

Supplementary material for:

Occurrence and recent long-distance dispersal of deep-sea hydrothermal vent shrimps

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Figure S1

Unrooted neighbour-joining phylogenetic tree of the crustacean decapods inferred from 18S rDNA sequences. The infraorder and common names are shown beside the tree. Numbers of each node represent bootstrap percentage values from neighbour-joining and maximum parsimony analyses, respectively. The bootstrap percentages less than 50% are not shown. Bar indicates 0.02 substitutions per site.

Figure S2

Multiple alignment of 870 bp nucleotide sequences of 18S rDNA among caridean shrimps. At least 15 indels are observed among the aligned sequences within caridean sequences and 817 unambiguously aligned positions with the corresponding sequences of other decapods were used for phylogenetic analyses.

Figure S3

Multiple alignment of 590 bp *COI* nucleotide sequences among *Alvinocaris* sp. of Sagami Bay, *A. longirostris* of the Hatoma Knoll haplotype 1 and 2 and *A. lusca* that has been reported from Galapagos Rift. *A. longirostris* *COI* haplotype 1 shows the identical nucleotide sequence to that of Sagami Bay, while the haplotype 2 reveals only two

nucleotide substitutions. On the other hand, both the haplotype 1 of *A. longirostris* and that of Sagami Bay revealed 4.9% differences (34 nucleotide substitutions) to the most closely related *A. lusca* (see figure 1b). For number of nucleotide substitutions or informative sites within the *COI* sequences of Bresiliidae, please refer to Shank *et al.* (1999).

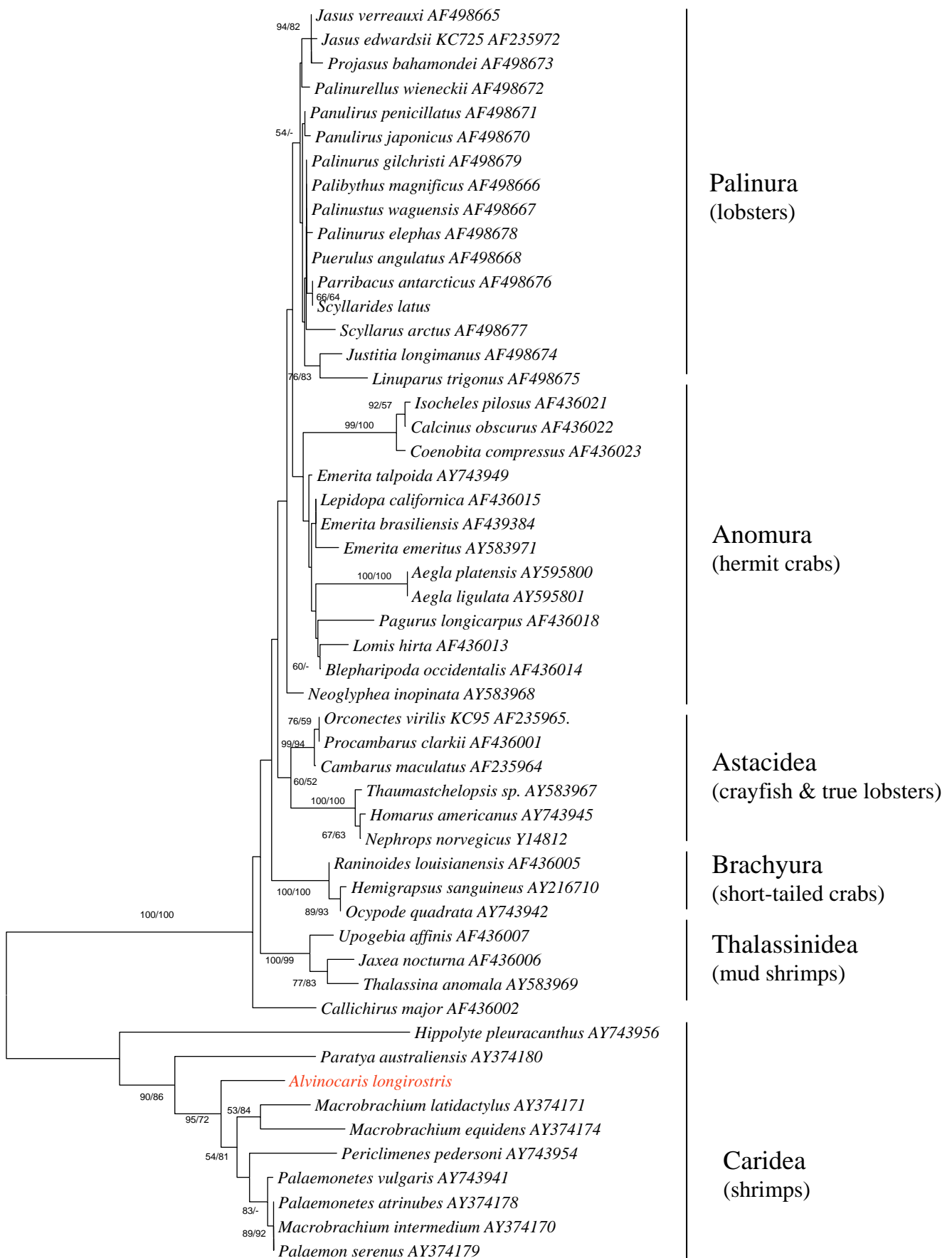


Figure S1

Haplotype2 TAGTTGGAAC TGCCCTTAGTCTCCTCATTGAGCAGAACTGGGCCAACAGGAAGACTTATTGGAAATGACCAAATTTACAATGTTATTGTCACCGCCCA
Haplotype1 TAGTTGGAAC TGCCCTTAGTCTCCTCATTGAGCAGAACTGGGCCAACAGGAAGACTTATTGGAAATGACCAAATTTACAATGTTATTGTCACCGCCCA
Sagami-Bay TAGTTGGAAC TGCCCTTAGTCTCCTCATTGAGCAGAACTGGGCCAACAGGAAGACTTATTGGAAATGACCAAATTTACAATGTTATTGTCACCGCCCA
A.lusca TAGTTGGGACTGCCCTTAGTCTCCTCATTGAGCAGAACTAGGTCAACCAGGAAGACTTATTGGAAATGACCAAATTTACAATGTTATTGTTACCTGCCA

Haplotype2 TGCCTTTGTCATAAATTTCTTTATAGTTATACCTATTATAATAGGTGGATTTGGAAATGACTACTTCCCTTATACTTGGTGCCCCAGATATAGCCTTC
Haplotype1 TGCCTTTGTCATAAATTTCTTTATAGTTATACCTATTATAATAGGTGGATTTGGAAATGACTACTTCCCTTATACTTGGTGCCCCAGATATAGCCTTC
Sagami-Bay TGCCTTTGTCATAAATTTCTTTATAGTTATACCTATTATAATAGGTGGATTTGGAAATGACTACTTCCCTTATACTTGGTGCCCCAGATATAGCCTTC
A.lusca TGCCTTTGTCATAAATTTCTTTATAGTATACCTATTATAATAGGTGGATTTGGAAATGACTACTTCCCTTATACTGGGTGCCCCAGATATAGCCTTT

Haplotype2 CCCCGAATAAATAACATAAGATTCTGGCTTCTCCCTCCCTCTCTCACCCTTCTACTCTCCAGAGGAATAGTAGAAAGGGGGGTGGGCAGGATGAAC TG
Haplotype1 CCCCGAATAAATAACATAAGATTCTGGCTTCTCCCTCCCTCTCTCACCCTTCTACTCTCCAGAGGAATAGTAGAAAGGGGGGTGGGCAGGATGAAC TG
Sagami-Bay CCCCGAATAAATAACATAAGATTCTGGCTTCTCCCTCCCTCTCTCACCCTTCTACTCTCCAGAGGAATAGTAGAAAGGGGGGTGGGCAGGATGAAC TG
A.lusca CCCCGAATAAATAACATAAGATTCTGACTCCTCCCCCTCCCTCAGCCTTCTACTCTCCAGAGGAATAGTAGAAAGGGGGGTGGGCAGGATGAAC TG

Haplotype2 TTTATCCACCGCTAGCAGCAGGAATTGCCACGCTGGAGCATCTGTTGACATAGCAATTTTTTCACTCCACCTTGCAGGAGTATCTTCAATCCTCGGTGC
Haplotype1 TTTATCCACCGCTAGCAGCAGGAATTGCCACGCTGGAGCATCTGTTGACATAGCAATTTTTTCACTCCACCTTGCAGGAGTATCTTCAATCCTCGGTGC
Sagami-Bay TTTATCCACCGCTAGCAGCAGGAATTGCCACGCTGGAGCATCTGTTGACATAGCAATTTTTTCACTCCACCTTGCAGGAGTATCTTCAATCCTCGGTGC
A.lusca TTTATCCGCCCCTAGCAGCGGGAATTGCTCAGCCGGAGCATCTGTTGACATAGCAATTTTTTTCGCTCCACCTTGCAGGAGTATCTTCAATCCTCGGTGC

Haplotype2 CGTCAATTTTATAACTACATGCATTAACATGCGAACAAAGAGGGATAACGATAGATCGTATGCCCTTTTTGTGTGATCAATTTTTTTAACGGCTATCCTA
Haplotype1 CGTCAATTTTATAACTACATGCATTAACATGCGAACAAAGAGGGATAACGATAGATCGTATGCCCTTTTTGTGTGATCAATTTTTTTAACGGCTATCCTA
Sagami-Bay CGTCAATTTTATAACTACATGCATTAACATGCGAACAAAGAGGGATAACGATAGATCGTATGCCCTTTTTGTGTGATCAATTTTTTTAACGGCTATCCTA
A.lusca CGTCAATTTTATAACCACATGCATTAATATGCGAACAAAGAGGGATAACGATAGATCGTATGCCCTTTTTGTGTGGTCAATTTTTTTAACGGCTATCCTA

Haplotype2 CTCCCTCTCTCACTCCCAGTTTTAGCAGGAGCTATTACCATACTACTAACAGATCGTAACCTTAATACTTCAATCTTTGACCCCTGCCGGGGGAGGGG
Haplotype1 CTCCCTCTCTCACTCCCAGTTTTAGCAGGAGCTATTACCATACTACTAACAGATCGTAACCTTAATACTTCAATCTTTGACCCCTGCCGGGGGAGGGG
Sagami-Bay CTCCCTCTCTCACTCCCAGTTTTAGCAGGAGCTATTACCATACTACTAACAGATCGTAACCTTAATACTTCAATCTTTGACCCCTGCCGGGGGAGGGG
A.lusca CTCCCTCTCTCCCTCCCAGTTTTAGCAGGAGCTATTACCATACTACTAACAGATCGTAACCTTAATACTTCAATCTTTGACCCCTGCCGGGGGAGGGG

Figure S3