Supplementary Materials

Unique Skin Microbiome: Insights to Understanding Bacterial Symbionts in Octopuses

Authors and Affiliations
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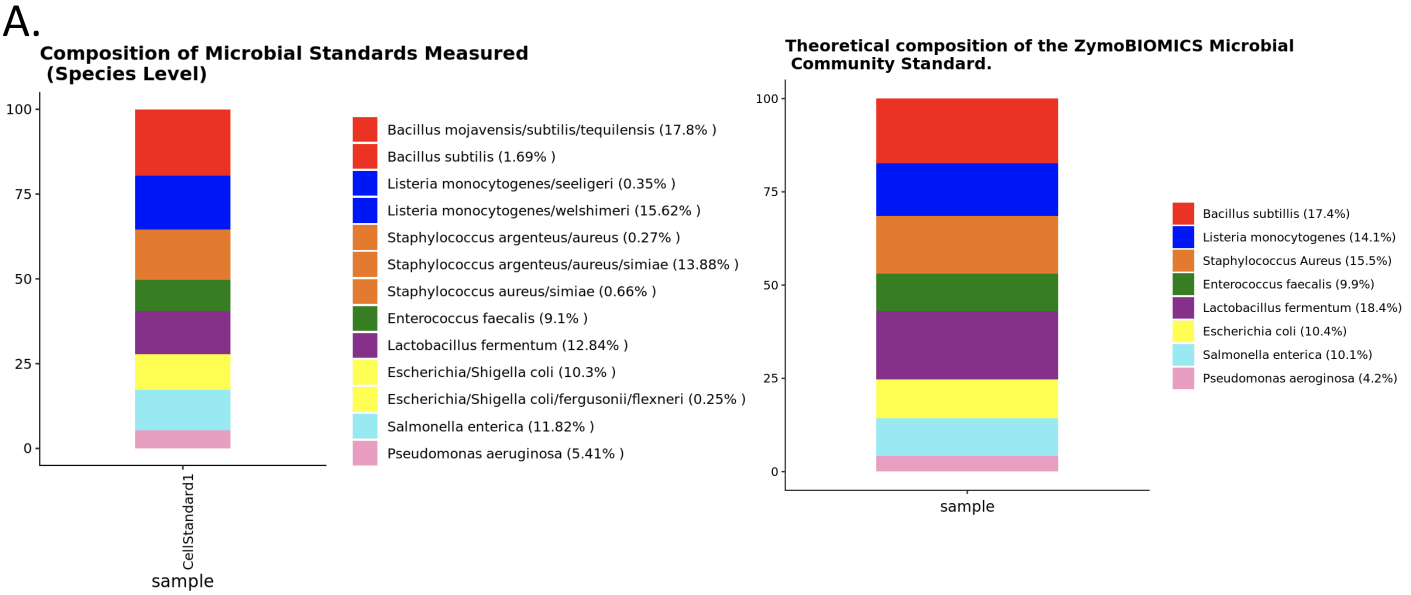
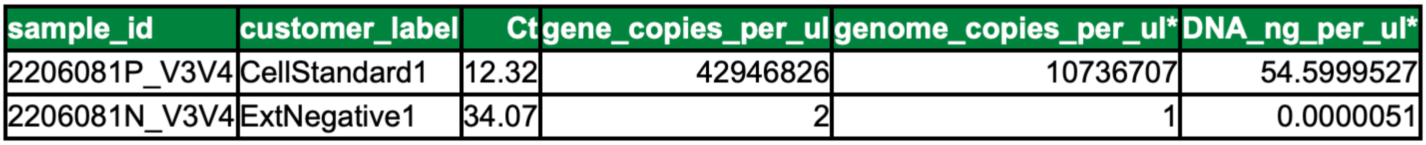


B.



sample_id	customer_label	Ct	gene_copies_per_ul	genome_copies_per_ul*	DNA_ng_per_ul*
2206081P_V3V4	CellStandard1	12.32	42946826	10736707	54.5999527
2206081N_V3V4	ExtNegative1	34.07	2	1	0.0000051

Figure 1: (A) The percent microbial composition of ZymoBIOMICS® Microbial Community measured (species level) in this project for the positive control compared to the theoretical composition of the ZymoBIOMICS® microbial community standard. The positive control utilizes a mock microbial community of well-defined composition to ensure the data generated are representative of the analyzed microbial samples. (B) Absolute abundance data for the ZymoBIOMICS® Microbial Community Standards processed, as positive control (CellStandard1) and negative control (ExtNegative1) with the cycle at which sample amplified for absolute abundance quantification (Ct). *Genome copies per microliter and DNA ng per microliter are calculated from the gene copies per microliter measured in the sample.

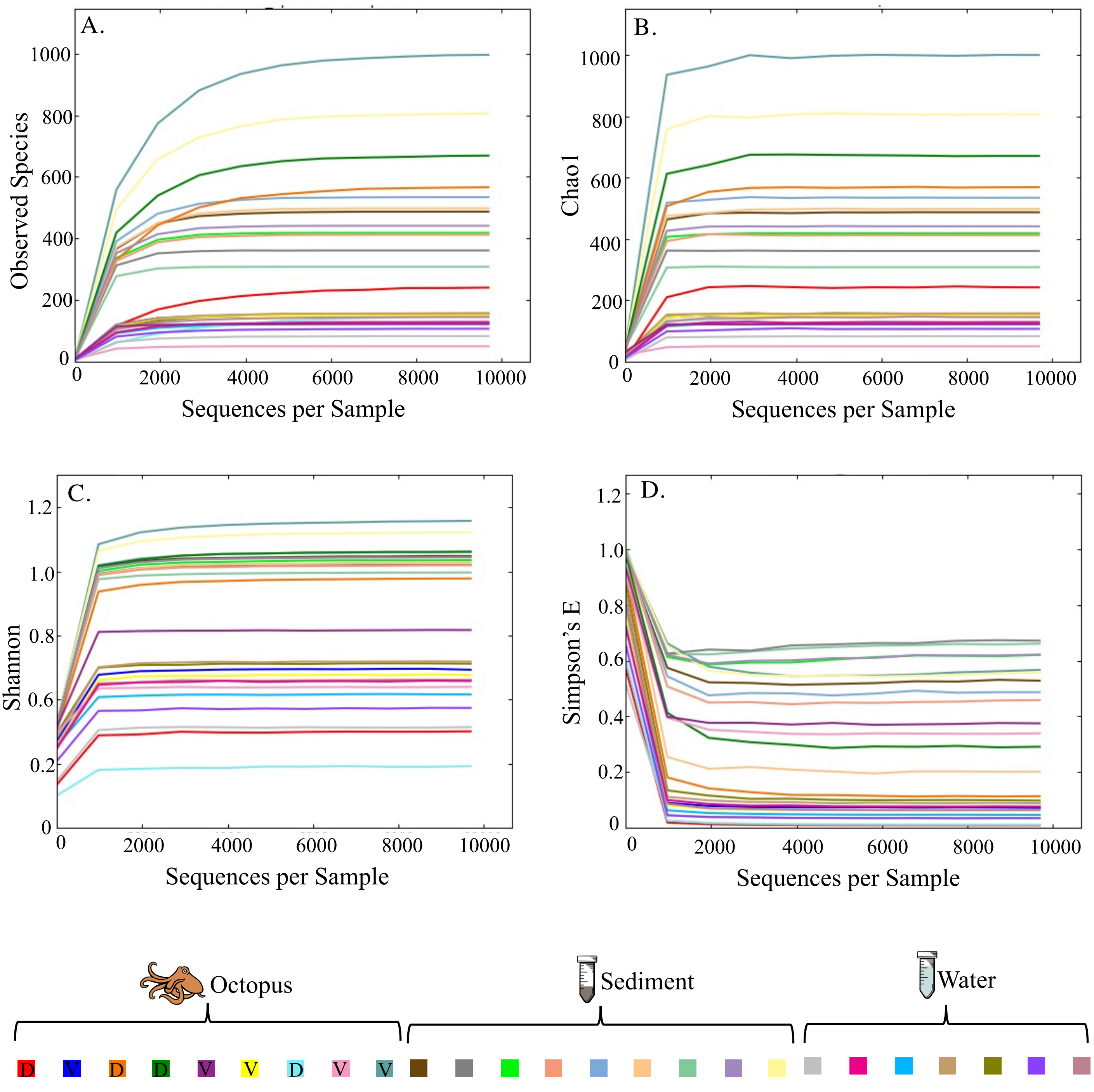


Figure 2: Rarefaction curves for alpha diversity (A. Observed species, B. Chao1, C. Shannon, D. Simpson's E) for octopus skin (n = 9), sediment (n = 9), and seawater (n = 7) within the Lake Worth Lagoon, FL. Each curve in the graph represents a different sample and is shown in a different color. For octopus samples, octopus species is indicated by a "V" for *Octopus vulgaris* or by a "D" for *Macrotritopus defilippi* in the legend. As the sequencing depth increased, the number of ASVs also increased. Eventually the curves plateau, indicating the gain of newly discovered ASVs is limited.

Table 1: Microbial composition for *Octopus vulgaris* (n = 5) and *Macrotritoups defilippi* (n = 4) at the family and genus levels to summarize potential overlap and species-specific microbial symbionts for two sympatric octopuses. Taxa are represented as percent average relative abundance with number of octopus individual incidences in paratheses. Bacteria groups included were > 1% for either octopus species in percent average relative abundance.

Families	***O. vulgaris***	***M. defilippi***
Flavobacteriaceae	21.5%, (5/5)	30.3%, (4/4)
Rhodobacteraceae	4.6%, (5.5)	6.9%, (4.4)
Halomonadaceae	4.9%, (2/5)	2.6%, (3/4)
Saprospiraceae	3.6%, (4/5)	3.0%, (4/4)
Pseudoalteromonadaceae	7.4%, (3/5)	1.0%, (4/4)
Cryomorphaceae	4.2%, (4/5)	1.5%, (4/4)
Rubritaleaceae	3.9%,(5/5)	<0.1%, (2/4)
Acidimicrobiaceae	3.2%,(4/5)	0.1%, (3/4)
Halieaceae	3.0%, (5/5)	0.2%, (3/4)
FamilyI	2.4%, (3/5)	0.8%, (4/4)
Chitinophagaceae	2.3%, (3/5)	0.3%, (2/4)
Vibrionaceae	0.6 %, (4/5)	1.6%, (4/4)
Chromatiaceae	1.2%, (2/5)	0.1%, (3/4)
Flammeovirgaceae	1.0%, (3/5)	0.5%, (4/4)
Salinisphaeraceae	0.0%, (0/5)	1.3%, (2/4)
Alteromonadaceae	0.4%, (3/5)	1.0%, (4/4)

Genera	***O. vulgaris***	***M. defilippi***
Tenacibaculum	3.3%, (4/5)	26.6%, (5/5)
Pseudoalteromonas	7.4%, (3/5)	1.0%, (5/5)
Polaribacter	6.7%, (5/5)	0.1%, (3/4)
Psychroserpens	6.3%, (3/5)	<0.1%, (1/4)
Cobetia	4.9%, (1/5)	1.1%, (3/4)
Rubritalea	3.9%, (5/5)	<0.1%, (2/4)
Illumatobacter	3.1%, (3/5)	0.1%, (2.4)
Prochlorococcus	2.4%, (2/5)	0.3%, (4/4)
Crocinitomix	2.2%, (4/5)	0.1, (3/4)
Saprospira	2.1%, (3/5)	0.0%, (0/4)
Nitrosococcus	1.2%, (2/5)	0.1%, (2/4)
Formosa-Fulvibacter	1.1%, (1/5)	0.0%, (0/4)
Halomonas	<0.1%, (2/5)	1.5%, (2/4)
Vibrio	0.4%, (3/5)	1.4%, (4/4)
Marinicella	0.7%, (3/5)	1.3%, (4/4)
Lewinella	0.1%, (1/5)	1.3%, (3/4)