

Possible links between white plague-like disease, scleractinian corals, and a cryptochirid gall crab

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Table S1. Read abundance, quality statistics, and Shannon-Weiner Index (based upon class) for all samples

Sample	Number of raw reads per Ion 316 Chip	Quality reads (QC > 20) per barcode		Quality reads determined by MG-RAST QC		% GC	Number of ribosomal reads (from Column 3)	Shannon-Weiner index
		Number	Avg. length (bp)	Number	Avg. length (bp)			
Crab	2837430	593337	256 ± 97	527016	189 ± 83	47 ± 9	330619	0.846
Crab lesion		1026498	268 ± 94	878049	188 ± 85	49 ± 10	639497	0.822
Lesion		1156475	251 ± 104	985678	191 ± 87	49 ± 9	669679	0.805
Total		2776310	258 (avg.)	2390743	189 (avg.)	48 (avg.)	1639795	0.824 (avg.)

Table S2. OTUs of interest from four bacterial communities: the Chryptochiridae gall crab (crab), lesions caused by the crab (crab lesion), lesions caused by possible white plague (disease lesion), and apparently healthy *D. labyrinthiformis*, manually curated from the MG-RAST read table

Class	Order	Family	Genus and species	Meta-genome	% Abundance	Avg. e-value	Avg. ident. (%)
Actinobacteria	Actinomycetales	Kineosporiaceae	<i>Kineococcus radiotolerans</i>	Apparently healthy	3.20	-7.93	72.64
Actinobacteria	Actinomycetales	Kineosporiaceae	<i>Kineococcus radiotolerans</i>	Crab	1.20	-6.86	72.26
Actinobacteria	Actinomycetales	Kineosporiaceae	<i>Kineococcus radiotolerans</i>	Crab lesion	1.00	-9.76	69.98
Actinobacteria	Actinomycetales	Kineosporiaceae	<i>Kineococcus radiotolerans</i>	Disease lesion	1.23	-7.3	74.11
Cyanobacteria	Oscillatoriales	unclassified (derived from Oscillatoriiales)	<i>Trichodesmium erythraeum</i>	Apparently healthy	1.71	-7.88	70.94
Cyanobacteria	Oscillatoriales	unclassified (derived from Oscillatoriiales)	<i>Trichodesmium erythraeum</i>	Crab	0.04	-10.3	70.49
Cyanobacteria	Oscillatoriales	unclassified (derived from Oscillatoriiales)	<i>Trichodesmium erythraeum</i>	Crab lesion	0.13	-5.01	84.69
Cyanobacteria	Oscillatoriales	unclassified (derived from Oscillatoriiales)	<i>Trichodesmium erythraeum</i>	Disease lesion	0.04	-51.55	97.59
Bacilli	Lactobacillales	Lactobacillaceae	<i>Lactobacillus vaginalis</i>	Apparently healthy	20.47	-5.51	86.4
Bacilli	Lactobacillales	Lactobacillaceae	<i>Lactobacillus vaginalis</i>	Crab	12.13	-5.64	84.74
Bacilli	Lactobacillales	Lactobacillaceae	<i>Lactobacillus vaginalis</i>	Crab lesion	8.55	-6.23	86.24
Bacilli	Lactobacillales	Lactobacillaceae	<i>Lactobacillus vaginalis</i>	Disease lesion	8.33	-5.88	83.71
Clostridia	Clostridiales	Syntrophomonadaceae	<i>Dethiobacter alkaliphilus</i>	Apparently healthy	15.35	-5.47	78.34
Clostridia	Clostridiales	Syntrophomonadaceae	<i>Dethiobacter alkaliphilus</i>	Crab	4.89	-5.18	78.23
Clostridia	Clostridiales	Syntrophomonadaceae	<i>Dethiobacter alkaliphilus</i>	Crab lesion	4.98	-5.21	78.25
Clostridia	Clostridiales	Syntrophomonadaceae	<i>Dethiobacter alkaliphilus</i>	Disease lesion	1.17	-15.21	80.23
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Dinoroseobacter shibae</i>	Crab	1.75	-47.34	95.94
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Dinoroseobacter shibae</i>	Crab lesion	0.48	-19.92	83.38
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Dinoroseobacter shibae</i>	Disease lesion	1.98	-35.62	89.02
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Rhodobacter sphaeroides</i>	Crab	1.88	-39.63	92.44
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Rhodobacter sphaeroides</i>	Crab lesion	0.75	-19.87	85.75
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Rhodobacter sphaeroides</i>	Disease lesion	4.99	-43.85	89.31
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Roseobacter denitrificans</i>	Crab	4.83	-62.02	97.24

Class	Order	Family	Genus and species	Meta-genome	% Abundance	Avg. e-value	Avg. ident. (%)
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Roseobacter denitrificans</i>	Crab lesion	5.96	-50.01	93.5
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Roseobacter denitrificans</i>	Disease lesion	9.03	-68.66	98.05
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Roseobacter litoralis</i>	Crab	0.22	-22.75	70.58
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Roseobacter litoralis</i>	Crab lesion	0.19	-32.08	85.94
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Roseobacter litoralis</i>	Disease lesion	0.07	-19.57	87.13
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Roseobacter sp. AzwK-3b</i>	Crab	0.13	-7.31	73.66
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Roseobacter sp. AzwK-3b</i>	Crab lesion	3.84	-58.46	97.62
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Roseobacter sp. AzwK-3b</i>	Disease lesion	0.62	-38.29	89.42
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Roseobacter sp. BS90</i>	Disease lesion	0.06	-49.72	95.93
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Roseobacter sp. CCS2</i>	Crab	1.20	-43.99	95.22
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Roseobacter sp. CCS2</i>	Crab lesion	0.01	-8.14	65.36
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Roseobacter sp. CCS2</i>	Disease lesion	0.65	-46.34	93.5
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Roseobacter sp. COLSP</i>	Crab	0.05	-20.48	91.61
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Roseobacter sp. COLSP</i>	Crab lesion	0.04	-15.36	92.92
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Roseobacter sp. COLSP</i>	Disease lesion	0.09	-17.1	94.2
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Roseobacter sp. GAI101</i>	Crab	1.74	-35.24	91.2
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Roseobacter sp. GAI101</i>	Crab lesion	0.04	-26.67	88.21
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Roseobacter sp. GAI101</i>	Disease lesion	0.01	-13.1	78.8
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Roseobacter sp. MED193</i>	Crab	0.28	-9.25	68.91
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Roseobacter sp. MED193</i>	Crab lesion	0.16	-20.69	82.3
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Roseobacter sp. MED193</i>	Disease lesion	0.09	-13.14	87.08
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Roseobacter sp. SK209-2-6</i>	Crab lesion	0.09	-18.85	75.34
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Roseobacter sp. SK209-2-6</i>	Disease lesion	0.01	-15.67	83.8
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Roseobacter sp. SYOPI</i>	Crab	0.06	-49.72	95.93
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Roseobacter sp. SYOP2</i>	Disease lesion	0.06	-49.72	95.93
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Roseovarius sp.</i>	Disease lesion	0.00	-24	94.55
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Roseovarius nubinhibens</i>	Crab	0.61	-11.96	85.32
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Roseovarius nubinhibens</i>	Crab lesion	0.14	-19.97	87.95
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Roseovarius nubinhibens</i>	Disease lesion	0.13	-15.3	86.62
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Roseovarius sp. 217</i>	Crab	0.24	-9.25	90.91
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Roseovarius sp. 217</i>	Crab lesion	1.15	-44.8	89.61
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Roseovarius sp. 217</i>	Disease lesion	0.40	-25.4	85.37
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Roseovarius sp. TM1035</i>	Crab	0.12	-9.4	71.79
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Roseovarius sp. TM1035</i>	Crab lesion	0.33	-14.07	79.55
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Roseovarius sp. TM1035</i>	Disease lesion	0.04	-12.04	78.22
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Ruegeria lacuscaerulensis</i>	Crab	0.14	-18.11	82.33
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Ruegeria lacuscaerulensis</i>	Crab lesion	2.58	-17.71	92.17
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Ruegeria lacuscaerulensis</i>	Disease lesion	0.23	-23.68	90.96
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Ruegeria pomeroyi</i>	Crab	0.25	-17.68	79.58

Class	Order	Family	Genus and species	Meta-genome	% Abundance	Avg. e-value	Avg. ident. (%)
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Ruegeria pomeroyi</i>	Crab lesion	1.50	-22.4	86.43
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Ruegeria pomeroyi</i>	Disease lesion	0.58	-17.22	83.97
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Ruegeria sp. PR1b</i>	Disease lesion	0.00	-19.5	86.26
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Ruegeria sp. R11</i>	Crab	0.10	-25.15	86.24
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Ruegeria sp. R11</i>	Crab lesion	0.04	-23.33	79.98
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Ruegeria sp. R11</i>	Disease lesion	0.06	-28.65	85.09
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Ruegeria sp. TM1040</i>	Crab	1.01	-15.84	84.45
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Ruegeria sp. TM1040</i>	Crab lesion	5.33	-20.4	91.06
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Ruegeria sp. TM1040</i>	Disease lesion	0.49	-25.32	83.06
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Silicibacter sp. TrichCH4B</i>	Crab	0.05	-13.58	82.72
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Silicibacter sp. TrichCH4B</i>	Crab lesion	0.70	-32.09	97.55
Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Silicibacter sp. TrichCH4B</i>	Disease lesion	0.03	-16.17	76.76
Deltaproteobacteria	Syntrophobacterales	Syntrophaceae	<i>Syntrophus aciditrophicus</i>	Apparently healthy	5.33	-5.95	70.66
Deltaproteobacteria	Syntrophobacterales	Syntrophaceae	<i>Syntrophus aciditrophicus</i>	Crab	3.54	-5.75	72.04
Deltaproteobacteria	Syntrophobacterales	Syntrophaceae	<i>Syntrophus aciditrophicus</i>	Crab lesion	0.81	-5.65	71.15
Deltaproteobacteria	Syntrophobacterales	Syntrophaceae	<i>Syntrophus aciditrophicus</i>	Disease lesion	0.74	-6.02	75.43
Gammaproteobacteria	unclassified (derived from Gammaproteobacteria)	unclassified (derived from Gammaproteobacteria)	<i>Reinekea blandensis</i>	Apparently healthy	17.48	-6.99	82.06
Gammaproteobacteria	unclassified (derived from Gammaproteobacteria)	unclassified (derived from Gammaproteobacteria)	<i>Reinekea blandensis</i>	Crab	14.11	-10.74	80.75
Gammaproteobacteria	unclassified (derived from Gammaproteobacteria)	unclassified (derived from Gammaproteobacteria)	<i>Reinekea blandensis</i>	Crab lesion	10.39	-16.51	81.9
Gammaproteobacteria	unclassified (derived from Gammaproteobacteria)	unclassified (derived from Gammaproteobacteria)	<i>Reinekea blandensis</i>	Disease lesion	10.01	-11.51	78.59
Gammaproteobacteria	Vibrionales	Vibrionaceae	<i>Vibrio alginolyticus</i>	Crab lesion	0.00	-5	64.71
Gammaproteobacteria	Vibrionales	Vibrionaceae	<i>Vibrio brasiliensis</i>	Crab lesion	0.00	-29	98.33
Gammaproteobacteria	Vibrionales	Vibrionaceae	<i>Vibrio cholerae</i>	Crab	0.00	-21	76.81
Gammaproteobacteria	Vibrionales	Vibrionaceae	<i>Vibrio cholerae</i>	Crab lesion	0.03	-18.42	70.71
Gammaproteobacteria	Vibrionales	Vibrionaceae	<i>Vibrio cholerae</i>	Disease lesion	0.00	-16	83.96
Gammaproteobacteria	Vibrionales	Vibrionaceae	<i>Vibrio diazotrophicus</i>	Disease lesion	0.01	-32	95.46
Gammaproteobacteria	Vibrionales	Vibrionaceae	<i>Vibrio furnissii</i>	Crab lesion	0.00	-7	66.67
Gammaproteobacteria	Vibrionales	Vibrionaceae	<i>Vibrio harveyi</i>	Crab	0.01	-11.93	96.67
Gammaproteobacteria	Vibrionales	Vibrionaceae	<i>Vibrio harveyi</i>	Crab lesion	1.66	-7.12	79.46
Gammaproteobacteria	Vibrionales	Vibrionaceae	<i>Vibrio harveyi</i>	Disease lesion	0.06	-7.01	80.38
Gammaproteobacteria	Vibrionales	Vibrionaceae	<i>Vibrio orientalis</i>	Crab	0.00	-7	69.23
Gammaproteobacteria	Vibrionales	Vibrionaceae	<i>Vibrio orientalis</i>	Crab lesion	0.01	-5	70
Gammaproteobacteria	Vibrionales	Vibrionaceae	<i>Vibrio parahaemolyticus</i>	Crab	0.24	-15.33	77.38
Gammaproteobacteria	Vibrionales	Vibrionaceae	<i>Vibrio parahaemolyticus</i>	Crab lesion	1.67	-15.5	84.99
Gammaproteobacteria	Vibrionales	Vibrionaceae	<i>Vibrio parahaemolyticus</i>	Disease lesion	0.06	-8.66	87.45
Gammaproteobacteria	Vibrionales	Vibrionaceae	<i>Vibrio sp.</i>	Crab lesion	0.01	-19.75	76.17
Gammaproteobacteria	Vibrionales	Vibrionaceae	<i>Vibrio sp. MED222</i>	Disease lesion	0.00	-12	74
Gammaproteobacteria	Vibrionales	Vibrionaceae	<i>Vibrio sp. RC586</i>	Crab lesion	0.01	-19.75	76.17
Gammaproteobacteria	Vibrionales	Vibrionaceae	<i>Vibrio splendidus</i>	Crab lesion	0.00	-19	60.53
Gammaproteobacteria	Vibrionales	Vibrionaceae	<i>Vibrio splendidus</i>	Disease lesion	0.00	-12	74
Gammaproteobacteria	Vibrionales	Vibrionaceae	<i>Vibrio vulnificus</i>	Crab lesion	0.03	-11.99	81.34
Gammaproteobacteria	Vibrionales	Vibrionaceae	<i>Vibrio vulnificus</i>	Disease lesion	0.00	-8	82.38