

# Supporting Information

Campbell et al. 10.1073/pnas.1101405108

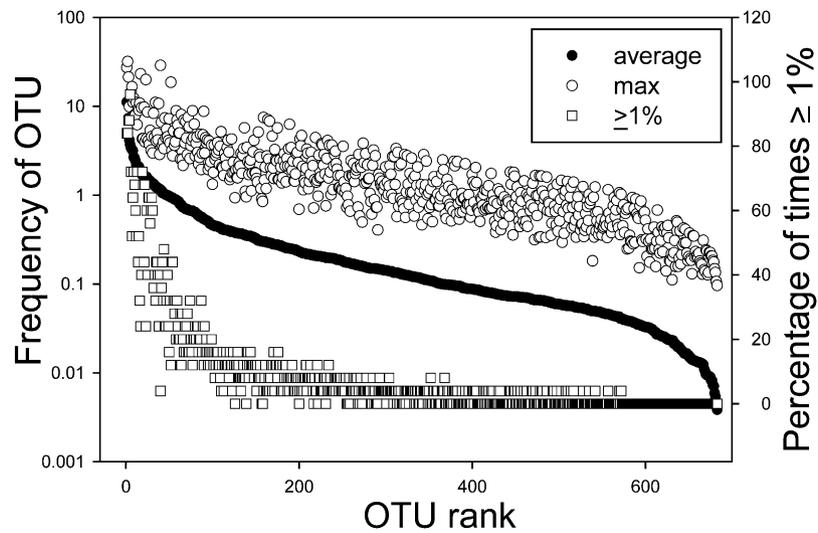


Fig. S1. Rank abundance curve of bacterial OTUs defined by 16S rDNA pyrosequencing of 25 Delaware coastal site surface water samples taken monthly over 3 y. Average (●) and maximum frequencies (○) of each OTU are plotted. The percentage of times the OTU frequency was equal to or above 1% (□).

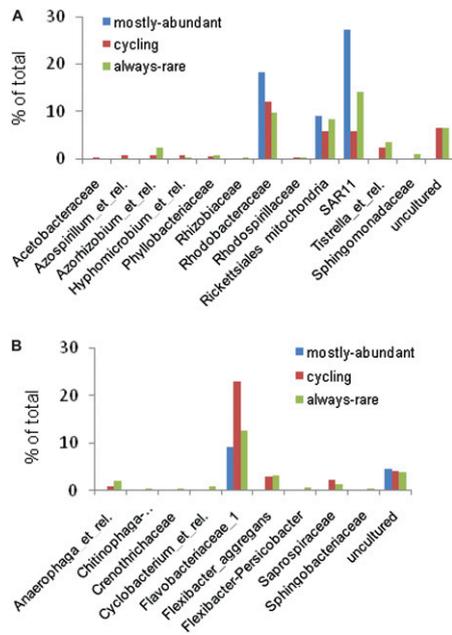
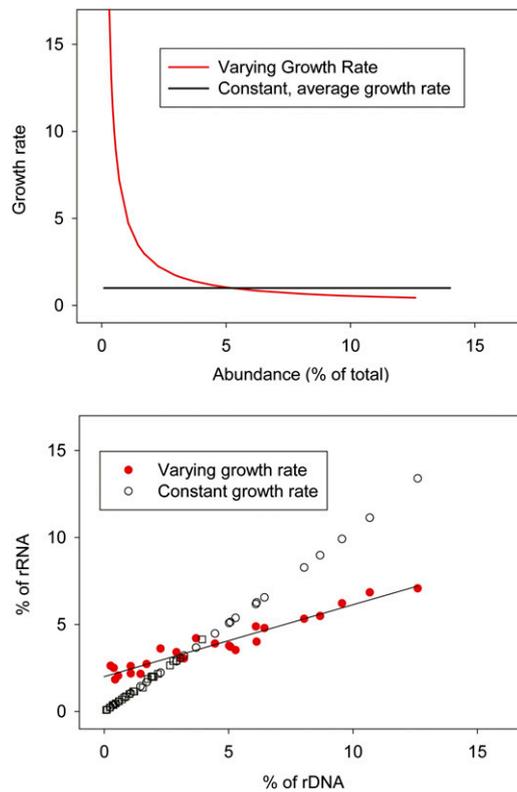


Fig. S2. Phylogenetic classification of bacterial OTUs found in Delaware coastal surface waters. Members of the (A) *Alphaproteobacteria* and (B) *Bacteroidetes*. The groups' percentage was divided into three categories: mostly abundant (occurring >50% of the time), cycling (<50% of the time), and always rare.





**Fig. S5.** To explore the effect of varying growth rates on the relationship between rRNA and rDNA, we took the original sequence numbers generated for all ribotypes. The community consisted of 685 ribotypes varying in abundance as described in the main text. This distribution of sequence numbers was assumed to approximate the distribution of ribotypes in the actual community, in effect assuming one operon per ribotype for this exercise. All of the ribotypes were assumed to grow at the same, constant growth rate, except for one ribotype whose growth rate was very high at low abundances and low at high abundances (*Upper*). The growth rates, i.e., rRNA:rDNA ratios (*Upper*), were then used to calculate the rRNA numbers as abundance varied. The absolute abundance of rRNA and rDNA was then used to calculate the percent of the total rRNA and the percent of total rDNA made up by all ribotypes (*Lower*). The data for two ribotypes are plotted, one whose growth rate varies and another with a constant growth rate. Note that the intercept varies for the two ribotypes; it is zero for the ribotype with a constant growth rate, and it is greater than zero for the ribotype whose growth rate increases as abundance decreases.

