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Patchiness of deep-sea communities in Papua New Guinea and potential susceptibility to anthropogenic disturbances illustrated by seep organisms.

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Abstract

The deep-sea part of the "Papua Niugini Biodiversity Expedition" surveyed the deep-sea environments along the coasts of New Guinea Island in the Bismarck Sea, from the Vitiaz Strait to the border between Papua New Guinea (PNG) and Irian Jaya. This expedition was a follow-up of the BIOPAPUA cruise (2010) that gave some of the first insights into the diversity of the deep-sea fauna of the Bismarck and Solomon Seas for environments other than deep-sea hydrothermal vents. The main targets of the cruise were to survey the diversity of the fauna of (i) hard bottoms that are typically found on deep seamounts, (ii) Astrolabe Bay from 200 m to about 1000 m, (iii) the chemosynthetic environments of the deep sea, including cold-seep environments and plant debris. The Astrolabe Bay was one of our targets because its topography allows sampling over the complete bathymetric gradient covered by our sampling gears (down to 1000 m depth), and the recent start of nickel refining activities in the bay is a potential threat to a marine fauna for which little reference data are available. Sampling in the bay has revealed not only a diversified fauna associated with soft bottoms and plant debris, but also a chemosynthetic fauna typical of cold-seep environments (e.g. siboglinid worms and bathymodioline mussels) below the Ramu refinery. Although the refinery activities had officially started just one week before our work in the area, an impact of its activities is already observed. Our molecular work indicates that the siboglinid tubeworm species and one of the two mussel species collected below the Ramu refinery have so far only been documented from this location, despite an important sampling effort. This illustrates the potential destructive effects of human activities in areas where the diversity and uniqueness of deep-sea communities are poorly understood.

INTRODUCTION

Despite some significant exploration efforts notably during the last decade (e.g. Costello et al. 2010), the deep-sea realm remains among the least known biodiversity compartments on Earth, even for macro-organisms. Because it is difficult to protect what we do not know exists, this knowledge gap makes the deep sea particularly vulnerable to human disturbances. Pioneering work in the 1960's with the development of appropriate tools revealed that deep-sea biodiversity was greatly underestimated and rivals that of shallow tropical communities (e.g. Hessler and Sanders, 1967). Later studies also revealed that deep-sea assemblages are far from homogenous, with strong between-site differences, and some endemism (Brandt et al. 2007; Levin et al. 2001). Despite ongoing efforts to describe deep-sea biodiversity, working in this environment is challenging and much remains to be learned.

As a result of this knowledge gap, many common assumptions on the structure of deep-sea biodiversity, on which many environmental policies are based, are questionable. Among them, the seemingly uniform nature of the deep sea ('everything is everywhere') is potentially one of the most damaging assumptions. This assumption is mainly based on the observation that many deep-sea organisms have a cosmopolitan distribution. However, most of these cosmopolitan species are patchily distributed over their wide geographic range (McClain & Hardy, 2010 and references therein). More generally, recent studies revealed an unexpected heterogeneity of deep-sea habitats linked to geomorphological, geochemical and hydrographic features and stressed the resulting vulnerability of associated communities to human activities (e.g. Levin & Dayton, 2009; Levin & Sibuet, 2012). Thus, considering that 'everything is everywhere' minimizes the potential effect of the destruction of discrete habitats. In this communication we illustrate this problem by reporting the discovery of two chemosynthetic sites in Papua New Guinea (PNG), one of them being impacted by the tailings rejected by a nickel mine refinery.

The first chemosynthetic site was discovered during the BIOPAPUA cruise off the Sepik River (Pante et al. 2012). The discovery of the impacted site, in the Basamuk canyon near the Astrolabe Bay, occurred during the deep-sea leg of the 'Papua Niugini Biodiversity Expedition,' (hereafter PAPUA NIUGINI) the latest expedition of 'Our planet reviewed' programme (www.laplaneterevisitee.org). This programme is an international scientific project whose goals are to provide better estimates of the magnitude of biodiversity worldwide, to provide baseline data for several sites that are particularly rich or vulnerable on our planet. The most recent expedition of the programme targeted PNG and the surrounding Bismarck and Solomon Seas. PNG is located in the Coral Triangle, a region of exceptional zooxanthellate coral diversity (Veron et al. 2009). Its forests count among the most important in the world in terms of diversity of plant species (Joppa et al. 2011). The marine part of the expedition included a shallow-water sampling workshop and a deep-sea cruise. Over 3 months, the marine expedition involved a total of 88 scientists from 18 countries, in addition to 51 trainees, media, logistics coordinators and visitors. Prior to this expedition, exploration of PNG's marine biodiversity has been minimal, and has mostly focused on shallow-water coral reefs (e.g. Drew et al. 2012) and hydrothermal vents in the Manus Basin (e.g. Levin et al. 2009). Other deep-sea habitats of PNG waters were particularly poorly explored, including during great historical expeditions (Pante et al. 2012)

The BIOPAPUA cruise and the deep-sea part of the 2012 marine expedition used the RV *Alis* for deploying hauls from 100 to 1000 meters depth. The BIOPAPUA cruise covered a wide area surrounding the Bismarck Sea and the Solomon Sea (Pante et al. 2012). The 2012 (PAPUA NIUGINI) cruise surveyed the deep-sea environments along the coasts of New Guinea Island in the Bismarck Sea, from the Vitiaz Strait to the border between PNG and Irian Jaya. Both expeditions aimed at covering at best the diversity of deep-sea habitats and had three main targets. First, seamounts were one of the targets because they generally offer

74 hard bottoms with a fauna dominated in terms of biomass by [suspension](#)-feeding organisms
75 that shelter an important diversity of associated organisms. The second goal was to sample the
76 organisms associated with soft bottoms that can be found in accumulation basins separating
77 islands, or, when the topography allows the accumulation of sediments, on islands slopes.
78 Preliminary work during the BIOPAPUA cruise allowed us to focus in 2012 the sampling of
79 the fauna of soft bottoms in the Astrolabe Bay. Additionally, starting refinery activities had
80 already been identified as a potential threat to the marine fauna but little biological data were
81 available (e.g. Reichelt-Brushett, 2012). Finally, we targeted chemosynthetic habitats as they
82 are among the most productive environments in the deep sea. In PNG, hydrothermal vents are
83 easily accessible, and have been intensively studied for many years (e.g. Erickson et al. 2009,
84 Levin et al. 2009). For the same reason of accessibility, [the hydrothermal deposits](#)
85 [characterized by a high grade of precious ore](#), in the Bismarck Sea represent a prime target for
86 deep-sea refinery activities (Van Dover et al. 2011). [Other types of deep-sea chemosynthetic](#)
87 [environments \(i.e. cold seeps and accumulations of decaying terrestrial plant debris\)](#) remain
88 [poorly surveyed in PNG, even if geological surveys in this active area provided sporadic](#)
89 [records of cold-seep environments \(e.g. Tappin et al. 2001\).](#) The BIOPAPUA cruise allowed
90 [us to discover a site off the Sepik River \(facing Broken Water Bay\), at about 400 meters](#)
91 [depth, with fauna typically associated with cold-seep environments.](#) This area, which we
92 [revisited during the 2012 cruise, is close to the area detected by the JAMSTEC cruise \(Tappin](#)
93 [et al. 2001\), providing the only report of chemosynthetic organisms from cold-seep](#)
94 [environments in PNG waters \(e.g. Kuyno et al. 2009 for bathymodiolinae, Kojima et al. 2003](#)
95 [for siboglinidae\).](#) Additionally, the deeper operations off the Ramu refinery unexpectedly
96 [brought back bathymodioline mussels and siboglinid tubeworms, revealing a new location of](#)
97 [chemosynthetic habitat.](#)

In these poorly-explored deep-sea regions, chemosynthetic organisms are perhaps the best studied, especially at vents in the Manus Basin. The two seep sites sampled in 2012, in combination with the data available from the Japanese geological surveys and the 2010 data from BIOPAPUA cruise, offered the opportunity of comparing the specific diversity of bathymodioline mussels and siboglinid tubeworms at a relatively small spatial scale (the Astrolabe Bay and Broken Water Bay sites are separated by only about 250 km). Moreover, operations off the Ramu refinery revealed the presence of a brick-red deposit. The activities of the Ramu refinery started by the end of November 2012, and tailings were announced to be released from the refinery at 200 meters depth. The deposits observed off the Ramu refinery have been found nowhere else during either the BIOPAPUA cruise or the PAPUA NIUGINI expedition. Dredging operations brought back a dark gray mud (as found in many other locations) but overlaid by a brick-red deposit, consistent with the release of tailings from the refinery, suggesting that the newly discovered site is potentially threatened by rapidly accumulating tailings from the refinery.

The bathymodioline mussels and siboglinid worms sampled in the two discovered seep sites in PNG waters offer the opportunity of illustrating the patchiness of distribution of organisms, even at small scales, and to question some common misconceptions about the pattern of diversity in the deep sea that result from the paucity of available knowledge.

MATERIAL AND METHODS

Sampling

During the deep-sea leg of the 2012 expedition, 137 hauls (92 trawling and 45 dredging operations) were conducted. These samples were added to the ones collected the during

BIOPAPUA cruise (Pante et al. 2012). Out of all 2012 sampling operations (Fig 1), five contained fauna typically found in cold-seep environments, and in particular representatives of the Siboglinidae (Polychaeta) and Bathymodiolinae (Bivalvia). Three were conducted in Broken Water Bay, off the Sepik River (stations CP4040, CP4042, CP4043, depth range 400-800 meters), a site where cold seeps were discovered during a previous expedition in 2010 (BIOPAPUA, stations CP3703 and CP3704, depth range 400-800), and two in the Basamuk canyon facing the Ramu refinery, near the Astrolabe Bay (stations CP4020 and CP4081, depth range 400-860 meters). During the 2012 cruise, a total of 16 *Lamellibrachia* (siboglinid tubeworms), and 52 bathymodioline mussels (Table 1), were preserved in 90% alcohol for molecular analyses. Out of the 11 Siboglinidae in the small aggregation sampled in the Basamuk Bay, however, only 4 provided DNA that could be amplified. These animals are thought to have been dead, buried under an accumulation of tailings. To facilitate preservation of tissues in alcohol, mussels were first microwaved following the procedure described in Galindo et al. (2014).

DNA amplification and sequencing

DNA from mussel specimens was extracted using the QIAmp® DNA Micro Kit (Qiagen, Valencia, CA). After removal of excess ethanol, total DNA from tubeworms was isolated following a CTAB + PVPP extraction protocol (Doyle and Doyle 1987). For the Siboglinidae, only the barcode fragment of the COI gene was amplified using the Folmer primers LCO1490 and HCO2198 (Folmer et al. 1994). For the Bathymodiolinae both the barcode fragment of the COI gene and a fragment of the rDNA 28S gene were amplified using the Folmer primers and the C1 and D2 primers (Jovelín & Justine, 2001), respectively. All PCR reactions were performed in 20 µl, using 3 ng of DNA, 10X reaction buffer containing 15 mM MgCl₂, 0.26

mM dNTP, 0.3 μ M of each primer, 5% DMSO, 1 mg/ml BSA, and 1 unit of QBIotaq (MP Biomedicals, Illkirch Graffenstaden, France). Amplification consisted of an initial denaturation step at 95°C for 5 min, followed by 40 cycles of denaturation at 95°C for 1 min, annealing at 48°C for the COI gene and 55°C for the 28S gene for 30 s, followed by extension at 72°C for 30 s. The final extension was at 72°C for 5 min. PCR products were purified and sequenced in both forward and reverse directions by the Genoscope or the Eurofins sequencing facilities.

Phylogenetic analyses

Sequences were aligned automatically using Muscle 3.8.31 (Edgar 2004). Both maximum likelihood (ML) and Bayesian analyses (BA) were performed for the inference of phylogenetic relationships. ML analyses were performed using RAxML 7.0.4 (Stamatakis, 2006), with a GAMMAI model. Three partitions were defined for the COI gene, corresponding to each position of the codon. RaxML analyses were performed on the Cipres Science Gateway (<http://www.phylo.org/portal2/>) using the RAxML-HPC2 on TG Tool (Miller et al. 2010). Node support was estimated by bootstrapping (1000 replicates). For the Bathymodiolinae, a concatenated dataset (COI+28S) was also analysed, with four partitions defined (the three codon position of the COI, and one for the 28S). Bayesian Analyses (BA) were performed running two parallel analyses in MrBayes (Huelsenbeck et al. 2001), consisting each of four Markov chains of 30 million generations each with a sampling frequency of one tree each thousand generations. The number of swaps was set to two, and the chain temperature to 0.02. Similarly to the ML approach, unlinked models (each with six substitution categories, a gamma-distributed rate variation across sites approximated in four discrete categories and a proportion of invariable sites estimated during the analysis) were applied for each partition. Convergence of each analysis was evaluated using Tracer 1.4.1

(Rambaut and Drummond, 2007), and analyses were terminated when ESS values were all superior to 200. A consensus tree was then calculated after omitting the first 25% trees as a burn-in.

Additional sequences from GenBank and outgroups

Within the Siboglinidae, vestimentiferans constitute a monophyletic group (*e.g.* Eichinger et al. 2013). We thus downloaded all the COI sequences of vestimentiferans from GenBank. Four sequences (GU059239.1, GU059172.1, GU059250.1 and GU059230.1), obviously contaminated or misidentified (they clustered within groups of specimens with different species and genus names) were removed from the dataset. To reduce computational times, 215 *Ridgeia piscesae* sequences (EU190494.1-EU190709.1, all highly similar) were removed from the dataset (one sequence from the popset was kept). In total 283 COI sequences from GenBank were included in the alignment (Table 1). COI sequences of *Sclerolinum* were used as closely related outgroups, and a sequence of *Osedax roseus* was used to artificially root the tree, following the results of Eichinger et al. (2013). Also, two sequences obtained from two escarpiid collected in 2010 during the BIOPAPUA cruise, collected in the Broken Water Bay, off the Sepik River (stations CP3703 and CP3704) were added to the dataset (Table 1). For the Bathymodiolinae, we used the dataset from Thubaut et al. (2013), representative of the known diversity the sub-family (Table 1). *Modiolus modiolus* was used as an outgroup.

RESULTS AND DISCUSSION

New data and collections of deep-sea habitats in PNG

Due to a very active tectonic regime, the PNG bottom topography is very uneven. Bathymetric datasets are also scarce. The 2012 deep-sea expedition largely took advantage of the deep-sea results of the BIOPAPUA cruise that both allowed us to identify the most

interesting spots and provided preliminary bathymetric maps that were added to during the 2012 expedition. During each cruise, when the topology of the bottom allowed, each selected spot was explored over a depth range of 100 to 1000 meters. Depending of the topology and the kind of substrates (*i.e.* hard or soft bottom), either a trawl or a dredge was used. Each collection was sieved on board, using seawater to separate animals from the substrate in different size classes. Specimens were then quickly sorted and preserved. All invertebrates were then integrated into the collections of Muséum national d'histoire naturelle (MNHN) in Paris and then distributed over an international network of taxonomists for study (Bouchet et al. 2008; Richer de Forges et al. 2013).

Seamounts were particularly difficult to localize and to sample, but a diversified fauna was obtained when operations were successful. On island slope, from the Sepik River to Vanimo, collections were characterized by soft bottom associated with low diversity vastly dominated in biomass by irregular sea-urchins (morphologically resembling *Sarsiaster greigii*, SH pers. obs.), most of which contained an Amphinomidae (Annelida) in the terminal portion of their digestive tube. Sunken plant remains associated with their typical fauna were present in most of the operations. The typical fauna associated with cold-seep environments was only found in a very restricted area off Broken Water Bay. From Manam Island to the Vitiaz Strait, *i.e.* the limit between the Bismark and Solomon Seas, island slopes are very steep. Consequently hauls mainly contained round stones suggesting that strong currents do not allow settlement of sessile organisms or sediment accumulation. When terrestrial plant remains were found, these were large pieces of wood, in early stages of decomposition but greatly abraded. Accumulations of sediments and/or of terrestrial plant remains were mostly found in small canyons and in large bays, notably in the Astrolabe Bay.

Fauna sampled off Broken Water Bay (Sepik River)

In a very restricted area at the Sepik site, off Broken Water Bay, at stations dominated by irregular sea urchins (*cf. Sarsiaster greigii*), a fauna typical of cold seeps was collected (figure 2), including Bathymodiolinae mussels and siboglinid tubeworms (sampled during both the BIOPAPUA cruise (2010) and Niugini (2012) Expedition). Irregular sea urchins are often found at seeps, although rarely properly identified (e.g. Cordes et al. 2009, Olu-Le Roy et al. 2004). The other bivalves sampled at this location were typical of seep environments. Among these, Rudo Von Cosel (pers. com.) identified two species of Vesicomyidae, one species of Thyasiridae attributed to the genus *Conchocele*, and one species of Nuculidae attributed to the genus *Acila*. Among gastropods, predatory snails attributed to the genera *Phymorhynchus* (Raphitomidae) and *Manaria* sp. (Buccinidae closely related to *Eosipho*) are also typical of chemosynthetic environments (Warén 2011, et al. 2009, Kantor et al. 2013). Among the Nassariidae, this location was the only one where a specimen attributed to the genus *Profundinassa* was sampled. For the crustacean fauna, a hippolytid shrimp typical of deep-sea reducing environments, attributed to the genus *Lebbeus*, was identified (Komai et al. 2012, Nye et al. 2012), while other specimens were not typical of chemosynthetic environments. The ethusid crab *Ethusa curvipes*, a species typical of muddy deep-sea bottoms (P. Castro, pers. com.), was also found among the animals collected.

Fauna sampled below the Ramu refinery

Off the Ramu refinery, specimens were sampled from 200 to 1000 meters depth. The samples contained fauna associated with both soft bottom and plant remains. Sampling off the Ramu refinery showed a heavy release of tailings (figure 3) although refining activities had only started 10 days prior to our sampling operations. These tailings formed a layer of color and texture consistent with the known nickel refining protocols used at the Ramu refinery. The tailings overlay the otherwise grey sediment, very similar to sediment sampled elsewhere

during the expedition, including the Broken Water Bay cold-seep site. Shallower operations (ca. 250-400 m) brought back sediments only slightly stained by the tailings (figure 3A), while deeper collections (400-700 m), sediments were covered by a thick layer of red sediment (figure 3B). In the impacted sediments, we notably sampled polychaete tubes that had incorporated red particles over a few centimeters. The topography of the Basamuk canyon, off the Ramu refinery rendered the operations difficult, with many instances of damage to the trawls for the deeper sites (hard bottoms). Although the catch was not very abundant in this canyon we unexpectedly captured organisms typical of cold-seep environments (Bathymodioline mussels and Siboglinidae tubeworms; Figure 4). As for the Broken Water Bay, other fauna typical of seep environments was identified, notably bivalves of the families Thyasiridae and Nuculidae (genus *Acila*). The crustacean fauna was mostly composed of species that were not specific to reducing environments (e.g. *Ethusa curvipes* as in the Broken Water Bay), with the exception of the hippolytid shrimp *Lebbeus* sp. (also found in the Broken Water Bay). The squat-lobster *Munidopsis andamanica*, largely distributed in the Indo-Pacific and frequently found associated with sunken wood (Hoyoux et al. 2009), was also found in these samples.

Bathymodioline mussel diversity

All phylogenetic trees (COI, 28S and COI+28S) are very congruent. Specimens collected in the Broken Water Bay (Sepik) and in the Basamuk canyon (Astrolabe Bay) cluster into four distinct groups (Figure 5), some of which also include sequences from GenBank. The specimens from Broken Water Bay (Sepik station CP4042), are divided into three groups. One well-supported clade (three specimens) is sister to *Gigantidas taiwanensis*. This new clade is closely related but distinct from *G. taiwanensis* which is only known from a shallow vent off Taiwan. The second group clusters 39 newly-collected specimens, including one

collected during the BIOPAPUA cruise in the Broken Water Bay (labeled in Thubaut et al. 2013 as “*Gigantidas* sp 1 Broken Bay”). Finally, one specimen clustered with one specimen collected in 2010 (labeled “*Gigantidas* sp. 2 Broken Bay” in Thubaut et al. 2013). Interestingly this cluster also included one sequence from a specimen collected in the Basamuk canyon (CP4042). Based on COI data, this species was also collected earlier in a site after the nearby Aitape village, at 420 m depth (Kyuno et al. 2009). The 2012 expedition also explored the Aitape area but did not bring back any catch of fauna typical of seep environments. In this area, two additional undescribed *Gigantidas* species (assignment based on COI data) were collected deeper during the Japanese cruise (1600-1900 m, Kyuno et al. 2009). These species were not collected again during our expeditions, probably because they live deeper than the explored bathymetric range. The eight other specimens from Basamuk canyon (CP4020) cluster into a distinct group and form a well-supported group, sister to *Nypamodiolus longissimus*. These specimens are thus attributed to a potential new species of the genus *Nypamodiolus*.

If we consider the high genetic distances found within and among these clusters, and the fact that the phylogenetic information from mitochondrial and nuclear genes is congruent, we can conclude that four putative species were found at the Broken Water Bay site and in the Basamuk canyon, and two of these were previously collected during the BIOPAPUA cruise. Overall, the three explorations in this area (JAMSTEC cruise, BIOPAPUA cruise and PAPUA NIUGINI expedition) identified five different *Gigantidas* species and one *Nypamodiolus* species. Interestingly, only one of these species was found at all locations (including at Aitape), the five others being each restricted to a single location. Similarly, *Nipponiomodiolus manusensis* (new genus under description, Cosel & Thubaut) has only been found at hydrothermal vent sites in the Manus Basin and was not found in our cold-seep collections (Thubaut et al. 2013).

The genus *Nypamodiolus* contains species that are very ecologically diverse (i.e. associated to plant remains, whale bones or seep environments over a wide bathymetric range). For example the geographic range *N. longissimus* coincides with that of the *Nypa* palm, even if it is sometimes associated with other types of wood; *N. simpsoni* has been collected in both the Mediterranean and in the Atlantic, over a wide range of depths, and associated with whale carcasses, sunken wood, and cold seeps (Thubaut et al. 2013). The specimens attributed to *Nypamodiolus* collected below the Ramu refinery, belong to [an unknown](#) species: they have never been found elsewhere in our collections (neither in the Astrolabe Bay in general nor on the abundant plant debris often collected at other sites during our expeditions).

Siboglinidae diversity

Siboglinid tubeworms were only found at two locations (Broken Water Bay and Astrolabe Bay sites). In the Astrolabe Bay, tubeworms were only found in the Basamuk canyon off the Ramu refinery. Part of COI was sequenced for a total of 11 siboglinid specimens collected from these locations. Specimens fall into three distinct lineages (Figure 6) that are not shared between locations: two of these clades are only found at the Sepik River site and the third has only been collected at the Astrolabe site during our expeditions.

Two specimens from the BrokenWater Bay collections (BIOPAPUA cruise) cluster among escarpiids, but clearly form a separate clade. Although clearly distinct, the sequences of the Broken Water Bay escarpiid species most closely resembles that of a distinct isolate of an animal identified as *Paraescarpia* cf. *echinospica* (isolate E1) collected near Japan (Andersen et al. 2004). Sequences from two other specimens of *Paraescarpia* cf. *echinospica*, also collected near Japan, however form a different clade. [Closer examination of the morphology of all these worms \(if vouchers are available\) will be necessary to determine species identities.](#)

322 The sequences for five specimens of *Lamellibrachia* from the Broken Water Bay site most
323 closely cluster with the sequence of a *Lamellibrachia* specimen collected about 325 km west
324 of the Broken Water Bay collection site (Aitape site *Lamellibrachia* L6 in Kojima et al.
325 2003). Although distinct in sequence, two other species of *Lamellibrachia* are closely related
326 to this group: *L. sp. L4*, from the PACMANUS vent site in the Manus Basin (about 650 km
327 east of the Broken Water Bay site), and *L. sp. L5*, from the cold-seep sites of Kuroshima
328 Knoll, about 3 000 km north-northwest of the Broken Water Bay site (Kojima et al. 2001).
329 Additional samples from the different locations will be necessary to further study this lineage
330 and determine whether there is genetic continuity between the groups identified.

331 Sequences from Basamuk canyon specimens all cluster with different haplotypes of
332 *Lamellibrachia juni*, including four specimens collected from the DESMOS hydrothermal
333 vent site in the Manus Basin, about 770 km to the East. However, some genetic structure
334 exists in this clade, and the haplotype network produced for this lineage (Figure 7) revealed
335 some geographic patterns that could correspond to different species occupying different
336 locations. Basamuk canyon specimens (n=4) represent 3 distinct haplotypes differing by 2
337 mutations at the most. These differ from the DESMOS specimens (n=4) by at least 10 fixed
338 mutational steps. Sequences from specimens collected 1600 km to the North (TOTO Caldera,
339 South Mariana) differ from Basamuk canyon sequences by 6 fixed mutational steps. At the
340 Brothers Caldera (4600 km Southeast of the TOTO Caldera, and 3500 km Southeast of the
341 Astrolabe Bay), there are two haplotype groups, one of which only differs from the TOTO
342 haplotype by a single mutational step, possibly corresponding to a single species. The other
343 haplotypic group from Brothers Caldera differs from all the other haplotypes by at least 4
344 fixed mutational steps.

345 For at least two clades, even though sequence polymorphism does exist, interspecific
346 variation is no greater than intraspecific variation (Miglietta et al. 2010). This observation

does not reflect within-species morphological variation but a reduced divergence of the mitochondrial genome (Miglietta et al. 2010; Cowart et al. 2013). The COI marker thus offers a very conservative estimation of specific diversity in Siboglinidae. Based solely on COI sequence data, there is therefore little doubt that the species studied here represent new species that have only been collected in the sampled area so far. The *Lamellibrachia* specimens collected at Broken Water Bay probably correspond to the same species as the specimen collected at the Aitape site, further west on the PNG coast (Kojima et al. 2001, 2003). A population genetics study including more variable markers (e.g. microsatellites) could reveal whether these populations separated by 350 km are genetically connected. The number of specimens collected in Basamuk canyon (*Lamellibrachia juni* clade), and other specimens of the same clade from different locations was sufficient to initiate a study of connectivity. The specimens from the Astolabe Bay were only found at the site below the Ramu refinery. Although close to *L. juni*, there are some fixed differences in the COI sequences that strongly suggest that this lineage should be separated into at least four species (non-interbreeding populations), two of which are found in Papua-New Guinea. Except for the Brothers Caldera site where two species co-occur, only a single haplotypic group (=species) occurs at each site. Even within the Manus Basin, the sequences of the specimens from the hydrothermal vent site DESMOS are 10 mutational steps distant from the sequences of the specimens collected at the cold-seep site in the Astolabe Bay, indicating that they belong to reproductively isolated evolutionary units.

CONCLUDING REMARKS

Deep-sea chemosynthetic environments are rare and very patchy (Levin & Sibuet 2012, Van Dover et al. 2012). Some organisms can live in several types of chemosynthetic environments (e.g. *Idas washingtonius* is present at vents and on sunken wood or bones in the Eastern

Pacific; *Gigantidas platifrons* is present both at vent and seep environments in the western Pacific, Thubaut et al. 2013; *Pyropelta musaica* is found at cold seeps, hot vents and on sunken whale carcasses, Smith & Baco, 2003), and some have a very wide distribution, sometimes spanning thousands of kilometers (e.g. *Rimicaris exoculata* on the Mid-Atlantic Ridge, Teixeira et al. 2013). In the Atlantic Ocean, the among-site faunal similarity is better explained by depth than by geographic distances (Olu et al. 2010). The potential threat to the fauna associated with deep-sea chemosynthetic habitats should therefore take into account a complex pattern of patchiness and connectivity at small and large geographic scales.

Although intensive, our sampling in the area has probably missed some chemosynthetic sites. For instance, we re-visited the Aitape site sampled earlier with a remotely operated vehicle (Tappin et al. 2001), and did not find any fauna typical of cold seeps in our collections. The area is characterized by very complex bottom structures that are difficult to sample using dredges and trawls. In addition, the sampled animals formed very small clumps (Tappin et al. 2001) that are easily missed. It is therefore very likely that there are sites with chemosynthetic fauna elsewhere in the sampled area.

However, the collections so far clearly reveal not only the great patchiness in the distribution of different environments (cold-seeps, hydrothermal vents, sedimentary areas, rubble, plant debris) that has a direct effect on the distribution of species, but also differences in the species that occupy different sites of the same habitat type, in particular for the cold-seep sites studied so far in PNG.

In other words, even if some species are shared between the two locations sampled, each location is also characterized by unique assemblages. The Broken Water Bay site does share some species with the Aitape site (*Lamellibrachia* L6 and *Gigantidas* sp. 2, this latter also found in the Astrolabe Bay) but the Astrolabe Bay site is characterized by some species that have so far only been found there. Interestingly, the Northern sites (Aitape and Broken Water

Bay) receive currents from the Northwest (with occasional upwellings) while the Astrolabe Bay receives currents coming from the Southeast through the Vitiaz Strait (Hasegawa et al. 2011), suggesting each location could receive larvae from different sources. Our results however provide clear evidence of the patchiness of the cold-seep habitats in PNG and of the limited connectivity between the two studied sites. Although more exploration remains to be performed, it is clear that the assertions that impact of human activities on deep-sea species is limited because the deep sea is uniform and that all species are present everywhere, are inherently wrong. In case the of the Ramu refinery in the Astrolabe Bay, we could not exclude that the major impact it has on the local deep-sea habitat in the Basamuk Bay would actually correspond to local species extinction. These concerns call for major exploration efforts and studies of connectivity in the hotspot of biodiversity that PNG represents.

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FIGURE CAPTION

Figure 1: Map of Papua New Guinea with locations of stations sampled during the BIOPAPUA (2010) cruise and PAPUA NIUGINI expedition (2012). Stations where cold seep organisms were found are represented by white squares (left of arrows: station numbers).

Other stations are represented by grey circles. The map was prepared based on NOAA's ETOPO1 data using the *marmap* package in R (Pante and Simon-Bouhet 2013). Stations CP4020 and 4081: Basamuk canyon, canyon below the Ramu refinery. Stations CP3703, 3704, 4040, 4042, and 4043: Broken Water Bay, Sepik site.

Figure 2: Broken Water Bay fauna. Photos taken on board. A- Bathymodiolinae mussels, PAPUA NIUGINI, CP4042; B-*Gigantidas* sp 2 Broken Bay BIOPAPUA, CP3703; C-*Gigantidas* sp 1 Broken Bay, BIOPAPUA, CP3703; D-*Lamellibrachia* sp., BIOPAPUA, CP3703; E- *Acila* sp., BIOPAPUA, CP3703; F- *Conchocele* sp., BIOPAPUA CP3703; G- Buccinidae gastropod *Manaria* sp. , PAPUA NIUGINI, CP4042

Figure 3: Basamuk Canyon, below the Ramu refinery. A- Muddy sediment collected 50 m below pipe opening (DW 4018) B- Red muddy sediment collected 200 m below pipe opening (DW 4019). C- *Goniopugettia sagamiensis*. D- *Ethusa curvipes*. Illustrations of the red mineral deposit covering animals. Specimens on the left collected outside the refinery area. Specimens on the right collected at station CP4081.

Figure 4: Basamuk Canyon fauna (PAPUA NIUGINI, CP4081). A-B Siboglinidae (*Lamellibrachia* sp.), C-Bathymodiolinae (*Gigantidas* sp.), D- *Lebbeus* sp.; E- *Munidopsis andamanica*. The red coloration of the specimens is due to the Ramu refinery tailings.

Figure 5: COI (A), 28S (B) and COI+28S (C) Bayesian phylogenetic trees obtained from 105 Bathymodiolinae. Posterior Probabilities (> 0.90) and Bootstraps (> 75%) are shown for each node. *: Posterior Probabilities > 0.98 and Bootstraps > 95%. For clarity purpose, supports for

within species relationships are not shown. Specimens from the PAPUA NIUGINI are in **BOLD**.

Figure 6: Bayesian phylogenetic tree obtained from 298 Vestimentifera COI sequences. Posterior Probabilities (> 0.85) and Bootstraps ($> 75\%$) are shown for each node. *: Posterior Probabilities > 0.98 and Bootstraps $> 95\%$. For clarity purpose, supports for within species relationships are not shown and clades that included sequences from the same species or the same species complex were collapsed in triangles (as long as they did not include Papua Niugini sequences). Specimens from the PAPUA NIUGINI are in **BOLD**. Specimens of the species *Gigantidas* sp. 1 Broken Water Bay were collapsed into a triangle (details in table 1).

Figure 7: Sampling locations (left) and TCS haplotype network (Clement et al. 2000) of the *Lamellibrachia juni* clade (right). Circles on the network represent unique mtCOI haplotypes, circle diameter proportional to number of individuals (key: bottom right). Intermediate mutations (*i.e.* unsampled haplotypes) are represented by small white circles. Site colors on the map correspond to circle colors on the network. The map was prepared based on NOAA's ETOPO1 data using the *marmap* package in R (Pante and Simon-Bouhet, 2013).

Table 1: List of analyzed specimens.

MNHN #	Group	ID	Expedition	Station	GenBank COI
IM_2013_17293	Bathymodiolinae	<i>Gigantidas</i> sp. 1 Broken Bay	PAPUA NIUGINI	CP4042	submitted
IM_2013_17294	Bathymodiolinae	<i>Gigantidas</i> sp. 1 Broken Bay	PAPUA NIUGINI	CP4042	submitted
IM_2013_17295	Bathymodiolinae	<i>Gigantidas</i> sp. 1 Broken Bay	PAPUA NIUGINI	CP4042	submitted
IM_2013_17296	Bathymodiolinae	<i>Gigantidas</i> sp. 1 Broken Bay	PAPUA NIUGINI	CP4042	submitted
IM_2013_18626	Bathymodiolinae	<i>Gigantidas</i> sp. 1 Broken Bay	PAPUA NIUGINI	CP4042	submitted
IM_2013_18628	Bathymodiolinae	<i>Gigantidas</i> sp. 1 Broken Bay	PAPUA NIUGINI	CP4042	submitted
IM_2013_18629	Bathymodiolinae	<i>Gigantidas</i> sp. 2 Broken Bay	PAPUA NIUGINI	CP4042	submitted
IM_2013_18630	Bathymodiolinae	<i>Gigantidas</i> sp. 1 Broken Bay	PAPUA NIUGINI	CP4042	submitted
IM_2013_18631	Bathymodiolinae	<i>Gigantidas</i> sp. 1 Broken Bay	PAPUA NIUGINI	CP4042	submitted
IM_2013_18632	Bathymodiolinae	<i>Gigantidas</i> sp. 1 Broken Bay	PAPUA NIUGINI	CP4042	submitted
IM_2013_18634	Bathymodiolinae	<i>Gigantidas</i> sp. 1 Broken Bay	PAPUA NIUGINI	CP4042	submitted
IM_2013_18656	Bathymodiolinae	<i>Gigantidas</i> sp. 1 Broken Bay	PAPUA NIUGINI	CP4042	submitted
IM_2013_18670	Bathymodiolinae	<i>Gigantidas</i> sp. 1 Broken Bay	PAPUA NIUGINI	CP4042	submitted
IM_2013_18674	Bathymodiolinae	<i>Gigantidas</i> sp. 1 Broken Bay	PAPUA NIUGINI	CP4042	submitted
IM_2013_18675	Bathymodiolinae	<i>Gigantidas</i> sp. 1 Broken Bay	PAPUA NIUGINI	CP4042	submitted
IM_2013_18717	Bathymodiolinae	<i>Gigantidas</i> sp. 1 Broken Bay	PAPUA NIUGINI	CP4042	submitted
IM_2013_18719	Bathymodiolinae	new species 2	PAPUA NIUGINI	CP4042	submitted
IM_2013_18722	Bathymodiolinae	<i>Gigantidas</i> sp. 1 Broken Bay	PAPUA NIUGINI	CP4042	submitted
IM_2013_18723	Bathymodiolinae	<i>Gigantidas</i> sp. 1 Broken Bay	PAPUA NIUGINI	CP4042	submitted
IM_2013_18724	Bathymodiolinae	<i>Gigantidas</i> sp. 1 Broken Bay	PAPUA NIUGINI	CP4042	submitted
IM_2013_18725	Bathymodiolinae	<i>Gigantidas</i> sp. 1 Broken Bay	PAPUA NIUGINI	CP4042	submitted
IM_2013_18726	Bathymodiolinae	<i>Gigantidas</i> sp. 1 Broken Bay	PAPUA NIUGINI	CP4042	submitted
IM_2013_18727	Bathymodiolinae	<i>Gigantidas</i> sp. 1 Broken Bay	PAPUA NIUGINI	CP4042	submitted
IM_2013_18728	Bathymodiolinae	<i>Gigantidas</i> sp. 1 Broken Bay	PAPUA NIUGINI	CP4042	submitted
IM_2013_18729	Bathymodiolinae	<i>Gigantidas</i> sp. 1 Broken Bay	PAPUA NIUGINI	CP4042	submitted
IM_2013_18730	Bathymodiolinae	<i>Gigantidas</i> sp. 1 Broken Bay	PAPUA NIUGINI	CP4042	submitted
IM_2013_18731	Bathymodiolinae	<i>Gigantidas</i> sp. 1 Broken Bay	PAPUA NIUGINI	CP4042	submitted
IM_2013_18732	Bathymodiolinae	<i>Gigantidas</i> sp. 1 Broken Bay	PAPUA NIUGINI	CP4042	submitted
IM_2013_18733	Bathymodiolinae	<i>Gigantidas</i> sp. 1 Broken Bay	PAPUA NIUGINI	CP4042	submitted
IM_2013_18734	Bathymodiolinae	<i>Gigantidas</i> sp. 1 Broken Bay	PAPUA NIUGINI	CP4042	submitted
IM_2013_18735	Bathymodiolinae	<i>Gigantidas</i> sp. 1 Broken Bay	PAPUA NIUGINI	CP4042	submitted
IM_2013_18736	Bathymodiolinae	<i>Gigantidas</i> sp. 1 Broken Bay	PAPUA NIUGINI	CP4042	submitted
IM_2013_18737	Bathymodiolinae	<i>Gigantidas</i> sp. 1 Broken Bay	PAPUA NIUGINI	CP4042	submitted
IM_2013_18738	Bathymodiolinae	<i>Gigantidas</i> sp. 1 Broken Bay	PAPUA NIUGINI	CP4042	submitted

IM_2013_18739	Bathymodiolinae	<i>Gigantidas</i> sp. 1 Broken Bay	PAPUA NIUGINI	CP4042	submitted
IM_2013_18740	Bathymodiolinae	<i>Gigantidas</i> sp. 1 Broken Bay	PAPUA NIUGINI	CP4042	submitted
IM_2013_18741	Bathymodiolinae	<i>Gigantidas</i> sp. 1 Broken Bay	PAPUA NIUGINI	CP4042	submitted
IM_2013_18742	Bathymodiolinae	<i>Gigantidas</i> sp. 1 Broken Bay	PAPUA NIUGINI	CP4042	submitted
IM_2013_18743	Bathymodiolinae	<i>Gigantidas</i> sp. 1 Broken Bay	PAPUA NIUGINI	CP4042	submitted
IM_2013_18744	Bathymodiolinae	<i>Gigantidas</i> sp. 1 Broken Bay	PAPUA NIUGINI	CP4042	submitted
IM_2013_18745	Bathymodiolinae	<i>Gigantidas</i> sp. 1 Broken Bay	PAPUA NIUGINI	CP4042	submitted
IM_2013_18746	Bathymodiolinae	new species 2	PAPUA NIUGINI	CP4042	submitted
IM_2013_18747	Bathymodiolinae	new species 2	PAPUA NIUGINI	CP4042	submitted
IM_2013_19398	Bathymodiolinae	new species 1	PAPUA NIUGINI	CP4020	submitted
IM_2013_19399	Bathymodiolinae	new species 1	PAPUA NIUGINI	CP4020	submitted
IM_2013_19400	Bathymodiolinae	new species 1	PAPUA NIUGINI	CP4020	submitted
IM_2013_19401	Bathymodiolinae	new species 1	PAPUA NIUGINI	CP4020	submitted
IM_2013_19403	Bathymodiolinae	new species 1	PAPUA NIUGINI	CP4020	submitted
IM_2013_19406	Bathymodiolinae	new species 1	PAPUA NIUGINI	CP4020	submitted
IM_2013_19408	Bathymodiolinae	new species 1	PAPUA NIUGINI	CP4020	submitted
IM_2013_19409	Bathymodiolinae	<i>Gigantidas</i> sp. 2 Broken Bay	PAPUA NIUGINI	CP4020	submitted
IM_2013_19411	Bathymodiolinae	new species 1	PAPUA NIUGINI	CP4020	submitted
GenBank	Bathymodiolinae	<i>Terua arcuatilis</i>			FJ937033
GenBank	Bathymodiolinae	<i>Gigantidas crypta</i> B'			EU702319
GenBank	Bathymodiolinae	<i>Gigantidas crypta</i> B''			EU702315
GenBank	Bathymodiolinae	<i>Idas iwaotakii</i> A'			EU702333
GenBank	Bathymodiolinae	<i>Idas iwaotakii</i> A''			EU702322
GenBank	Bathymodiolinae	<i>Benthomodiolus lignocola</i>			AY275545
GenBank	Bathymodiolinae	<i>Bathymodiolus boomerang</i>			FJ890503
GenBank	Bathymodiolinae	<i>Bathymodiolus aff. thermophilus</i>			AF456317
GenBank	Bathymodiolinae	<i>Bathymodiolus azoricus</i>			AY649795
GenBank	Bathymodiolinae	<i>Bathymodiolus brevior</i>			AY649799
GenBank	Bathymodiolinae	<i>Bathymodiolus brooksi</i>			AY649798
GenBank	Bathymodiolinae	<i>Bathymodiolus heckerae</i>			AY649794
GenBank	Bathymodiolinae	<i>Bathymodiolus puteoserpentis</i>			AY649796
GenBank	Bathymodiolinae	<i>Gigantidas tangaroa</i>			AY608439
GenBank	Bathymodiolinae	<i>Vulcanidas</i> ESU E			FJ937079
GenBank	Bathymodiolinae	<i>Vulcanidas</i> ESU F			FJ937127
GenBank	Bathymodiolinae	<i>Lignomodiolus</i> ESU G			FJ937161
GenBank	Bathymodiolinae	<i>Nypamodiolus</i> ESU H			FJ937073
GenBank	Bathymodiolinae	<i>Nypamodiolus</i> ESU I			FJ937188
GenBank	Bathymodiolinae	<i>Nypamodiolus</i> ESU J			FJ937189

GenBank	Bathymodiolinae	<i>Idas</i> ESU K			FJ937192
GenBank	Bathymodiolinae	<i>Idas</i> ESU L			FJ937193
GenBank	Bathymodiolinae	<i>Idas</i> ESU M			FJ937202
GenBank	Bathymodiolinae	<i>Idas</i> ESU N			FJ937205
GenBank	Bathymodiolinae	<i>Idas</i> ESU O			FJ937211
GenBank	Bathymodiolinae	<i>Idas</i> ESU P			FJ937222
GenBank	Bathymodiolinae	<i>Lignomodiolus</i> ESU Q			FJ937230
GenBank	Bathymodiolinae	<i>Lignomodiolus</i> ESU R			FJ937239
GenBank	Bathymodiolinae	<i>Lignomodiolus</i> ESU S'			FJ937240
GenBank	Bathymodiolinae	<i>Lignomodiolus</i> ESU S''			FJ937258
GenBank	Bathymodiolinae	<i>Terua</i> ESU T			FJ937283
GenBank	Bathymodiolinae	<i>Gigantidas gladius</i>			AY649802
GenBank	Bathymodiolinae	<i>Idas macdonaldi</i>			AY649804
GenBank	Bathymodiolinae	<i>Idas modiolaeformis</i>			FJ158585
GenBank	Bathymodiolinae	<i>Idas</i> sp. C			EU702376
GenBank	Bathymodiolinae	<i>Idas</i> sp. D			EU702357
GenBank	Bathymodiolinae	<i>Idas washingtonius</i>			AY275546
GenBank	Bathymodiolinae	<i>Benthomodiolus</i> sp. Juan de Fuca			KF611694
GenBank	Bathymodiolinae	<i>Nypamodiolus longissimus</i>			DQ340773
GenBank	Bathymodiolinae	<i>Nipponiiodiolus manusensis</i>			GU966637
GenBank	Bathymodiolinae	<i>Gigantidas mauritanicus</i>			FJ890502
GenBank	Bathymodiolinae	<i>Idas</i> SAL1			DQ340775
GenBank	Bathymodiolinae	<i>Vulcanidas</i> SAL3			DQ340772
GenBank	Bathymodiolinae	<i>Lignomodiolus</i> SAL4			DQ340776
GenBank	Bathymodiolinae	<i>Nypamodiolus simpsoni</i>			KF611695
GenBank	Bathymodiolinae	<i>Gigantidas</i> sp. 1 Broken Bay			KF611693
GenBank	Bathymodiolinae	<i>Gigantidas</i> sp. 2 Broken Bay			KF611692
GenBank	Bathymodiolinae	<i>Benthomodiolus</i> sp. South Atlantic			KF611691
GenBank	Bathymodiolinae	<i>Gigantidas taiwanensis</i>			GU966638
GenBank	Bathymodiolinae	<i>Bathymodiolus thermophilus</i>			GU966639
GenBank	Bathymodiolinae	<i>Tamu fisheri</i>			AY649803
GenBank	Bathymodiolinae	<i>Vulcanidas insolatus</i>			FJ767936
GenBank	OUTGROUP (Mytilidae)	<i>Modiolus modiolus</i>			FJ890501
	Vestimentifera	Escarpia	BIOPAPUA	CP3703	submitted
	Vestimentifera	Escarpia	BIOPAPUA	CP3704	submitted
	Vestimentifera	Lam1	PAPUA NIUGINI	CP4040	submitted
	Vestimentifera	Lam2	PAPUA NIUGINI	CP4040	submitted
	Vestimentifera	LamB	PAPUA NIUGINI	CP4042	submitted

	Vestimentifera	LamC	PAPUA NIUGINI	CP4042	submitted
	Vestimentifera	LamD	PAPUA NIUGINI	CP4043	submitted
	Vestimentifera	LamC	PAPUA NIUGINI	CP4081	submitted
	Vestimentifera	LamD	PAPUA NIUGINI	CP4081	submitted
	Vestimentifera	LamE	PAPUA NIUGINI	CP4081	submitted
	Vestimentifera	LamF	PAPUA NIUGINI	CP4081	submitted
GenBank	Vestimentifera	<i>Lamellibrachia</i> sp L4			AB0552091
GenBank	Vestimentifera	<i>Lamellibrachia</i> sp L5			AB0552101
GenBank	Vestimentifera	<i>Arcovestia ivanovi</i>			AB0734911
GenBank	Vestimentifera	<i>Cf Alaysia</i> sp A1			AB0886701
GenBank	Vestimentifera	<i>Cf Alaysia</i> sp A2			AB0886711
GenBank	Vestimentifera	<i>Cf Alaysia</i> sp A3			AB0886721
GenBank	Vestimentifera	<i>Cf Alaysia</i> sp A4			AB0886731
GenBank	Vestimentifera	<i>Lamellibrachia</i> sp L6			AB0886741
GenBank	Vestimentifera	<i>Lamellibrachia</i> sp L7			AB0886751
GenBank	Vestimentifera	<i>Lamellibrachia</i> sp L1 DH-2004			AB1811611
GenBank	Vestimentifera	<i>Oasisia fujikurai</i>			AB2428571
GenBank	Vestimentifera	<i>Lamellibrachia juni</i>			AB2428581
GenBank	Vestimentifera	<i>Lamellibrachia juni</i> haplotype1			AB2646011
GenBank	Vestimentifera	<i>Lamellibrachia juni</i> haplotype2			AB2646021
GenBank	Vestimentifera	<i>Lamellibrachia juni</i> haplotype3			AB2646031
GenBank	Vestimentifera	<i>Lamellibrachia juni</i> haplotype4			AB2646041
GenBank	Vestimentifera	<i>Lamellibrachia juni</i> haplotype5			AB2646051
GenBank	Vestimentifera	<i>Lamellibrachia satsuma</i> haplotype 1			AB7214791
GenBank	Vestimentifera	<i>Lamellibrachia satsuma</i> haplotype 2			AB7214801
GenBank	Vestimentifera	<i>Lamellibrachia satsuma</i> haplotype 3			AB7214811
GenBank	Vestimentifera	<i>Lamellibrachia satsuma</i> haplotype 4			AB7214821
GenBank	Vestimentifera	<i>Lamellibrachia satsuma</i> haplotype 5			AB7214831
GenBank	Vestimentifera	<i>Lamellibrachia satsuma</i> haplotype 6			AB7214841
GenBank	Vestimentifera	<i>Lamellibrachia satsuma</i> haplotype 7			AB7214851
GenBank	Vestimentifera	<i>Lamellibrachia satsuma</i> haplotype 8			AB7214861
GenBank	Vestimentifera	<i>Lamellibrachia satsuma</i> haplotype 9			AB7214871
GenBank	Vestimentifera	<i>Lamellibrachia satsuma</i> haplotype 10			AB7214881
GenBank	Vestimentifera	<i>Lamellibrachia satsuma</i> haplotype 11			AB7214891
GenBank	Vestimentifera	<i>Lamellibrachia satsuma</i> haplotype 12			AB7214901
GenBank	Vestimentifera	<i>Lamellibrachia satsuma</i> haplotype 13			AB7214911
GenBank	Vestimentifera	<i>Lamellibrachia satsuma</i> haplotype 14			AB7214921
GenBank	Vestimentifera	<i>Lamellibrachia satsuma</i> haplotype 15			AB7214931

GenBank	Vestimentifera	<i>Lamellibrachia satsuma</i> haplotype 16	AB7214941
GenBank	Vestimentifera	<i>Lamellibrachia satsuma</i> haplotype 17	AB7214951
GenBank	Vestimentifera	<i>Lamellibrachia satsuma</i> haplotype 18	AB7214961
GenBank	Vestimentifera	<i>Ridgeia piscesae</i>	AF0222331
GenBank	Vestimentifera	<i>Ridgeia piscesae</i>	AF0222341
GenBank	Vestimentifera	<i>Ridgeia piscesae</i>	AF0222351
GenBank	Vestimentifera	<i>Seepiophila jonesi</i>	AF3172871
GenBank	Vestimentifera	<i>Seepiophila jonesi</i> isolate GB425	AF3172881
GenBank	Vestimentifera	<i>Seepiophila jonesi</i> isolate GC234	AF3172891
GenBank	Vestimentifera	<i>Seepiophila jonesi</i> isolate TAMU-17	AF3172901
GenBank	Vestimentifera	<i>Lamellibrachia satsuma</i>	AF3426711
GenBank	Vestimentifera	<i>Seepiophila jonesi</i> individual 2	AY1291211
GenBank	Vestimentifera	<i>Seepiophila jonesi</i> isolate GC354	AY1291221
GenBank	Vestimentifera	<i>Seepiophila jonesi</i> isolate GB535	AY1291231
GenBank	Vestimentifera	<i>Lamellibrachia cf luymesii</i> individual 6	AY1291241
GenBank	Vestimentifera	<i>Seepiophila jonesi</i> individual 1	AY1291251
GenBank	Vestimentifera	<i>Lamellibrachia cf luymesii</i> isolate GC354	AY1291261
GenBank	Vestimentifera	<i>Seepiophila jonesi</i> individual 3	AY1291271
GenBank	Vestimentifera	<i>Escarpiella laminata</i> individual 41314	AY1291281
GenBank	Vestimentifera	<i>Escarpiella laminata</i> individual 35-11	AY1291291
GenBank	Vestimentifera	<i>Escarpiella laminata</i> individual 35-2	AY1291301
GenBank	Vestimentifera	<i>Escarpiella laminata</i> individual 2	AY1291311
GenBank	Vestimentifera	<i>Lamellibrachia cf luymesii</i> individual 1	AY1291321
GenBank	Vestimentifera	<i>Lamellibrachia cf luymesii</i> individual 2	AY1291331
GenBank	Vestimentifera	<i>Escarpiella</i> sp GB425-GoM	AY1291341
GenBank	Vestimentifera	<i>Lamellibrachia cf luymesii</i> isolate GB425	AY1291351
GenBank	Vestimentifera	<i>Lamellibrachia cf luymesii</i> isolate GC234	AY1291361
GenBank	Vestimentifera	<i>Lamellibrachia barhami</i> individual 10	AY1291371
GenBank	Vestimentifera	<i>Lamellibrachia barhami</i> individual 11	AY1291381
GenBank	Vestimentifera	<i>Lamellibrachia cf luymesii</i>	AY1291391
GenBank	Vestimentifera	<i>Seepiophila jonesi</i> isolate TAMU-17	AY1291401
GenBank	Vestimentifera	<i>Lamellibrachia barhami</i> individual 9	AY1291411
GenBank	Vestimentifera	<i>Seepiophila jonesi</i>	AY1291421
GenBank	Vestimentifera	<i>Seepiophila jonesi</i> isolate GB425	AY1291431
GenBank	Vestimentifera	<i>Seepiophila jonesi</i> isolate GC234	AY1291441
GenBank	Vestimentifera	<i>Lamellibrachia barhami</i> individual 8	AY1291451
GenBank	Vestimentifera	<i>Lamellibrachia barhami</i> individual 7	AY1291461
GenBank	Vestimentifera	<i>Lamellibrachia barhami</i> individual 4	AY1291471

GenBank	Vestimentifera	<i>Escarpia southwardae</i> haplotype 2	AY3263031
GenBank	Vestimentifera	<i>Escarpia southwardae</i> haplotype 1	AY3263041
GenBank	Vestimentifera	<i>Riftia pachyptila</i> haplotype A	AY6459891
GenBank	Vestimentifera	<i>Riftia pachyptila</i> haplotype B	AY6459901
GenBank	Vestimentifera	<i>Riftia pachyptila</i> haplotype C	AY6459911
GenBank	Vestimentifera	<i>Tevnia jerichonana</i> haplotype A	AY6459921
GenBank	Vestimentifera	<i>Tevnia jerichonana</i> haplotype B	AY6459931
GenBank	Vestimentifera	<i>Tevnia jerichonana</i> haplotype C	AY6459941
GenBank	Vestimentifera	<i>Tevnia jerichonana</i> haplotype D	AY6459951
GenBank	Vestimentifera	<i>Tevnia jerichonana</i> haplotype E	AY6459961
GenBank	Vestimentifera	<i>Tevnia jerichonana</i> haplotype F	AY6459971
GenBank	Vestimentifera	<i>Tevnia jerichonana</i> haplotype G	AY6459981
GenBank	Vestimentifera	<i>Tevnia jerichonana</i> haplotype H	AY6459991
GenBank	Vestimentifera	<i>Tevnia jerichonana</i> haplotype I	AY6460001
GenBank	Vestimentifera	<i>Oasisia alvinae</i> haplotype A	AY6460011
GenBank	Vestimentifera	<i>Oasisia alvinae</i> haplotype B	AY6460021
GenBank	Vestimentifera	<i>Oasisia alvinae</i> haplotype C	AY6460031
GenBank	Vestimentifera	<i>Oasisia alvinae</i> haplotype D	AY6460041
GenBank	Vestimentifera	<i>Oasisia alvinae</i> haplotype E	AY6460051
GenBank	Vestimentifera	<i>Oasisia alvinae</i> haplotype F	AY6460061
GenBank	Vestimentifera	<i>Oasisia alvinae</i> haplotype G	AY6460071
GenBank	Vestimentifera	<i>Oasisia alvinae</i> haplotype H	AY6460081
GenBank	Vestimentifera	<i>Oasisia alvinae</i> haplotype I	AY6460091
GenBank	Vestimentifera	<i>Oasisia alvinae</i> haplotype J	AY6460101
GenBank	Vestimentifera	<i>Oasisia alvinae</i> haplotype K	AY6460111
GenBank	Vestimentifera	<i>Oasisia alvinae</i> haplotype L	AY6460121
GenBank	Vestimentifera	<i>Oasisia alvinae</i> haplotype M	AY6460131
GenBank	Vestimentifera	<i>Oasisia alvinae</i> haplotype N	AY6460141
GenBank	Vestimentifera	<i>Oasisia alvinae</i> haplotype O	AY6460151
GenBank	Vestimentifera	<i>Oasisia alvinae</i> haplotype P	AY6460161
GenBank	Vestimentifera	<i>Oasisia alvinae</i> haplotype Q	AY6460171
GenBank	Vestimentifera	<i>Oasisia alvinae</i> haplotype R	AY6460181
GenBank	Vestimentifera	<i>Oasisia alvinae</i> haplotype S	AY6460191
GenBank	Vestimentifera	<i>Oasisia alvinae</i> haplotype T	AY6460201
GenBank	Vestimentifera	<i>Riftia pachyptila</i>	AY7416621
GenBank	Vestimentifera	<i>Lamellibrachia</i> sp	D380292
GenBank	Vestimentifera	<i>Lamellibrachia satsuma</i>	D380302
GenBank	Vestimentifera	<i>Lamellibrachia</i> sp	D505922

GenBank	Vestimentifera	<i>Paraescarpia cf echinospica</i> isolateE1	D505932
GenBank	Vestimentifera	<i>Paraescarpia cf echinospica</i> isolateE2	D505942
GenBank	Vestimentifera	<i>Paraescarpia cf echinospica</i>	D505951
GenBank	Vestimentifera	<i>Lamellibrachia columna</i> isolate Lcolumna C JII145	DQ9966451
GenBank	Vestimentifera	<i>Lamellibrachia</i> sp SMH-2007a	EU0466161
GenBank	Vestimentifera	<i>Ridgeia piscesae</i> isolate T449A1-1	EU1904941
GenBank	Vestimentifera	<i>Riftia pachyptila</i> isolate 97	FJ6675291
GenBank	Vestimentifera	<i>Arcovestia ivanovi</i> isolate JII142	FJ6675301
GenBank	Vestimentifera	<i>Tevnia jerichonana</i> isolate 92	FJ6675311
GenBank	Vestimentifera	<i>Tevnia jerichonana</i> isolate 351	FJ6675321
GenBank	Vestimentifera	<i>Oasisia</i> sp SBJ-2009 isolate NZ	FJ6675331
GenBank	Vestimentifera	<i>Oasisia</i> sp SBJ-2009 isolate S	FJ6675341
GenBank	Vestimentifera	<i>Oasisia</i> sp SBJ-2009 isolate 2S	FJ6675351
GenBank	Vestimentifera	<i>Alaysia</i> sp SBJ-2009 isolate JII145	FJ6675361
GenBank	Vestimentifera	<i>Escarpia spicata</i> isolate T548	FJ6675371
GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate AC818 E6 1	GU0591631
GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate GB697 E20S 10	GU0591641
GenBank	Vestimentifera	<i>Lamellibrachia</i> sp 1 MPM-2010 isolate WR269 102	GU0591651
GenBank	Vestimentifera	<i>Lamellibrachia</i> sp 1 MPM-2010 isolate AT340 L1	GU0591661
GenBank	Vestimentifera	<i>Lamellibrachia</i> sp 1 MPM-2010 isolate WR269 L9 104	GU0591671
GenBank	Vestimentifera	<i>Lamellibrachia</i> sp 1 MPM-2010 isolate WR269 L2 105	GU0591681
GenBank	Vestimentifera	<i>Lamellibrachia</i> sp 1 MPM-2010 isolate AC601 L13 107	GU0591691
GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate GB829 E4 11	GU0591701
GenBank	Vestimentifera	<i>Lamellibrachia</i> sp 1 MPM-2010 isolate AC601 L2 110	GU0591711
GenBank	Vestimentifera	<i>Lamellibrachia</i> sp 2 MPM-2010 isolate GC852 L5 118	GU0591731
GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate GB829 E5 12	GU0591741
GenBank	Vestimentifera	<i>Lamellibrachia</i> sp 2 MPM-2010 isolate AT340 L39 122	GU0591751
GenBank	Vestimentifera	<i>Lamellibrachia</i> sp 2 MPM-2010 isolate WR269 123	GU0591761
GenBank	Vestimentifera	<i>Lamellibrachia</i> sp 2 MPM-2010 isolate AC601 L1 124	GU0591771
GenBank	Vestimentifera	<i>Lamellibrachia</i> sp 2 MPM-2010 isolate AC601 L81 126	GU0591781
GenBank	Vestimentifera	<i>Lamellibrachia</i> sp 1 MPM-2010 isolate AT340 L2 128	GU0591791
GenBank	Vestimentifera	<i>Seepiophila jonesi</i> isolate GB697 S3 130	GU0591801
GenBank	Vestimentifera	<i>Seepiophila jonesi</i> isolate GB647 S10 131	GU0591811
GenBank	Vestimentifera	<i>Seepiophila jonesi</i> isolate GC234 LV3 132	GU0591821
GenBank	Vestimentifera	<i>Seepiophila jonesi</i> isolate GC234 EV3 134	GU0591831
GenBank	Vestimentifera	<i>Seepiophila jonesi</i> isolate GC234 EV7 134b	GU0591841
GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate GC852 E23B 14	GU0591851
GenBank	Vestimentifera	<i>Seepiophila jonesi</i> isolate GB647 S12 141	GU0591861

GenBank	Vestimentifera	<i>Seepiophila jonesi</i> isolate GB647 S6 143	GU0591871
GenBank	Vestimentifera	<i>Seepiophila jonesi</i> isolate GB647 S5 144	GU0591881
GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate AC818 E5 145	GU0591891
GenBank	Vestimentifera	<i>Seepiophila jonesi</i> isolate GB647 S11 147	GU0591901
GenBank	Vestimentifera	<i>Seepiophila jonesi</i> isolate GB647 S7 148	GU0591911
GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate GC852 E47 17	GU0591921
GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate GC852 E35 18	GU0591931
GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate GC852 newVest 19	GU0591941
GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate AC818 E93 19B	GU0591951
GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate AC818 E2 2	GU0591961
GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate WR269 E4 20	GU0591971
GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate WR269 E5 21	GU0591981
GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate WR269 E6 22	GU0591991
GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate WR269 E7S 23	GU0592001
GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate WR269 E9S 24	GU0592011
GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate AT340 Efat 27	GU0592021
GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate AT340 E2 28	GU0592031
GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate AT 340 E4 29	GU0592041
GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate AC818 E2 3	GU0592051
GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate AT340 E1 30	GU0592061
GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate AT340 E5 31	GU0592071
GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate AT341 E2 32	GU0592081
GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate AT340 E6 33	GU0592091
GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate WR269 E5 35	GU0592101
GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate AC601 E3 37	GU0592111
GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate AC601 E4 38	GU0592121
GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate AC601 L2 39	GU0592131
GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate AC818 E3 4	GU0592141
GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate AC601 E3 40	GU0592151
GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate AC602 E5 42	GU0592161
GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate AC601 E2 43	GU0592171
GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate AC602 E6 44	GU0592181
GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate AC601 E4 45	GU0592191
GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate AC601 L2 47	GU0592201
GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate AC601 E9 49	GU0592211
GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate AC818 E4 5	GU0592221
GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate AC601 L7 50	GU0592231
GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate AC601 E1 54	GU0592241

GenBank	Vestimentifera	<i>Lamellibrachia luymesii</i> isolate BH L7 55	GU0592251
GenBank	Vestimentifera	<i>Lamellibrachia luymesii</i> isolate GC234 V1 57	GU0592261
GenBank	Vestimentifera	<i>Lamellibrachia</i> sp 1 MPM-2010 isolate GC852 L33 58	GU0592271
GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate AC818 E6 6	GU0592281
GenBank	Vestimentifera	<i>Lamellibrachia luymesii</i> isolate BH LA V9 62	GU0592291
GenBank	Vestimentifera	<i>Lamellibrachia luymesii</i> isolate BH LV1 66	GU0592311
GenBank	Vestimentifera	<i>Lamellibrachia luymesii</i> isolate BH V2 68	GU0592321
GenBank	Vestimentifera	<i>Lamellibrachia luymesii</i> isolate BH V3 69	GU0592331
GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate AC818 E4 7	GU0592341
GenBank	Vestimentifera	<i>Lamellibrachia luymesii</i> isolate BH V4 70	GU0592351
GenBank	Vestimentifera	<i>Lamellibrachia luymesii</i> isolate BP LV8 72	GU0592361
GenBank	Vestimentifera	<i>Lamellibrachia</i> sp 1 MPM-2010 isolate GB697 L13S 73	GU0592371
GenBank	Vestimentifera	<i>Lamellibrachia</i> sp 1 MPM-2010 isolate GB829 L1 76	GU0592381
GenBank	Vestimentifera	<i>Lamellibrachia luymesii</i> isolate GC234 LV5 83	GU0592401
GenBank	Vestimentifera	<i>Lamellibrachia luymesii</i> isolate GC234 LV6 86	GU0592411
GenBank	Vestimentifera	<i>Lamellibrachia</i> sp 1 MPM-2010 isolate GC600 L4 88	GU0592421
GenBank	Vestimentifera	<i>Lamellibrachia</i> sp 1 MPM-2010 isolate GC600 L5 89	GU0592431
GenBank	Vestimentifera	<i>Lamellibrachia</i> sp 1 MPM-2010 isolate GC852 L4 90	GU0592441
GenBank	Vestimentifera	<i>Lamellibrachia</i> sp 1 MPM-2010 isolate GC852 L6 92	GU0592451
GenBank	Vestimentifera	<i>Lamellibrachia luymesii</i> isolate BH V10 93	GU0592461
GenBank	Vestimentifera	<i>Lamellibrachia luymesii</i> isolate GC234 V4L 99	GU0592471
GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate AC601 L8 95 149	GU0592481
GenBank	Vestimentifera	<i>Lamellibrachia</i> sp 1 MPM-2010 isolate GB697 L13 157	GU0592491
GenBank	Vestimentifera	<i>Seepiophila jonesi</i> isolate GB697 L5 160	GU0592511
GenBank	Vestimentifera	<i>Seepiophila jonesi</i> isolate GB697 S3P 160	GU0592521
GenBank	Vestimentifera	<i>Lamellibrachia luymesii</i> isolate GC234 LaV2 152	GU0592531
GenBank	Vestimentifera	<i>Lamellibrachia</i> sp 1 MPM-2010 isolate GC600 L3 417 153	GU0592541
GenBank	Vestimentifera	<i>Escarpiid</i> sp n MPM-2010 isolate GB425 154	GU0592551
GenBank	Vestimentifera	<i>Escarpiid</i> sp n MPM-2010 isolate GC234 155	GU0592561
GenBank	Vestimentifera	<i>Lamellibrachia</i> sp Lam1	HQ1545251
GenBank	Vestimentifera	<i>Lamellibrachia</i> sp Lam2	HQ1545261
GenBank	Vestimentifera	<i>Lamellibrachia</i> sp DBUA 1146	HQ3968911
GenBank	Vestimentifera	<i>Escarpia</i> sp 1 JMP-2012	JN0212671
GenBank	Vestimentifera	<i>Escarpia</i> sp 2 JMP-2012	JN0212681
GenBank	Vestimentifera	<i>Escarpia</i> sp 3 JMP-2012	JN0212691
GenBank	Vestimentifera	<i>Escarpia</i> sp 4 JMP-2012	JN0212701
GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate AC601-S03-41	KC3573211
GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate DC673-S10-14	KC3573221

GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate DC673-S10-17	KC3573231
GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate DC673-S10-18	KC3573241
GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate DC673-S10-19	KC3573251
GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate DC673-S10-45	KC3573261
GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate DC673-S10-7	KC3573271
GenBank	Vestimentifera	<i>Escarpia laminata</i> isolate DC673-S10-9	KC3573281
GenBank	Vestimentifera	<i>Escarpia spicata</i> isolate TF4-S11-102	KC3573291
GenBank	Vestimentifera	<i>Escarpia spicata</i> isolate TF4-S11-103	KC3573301
GenBank	Vestimentifera	<i>Escarpia spicata</i> isolate TF4-S11-107	KC3573311
GenBank	Vestimentifera	<i>Escarpia spicata</i> isolate TF4-S11-92	KC3573321
GenBank	Vestimentifera	<i>Escarpia spicata</i> isolate TF4-S11-94	KC3573331
GenBank	Vestimentifera	<i>Escarpia southwardae</i> isolate Regab-S11-19	KC3573341
GenBank	Vestimentifera	<i>Escarpia southwardae</i> isolate Regab-S11-21	KC3573351
GenBank	Vestimentifera	<i>Escarpia southwardae</i> isolate Regab-S11-27	KC3573361
GenBank	Vestimentifera	<i>Escarpia southwardae</i> isolate Worm Hole-S11-35	KC3573371
GenBank	Vestimentifera	<i>Escarpia southwardae</i> isolate Worm Hole-S11-40	KC3573381
GenBank	Vestimentifera	<i>Escarpia southwardae</i> isolate Worm Hole-S11-43	KC3573391
GenBank	Vestimentifera	<i>Escarpia southwardae</i> isolate Worm Hole-S11-45	KC3573401
GenBank	Vestimentifera	<i>Escarpia southwardae</i> isolate Worm Hole-S11-47	KC3573411
GenBank	Vestimentifera	<i>Escarpia southwardae</i> isolate Worm Hole-S11-50	KC3573421
GenBank	Vestimentifera	<i>Escarpia southwardae</i> isolate Worm Hole-S11-58	KC3573431
GenBank	Vestimentifera	<i>Escarpia southwardae</i> isolate Baboon-S11-83	KC3573441
GenBank	Vestimentifera	<i>Escarpia southwardae</i> isolate Baboon-S11-62	KC8709531
GenBank	Vestimentifera	<i>Escarpia southwardae</i> isolate Baboon-S11-61	KC8709541
GenBank	Vestimentifera	<i>Escarpia southwardae</i> isolate Worm Hole-S11-37	KC8709551
GenBank	Vestimentifera	<i>Escarpia southwardae</i> isolate Worm Hole-S11-33	KC8709561
GenBank	Vestimentifera	<i>Escarpia southwardae</i> isolate Regab-S11-16	KC8709571
GenBank	Vestimentifera	<i>Escarpia southwardae</i> isolate Worm Hole-S11-31	KC8709581
GenBank	Vestimentifera	<i>Escarpia spicata</i> isolate TF4-S11-101	KC8709591
GenBank	Vestimentifera	<i>Escarpia spicata</i> isolate TF4-S11-110	KC8709601
GenBank	Vestimentifera	<i>Escarpia spicata</i> isolate TF4-S11-116	KC8709611
GenBank	Vestimentifera	<i>Lamellibrachia anaximandri</i> isolate Eratosthenes	KF1992561
GenBank	Vestimentifera	<i>Lamellibrachia anaximandri</i> isolate Palmachim 1	KF1992571
GenBank	Vestimentifera	<i>Lamellibrachia anaximandri</i> isolate Palmachim 2	KF1992581
GenBank	Vestimentifera	<i>Lamellibrachia anaximandri</i> isolate Palinuro 1	KF1992591
GenBank	Vestimentifera	<i>Lamellibrachia anaximandri</i> isolate Palinuro 2	KF1992601
GenBank	Vestimentifera	<i>Lamellibrachia anaximandri</i> isolate Palinuro 3	KF1992611
GenBank	Vestimentifera	<i>Riftia pachyptila</i>	U740531

GenBank	Vestimentifera	<i>Lamellibrachia barhami</i>	U740541
GenBank	Vestimentifera	<i>Lamellibrachia barhami</i>	U740551
GenBank	Vestimentifera	<i>Ridgeia</i> sp Southern Explorer Ridge	U740561
GenBank	Vestimentifera	<i>Ridgeia piscesae</i>	U740571
GenBank	Vestimentifera	<i>Lamellibrachia columna</i>	U740611
GenBank	Vestimentifera	<i>Escarpia laminata</i>	U740631
GenBank	Vestimentifera	<i>Escarpia spicata</i>	U740641
GenBank	Vestimentifera	<i>Escarpia spicata</i>	U740651
GenBank	Vestimentifera	<i>Oasisia alvinae</i>	U740691
GenBank	Vestimentifera	<i>Ridgeia piscesae</i>	U740731
GenBank	Vestimentifera	<i>Riftia pachyptila</i>	U740741
GenBank	Vestimentifera	<i>Tevnia jerichonana</i>	U740751
GenBank	Vestimentifera	<i>Basibranchia</i> sp Mariana Trough	U740781
GenBank	Vestimentifera	<i>Escarpia spicata</i>	U842621
GenBank	Vestimentifera	<i>Ridgeia piscesae</i>	U879751
GenBank	Vestimentifera	<i>Ridgeia piscesae</i>	U879761
GenBank	Vestimentifera	<i>Ridgeia piscesae</i>	U879771
GenBank	Vestimentifera	<i>Ridgeia piscesae</i>	U879781
GenBank	Vestimentifera	<i>Ridgeia piscesae</i>	U879791
GenBank	OUTGROUP (Siboglinidae)	<i>Pogonophora</i> sp Kushiro-SK-2003	D505982
GenBank	OUTGROUP (Siboglinidae)	<i>Osedax roseus</i>	JF5099491
GenBank	OUTGROUP (Siboglinidae)	<i>Sclerolinum brattstromi</i>	FJ3476441
GenBank	OUTGROUP (Siboglinidae)	<i>Sclerolinum contortum</i> Scon COI-1	FM1784801
GenBank	OUTGROUP (Siboglinidae)	Loihi Seamount perviate pogonophoran	U740681

Fig 1

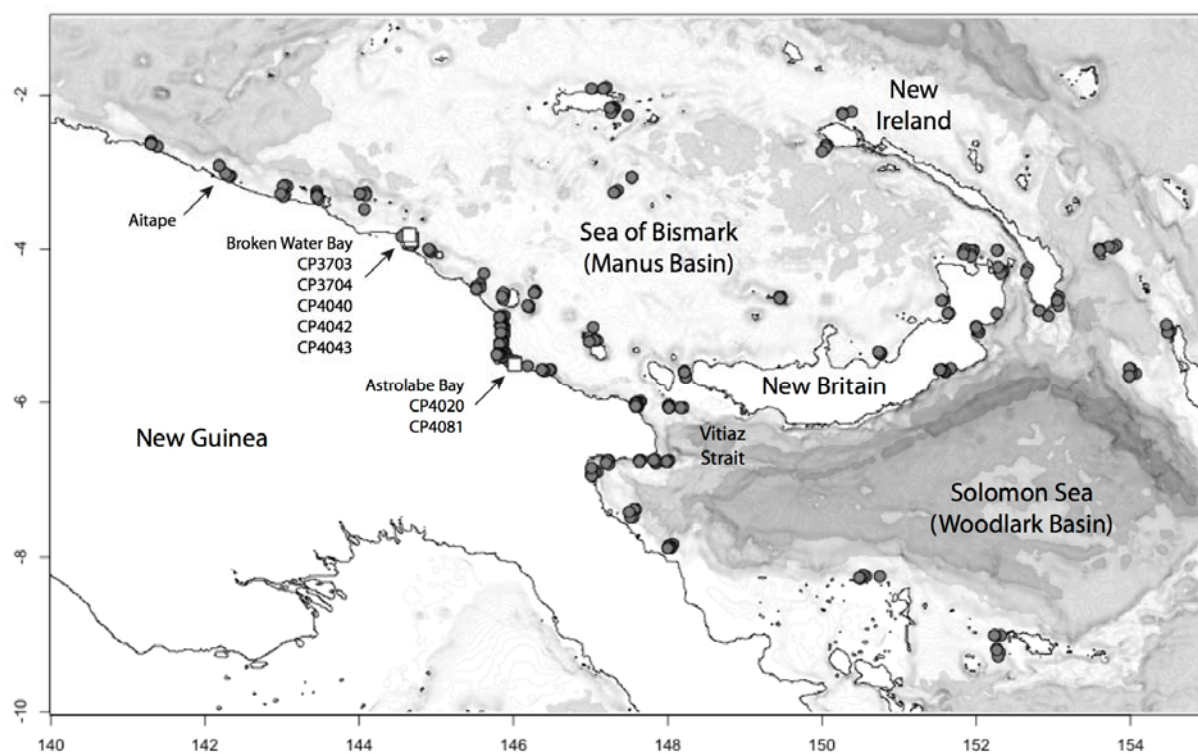


Fig 2

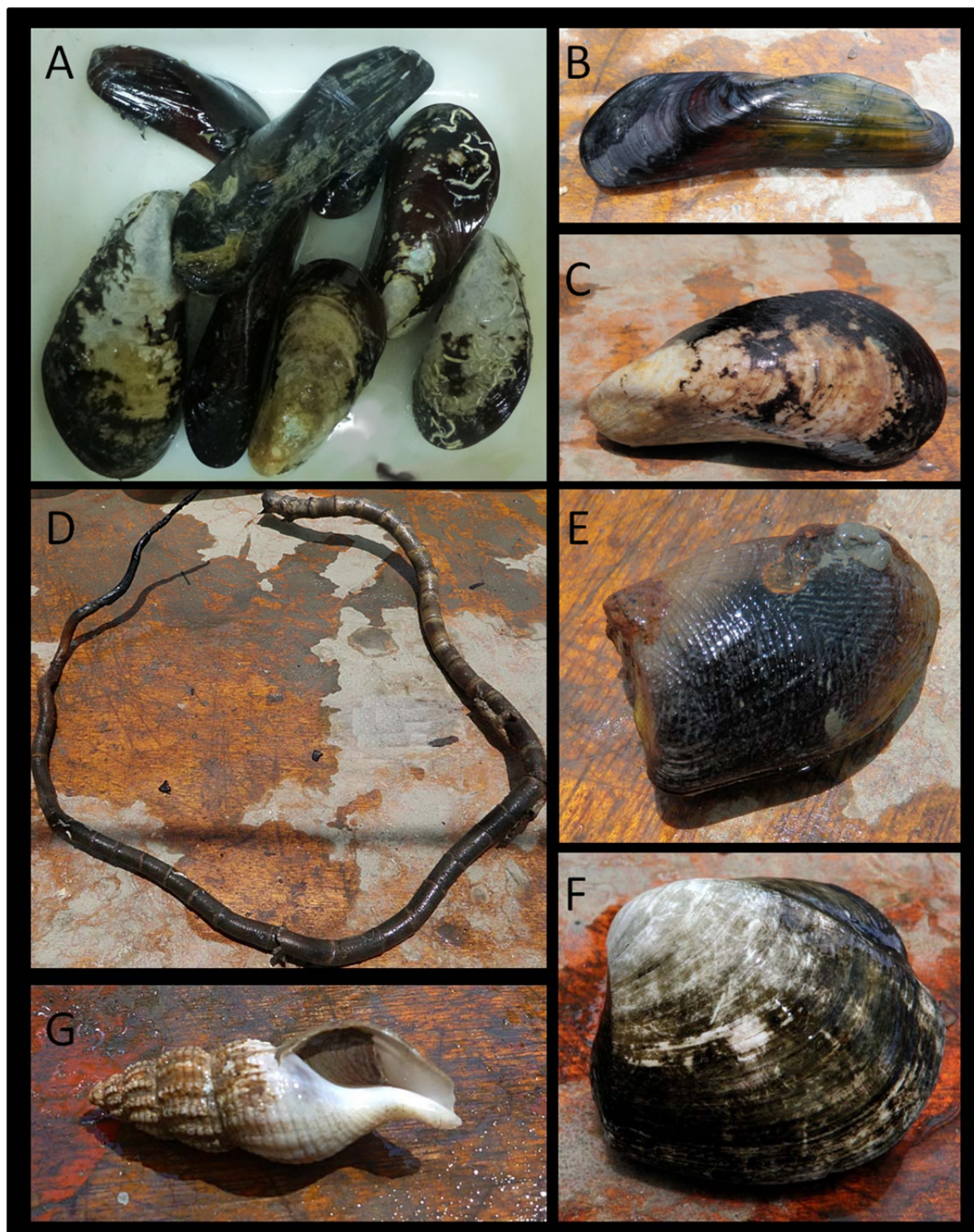


Fig 3

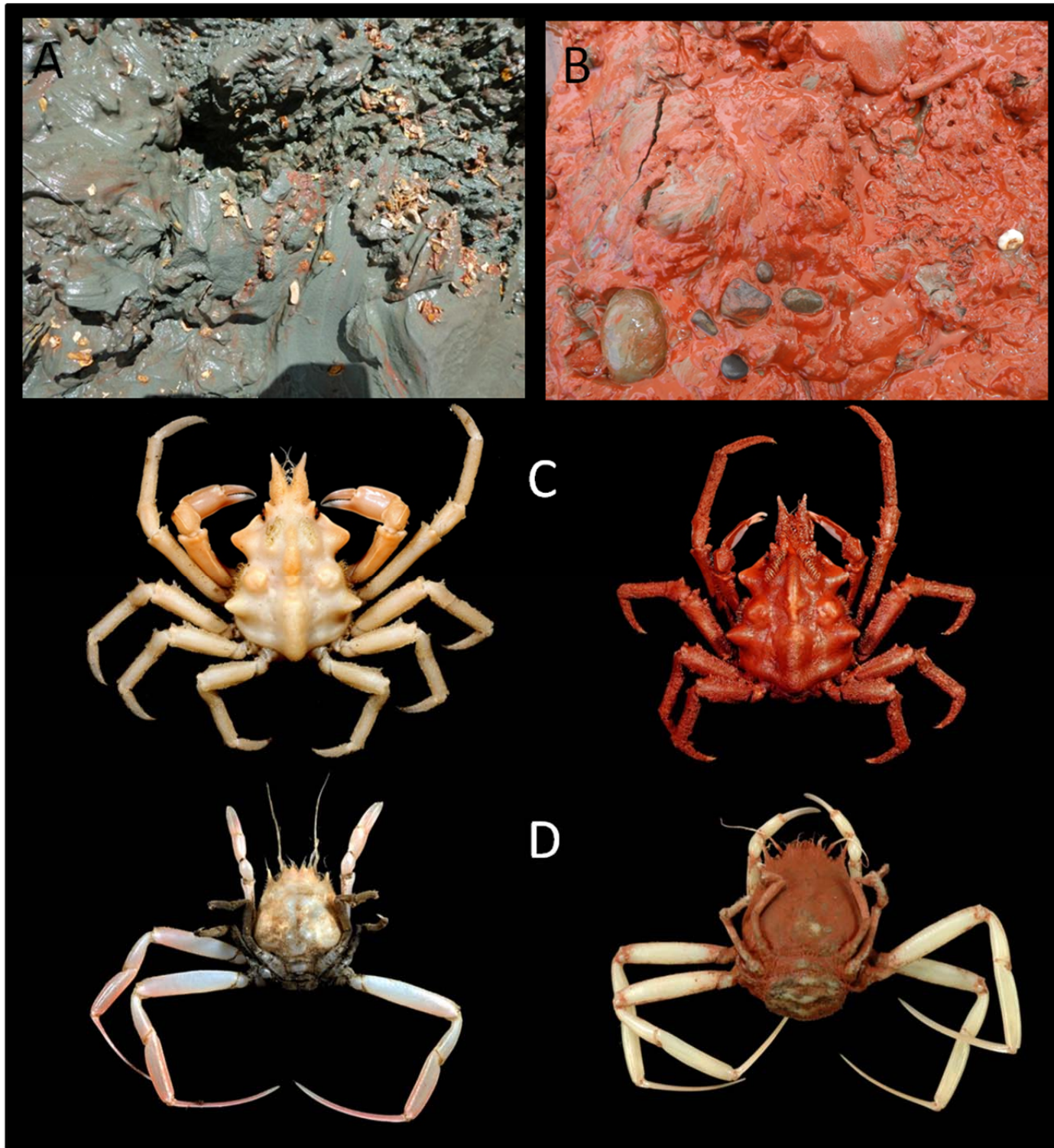


Fig 4

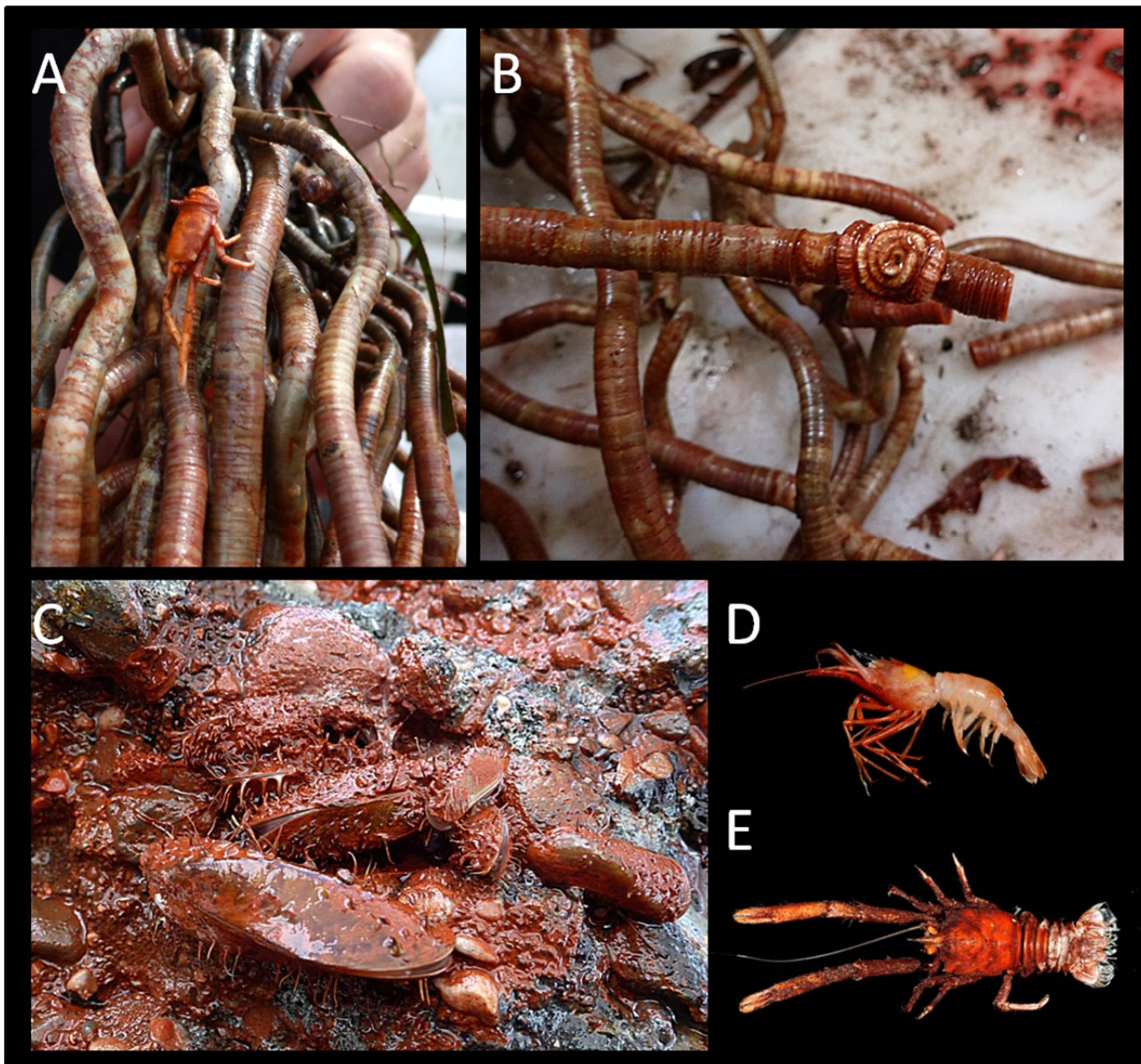


Fig 6

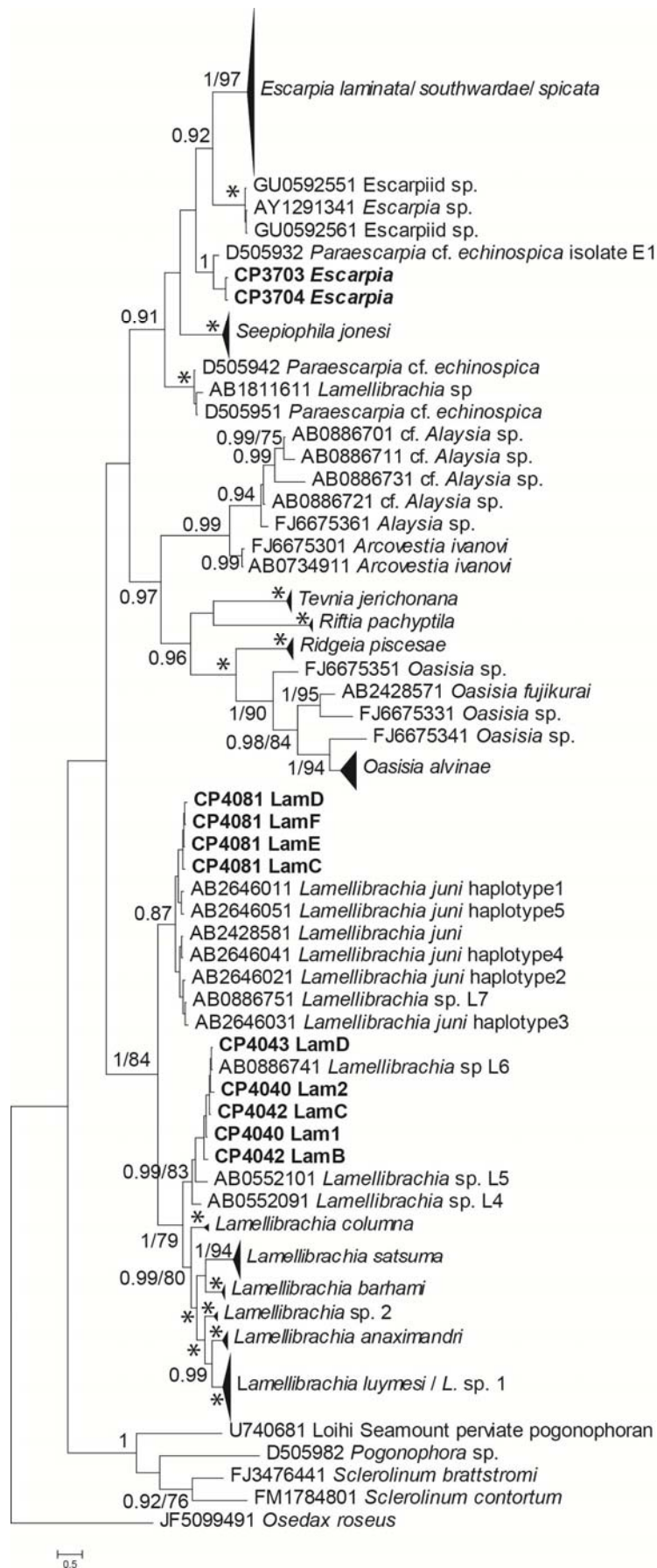


Figure 7

