



HOKKAIDO UNIVERSITY

Title	Integrative taxonomy of <i>Pseudolepeophtheirus longicauda</i> (Crustacea: Copepoda: Caligidae) parasitic on <i>Platichthys stellatus</i> (Actinopterygii: Pleuronectidae)
Author(s)	Homma, Riko; Uyeno, Daisuke; Kakui, Keiichi
Citation	Parasitology International, 78, 102135 https://doi.org/10.1016/j.parint.2020.102135
Issue Date	2020-10
Doc URL	https://hdl.handle.net/2115/82838
Rights	©2020. This manuscript version is made available under the CC-BY-NC-ND 4.0 license https://creativecommons.org/licenses/by-nc-nd/4.0/
Rights(URL)	https://creativecommons.org/licenses/by/4.0/
Type	journal article
File Information	Parasitology International_2020.pdf



This is an Accepted Manuscript of an article published by Elsevier in *Parasitology International* on 13 May 2020, available online: <https://doi.org/10.1016/j.parint.2020.102135>

©2020. This manuscript version is made available under the CC-BY-NC-ND 4.0 license <http://creativecommons.org/licenses/by-nc-nd/4.0/>

Integrative taxonomy of *Pseudolepeophtheirus longicauda* (Crustacea: Copepoda: Caligidae)

parasitic on *Platichthys stellatus* (Actinopterygii: Pleuronectidae)

Riko Homma^{a,1}, Daisuke Uyeno^b, Keiichi Kakui^{c,*}

^a*Department of Natural History Sciences, Graduate School of Science, Hokkaido University,*

N10 W8 Kita-ku, Sapporo 060-0810, Japan

^b*Graduate School of Science and Engineering, Kagoshima University, 1-21-40 Korimoto,*

Kagoshima 890-0065, Japan

^c*Department of Biological Sciences, Faculty of Science, Hokkaido University, N10 W8*

Kita-ku, Sapporo 060-0810, Japan

¹Present address. Graduate School of Agriculture, Hokkaido University, N9 W9 Kita-ku,

Sapporo 060-8589, Japan

*Corresponding author.

E-mail address: keiichikakui@gmail.com (K. Kakui).

20 ABSTRACT

21 Based on specimens from the gill cavities of one *Platichthys stellatus* individual collected in
22 the Sea of Japan, we investigated the taxonomic status of the enigmatic caligid genus
23 *Pseudolepeophtheirus* and its type species, *Pseudolepeophtheirus longicauda*. In a maximum
24 likelihood (ML) tree based on 18S rRNA gene sequences, the sequence from our sample was
25 nested in a well-supported *Lepeophtheirus* clade, along with the type species, confirming that
26 *Pseudolepeophtheirus* should be considered a junior synonym of *Lepeophtheirus*; our
27 morphological data support this synonymy. Although a previous study had synonymized
28 *Pseudolepeophtheirus longicauda* with *Lepeophtheirus parvicruris*, we found that the former
29 differs morphologically from the latter in having a short leg-4 exopod, with the articulation
30 between the first and second segments not evident (the shape of the posterior striated
31 membrane on the leg-2 intercoxal sclerite also differs between two species), and detected
32 slight differences in 18S rRNA sequences between two taxa. We thus concluded that this
33 synonymy is invalid, and reinstate *Lepeophtheirus longicauda* as a valid species. A ML
34 analysis of COI sequences from *Pl. stellatus* (the host fish for both *L. longicauda* and *L.*
35 *parvicruris*) showed the host species to comprise distinct northwestern- and
36 northeastern-Pacific clades. *Lepeophtheirus longicauda* is distributed in the northwestern
37 Pacific and *L. parvicruris* in the northeastern Pacific, indicating co-divergence of the two
38 copepod species with the host lineages.

39

40 *Keywords:*

41 Siphonostomatoida, sea lice, ectoparasite, phylogeny, COX1, redescription

42

43

44 **1. Introduction**

45

46 Copepods in the family Caligidae, known as sea lice, are ectoparasites mainly on
47 marine fishes. Using their ventrally concave, discoid cephalothorax as a sucker
48 (“cephalothoracic sucker” sensu [1]), they slide smoothly over the surface of the attachment
49 sites (gill filaments, buccal cavity, operculum, skin, etc.) of their host and feed on the host’s
50 mucus, epithelial tissues, and sometimes blood by rasping, scraping, and sucking [2]. Severe
51 infections by caligids cause serious damage to farmed fishes [3,4]. With more than 500
52 species, the Caligidae is the most species-rich family in the Siphonostomatoida [5]. Dojiri
53 and Ho [6] recently revised the taxonomy of this family based on morphology, but the
54 taxonomic status of some genera remains unclear.

55 Markevich [7] established the caligid genus *Pseudolepeophtheirus* for *P. longicauda*

56 Markevich, 1940, based on the morphology of the specimens collected from the gill cavity of

57 *Platichthys stellatus* (Pallas, 1788) (Pleuronectidae) collected from the Sea of Japan near

58 Vladivostok [8] (Fig. 1; cf. [6,7,9–11]). The second member of the genus, *P. schmidt* Gusev,
 59 1951, was described from the pleuronectid *Limanda punctatissima* (Steindachner, 1879)
 60 collected from Nakhodka Bay in the Sea of Japan; it differs from *P. longicauda* in having 1)
 61 the abdomen slightly shorter than the genital complex and 2) leg 4 in the form of a small
 62 papilla [8]. The third species discovered, *P. mediterraneus* Paperna, 1964, described from
 63 chalimus-stage specimens found on gills of the mugilid *Chelon ramada* (Risso, 1827)
 64 collected in the Mediterranean [13], was later synonymized with *Pseudocaligus apodus* Brian,
 65 1924 (currently accepted as *Caligus apodus*) [14]. *Pseudolepeophtheirus* closely resembles
 66 the confamilial genus *Lepeophtheirus* von Nordmann, 1832, but differs in having the exopod
 67 of leg 4 so much reduced that it is referred to as “a small two-segmented process” in *P.*
 68 *longicauda*, and “a small papilla” in *P. schmidt* (p. 227 in [8]).

69 In the Caligidae, the reduced leg 4 has been used as one of the characters
 70 distinguishing among closely similar genera, e.g., *Pseudocaligus* from *Caligus*,
 71 *Pseudolepeophtheirus* from *Lepeophtheirus* [7,15], but Kabata [16] questioned its validity for
 72 that purpose and suggested that *Pseudocaligus* and *Pseudolepeophtheirus* should be relegated
 73 to synonymy with *Caligus* and *Lepeophtheirus*, respectively. Dojiri and Ho [6] followed
 74 Kabata’s [16] suggestion and synonymized both pairs of genera. They also synonymized *P.*
 75 *longicauda* with *Lepeophtheirus parvicruris* Fraser, 1920, which was originally described
 76 from *Pl. stellatus* collected around Vancouver Island, northeastern Pacific [10]. As Dojiri and

Ho [6] could not find any specimens or illustrations of *P. longicauda*—Markevich [7] did not illustrate the species, and the type specimens had been lost—this synonymy was based only on the text descriptions by Markevich.

In a report on caligids attached to coastal fishes from the Sea of Japan and Sea of Okhotsk around Sakhalin Island (Fig. 1), Vinogradov [9] included two *Pseudolepeophtheirus* species, one of which (collected from *Pleuronectes stellatus*) he identified as "*Pseudolepeophtheirus parvicruris* Fraser, 1920" (p. 259 in [9]). An illustration of leg 4 (fig. 9M of [9]) shows a short exopod (2.3 times longer than wide), with no articulation evident between first and second exopodal segments. In contrast, the exopod of leg 4 in *L. parvicruris* reported from the northeastern Pacific is longer (3.6 times or more longer than wide), and the two exopodal segments are articulated [6,9,10]. This morphological difference, along with the locality and host fish, suggest that Vinogradov's [9] *P. parvicruris* was actually *P. longicauda*. The other *Pseudolepeophtheirus* species that Vinogradov [9] reported was *P. schmidtii* (collected from *Limanda punctatissima*), with leg 4 in the form of a one-segmented appendage (fig. 9E of [9]).

The synonymy [6] of *P. longicauda* with *L. parvicruris* lacked adequate morphological data for the former species and has not been tested molecularly. Furthermore, the morphology of *P. parvicruris* sensu [9] suggests that *P. longicauda* and *L. parvicruris* may not be conspecific. Our study deals with copepod specimens recently obtained from *Pl.*

stellatus, collected from the Sea of Japan off the northwestern coast of Hokkaido, which seemed to be conspecific to *P. parvicruris* sensu [9], i.e., *P. longicauda*. Through morphological observations and a molecular phylogeny, we elucidate the taxonomic status of *Pseudolepeophtheirus* and *P. longicauda*.

2. Materials and methods

2.1. Sampling and morphological observation

A fresh individual of *Platichthys stellatus* (total length, 32.1 cm), collected in the Sea of Japan and landed at Asari, Hokkaido, northern Japan (43°10'37.5"N 141°03'55.6"E; Fig. 1), was obtained on 23 May 2017. Ten female caligids (hereafter referred to as “Caligid sp. A”) were collected from the inner surface of the left and right opercula of the fish and were fixed and preserved in 70% ethanol. The methods used in dissection, specimen preparation, light microscopy, scanning electron microscopy (SEM), and drawing were as described in [17]. The following caligid measurements were taken from digital images by using ImageJ [18]: total body length (TL: length from the anterior margin of the frontal plate to the posterior margin of the caudal ramus); cephalothorax length (CL) and width (CW); genital-complex length (GL) and width (GW); abdomen length (AL) and width (AW); caudal-ramus length

(CrL) and width (CrW). In some specimens, measurements were not made when the relevant structures were strongly deformed by fixation or dissection. The length of the exopod on leg 4 corresponds to the combined length of first and second segments; its width was measured at the widest part of the second segment. Specimens studied were deposited in the Invertebrate Collection of the Hokkaido University Museum (ICHUM), Sapporo, Japan.

2.2. DNA extraction and sequence determination

Total DNA was extracted from the egg-sac of three copepod specimens and a piece of host muscle by using a NucleoSpin Tissue XS Kit (TaKaRa Bio, Japan). Table 1 lists the primers used in this study (cf. [19–22]). PCR amplification conditions for part of the cytochrome *c* oxidase subunit I (COI) gene with TaKaRa Ex taq DNA polymerase (TaKaRa Bio) were 94°C for 1 min; 35 cycles of 98°C for 10 s, 50°C (copepods) or 64°C (fish) for 30 s, and 72°C for 50 s; and 72°C for 2 min. Conditions for amplification of the nearly complete 18S rRNA (18S) gene from copepods with KOD FX Neo polymerase (Toyobo, Japan) were 94°C for 2 min; 45 cycles of 98°C for 10 s, 65°C for 30 s, and 68°C for 1 min; and 68°C for 2 min. Nucleotide sequences were determined by direct sequencing with a BigDye Terminator Kit ver. 3.1 and a 3130 or 3730 Genetic Analyzer (Life Technologies, California, USA), and fragments were concatenated by using MEGA7 [23]. The sequences we obtained were

deposited in the International Nucleotide Sequence Database (INSD) through the DNA Data Bank of Japan (DDBJ), under accession numbers LC512439–512441 (copepod COI), LC512442–512444 (copepod 18S), and LC515810 (fish COI).

2.3. Phylogenetic analyses

A copepod 18S dataset comprising 28 terminal copepod taxa, including *Caligid* sp. A, other caligids, and three outgroup taxa from Dissonidae and Pandaridae (Table 2: cf. [12,24–28]), was aligned by using MAFFT ver. 7 [29] with the “Q-INS-i” strategy [30]; the aligned sequences were trimmed in MEGA7 to the shortest length among the sequences (1675 nt). The optimal substitution model was GTR + I + G, determined under the corrected Akaike information criterion (AIC) with PartitionFinder 2.1.1 [31]. A maximum likelihood (ML) analysis was conducted in RAxML ver. 8.1.5 [32], and nodal support values were obtained through ML analyses of 1000 bootstrap pseudoreplicates [33]. A fish COI dataset comprising 17 *Pl. stellatus* sequences (including one from our host fish; Table 3; cf. [34–36]) and one *Pl. flesus* (Linnaeus, 1758) sequence was aligned by using MAFFT ver. 7 with the “Auto” strategy (“L-INS-i” selected; [37]); the aligned sequences were trimmed in MEGA7 to the shortest length among the sequences (558 nt). The optimal substitution models for different partitions determined under the corrected AIC with PartitionFinder 2.1.1 were F81 for the

first and second codons, and TrN for the third codon. A partitioned ML analysis was conducted in IQ-TREE ver. 1.6.8 [38,39], with nodal support values obtained by ultrafast bootstrap analysis of 1000 pseudoreplicates [40].

The 18S sequences from Caligid sp. A and two closely related taxa indicated by our ML analysis were realigned by eye according to the secondary structure of the honeybee 18S sequence [41]; the secondary structure of the “variable area” [42] with indels was predicted with CentroidFold [43] to check the indels’ position in the area.

Kimura [44] 2-parameter (K2P) distances among copepod sequences were calculated with MEGA7.

3. Results

3.1. Morphological description

Order Siphonostomatoida

Family Caligidae

Caligid sp. A (Figs. 2–5)

Host: *Platichthys stellatus* (Actinopterygii: Pleuronectidae).

172 Sampling locality: Sea of Japan off Asari, Hokkaido, Japan; depth unknown; GPS

173 data not available.

174 Attachment site: inner surface of left and right opercula.

175 Material examined (10 females): ICHUM6041, dissected, 1 vial and 6 slides;

176 ICHUM6042, dissected, 1 vial and 4 slides; ICHUM6043, dissected, 1 vial and 2 slides;

177 ICHUM6044, dissected, 1 vial and 2 slides; ICHUM6045, dissected, 1 vial and 1 slide, INSD

178 accession numbers LC512439 (COI) and LC512442 (18S); ICHUM6046, dissected, 1 vial

179 and 1 slide, LC512440 (COI) and LC512443 (18S); ICHUM6047, intact, 1 vial, LC512441

180 (COI) and LC512444 (18S); ICHUM6048, dissected, 1 vial and 1 slide; ICHUM6049,

181 dissected, 1 vial and 2 slides; ICHUM6050, dissected, 1 vial, 2 slides, and 3 SEM stubs.

182 Measurements: see Table 4.

183

184 3.1.1. *Description of adult females*

185 Body (Figs. 2, 3A) TL 6.6–8.3 mm (mean 7.7 mm; $n = 10$). Dorsal cephalothoracic

186 shield subcircular (CL/CW, 0.94–1.18; mean CL/CW, 1.08; $n = 9$), comprising about 30% of

187 TL. Free posterior margin of dorsal thoracic zone of shield slightly extending beyond

188 posterior end of lateral zones. Frontal plates without lunules. Genital complex fused with

189 fourth pedigerous somite, longer than wide (GL/GW, 1.06–1.22; mean GL/GW, 1.12; $n = 6$),

190 comprising about 30% of TL, with short posterolateral protrusion. Copulatory pores located

near base of leg 5. Abdomen 1-segmented (constriction in subposterior region found), longer than wide (AL/AW, 3.75–4.61; mean AL/AW, 4.27; $n = 6$), longer than genital complex (AL/GL, 1.15–1.65; mean AL/GL, 1.31; $n = 10$), comprising about 40% of TL, with terminal anal slit. Caudal rami with parallel sides, about 1.4 times longer than wide (CrL/CrW, 1.38–1.45; mean CrL/CrW, 1.41; $n = 10$). Each ramus with six plumose setae and ornamented with fine setules.

Antennule (Fig. 3C) 2-segmented; proximal segment with 26 or 27 plumose setae and small distal protrusion (Fig. 3C, arrow); distal segment bearing 12 distal elements and subdistal seta (possibly 1 distal element lost during dissection). Antenna (Fig. 3D) 3-segmented; proximal segment with spatulate, posteriorly-directed process; middle segment subrectangular, with small corrugated pad ventrally; distal segment forming recurved, tapering claw with proximal seta at base and longer middle seta. Post-antennal process (Fig. 3D) robust, weakly curved, carrying 2 basal papillae each with 3 sensillae; similar, adjacent papilla with 2 sensillae located on ventral surface of cephalothorax. Small, rounded cuticular swelling (Fig. 3D) present between antenna and post-antennal process.

Mandible (Fig. 3E) stylet-like, with 12 marginal teeth. Maxillule (Fig. 3F) comprising anterior papilla bearing 3 unequal setae and bifid posterior process with subspherical knob on base. Maxilla (Fig. 3G) 2-segmented, brachiform; proximal segment (lacertus) robust and unarmed; distal segment (brachium) slender, bearing large flabellum on mid-inner margin

210 plus bilaterally-serrate short canna and long calamus distally. Maxilliped subchelate (Fig. 3H,
 211 I); proximal segment robust with smooth myxal margin and 2 dorsal patches of scale-like
 212 processes; distal subchela sharply pointed, with long claw indistinctly fused to short shaft and
 213 proximal seta at base of claw. Sternal furca (Fig. 3J) with short, broad divergent tines bearing
 214 lamellar flange and bluntly rounded tip.

215 Leg 1 (Figs. 3K, 4A) biramous, with 2-segmented exopod and vestigial endopod.
 216 Intercoxal sclerite elongate, unarmed. Protopod with 1 outer and 1 posterior plumose setae.
 217 First exopodal segment with outer distal naked spine and posterior row of setules. Second
 218 exopod segment with 3 inner long plumose setae, subdistal short plumose seta, and 3 distal
 219 spines; spines except outermost one with accessory process (Fig. 4A). Endopod with
 220 bifurcate tip.

221 Leg 2 (Figs. 3L, 5A) biramous, with 3-segmented rami. Intercoxal sclerite rectangular,
 222 wider than long, with extensive striated membrane along posteriormargin; membrane
 223 strongly expanded in mid-line and as long as or longer than sclerite (Fig. 5A). First
 224 protopodal segment with posterior plumose seta and ventral spinule-bearing papilla. Second
 225 protopodal segment with outer distal plumose seta, posterior setule-bearing papilla, and outer
 226 and posterior striated membranes. First exopodal segment with inner distal plumose seta,
 227 outer distal bilaterally-serrate spine, outer distal and inner rows of setules, and outer striated
 228 membrane. Second exopodal segment with inner distal plumose seta, outer distal

229 bilaterally-serrate spine, and inner row of setules. Third exopodal segment with 5 plumose
 230 setae and 3 outer spines; proximal spine bilaterally-serrate, middle spine fringed with hyaline
 231 membrane, and distal spine with outer hyaline membrane and inner row of setules. First
 232 endopodal segment with inner plumose seta and outer row of setules. Second endopodal
 233 segment with 2 inner plumose setae and outer and inner rows of setules. Third endopodal
 234 segment with 6 plumose setae and outer and inner rows of setules.

235 Leg 3 (Figs. 3M, 4B, 5B) biramous, with 3-segmented exopod and 2-segmented
 236 endopod. Intercoxal sclerite trapezoid, with subrectangular striated membrane along posterior
 237 margin; membrane shorter than sclerite (Fig. 5B). Protopod large, modified to apron, with 1
 238 postero-inner and 1 outer plumose setae, 5 ventral setule-bearing papillae, outer and
 239 posterior striated membranes, and outer antero-dorsal corrugated pad. First exopodal segment
 240 with inner plumose seta and exopod spine fringed with hyaline membrane. Second exopodal
 241 segment with inner plumose seta, outer distal naked spine (absent in illustrated leg; but see
 242 Fig. 4B), and outer row of setules. Third exopodal segment with 4 plumose setae, 3 distal
 243 naked spines, and outer row of setules. First endopodal segment with inner plumose seta and
 244 outer row of setules. Second endopodal segment with 6 plumose setae and outer and inner
 245 rows of setules.

246 Leg 4 (Figs. 3N, 4C–E) uniramous, with 2-segmented exopod with articulation
 247 between first and second exopodal segments not evident (Fig. 4C–E). Protopod with outer

distal plumose seta. Exopod 2.2–2.9 (mean 2.47; $n = 7$) times longer than wide; first segment with outer distal naked spine; second segment with 2 or 3 distal bilaterally-serrate spines (spine-length decreasing from inner to outer; innermost spine 2 times or more longer than other(s)).

Leg 5 (Fig. 3O) composed of trifold process located near egg-sac attachment area of genital complex, with 3 plumose setae; papilla bearing plumose seta present on adjacent ventral surface of genital complex.

Variation. Among six leg-3 samples we observed (left and right of ICHUM6041, 6043, and 6050), one lacked any spines (right of ICHUM6041; cf. Fig. 3M) but the others had one outer distal naked spine (cf. Fig. 4B); the former may be an abnormal state. Among seven leg-4 samples we observed (left and right of ICHUM6044 and 6050; right of ICHUM6042, 6043, and 6046), three have 3 distal spines (cf. Fig. 3N) and the others have 2 distal spines (cf. Fig. 4C).

3.2. Molecular phylogenetic analysis of the caligid copepods

We obtained partial COI and nearly complete 18S sequences from three specimens of *Caligid* sp. A (ICHUM6045, 6046, 6047). The three COI sequences (LC512439–512441) were 658 nt long, translating to 219 amino acids. The maximum K2P distance among these

was 0.61%, representing four nucleotide substitutions. The sequence in the INSD most similar to our COI sequences, as determined by BLAST searches [45], was from *Lepeophtheirus hospitalis* Fraser, 1920 (accession number HM582235; identity score 84.32%, query cover 99%; [46]); the K2P distances between our sequences and the *L. hospitalis* sequence were 18.1–18.9%. To date, no COI sequences from *L. parvicruris* have been deposited in public databases [47].

The three 18S sequences (LC512442–512444) were identical and 1760 nt long. The 18S sequence includes one site in the V7 variable area (Fig. 6A) that was dimorphic (Y, i.e., C or T) in all three sequences we determined. In the ML tree (1675 nt; Fig. 7), all *Lepeophtheirus* sequences except *L. natalensis* Kensley and Grindley, 1973 formed a clade with 98% bootstrap support (BS). The clade included a sequence from *L. pectoralis* (O.F. Müller, 1776), the type species of *Lepeophtheirus*, and *Caligid* sp. A. *Caligid* sp. A forms a moderately supported (BS 74%) clade with *L. parvicruris* and *L. thompsoni* Baird, 1850. Aligned 18S sequences from *Caligid* sp. A, *L. parvicruris*, and *L. thompsoni* showed one indel and one incongruent site (Y vs. T) in the V7 variable area among the three taxa (Fig. 6B–D).

3.3. Phylogenetic relationships within the host fish, *Platichthys stellatus*

We obtained a partial COI sequence (619 nt; LC515810) from the host fish of our caligid specimens. In the ML tree (558 nt; Fig. 8), 17 *Pl. stellatus* sequences were divided into two clades. One clade included sequences from northeastern Pacific specimens with 62% ultrafast bootstrap support (uBS). The other comprised northwestern Pacific sequences, including our fish sequence, with 90% uBS. K2P distances between two clades were 0.7–1.3%; those among sequences within the northeastern and northwestern Pacific clades were 0.0–0.4% and 0.0–0.5%, respectively.

4. Discussion

Based on its locality (Sea of Japan), host fish (*Pl. stellatus*), and morphological features (e.g., body shape, and leg 4 bearing a short exopod, ca 2.5 times longer than wide), we concluded that Caligid sp. A is conspecific with *Pseudolepeophtheirus parvicruris* sensu [9] and *Pseudolepeophtheirus longicauda*. Here we have presented the first information on the armature of most appendages and the segmentation of the abdomen.

In the 18S ML tree, Caligid sp. A (= *P. longicauda*) formed a moderately supported (BS 74%) clade with *L. parvicruris* and *L. thompsoni*, which was nested in the clade containing all *Lepeophtheirus* except for *L. natalensis* (Fig. 7). The *Lepeophtheirus* clade included a sequence from *L. pectoralis*, the type species of *Lepeophtheirus*. Our results thus

305 molecularly confirm the synonymy of *Pseudolepeophtheirus* with *Lepeophtheirus* [6].

306 Although Dojiri and Ho [6] synonymized *Pseudolepeophtheirus longicauda* (now
 307 *Lepeophtheirus longicauda*) with *Lepeophtheirus parvicruris*, we concluded these are
 308 different species. Among 126 valid species and two recognized subspecies in *Lepeophtheirus*,
 309 including two species formerly placed in *Pseudolepeophtheirus* ([4,48,49], this study), *L.*
 310 *longicauda* shares the following combination of characters with *L. parvicruris* and three other
 311 species (*L. longiventralis* Yü & Wu, 1932; *L. marcepes* C.B. Wilson, 1944; and *L. schmidtii*
 312 (formerly *Pseudolepeophtheirus schmidtii*): 1) the abdomen is about as long as, or longer
 313 than, the genital complex (Kabata's [11] "long abdomen"); 2) CL is far shorter than GL+AL,
 314 with CL/(GL+AL) around 0.5; and 3) the number of exopodal segments in leg 4 is 2 or less
 315 [6,8,9,11,50,51]. *Lepeophtheirus longicauda* strongly resembles *L. parvicruris*, but differs in
 316 having a shorter leg-4 exopod, with the length ca. 2.5 times the width (more than 3.6 times
 317 the width in *L. parvicruris* [6,10,11]), and a leg-4 exopod with the articulation between the
 318 first and second segments not evident (present in *L. parvicruris* [6,10,11]) (Table 5); these
 319 characters are consistent among specimens collected from distant localities in each species
 320 (from off Sakhalin to off Hokkaido in *L. longicauda*; from off Alaska to off Vancouver in *L.*
 321 *parvicruris*; Fig. 1). Additionally, although available data are limited for each species, the
 322 shape of a posterior striated membrane on the leg-2 intercoxal sclerite of *L. longicauda*
 323 differs from that of *L. parvicruris* illustrated by [6]: it strongly expands in mid-line and is as

long as or longer than the sclerite-length in the former; curved rectangle and shorter than half length of sclerite in *L. parvicruris* (this study, [6]). To say whether the condition of this character is consistent within a species, data from more specimens from more sampling localities are necessary. *Lepeophtheirus longicauda* differs from *L. longiventralis* in having 1) short posterolateral protrusions on the genital complex and 2) a trifid leg 5; from *L. marcepes* in having 1) the second exopodal segment of leg 1 with three spines and four setae and 2) the leg-4 protopod with one outer seta; and from *L. schmidtii* in having leg 4 with an exopod (Table 5).

Among sequences deposited in INSD, the 18S sequence from *L. longicauda* was most similar to those from *L. parvicruris* and *L. thompsoni*; it was one nucleotide shorter than the latter two (i.e., one indel was observed), and differed at one nucleotide position (Fig. 6B). No sequences from *L. longiventralis*, *L. marcepes*, or *L. schmidtii* were found in the public database [47]. Unfortunately, no COI sequences from any of these five other species have yet been deposited in public databases [47].

Our host-fish sequence data also support the conclusion that *L. longicauda* is distinct from *L. parvicruris*. Both species utilize the same flatfish, *Pl. stellatus*. This nominal species has a wide distribution from the northwestern to the northeastern Pacific (from Korea to California) at depths shallower than 300 m [52], but Vinnikov et al. [34] suggested that it may harbor cryptic species. Our COI tree corroborates the multilocus phylogenetic analyses by [34]

that showed *Pl. stellatus* sequences grouping into separate northwestern and northeastern Pacific clades (Fig. 8). *Lepeophtheirus longicauda* and *L. parvicruris* were originally described from the Sea of Japan and the northeastern Pacific (Vancouver Island vicinity), respectively. Although we have no information on *Pl. stellatus* or the two copepod species from the Bering Sea, *Pl. stellatus* may actually comprise divergent northwestern and northeastern Pacific populations (or species), each acting as host to a co-divergent copepod species.

Acknowledgments

We thank Naohiro Hasegawa for help in sampling; Hiroko Uyeno for help in observation; and Matthew H. Dick for reviewing the manuscript and editing our English.

References

- [1] Z. Kabata, Copepoda (Crustacea) parasitic on fishes: problems and perspectives, Adv. Parasitol. 19 (1982) 1–71, [https://doi.org/10.1016/S0065-308X\(08\)60265-1](https://doi.org/10.1016/S0065-308X(08)60265-1)
- [2] C.-L. Lin, J.-S. Ho, S.-N. Chen, Two species of Caligidae (Copepoda) parasitic on cultured rabbit fish (*Siganus fuscescens*) in Taiwan, Fish Pathol. 31 (1996) 129–139.
- [3] S.C. Johnson, J.W. Treasurer, S. Bravo, K. Nagasawa, Z. Kabata, A review of the impact

- of parasitic copepods on marine aquaculture, Zool. Stud. 43 (2004) 229–243.
- [4] G. Boxshall, The sea lice (Copepoda: Caligidae) of Moreton Bay (Queensland, Australia), with descriptions of thirteen new species, Zootaxa 4398 (2018) 1–172.
<https://doi.org/10.11646/zootaxa.4398.1.1>.
- [5] A.A. Özak, Y. Sakarya, G.A. Boxshall, *Caligus adanensis* sp. nov. (Copepoda: Caligidae Burmeister, 1835) parasitic on garfish, *Belone belone* (Linnaeus, 1760), from the eastern Mediterranean Sea, off the Turkish coast, Mar. Biodivers. 49 (2019) 1877–1890.
- [6] M. Dojiri, J.-S. Ho, Systematics of the Caligidae, Copepods Parasitic on Marine Fishes, Brill, Leiden, 2013.
- [7] A.P. Markevich, Novi vidi parazitichnykh Copepoda, Depovidi Akademiyi Nauk USSR 11 (1940) 11–21.
- [8] A.P. Markevich, Parasitic Copepodes on the Fishes of the USSR, Indian National Scientific Documentation Centre, New Delhi, 1976 (Translated from Russian).
- [9] S.A. Vinogradov, Parasitic copepods of family Caligidae from fishes of coastal waters at Sakhalin, Izvestia TINRO 168 (2012) 243–261.
- [10] C.M. Fraser, Copepods parasitic on fish from the Vancouver Island region, Proc. Trans. Roy. Soc. Can. Ser 3 13 (1920) 45–67 + 8 pls.
- [11] Z. Kabata, The species of *Lepeophtheirus* (Copepoda: Caligidae) from fishes of British Columbia, J. Fish. Res. Board Can. 30 (1973) 729–759.

- 381 [12] S.R. Jones, G. Prosperi-Porta, E. Kim, P. Callow, B. Hargreaves, The occurrence of
 382 *Lepeophtheirus salmonis* and *Caligus clemensi* (Copepoda: Caligidae) on three-spine
 383 stickleback *Gasterosteus aculeatus* in coastal British Columbia, J. Parasitol. 92 (2006)
 384 473–480.
- 385 [13] I. Paperna, Parasitic Crustacea (Copepoda and Branchiura) from inland water fishes of
 386 Israel, Israel J. Zool. 13 (1964) 58–68.
- 387 [14] I. Paperna, M. Lahav, Mortality among gray mullets in a seawater pond due to caligiid
 388 parasitic copepod epizootic, Bamidgeh: Bull. Fish Cult. Israel 26 (1974) 12–15.
- 389 [15] A. Scott, Some additions to the fauna of Liverpool Bay, Proc. Trans. Liverpool Biol. Soc.
 390 15 (1901) 342–353.
- 391 [16] Z. Kabata, Copepoda parasitic on Australian fishes. III. Genera *Dentigryps*,
 392 *Heniochophilus* and *Pseudanuretes* (Caligidae), Ann. Mag. Nat. Hist., Ser. 13 (1965) 19–
 393 31.
- 394 [17] K. Kakui, S. Angsupanich, *Birdotanaïs songkhlaensis*, a new genus and species of
 395 Nototanaidae (Crustacea: Tanaidacea) from Thailand, Raffles Bull. Zool. 60 (2012) 421–
 396 432.
- 397 [18] W.S. Rasband, ImageJ. <https://imagej.nih.gov/ij/>, 2019 (accessed 2 July 2019).
- 398 [19] O. Folmer, M. Black, W. Hoeh, R. Lutz, R. Vrijenhoek, DNA primers for amplification
 399 of mitochondrial cytochrome c oxidase subunit I from diverse metazoan invertebrates,

- 400 Mol. Mar. Biol. Biotechnol. 3 (1994) 294–299.
- 401 [20] T. Nakayama, S. Watanabe, K. Mitsui, H. Uchida, I. Inoue, The phylogenetic
402 relationship between the Chlamydomonadales and Chlorococcales inferred from
403 18SrDNA data, Phycol. Res. 44 (1996) 47–55.
- 404 [21] T. Puitika, Y. Kasahara, N. Miyoshi, Y. Sato, S. Shimano, A taxon-specific
405 oligonucleotide primer set for PCR-based detection of soil ciliate, Microbes Environment.
406 22 (2007) 78–81.
- 407 [22] M. Maraun, G. Erdmann, G. Schulz, R.A. Norton, S. Scheu, K. Domes, Multiple
408 convergent evolution of arboreal life in oribatid mites indicates the primacy of ecology,
409 Proc. Roy. Soc. B 276 (2009) 3219–3227.
- 410 [23] S. Kumar, G. Stecher, K. Tamura, MEGA7: Molecular evolutionary genetics analysis
411 version 7.0 for bigger datasets, Mol. Biol. Evol. 33 (2016) 1870–1874.
- 412 [24] Ø. Øines, T. Schram, Intra- or inter-specific difference in genotypes of *Caligus elongatus*
413 Nordmann 1832?, Acta Parasitol. 53 (2008) 93–105.
- 414 [25] R. Huys, J. Llewellyn-Hughes, P.D. Olson, K. Nagasawa, Small subunit rDNA and
415 Bayesian inference reveal *Pectenophilus ornatus* (Copepoda *incertae sedis*) as highly
416 transformed Mytilicolidae, and support assignment of Chondracanthidae and Xarifiidae to
417 Lichomolgoidea (Cyclopoida), Biol. J. Linn. Soc. 87 (2006) 403–425.
- 418 [26] M.A. Freeman, H. Anshary, K. Ogawa, Multiple gene analyses of caligid copepods

- 419 indicate that the reduction of a thoracic appendage in *Pseudocaligus* represents
420 convergent evolution, *Parasite Vector* 6 (2013) 336.
421 <https://doi.org/10.1186/1756-3305-6-336>.
- 422 [27] R. Huys, J. Llewellyn-Hughes, S. Conroy-Dalton, P.D. Olson, J.N. Spinks, D.A.
423 Johnston, Extraordinary host switching in siphonostomatoid copepods and the demise of
424 the Monstrilloidea: integrating molecular data, ontogeny and antennular morphology, *Mol.*
425 *Phylogenet. Evol.* 43 (2007) 368–378.
- 426 [28] S.M. Dippenaar, Estimated molecular phylogenetic relationships of six
427 siphonostomatoid families (Copepoda) symbiotic on elasmobranchs, *Crustaceana* 82
428 (2009) 1547–1567.
- 429 [29] K. Katoh, D.M. Standley, MAFFT multiple sequence alignment software version 7:
430 improvements in performance and usability, *Mol. Biol. Evol.* 30 (2013) 772–780.
- 431 [30] K. Katoh, H. Toh, Recent developments in the MAFFT multiple sequence alignment
432 program, *Brief. Bioinform.* 9 (2008) 286–298.
- 433 [31] R. Lanfear, P.B. Frandsen, A.M. Wright, T. Senfeld, B. Calcott, PartitionFinder 2: new
434 methods for selecting partitioned models of evolution for molecular and morphological
435 phylogenetic analyses, *Mol. Biol. Evol.* 34 (2016) 772–773.
- 436 [32] A. Stamatakis, RAxML version 8: a tool for phylogenetic analysis and post-analysis of
437 large phylogenies, *Bioinformatics* 30 (2014) 1312–1313.

- 438 [33] J. Felsenstein, Confidence limits on phylogenies: an approach using the bootstrap,
439 Evolution 39 (1985) 783–791.
- 440 [34] K.A. Vinnikov, R.C. Thomson, T.A. Munroe, Revised classification of the righteye
441 flounders (Teleostei: Pleuronectidae) based on multilocus phylogeny with complete taxon
442 sampling, Mol. Phylogenet. Evol. 125 (2018) 147–162.
- 443 [35] D. Steinke, T.S. Zemlak, J.A. Boutillier, P.D.N. Hebert, DNA barcoding of Pacific
444 Canada’s fishes, Mar. Biol. 156 (2009) 2641–2647.
- 445 [36] Y.P. Kartavtsev, S.N. Sharina, K. Saitoh, J.M. Imoto, N. Nanzawa, A.D. Redin,
446 Phylogenetic relationships of Russian far eastern flatfish (Pleuronectiformes,
447 Pleuronectidae) based on two mitochondrial gene sequences, *Co-1* and *Cyt-b*, with
448 inferences in order phylogeny using complete mitogenome data, Mitochondr. DNA Pt. A
449 27 (2016) 667–678.
- 450 [37] K. Katoh, K. Kuma, H. Toh, T. Miyata, MAFFT version 5: improvement in accuracy of
451 multiple sequence alignment, Nucleic Acids Res. 33 (2005) 511–518.
- 452 [38] L.-T. Nguyen, H.A. Schmidt, A. von Haeseler, B.Q. Minh, IQ-TREE: a fast and effective
453 stochastic algorithm for estimating maximum likelihood phylogenies, Mol. Biol. Evol. 32
454 (2015) 268–274.
- 455 [39] O. Chernomor, A. von Haeseler, B.Q. Minh, Terrace aware data structure for
456 phylogenomic inference from supermatrices, Syst. Biol. 65 (2016) 997–1008.

- 457 [40] D.T. Hoang, O. Chernomor, A. von Haeseler, B.Q. Minh, L.S. Vinh, UFBoot2:
458 improving the ultrafast bootstrap approximation, *Mol. Biol. Evol.* 35 (2018) 518–522.
- 459 [41] J.J. Gillespie, J.S. Johnston, J.J. Cannone, R.R. Gutell, Characteristics of the nuclear
460 (18S, 5.8S, 28S and 5S) and mitochondrial (12S and 16S) rRNA genes of *Apis mellifera*
461 (Insecta: Hymenoptera): structure, organization, and retrotransposable elements, *Insect*
462 *Mol. Biol.* 15 (2006) 657–686.
- 463 [42] J.-M. Neefs, Y. van de Peer, L. Hendriks, R. de Wachter, Compilation of small ribosomal
464 subunit RNA sequences, *Nucleic Acids Res.* 18 (Suppl) (1991) 2237–2317.
- 465 [43] K. Sato, M. Hamada, K. Asai, T. Mituyama, CentroidFold: a web server for RNA
466 secondary structure prediction. *Nucleic Acids Res.* 37 (2009) W277–W280.
- 467 [44] M. Kimura, A simple method for estimating evolutionary rates of base substitutions
468 through comparative studies of nucleotide sequences, *J. Mol. Evol.* 16 (1980) 111–120.
- 469 [45] S.F. Altschul, W. Gish, W. Miller, E.W. Myers, D.J. Lipman, Basic local alignment
470 search tool, *J. Mol. Biol.* 215 (1990) 403–410.
- 471 [46] S.R.M. Jones, G. Prosperi-Porta, The diversity of sea lice (Copepoda: Caligidae)
472 parasitic on threespine stickleback (*Gasterosteus aculeatus*) in coastal British Columbia, *J.*
473 *Parasitol.* 97 (2011) 399–405.
- 474 [47] DDBJ, DNA Data Bank of Japan. <https://www.ddbj.nig.ac.jp/index-j.html>, 2019
475 (accessed 2 July 2019).

- 476 [48] J.K. Passarelli, D. Tang, A new species of *Lepeophtheirus* (Copepoda; Caligidae)
477 parasitic on three kelpfish species (Clinidae) from the southern California coast, Bull. S.
478 Calif. Acad. Sci. 116 (2017) 1–16.
- 479 [49] A.A. Özak, A.M.V. Rodrigues, N.S.S. Vieira, R.M.G. Rosa, A. Yanar, E. Koyuncu, G.A.
480 Boxshall, *Lepeophtheirus azoricus* n. sp. (Copepoda: Caligidae) parasitic on dusky
481 grouper, *Epinephelus marginatus*, from Atlantic waters off the Azores, Portugal, Mar.
482 Biodiv. 48 (2018) 1045–1055.
- 483 [50] J.-S. Ho, S. Gómez, K. Ogawa, M. Aritaki, Two species of parasitic copepods
484 (Caligidae) new to Japan, Syst. Parasitol. 57 (2004) 19–34.
- 485 [51] C.B. Wilson, Parasitic copepods in the United States National Museum, Proc. U. S. Natl.
486 Mus. 94 (1944) 529–582 + pls. 21–34.
- 487 [52] A.J. Allen, G.B. Smith, Atlas and zoogeography of common fishes in the Bering Sea and
488 northeastern Pacific, NOAA Tech. Rep. NMFS 66 (1988) 1–151.
- 489

Figure legends

Fig. 1. Map showing collection localities for caligid specimens relevant to this study. Circles, *Pseudolepeophtheirus longicauda* of [7], *P. parvicruris* of [9], and Caligid sp. A (this study); triangles, *Lepeophtheirus parvicruris* of [6,10–12].

Fig. 2. Caligid sp. A, female (ICHUM6045), fixed specimen, dorsal view. Scale bar = 1 mm.

Fig. 3. Caligid sp. A, female, ICHUM6041 (A, B, D, G–M), ICHUM6045 (C); ICHUM6042 (E, F, N, O). A, Habitus, dorsal; B, caudal rami; C, antennule, ventral (arrow, small protrusion); D, antenna, post-antennal process, and round process, ventral; E, mandible; F, maxillule; G, maxilla (arrow, partly broken portion); H, I, maxilliped, ventral (H), dorsal (I); J, sternal furca, ventral; K–O, legs 1–5, ventral, with most of posterior striated membranes on intercoxal sclerite and protopod of leg 3 omitted. Scale bars: 1 mm (A), 0.1 mm (others).

Fig. 4. SEM images of Caligid sp. A, female, ICHUM6050. A, Distal region of second exopodal segment of right leg 1, ventral; B, exopod spine on first exopodal segment of left leg 3, ventral; C, left leg 4, ventral; D, E, exopod of left leg 4, ventral (D) and dorsal (E). Abbreviations: *ap*, accessory process; *sp*, spine on outer distal corner of second exopodal segment of left leg 3. Scale bars: 25 μ m.

Fig. 5. Intercoxal sclerite and posterior striated membrane of leg 2 (A, ICHUM6041) and leg 3 (B, ICHUM6043) in Caligid sp. A, female. Intercoxal sclerite of leg 3 partly broken. Abbreviations: *is*, intercoxal sclerite; *sm*, striated membrane. Scale bar: 0.1 mm.

Fig. 6. Comparison of part of 18S sequence from Caligid sp. A, *L. parvicruris*, and *L. thompsoni*. A, Chromatogram showing the dimorphic site in the 18S sequence of Caligid sp. A (Y indicates that both T and C peaks were detected); B, part of aligned 18S sequences from the three species; C, D, secondary structure of the V7 variable area in 18S from *L. parvicruris* and *L. thompsoni* (C) and Caligid sp. A (D), predicted with CentroidFold, inference engine = “McCaskill(BL)”, weight of base pairs = “2²” (black arrow, dimorphic site; white arrow, non-dimorphic site; arrowheads, nucleotide present in *L. parvicruris* and *L. thompsoni* (black), lacking in Caligid sp. A (white)).

523 **Fig. 7.** ML tree for copepod 18S sequences (1675 nt). Numbers near nodes are bootstrap
524 values in percent; values less than 70 are not shown. The scale indicates branch length in
525 number of substitutions per site.

526

527 **Fig. 8.** ML tree for COI sequences (558 nt) from 17 *Platichthys stellatus* and an outgroup
528 taxon, *Platichthys flesus*. Numbers near nodes are ultrafast bootstrap values in percent. The
529 scale indicates branch length in number of substitutions per site.

530

Table 1

List of PCR and cycle sequencing (CS) primers used in this study.

Marker	Primer	Primer sequence	Reaction	Source
COI (copopod)	LCO1490	GGTCAACAAATCATAAAGATATTGG	PCR & CS	[19]
	HCO2198	TAAACTTCAGGGTGACCAAAAAATCA	PCR & CS	[19]
COI (fish)	COI_ff_F	CAAAGACATCGGCACCCTCT	PCR & CS	This study
	COI_ff_R	GGTAGAGGATGGGGTCACCT	PCR & CS	This study
18S	SR1	TACCTGGTTGATCCTGCCAG	PCR	[20]
	SR8	GGATTGACAGATTGAGAGCT	CS	[20]
	SR9	AACTAAGAACGGCCATGCAC	CS	[20]
	SR10	AGGTCTGTGATGCCCTTAGA	CS	[20]
	SR12	CCTTCCGCAGGTTACCTAC	PCR & CS	[20]
	EU929R	TTGGCAAATGCTTTTCGC	CS	[21]
	18S554f	AAGTCTGGTGCCAGCAGCGCG	CS	[22]
	18S614r	TCCAACACTACGAGCTTTTAAACC	CS	[22]

535 **Table 2**

536 Copepod species included in the 18S analysis in this study.

Family	Taxon	Accession no.	Source
CALIGIDAE	<i>Caligus clemensi</i>	DQ123833	[12]
	<i>Caligus curtus</i>	EF088407	[24]
	<i>Caligus elongatus</i>	AY627020	[25]
	<i>Caligus fugu</i>	KC569364	[26]
	<i>Caligus gurnardi</i>	EF088410	[24]
	<i>Caligus pelamydis</i>	EF088411	[24]
	<i>Caligus punctatus</i>	KR048777	Unpublished
	<i>Caligus quadratus</i>	EF088412	[24]
	<i>Caligus uniartus</i>	KC569363	[26]
	<i>Caligus brevipedis</i>	EF088416	[24]
	<i>Caligus</i> sp1JYW2010	HM545887	Unpublished
	<i>Gloiopotes watsoni</i>	AY627019	[25]
	<i>Gloiopotes huttoni</i>	KF667350	Unpublished
	<i>Lepeophtheirus goniistii</i>	KR048779	Unpublished
	<i>Lepeophtheirus</i> <i>hippoglossi</i>	DQ538503	[27]
	<i>Lepeophtheirus hospitalis</i>	DQ123831	[12]
	<i>Lepeophtheirus natalensis</i>	FJ447440	[28]
	<i>Lepeophtheirus</i> <i>parvicruris</i>	DQ123830	[12]
	<i>Lepeophtheirus</i> <i>parviventris</i>	KR048780	Unpublished
	<i>Lepeophtheirus pectoralis</i>	EF088413	[24]
	<i>Lepeophtheirus</i> <i>pollachius</i>	EF088414	[24]
	<i>Lepeophtheirus salmonis</i>	DQ123829	[12]
	<i>Lepeophtheirus</i> <i>thompsoni</i>	EF088415	[24]
	<i>Paralebion elongatus</i>	FJ447441	[28]
	Caligid sp. A	LC512442	This study

DISSONIDAE	<i>Dissonus manteri</i>	DQ538500	[27]
PANDARIDAE	<i>Dinemoura latifolia</i>	DQ538501	[27]
	<i>Perissopus dentatus</i>	FJ447453	[28]

537

538

Table 3

Fish sequences included in the COI analysis in this study.

Species	Accession	Locality	Source
<i>Pl. stellatus</i>	KF930268	NE Pacific (USA: California)	Unpublished
	GU440461	NE Pacific (USA: Washington: Puget Sound)	Unpublished
	GU440462	NE Pacific (USA: Washington: Puget Sound)	Unpublished
	MH032494	NE Pacific (USA: Washington: Puget Sound)	[34]
	FJ165021	NE Pacific (Canada: British Columbia)	[35]
	FJ165020	NE Pacific (Canada: British Columbia)	[35]
	KF930269	NE Pacific (USA: Alaska: Gulf of Alaska)	Unpublished
	MH032495	NE Pacific (USA: Alaska: Gulf of Alaska)	[34]
	MH032493	NW Pacific (Japan: Miyagi)	[34]
	MH032492	NW Pacific (Japan: Miyagi)	[34]
	KF386375	NW Pacific (Russia: Sea of Japan: Vostok Bay)	[36]
	KF386374	NW Pacific (Russia: Sea of Japan: Vostok Bay)	[36]
	LC515810	NW Pacific: Sea of Japan (Japan: Asari)	This study
	KT920091	NW Pacific (China: Yellow Sea: RiZhao)	Unpublished
	KT920090	NW Pacific (China: Yellow Sea: RiZhao)	Unpublished
	KT920044	NW Pacific (China: Yellow Sea: JiangSu)	Unpublished
	KT920043	NW Pacific (China: Yellow Sea: JiangSu)	Unpublished
<i>Pl. flesus</i>	MH032490	Atlantic: Baltic Sea	[34]

Table 4

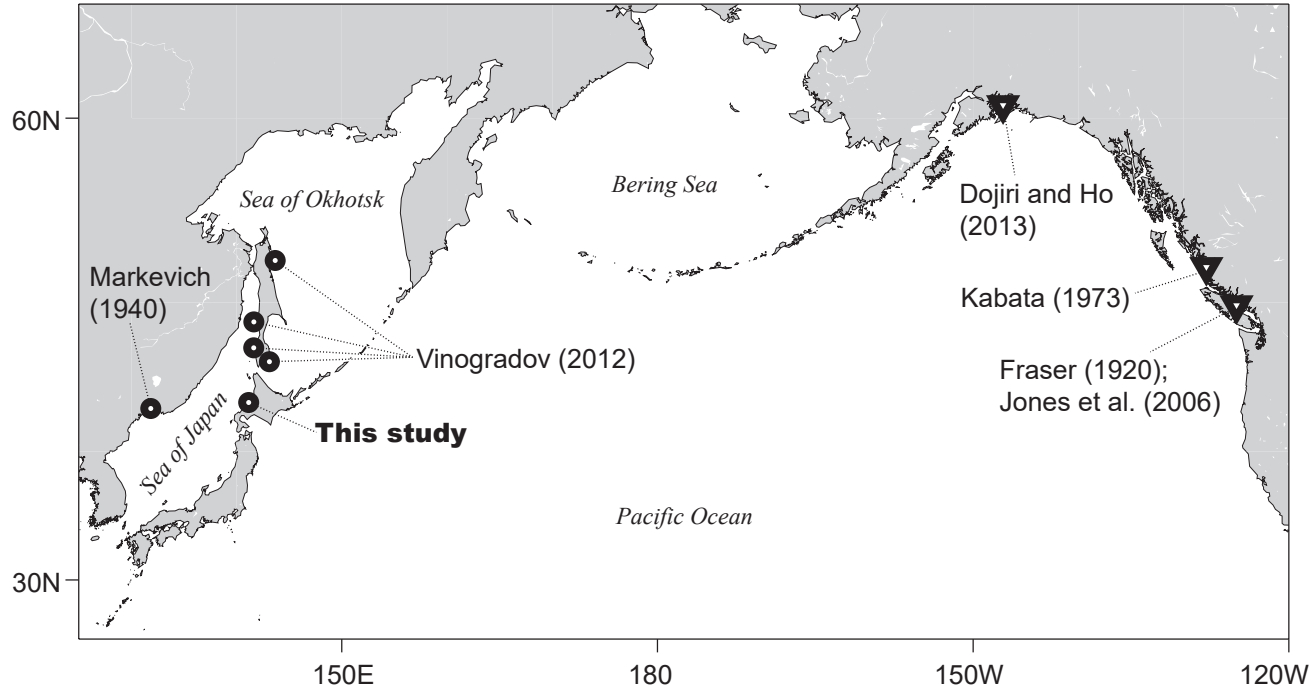
Measurements for *Caligid* sp. A specimens. Values are in millimeters, except for ratios. CL, CrL, GL, AL, length of cephalothorax, caudal ramus, genital complex, and abdomen; CW, CrW, GW, AW, maximum width of cephalothorax, caudal ramus, genital complex, and abdomen; TL, total body length. –, no data

Specimen Number	TL	CL	CW	GL	GW	AL	AW	CrL	CrW	CL/(GL+AL)	CrL/CrW
ICHUM6041	6.99	2.38	2.25	1.93	–	2.43	–	0.11	0.08	0.52	1.45
ICHUM6042	7.47	2.55	2.45	1.80	–	2.75	–	0.12	0.09	0.58	1.40
ICHUM6043	8.09	2.35	2.22	2.09	–	3.44	–	0.12	0.08	0.41	1.41
ICHUM6044	6.62	2.25	2.38	1.69	–	2.46	–	0.11	0.08	0.53	1.39
ICHUM6045	8.28	2.43	2.25	2.31	2.05	3.18	0.69	0.11	0.08	0.40	1.39
ICHUM6046	7.77	2.31	–	2.27	2.09	2.96	0.66	0.10	0.07	0.38	1.38
ICHUM6047	8.11	2.58	2.21	2.44	2.14	2.81	0.75	0.12	0.08	0.46	1.41
ICHUM6048	7.84	2.41	2.04	2.25	2.09	2.88	0.72	0.11	0.08	0.45	1.40
ICHUM6049	7.46	2.31	2.04	2.06	1.69	2.80	0.62	0.11	0.08	0.45	1.40
ICHUM6050	8.34	2.58	2.39	2.29	2.16	3.14	0.74	0.13	0.09	0.44	1.45
Mean	7.70	2.42	2.25	2.11	2.04	2.89	0.70	0.11	0.08	0.46	1.41

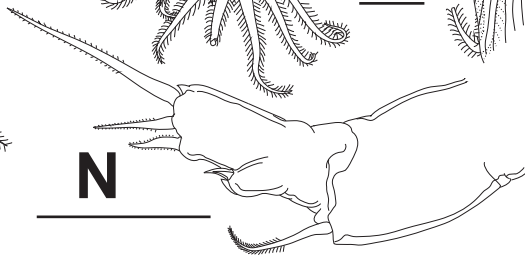
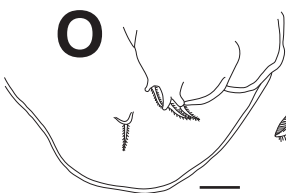
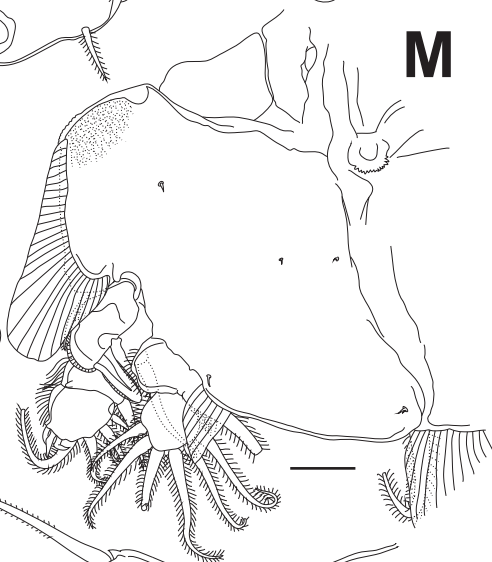
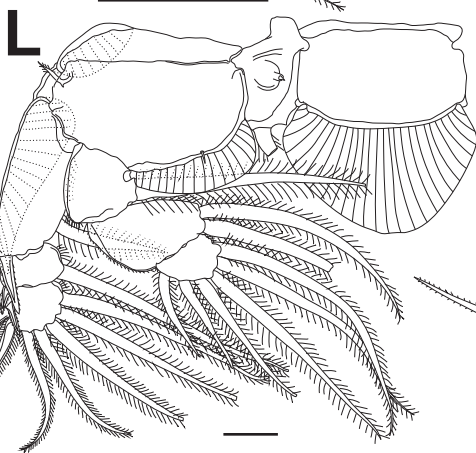
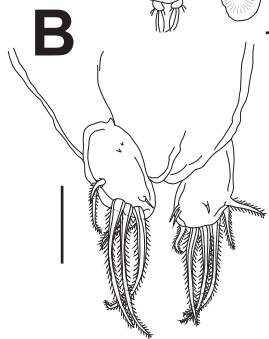
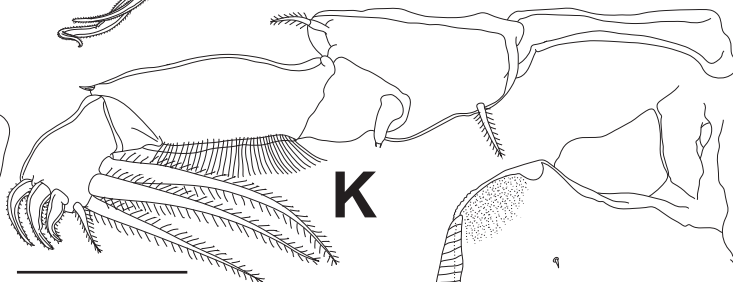
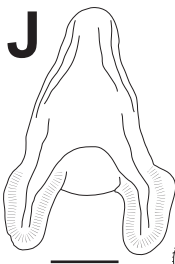
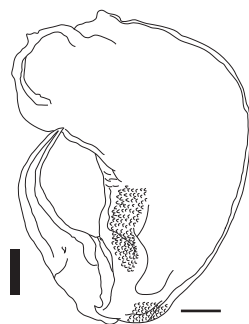
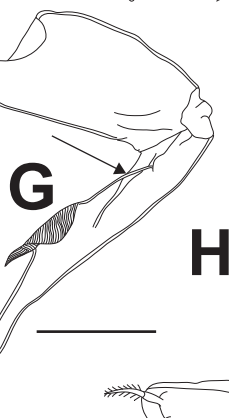
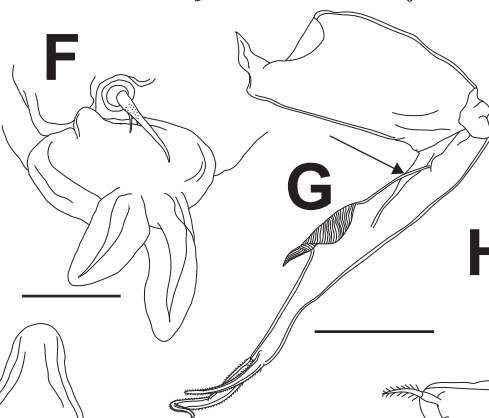
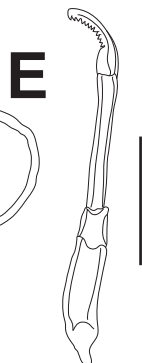
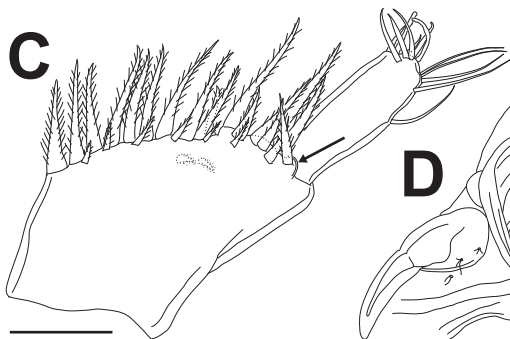
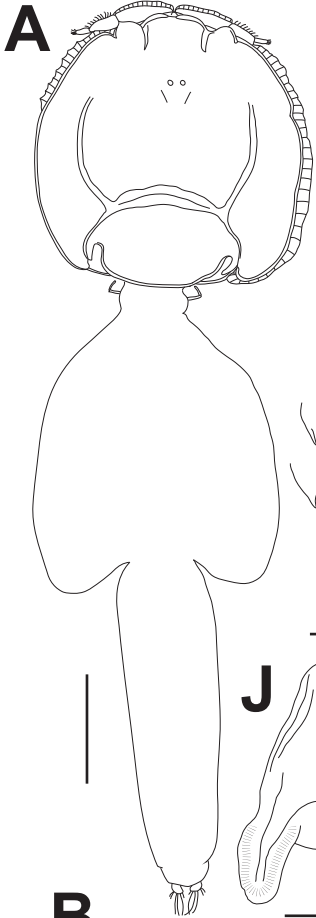
Table 5

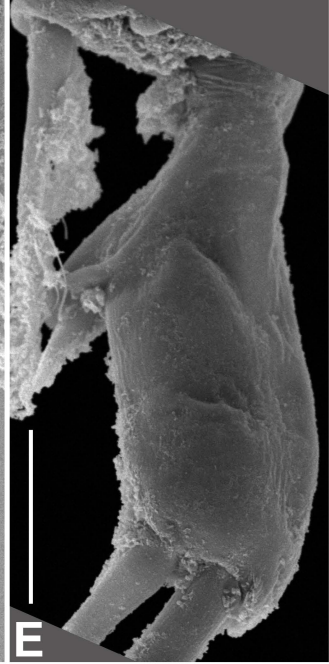
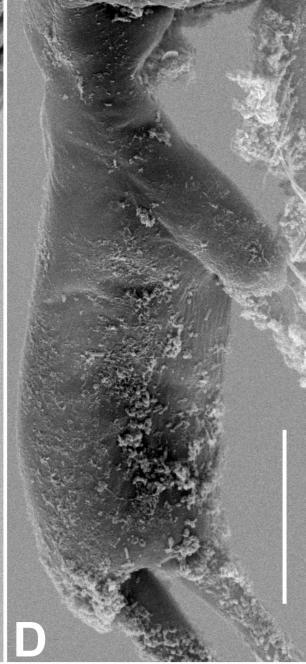
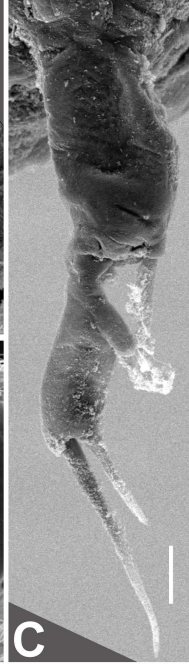
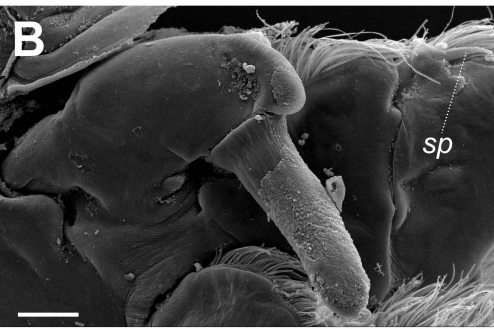
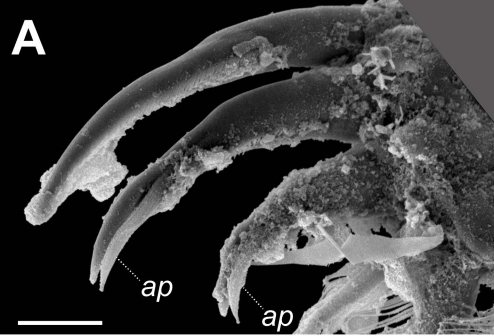
Comparison of selected characters for five *Lepeophtheirus* species. L, length; W, width. Arm, armature (number of setae in Arabic numbers; number of spines in Roman numbers; numbers left to hyphen for outer setae/spines, the others for inner ones); Prp, protopod; Exp, exopod. ^aArticulation between first and second exopodal segments not evident.

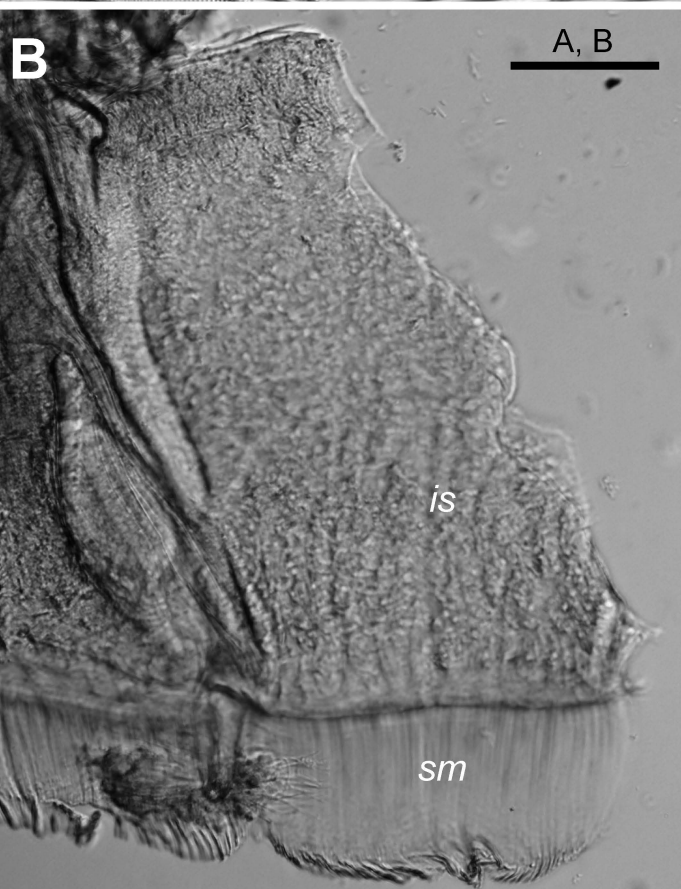
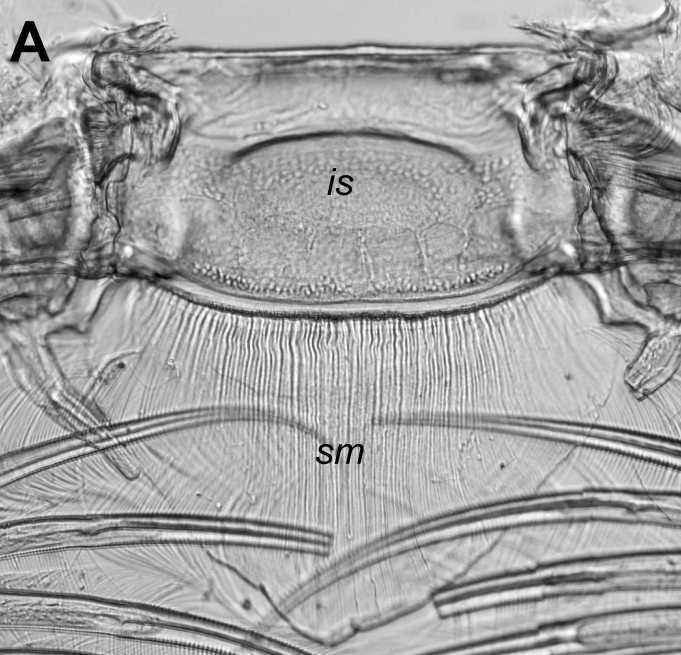
Taxon	Leg 1	Leg 4			Leg 5	Genital complex	Host	Type Locality	Source(s)
	Arm of Exp	Arm of Prp	Exp segments	L/W of Exp	Shape	Posterolateral protrusion			
Caligid sp. A (= <i>L. longicauda</i>)	I-0; III,1,3	1-0	2 ^a	ca 2.5	trifid	short	<i>Platichthys stellatus</i>	Vladivostok, Sea of Japan	[9]; this study
<i>L. longiventralis</i>	1-0; III,1,3	1-0	2	4.3	triangular	long	<i>Verasper variegatus</i>	Yen-Dai, Yellow Sea	[50]
<i>L. marcepes</i>	0-0; III,0,3	0-1	2	2.4	nd	short	<i>Pleuronectes quadrituberculatus</i>	Alitak Bay, Kodiak Island, NE Pacific	[51]
<i>L. parvicurris</i>	1-0; III,1,3	1-0	2	3.6 or more	trifid	short	<i>Platichthys stellatus</i>	Vancouver Island, NE Pacific	[6,10,11]
<i>L. schmidtii</i>	1-0; III,1,3	1	0	-	nd	slight	<i>Limanda punctatissimus</i>	Nakhodka Bay, Sea of Japan	[8,9]

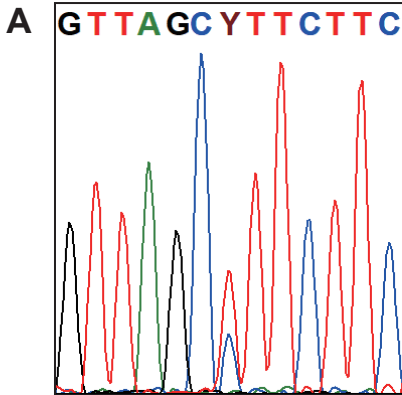






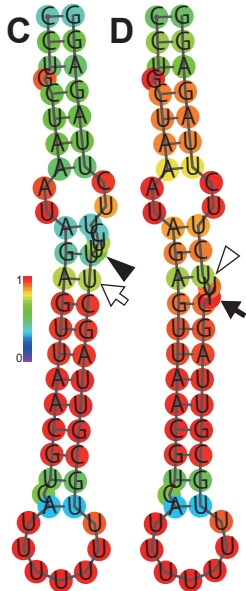


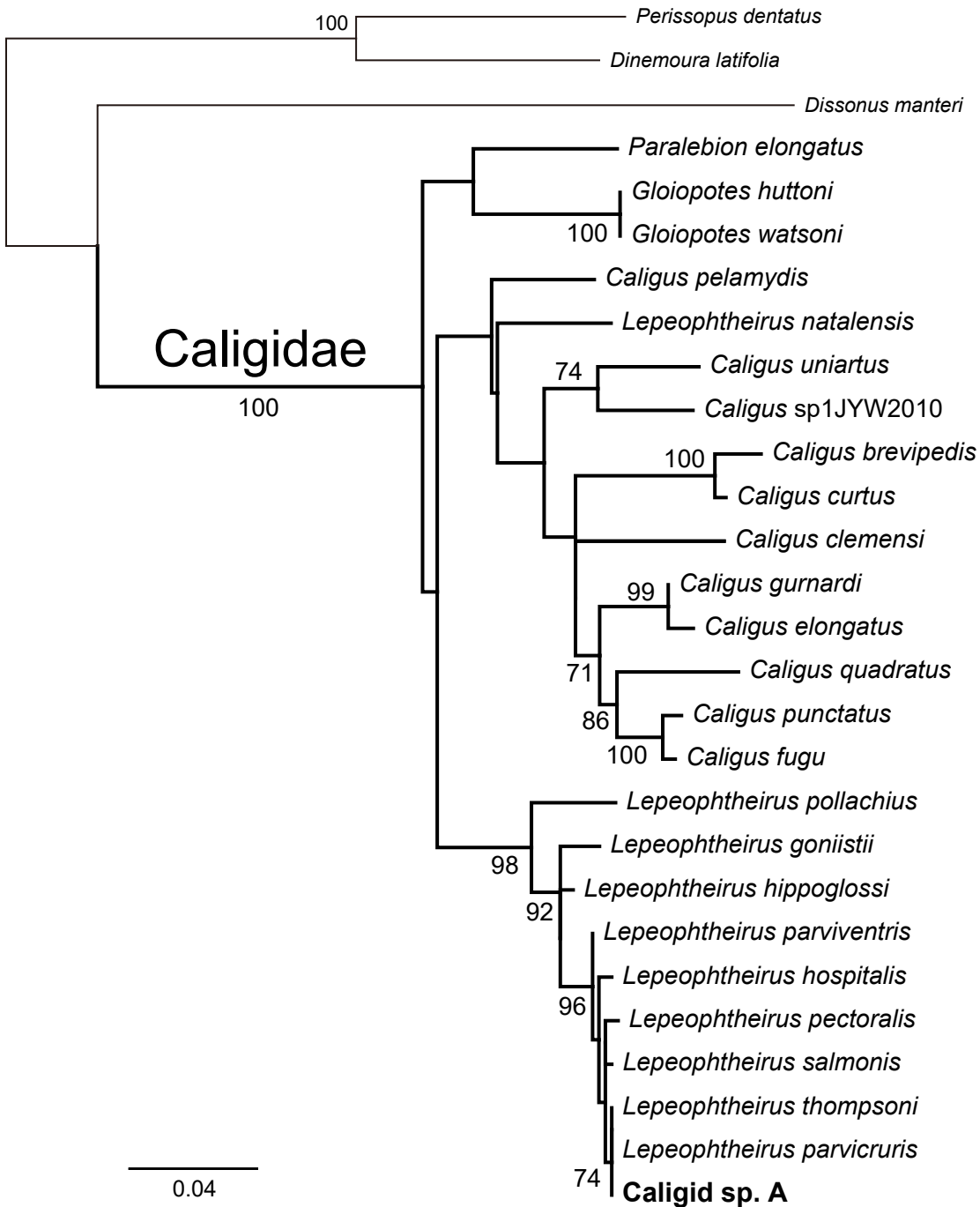




B

Species/Abbrv	*	*	*	*	*	*	*	*	*	*	*	*	*	*
1. <i>L. parvicurris</i>	G	T	T	A	G	C	T	T	T	T	C	T	T	C
2. <i>L. thompsoni</i>	G	T	T	A	G	C	T	T	T	T	C	T	T	C
3. <i>Caligid</i> sp. A	G	T	T	A	G	C	Y	T	-	T	C	T	T	C





P. flesus

GU440461 Washington, USA

GU440462 Washington, USA

KF930269 Gulf of Alaska

FJ165021 British Colombia, Canada

FJ165020 British Colombia, Canada

MH032495 Gulf of Alaska

KF930268 California, USA

MH032494 Washington, USA

NE Pacific

72 MH032492 Miyagi, Japan

KF386374 Sea of Japan

KT920044 Yellow Sea

KT920043 Yellow Sea

KT920090 Yellow Sea

KT920091 Yellow Sea

KF386375 Sea of Japan

MH032493 Miyagi, Japan

NW Pacific

0.002

Host of Caligid sp. A