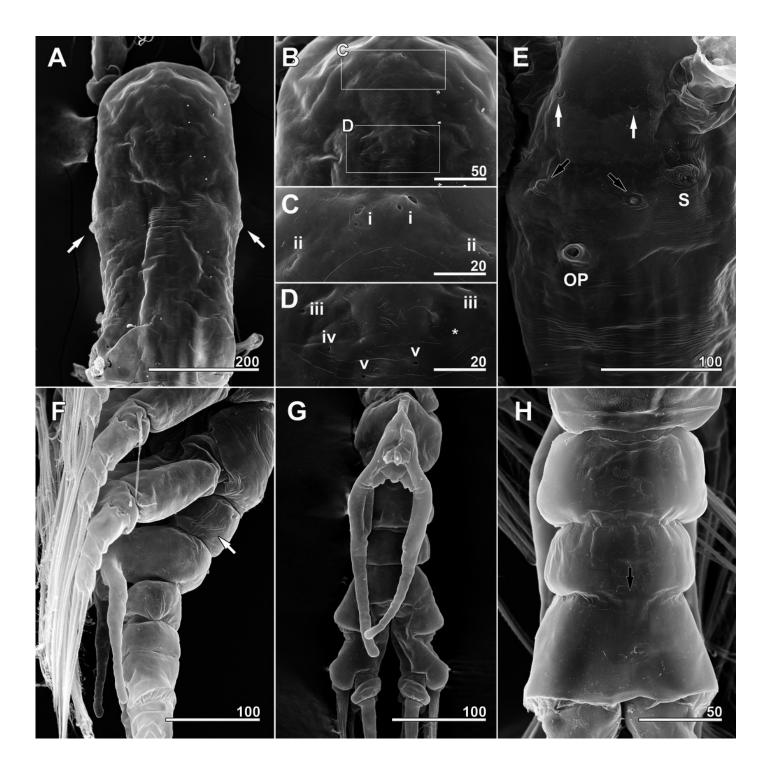
(A) Leg 1, left, anterior. (B) Leg 2, right, anterior. (C) Leg 3 with well-developed basal seta (arrow), left, anterior. (D) Leg 4, right, anterior. Scale bars in μ m.





Monstrillopsis longilobata Lee, Kim & Chang, 2016, male, SEM.

(A) Cephalothorax, dorsal, showing dorsal band of striations and crumpled lateral areas (arrows). (B) Anterior dorsum of cephalothorax, dorsal, showing general arrangement of simple pores. (C) Detail of anterior pore group in B, showing pores i and ii. (D) Detail of posterior pore group in B, showing pores iii-v, with presumed site of missing right pore iv marked by asterisk (*). (E) Anterior ventral surface of cephalothorax showing scar (S), oral papilla (OP), and pores (arrows). (F) Urosome, lateroventral, showing lateral striation on first urosomal somite (arrow). (G) Urosome with extremely elongated genital lappets, ventral. (H) Urosomal somites, dorsal, showing area of partial fusion between penultimate somite and anal somite (arrow). Scale bars in µm.



Monstrillopsis longilobata Lee, Kim & Chang, 2016, male (A-D) and female (E), SEM.

(A) Incorporated first pediger, left side, dorsal, showing arrangement of pit-setae 1–5. (B)
First urosomal somite, dorsal, showing odd number (3) simple pores (i, ii). (C) Caudal rami, dorsal, each armed with four well-developed setae (arrow indicating socket of fellen seta).
(D) Legs 4 joined by rectangular intercoxal sclerite (arrow), posterior. (E) Female legs 4 joined by wide intercoxal sclerite (arrow), anterior. Scale bars in μm.

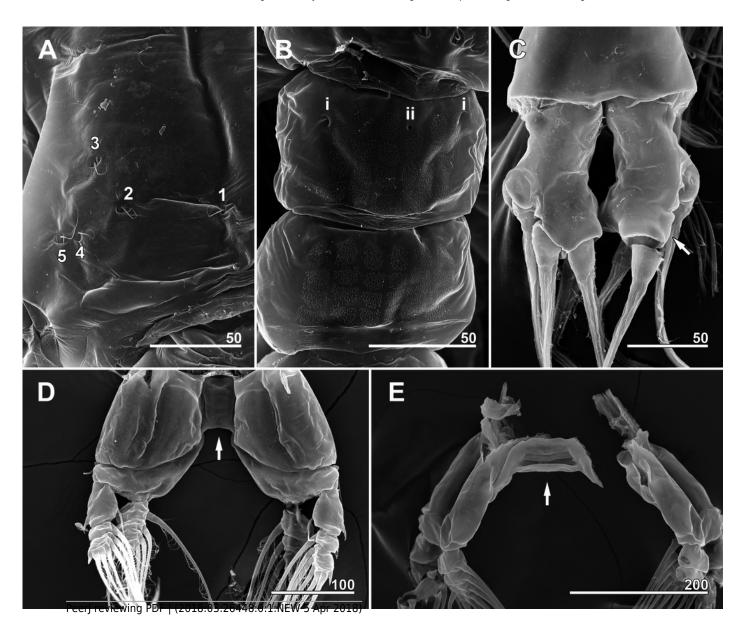




Table 1(on next page)

Information of primers used for PCR amplifications and thermal cycling profiles.

Primer sequences are given based on the nucleic acid notation formalized by the International Union of Pure and Applied Chemistry (IUPAC).

Gene	Primer	Primer sequence (5'-3') and thermal cycling profile	Reference
	XcoiF	ATAACRCTGTAGTAACTKCTCAYGC	This study
mtCOI	HCO2198	TAAACTTCAGGGTGACCAAAAAATCA	Folmer et al., 1994
		94 °C, 5 min + [94 °C, 40 sec; 50 °C, 45 sec; 72 °C, 45 sec] ₄₀ + 72 °C, 7 min	
	ITS5	GGAAGTAAAAGTCGTAACAAGG	White et al., 1990
ITS1-5.8S-ITS2	ITS4	TCCTCCGCTTATTGATATGC	White et al., 1990
		94 °C, 5 min + [94 °C, 1 min; 48 °C, 1.5 min; 72 °C, 1.5 min] ₃₅ + 72 °C, 7 m	in
	28S-F1a	GCGGAGGAAAAGAAACTAAC	Ortman, 2008
28S rRNA	28S-R1a	GCATAGTTTCACCATCTTTCGGG	Ortman, 2008
		94 °C, 5 min + [94 °C, 1 min; 50 °C, 1 min; 72 °C, 1 min] ₃₅ + 72 °C, 7 min	



Table 2(on next page)

List of specimens used for molecular analysis with GenBank Accession numbers.

Con a airm an	Sex	Specimen voucher	GenBank accession number		
Specimen			mtCOI	ITS1-5.8S-ITS2	28S rRNA
Monstrillopsis longilobata	female	HYU-Mon0033	nd	nd	KY563308
Monstrillopsis longilobata	female	HYU-Mon0034	nd	MG645220	KY563309
Monstrillopsis longilobata	female	HYU-Mon0035	KY553229	MG645221	KY563310
Monstrillopsis longilobata	male	HYU-Mon0036	nd	MG645222	KY563311
Monstrillopsis longilobata	male	HYU-Mon0037	KY553230	MG645223	KY563312
Monstrillopsis longilobata	male	HYU-Mon0038	nd	MG645224	KY563313
Monstrillopsis longilobata	female	HYU-Mon0042	MF447158	MG645225	MF447164
Monstrillopsis longilobata	female	HYU-Mon0043	MF447159	MG645226	MF447165
Monstrillopsis longilobata	female	HYU-Mon0044	MF447160	MG645227	MF447166
Monstrillopsis longilobata	male	HYU-Mon0045	MF447161	MG645228	nd
Monstrillopsis longilobata	male	HYU-Mon0046	MF447162	nd	MF447167
Monstrillopsis longilobata	male	HYU-Mon0047	MF447163	nd	MF447168

nd: no data; accession numbers for newly obtained sequences presented in bold.