

# Microbiome landscape changes of the coastal of Yucatán

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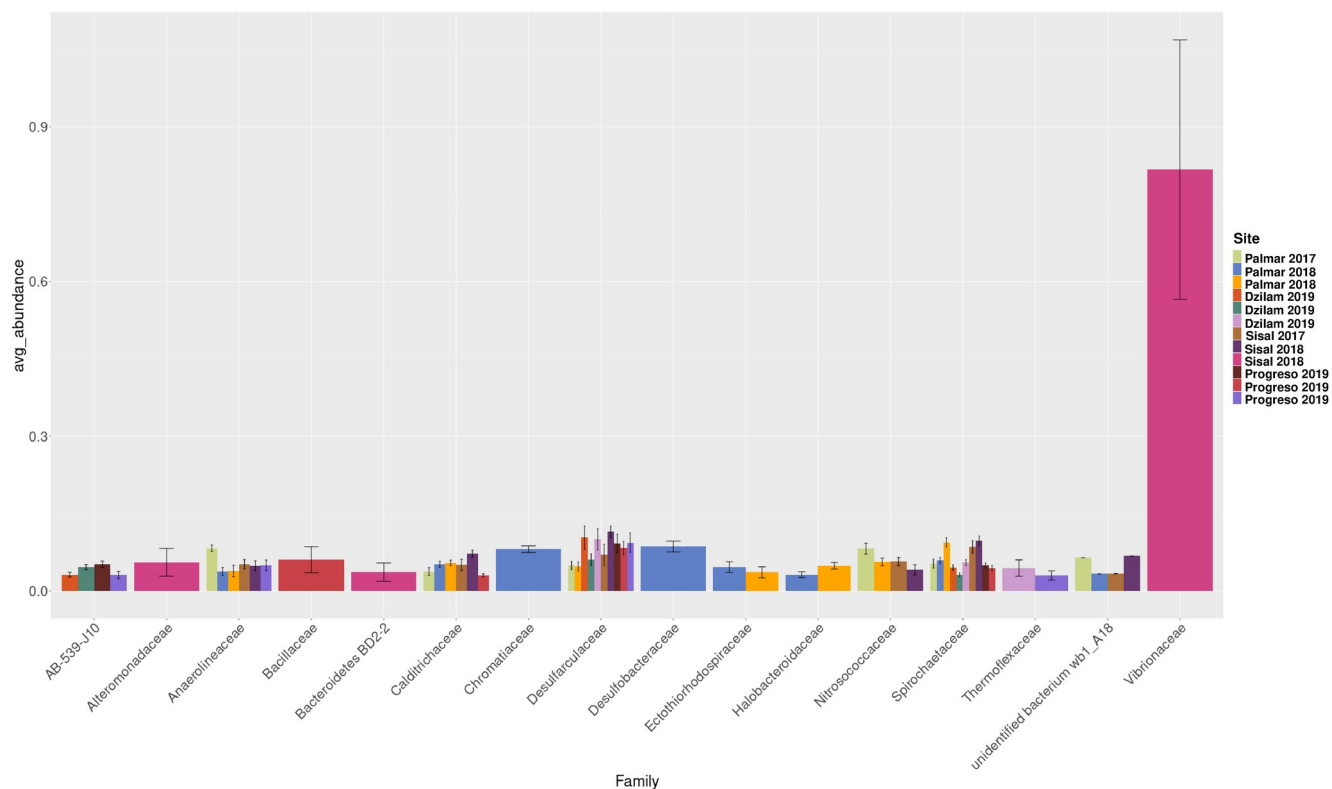
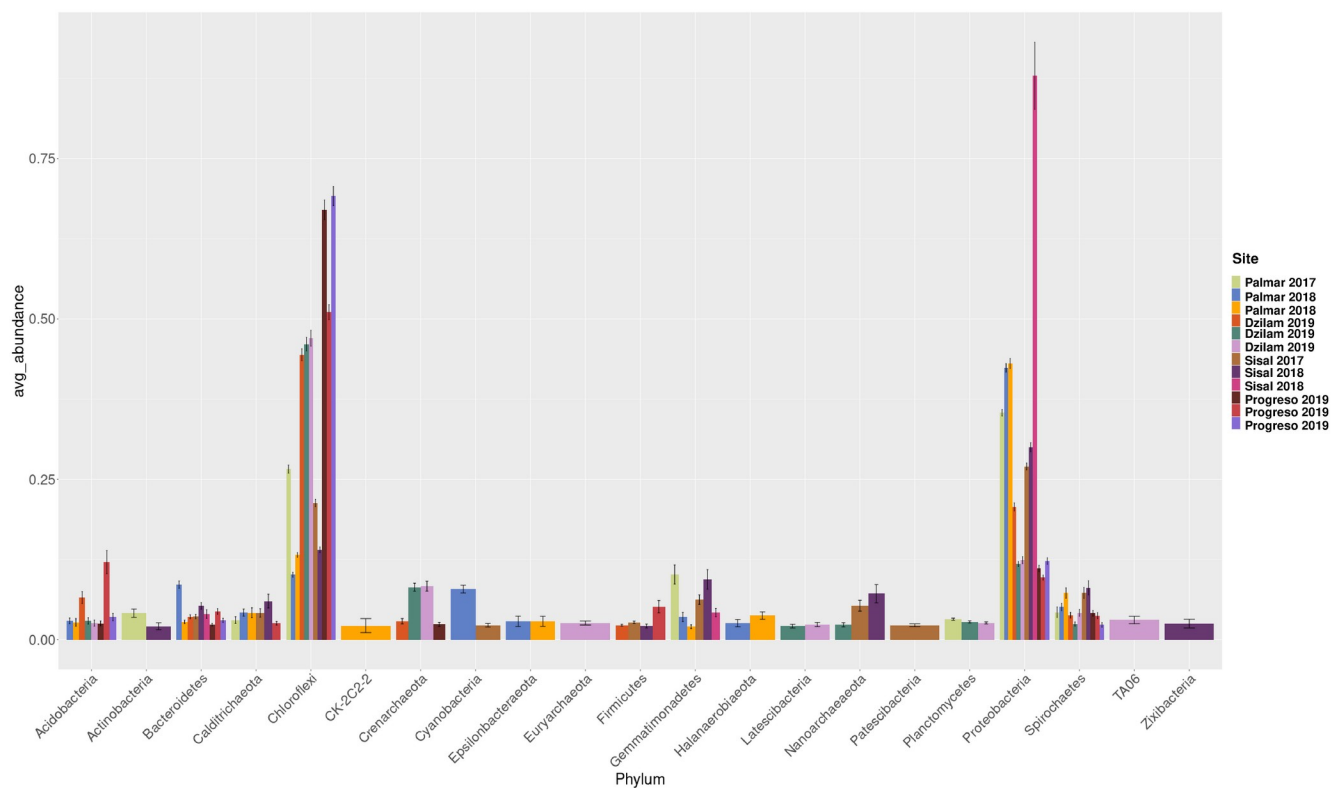
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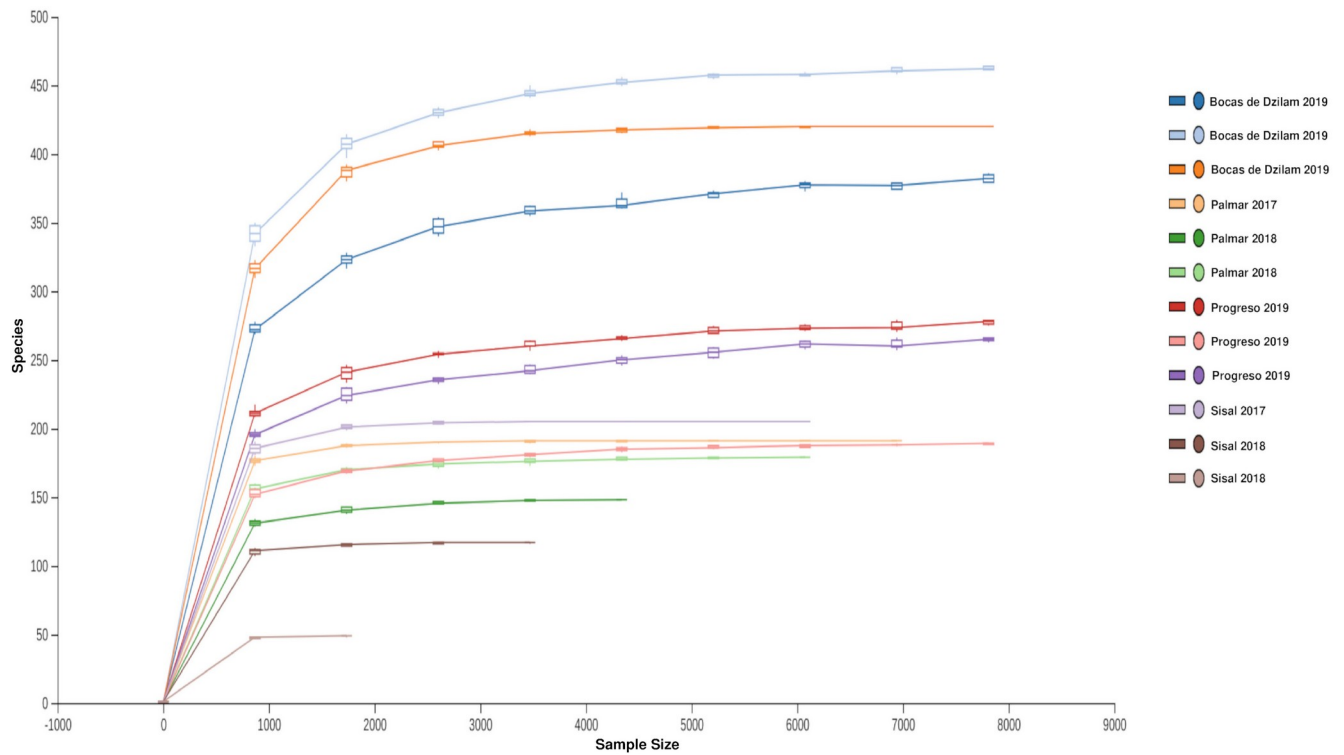
## Supplementary Figures.



**Supplementary Figure S1.** Sampled sites at Sisal (left) and Progreso (right). The garbage deposited in the wetlands by the residents can be observed.

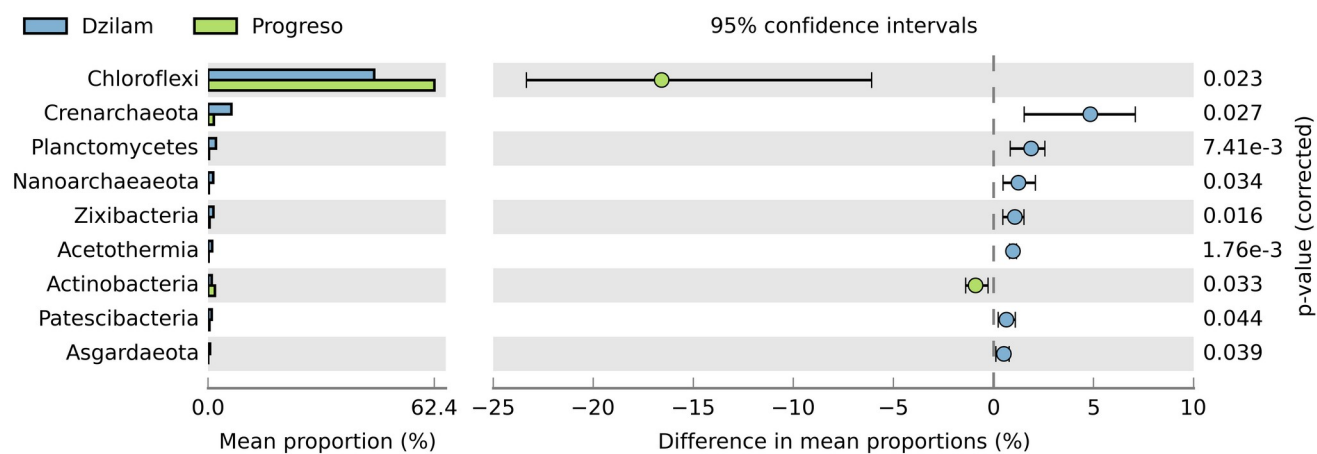


**Supplementary Figure S2.** Relative abundance of bacteria composition and their standard deviation across the four wetland sampling sites at (upper) phylum and (bottom) family levels. Bocas de Dzilam: conserved site; El Palmar: conserved site; Progreso: contaminated site; Sisal: contaminated site. X-axis: taxon. Y-axis: relative abundance of taxon.

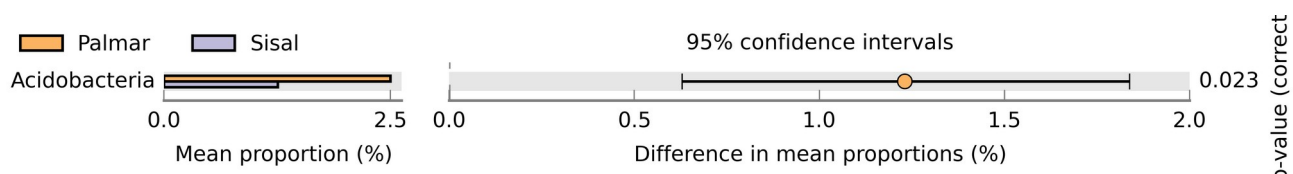


**Supplementary Figure S3.** Rarefaction curves-based of the phylogenetic prokaryotic diversity of the studied sites. X-axis: Number of species annotated. Y-axis: Sample size as number of reads obtained from sequencing.

**A**

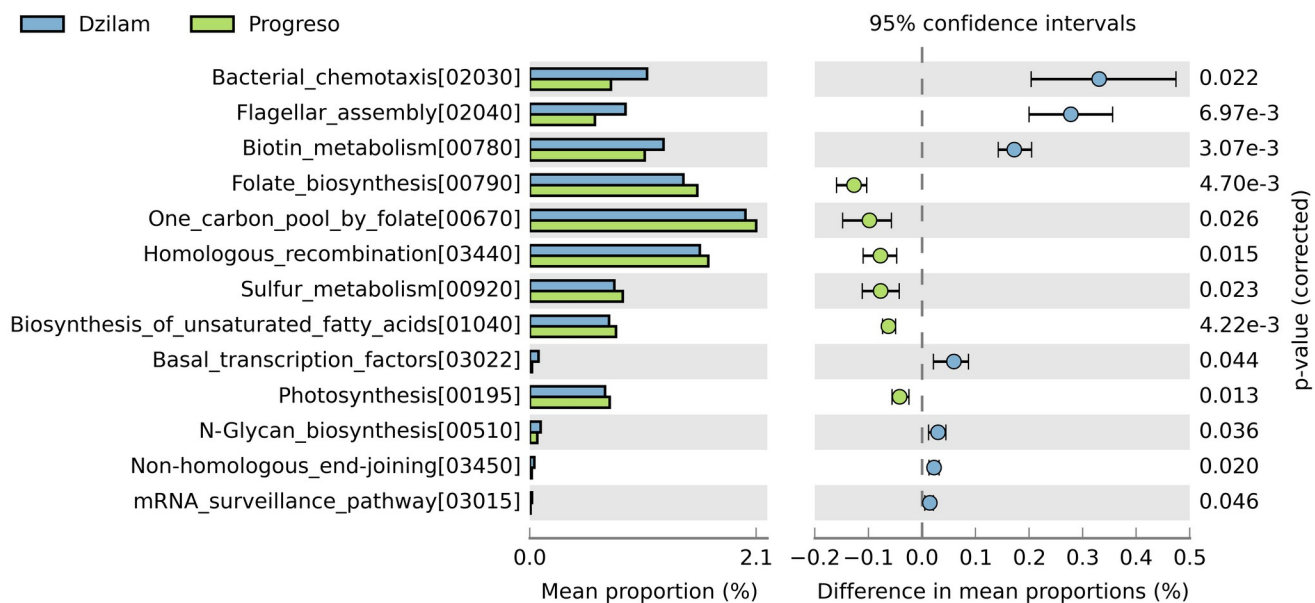


**B**

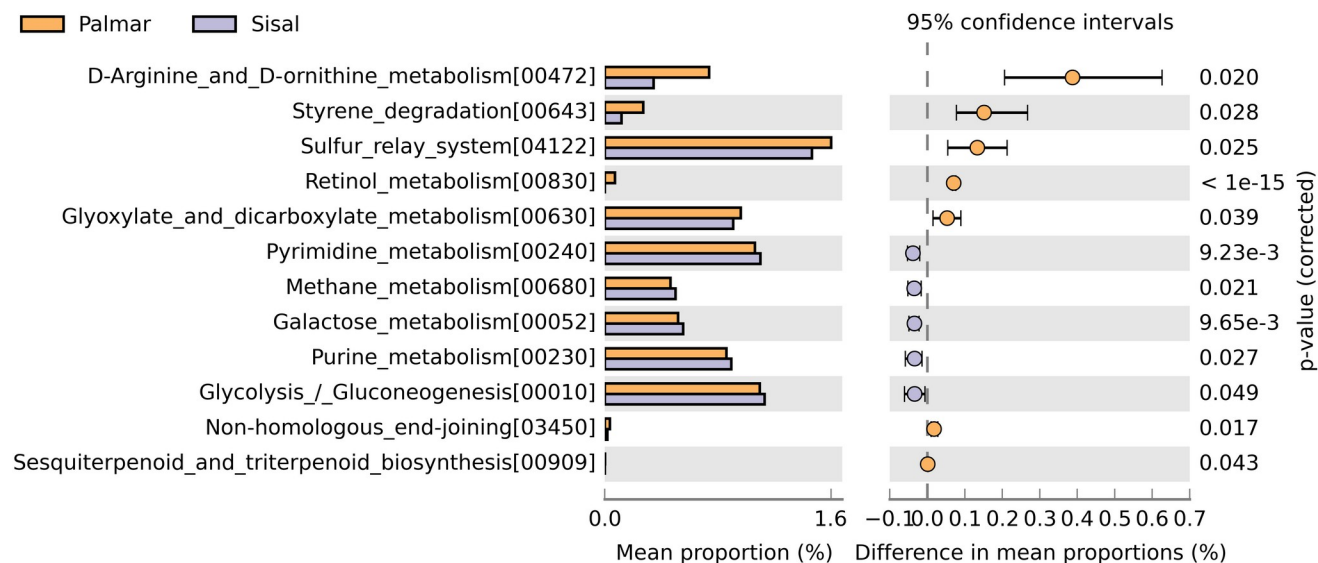


**Supplementary Figure S4.** Metataxonomic profile comparisons of differentially phylotypes between conserved sites (Bocas de Dzilam and El Palmar) and contaminated sites (Progreso and Sisal) using STAMP analysis. **A:** analysis at phylum level of Bocas de Dzilam and Progreso samples. **B:** analysis at phylum level of Palmar and Sisal samples.

A



B



**Supplementary Figure S5.** Metabolic pathways profile comparisons between study sites. **A:** Bocas de Dzilam and Progreso. Blue bar: conserved site; green bar: contaminated site. **B:** El Palmar and Sisal. Orange bar: conserved site; purple bar: contaminated site. Statistical analyzes were done with STAMP analysis. Analyses were carried out at level 3 of specific pathway associated with a specific function using KEGG database.