

Table S1. Fraction of parsimony informative characters out of the total characters for each gene of the nucleotide and amino acid datasets. The three-outgroup analysis was with *Euphausia pacifica*, *Cymothoa indica*, and *Neomysis japonica*.

Gene	<i>Hemisquilla</i> Outgroup Nucleotide Dataset	<i>Hemisquilla</i> Outgroup Amino Acid/Nucleotide Dataset	3 Outgroups Nucleotide Dataset	3 Outgroups Amino Acid/Nucleotide Dataset
ATP6	0.414	0.133	0.481	0.259
ATP8	0.516	0.442	0.566	0.509
COX1	0.359	0.064	0.404	0.128
COX2	0.379	0.114	0.455	0.194
COX3	0.383	0.129	0.432	0.185
CYTB	0.385	0.079	0.451	0.203
ND1	0.423	0.140	0.480	0.244
ND2	0.518	0.347	0.614	0.490
ND3	0.433	0.168	0.504	0.267
ND4	0.439	0.195	0.527	0.326
ND4L	0.363	0.121	0.467	0.323
ND5	0.444	0.200	0.535	0.315
ND6	0.488	0.326	0.590	0.492

Table S2. Models used for each gene in the datasets for maximum likelihood analyses. The models were chosen by ModelTest-NG. The three-outgroup analysis was with *Euphausia pacifica*, *Cymothoa indica*, and *Neomysis japonica*.

Genes	<i>Hemisquilla</i> Outgroup Nucleotide Only Dataset	<i>Hemisquilla</i> Outgroup Amino Acid/Nucleotide Dataset	3 Outgroups Nucleotide Dataset	3 Outgroups Amino Acid/Nucleotide Dataset	<i>Euphausia</i> Outgroup Amino Acid/Nucleotide Dataset	<i>Neomysis</i> Outgroup Amino Acid/Nucleotide Dataset	<i>Cymothoa</i> Outgroup Amino Acid/Nucleotide Dataset
ATP6	TVM+I+G	MTMAM	TVM+I+G	MTMAM	MTMAM	MTMAM	MTMAM
ATP8	TPM3uf+I+G	MTREV	TPM3uf+I+G	MTREV	MTREV	MTREV	MTREV
COX1	TN93+I+G	MTZOA	TIM2+I+G	MTZOA	MTZOA	MTZOA	MTZOA
COX2	GTR+I+G	MTZOA	TVM+I+G	MTZOA	MTZOA	MTZOA	MTART
COX3	TPM2uf+I+G	MTZOA	TVM+I+G	MTZOA	MTZOA	MTZOA	MTZOA
CYTB	TPM2uf+I+G	MTZOA	TIM2+I+G	MTZOA	MTZOA	MTZOA	MTZOA
ND1	GTR+I+G	MTZOA	GTR+I+G	MTART	MTZOA	MTART	MTZOA
ND2	TIM2+I+G	MTZOA	GTR+I+G	MTMAM	MTZOA	MTZOA	MTMAM
ND3	TPM2uf+I+G	MTZOA	TIM2+I+G	MTMAM	MTMAM	MTZOA	MTMAM
ND4	GTR+I+G	MTZOA	GTR+I+G	MTZOA	MTZOA	MTZOA	MTZOA
ND4L	TVM+I+G	MTZOA	TPM3uf+G	MTZOA	MTZOA	MTZOA	MTZOA
ND5	GTR+I+G	MTZOA	GTR+I+G	MTZOA	MTZOA	MTZOA	MTZOA
ND6	GTR+I+G	MTMAM	GTR+I+G	MTREV	MTMAM	MTREV	MTREV
16S	TIM3+I+G	TIM3+I+G	TIM3+I+G	TIM3+I+G	TIM3+I+G	TIM3+I+G	TIM2+I+G
12S	TIM2+I+G	TIM2+I+G	TPM2uf+G	TPM2uf+G	TIM2+I+G	TPM2uf+I+G	TPM2uf+I+G
18S	TN93+I+G	TN93+I+G	TIM3+I+G	TIM3+I+G	TIM3+I+G	TN93+I+G	TN93+I+G

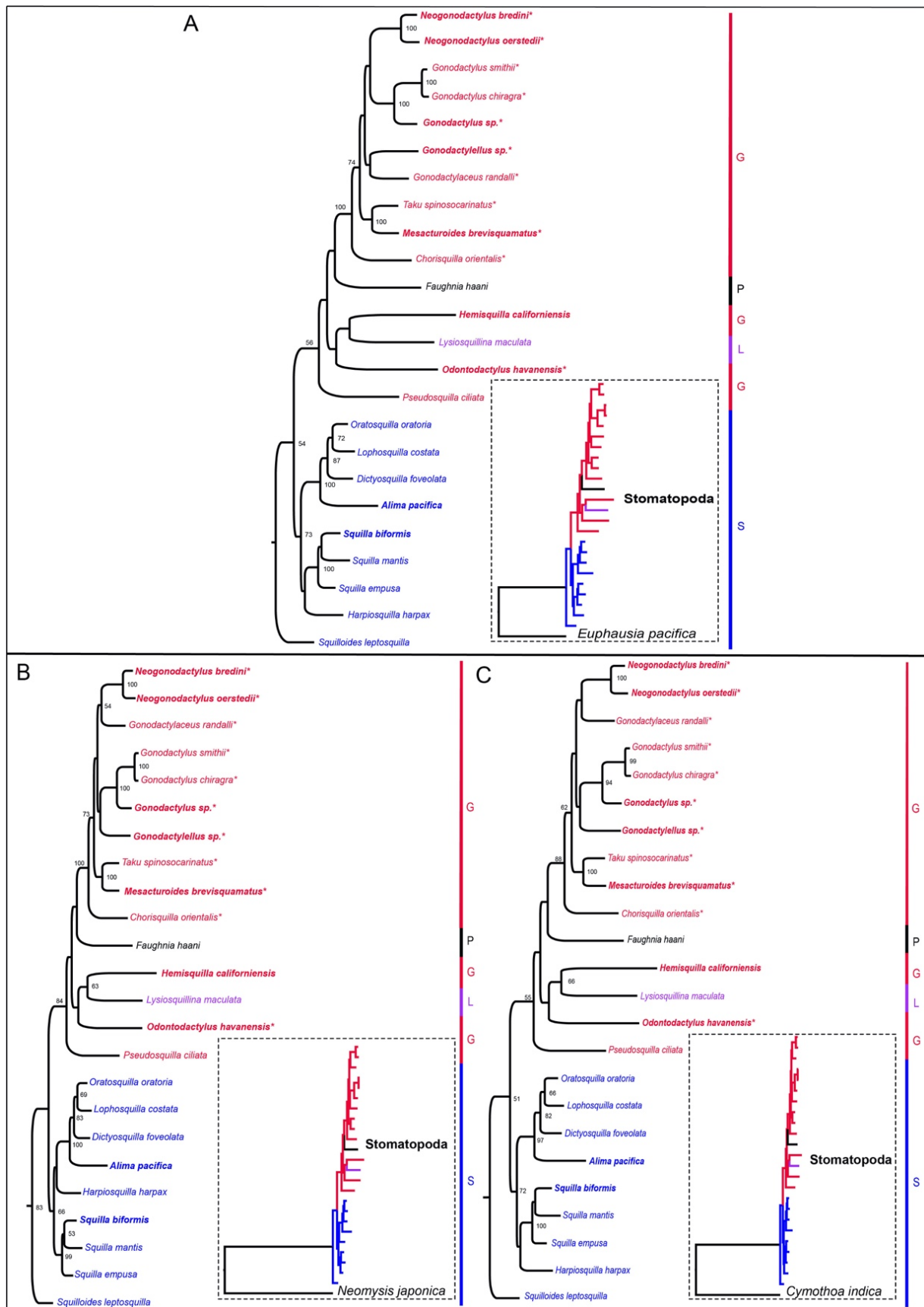


Figure S1. Stomatopoda phylogeny based on the concatenated mitochondrial genes and 18S rRNA sequences. Maximum likelihood tree topologies from the mixed amino acid and nucleotide dataset analysed with three different outgroups. Newly sequenced species are in bold. Each superfamily is coded by color of the taxon name. Superfamily abbreviations are G: Gonodactyloidea, L: Lysiosquilloidea, S: Squilloidea, P: Parasquilloidea. Asterisks in the taxon name denote smashers. Values at the nodes represent the bootstrap scores, blank if below 50. (A) *Euphausia pacifica* as outgroup (B) *Neomysis japonica* as outgroup. (C) *Cymothoa indica* as outgroup.