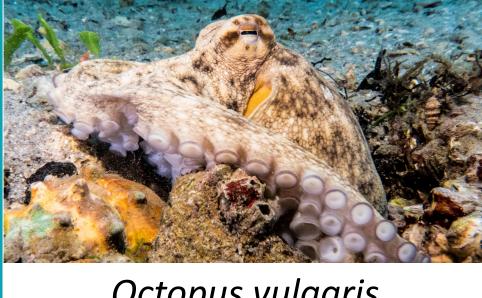
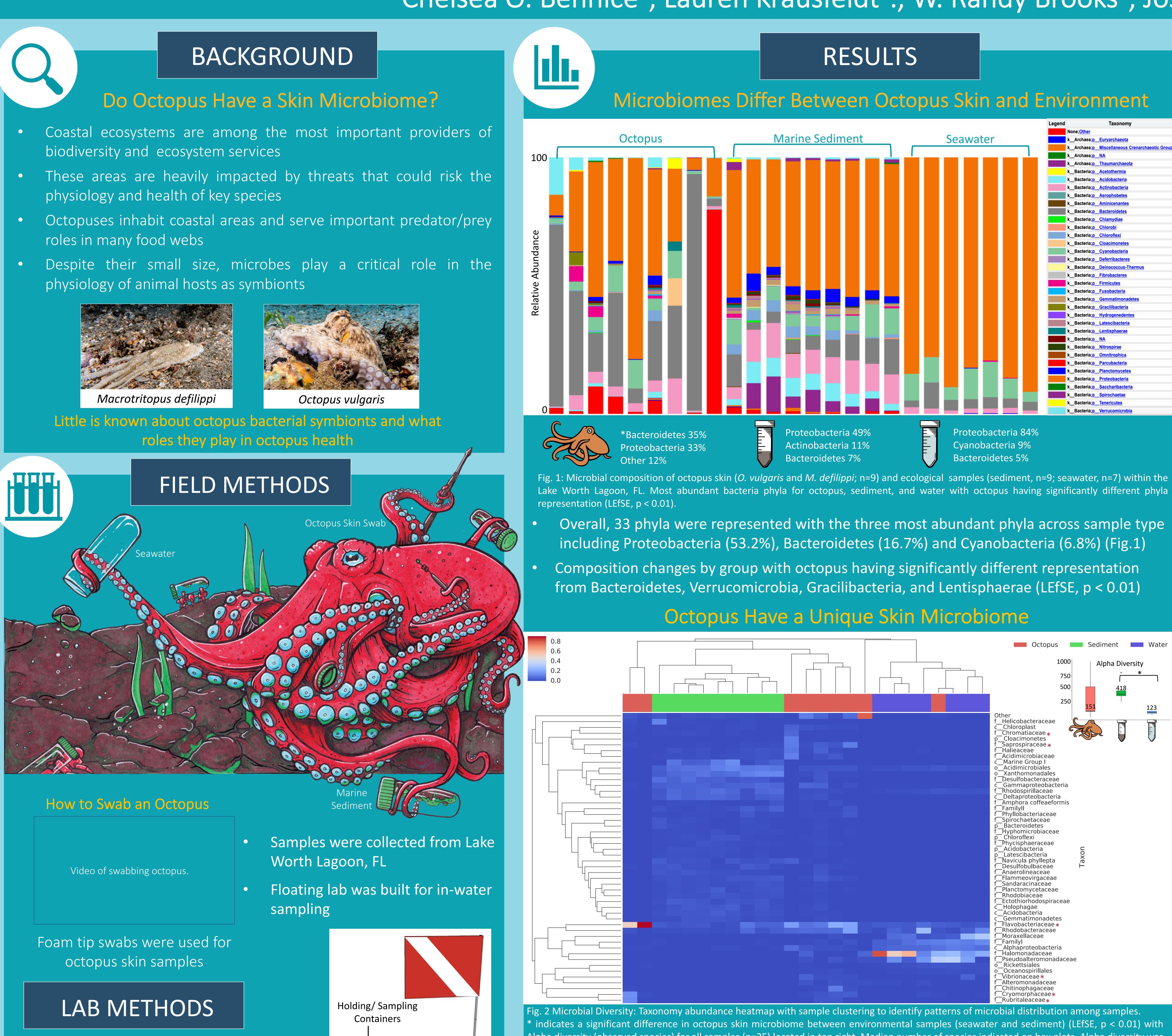
### Unique Skin Microbiome: Insights to Understanding Octopus Health FAI in a South Florida Lagoon FLORIDA ATLANTIC **UNIVERSITY** \*Chelsea O. Bennice<sup>1</sup>, Lauren Krausfeldt<sup>2</sup>., W. Randy Brooks<sup>1</sup>, Jose V. Lopez<sup>2</sup>



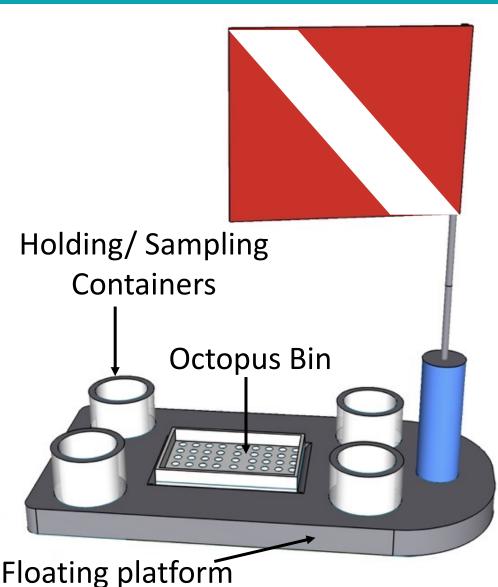
- biodiversity and ecosystem services
- physiology and health of key species
- roles in many food webs
- physiology of animal hosts as symbionts







- DNA Extraction with DNeasy PowerSoil Kit
- DNA sequencing using Illumina MiSeq
- Bacterial 16S rRNA gene V3-V4 region



Alpha diversity (observed species) for all samples (n=25) located in top right. Median number of species indicated on box plots. Alpha diversity was different between seawater and sediment samples (ANOVA, Games-Howell's multiple comparisons; \* indicates a significant difference p < 0.05).

Microbial species richness was greatest for sediment followed by octopus then water

Octopuses have unique taxa comprising their microbiome from 6 phyla, 17 families, 25 genera, 13 identifiable species (top families shown in Fig. 2)

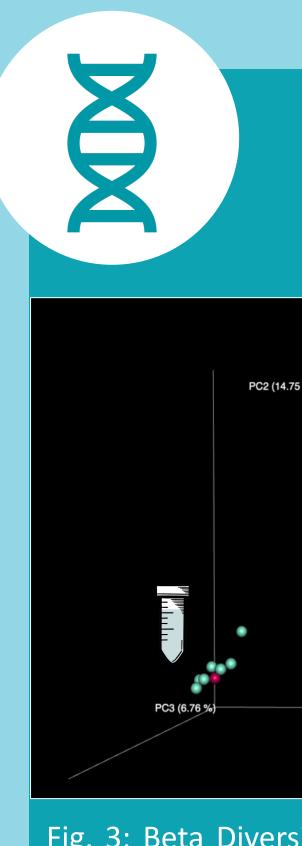


Fig. 3: Beta Diversity Plot (PCA, Bray-Curtis dissimilarity) for differences across microbiome samples plotted (ANOSIM; R = 0.76, p = 0.001) and Table 1: Bacteria by family, genus, and species (if identifiable) associated with octopus species (*M. defilippi*, n = 4; *O. vulgaris*, n = 5). \* indicates significance (LEfSE, p < 0.05).



- Octopuses have a unique microbiome that differs from their environment which is dominated by Bacteroidetes
- Bacterial symbionts consisted of both non-pathogenic and possibly pathogenic bacteria
- Flavobacteriaceae, Rubritaleaceae, Vibrionaceae
- Some members of the octopus skin microbiome were species-specific
- Saprospiraceae could be involved in the organic Carbon breakdown on *M. defilippi*

Symbiotic microbes were identified and may aid in protecting octopuses, a key player in many marine foods webs





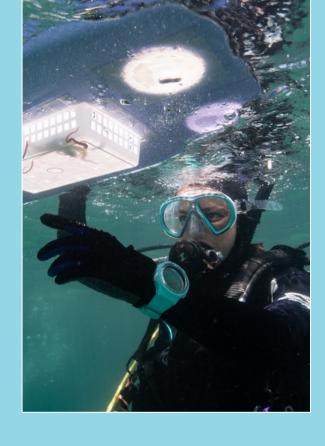
## RESULTS

### Octopus Species-Specific Microbiome

		Family	Genus species	*Octopus
%)		Flavobacteriaceae	Winogradskyella echinorum	M. defilippi
			Tenacibaculum mesophilum	M. defilippi
		Saprospiraceae	Portibacter sp18825	M. defilippi
			NA. sp18863	M. defilippi
			NA. sp18874	M. defilippi
		Vibrionaceae	Vibrio harveyi	M .defilippi
	PC1 (41.05 %)	Cryomorphaceae	Crocinitomix sp16188	M. defilippi
		Flavobacteriaceae	Polaribacter sp17445	O. vulgaris
		Rubritaleaceae	Rubritalea sp69326	O. vulgaris

Microbial community composition differs across groups (Fig.3) Octopus species have similar contributing bacteria to microbiome on the family level, with the exception of Rubitaleaceae (O. vulgaris) Microbiomes differ at the genus and/or species level for octopuses M. defilippi has more unique bacteria contributing to its microbiome than *O. vulgaris* 









# TAKEAWAYS

## Octopus Microbiome May Play a Role in Lifestyle

• Group containing pathogen-suppressing bacteria

\*Chelsea Bennice, Presenter





cbennice@fau.edu