

## 16s rDNA Characterization of Epiphytic Bacteria on Seagrasses from an Estuary and a Hypersaline Lagoon on the South Texas Coast

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There is concern for the global decline of seagrass beds due to their ecological importance. Epiphytic biofilms of bacteria and algae may contribute to the decline of seagrasses by shading the light required for photosynthesis. Eutrophication and other environmental changes may affect the overall quantity, diversity and species richness of these epiphytes. Because microbial populations can be indicators of biogeochemical conditions, characterization of the epiphytic organisms, particularly bacteria, will provide insight into environmental conditions.

Representative bacterial epiphyte species assemblages on both *Halodule wrightii* and cellulosic substrates were compared between the Corpus Christi Bay estuary (East Flats) and a hypersaline lagoon (Upper Laguna Madre). Species assemblage profiles were generated by denaturing gradient gel electrophoresis (DGGE) following amplification of 16S rDNA genes using primers for alphaproteobacteria, gammaproteobacteria, cyanobacteria, and bacteroidetes.

Unique diversity and richness were observed for bacterial assemblages from the estuary and hypersaline lagoon, whereas assemblages taken from seagrass leaves and substrates appeared to have mostly similar diversity. A striking difference between seagrass leaf and substrate for a cyanobacterial amplicon suggests a host-specific preference. Some DGGE bands were excised, re-amplified, cloned, and sequenced. Comparison of a clone library to Ribosomal Database Project II identified species indicative of an interface between aerobic and anaerobic conditions.