

Nature's ultimate environmental sampler: a look at the stomach content of Gulf Menhaden using molecular signatures

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Menhaden are a key forage fish species that feed by filtering the water column primarily based on size. This makes menhaden excellent environmental samplers through analyzing their stomach contents. However, this is difficult because organisms are small and fairly easily digested. By combining mass-amplification of short DNA sequences and high-throughput sequencing of DNA signatures, a fairly unbiased estimate of microbial diversity can be made. Using Illumina NextGen sequencing, DNA from the stomachs of *Brevoortia patronus* (Gulf menhaden) from high (HS) and low (LS) salinity sites were sequenced. The sequences were then quality filtered, assembled and assigned taxonomic classification using Quantitative Insights Into Microbial Ecology (QIIME). Using R packages, alpha diversity metrics analyzing taxonomic richness and evenness showed that LS samples had a higher level of richness despite being dominated by 2-3 operational taxonomic units (OTUs) and contained several unique OTUs. In contrast HS samples had a higher level of evenness. Furthermore there was an enrichment of several taxa in the HS samples but an enrichment of only one taxa in the LS samples. HS samples are dominated by the group Metazoa. LS samples are dominated by Alveolata. For both datasets, there appears to be a relationship between items and salinity.