

**Fishing for scavengers: An integrated study to amphipod (Crustacea: Lysianassoidea)
diversity of Potter Cove (South Shetland Islands, Antarctica)**

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Abstract

Amphipoda from the superfamily Lysianassoidea Dana, 1849 play an important role in Southern Ocean benthic food webs due to their high biomass, abundance and predominantly scavenging mode of feeding. Our knowledge on the lysianassoid fauna, even in well-studied areas of the Western Antarctic Peninsula, is incomplete. Here we report the findings of an integrated study of lysianassoid amphipods of Potter Cove, King George Island/ Isla 25 de Mayo (KGI), combining morphological and molecular species identification (*COI* barcoding) methods, investigating more than 41,000 specimens from baited traps. For comparison, 2039 specimens from the adjacent Marian Cove were analysed. Ten lysianassoid species were recorded in the deeper outer Potter Cove, whereas the inner cove (<50 m) was dominated by a single species, *Cheirimedon femoratus* Pfeffer, 1888 (99.44% relative abundance). It is hypothesized that the impoverished lysianassoid fauna inside the meltwater-influenced inner cove represents a model for future conditions along the Western Antarctic Peninsula under conditions of increased glacial melting.

Abyssorhomene charcoti (Chevreux, 1912) and *Orchomenella pinguides* Walker, 1903 were recorded in KGI waters for the first time. Furthermore, one new lysianassoid amphipod species of the genus *Orchomenella* Sars, 1890 is described: *Orchomenella infinita* sp. n. Seefeldt, 2017. First-time DNA barcode data was established for *Cheirimedon femoratus*, *Hippomedon kergueleni* Miers, 1875, *Orchomenella rotundifrons* K.H. Barnard, 1932 and *Orchomenella infinita* sp. n.

Keywords

Biodiversity inventory; DNA barcoding; Lysianassidae; Taxonomy; New species; Southern Ocean; Glacier retreat

This article is registered in ZooBank under urn:lsid:zoobank.org: pub: 829D1ED2-936D-4121-9D2E-3C65D4BCE63A

Acknowledgments

The authors thank the DNA/IAA and the staff of *Carlini* station 2014/2015 and 2015/2016 for logistics and support. We would like to thank particularly E. Barrera-Oro, O. Gonzáles, C. Bellisio, J. Movilla, L. Torre, J. Piscicelli, G. Alurralde for help in the field and lab. A sincere gratitude is owed to D. Abele for supporting this project. Furthermore, we want to thank R. Tollrian for his encouragement and the provision of technical equipment, M. Schweinsberg and K. Lampert for assistance in the laboratories at RUB. We are grateful to K. Jerosch for generating the maps. We thank A. Feuring for her help in sorting some samples. We greatly acknowledge the constructive comments of two anonymous reviewers. The first author particularly expresses her deep gratitude to H. Kiepe and team for support and logistics.

This study was funded by the German Research Foundation (DFG) with the project TO 171/9-1, HE 3391/7-1 and C. Havermans with the project HA 7627/1-1 funded through the Priority Programme 1158 on Antarctic Research.

The present manuscript also presents an outcome of the EU research network IMCONet funded by the Marie Curie Action International Research Staff Exchange Scheme (FP7 IRSES, Action No. 319718).

Introduction

Understanding the eco-functional role of species, communities, and ecosystems are prerequisites for biodiversity conservation. This is particularly true for remote and vulnerable environments, such as the Western Antarctic Peninsula (WAP) region. The WAP region belongs to one of the most rapidly changing environments worldwide caused, inter alia, by the increase of air temperatures and its consequences such as rapid glacier retreats and loss of sea ice (see e.g. Gutt 2016; Turner et al. 2005, 2014). Thus, an accurate assessment of species diversity and community composition is needed. The Antarctic marine biota is characterized by a surprisingly high species richness and a high rate of species endemism, which is generally assumed to be a consequence of the isolating effect of the Antarctic Circumpolar Current (Arntz et al. 1997; Brandt 1999; Poulin 2002; Clarke and Johnston 2003) as well as the effect of glacial and interglacial periods, subsequently isolating and reconnecting shelf populations and those on the surrounding slope and in the deep sea (Clarke and Crame 1989; Allcock and Strugnell 2012). With over 900 species recorded in the Southern Ocean and more than 500 species in the Antarctic region, amphipods represent the dominant taxon among peracarid crustaceans (De Broyer et al. 2007). The superfamily Lysianassoidea is one of the key amphipod taxa with respect to species richness, abundance and ecological importance in the region. Many lysianassoid species are scavengers, known to gather in enormous numbers on large carcasses which they are able to devour within hours or days (e.g. Slattery and Oliver 1986). At the same time, they function as an important food source for higher taxa particularly fish, birds and mammals (Dauby et al. 2001; De Broyer et al. 2004; Moreira 2015; Moreira et al. 2016). The amphipod scavenger fauna can be easily sampled and studied by the deployment of baited traps, an approach which has a century-long history of investigations on scavenging amphipods of the world-wide oceans from the shelf to the deep sea (e.g. Arntz and Gutt, 1997; De Broyer et al. 2004; Horton et al. 2013; Hurley, 1965; Ingólfsson and Agnarsson, 1999; Legeżyńska et al. 2000; Presler, 1986; Walker, 1907; Wickins, 1982). These trap deployments, with which huge numbers of specimens could be sampled and new species described, served investigations on marine biodiversity in the WAP area from the very beginning of Antarctic research to nowadays (for an overview see De Broyer et al. 2011).

King George Island (KGI) is the largest island of the South Shetland Islands and has three bays: King George Bay, Admiralty Bay and Maxwell Bay. The latter two bays consist of many fjord-like inlets. Amongst others, the Argentinean scientific station *Carlini* (formerly known as Jubany), where also the Argentinean-German *Dallmann Laboratory* is situated, is located in Potter Cove, Maxwell Bay. For the last three decades, international research has focused on environmental changes caused by the climate-driven retreat of the

Fourcade Glacier, increase of water temperature and its consequences, including freshwater runoff, high sedimentation and benthic community shifts (e.g. Wiencke et al. 1998, 2008; Rückamp et al. 2011, Quartino et al. 2013; Pasotti et al. 2014; Schloss et al. 2014; Falk et al. 2015, Sahade et al. 2015; Fuentes et al. 2016).

Extensive research data already exists for the amphipod fauna of Admiralty Bay (e.g. Jazdzewski 1981; Presler 1986; Jazdzewski et al. 1991, 1992, 1995, 2001; Chapelle and Peck 1995; Jazdzewski and Konopacka 1999; Jazdzewska 2011), primarily acquired by scientists from the Polish *Arctowski* station and the Brazilian *Comandante Ferraz Antarctic Station*. The *Admiralty Bay Benthos Diversity Database* web page (ABBED, www.abbed.uni.lodz.pl; Siciński et al. 2011) lists 172 amphipod species, of which 29 belong to the superfamily Lysianassoidea (pers. communication A. Jazdzewska), representing six families. Kim et al. (2014) published the first amphipod checklist of the sublittoral zone of Marian Cove, one of several fjord-like inlets situated in Maxwell Bay. The authors listed 22 amphipod species belonging to twelve families, including two lysianassid species. In the studies of Rauschert (1988, 1989, 1990, 1991), focussing on the Fildes Peninsula shore, the south western part of KGI, and the Fildes Strait, amphipod data has been published, listing 103 species. However, the presence of some of these amphipod species is questionable and needs reevaluation. For example, Rauschert (1990, 1991) reported the occurrence of *Tryphosella* cf. *sarsi* Bonnier, 1893, a lysianassid species previously only known from the North Sea and North Atlantic, and Casaux et al. (1990) as well as Momo et al. (1998) reported the occurrence of the deep-sea species *Valettia coheres* Stebbing, 1888 (moved to the family Valettidae by Thurston, 1989) in Potter Cove.

Due to conservative and often slight morphological diagnostic characteristics, species identification of lysianassoid amphipods is error-prone. At the same time, accurate species identifications are paramount for a multitude of downstream analyses dealing with or relying on ecological and biodiversity data. Here we report the results of the first integrative taxonomic study of lysianassoid amphipods of Potter Cove (KGI, Antarctica), applying morphological and molecular data to provide up-to-date species delimitation hypotheses and examination of the taxonomy of an important group in the Potter Cove scavenging guild. Furthermore, the new lysianassid species *Orchomenella infinita* sp. n. Seefeldt, 2017 is described and species diversity and taxonomic composition compared to the lysianassoid amphipod fauna of the adjacent Maxwell Bay and Admiralty Bay.

Material & Methods

Study area and sampling

The study was conducted at the Argentinean-German *Dallmann Laboratory* at the Argentinean scientific research station *Carlini* situated at Potter Cove, Maxwell Bay, on King George Island. Potter Cove is divided into an outer and inner cove defined by an underwater sill at 30 m depth. While the outer cove is characterized by a depth up to 200 m and mainly rocky hard substrate, the inner cove has a maximal depth of 50 m and is dominated by soft sediments. Further detailed hydrographical and biological features of the cove can be found in Klöser et al. (1994), Wiencke et al. (1998) and Wölfl et al. (2014).

Scavenging amphipods were sampled using traps made of a perspex hollow cylinder (50 cm length, 10 cm diameter, 5 mm wall thickness) closed on one side and equipped with a funnel-shaped entrance on the other side (1 cm diameter entrance). The traps were baited with accessible, either entire but dissected or pieces of dead Antarctic fish (Notothenioidei: *Notothenia rossii* Richardson, 1844; *N. coriiceps* Richardson, 1844; *Chaenocephalus aceratus* (Lönnberg, 1906)) of variable weights (100-250 g). To avoid unnecessarily killings of fish specimens as bait, and the given opportunity of a reutilisation of fish specimens from another project on-site, the variation of bait species and quantity was depending on their availability. Traps were deployed from a zodiac boat in the Antarctic spring/summer season 2014/2015 and summer season 2016 at depths between 12 and 43 m depth, positioned at 1 m above the bottom (Fig. 1, Table 1). Due to unpredictable weather conditions, which limited the ability of trap recovery, the duration of deployment varied from 44 hours to 65 hours with one extreme deviation of 8 days (Table 1; Station ID 02). A comparable number of traps were deployed in the outer and inner cove (11 and 9, respectively). In addition, four baited traps were deployed in Marian Cove at depths between 20 and 40 m to serve as a comparison with the recent study of Kim et al. (2014).

Identification and species description

Specimens were identified morphologically using original species descriptions, taxonomic revisions and redescrptions including Barnard K.H. (1932), Bellan-Santini (1972), d'Udekem d'Acoz and Havermans (2012). Sorting, identification and counting were performed using the stereomicroscopes Olympus SZH10 and ZEISS Stemi. Prior to preservation, selected animals were photographed using an Olympus DP21 camera attached to the stereomicroscope Olympus SZ-DF or with the digital camera Olympus OM-D EM-5 using a 60 mm macro lens. In particular cases, preserved specimens were pictured using the camera Olympus SDF attached to the stereomicroscope Olympus SZX16. All specimens were fixed and preserved predominantly in 96% undenatured

ethanol. For species description, appendages (except uropods) of the left side of the body of the female holotype specimen were dissected and temporary glycerine slides of appendages were prepared. As some characters of the holotype specimen were not in a sufficient condition, complementary drawings of the pleon and antenna 1 as well as a description of epimerons of a male paratype specimen (ZMB 30508) were additionally prepared. The pencil drawings were produced using Olympus BX40, Olympus SZH10 and LEICA MZ16 camera lucidas attached. Drawings were digitized using Adobe Illustrator CS4 following the instructions and settings of Coleman (2003, 2009) using WACOM Intuos tablets 3 and 5.

The terminology for setae and spines used in the species description follows the suggestions of d'Udekem d'Acoz (2010) and Krapp-Schickel (2011) where spines are defined as stout, articulated, inflexible structures and setae being slender, flexible and articulated structures.

The following abbreviations are used in figures 8-10: A1-2: antennae 1-2; Mx1-2: maxillae 1-2; MD: mandible; Mxp: maxilliped; Gn1-2: gnathopods 1-2; P3-7: pereopods 3-7; Cx: coxa; Ba: basis; Ca: carpus; Pr: propodus; D: dactylus; Ep1-3: epimerons 1-3; Uros1-3: urosomites 1-3; U1-3: uropods 1-3

DNA isolation, PCR and sequence processing

Specimens from Potter Cove used for molecular analyses were sorted to morphotypes and are registered and deposited at the Museum für Naturkunde, Leibniz-Institut für Evolutions- und Biodiversitätsforschung, Berlin, Germany (ZMB, Table 2). For DNA isolation, three pairs of pleopods and in cases of small specimens (approx. 5 mm - 1 cm) also pereopods from one side of the body were used to ensure a sufficient amount of DNA. Extraction followed the Blood & Tissue DNeasy Kit (Qiagen) manufacturer's protocol. Only 100 µL TE buffer were used for sample elution. PCR-amplification of the *COI* barcoding region (i.e. Folmer fragment of the Cytochrome C Oxidase subunit I gene) was carried out by using the modified Folmer-primers LCO1490-JJ (5'-CHACWAAAYCATAAAGATATYGG-3') and HCO2198-JJ (5'-AWACTTCVGGRTGVCCAAARAATCA-3') of Astrin and Stüben (2008). The premix for polymerase chain reaction consisted of a total volume of 25 µL containing 2.5 µL 10X PCR buffer, 2.5 µL dNTPs (2 mM), 0.125 µL of each primer (100 pmol/µL), 0.125 µL of HotMaster Taq DNA Polymerase (5 U/µL, 5 PRIME GmbH, Hamburg, Germany), 2 µL or 5 µL of template DNA and replenished with 17.625 µL or 14.625 µL molecular grade water. PCR settings for *COI* amplification were: initial denaturation at 94 °C for 120 s; 36 cycles of denaturation at 94 °C for 40 s, annealing at 52.5 °C for 40s, extension at 65 °C for 120 s; final extension at 65 °C for 8 min. The PCR products were sequenced with terminal primers using the sequencing services of EUROFINS (Germany), and GATC Biotech AG (Konstanz,

Germany). Sequence chromatograms were edited and assembled in Geneious 5.6.7 (Kearse et al. 2012). The *COI* alignment was constructed using the Geneious-plugin MAFFT v7.017 under the G-INS-i option recommended for sequences with global homology (Katoh et al. 2002).

Genetic diversity

Since two pseudo-cryptic lineages of *Waldeckia obesa* (Chevreux, 1905) are known (Havermans 2012), we included as references a total of ten sequences of *Waldeckia obesa* cluster ‘A’ and ‘B’ sensu Havermans (2012) in the analyses (Table 2). Mean genetic diversity for each species (intraspecific) and between species (interspecific) were calculated in MEGA 6.06 (Tamura et al. 2013) under the Kimura-2 parameter (K2P) substitution model generally used for DNA barcode data and the pairwise deletion option. A trimmed 544 bp *COI* alignment was used, as some sequences demonstrated missing data at either the 5’ or 3’ end. In the final alignment, all except two sequences were of full length, i.e. MT002Ppl001 (70 bp shorter at 5’ end) and MT002Oro013 (6 bp shorter at 3’ end). A *COI* neighbour-joining tree was generated in MEGA 6.06 using the K2P substitution model including transitions and transversions, 1000 bootstrap replicates and midpoint rooting. All DNA barcodes are cross-checked against the Barcode of Life Data System (BOLD, <http://www.barcodinglife.org>). DNA barcode data (i.e. sequences and additional information) of all genetically analysed specimens are stored and publically available in the project *LYAPO* (Lysianassoid Amphipods of Potter Cove) of the Barcode of Life Data System (BOLD, Ratnasingham and Hebert 2007) as well as in the public database of the National Centre for Biotechnology Information (NCBI).

Results

Species composition and morphological diversity

A total of more than 43,900 lysianassoid amphipod specimens (suppl. material 1) were sampled in 24 deployed baited traps. In the 20 analysed traps deployed throughout Potter Cove, 41,898 specimens of eleven distinct lysianassoid morphospecies were recorded, of which nine could be identified as known species (Fig. 2, Fig. 3). The two species *Abyssorhomene charcoti* (Chevreux, 1912) and *Orchomenella pinguides* Walker, 1903 were recorded in KGI waters for the first time. One new species – *Orchomenella infinita* sp. n. – is described herein. Individuals of *Hippomedon kergueleni* (Miers, 1875) demonstrated different colour patterns (morphotypes)

indicating that specimens may belong to two distinct species. While some *H. kergueleni* specimens had an off-white body colour (white morphotype), others were of a darker yellow colour with reddish pigmentation dorsally on pereonites and pleonites as well as on peduncle of antenna 1 and dorsal parts of the coxal plates (red morphotype) (Fig. 2a, b). This colour pattern was consistent for both sexes.

Some specimens of *Orchomenella rotundifrons* K.H. Barnard, 1932 showed morphological variations, sharing some character states with *Orchomenella denticulata* Rauschert, 1995, i.e. a serrated posterior margin of epimeral plate 3 and intermediate forms of dorsal humps and carinations on urosomite 1. For this reason some individuals were determined as *O. cf. rotundifrons*, designated as ‘Oxx’ (Table 2) and included in the barcoding analyses in order to clarify their taxonomic status.

Two lineages (cluster ‘A’, and ‘B’) of *Waldeckia obesa* were revealed by Havermans (2012). Our morphological reexamination of specimens from these lineages were compared and both comparisons with the original description and redescription of *W. obesa* in the publications of Chevreux (1905, 1906) as well as the recent revision of the genus *Waldeckia* by Lowry and Kilgallen (2014), enabled us to identify morphological evidence for considering the clusters as two distinct species. While the nominal *W. obesa* (cluster ‘A’, sensu Havermans 2012) has a labrum with a separate epistome and upper lip, a relatively short, acute hump on urosomite 1 and the posterolateral corner of epimeron 3 sickle-shaped and hooked, specimens belonging to cluster ‘B’ bear a longer, more curved hump on urosomite 1 with a flattened notch before ending into a small tooth. The labrum, epistome and upper lip are fused. Since specimens from cluster ‘B’ do not resemble any other described species of the genus *Waldeckia*, this is here confirmed as new to science and will be described elsewhere. Finally, all morphospecies, but not morphotypes, for which *COI* sequence data were obtained, were also supported as distinct taxa by molecular data (Fig. 4).

Genetic diversity and DNA barcode data

COI sequences (i.e. DNA barcodes) were generated for all species except *Orchomenella pinguides* and *Pseudorchomene coatsi* (Tab.2). The total molecular dataset comprised 79 sequences, of which 69 have been newly generated from Potter Cove. Those comprise eight morphospecies including a red coloured (11 specimens) and a white coloured (8 specimens) morphotype of *Hippomedon kergueleni* Miers, 1875. The dataset was complemented with two sequences of *Waldeckia obesa* cluster ‘A’ and eight sequences of the pseudo-cryptic and co-occurring lineage cluster ‘B’ sensu Havermans (2012) from different localities of the Southern Ocean.

Existing *COI* sequences data in BOLD is augmented for *P. rossi* (Barcode Index Number [BIN]: *BOLD:AAG7165*, identified in BOLD as *Abyssorchomene rossi*), *P. plebs* (*BOLD:AAL8109*), *A. charcoti* (*BOLD:AAN0316*) and *W. obesa*. Our sequences of *W. obesa* from Potter Cove demonstrate only max. 86.6% identity with two sequences taxonomically designated as *W. obesa* in BOLD. Since they are not yet publically available, no further information could be retrieved. However, 100% and 99.1% sequence identity is achieved with two single-specimen BINs (*BOLD:AAL8112*) and (*BOLD:AAL8113*) currently identified only as ‘Amphipoda’ in BOLD. These two specimens originate from Moon Bay (Livingston Island, South Shetland Islands). For *H. kergueleni*, *O. rotundifrons*, *Cheirimedon femoratus* and *O. infinita* sp. n. we establish first-time DNA barcode data.

Intraspecific genetic diversity is generally low (Table 3, Fig. 5), with the highest value observed for *W. obesa* cluster ‘A’ (2.8%). Interspecific genetic diversity ranges from 10.2% (*A. charcoti* / *O. rotundifrons*) to 40.1% (*Waldeckia obesa* cluster ‘B’ / *O. infinita* sp. n.). Specimens of *H. kergueleni* with red and white morphotypes possess identical *COI* sequences, as do all analysed specimens of *O. rotundifrons* bearing morphological variations as indicated earlier (Fig. 4).

Relative abundances

The analysis of the sampled amphipod specimens demonstrated clear patterns in distribution and species composition. The omnivore lysianassid *Cheirimedon femoratus* (Pfeffer, 1888) represented 79.81% of all collected specimens and was the most abundant species in Potter Cove (Table 4, Fig. 6) followed by *Hippomedon kergueleni* (Miers, 1875) (13.86%), *Orchomenella rotundifrons* K.H. Barnard, 1932 (5.04%) and *Waldeckia obesa* (Chevreux, 1905) (1.25%). *Orchomenella infinita* sp. n., *O. pinguides*, *Pseudorchomene coatsi* (Chilton, 1912), *Pseudorchomene plebs* (Hurley, 1965), *Pseudorchomene rossi* (Walker, 1903), and *Abyssorchomene charcoti* contributed only with less than 0.01% to the total number of specimens sampled in Potter Cove. Considering the relative abundances of lysianassid amphipods in the inner cove only, *C. femoratus* reached the highest proportion of 99.44%, whereas the other seven trapped species occurred in far lower abundances (Table 4: from 0.38% to <0.01%). The highest number of *C. femoratus* individuals per trap (11,922 specimens, suppl. material 1) was found at 12 m depth at approximately 60 m distance from the glacier. The species composition and relative abundances of the outer cove differed from the inner cove in that besides *C. femoratus* (67.61%) also *H. kergueleni* (22.25%), *O. rotundifrons* (8.07%) and *W. obesa* (2.02%) occurred at higher relative abundances in the outer cove (Table 4). In the adjacent Marian Cove the relative abundances of species differ compared to Potter Cove. Here, 2,039 specimens of four lysianassid species were found: *W. obesa*

dominated with 87.00% , while *C. femoratus* (12.75%), *H. kergueleni* (1.47%) and *P. rossi* (0.10%) occurred in much lower relative abundances.

Taxonomy

Order. Amphipoda Latreille, 1816

Superfamily. Lysianassoidea Dana, 1849

Family. Lysianassidae Dana, 1849

Subfamily. Tryphosinae Lowry and Stoddart, 1997

Genus. *Orchomenella* Sars, 1890

Type species. *O. minuta* Sars, 1890

Species composition. After Horton et al. (2016): *Orchomenella aahu* (Lowry and Stoddart, 1983); *O. acanthurus* (Schellenberg, 1931); *O. cavimanus* (Stebbing, 1888); *O. chelipes* Walker, 1906; *O. chilensis* (Heller, 1868); *O. decipiens* Hurley, 1963; *O. denticulata* Rauschert, 1995; *O. franklini* Walker, 1903; *O. goniops* (Walker, 1906); *O. guillei* De Broyer, 1985; *O. hiata* (Andres, 1983); *O. holmesi* Hurley, 1963; *O. hureaui* (De Broyer, 1973); *O. japonica* Gurjanova, 1962; *O. kryptopinguides* (Andres, 1983); *O. lepidula* Gurjanova, 1962; *O. littoralis* Nagata, 1965; *O. macrophthalma* (Birstein and Vinogradov, 1962; *O. minuta* (Krøyer, 1846); *O. obtusa* (G.O. Sars, 1891); *O. pacifica* Gurjanova, 1938; *O. perdido* Lowry and Stoddart, 1997; *O. pinguides* Walker, 1903; *O. pinguis* (Boeck, 1861); *O. rotundifrons* K.H. Barnard, 1932; *O. tabasco* (J.L. Barnard, 1967); *O. thomasi* Lowry and Stoddart, 1997; *O. ultima* (Bellan-Santini, 1972); *O. zschau* (Pfeffer, 1888)

Remarks. Currently, 29 species are attributed to the genus *Orchomenella* Sars, 1890, of which 15 are distributed in the Southern Ocean (De Broyer et al. 2007; Horton et al. 2016). The phylogenetic relationships between many lysianassoid families and genera remain unsolved. Molecular studies revealed the polyphyly of the genera *Orchomenella* and *Abyssorchomene* De Broyer, 1984 (Corrigan et al. 2014; Havermans et al. 2010). D'Udekem d'Acoz and Havermans (2012) made a detailed listing on the systematic history of the genus *Tryphosa* Boeck, 1871 also summarizing the phylogenetic relationship to *Orchomenella*. Resolution of phylogenetic relationships within the Lysianassoidea is beyond the scope of this paper and therefore our new species is placed in the currently defined genus *Orchomenella*. However, it should be stated that some morphological differences are apparent between our species and the current diagnosis of *Orchomenella*. The antenna 1 peduncle article 3 is well-developed and unusually long and the first article of the flagellum is not elongate in *O. infinita*.

***Orchomenella infinita* sp. n. Seefeldt**

(Figs. 3, 7-10; Tables 2-4)

Orchomenella cf. *ultima*– Jażdżewski et al. 1991:109–110, 112, 115

Orchomenella cf. *ultima*– Jażdżewski et al. 1995:371

Orchomenella cf. *ultima*– Jażdżewski et al. 2001:910–917 (eco)

Orchomenella sp.– Barrera-Oro and Piacentino 2007:792

Orchomenella (*Orchomenella*) cf. *ultima*– ABBED, www.abbed.uni.lodz.pl; Siciński et al. 2011

Orchomenella cf. *ultima*– Siciński et al. 2012:359–360, 365

Orchomenella cf. *ultima*– Kim et al. 2014:106, 108–109, 111, Fig 5 G

Lysianassid sp.– Moreira 2015

Orchomenella sp. n.– Barrera-Oro et al. (in prep.)

Type material. 1 HOLOTYPE female, 5.5 mm. ZMB 30506, dissected preserved in 70% ethanol (temporarily stored in 1:1 glycerin-ethanol (70%)) , King George Island, Potter Cove, sta.9, 62°14'23.43"S 58°41'52.3"W, baited trap, 39 m, 16.12.2014. Pleopods and right pereopods were used for DNA extractions, specimen ID MT009Oul006; BOLD ID: LYAPO020-16. PARATYPE specimens in 96% ethanol; BOLD ID LYAPO021-16 (MT002Oul014, ZMB 30507): female, 4 mm, sta. 2, 62°14'21.5"S 58°41'52.5"W, baited trap, 30 m, 14.11.2014; LYAPO022-16 (MT014Oul001, ZMB 30508): male, 4 mm, sta. 14, 62°14'23.4"S 58°41'52.5"W, baited trap, 40 m, 20.12.2014; MT014Oul003, ZMB 30593: male, 4 mm sta. 14, 62°14'23.4"S 58°41'52.5"W, baited trap, 40 m, 20.12.2014; MT002Oul015, ZMB 30592: female, 5 mm, sta. 2, 62°14'03.2"S 58°39'17.3"W, baited trap, 30 m, 14.11.2014.

Type locality. Potter Cove, King George Island, South Shetland Islands, Antarctica (62° 14'S 58°41"W).

Etymology. The epitheton *infinita* (latin: boundless, unlimited, endless, infinite) refers to the seemingly endless discovery of new species and the never ending chaos within the group of 'orchomenids'. It expresses the opposite to the morphologically most similar species, *O. ultima*, whose name could be misleadingly interpreted as the last species ever described in that genus.

Diagnosis: Eye blazing red when alive. Antenna 1 peduncle article 3 well-developed, unusually long; first article of flagellum not elongate; article 1 of accessory flagellum not strongly elongate; gnathopod 1 basis slender, palm concave; urosomite 1 no dorsal depression, without carina, keel or hump; somites of pereon and pleon with brownish pigmentation forming transversal striped colour patterns, some merging until dorsal parts of coxae (may vanish in alcohol).

Description. Based on HOLOTYPE female, ZMB 30506. *Body:* typical lysianassoid appearance in shape. *Head:* as broad as long, lateral cephalic lobes convex. Eyes large, somewhat pyriform, well-developed ommatidia, blazing red in living organism, colour is fading when preserved in alcohol. *Antenna 1:* subequal in length to Antenna 2; primary flagellum 11-articulate, first article not elongate, broader than long; accessory flagellum present, 4- articulated, first article not strongly elongated, 2.5x longer than broad; calceoli absent. *Antenna 2:* calceoli absent; flagellum 9-articulate. *Mouthparts:* subquadrate. *Labrum (Epistome and upper lip):* separate; epistome produced subequally, slightly convex. *Mandible:* incisor with smooth edge with a small denticle on each side; lacinia mobilis present on the left side, slender peg; molar process oval, ridged and fully triturating; palp 3- articulated, attached proximal, markedly below molar process, article 2 slender (7.3x longer than broad), article 3 slender (4x longer than broad) and bent in a sickle shape. *Maxilla 1:* inner plate elongate, bearing two stout plumose setae distally, equal in size; outer plate with 11 spines (setal-teeth, ST), (modified 6/5 arrangement), ST1-ST5 stout, ST6-ST7 very stout, ST1 three-cuspidate, ST2 four-cuspidate, ST3 four-cuspidate, ST4; ST5 five-cuspidate; ST6 multicuspidate; ST7 multicuspidate, slightly displaced from ST6, STA-D more slender than ST1-ST7, STA five-cuspidate, STB, four-cuspidate, STC six-cuspidate, STD six-cuspidate, palp distal margin with five cuspidate spines and one antero-distal flag seta. *Maxilla 2:* inner plate slightly shorter than outer plate; outer plate with long denticulate and simple setae distally; inner plate with long plumose setae. *Maxilliped:* inner and outer plate well-developed; inner plate narrow, with few plumose setae medially; outer plate reaching halfway along 3rd article of palp, bearing two larger stout, nodular spines distally, several shorter stout, nodular spines along medial margin; palp 4- articulated, dactylus long, well-developed. *Gnathopod 1:* subchelate; coxa large, shorter than coxa 2, subrectangular, not tapering, anterior and posterior margins almost parallel, anterodorsal margin slightly concave, basis elongate and slender (3.5x longer than broad); ischium short; merus missing/broken, carpus subtriangular, subequal in length to propodus; propodus subrectangular, margins subparallel; palm transverse and concave, minutely serrate bearing two long, stout spines at the posteroventral corner; dactylus stout but simple *Gnathopod 2:* minutely chelate; coxa large, subrectangular, subequal in size to coxa 3; basis elongate, long (8x longer than broad); ischium long (4x longer than broad); posterior margin of merus with several long, simple setae and short brush setae; carpus 2.3x as long as wide, 2.3x as long as propodus, posterior margin lobate, from midway to distal end of posterior margin with area of dense, very short setae, anterior distal margin with several longer setae; propodus subquadrate, length 1.6x breadth, anterodistal with many long setae, posterior margin with long setae; dactylus reaching beyond posterior margin of propodus; palm concave. *Pereopod 3:* coxa large, subrectangular; basis slender (3x longer than broad); anterior margin of merus convex, posterior margin with a few, long setae. *Pereopod 4:* coxa 1.5x deeper than

broad, posteroventral lobe well-developed (1.5x broader than deep), posteroventral corner of lobe rounded; basis slender (3.3x longer than broad), no setae visible; ischium and merus similar to Pereopod 3. *Pereopod 5*: shorter than pereopod 6 and 7; coxa posteriolobate; basis expanded posteriorly, broadly rounded, posterior margin crenate with one short, simple seta in each notch, anterior margin with several short, cone-shaped spines and one longer spine at the anteroventral corner; merus expanded posteriorly longer than broad; carpus longer than broad; propodus 6x longer than broad bearing spines on the anterior margin, anteroventral and posteroventral corner; dactylus slender and curved. *Pereopod 6*: coxa distinctly smaller than coxa 5, posteriorlobate; basis longer than pereopod 5 basis, expanded posteriorly, posterior margin crenate with one short, simple seta in each notch, anterior margin with cone-shaped spines from midway until just before anteroventral corner, anteroventral corner with two long, stout setae and two slender setae, posteroventral lobe well-developed; merus longer than broad, posterior margin expanded with two crenations, posteroventral corner produced bearing a cone-shaped spine, anterior margin with one long and one short cone-shaped spine, anteroventral corner with one long seta; carpus longer than broad, posterior margin slightly convex, anterior margin with one large cone-shaped spine; propodus much longer than broad, anterior margin with five cone-shaped spines; dactylus, slender and curved. *Pereopod 7*: coxa round, small; basis expanded, posterior margin convex, crenate with one short, simple seta in each notch, anterior margin with cone-shaped spine from midway until just before anteroventral corner, anteroventral corner with one stout spine, posteroventral lobe well-developed; ischium missing/broken; merus longer than broad, expanded, anterior margin straight, posterior margin convex, with one crenation bearing one cone-shaped spine, posteroventral corner with one stout spine, anteroventral corner with one stout spine; carpus longer than broad, anteroventral corner with spines, posteroventral corner with setae; propodus 5.7x longer than broad, slender anterior margin crenate with stout, cone-shaped spines; dactylus slender and curved. *Urosome*: urosomite 1 flat, no carina nor hump, nor keel. *Uropod 1*: peduncle, 1.12x longer than outer ramus with three lateral spines; outer ramus 1.15x longer than inner ramus with three dorsomedial spines; inner ramus, with two dorso medial spines. *Uropod 2*: peduncle, length, 0.94x than outer ramus; outer ramus longer than inner, length 1.35x inner, with four dorsomedial spines, without constriction; inner ramus with two dorsomedial spines, without constriction. *Uropod 3*: peduncle short, length 0.78x outer ramus; rami stout without plumose setae; outer ramus 2-articulate, article 2 very short, length 0.25x article 1, with two apical spines; inner ramus distinctly shorter than outer, length 0.74x outer ramus. *Telson*: 1.3x longer than broad, half length cleft (50%), reaching just past peduncle of uropod 3.

Complementary description. Due to insufficient character condition of epimeron of the holotype specimen a complementary description of a paratype male (ZMB 30508) is given.

Epimeron 1: anterior margin slightly concave; anteroventral corner rounded; posteroventral corner convex, broadly rounded. *Epimeron 2*: anteroventral corner convex, rounded; posteroventral corner bluntly subquadrate. *Epimeron 3*: anteroventral corner convex, broadly rounded; posterior margin straight; posteroventral corner subacutely rounded, not produced.

Colour pattern. This species has brownish pigmentation forming transverse stripes on each segment of the pereon and pleon (Fig. 3a). This colour pattern might fade or disappear altogether following preservation.

Size. 4.0-5.5 mm (based on type series).

Sexual dimorphism. In males antenna 2 is longer than antenna 1, while in females antenna 2 is subequal to antenna 1. Moreover, males bear calceoli on antennae 1 and 2, whereas females lack calceoli on antennae 1 and 2.

Distribution and depth. King George Island, Potter Cove (30-40 m, present study), Marian Cove (0.5 m, Kim et al. 2014), Admiralty Bay (10 m, Jażdżewski et al. 1991; 5-10 cm, underneath waterline, Jażdżewski et al. 2001).

Biology. The scavenger status of this species remains unclear since the species did only occur in very low numbers in baited traps in this study. Due to the fact that it was attracted to bait bearing mouthparts typical for feeding on animal carcasses it is assumed that *O. infinita* is, at least, a facultative carrion-feeder. Jażdżewski et al. (2001) reported this species as an epibenthic dweller being also able to burrow in sediments.

Remarks. *O. infinita* sp. n. is most closely related to *O. ultima* but differs from this species in having the anterior margin of lateral lobe of the head broader and more convex, article 1 of the flagellum of antenna 1 is much shorter, not elongate (broader than long, not longer than broad as in *O. ultima*) and article 1 of the accessory flagellum is not strongly elongated (2.5x longer than broad) as it is in *O. ultima* (5x longer than broad). Urosomite 1 has no dorsal depression, no carina or hump while *O. ultima* has a deep dorsal depression followed by a prominent rounded dorsal hump.

The newly described species *O. infinita* has been detected in several earlier studies (e.g. Jażdżewski et al. 1991; Jażdżewski et al. 2001; Kim et al. 2014). It was identified as *Orchomenella* cf. *ultima* and morphological differences were already discussed by Jażdżewski et al. (1991) and Kim et al. (2014). After a detailed examination of the holotype of *O. ultima*, the original description of Bellan-Santini (1972), and a careful examination of the specimens within this study, the morphological differences between our specimens and *O. ultima* are evident and justify the description of a new species. Since the holotype specimen of *O. ultima*, stored at Museo Civico di Storia Naturale, Verona, Italy, MSNVRCr479, is in a fragile condition and the history of fixation is unknown, we decided not to risk a destruction of the valuable material for DNA extraction.

Discussion

Species inventory and identification

Taxonomic misidentifications can have serious consequences for subsequent data analyses especially for population assessments and conservation managements (Metcalf et al. 2007; Beerkircher et al. 2009), but also for evolutionary and ecology-based research (Bortolus 2008). It is therefore recommended that an integrative taxonomic approach should be conducted whenever possible. Our results are in large agreement with the general performance of DNA barcoding data in marine metazoans (Bucklin et al. 2011), crustaceans (Costa et al. 2007) including marine amphipods and demonstrated the identification potential of an integrative approach combining morphology and genetics (Radulovici et al. 2009; Havermans et al. 2010, 2011; Havermans 2012).

In our integrated study of scavenging lysianassoid amphipods from Potter Cove we contributed to the biodiversity inventory of the Antarctic marine fauna by analysing more than 43,900 amphipod specimens representing ten lysianassoid species in two families. Momo et al (1998) investigated the amphipod species composition from outer Potter Cove only. In their study they recorded three lysianassid species: *Cheirimedon dentimanus* Chevreux, 1905, *Valettia coheres* Stebbing, 1888 and *Orchomenella acanthurus* (Schellenberg, 1931). *C. dentimanus* is a junior synonym of *C. femoratus* (Chilton 1913; Lowry 2010). The record of *V. coheres* is very likely the result of a misidentification. This species belongs to a little known deep-sea genus, comprising only two species. In the study of Casaux et al. (1990) the occurrence of *V. coheres* was reported as a component of the algal bed fauna in Potter Cove, without giving any evidence and reference for this. Besides the questionable records of Casaux et al. (1990) and Momo et al. (1998), only one specimen of *V. coheres* is known, subsequently designated as the holotype (Thurston and Allen, 1969). The sibling species *Valettia hystrix* Thurston, 1989 is only known from the alimentary canal of two species of holothurian collected in the North East Atlantic Ocean (Thurston 1989). In addition, the type locality of *V. coheres* is in the Southern Ocean Indian Ocean sector but at more than 3600 m depth (Stebbing, 1888). For this reason, it is very unlikely that *V. coheres* is found sub-littorally and not more frequently in an Antarctic sampling hotspot such as the western Antarctic islands. It is herein postulated that the records of *V. coheres* by Casaux et al. (1990) and Momo et al. (1998) are misidentifications.

Intra- or interspecific morphological variation?

We investigated if two colour morphs (red and white) of *H. kergueleni* might represent two distinct species.

Species delimitation has been carried out successfully on the basis of colouration and subsequently supported by molecular data in the amphipod *Paramphithoe hystrix* complex (Schnabel and Hebert 2003) as well as in the decapod *Petrolisthes galathinus* complex (Hiller et al. 2006, Hiller and Werding 2007). However, in our study, both colour morphs of *H. kergueleni* can not be distinguished by molecular data. A similar case of a species bearing distinct morphotypes, but with pairwise genetic divergence values within the intraspecific range (max. 4% K2P distance) both in mitochondrial (*COI*, 16S rDNA; 0-1% mean K2P distance) as well as in nuclear marker (28S rDNA; 0% mean K2P distance) was described for the Antarctic deep-sea lysianassoid *Eurythenes andhakarae* D'Udekem d'Acoz and Havermans, 2015 (Havermans et al. 2013; d'Udekem d'Acoz and Havermans, 2015). D'Udekem d'Acoz and Havermans (2015) explained the differences in colour patterns as a result of the interdependence between pigmentation and moult and intermoult stages – a phenomenon already known from the shore crab *Carcinus maenas* (Linnaeus, 1758) (Baldwin and Smith 1987; Reid et al. 1997; Styrrishave et al. 2004; Lewis 2011). This is likely also the case for the two detected morphotypes of *H. kergueleni*.

The species *Orchomenella rotundifrons* represents another case of a species with a high morphological variability. Due to the fact that some specimens of *O. rotundifrons* share morphological traits fitting to the characteristics of *O. denticulata* without being genetically distinct, we can assume that *O. denticulata* might represent a morphotype within the variability range of *O. rotundifrons*. However, it should be noted that investigations of DNA barcode data or mitochondrial DNA can be misleading or wrong in cases of relatively recent speciation or introgression events (Moritz and Cicero 2004). More detailed analyses with the integration of nuclear data should address the aforementioned taxonomic issues. On the other hand, *COI* data can highlight cases of cryptic species complexes, for which amphipods provide well-known examples (e.g. see Costa et al. 2007; Havermans et al. 2011; Havermans 2012; Katouzian et al. 2016). Havermans (2012) revealed two genetically distinct clusters of *W. obesa* (>15% K2P distance) which we could corroborate with new morphological data, thus supporting their interpretation as reproductively isolated species (nominal *W. obesa* cluster 'A' and *W. obesa* cluster 'B'). We included sequences of nominal *W. obesa* and *W. obesa* cluster 'B' sensu Havermans (2012) in our study and have obtained evidence for the occurrence of nominal *W. obesa* in Potter Cove.

The influence of sampling method and environmental factors on species occurrences and abundances

In previous studies in which the amphipod scavenging fauna has been investigated by baited traps, the number of species reported was related to the sampling effort and coverage area. De Broyer et al. (2004) recorded for a sampling effort of 31 baited traps covering the eastern and western Weddell Sea, including King George Island, 37 lysianassoid species from the 70,000 specimens investigated up to 1000m depth. A study on deep-sea lysianassoid scavengers from the Mid-Atlantic Ridge (Horton et al. 2013) has given an account of 31 species out of more than 250,000 specimens sampled from sixteen baited trap deployments over a 4-year study period. Results of biodiversity assessments often vary according to the sampling methods and the sample sizes used. In this context, the use of baited traps as a non-quantitative and selective method presents difficulties when estimating species abundances. Scavengers are specifically attracted by chemical cues and the challenges of defining the certain area of attraction has been made a subject of discussion (Gros and Santarelli, 1986; Ingram and Hessler, 1983; Premke et al. 2003; Sainte-Marie and Hargrave, 1987). Sainte-Marie and Hargrave (1987) made an attempt to develop a model for estimating amphipod species abundances inferred from baited traps. They stated that variables such as species-specific swimming speeds, current velocity, site specific eddy diffusivity, bait-specific odour leaking rate and species-specific chemosensory thresholds are critical parameters for estimation models. Without these information the estimation of species abundances inferred from baited traps will not be accurate. Furthermore, bait size, daytime (Sainte-Marie, 1986) and entrance size of the trap also affect the sampling results. However, the use of baited traps for collecting scavenging, mobile organisms such as amphipods helps to avoid sources of errors such as gear avoidance or inefficient retention of (smaller) organisms associated with other commonly used sampling methods (hand nets, Van Veen grabs, epibenthic sledges, trawls). Indeed, these could introduce a sampling bias of unknown magnitude.

The omnivorous scavenger *C. femoratus* is ubiquitously distributed both in the soft sediment dominated part of Potter Cove (inner cove) as well as in the hard substrated area (outer cove). Moreover, *C. femoratus* occupied a dominant role among scavenging lysianassoids in the inner cove being the only species occurring in high relative abundances and particularly in the recently ice-free areas of Potter Cove. These areas are greatly influenced by the retreat of the Fourcade Glacier as well as by high rates of freshwater run-off and sedimentation caused by the meltwater creeks disemboguing into the cove. This has already led to shifts in the benthic communities and has also created new habitats available for colonization (Quartino et al. 2013; Sahade et al. 2015; Deregibus et al. 2016). Pioneer species as well as species with a broad ecological niche, are expected to occupy new areas within

the succession process. The sporadic and rare occurrence of other lysianassoid species suggests that the inner cove is not a favourable habitat although potential candidate colonizers are present in the outer cove. Hence, it is very likely that *C. femoratus* is a pioneer species of sublittoral coastal systems, with a broad ecological niche. When compared to the inner cove, the outer cove seems to provide a more suitable habitat for other lysianassoid amphipod species, and this is where the highest numbers of lysianassoid amphipod species were found. This finding indicates that some or all of the conditions present in the inner cove may be challenging to lysianassoid amphipods: shallower depths, the strong influence of sedimentation processes, fluctuating salinity, predominantly soft sediment and low coverage of macroalgae beds (Barrera-Oro and Casaux 1990; Quartino et al. 2013; Sahade et al. 2015). Most of the less abundant species found in our study such as *P. plebs*, *P. rossi*, *P. coatsi*, *A. charcoti* and *W. obesa* have been frequently reported at greater depths (De Broyer et al. 2004, 2007; Presler 1986) indicating a preference for deeper waters. However, the conclusion of the aforementioned records could also be biased due to the restricted sampling possibilities for shallow-water samplings on board of a research vessel.

C. femoratus plays an important role in the shallow-water benthic communities of Maxwell Bay, being the only scavenging amphipod species found in high numbers compared to other amphipods (Rauschert 1991; Siciński et al. 2012; Kim et al. 2014). Siciński et al. (2011) reported *C. femoratus* dominating the necrophagous benthic community of Admiralty Bay in winter while being replaced in summers by *H. kergueleni*. A similar seasonal species shift was revealed by Smale et al. (2007) in which a replacement of *C. femoratus* in summers by the nemertean *Parborlasia corrugatus* (McIntosh, 1876) was reported. Our data did not corroborate this species shift: we found *C. femoratus* in higher numbers than *H. kergueleni* in our summer samples. Finally, and in addition to the findings of Kim et al. (2014), who only reported *C. femoratus* and *O. infinita* sp. n., we now can add *H. kergueleni* as well as *O. rotundifrons* to the species list of the sublittoral of Maxwell Bay.

In a compilation of thirty years of benthic biodiversity research from Admiralty Bay, Siciński et al. (2011) listed 27 lysianassoid amphipod species (subsequently corrected into 29 species; pers. communication A. Jażdżewska) sampled by various methods. Eight of the ten lysianassoid species we detected for Potter Cove are also known from Admiralty Bay, while *A. charcoti* and *O. pinguides* were reported for KGI for the first time. The higher species number for lysianassoid amphipods in Admiralty Bay is not surprising given that a) the amphipod community in Admiralty Bay has been studied for more than 30 years and therefore likely higher due the greater number of total samples investigated, b) the use of additional sampling methods (e.g. netting, van Veen grabs), and c) the larger size of Admiralty Bay (25.3 km coastline) and greater depths (up to 535 m), which might favour

a higher alpha diversity by providing more microhabitats (Siciński et al. 2011). Moreover, variations in soak time, bait quantity and the limited size of trap entrance could have also affected the number of sampled species from Potter Cove. However, assuming that abiotic conditions (e.g. sedimentation, freshwater input) are one of the major limiting factors of the taxonomic diversity of scavenging amphipods in the shallower inner Potter Cove, the increased influence of meltwater-related conditions along the Antarctic Peninsula could lead to similarly impoverished communities in affected habitats. A continuation of studying scavenging amphipods from Potter Cove and understanding the reason for the broad ecological niche of *C. femoratus* will improve future species distribution modelling and predictions on the effects of ongoing and future environmental changes.

Outlook

As an omnivorous scavenger, the lysianassoid amphipod *C. femoratus* is a key species Potter Cove food web, illustrated by its wide distribution and high abundances in both the outer and inner cove. It is an important element for the decomposition of organic matter in Potter Cove. A recent study of fish gut content analyses showed that *C. femoratus* is also an important food source for the locally abundant Antarctic fish species *Notothenia rossii* Richardson, 1844 at 10 and 20 m depths (Index of relative importance, IRI%= 19.24; 9.47) as well as for *Notothenia coriiceps* Richardson, 1844 at 10 and 20 m depths (IRI%= 4.52; 9.25) (Barrera-Oro et al. unpubl. data). The ecological role of lysianassoid amphipods, but particularly the trophic position of *C. femoratus* in the food web of Potter Cove needs more detailed study as omnivorous species in general do not necessarily have a flexible position in food webs (Johnston et al. 2011). Studies addressing species-specific feeding and decomposition rates (Lastra et al. 2014) as well as stable isotope and fatty acid analyses (Nyssen et al. 2002, 2005) are needed to further elucidate the role and importance of lysianassoid amphipods in the coastal Antarctic ecosystem, which are exposed to a rapidly changing environment due to climate-induced glacier retreat.

Conflict of Interest: The authors declare that they have no conflict of interest.

Ethical approval: All applicable international, national, and/or institutional guidelines for the care and use of animals were followed.

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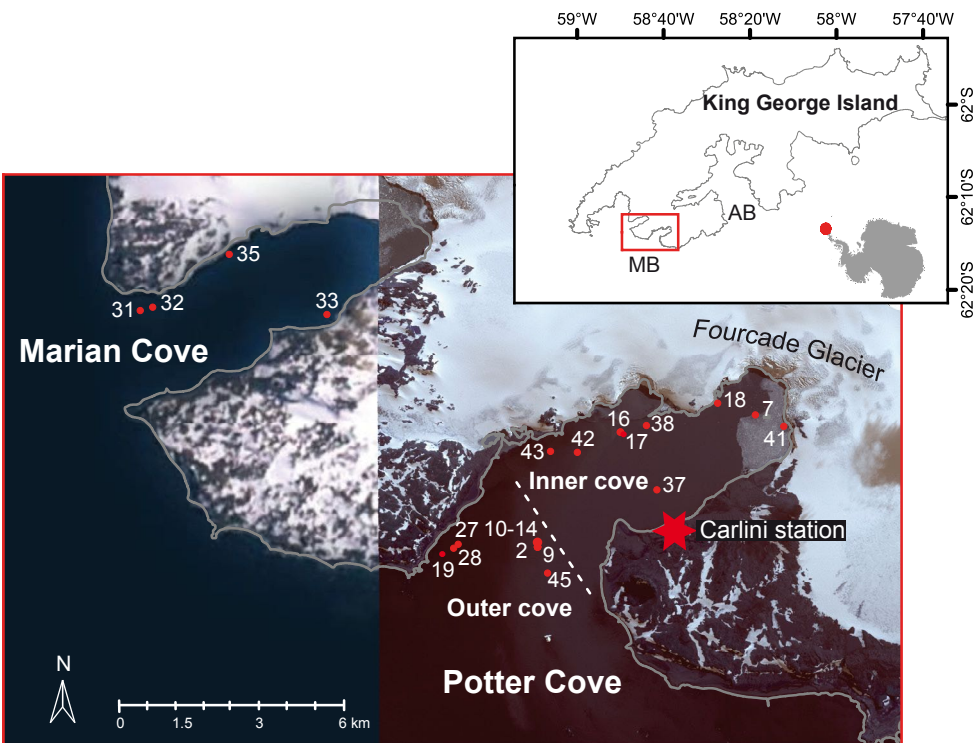


Fig. 1 Sampling stations in Potter Cove and Marian Cove.

MB: Maxwell Bay; AB: Admiralty Bay.

Map data: DIGITALGLOBE 2014, WorldView-2 scene

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Catalog ID: 103001001F612100, Acq Date: 2013/03/07,

Sensor: WV02, Band Info: Pan_MS1_MS2, Resolution 0.5*0.5m;

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swisstopo, and the GIS User Community



Fig. 2 Lysianassoid amphipod species of Potter Cove. Scale bars correspond to 1 mm. f, i, j) post mortem

a) <i>Hippomedon kergueleni</i> white colour morph	d) <i>Cheirimedon femoratus</i>
b) <i>Hippomedon kergueleni</i> red colour morph	f) <i>Orchomenella pinguides</i>
c) <i>Abyssorchomene charcoti</i>	h) <i>Waldeckia obesa</i>
e) <i>Orchomenella rotundifrons</i>	j) <i>Pseudorchomene plebs</i>
g) <i>Pseudorchomene rossi</i>	
i) <i>Pseudorchomene coatsi</i>	

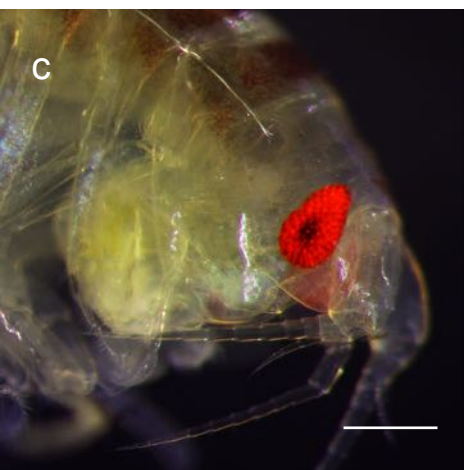
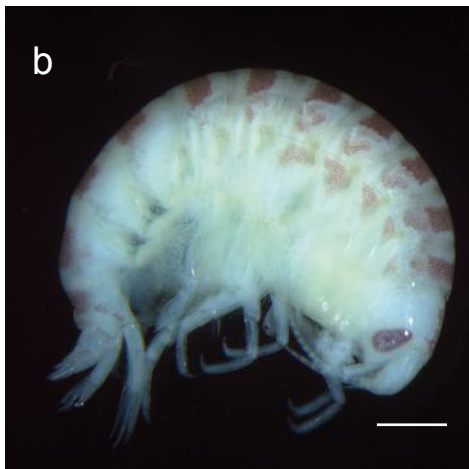


Fig. 3 *Orchomenella infinita* sp. n., holotype, female, 5.5 mm; Potter Cove, station 9. a, c, d) in vivo b) preserved in ethanol. a +b) habitus and colour pattern, scale bars correspond to 1 mm. c+d) scale bars correspond to 250 μ m c) emphasizing antenna 1 d) emphasizing epistome and upper lip and chelation of gnathopod 2

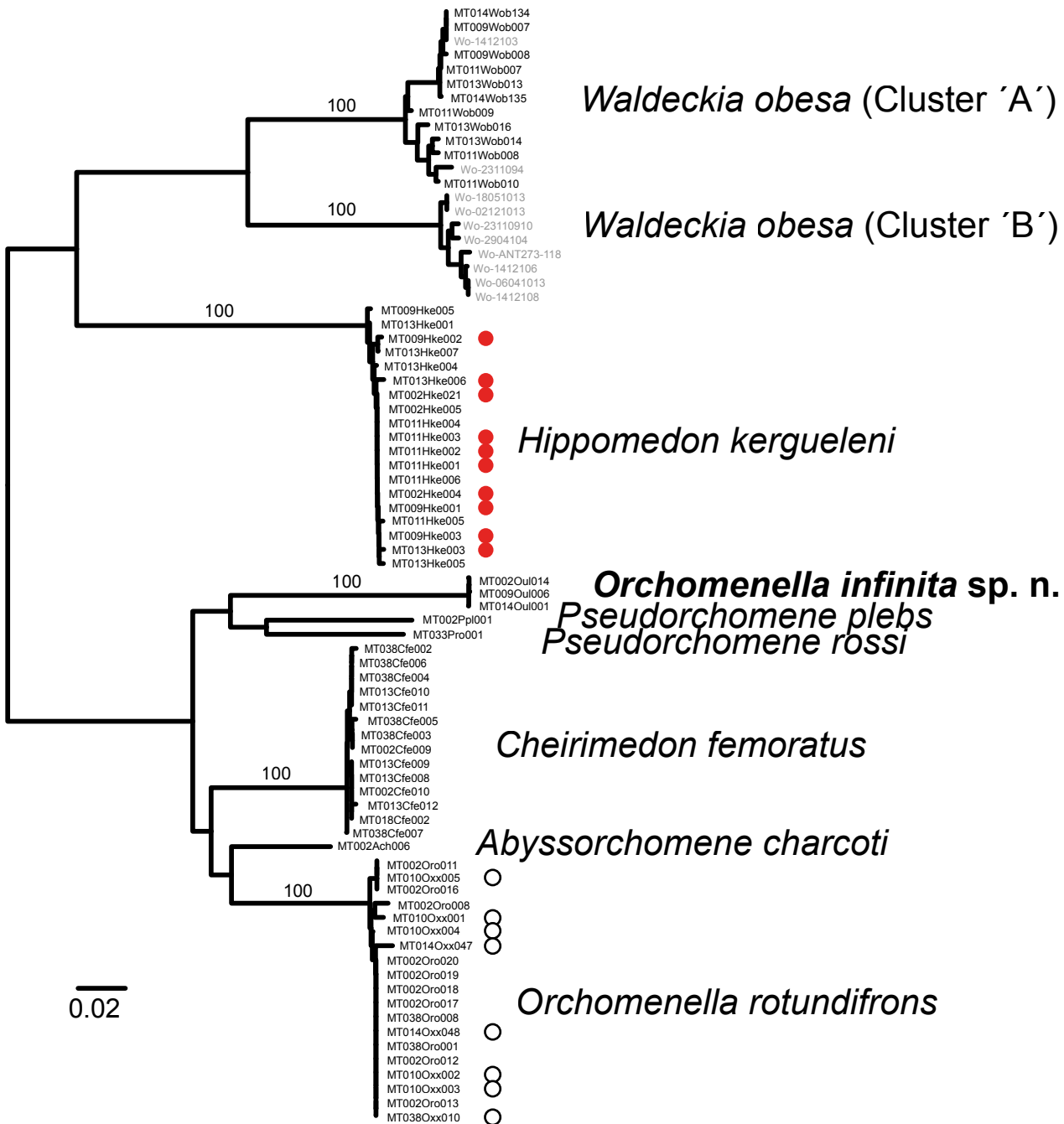


Fig. 4 Mid point rooted neighbour-joining tree of COI sequences of lysianassoid species based on K2P distances. Bootstrap values with full support are shown (number of replicates= 1000). Red dot: red colour morph in *Hippomedon kergueleni*. White dot: morphological variability present in *Orchomenella rotundifrons*. Sequences shown in light grey represent data from Havermans (2012). Specimen information can be found in Table 2

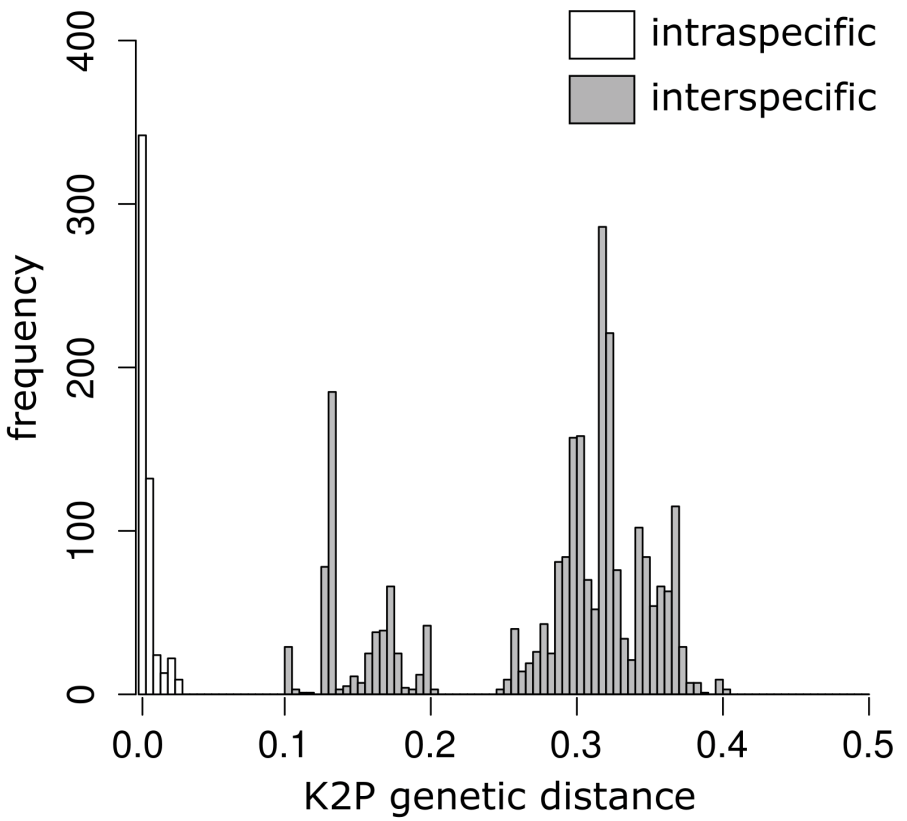


Fig. 5 Frequency distribution of pairwise K2P distances within and between Antarctic lysianassoid species

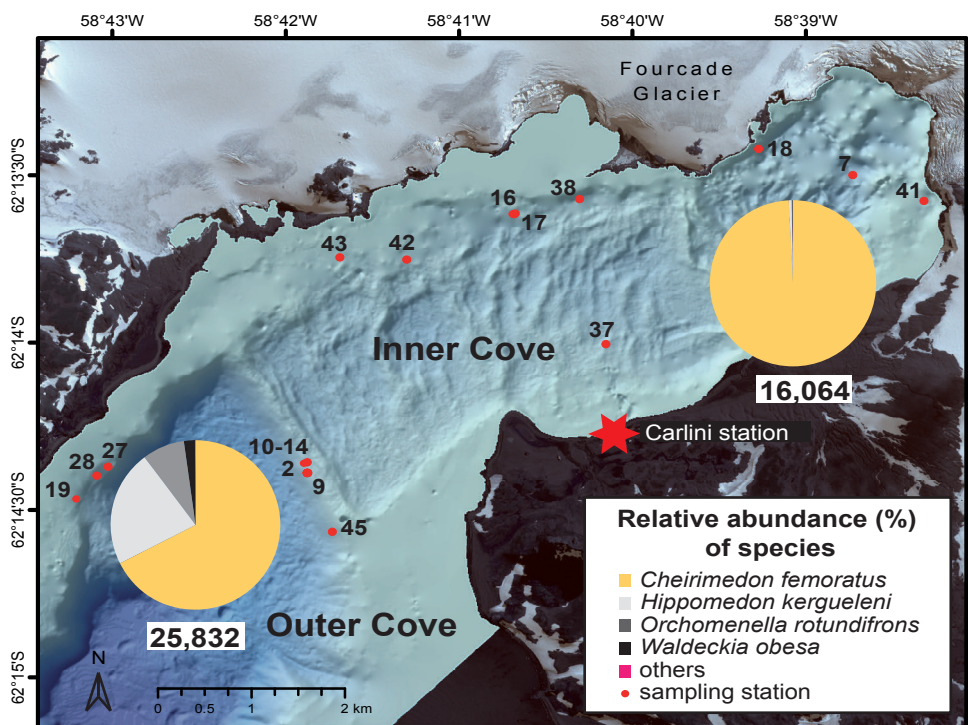


Fig. 6 Relative abundances (%) of lysianassoid amphipod species found in Potter Cove (outer cove, inner cove). Numbers below pie charts depict the total number of specimens found at respective locations. Further information can be found in Table 4 and supplementary material 1. Map data: DIGITALGLOBE 2014, WorldView-2 scene 103001001F612100, Image Courtesy of / Copyright © DigitalGlobe - Longmont, Colorado. All rights reserved.

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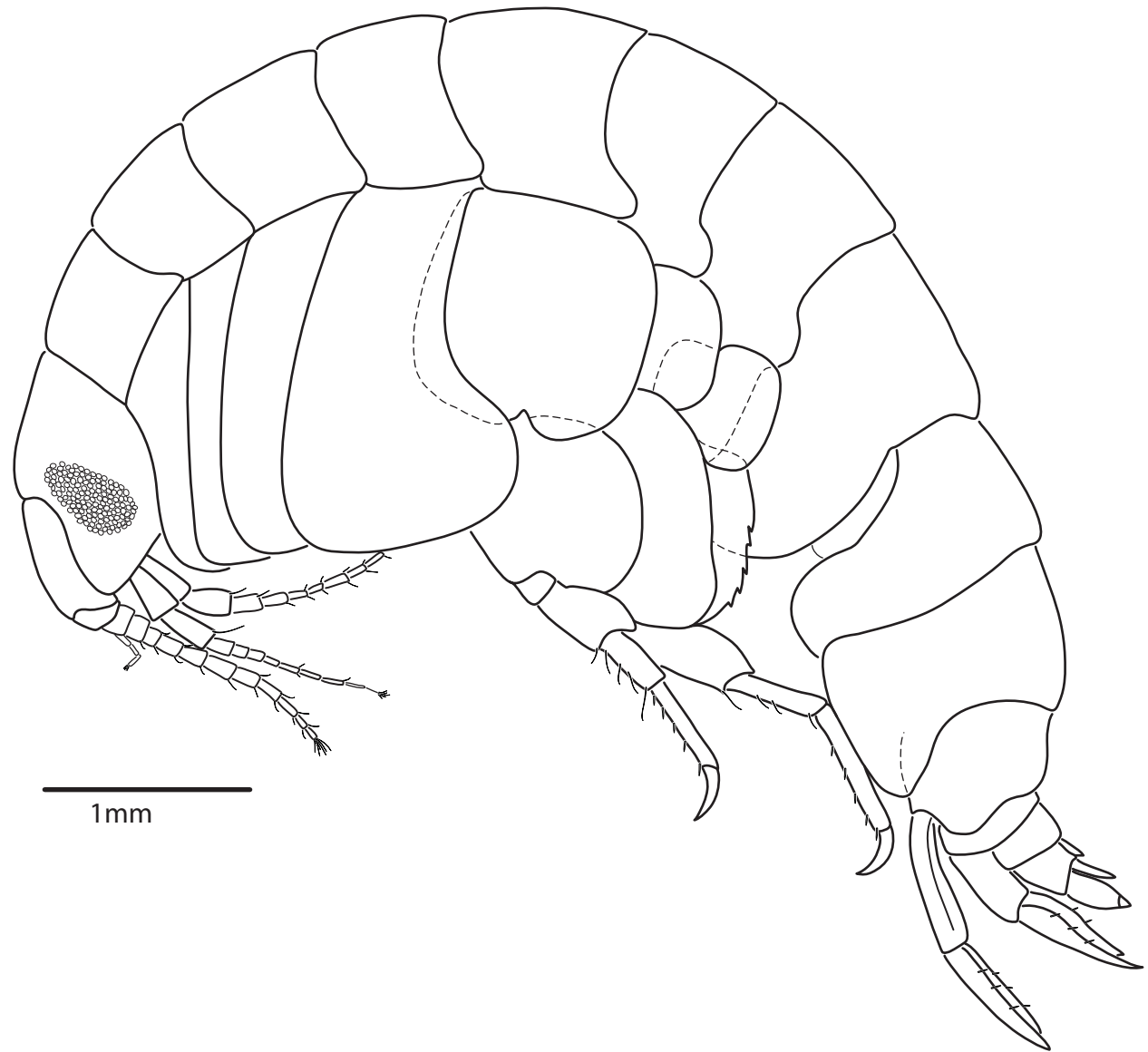


Fig. 7 Habitus of *Orchomenella infinita* sp. n., holotype, female, 5.5 mm; Potter Cove, station 9

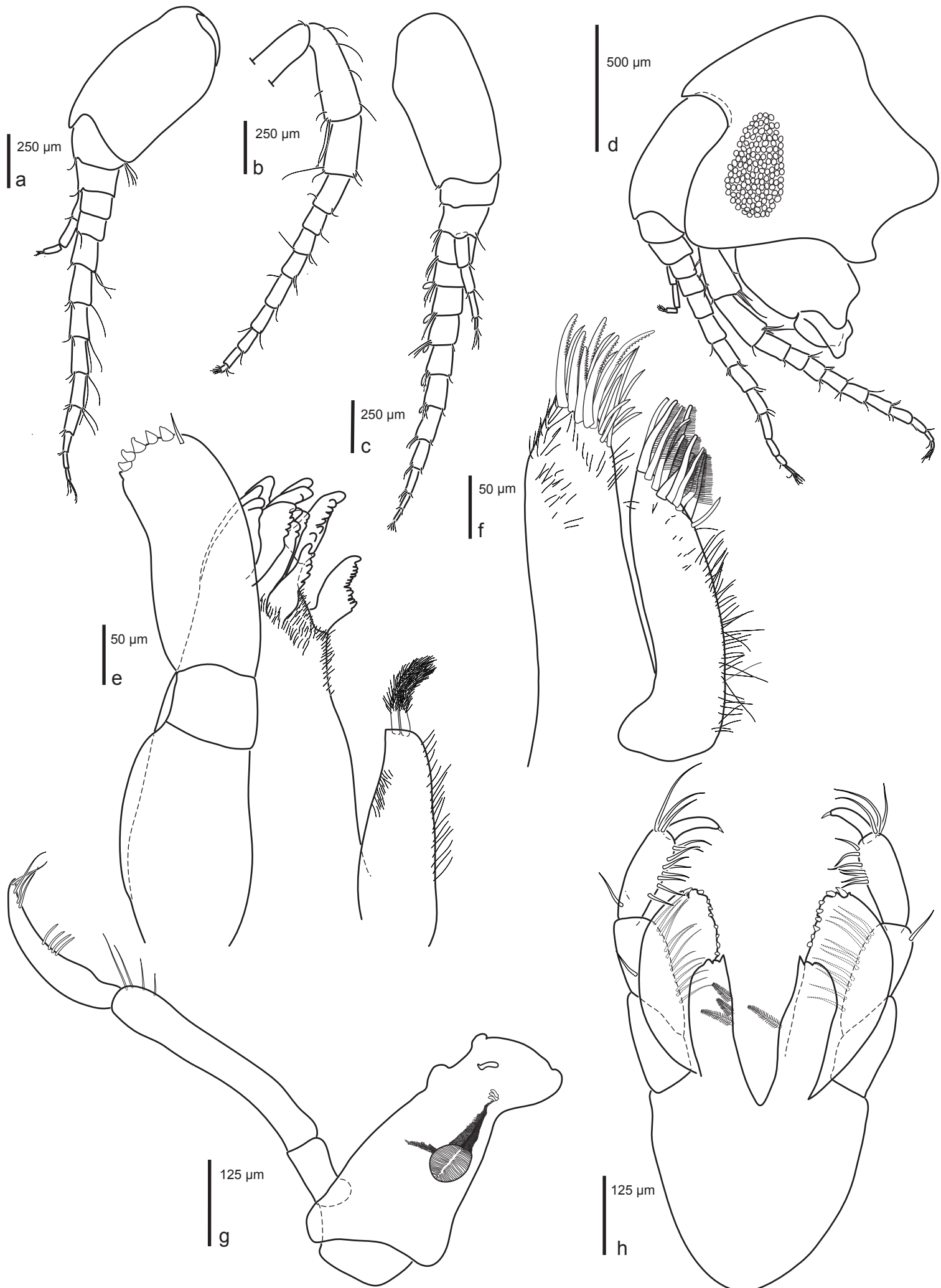


Fig. 8 *Orchomenella infinita* sp. n., holotype, female, 5.5 mm; Potter Cove, station 9. a) left A1 b) left A2 d) head, antennae, epistome and upper lip e) left Mx1 f) left Mx2 g) left MD h) Mxp. *Orchomenella infinita* sp. n., paratype, male, 4 mm; Potter Cove station 14. c) left A1

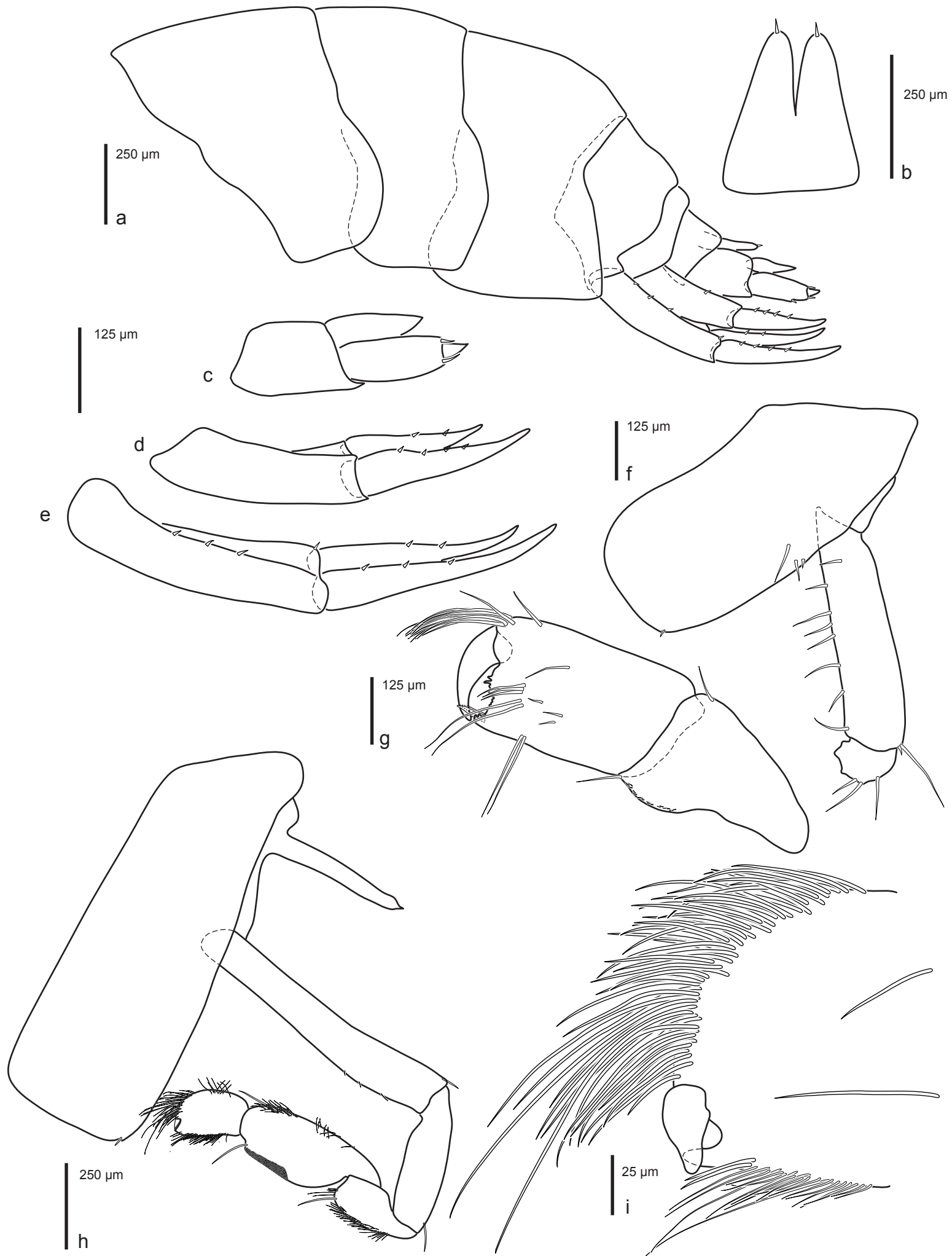


Fig. 9 *Orchomenella infinita* sp. n., holotype, female, 5.5 mm; Potter Cove, station 9. b) telson c) left U3 d) left U2 e) left U3 f) left Gn1: Cx, Ba, Is g) left Gn1 Ca, Pr h) left Gn2 i) left Gn2 distal part of Ca. *Orchomenella infinita* sp. n., paratype, male, 4 mm; Potter Cove station 14. a) Ep 1-3, Uros 1-3, U1-3

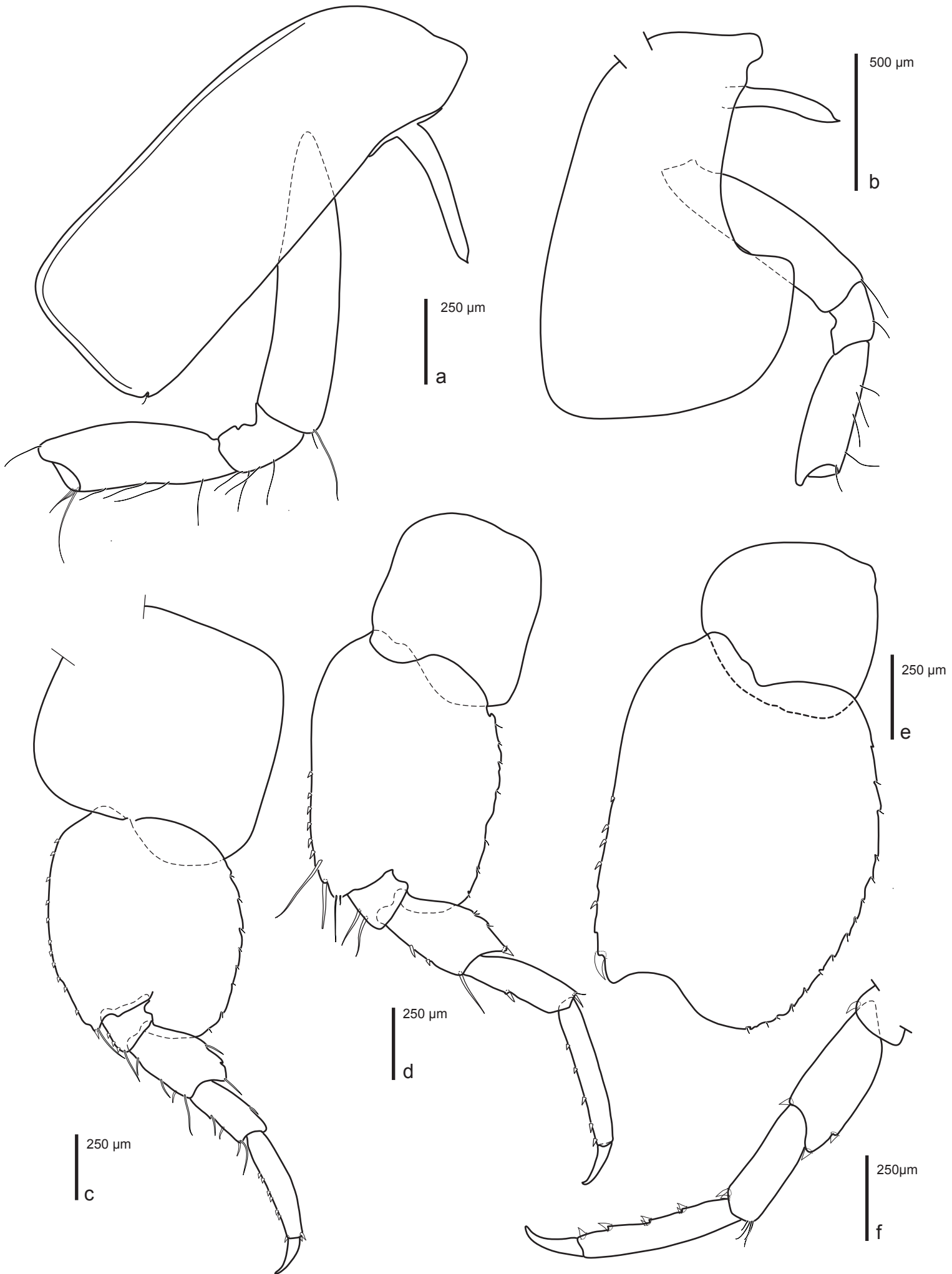


Fig. 10 *Orchomenella infinita* sp. n., holotype, female, 5.5 mm; Potter Cove, station 9. a) left P3: Cx, Ba, Is, Me b) left P4: Cx, Ba, Is, Me c) left P5 d) left P6 e) left P7:Cx, Ba f) left P7: Me, Ca, Pr, D

Table 1 Sampling stations in Potter Cove and Marian Cove analysed in the present study

Station ID	Locality	Coordinates	Depth	Date
02	King George Island, Potter Cove, outer cove	62° 14'03.2"S 58° 39'17.3"W	30 m	14.11.2014
07	King George Island, Potter Cove, inner cove	62° 13'30.1"S 58° 38'43.7"W	43 m	13.12.2014
09	King George Island, Potter Cove, outer cove	62° 14'23.4"S 58° 41'52.3"W	39 m	16.12.2014
10	King George Island, Potter Cove, outer cove	62° 14'23.4"S 58° 41'52.5"W	40 m	16.12.2014
11	King George Island, Potter Cove, outer cove	62° 14'23.4"S 58° 41'52.5"W	40 m	18.12.2014
12	King George Island, Potter Cove, outer cove	62° 14'23.4"S 58° 41'52.5"W	40 m	18.12.2014
13	King George Island, Potter Cove, outer cove	62° 14'23.4"S 58° 41'52.5"W	40 m	20.12.2014
14	King George Island, Potter Cove, outer cove	62° 14'23.4"S 58° 41'52.5"W	40 m	20.12.2014
16	King George Island, Potter Cove, inner cove	62° 13'36.9"S 58° 40'40.5"W	28 m	22.12.2014
17	King George Island, Potter Cove, inner cove	62° 13'37.0"S 58° 40'40.9"W	20 m	24.12.2014
18	King George Island, Potter Cove, inner cove	62° 13'25.3"S 58° 39'16.3"W	19 m	24.12.2014
19	King George Island, Potter Cove, outer cove	62° 14'23.6"S 58° 43'07.2"W	21 m	26.12.2014
27	King George Island, Potter Cove, outer cove	62° 14'22.3"S 58° 43'01.4"W	30 m	03.01.2015
28	King George Island, Potter Cove, outer cove	62° 14'23.9"S 58° 43'05.3"W	20 m	03.01.2015
31	King George Island, Marian Cove	62° 12'47.8"S 58° 47'37.1"W	30 m	08.01.2015
32	King George Island, Marian Cove	62° 12'46.5"S 58° 47'26.3"W	40 m	08.01.2015
33	King George Island, Marian Cove	62° 12'49.4"S 58° 44' 55.2"W	25 m	08.01.2015
35	King George Island, Marian Cove	62° 12' 25.1"S 58° 46' 19.9"W	20 m	10.01.2015
37	King George Island, Potter Cove, inner cove	62° 14' 00.3"S 58° 40' 09.1"W	30 m	10.01.2015
38	King George Island, Potter Cove, inner cove	62° 13' 34.3"S 58° 40' 18.2"W	20 m	10.01.2015
41	King George Island, Potter Cove, inner cove	62° 13' 34.6"S 58° 38' 19.1"W	12 m	24.02.2016
42	King George Island, Potter Cove, inner cove	62° 13' 45.1"S 58° 41' 18.0"W	20 m	01.03.2016
43	King George Island, Potter Cove, inner cove	62° 13' 44.7"S 58° 41' 41.2"W	13 m	01.03.2016
45	King George Island, Potter Cove, outer cove	62° 14' 33.9"S 58° 41' 43.8"W	35 m	24.02.2016

Table 2 Information of *COI* barcoded specimens including information of *W. obesa* (Cluster ‘A’ and ‘B’) generated by Havermans (2012)

Morphospecies	ID Code	BOLD ID	Museums ID ZMB	Locality	Expedition/ station ID	Coordinates	Depth
<i>Orchomenella</i> cf. <i>rotundifrons</i>	MT014Oxx047	LYAPO001-16	30509	Potter Cove, outer cove	Carlini 14-15 st 14	62°14'23.4"S, 58°41'52.5"W	40 m
<i>Orchomenella</i> cf. <i>rotundifrons</i>	MT010Oxx003	LYAPO002-16	30510	Potter Cove, outer cove	Carlini 14-15 st 10	62°14'23.4"S, 58°41'52.5"W	40 m
<i>Orchomenella rotundifrons</i>	MT038Oro008	LYAPO003-16	30511	Potter Cove, inner cove	Carlini 14-15 st 38	62°13'34.3"S 58°40'18.2"W	20 m
<i>Orchomenella rotundifrons</i>	MT038Oro001	LYAPO004-16	30512	Potter Cove, inner cove	Carlini 14-15 st 38	62°13'34.3"S 58°40'18.2"W	30 m
<i>Orchomenella rotundifrons</i>	MT002Oro019	LYAPO005-16	30513	Potter Cove, outer cove	Carlini 14-15 st 02	62°14'03.2"S, 58°39'17.3"W	20 m
<i>Orchomenella rotundifrons</i>	MT002Oro017	LYAPO006-16	30514	Potter Cove, outer cove	Carlini 14-15 st 02	62°14'03.2"S, 58°39'17.3"W	30 m
<i>Orchomenella</i> cf. <i>rotundifrons</i>	MT038Oxx010	LYAPO007-16	30515	Potter Cove, inner cove	Carlini 14-15 st 38	62°13'34.3"S 58°40'18.2"W	20 m
<i>Orchomenella rotundifrons</i>	MT002Oro012	LYAPO008-16	30516	Potter Cove, outer cove	Carlini 14-15 st 02	62°14'03.2"S, 58°39'17.3"W	30 m
<i>Orchomenella rotundifrons</i>	MT002Oro018	LYAPO009-16	30517	Potter Cove, outer cove	Carlini 14-15 st 02	62°14'03.2"S, 58°39'17.3"W	30 m
<i>Orchomenella rotundifrons</i>	MT002Oro020	LYAPO010-16	30518	Potter Cove, outer cove	Carlini 14-15 st 02	62°14'03.2"S, 58°39'17.3"W	30 m
<i>Orchomenella</i> cf. <i>rotundifrons</i>	MT010Oxx002	LYAPO011-16	30519	Potter Cove, outer cove	Carlini 14-15 st 10	62°14'23.4"S, 58°41'52.5"W	40 m
<i>Orchomenella rotundifrons</i>	MT002Oro013	LYAPO012-16	30520	Potter Cove, outer cove	Carlini 14-15 st 02	62°14'03.2"S, 58°39'17.3"W	30 m
<i>Orchomenella</i> cf. <i>rotundifrons</i>	MT014Oxx048	LYAPO013-16	30521	Potter Cove, outer cove	Carlini 14-15 st 14	62°14'23.4"S, 58°41'52.5"W	40 m
<i>Orchomenella rotundifrons</i>	MT002Oro008	LYAPO014-16	30522	Potter Cove, outer cove	Carlini 14-15 st 02	62°14'03.2"S, 58°39'17.3"W	30 m
<i>Orchomenella</i> cf. <i>rotundifrons</i>	MT010Oxx001	LYAPO015-16	30523	Potter Cove, outer cove	Carlini 14-15 st 10	62°14'23.4"S, 58°41'52.5"W	40 m
<i>Orchomenella</i> cf. <i>rotundifrons</i>	MT010Oxx004	LYAPO016-16	30524	Potter Cove, outer cove	Carlini 14-15 st 10	62°14'23.4"S, 58°41'52.5"W	40 m
<i>Orchomenella rotundifrons</i>	MT002Oro016	LYAPO017-16	30525	Potter Cove, outer cove	Carlini 14-15 st 02	62°14'03.2"S, 58°39'17.3"W	30 m
<i>Orchomenella</i> cf. <i>rotundifrons</i>	MT010Oxx005	LYAPO018-16	30526	Potter Cove, outer cove	Carlini 14-15 st 10	62°14'23.4"S, 58°41'52.5"W	40 m

<i>Orchomenella rotundifrons</i>	MT002Oro011	LYAPO019-16	30527	Potter Cove, outer cove	Carlini 14-15 st 02	62°14'03.2"S, 58°39'17.3"W	30 m
<i>Orchomenella infinita</i> sp.n.	MT009Oul006	LYAPO020-16	30506 holotype	Potter Cove, outer cove	Carlini 14-15 st 09	62°14'23.4"S, 58°41'52.3"W	39 m
<i>Orchomenella infinita</i> sp.n.	MT002Oul014	LYAPO021-16	30507 paratypes	Potter Cove, outer cove	Carlini 14-15 st 02	62°14'03.2"S, 58°39'17.3"W	30 m
<i>Orchomenella infinita</i> sp.n.	MT014Oul001	LYAPO022-16	30508 paratypes	Potter Cove, outer cove	Carlini 14-15 st 14	62°14'23.4"S, 58°41'52.5"W	40 m
<i>Cheirimedon femoratus</i>	MT038Cfe007	LYAPO023-16	30528	Potter Cove, inner cove	Carlini 14-15 st38	62°13'34.3"S 58°40'18.2"W	20 m
<i>Cheirimedon femoratus</i>	MT013Cfe011	LYAPO024-16	30529	Potter Cove, outer cove	Carlini 14-15 st 13	62°14'23.4"S, 58°41'52.5"W	40 m
<i>Cheirimedon femoratus</i>	MT038Cfe004	LYAPO025-16	30530	Potter Cove, inner cove	Carlini 14-15 st38	62°13'34.3"S 58°40'18.2"W	20 m
<i>Cheirimedon femoratus</i>	MT013Cfe010	LYAPO026-16	30531	Potter Cove, outer cove	Carlini 14-15 st 13	62°14'23.4"S, 58°41'52.5"W	40 m
<i>Cheirimedon femoratus</i>	MT038Cfe006	LYAPO027-16	30532	Potter Cove, inner cove	Carlini 14-15 st38	62°13'34.3"S 58°40'18.2"W	20 m
<i>Cheirimedon femoratus</i>	MT038Cfe002	LYAPO028-16	30533	Potter Cove, inner cove	Carlini 14-15 st38	62°13'34.3"S 58°40'18.2"W	20 m
<i>Cheirimedon femoratus</i>	MT038Cfe005	LYAPO029-16	30534	Potter Cove, inner cove	Carlini 14-15 st38	62°13'34.3"S 58°40'18.2"W	20 m
<i>Cheirimedon femoratus</i>	MT038Cfe003	LYAPO030-16	30535	Potter Cove, inner cove	Carlini 14-15 st38	62°13'34.3"S 58°40'18.2"W	20 m
<i>Cheirimedon femoratus</i>	MT002Cfe009	LYAPO031-16	30536	Potter Cove, outer cove	Carlini 14-15 st 02	62°14'03.2"S, 58°39'17.3"W	30 m
<i>Cheirimedon femoratus</i>	MT013Cfe012	LYAPO032-16	30537	Potter Cove, outer cove	Carlini 14-15 st 13	62°14'23.4"S, 58°41'52.5"W	40 m
<i>Cheirimedon femoratus</i>	MT002Cfe010	LYAPO033-16	30538	Potter Cove, outer cove	Carlini 14-15 st 02	62°14'03.2"S, 58°39'17.3"W	30 m
<i>Cheirimedon femoratus</i>	MT018Cfe002	LYAPO034-16	30539	Potter Cove, inner cove	Carlini 14-15 st 18	62°13'25.3"S, 58°39'16.3"W	19 m
<i>Cheirimedon femoratus</i>	MT013Cfe009	LYAPO035-16	30540	Potter Cove, outer cove	Carlini 14-15 st 13	62°14'23.4"S, 58°41'52.5"W	40 m
<i>Cheirimedon femoratus</i>	MT013Cfe008	LYAPO036-16	30541	Potter Cove, outer cove	Carlini 14-15 st 13	62°14'23.4"S, 58°41'52.5"W	40 m
<i>Abyssorchomene charcoti</i>	MT002Ach006	LYAPO037-16	30542	Potter Cove, outer cove	Carlini 14-15 st 02	62°14'03.2"S, 58°39'17.3"W	30 m
<i>Pseudorchomene plebs</i>	MT002Ppl001	LYAPO038-16	30543	Potter Cove, outer cove	Carlini 14-15 st 02	62°14'03.2"S, 58°39'17.3"W	30 m
<i>Pseudorchomene rossi</i>	MT033Pro001	LYAPO039-16	30544	Marian Cove	Carlini 14-15	62°12'49.4"S 58°44'55.2"W	25 m

					st 33		
<i>Hippomedon kergueleni</i>	MT013Hke006	LYAPO040-16	30545	Potter Cove, outer cove	Carlini 14-15 st 13	62°14'23.4"S, 58°41'52.5"W	40 m
<i>Hippomedon kergueleni</i>	MT013Hke004	LYAPO041-16	30546	Potter Cove, outer cove	Carlini 14-15 st 13	62°14'23.4"S, 58°41'52.5"W	40 m
<i>Hippomedon kergueleni</i>	MT009Hke001	LYAPO042-16	30547	Potter Cove, outer cove	Carlini 14-15 st 09	62°14'23.4"S, 58° 41'52.3"W	39 m
<i>Hippomedon kergueleni</i>	MT013Hke001	LYAPO043-16	30548	Potter Cove, outer cove	Carlini 14-15 st 13	62°14'23.4"S, 58°41'52.5"W	40 m
<i>Hippomedon kergueleni</i>	MT009Hke003	LYAPO044-16	30549	Potter Cove, outer cove	Carlini 14-15 st 09	62°14'23.4"S, 58° 41'52.3"W	39 m
<i>Hippomedon kergueleni</i>	MT013Hke003	LYAPO045-16	30550	Potter Cove, outer cove	Carlini 14-15 st 13	62°14'23.4"S, 58°41'52.5"W	40 m
<i>Hippomedon kergueleni</i>	MT013Hke005	LYAPO046-16	30551	Potter Cove, outer cove	Carlini 14-15 st 13	62°14'23.4"S, 58°41'52.5"W	40 m
<i>Hippomedon kergueleni</i>	MT009Hke002	LYAPO047-16	30552	Potter Cove, outer cove	Carlini 14-15 st 09	62°14'23.4"S, 58° 41'52.3"W	39 m
<i>Hippomedon kergueleni</i>	MT013Hke007	LYAPO048-16	30553	Potter Cove, outer cove	Carlini 14-15 st 13	62°14'23.4"S, 58°41'52.5"W	40 m
<i>Hippomedon kergueleni</i>	MT009Hke005	LYAPO049-16	30554	Potter Cove, outer cove	Carlini 14-15 st 09	62°14'23.4"S, 58° 41'52.3"W	39 m
<i>Hippomedon kergueleni</i>	MT002Hke004	LYAPO050-16	30555	Potter Cove, outer cove	Carlini 14-15 st 02	62°14'03.2"S, 58°39'17.3"W	30 m
<i>Hippomedon kergueleni</i>	MT002Hke005	LYAPO051-16	30556	Potter Cove, outer cove	Carlini 14-15 st 02	62°14'03.2"S, 58°39'17.3"W	30 m
<i>Hippomedon kergueleni</i>	MT011Hke001	LYAPO052-16	30557	Potter Cove, outer cove	Carlini 14-15 st 11	62°14'23.4"S, 58°41'52.5"W	40 m
<i>Hippomedon kergueleni</i>	MT002Hke021	LYAPO053-16	30558	Potter Cove, outer cove	Carlini 14-15 st 02	62°14'03.2"S, 58°39'17.3"W	30 m
<i>Hippomedon kergueleni</i>	MT011Hke003	LYAPO054-16	30559	Potter Cove, outer cove	Carlini 14-15 st 11	62°14'23.4"S, 58°41'52.5"W	40 m
<i>Hippomedon kergueleni</i>	MT011Hke006	LYAPO055-16	30560	Potter Cove, outer cove	Carlini 14-15 st 11	62°14'23.4"S, 58°41'52.5"W	40 m
<i>Hippomedon kergueleni</i>	MT011Hke002	LYAPO056-16	30561	Potter Cove, outer cove	Carlini 14-15 st 11	62°14'23.4"S, 58°41'52.5"W	40 m
<i>Hippomedon kergueleni</i>	MT011Hke005	LYAPO057-16	30562	Potter Cove, outer cove	Carlini 14-15 st 11	62°14'23.4"S, 58°41'52.5"W	40 m
<i>Hippomedon kergueleni</i>	MT011Hke004	LYAPO058-16	30563	Potter Cove, outer cove	Carlini 14-15 st 11	62°14'23.4"S, 58°41'52.5"W	40 m
<i>Waldeckia obesa</i> cluster 'A'	MT011Wob010	LYAPO059-16	30564	Potter Cove, outer cove	Carlini 14-15 st 11	62°14'23.4"S, 58°41'52.5"W	40 m

<i>Waldeckia obesa</i> cluster 'A'	MT013Wob014	LYAPO060-16	30565	Potter Cove, outer cove	Carlini 14-15 st 13	62°14'23.4"S, 58°41'52.5"W	40 m
<i>Waldeckia obesa</i> cluster 'A'	MT011Wob008	LYAPO061-16	30566	Potter Cove, outer cove	Carlini 14-15 st 11	62°14'23.4"S, 58°41'52.5"W	40 m
<i>Waldeckia obesa</i> cluster 'A'	MT013Wob016	LYAPO062-16	30567	Potter Cove, outer cove	Carlini 14-15 st 13	62°14'23.4"S, 58°41'52.5"W	40 m
<i>Waldeckia obesa</i> cluster 'A'	MT011Wob009	LYAPO063-16	30568	Potter Cove, outer cove	Carlini 14-15 st 11	62°14'23.4"S, 58°41'52.5"W	40 m
<i>Waldeckia obesa</i> cluster 'A'	MT013Wob013	LYAPO064-16	30569	Potter Cove, outer cove	Carlini 14-15 st 13	62°14'23.4"S, 58°41'52.5"W	40 m
<i>Waldeckia obesa</i> cluster 'A'	MT011Wob007	LYAPO065-16	30570	Potter Cove, outer cove	Carlini 14-15 st 11	62°14'23.4"S, 58°41'52.5"W	40 m
<i>Waldeckia obesa</i> cluster 'A'	MT009Wob008	LYAPO066-16	30571	Potter Cove, outer cove	Carlini 14-15 st 09	62°14'23.4"S, 58° 41'52.3"W	39 m
<i>Waldeckia obesa</i> cluster 'A'	MT014Wob135	LYAPO067-16	30572	Potter Cove, outer cove	Carlini 14-15 st 14	62°14'23.4"S, 58°41'52.5"W	40 m
<i>Waldeckia obesa</i> cluster 'A'	MT014Wob134	LYAPO068-16	30573	Potter Cove, outer cove	Carlini 14-15 st 14	62°14'23.4"S, 58°41'52.5"W	40 m
<i>Waldeckia obesa</i> cluster 'A'	MT009Wob007	LYAPO069-16	30574	Potter Cove, outer cove	Carlini 14-15 st 09	62°14'23.4"S, 58° 41'52.3"W	39 m
<i>Waldeckia obesa</i> cluster 'A'	Wo-1412103	LYAPO070-17	-	Antarctic Peninsula	ANT-XXIII-8 689-5	62°27"S, 55°25"W	211 m
<i>Waldeckia obesa</i> cluster 'A'	Wo-2311094	LYAPO071-17	-	Haakon VII Sea	BELARE AT	70°S, 5° E	130 m
<i>Waldeckia obesa</i> cluster 'B'	Wo-18051013	LYAPO072-17	-	Terre Adélie Coast	CEAMARC ST13A EV 465	66°08"S, 140°38"E	213 m
<i>Waldeckia obesa</i> cluster 'B'	Wo-02121013	LYAPO073-17	-	George V Coast	CEAMARC St47EV201(1243)	67°04"S, 144°39"E	194 m
<i>Waldeckia obesa</i> cluster 'B'	Wo-23110910-AMPBE019-10	AMPBE019-10	-	Haakon VII Sea Crown Bay	BELARE AT	70°S, 23°E	230
<i>Waldeckia obesa</i> cluster 'B'	Wo-2904104	LYAPO074-17	-	Amundsen Sea	JR179 BIOPEARL II KL-06-0769	n.a.	n.a.
<i>Waldeckia obesa</i> cluster 'B'	Wo-06041013-AMPBE044-10	AMPBE044-10	-	Eastern Weddell Sea	ANT XXVII-3 275-3 AGT	70° 56"S, 10°29"W	226 m
<i>Waldeckia obesa</i> cluster 'B'	Wo-ANT27 3-118	LYAPO075-17	-	Haakon VII Sea Crown Bay	BELARE AT	70°S, 5°E	130 m
<i>Waldeckia obesa</i> cluster 'B'	Wo-1412106	LYAPO076-17	-	Eastern Weddell Sea	ANT XXIV-2 48 AGT	70°24"S, 08°19"W	602 m
<i>Waldeckia obesa</i> cluster 'B'	Wo-1412108	LYAPO077-17	-	Eastern Weddell Sea	ANT XXIV-2 48 AGT	70°24"S, 08°19"W	602 m

Table 3 K2P genetic distances within and between species, Ach: *Abyssorchomene charcoti*, Cfe: *Cheirimedon femoratus*, Hke: *Hippomedon kergueleni*, Oul: *Orchomenella infinita* sp. n. Oro: *Orchomenella rotundifrons*, Ppl: *Pseudorchomene plebs*, Pro: *Pseudorchomene rossi*, Wob_A: *Waldeckia obesa* cluster ‘A’, Wob_B: *Waldeckia obesa* cluster ‘B’, n.a.: not applicable

	Ach	Cfe	Oin	Oro	Hke	Ppl	Pro	Wob_A	Wob_B
Ach	n.a.								
Cfe	10.3-10.7	0.0-0.7							
Oin	17.4-17.5	17.4-17.7	0.00						
Oro	10.2-11.3	12.9-13.8	19.5-20.3	0.0-1.5					
Hke	29.8-30.7	29.4-30.7	36.1-37.0	30.5-32.5	0.0-0.7				
Ppl	15.5	14.2-14.7	18.8	17.3-18.1	30.8-32.2	n.a.			
Pro	15.8	15.5-16.2	16.4-16.5	15.7-16.6	30.6-32.2	12.0	n.a.		
Wob_A	29.6-32.5	31.7-35.6	34.0-37.0	30.2-33.7	27.6-30.4	34.2-37.3	33.6-36.2	0.0-2.8	
Wob_B	33.3-35.4	34.4-37.2	37.3-40.1	34.1-37.8	24.8-28.2	37.3-38.9	34.8-37.4	15.0-18.1	0.0-1.7

Table 4 Relative and total abundances of lysianassoid amphipod species found in Potter Cove and Marian Cove

	Potter Cove		Outer cove		Inner cove		Marian Cove	
	<i>No of specimens</i>	<i>%</i>	<i>No of specimens</i>	<i>%</i>	<i>No of specimens</i>	<i>%</i>	<i>No of specimens</i>	<i>%</i>
<i>Cheirimedon femoratus</i>	33,440	79.81	17,466	67.61	15,974	99.44	260	12.75
<i>Hippomedon kergueleni</i>	5808	13.86	5747	22.25	61	0.38	3	1.47
<i>Orchomenella rotundifrons</i>	2110	5.04	2086	8.07	24	0.15	-	-
<i>Waldeckia obesa</i>	525	1.25	524	2.02	1	0.006	1774	87.00
<i>Orchomenella infinita</i> sp. n.	6	<0.01	5	0.02	1	0.006	-	-
<i>Pseudorchomene coatsi</i>	3	<0.01	-	-	3	0.02	-	-
<i>Pseudorchomene plebs</i>	2	<0.01	1	<0.01	1	0.006	-	-
<i>Abyssorchomene charcoti</i>	2	<0.01	2	<0.01	0	-	-	-
<i>Pseudorchomene rossi</i>	3	<0.01	-	-	1	0.006	2	0.1
<i>Orchomenella pinguides</i>	1	<0.01	1	<0.01	0	-	-	-
Total	41,898		25,832		16,064		2039	

Supplement material 1 Numbers of lysianassoid amphipod specimens per species and station in Potter Cove and Marian Cove. Yellow: Outer Potter Cove; Blue: Inner Potter Cove; Grey: Marian Cove

Station ID	<i>Cheirimedon femoratus</i>	<i>Waldeckia obesa</i>	<i>Hippomedon kergueleni</i>	<i>Orchomenella rotundifrons</i>	<i>Orchomenella infinita sp.n</i>	<i>Abyssorchomene charcoti</i>	<i>Pseudorchomene rossi</i>	<i>Pseudorchomene plebs</i>	<i>Pseudorchomene coatsi</i>	<i>Orchomenella pinguides</i>	
02	793	0	658	1589	2	2	0	1	0	0	
07	8	0	0	0	0	0	0	0	0	0	
09	404	196	275	2	1	0	0	0	0	0	
10	1664	2	2	23	0	0	0	0	0	0	
11	360	83	30	20	0	0	0	0	0	0	
12	3	7	29	3	0	0	0	0	0	0	
13	1082	123	55	34	0	0	0	0	0	0	
14	893	111	539	116	2	0	0	0	0	0	
16	536	0	6	1	0	0	0	0	0	0	
17	156	0	4	0	0	0	0	0	0	0	
18	227	0	0	0	0	0	0	0	0	0	
19	2667	2	978	195	0	0	0	0	0	0	
27	462	0	2790	63	0	0	0	0	0	0	
28	2004	0	346	29	0	0	0	0	0	0	
31	11	605	2	0	0	0	0	0	0	0	
32	78	856	1	0	0	0	0	0	0	0	
33	23	313	0	0	0	0	2	0	0	0	
35	148	0	0	0	0	0	0	0	0	0	
37	6	0	6	0	0	0	0	0	0	0	
38	2403	0	3	12	0	0	0	0	0	0	
41	11,922	0	0	0	0	0	0	0	0	0	
42	548	0	20	8	0	0	1	1	0	0	
43	168	1	22	3	1	0	0	0	3	0	
45	7134	0	45	12	0	0	0	0	0	1	
Total	33,700	2,299	5,811	2,110	6	2	3	2	3	1	43,937