

Effect of short-term, diel changes in environmental conditions on active microbial communities in a salt marsh pond

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Aquatic Microbial Ecology 80: 29–41 (2017)

Supplement 2: Supplemental figures

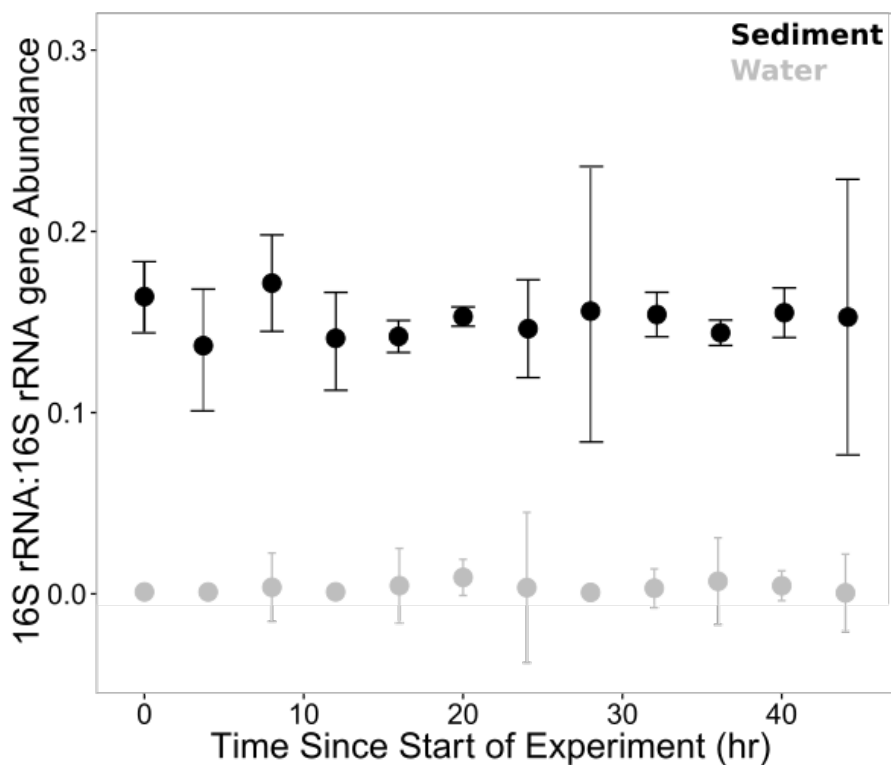


Fig. S1. Quantitative PCR (qPCR) results depicting the ratio of 16S rRNA:16S rRNA gene for sediment (black) and water (grey) communities. Points are the mean of three sites and the error bars are standard error of the mean

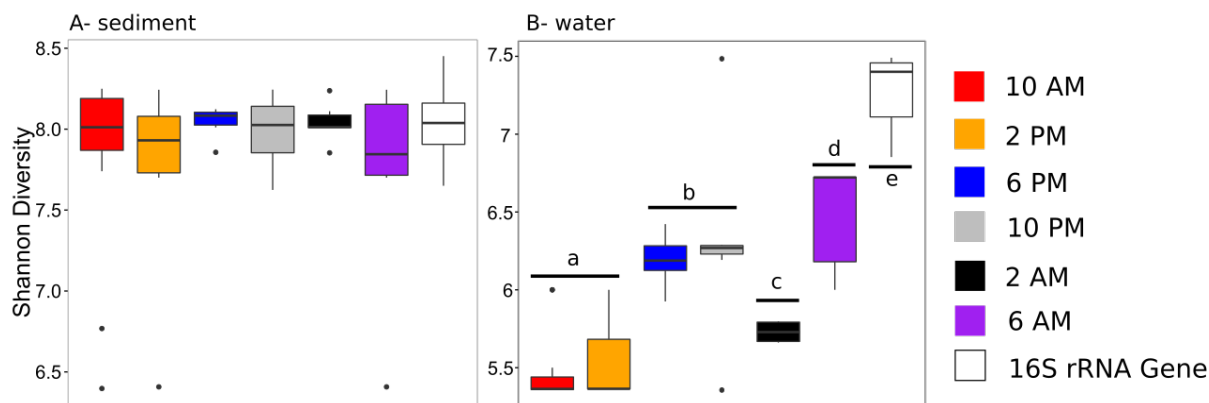


Fig. S2. Shannon Diversity values for sediment (A) and water (B) communities. Boxes represent 25-75% quartiles, the solid black line is the median value, and dots are outliers. Categories in (B) are significant ($p < 0.001$) based on a Tukey HSD correction for multiple comparisons

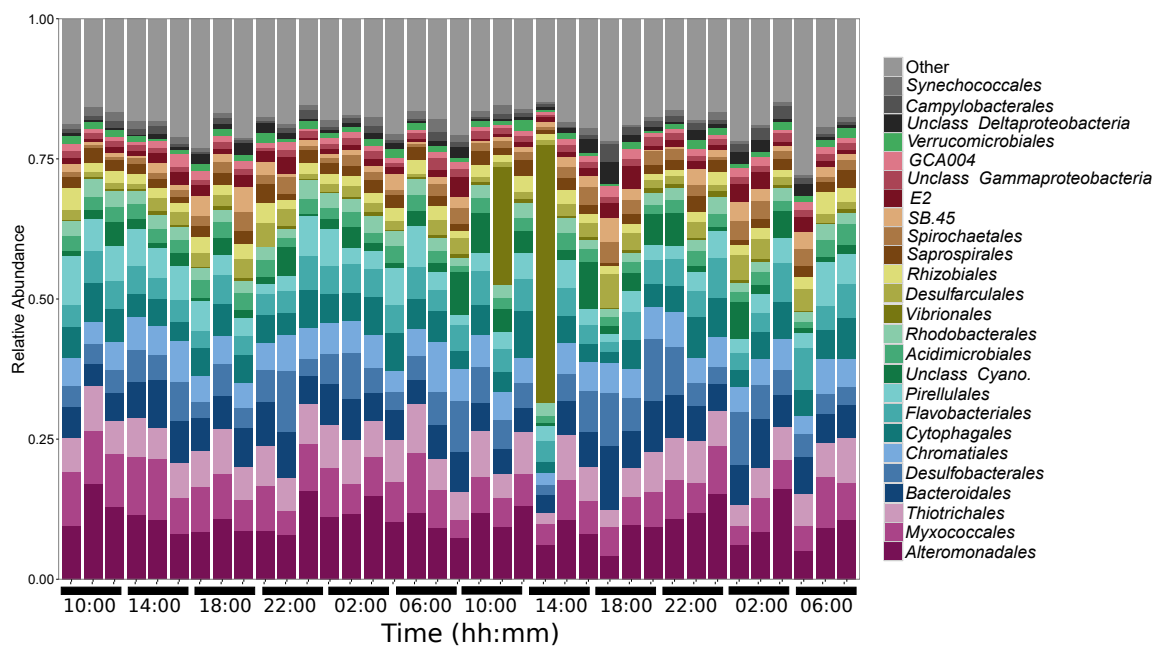


Fig. S3. Stacked bar plot of the top 25 most abundant microbial orders from the sediment 16S rRNA gene. The category 'Other' is the sum of the remaining microbial orders. Black bars are night time hours

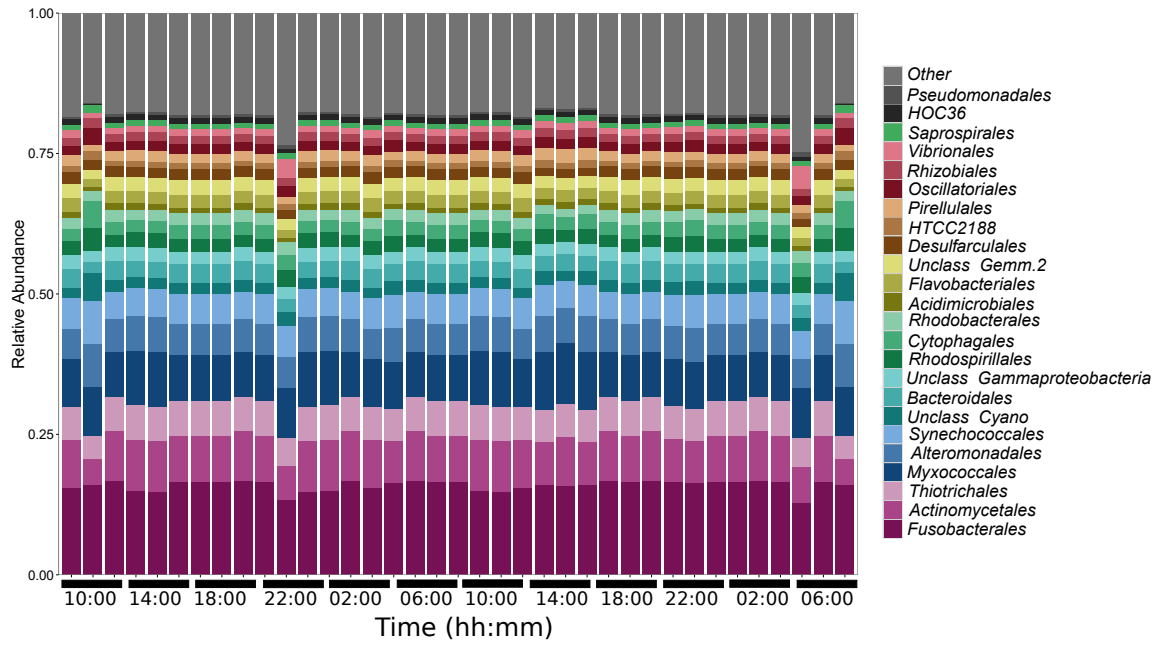


Fig. S4. Stacked bar plot of the top 25 most abundant microbial orders from the water 16S rRNA gene. The category 'Other' is the sum of the remaining microbial orders. Black bars are night time hours

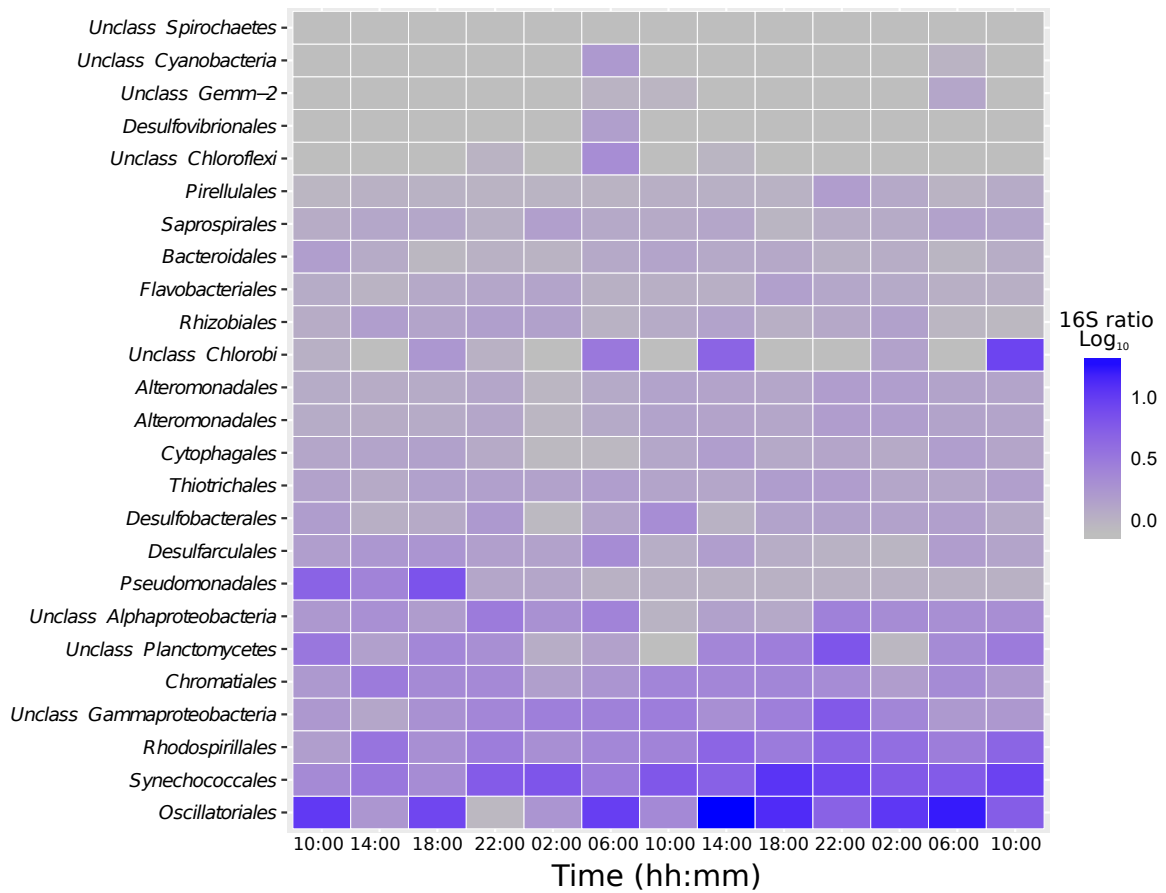


Fig. S5. Heat map showing the sum of the 16S rRNA:16S rRNA gene ratio for the 25 most active microbial orders in the sediment