

Supplementary Materials: Table S1: Summary of copepods gut bacterial communities identified from *Acartia hudsonica*, *Sinocalanus tenellus*, and *Pseudodiaptomus inopinus* in each site., Table S2: Summary of (A) common species and (B) unique species of the gut-bacterial communities among/in the copepod species (*Acartia hudsonica*, *Sinocalanus tenellus*, and *Pseudodiaptomus inopinus*). Composition (%) was calculated based on the all species that make up the gut-bacterial community identified from the copepods we targeted., Table S3: Summary of (A) common species and (B) unique species of the copepods gut-bacterial communities among/in the sites 1, 2, and 3. Composition (%) was calculated based on the all species that make up the copepods gut bacterial community identified from the sites we studied.

Supplementary Materials Legends

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Table S2. Summary of (A) common species and (B) unique species of the gut-bacterial communities among/in the copepod species (*Acartia hudsonica*, *Sinocalanus tenellus*, and *Pseudodiaptomus inopinus*). Composition (%) was calculated based on the all species that make up the gut-bacterial community identified from the copepods we targeted.

Table S3. Summary of (A) common species and (B) unique species of the copepods gut-bacterial communities among/in Sites 1, 2 and 3. Composition (%) was calculated based on the all species that make up the copepods gut-bacterial community identified from the sites we studied.

Table S1. Summary of copepods gut bacterial communities identified from *Acartia hudsonica*, *Sinocalanus tenellus*, and *Pseudodiaptomus inopinus* in each site.

Sample	Bacterial community		Accession number	Identities (%)	Number of reads	
	Phylum	Species/Genus/Family				
<i>A. hudsonica</i>	Site 1	Firmicutes	<i>Bacillus velezensis</i>	NR_075005.2	99	25
		Proteobacteria	<i>Novosphingobium capsulatum</i>	NR_113591.1	98	752
			Rhodobacteraceae	NR_159237.1	89	725
			<i>Bradyrhizobium cytisi</i>	NR_116360.2	99	36
			Muribaculaceae	NR_144616.1	89	22
	Site 2	Bacteroidetes	<i>Sediminibacterium roseum</i>	NR_159130.1	97	93
		Proteobacteria	<i>Novosphingobium capsulatum</i>	NR_113591.1	98	6813
			Rhodobacteraceae	NR_159237.1	89	5799
			<i>Bradyrhizobium cytisi</i>	NR_116360.2	99	596
			Bacteroidetes	<i>Sediminibacterium roseum</i>	NR_159130.1	97
	Site 3	Proteobacteria	<i>Novosphingobium capsulatum</i>	NR_113591.1	98	524
			Rhodobacteraceae	NR_159237.1	89	671
			<i>Bradyrhizobium cytisi</i>	NR_116360.2	99	30
			Bacteroidetes	<i>Muribaculum</i> sp.	NR_144616.1	90
		Firmicutes	<i>Bacillus velezensis</i>	NR_075005.2	99	70
<i>S. tenellus</i>	Site 1	Proteobacteria	<i>Aeromonas hydrophila</i>	NR_074841.1	99	13024
			<i>Novosphingobium capsulatum</i>	NR_113591.1	98	24
			Rhodobacteraceae	NR_159237.1	89	27
			<i>Brevundimonas bullata</i>	NR_113611.1	99	79
			<i>Novosphingobium capsulatum</i>	NR_113591.1	98	36
	Site 2	Proteobacteria	Rhodobacteraceae	NR_159237.1	89	54
			<i>Bradyrhizobium cytisi</i>	NR_116360.2	99	2
		Planctomycetes	Pirellulaceae	NR_043384.1	85	7
	Site 3	Bacteroidetes	<i>Sporocytophaga</i> sp.	NR_025463.1	93	1546
			<i>Muribaculum</i> sp.	NR_144616.1	91	10

<i>P. inopinus</i>		Firmicutes	<i>Bacillus velezensis</i>	NR_075005.2	99	1005
			<i>Aeromonas hydrophila</i>	NR_074841.1	99	369
		Proteobacteria	<i>Novosphingobium capsula-</i> <i>tum</i>	NR_113591.1	98	94
			Rhodobacteraceae	NR_159237.1	89	153
			<i>Phaselicystis</i> sp.	NR_044523.1	90	970
			<i>Bradyrhizobium cytisi</i>	NR_116360.2	99	3
			<i>Novosphingobium capsula-</i> <i>tum</i>	NR_113591.1	98	11
	Site 1	Proteobacteria	Rhodobacteraceae	NR_159237.1	89	25
			<i>Bradyrhizobium cytisi</i>	NR_116360.2	99	1
			<i>Brevundimonas denitrifi-</i> <i>cans</i>	NR_133989.1	99	373
			<i>Brevundimonas bullata</i>	NR_113611.1	99	8
				Bacteroidetes	<i>Polaribacter</i> sp.	NR_153703.1
			<i>Sediminibacterium roseum</i>	NR_159130.1	97	1
	Site 2	Proteobacteria	<i>Novosphingobium capsula-</i> <i>tum</i>	NR_113591.1	98	12
			Rhodobacteraceae	NR_159237.1	89	12
		Planctomycetes	Pirellulaceae	NR_043384.1	85	1
		Bacteroidetes	<i>Polaribacter</i> sp.	NR_153703.1	95	82
	Site 3	Proteobacteria	<i>Novosphingobium capsula-</i> <i>tum</i>	NR_113591.1	98	958
			Rhodobacteraceae	NR_159237.1	89	1131
			<i>Bradyrhizobium cytisi</i>	NR_116360.2	99	110
			<i>Hydrogenophaga taeniospi-</i> <i>ralis</i>	NR_114131.1	99	13
		Planctomycetes	Pirellulaceae	NR_043384.1	85	32

Table S2. Summary of (A) common species and (B) unique species of the gut-bacterial communities among/in the copepod species (*Acartia hudsonica*, *Sinocalanus tenellus*, and *Pseudodiaptomus inopinus*). Composition (%) was calculated based on the all species that make up the gut-bacterial community identified from the copepods we targeted.

Sample		Bacterial species		
		Phylum	Class	Family/Genus/Species
(A) Common species	Bacteroidetes	Bacteroidia	Muribaculaceae	3.56
		Chitinophagia	<i>Sediminibacterium roseum</i>	0.43
		Flavobacteriia	<i>Sporocytophaga</i> sp.	2.98
	Firmicutes	Bacilli	<i>Bacillus velezensis</i>	2.14
	Planctomycetes	Planctomycetia	Pirellulaceae	0.03
	Proteobacteria	Alphaproteobacteria	<i>Brevundimonas bullta</i>	0.16
			<i>Bradyrhizobium cytisi</i>	2.61
			Rhodobacteraceae	28.49
			<i>Novosphingobium capsulatum</i>	31.53
		Deltaproteobacteria	<i>Phaselicystis</i> sp.	1.87
		Gammaproteobacteria	<i>Aeromonas hydrophila</i>	35.08
(B) Unique species	<i>A. hudsonica</i>	There is no unique bacterial species.		
	<i>S. tenellus</i>	There is no unique bacterial species.		
	<i>P. inopinus</i>	Bacteroidetes	Flavobacteriia	<i>Polaribacter</i> sp.
Proteobacteria		Alphaproteobacteria	<i>Brevundimonas denitrificans</i>	0.24
		Betaproteobacteria	<i>Hydrogenophaga taeniospiralis</i>	0.01

Table S3. Summary of (A) common species and (B) unique species of the copepods gut-bacterial communities among/in Sites 1, 2 and 3. Composition (%) was calculated based on the all species that make up the copepods gut-bacterial community identified from the sites we studied.

Sample	Bacterial species			Composition (%)	
	Phylum	Class	Family/Genus/Species		
(A) Common species	Bacteroidetes	Bacteroidia	Muribaculaceae	4.78	
		Chitinophagia	<i>Sediminibacterium roseum</i>	0.29	
		Flavobacteriia	<i>Polaribacter</i> sp.	0.32	
	Firmicutes	Bacilli	<i>Bacillus velezensis</i>	2.88	
	Planctomycetes	Planctomycetia	Pirellulaceae	0.10	
	Proteobacteria	Alphaproteobacteria	<i>Bradyrhizobium cytisi</i>	2.04	
			Rhodobacteraceae	22.52	
			<i>Novosphingobium capsulatum</i>	24.16	
		Gammaproteobacteria	<i>Aeromonas hydrophila</i>	35.08	
(B) Unique species	Site 1	Proteobacteria	Alphaproteobacteria	<i>Brevundimonas bullata</i>	0.23
				<i>Brevundimonas denitrificans</i>	0.98
	Site 2	There is no unique bacterial species.			
	Site 3	Bacteroidetes	Cytophagia	<i>Sporocytophaga</i> sp.	4.05
		Proteobacteria	Deltaproteobacteria	<i>Phaselicystis</i> sp.	2.54
	Betaproteobacteria		<i>Hydrogenophaga taeniospiralis</i>	0.03	