

Belowground microbial ecosystems and aboveground vegetation associations at recently created tidal marshes differ from nearby natural marshes in Plaquemines Parish, Louisiana



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PRESENTED AT:



ABSTRACT

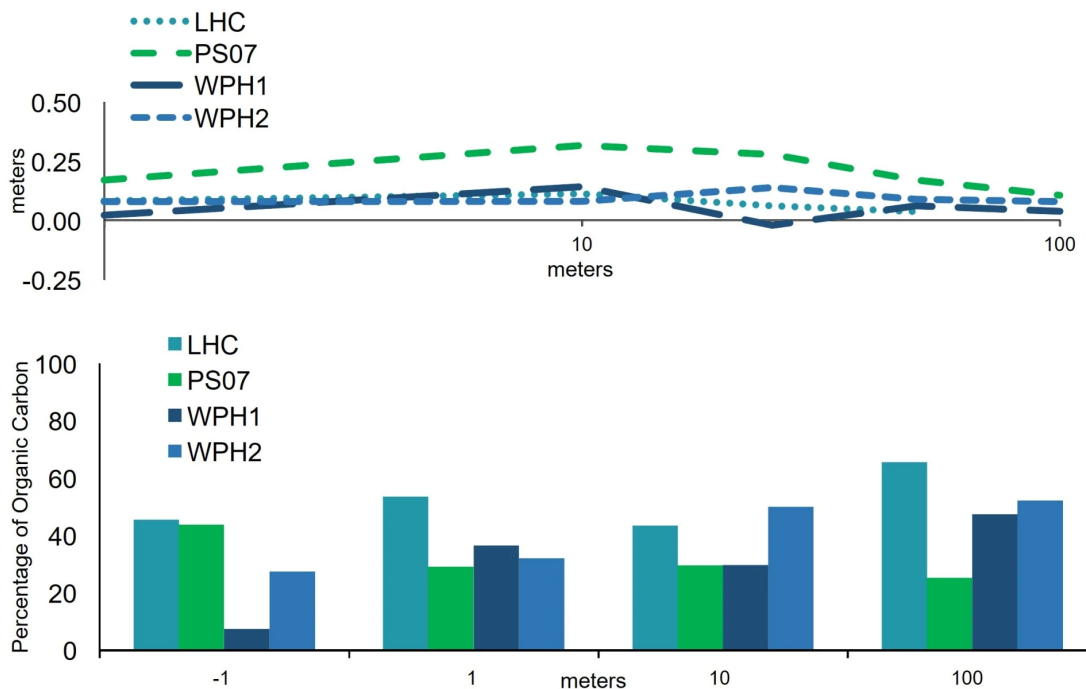
Tidal marsh construction projects in Louisiana, under the Coastal Wetlands Planning, Protection and Restoration Act, are meant to **restore critical habitat** for fisheries and to **combat erosion, land loss, and impacts from disturbance**. Monitoring restoration success typically includes evaluating survival/mortality of aboveground species. However, there has been **limited research to evaluate the microbiology, soil properties, biogeochemical processes, and microbial-vegetation associations of created marsh soils**, despite the important roles that soil microbes play in the recruitment and establishment of aboveground vegetation and the importance of specific plant species creating different belowground conditions (e.g., redox, nutrient availability). The purpose of this project was to assess soil microbial communities from natural marshes and nearby created marshes associated with the Plaquemines Parish Lake Hermitage Marsh Creation Project (LHMCP). LHMCP land creation was from 2012–2014. Marshes were sampled in 2018 (and 2019 and 2021), in transects up to 100 m inland. Soil organic C content and soil pH were consistently lower at LHMCP sites compared to natural marshes, but LHMCP soil microbial diversity was higher. LHMCP soil had different relative abundances of specific microbial groups associated with N and S cycling compared to natural marsh soils, and soil microbial diversity strongly correlated to plant type. Plant biomass was lower at LHMCP sites, but richness was comparable to or higher than natural marshes, although plant diversity was often non-traditional marsh species. **Natural marsh soil microbial diversity strongly correlated with typical marsh plants** (e.g., *Spartina alterniflora*, *Juncus roemerianus*), but LHMCP soil microbial diversity correlated to higher *Paspalum* spp. (crowngrass) and *Schoenoplectus pungens* (common bulrush) biomass. **The distinct plant-microbe associations at the created marshes likely affect habitability and sustainability for other marsh organisms**, but these relationships have yet to be explored. With time, the expectation would be that created marsh above and belowground biomass and microbial diversity would begin to mimic natural marshes, but continued monitoring will be necessary to understand how these linkages develop and affect basic soil processes.

NATURAL SITES

[VIDEO] https://res.cloudinary.com/amuze-interactive/video/upload/vc_auto/v1638563292/agu-fm2021/27-DB-58-B5-A6-C6-80-C5-D2-BE-D5-E1-16-40-D3-78/Video/2021-05-25_08.51.43_dvsaxd.mp4

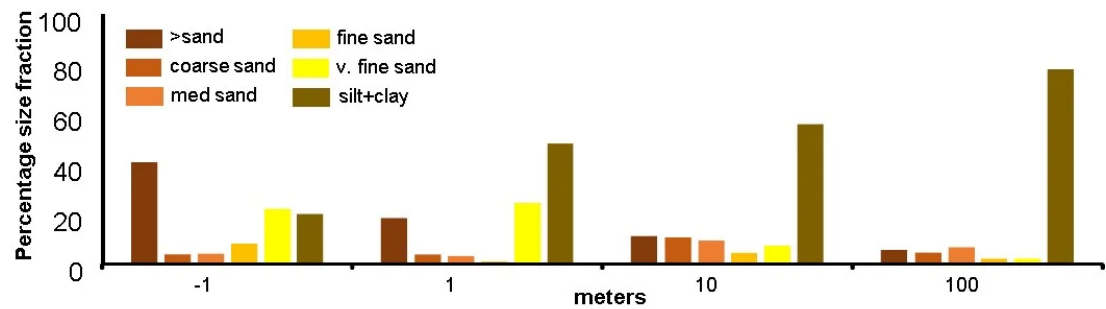
*Sampling a natural marsh (PS07) dominated by *Spartina alterniflora*. (Note: this video has background sound of us sampling in the marsh).*

- Mean **marsh elevations** (NAVD88) were from 0.05 m (WPH1) to 0.18 m (PS07)



Top: Marsh elevations; Bottom: Percentage of organic carbon content from sediments and soils.

- The organic carbon content, averaging above 20%, from natural marsh soils was significantly higher than the restored soils ($p = 0.0001$).
- Soil pH values averaged $6.35 (\pm 0.7)$, with $12.27 (\pm 2.4)$ mS/cm conductivity. Soil pH significantly differed between the surface and soil at depth ($p = 0.03$).
- Soil grain size was silt to mud, whereas offshore sediment was predominately sand.



Grain size distribution for natural marsh sites.

- Between 9 and 14 different plant species were identified at these natural sites, with the highest diversity 1 m inland for all sites.



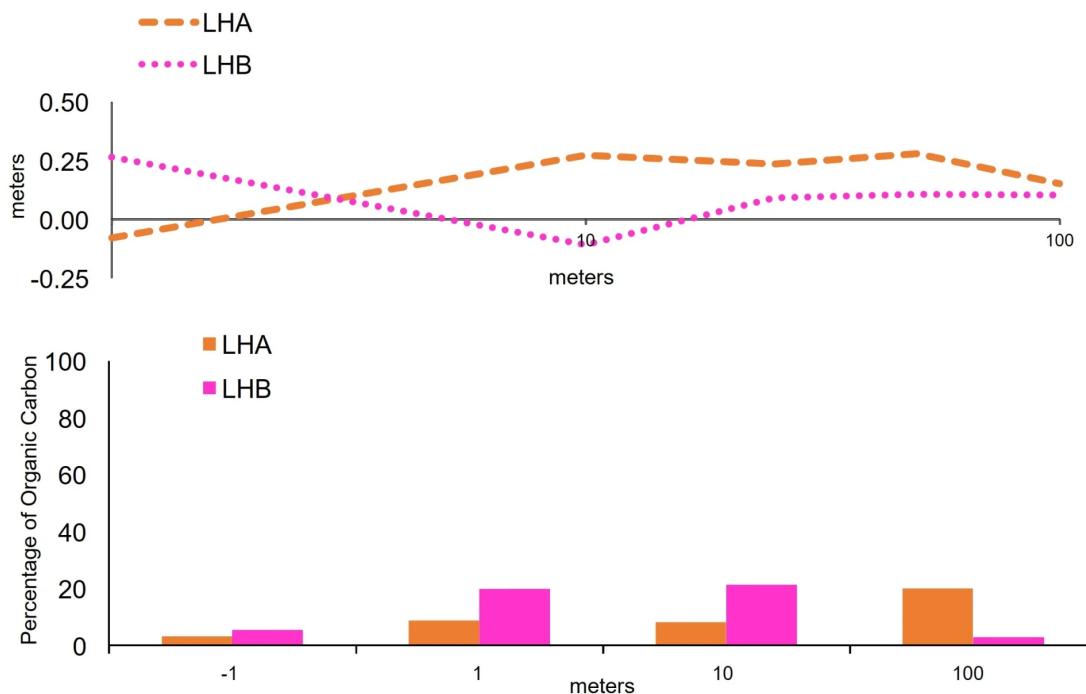
Natural marsh soil core, showing black color, predominately clay content mixed with organic matter.

RESTORED SITES

[VIDEO] https://res.cloudinary.com/amuze-interactive/video/upload/vc_auto/v1638562970/agu-fm2021/27-DB-58-B5-A6-C6-80-C5-D2-BE-D5-E1-16-40-D3-78/Video/2021-05-24_09.22.39_bkil7w.mp4

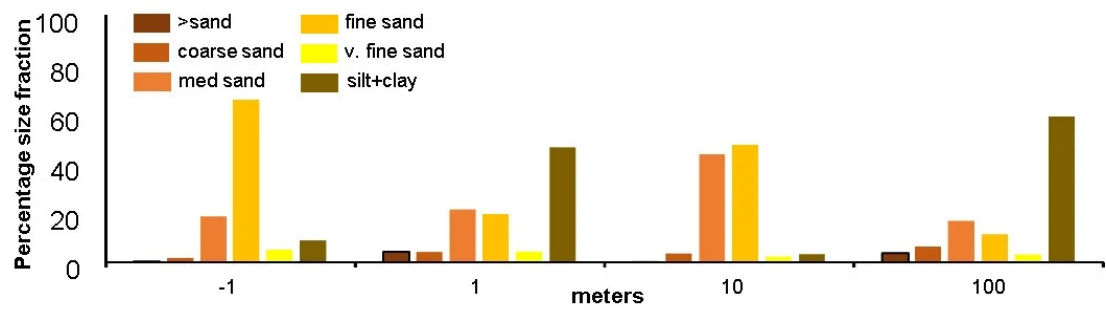
Sampling a restored marsh (LHA) dominated with *Paspalum spp. (crowngrass)* and *Schoenoplectus pungens (common bulrush)*. (Note: this video has background sound of us sampling in the marsh).

- Mean marsh elevation for LHA was ~0.23 m, and higher than LHB, and higher than natural marshes.



Top: Restored marsh elevations; Bottom: Percentage of organic carbon content from sediments and soils.

- Soils at these sites had less organic carbon content, averaging <10%, which was significantly different than the higher content from natural soils ($p = 0.0001$).
- Soil pH values averaged $7.05 (\pm 0.9)$, with $8.51 (\pm 2.6)$ mS/cm conductivity. Soil pH from the surface was significantly different than at depth ($p = 0.004$), and soil pH from restored sites was significantly different from natural soils at all depths ($p = 0.01$).
- The grain size of soil for the restored marshes, particularly on the marsh platform, was fine-grained sand. This is likely due to dredged material being used to construct the marsh land.



Grain size distribution for natural marsh sites.

- Plant diversity at these sites was higher at 1 m inland, and averaged 10.5 species between the two marsh locations.

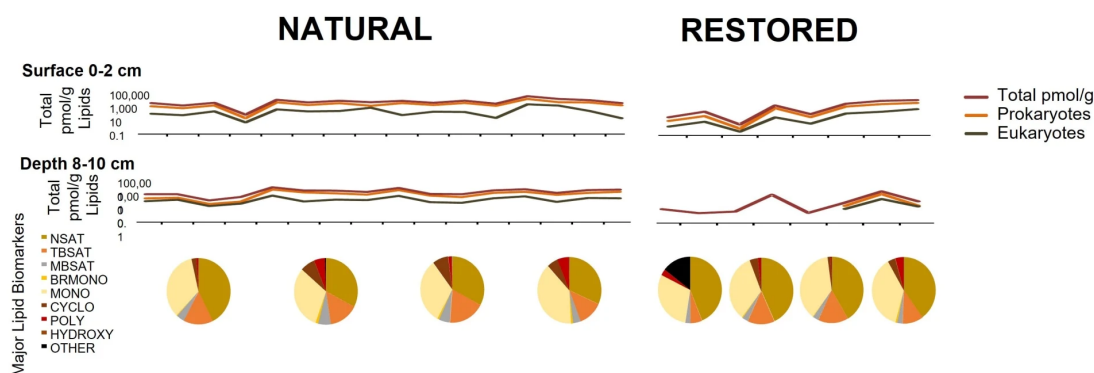


Restored soil core showing tan color and almost no organic matter mixed with fine sand.

MICROBIAL BIOMASS, DIVERSITY, & COMMUNITY STRUCTURE

MICROBIAL LIPID RESULTS

- Total microbial biomass differed for natural & restored surfaces ($p = 0.05$); total biomass was significantly different at depth between natural and restored soils ($p = 0.002$). **Restored marshes had less total microbial biomass.**



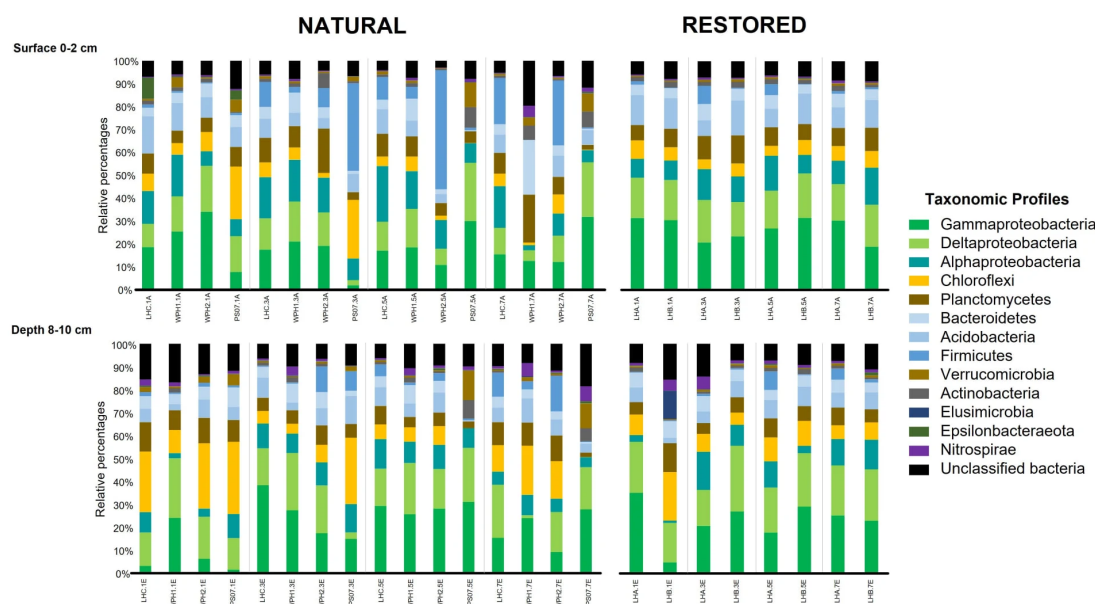
Membrane lipid results from all natural and all restored marshes, separated by soil depth (0-2 cm and 8-10 cm depth).

- Surface soil samples had higher relative abundances and diversity of eukaryotic FAME biomarkers ($\omega 6$ -animal and $\omega 3$ -plant) than deeper samples ($18:2$ $\omega 6$ dominated).
- Sulfate-reducers ($a15:0$, $i17:0$, and $10Me16:0$) were at depth, & actinomycetes and metal-reducers ($i15:0$, $Me18:0$'s, $Me17:0$, $br17:1$, and $Br19:1$) at the surface.
- Lipid analyses were done at the University of Tennessee, in Dr. Engel's lab, by Dr. Susan Pfiffner. Thanks, Susan!

MICROBIAL DIVERSITY RESULTS

- Taxonomic groups that had an average of $>0.1\%$ of the total microbial diversity in the dataset for all of the sites were included in detailed analyses.
- 11 major bacterial phyla were identified, and 116 orders, with most of the diversity being among three proteobacterial classes (Deltaproteobacteria, Alphaproteobacteria, and Gammaproteobacteria), Chloroflexi, Planctomycetes, and Bacteroidetes.

- 12 archeal phyla were retrieved from all the samples; however, Bathyarchaeia, Thermoplasmata, and Nanohaloarchaeia were the most abundant.
- The microbial diversity (based on relative abundances) from restored marshes was more homogenous than the diversity of natural marshes, which were more variable across salinity, distance into the marsh, and at depth. The restored bacterial communities were more similar to each other than to the natural marsh communities.
- The restored bacterial diversity from soil surface and depth samples was significantly different ($p = 0.04$). Although the surface soil bacterial communities from natural marshes was more variable at depth, there were no significant compositional differences between soil depths in natural marshes.

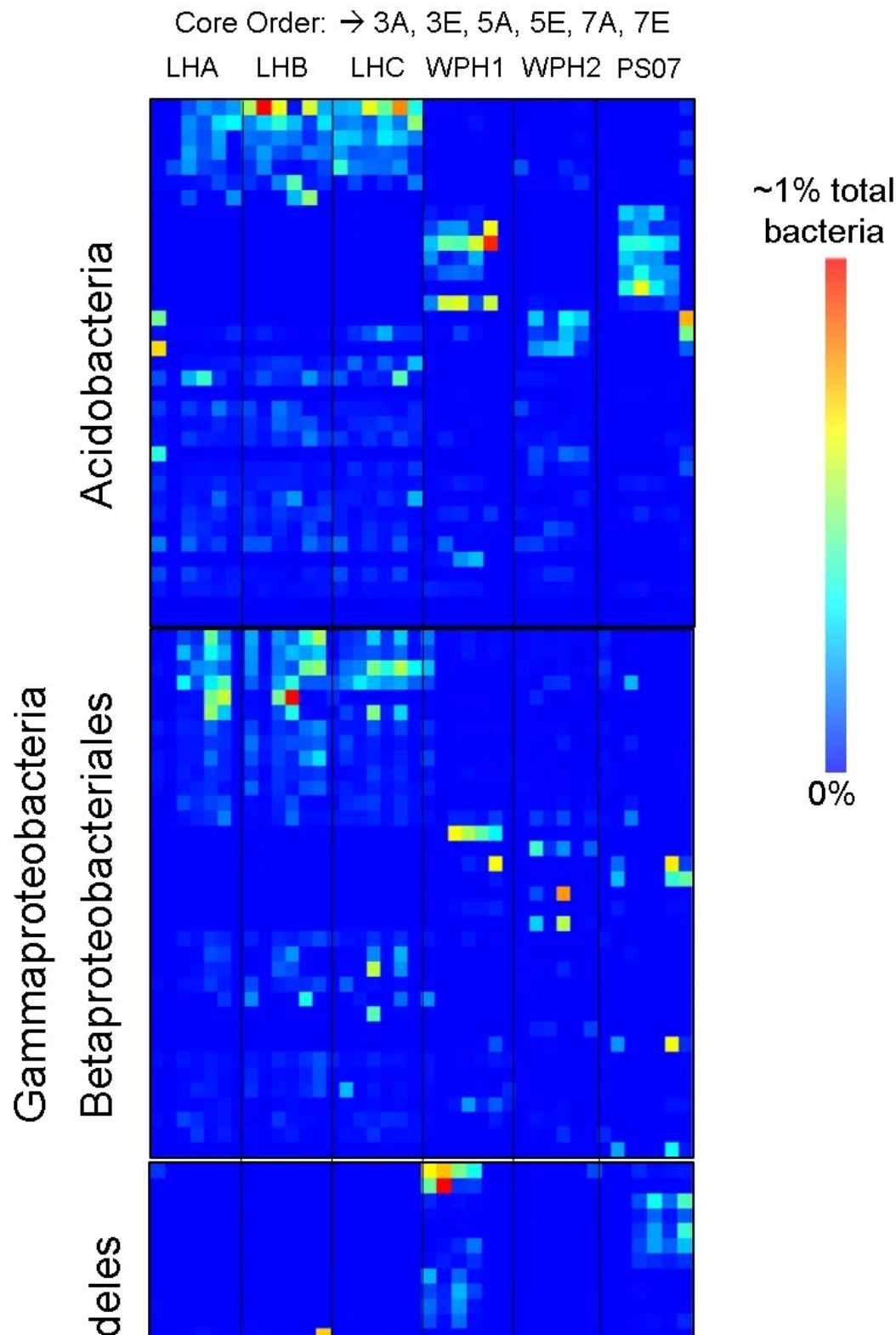


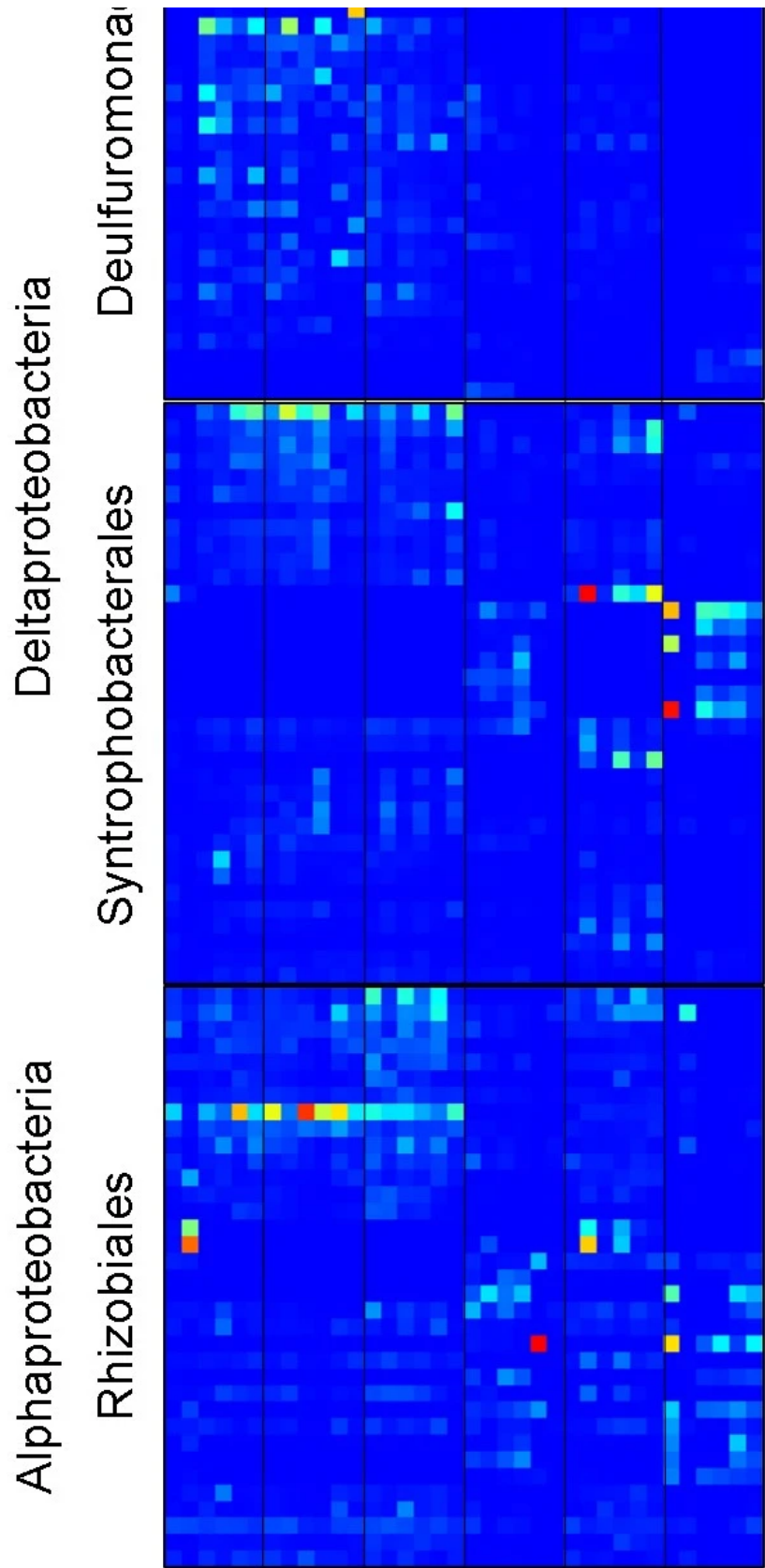
16S rRNA gene sequence results for major bacterial phyla from all natural and all restored marshes, separated by soil depth (0-2 cm and 8-10 cm depth).

SHARED MICROBIAL DIVERSITY

- Differences within communities were evident by comparing shared operational taxonomic units (OTUs).
- Even though major taxonomic groups (at the phylum level) were retrieved from all marsh locations and depths, there were genetic differences among OTUs.
- Some sites and soil depths were dominated by only a few OTUs within each taxonomic group, whereas other sites were dominated by different OTUs within the same taxonomic group.

- The restored sites shared more OTUs in common, as well as with a nearby natural marsh (LHC) compared to the OTUs that were shared with natural marshes.
- Differences in the number of shared OTUs indicated distinct functional groups within the marshes, including among sulfate-reducers and nitrogen-fixers.





Heatmaps of the top 35 shared OTUs (from 16S rRNA gene sequences) for prevalent taxonomic groups, as an example of the detailed analyses that are possible with this dataset. For each of the sites labelled, cores from 1, 10, and 100 m are shown from left to right.

STUDY AREA & METHODS OVERVIEW



RESTORE

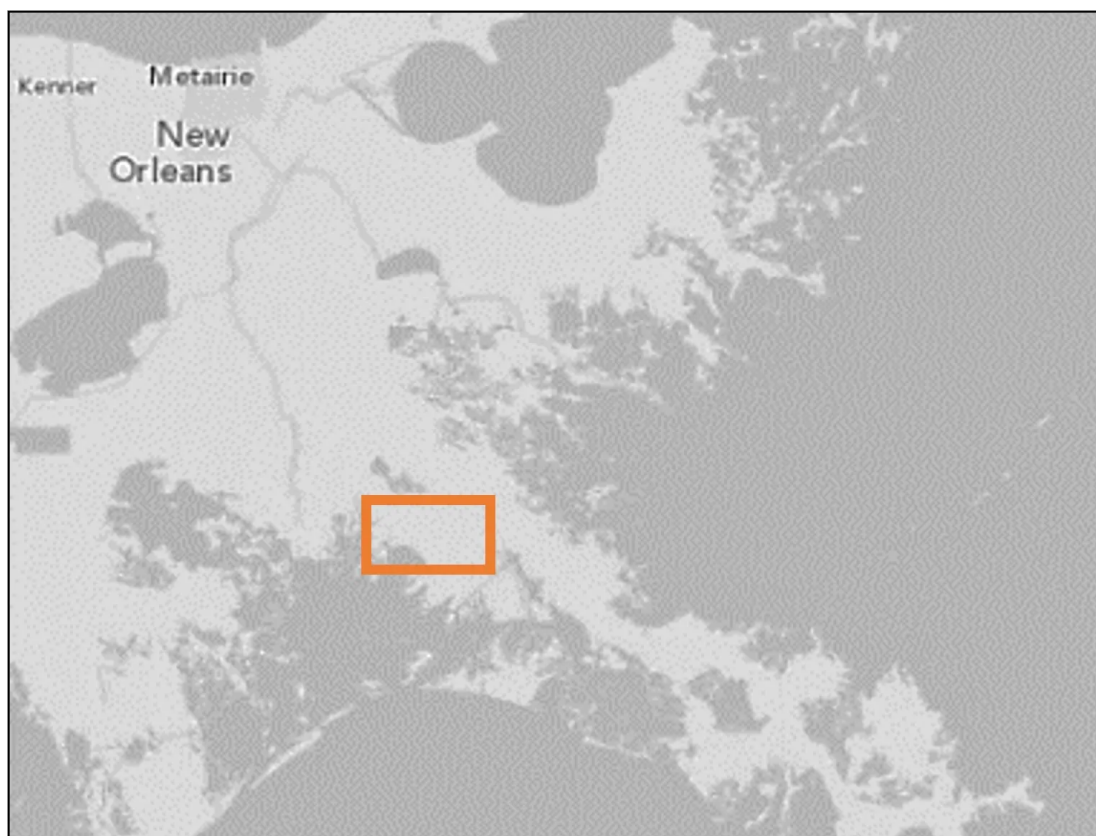
SCIENCE PROGRAM

- This research is part of a larger project, "*Linking community and food-web approaches to restoration: An ecological assessment of created and natural marshes influenced by river diversions*" (<https://restorefoodweb.lumcon.edu/>), funded by the NOAA RESTORE Science program.

More information can be found at:

https://restoreactscienceprogram.noaa.gov/projects/marshes#fvp_1,9s
(https://restoreactscienceprogram.noaa.gov/projects/marshes#fvp_1,9s)

- West Point a la Hache (WPH) area and **Lake Hermitage Marsh Creation Project**, within Barataria Bay, Plaquemines Parish, Louisiana



Location map, with New Orleans, Louisiana, in the upper-left. Orange box outlines the study area.

- Two created marshes (LHA & LHB) and one natural marsh (LHC) within the Lake Hermitage Marsh Creation Project area

1. LHA filled Aug 2012 – Oct 2013
2. LHB filled Dec 2013 – May 2014

- Three natural marshes at varying distances from the WPH siphon (WPH1, WPH2, PS07)



Sampling sites showing restored sites LHA and LHB (in yellow) and natural sites, LHC, WPH1, WPH2, and PS07 (in white). The siphon on the Mississippi River is in the upper-right, nearest to WPH1.

- Aboveground vegetation (g/m^2) was determined along three transects into the marsh at 1, 10, 25, 50, and 100 m inland. Data from 2018 are shown.
- At one representative transect per marsh location, soil electrical conductivity, pH, and temperature was measured from the surface (0-2 cm) and depth (8-10 cm) at 1, 10, 100 m inland for each marsh and 1 m off the marsh edge.
- Soil and sediment cores were collected and sectioned into 2-cm thicknesses in the field prior to being frozen.
- Microbial diversity determined after DNA extraction using a modified sucrose lysis method. V4 regions of bacterial and archaeal 16S rRNA genes were sequenced and taxonomy was assigned according to the Silva 132 database using the mother pipeline. Operational Taxonomic Units (OTUs) were determined to identify shared microbial groups. Data from 2018 are shown.
- Microbial biomass was estimated by phospholipid fatty acid methyl ester (FAME) analysis, and microbial community structure was evaluated according to FAME biomarkers. Data from 2018 are shown.

- Statistical analyses of field physicochemistry, vegetation, and microbial diversity results were done by using PAST, and included non-parametric multivariate analysis of variance (e.g., NPMANOVA) to compare the distribution of microbial taxa and Spearman's rho correlations.











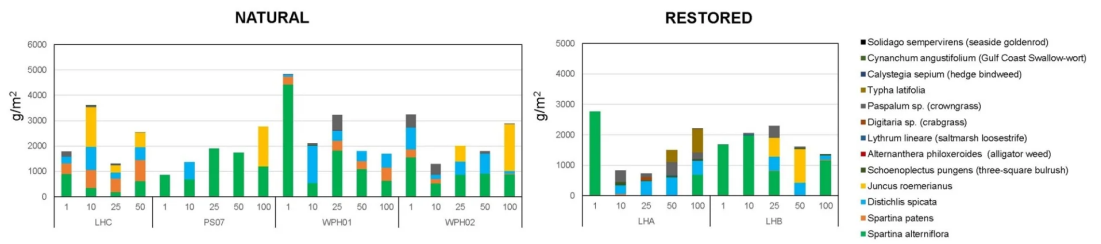
ACKNOWLEDGEMENTS

This research was made possible with funds from the National Oceanic and Atmospheric Administration's (NOAA) RESTORE Act Science Program, U.S. Department of Commerce, under award NA17NOS4510091 to Louisiana State University and associated subcontracts. **The statements, findings, conclusions, and recommendations are those of the authors and do not necessarily reflect the views of the NOAA RESTORE Act Science Program or the U.S. Department of Commerce.** Field work assistance was provided by Abigail Harmon and Stephanie Plaisance. Microbial sample processing was carried out with assistance from Abigail Harmon and Julie Coulombe at the University of Tennessee.

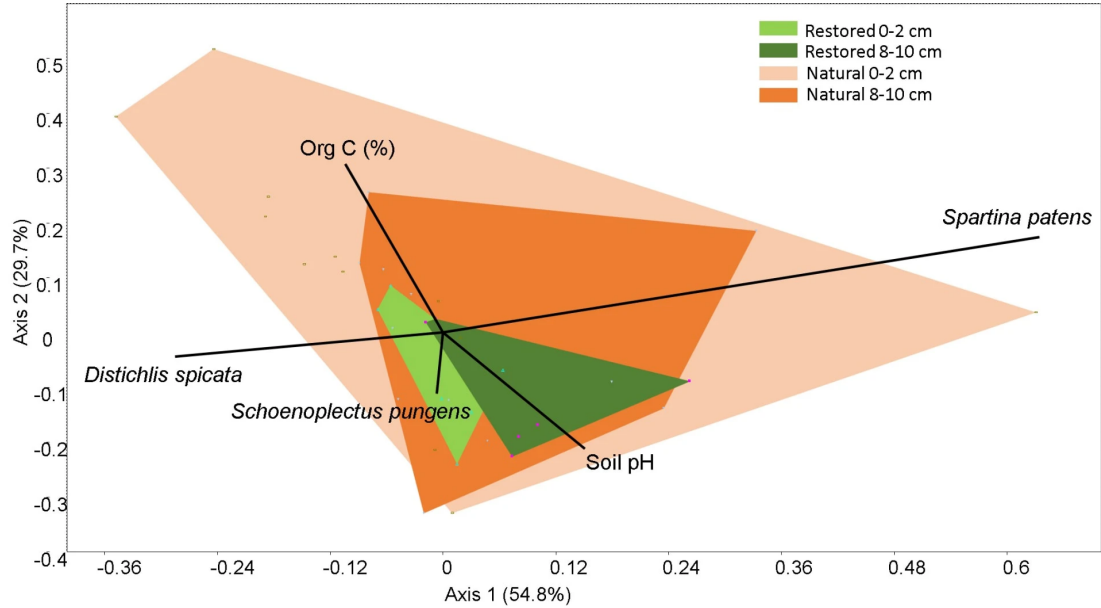
This research was done on the ancestral lands of the Chitimacha Tribe of Louisiana, Choctaw Nation, United Houma Nation, and others. We recognize and respect their cultural practices related to land stewardship and strive to understand the history of these lands, much of which has been impacted by centuries of colonization, racism, and violence.

MARSH VEGETATION & RELATIONSHIPS TO MICROBIAL COMMUNITIES

Aboveground plant biomass for the natural marshes was predominately *Spartina alterniflora*, with other marsh plant species like *Spartina patens* and *Distichlis spicata*. Restored marshes had less traditional marsh vegetation, despite efforts to plant and grow them on the newly constructed marsh platforms. The elevation of the restored marshes likely affects whether or not *S. alterniflora* is successful, as *S. alterniflora* dominates the plant community near the shoreline.



Aboveground biomass (in g/m²) for different plants found at the natural and restored marsh locations, with increasing distance inland.



Canonical correspondence analysis (CCA) ordination of microbial communities from natural and restored marsh soil samples against physicochemistry and vegetation (trace p = 0.05).

Controls on the microbial diversity of the restored marshes, being less variable than the natural marshes, can be explained by the presence of plants not considered as traditional marsh species, but also the lack of organic carbon and soil pH. The lower organic carbon content is likely due to the limited time that the marsh platform has been accumulating carbon, and the lower soil pH is likely due to the sandy sediment, sourced from nearby river channel, and limited mineralogic buffering capacity. The restored microbial communities occupied CCA space within the ordination space of deeper soil samples at natural marshes.

The spatial ordination of microbial community compositions from the natural marshes, being more variable, can be explained by the presence of traditional marsh plant species add a build-up of organic carbon.

The distinct plant-microbe associations at the created marshes likely affect habitability and sustainability for other marsh organisms, but these relationships have yet to be explored. Invertebrates relying on native vegetation for their diet may either not inhabit the restored marsh or adapt to available subsidies. With time, the expectation would be that restored marsh plant biomass and microbial diversity would mimic natural marshes, but continued monitoring will be necessary to understand how these linkages develop and affect basic soil processes.

AUTHOR INFORMATION

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ABSTRACT

Tidal marsh construction projects in Louisiana, under the Coastal Wetlands Planning, Protection and Restoration Act, are meant to restore critical habitat for fisheries and to combat erosion, land loss, and impacts from disturbance. Monitoring restoration success typically includes evaluating survival/mortality of aboveground species. However, there has been limited research to evaluate the microbiology, soil properties, biogeochemical processes, and microbial-vegetation associations of created marsh soils, despite the important roles that soil microbes play in the recruitment and establishment of aboveground vegetation and the importance of specific plant species creating different belowground conditions (e.g., redox, nutrient availability). The purpose of this project was to assess soil microbial communities from natural marshes and nearby created marshes associated with the Plaquemines Parish Lake Hermitage Marsh Creation Project (LHMCP). LHMCP land creation was from 2012–2014. Marshes were sampled in 2018, 2019, and 2021, in transects up to 100 m inland. Soil organic C content and soil pH were consistently lower at LHMCP sites compared to natural marshes, but LHMCP soil microbial diversity was higher. LHMCP soil had different relative abundances of specific microbial groups associated with N and S cycling compared to natural marsh soils, and soil microbial diversity strongly correlated to plant type. Plant biomass was lower at LHMCP sites, but richness was comparable to or higher than natural marshes, although plant diversity was often non-traditional marsh species. Natural marsh soil microbial diversity strongly correlated with typical marsh plants (e.g., *Spartina alterniflora*, *Juncus roemerianus*), but LHMCP soil microbial diversity correlated to higher *Paspalum* spp. (crowgrass) and *Schoenoplectus pungens* (common bulrush) biomass. The distinct plant-microbe associations at the created marshes likely affect habitability and sustainability for other marsh organisms, but these relationships have yet to be explored. With time, the expectation would be that created marsh above and belowground biomass and microbial diversity would begin to mimic natural marshes, but continued monitoring will be necessary to understand how these linkages develop and affect basic soil processes.