

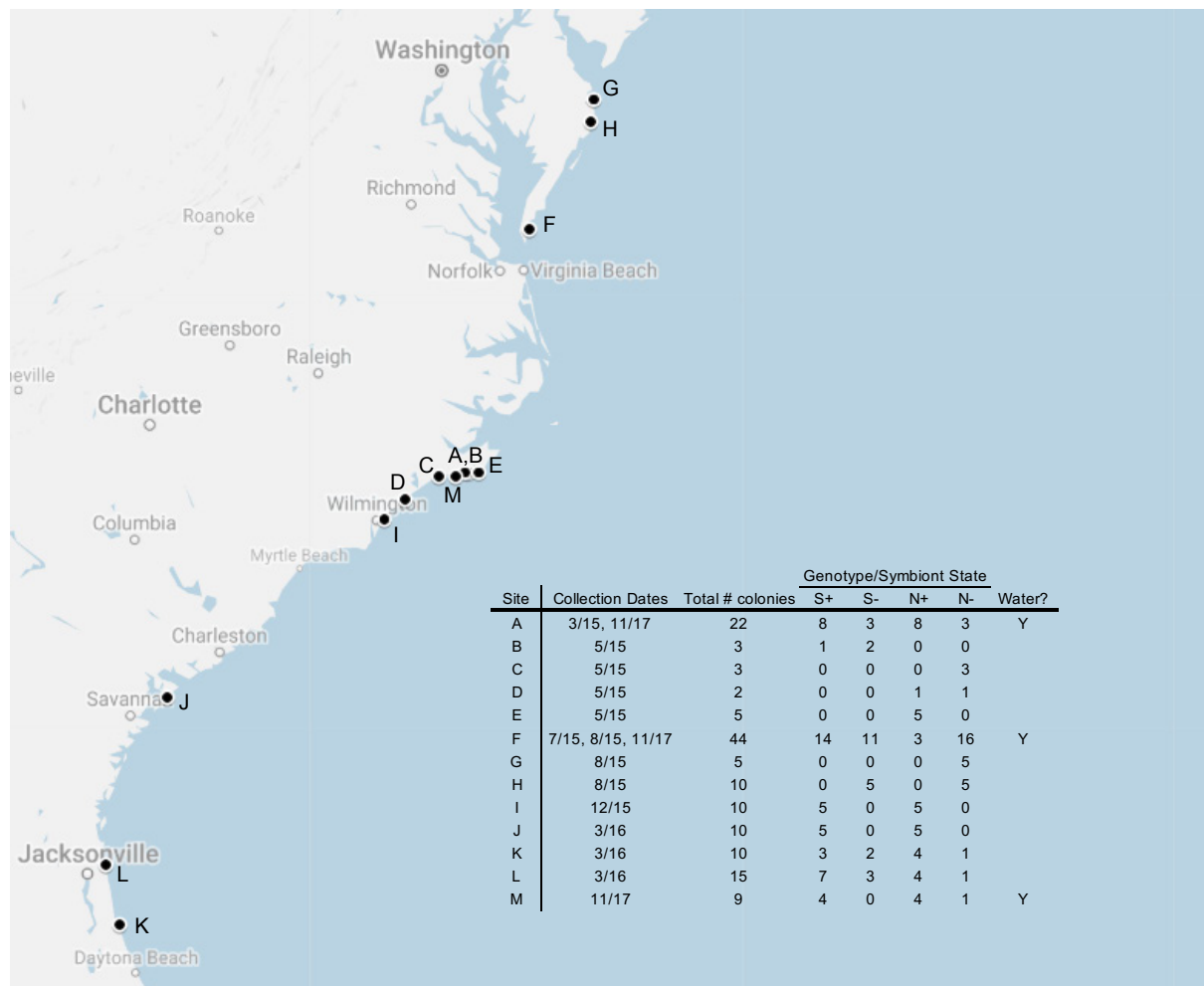
# Symbiont frequency predicts microbiome composition in a model bryozoan-bacterial symbiosis

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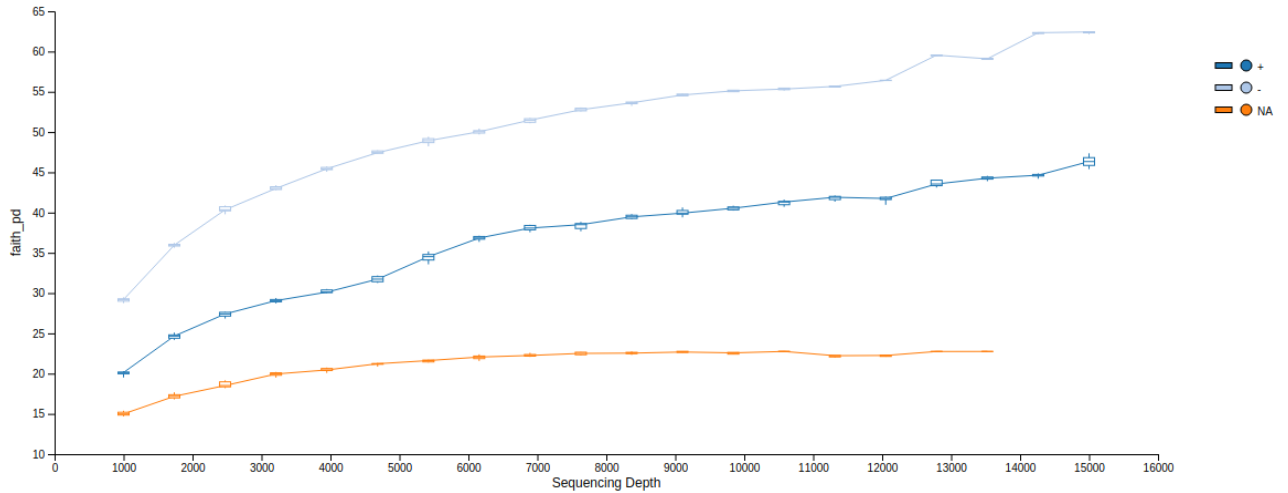
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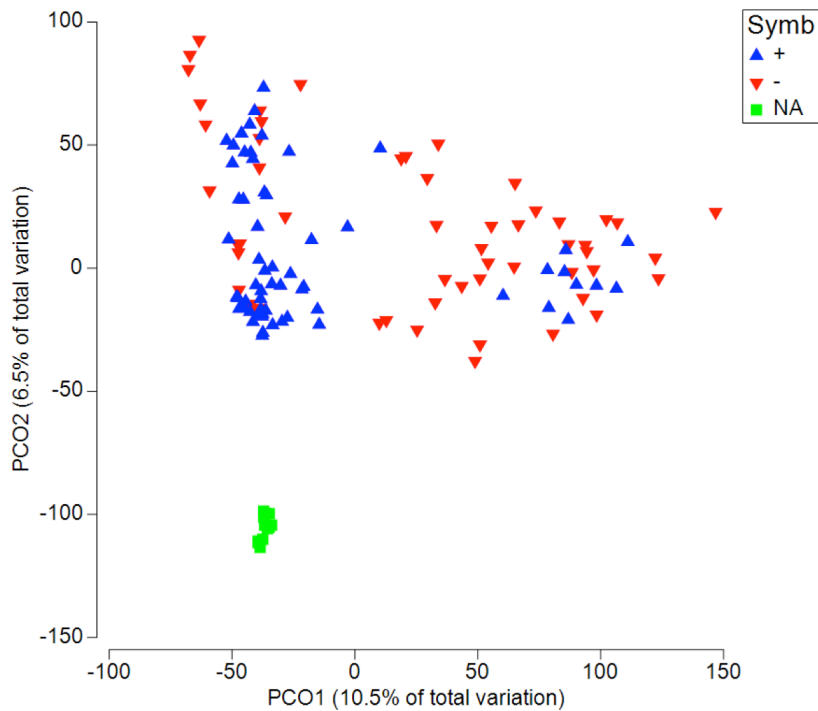
**Figure S1:** *B. neritina* colonies were sampled from sixteen locations along the East Coast of North America, ranging from Delaware to Florida.



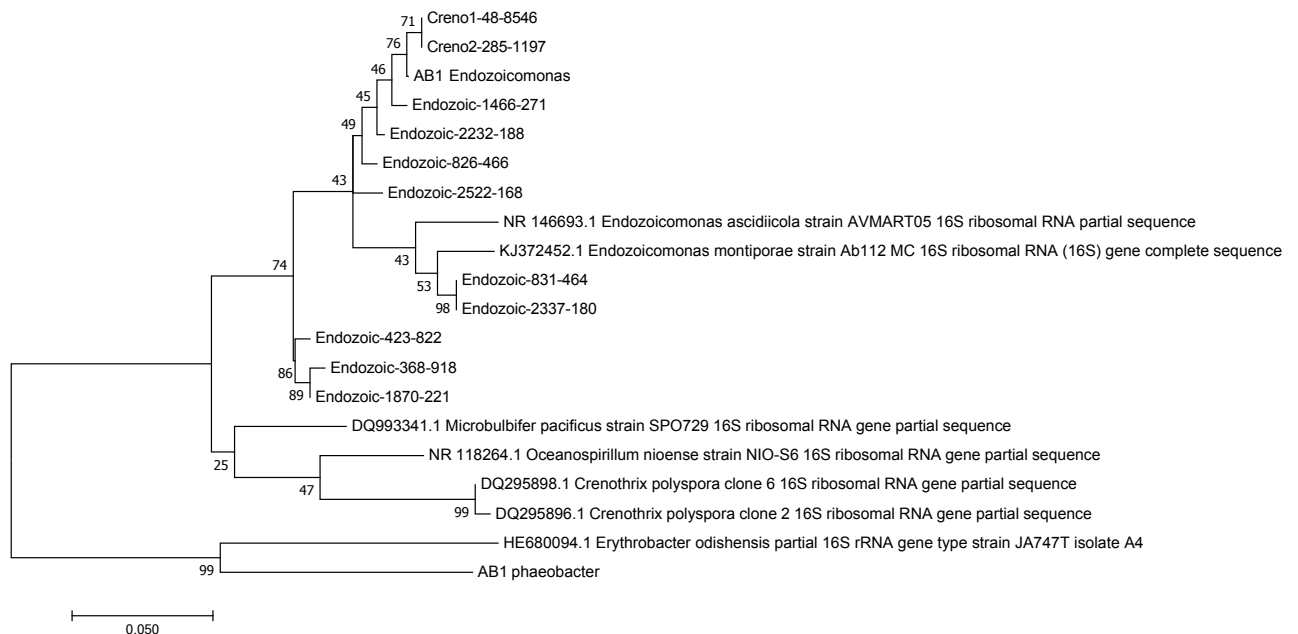
**Figure S2:** Alpha diversity differed among water samples (“NA”), *B. neritina* colonies enriched in *E. sertula* (“+”), and *B. neritina* colonies with <1% frequency of *E. sertula* (“-”). Rarefaction curves are based on Faith’s phylogenetic diversity metric subsampled at 20 steps between 1000 and 15000 read depth.



**Figure S3:** Water column microbiomes (green squares) clustered separately in ordination space from *B. neritina* microbiomes, which also clustered separately by *E. sertula* enrichment (red triangles) or absence (blue triangles). The plot is based on the Euclidean distances among rarefied and transformed data (full microbiomes).



**Figure S4:** Amplicons taxonomically classified as *Crenothrix* spp. are actually more closely related to the genus *Endozoicomonas*. The maximum likelihood phylogeny was constructed from full-length (251 bp) amplicons from our study and two 16S rRNA gene sequences from a recent metagenomic study of *B. neritina* [38], “AB1\_endozoicomonas” and “AB1\_phaeo.” Branch labels beginning with ‘Creno’ or ‘Endozoic’ are sequences from this study originally classified as *Crenothrix* sp. or *Endozoicomonas* sp., respectively, while labels beginning with “AB1” are the sequences from [38]. All other branches represent reference sequences downloaded from NCBI and are labeled with the accession number. *Erythrobacter odishensis* was used as an outgroup because it is a member of the Alphaproteobacteria, along with the “AB1\_phaeo” sequence (belonging to the genus *Phaeobacter*). All other taxa are Gammaproteobacteria. Nodes are labeled with bootstrap values generated from 999 iterations.



**Figure S5:** There was no observed clustering of *B. neritina* microbiome samples based on host genotype (blue triangles = Type N, red triangles = Type S). The plot is based on the Euclidean distances among rarefied and transformed data (complete microbiomes).

