

**Supplemental Tables S1-S2 and Figures S1-S2**

	<i>Elysia rufescens</i>			Mucus	
	ER1	ER2	ER3	M1	M2
<b>Number of Sequences w/o chloroplast</b>	4727	9108	803	6528	1539
<b>Number of OTUs</b>	485	650	168	1551	406
<b>Chao Estimator</b>	5339	6961	863	11605	3069
<b>Shannon Indices</b>	1.9	1.6	3.1	4.1	3.9
<b>Good's Coverage Estimator</b>	91%	93%	83%	79%	77%

Table S1. Number of 16S rRNA gene pyrosequences analyzed, the number of OTUs observed, and richness estimators from three individuals of *E. rufescens* and two replicate of its mucus at 3% clustering (distance 0.03).

	<i>E. rufescens</i>		
	Isolates & Clones	Isolates & Pyrosequences	Clones & Pyrosequences
<b>Shared OTUs</b>	1	2	5
<b>Classification of OTUs</b>	<u><i>γ-Proteobacteria</i></u> <i>Vibrio</i> sp.	<u><i>γ-Proteobacteria</i></u> <i>Vibrio</i> sp.	<u>4 <i>γ-Proteobacteria</i></u> 2 <i>Vibrio</i> sp. <i>Neptunomonas</i> sp. <i>Methylophaga</i> sp. <u><i>Tenericutes</i></u> <i>Mycoplasma</i> sp.
	<b>Mucus</b>		
	Isolates & Clones	Isolates & Pyrosequences	Clones & Pyrosequences
<b>Shared OTUs</b>	2	7	11
<b>Classification of OTUs</b>	<u>2 <i>γ-Proteobacteria</i></u> <i>Vibrio</i> sp.	<u><i>γ-Proteobacteria</i></u> 5 <i>Vibrio</i> sp. <i>Listonella</i> sp. <i>Photobacterium</i> sp.	<u>5 <i>γ-Proteobacteria</i></u> 3 <i>Vibrio</i> sp. <i>Neptunomonas</i> sp. <i>Methylophaga</i> sp. 2 <u><i>α-Proteobacteria</i></u> <i>Kiloniella</i> sp. <u>2 <i>Spirochaetes</i></u> <i>Exilispira</i> sp. <u><i>Chlamydia</i></u> <i>Simkania</i> sp. <u><i>Tenericutes</i></u> <i>Mycoplasma</i> sp.
<b><i>E. rufescens</i> and Mucus Pyrosequences</b>			
<b>Shared OTUs</b>	92		
<b>Classification of OTUs</b>	<u>27 <i>Tenericutes</i></u> <i>Mycoplasma</i> sp.  <u><i>Epsilonproteobacteria</i></u> <i>Helicobacter</i> sp. <u><i>Actinobacteria</i></u> <i>Rothia</i> sp. <u><i>Chlamydiae</i></u> <i>Simkania</i> sp. <u><i>Betaproteobacteria</i></u> <i>Neisseria</i> sp. <u><i>Fusobacteria</i></u> <i>Streptobacillus</i> sp. <u><i>Chrysiogenetes</i></u> <i>Chrysiogenes</i> sp.	20 <u><i>γ-Proteobacteria</i></u> 8 <i>Vibrio</i> sp. 5 <i>Neptunomonas</i> sp. 2 <i>Methylophaga</i> sp. <i>Teredinibacter</i> sp. 2 <i>Celerinatantimonas</i> sp. <i>Psychrosphaera</i> sp. <i>Cycloclasticus</i> sp.  13 <u><i>Firmicutes</i></u> 6 <i>Streptococcus</i> sp. 2 <i>Gemella</i> sp. 2 <i>Bulleidia</i> sp. <i>Oribacterium</i> <i>Oscillibacter</i> sp. <i>Veillonella</i> sp.	13 <u><i>α-Proteobacteria</i></u> 8 <i>Kiloniella</i> sp. 4 <i>Pseudorhodobacter</i> sp. <i>Hellea</i> sp.  4 <u><i>Bacteroidetes</i></u> 3 <i>Prevotella</i> sp. <i>Anaerorhabdus</i> sp.  5 <u><i>Spirochaetes</i></u> 4 <i>Exillispira</i> sp. <i>Turneriella</i> sp.

Table S2. Table summary of classification of shared OTUs between samples at 3% OTUs (distance = 0.03). Phyla and classes are underlined and species names are listed below.

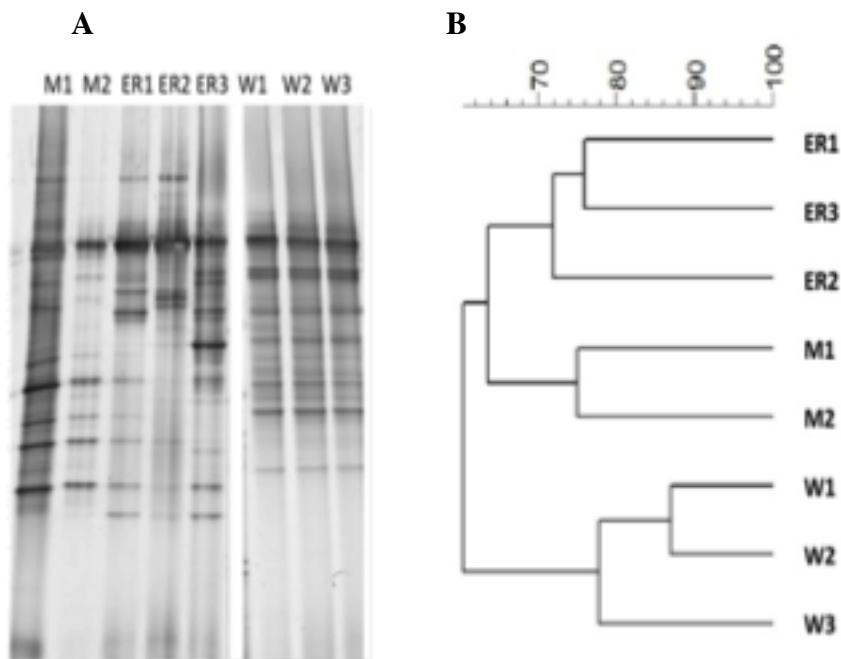


Figure S1. Bionumeric analysis of Denature Gradient Gel Electrophoresis (DGGE). Shown are the DGGE fingerprints of the bacterial communities associated with *E. rufescens* (ER1-ER3), secreted mucus from *E. rufescens* (M1, M2), and surrounding seawater samples (W1-W3) (A). UPGMA dendrogram showing clustering of normalized DGGE (B).

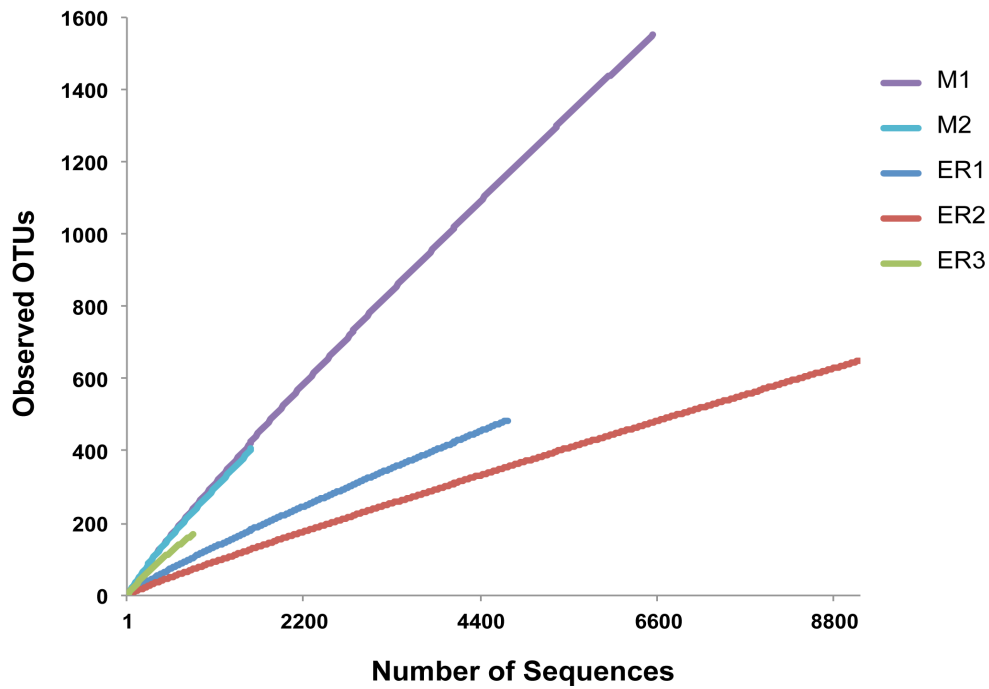


Figure S2. Rarefaction curves for *E. rufescens* and its mucus. Shown are rarefaction curves for the 16S rRNA gene sequences from *E. rufescens* (ER1, ER2, ER3) and secreted mucus from *E. rufescens* (M1 and M2) at the 3% OTUs (distance = 0.03).