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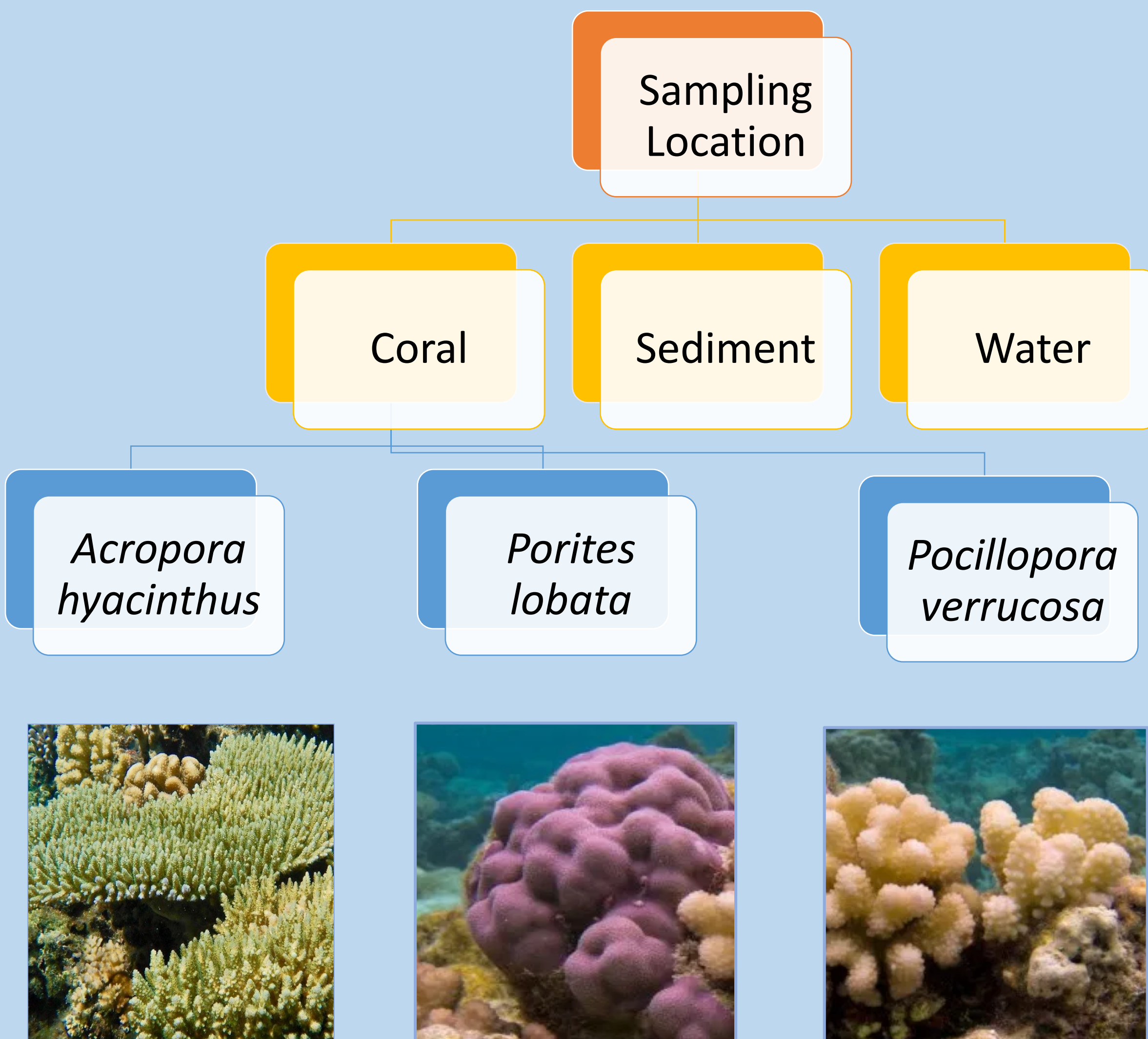
## MOTIVATION

Coral microbiomes— corals' symbiotic bacteria, archaea and eukaryota— are integral components of whole-organism persistence. Natural and human-induced change can alter microbiome communities, increasing coral vulnerability. Understanding inherent spatio-temporal variability of coral microbiomes is fundamental to our ability to quantify resilience and observe potential tipping points. Thus, we characterized microbiomes for the tropical south Pacific island of Mo'orea, French Polynesia (17.490° S, 149.826° W).

## HYPOTHESIS

Microbiome host, habitat and sampling location will house distinct microbiomes (beta diversity) that differ between seasons.

## SAMPLING DESIGN



Factors that distinguish microbiomes

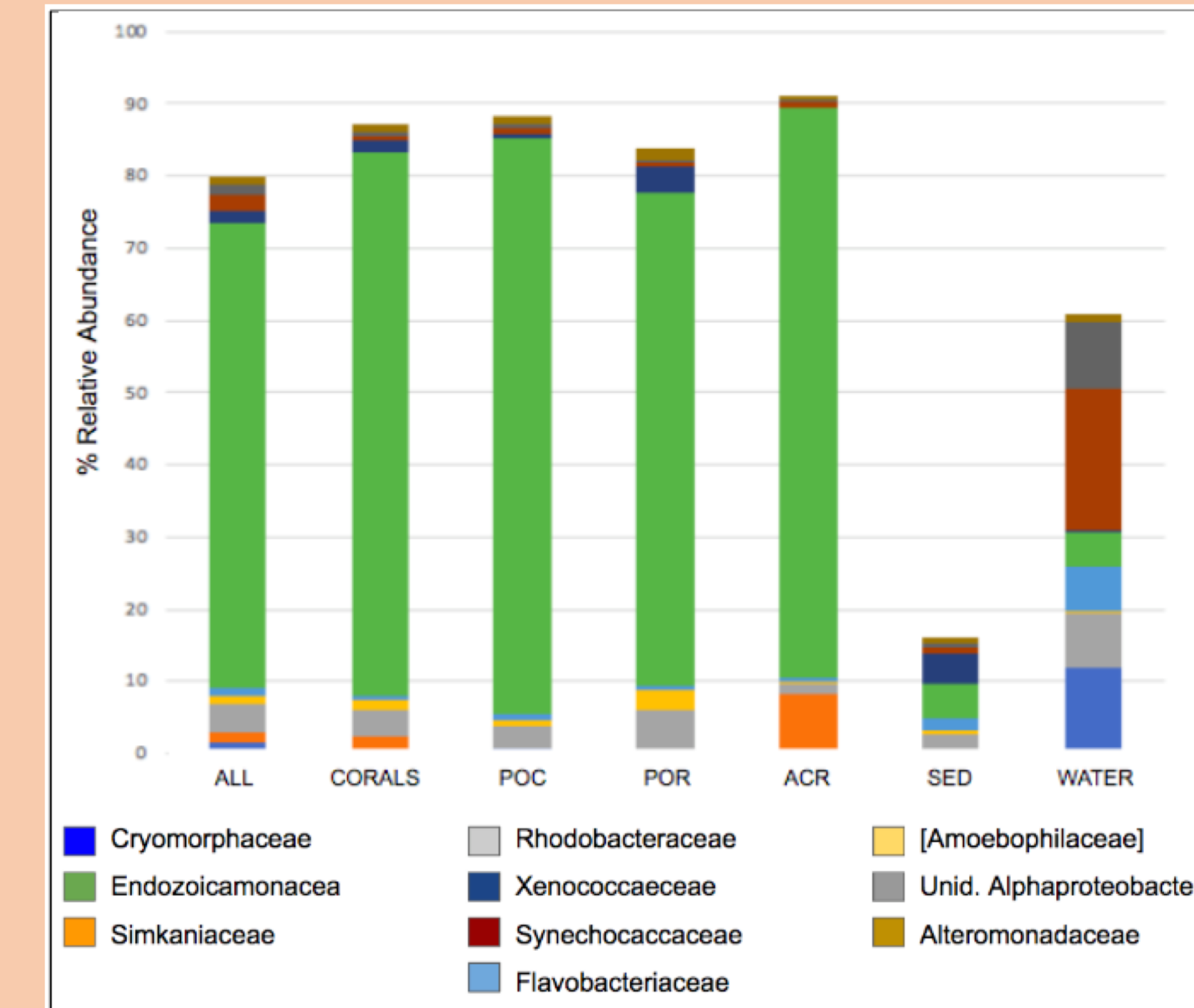
|                   | Sediment | Water | <i>P. verrucosa</i> | <i>P. lobata</i> | <i>A. hyacinthus</i> |
|-------------------|----------|-------|---------------------|------------------|----------------------|
| Host              | X        | X     | X                   | X                | X                    |
| Sampling Location | X        |       | X                   | X                | X                    |
| Habitat           | X        | X     | X                   | X                | X                    |
| Island Side       | X        | X     |                     | X                | X                    |
| Season            | X        | X     |                     | X                |                      |

Microbiomes are host/ feature specific and vary at different spatial scales. Coral microbiomes are distinct from those of sediment and water and are further distinguished by species. *Porites lobata* was the only coral with seasonally different microbiomes. The factor Season interacted with three spatial scales in Sediment microbiomes (highlighted red and yellow). X means PERMANOVA  $p < 0.05$ .

- Reef microbiomes are specific to their host, whether a reef feature or species
- Host microbiomes vary differently across island-wide scales, and fluctuate with the seasons differently--if at all.
- Fine-scale shifts in % abundance of taxa contribute to different microbiomes.
- The bacterial family *Endozoicamonaceae*, associated with carbon cycling, represented 75% of coral microbiomes and was the most deterministic in distinguishing groups (SIMPER analysis, cumsum < 0.44)
- Just 25% of coral microbiome sequence abundance represented the vast majority (99%) of the number of taxa present.

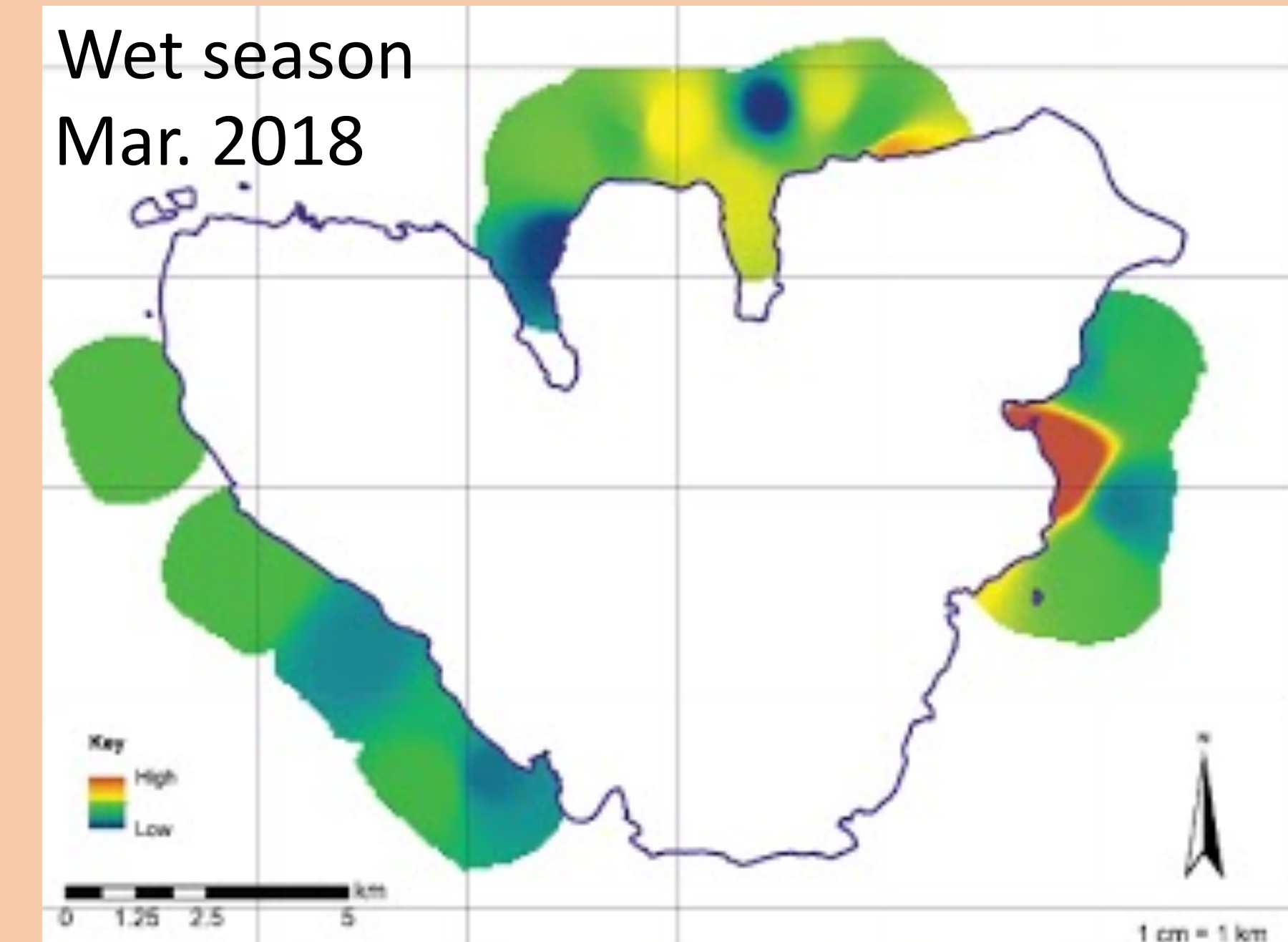
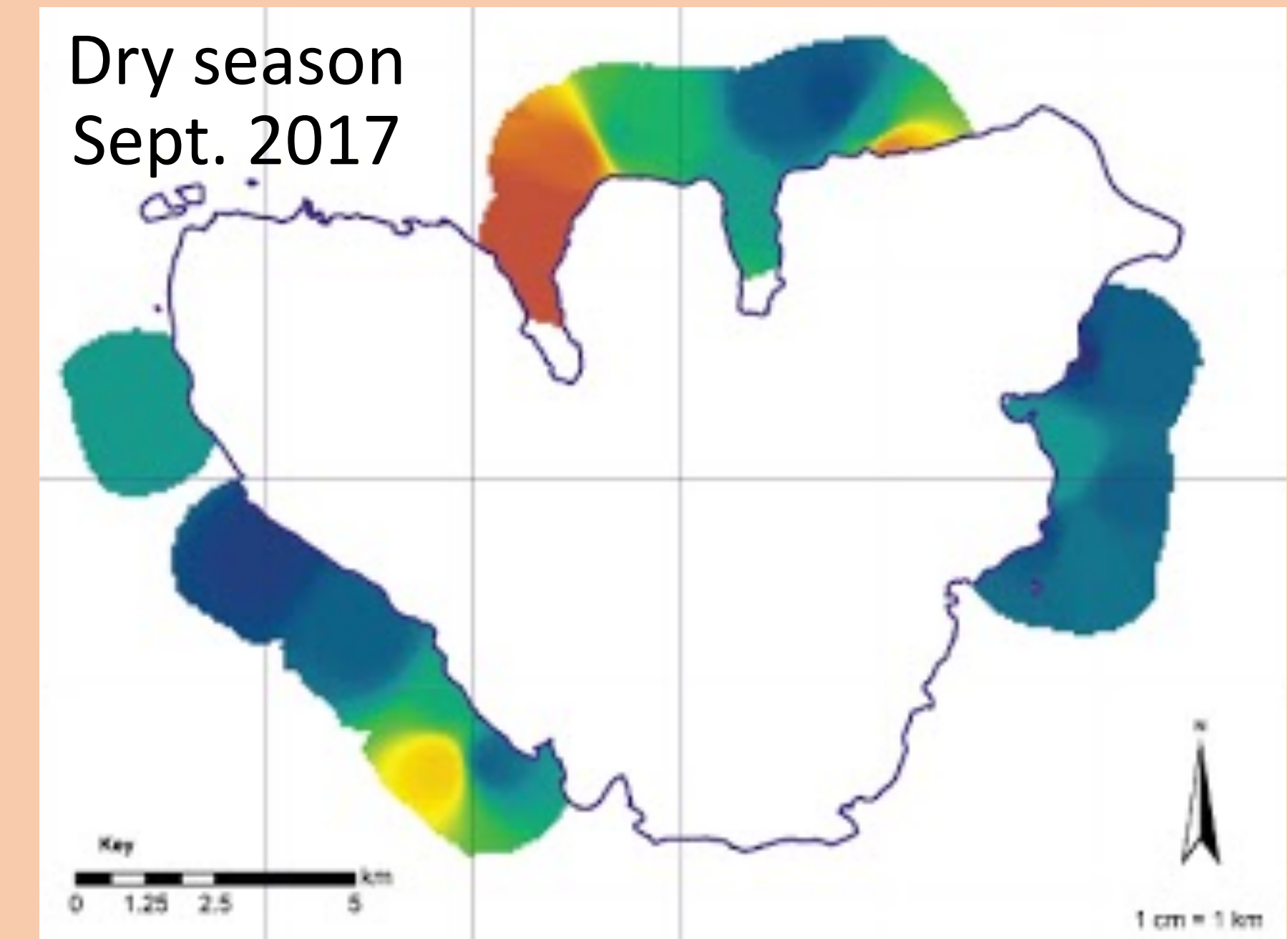
## RESULTS

% Abundance of Most Abundant Taxa



Top 10 most relatively abundant taxonomic families present in the sample pool 1) Microbiomes = all samples, 2) All coral samples. 3-6) Each coral species, POC = *P. verrucosa*, POR = *P. lobata*, ACR = *A. hyacinthus* 7) Sediment 8) Water samples.

Coral microbiome diversity peaks vary spatially and seasonally



Coral microbiome Chao1 diversity between seasons. Color scale by quartiles: red=upper, green=median, blue=lower. Additional maps of land use change, sedimentation, nitrogen, temperature & chlorophyll concentrations suggest coral microbiome diversity is affected by a combination of factors. (Visualization by Bran Black, OSU Geography PhD Candidate)

## ANALYSIS

We amplified the V4 region of the 16S rRNA gene (806R/515F) using modified Earth Microbiome Project protocols. Libraries were sequenced on the Illumina Mi-Seq at the CGRB of OSU. Quality control of raw reads and creation of Amplicon Sequence Variants (ASVs) was completed with Dada2 (in R). Taxonomy was assigned with Greengenes database v.13.8. 476 samples were rarefied to 1028 sequences using phyloseq. Permutational Analyses of Variance (PERMANOVA), pairwise comparisons (with Bonferroni correction) and SIMPER analyses were conducted using vegan and  $p < 0.05$ .

## DISCUSSION

Fine-scale spatial differences in microbiome composition allow us to interrogate factors driving microbiome shifts (including nutrient enrichment/pollution and sedimentation), helping to untangle host-specific trends and to better understand the overall causative factors of reef and island health.

Future detection of microbiome community shifts can provide indications of change and reveal anthropogenic signatures in the Mo'orea Island Socio-Ecological Coral Reef System. Scientists can partner with community members to highlight areas of interest for policy and management strategies.

Spatial variability was characterized within nested spatial scales of Island Side, Site, Reef Habitat and Sampling Locations that were distributed around Mo'orea island. At each Sampling Location seawater, sediment and 6 separate colonies of three species of prolific corals were sampled during one wet and one dry season of one year (September 2017 and March 2018).