Drivers of microbial community structure in a shallow estuary in the southeast that experiences seasonal hypoxia.

Weeks Bay is a shallow, tidally influenced estuary on the eastern shore of Mobile Bay in Alabama. *More text about the location and why it’s interesting*.

Triplicate surface water samples were taken seasonally at three sites along a transect from the mouth of the bay upstream to the Fish River. *Physiochemical analyses were performed, including TDN, TDP, etc*. Water was filtered in sterivex filters and the total DNA extracted from the filters. Genes for 16S rRNA and 18S rRNA were amplified and sequenced according to Earth Microbiome Project protocols. Amplicon data were analyzed with mothur (v.1.37.5) using the Silva database (v.123). Gene sequences were assembled into contigs and clustered into OTUs (0.03 dissimilarity).

Non-parametric statistical analysis of community composition and environmental data was performed using PRIMER (v7). Prokaryotes tended to cluster by date of sample collection. Within the parameter of station, BEST analysis, which searches for high matrix correlations, ranked, between community assemblage and environmental data. indicated that salinity, CDOM, and pH correlated best with community structure (Rho=0.921). Salinity is higher near the mouth of the bay and lower at the river, with the inverse being true for CDOM, so these results are not unexpected as the samples were on a transect from the mouth of the bay to the river. Within the parameter of date collected, BEST analysis indicated that TDN and salinity were the abiotic variables that correlated with the community structure when selecting for the least number of variables. However, six combinations of up to four variables produced identical correlations (Rho=0.773), with all four including TDN and salinity. Eukaryotes clustered primarily by date, but not as cleanly as the prokaryotes. Within the parameter of station, BEST analysis indicated that salinity alone provided the best correlation (Rho=0.921) to community structure of the eukaryotes. As with the prokaryotes, BEST analysis within the parameter of date of sample collection indicated what salinity and TDN had the highest correlation (Rho=0.854) with community structure.