Salt Marsh Protection by Soil Bacteria

Reference SON: *N/A*

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Research Need

Salt marshes are the most productive ecosystems in the biosphere and provide multiple public benefits such as: absorbing excess nitrogen and phosphorus from sewage and fertilizer run-off into rivers which prevents algal blooms and hypoxia in coastal waters; detoxification of run-off from industrial areas; providing habitat and shelter for many hundreds of species of shellfish, finfish, migratory and sedentary birds, and other marine animals.

There have been an increasing number of reports of salt marsh dieback (SMD) in the United States over the past decade. The Mississippi River deltaic plain experienced a sudden dieback event that affected over 100,000 ha of *Spartina alterniflora* dominated salt marsh in 2000. Affected areas showed a progression from yellow to brown leaves to bare mud as *S. alterniflora* died. Both abiotic and biotic mechanisms have been implicated as causes of dieback events.

Project Objectives & Plan

Project objectives include 1) isolation and characterization of beneficial root zone bacterial isolates with antagonistic activity towards *Fusarium* species associated with SMD, and 2) characterization of the impact of SMD on the composition of rhizosphere microbial communities in *S. alterniflora*. We anticipate releasing a technical note and manuscript to provide a basic framework for establishing procedures for revegetating areas already impacted by dieback.

Payoff

The results from this Ecosystem Management and Restoration Research Program (EMRRP) study will be beneficial in protecting salt marsh ecosystems from dieback by establishing procedures for revegetating areas already impacted by dieback.

Products

Journal Articles (JAs)

Mavrodi, O.V., Jung, C.M., Eberly, J.O., Hendry, S.V., Namjilsuren, S., Biber, P.D., Indest, K.J., and Mavrodi, D.V.

(2018). Rhizosphere Microbial Communities of *Spartina alterniflora* and *Juncus roemerianus* From Restored and Natural Tidal Marshes on Deer Island, Mississippi. Frontiers in Microbiology 9: 3049. doi: 10.3389/fmicb.2018.03049