

Microbial Composition in Soil and Water column of the Everglades Stormwater Treatment Areas



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Why study microbiome in the Everglades Stormwater Treatment Areas (STAs)?

STAs are designed to remove nutrients

Well controlled system

Lots of abiotic, biotic, and hydrology data available

Lack of research on microbiome



“Bacteria have sculpted the world we live in”

- Dianne Newman

Research goals

What is the structure of microbial communities in STAs?

Alpha-diversity

Beta-diversity

Why do these microbes have their particular distributions?

What are the functions of these microbes?

Methods

Sampling:

2 cells x 3 locations x 5 depths x 3 replicates

Methods:

DNA extractions

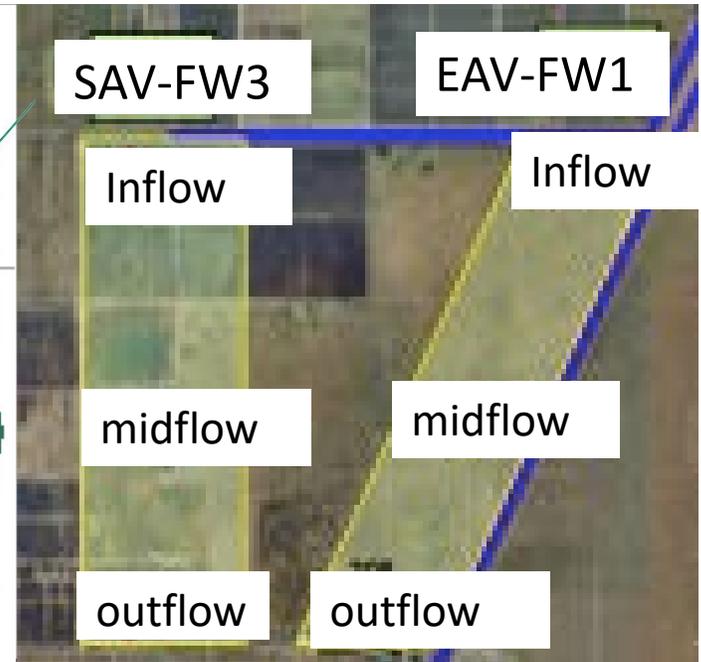
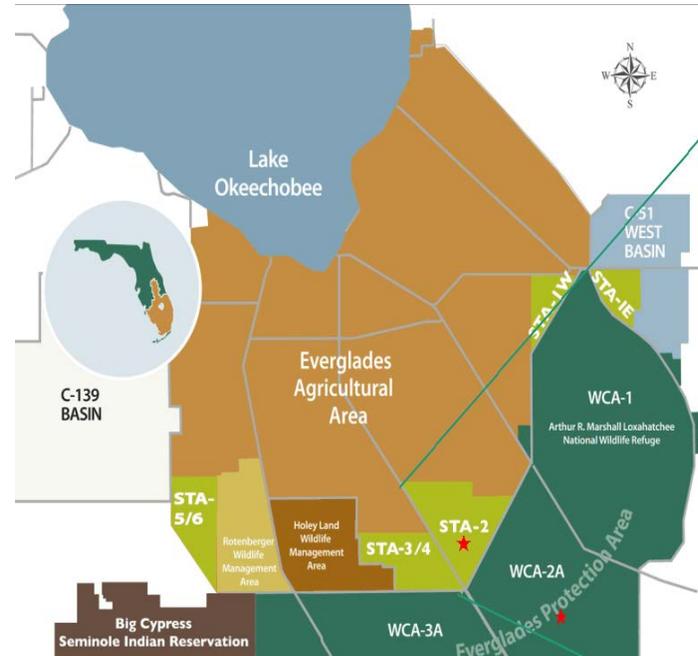
16S survey: V4

primers

Illumina sequencing

Bioinformatic

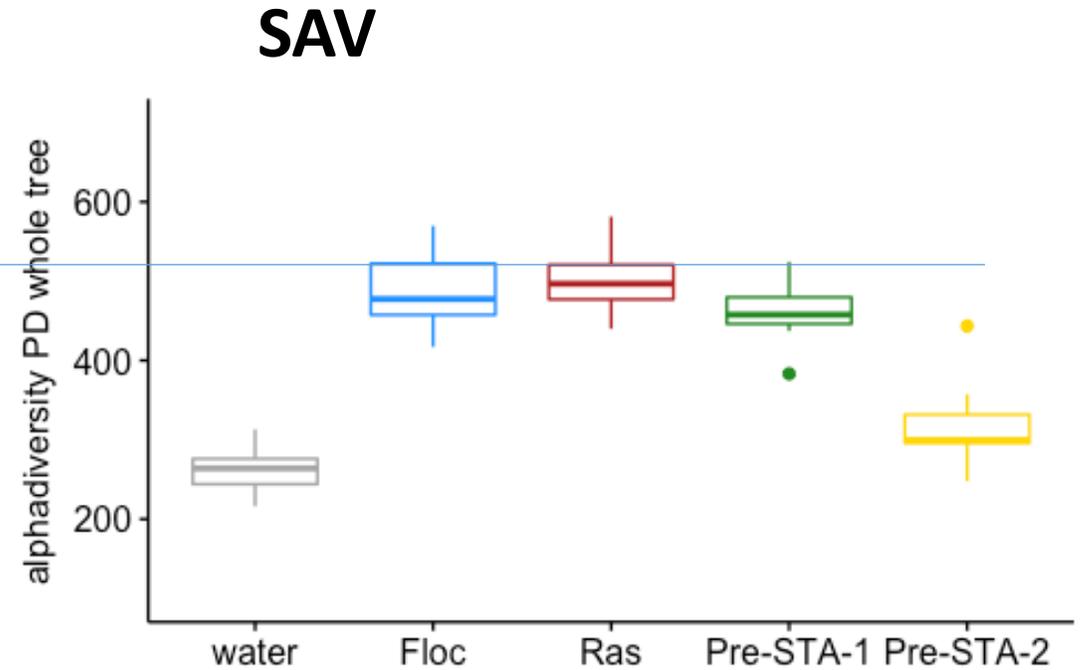
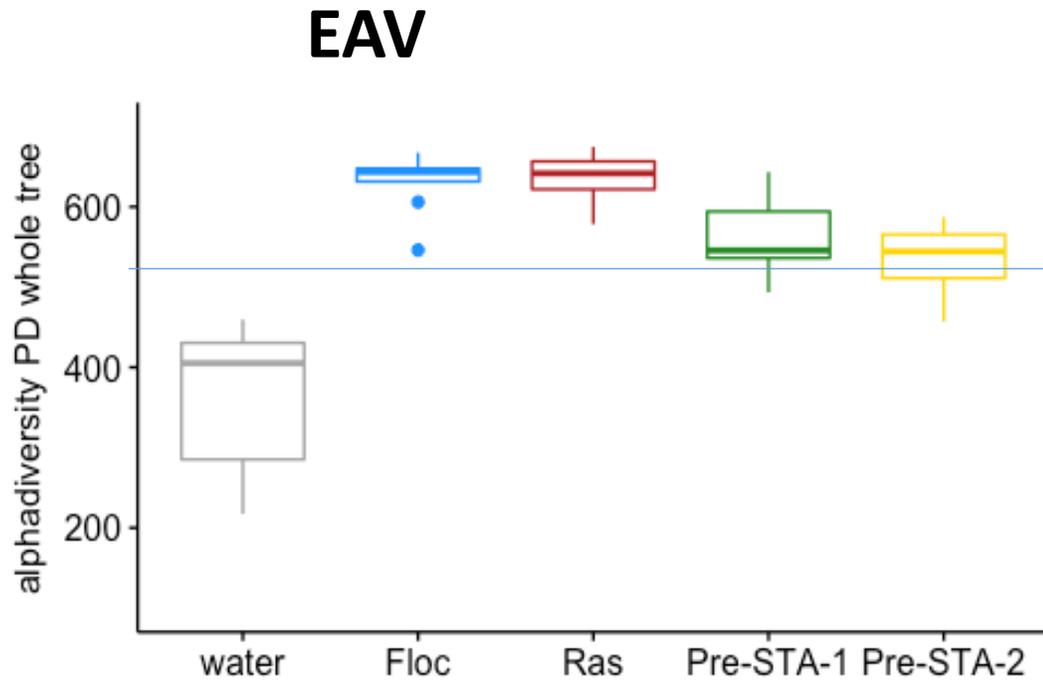
approaches: QIIME, R



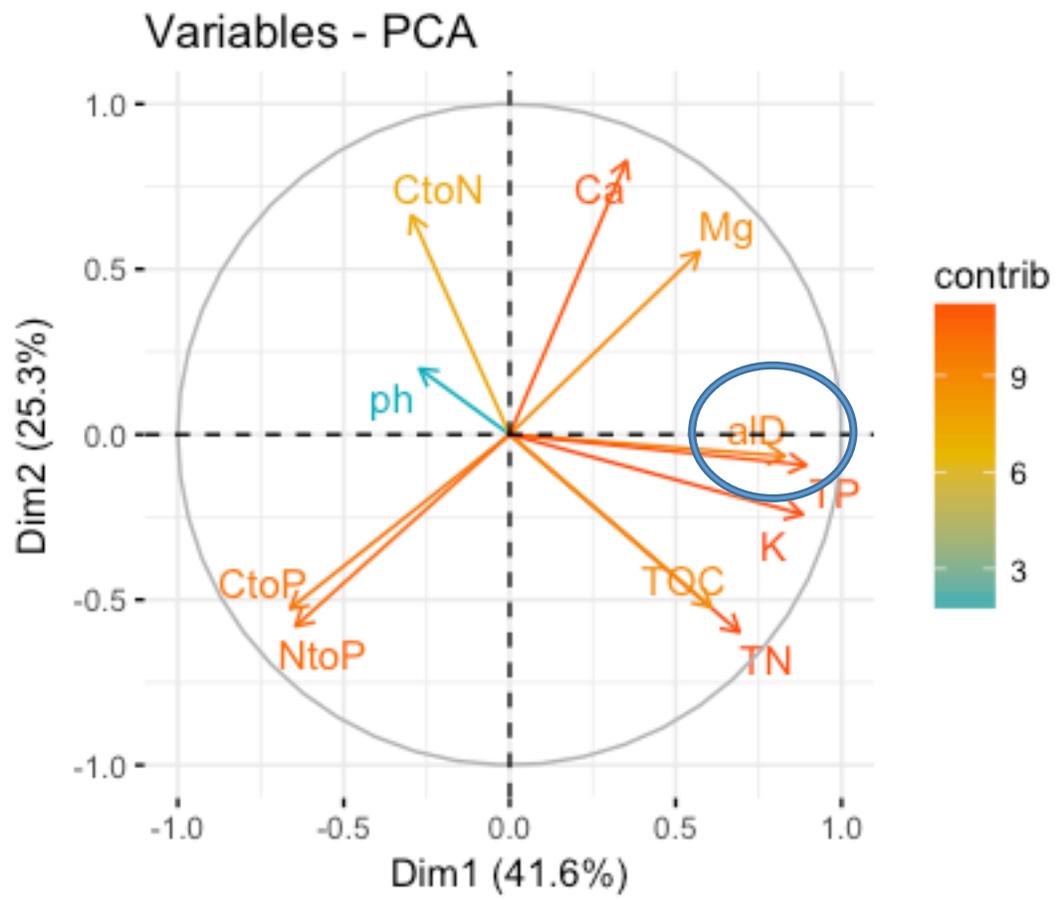
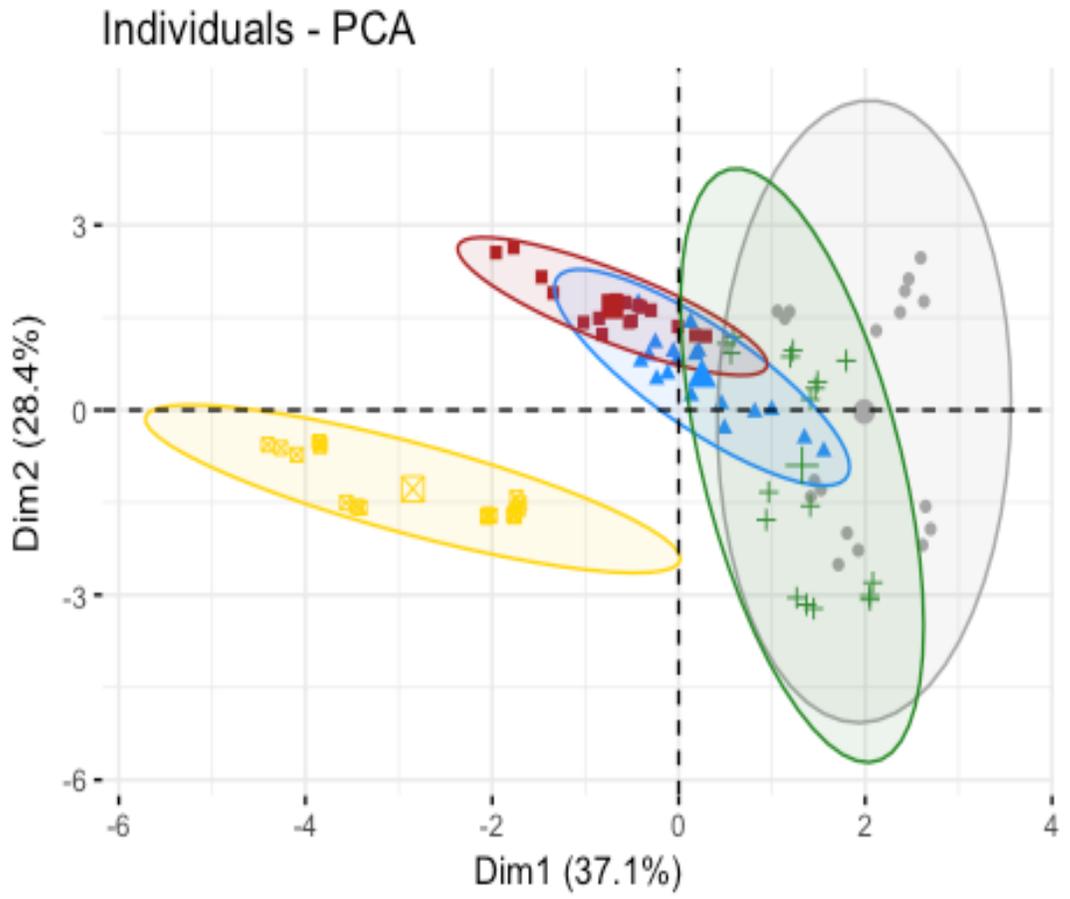
Concepts

- **Alpha-diversity**: how many species are there (measure of the diversity within sample)
- **Beta-diversity**: How one sample is different from others (measure of the difference between samples)
- **Phyla**: The highest classification level
- **OTU**: lowest classification level (unique sequences)

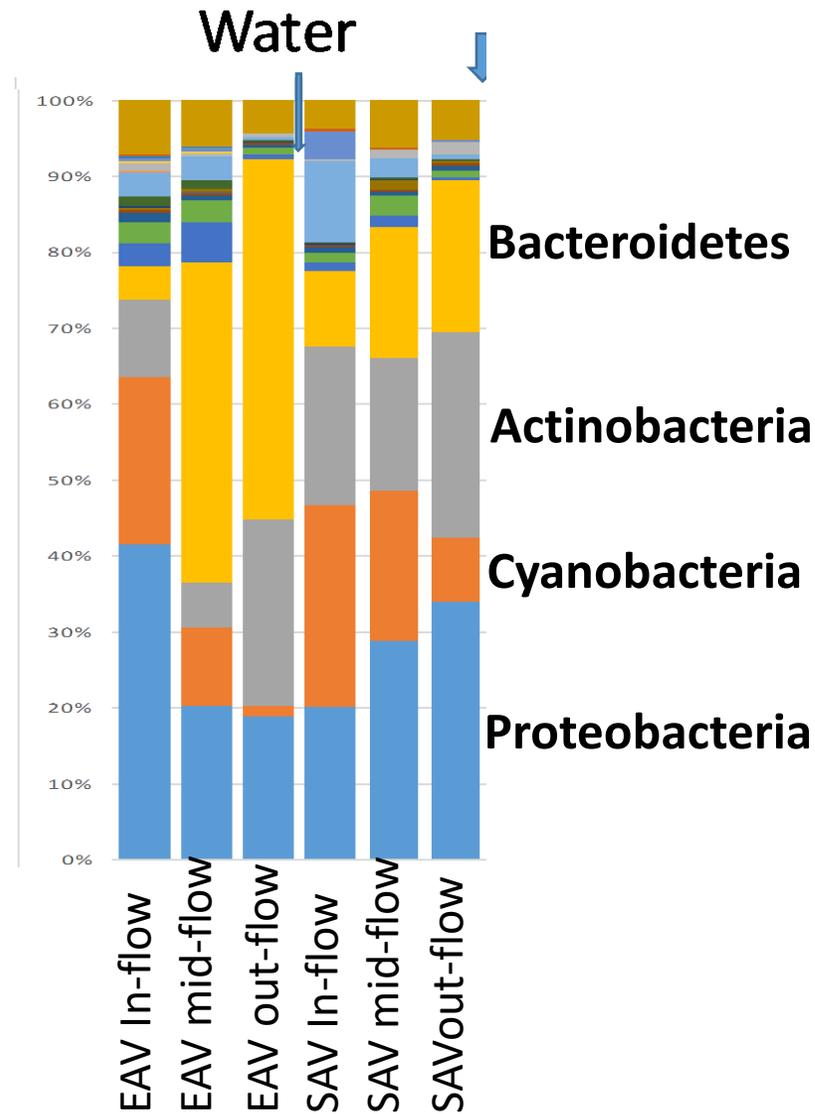
Higher Alpha-diversity in Floc~RAS > pre-STA1 > pre-STA-2 > water; EAV > SAV



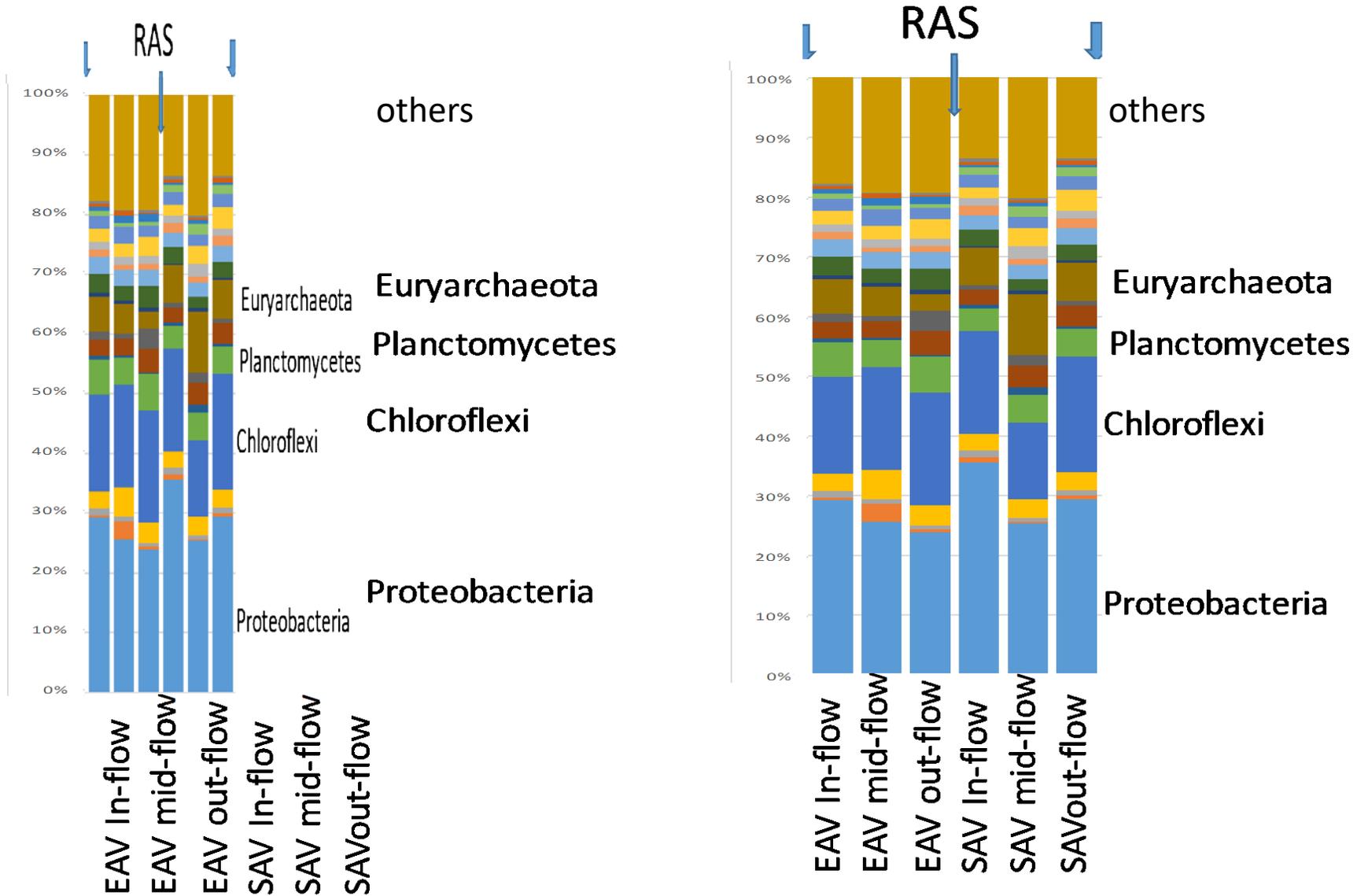
Alpha-diversity is highly correlated with TP



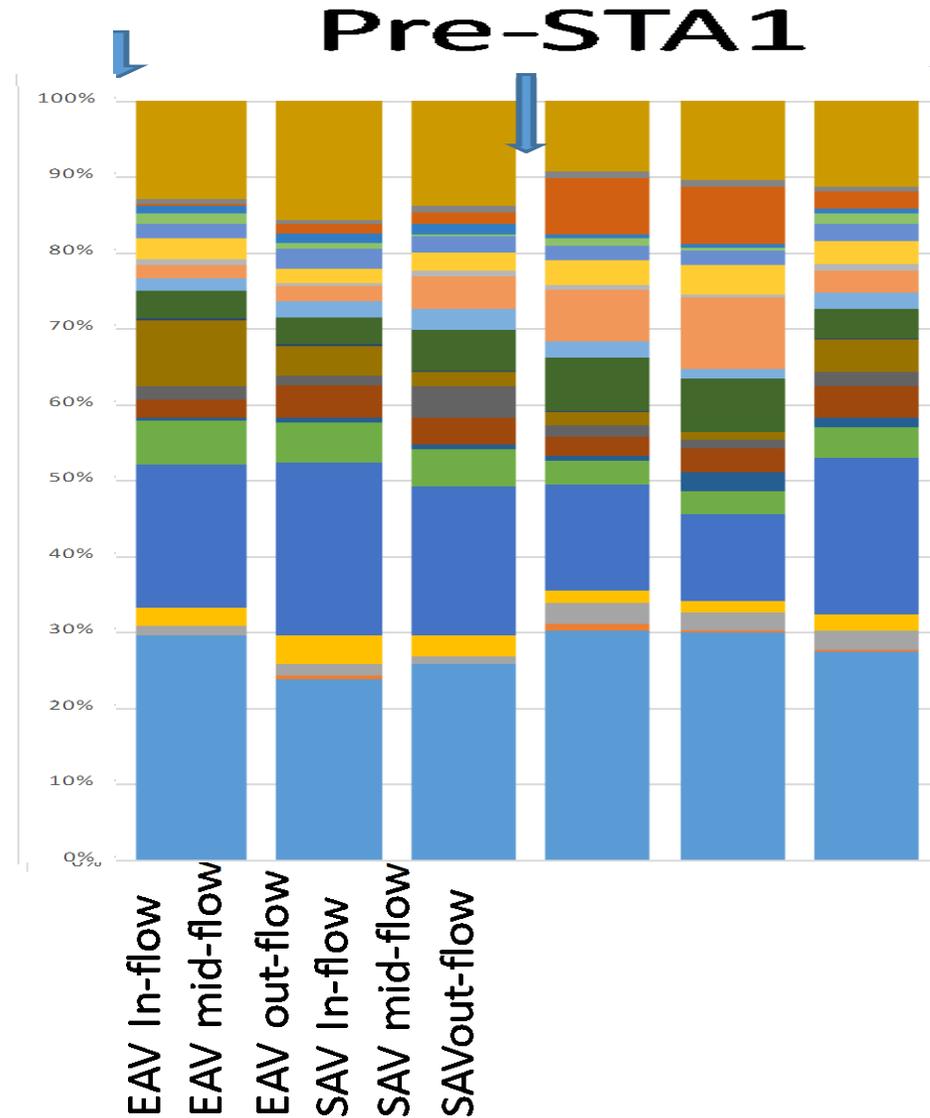
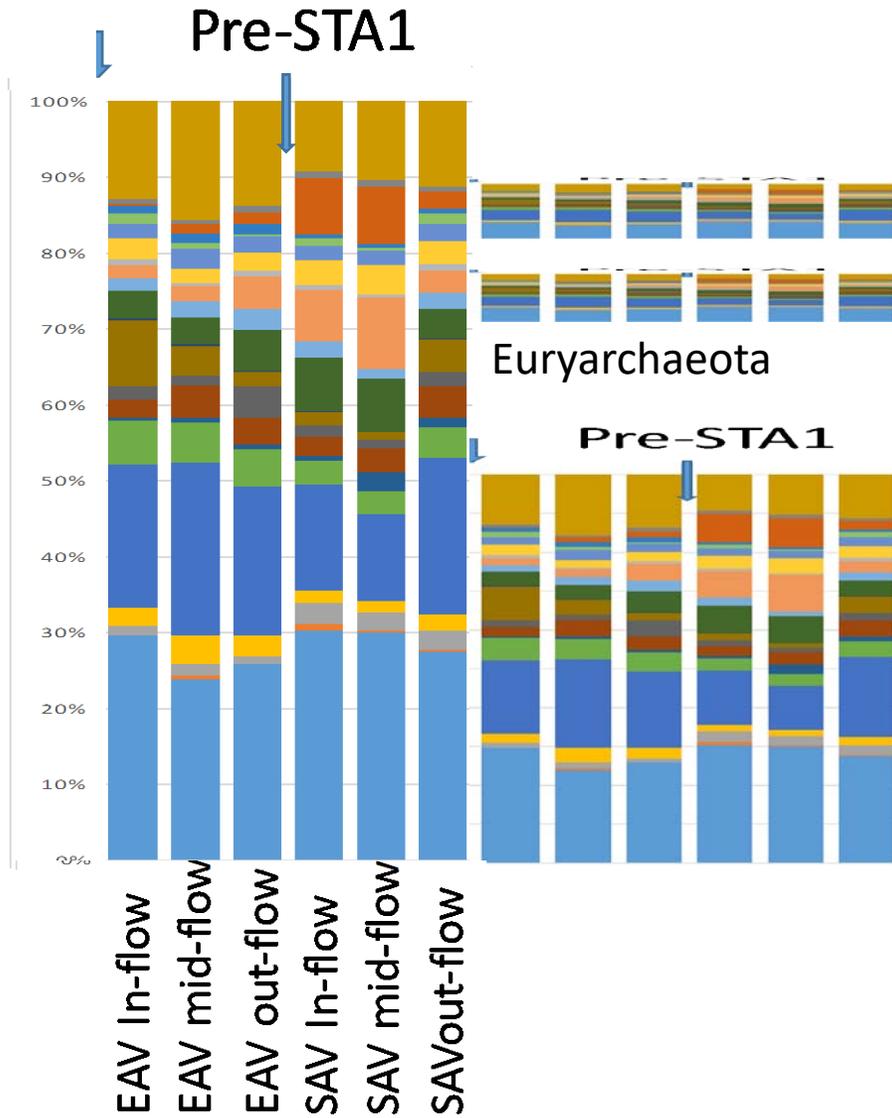
Four main phyla ~80% total relative abundance in water samples



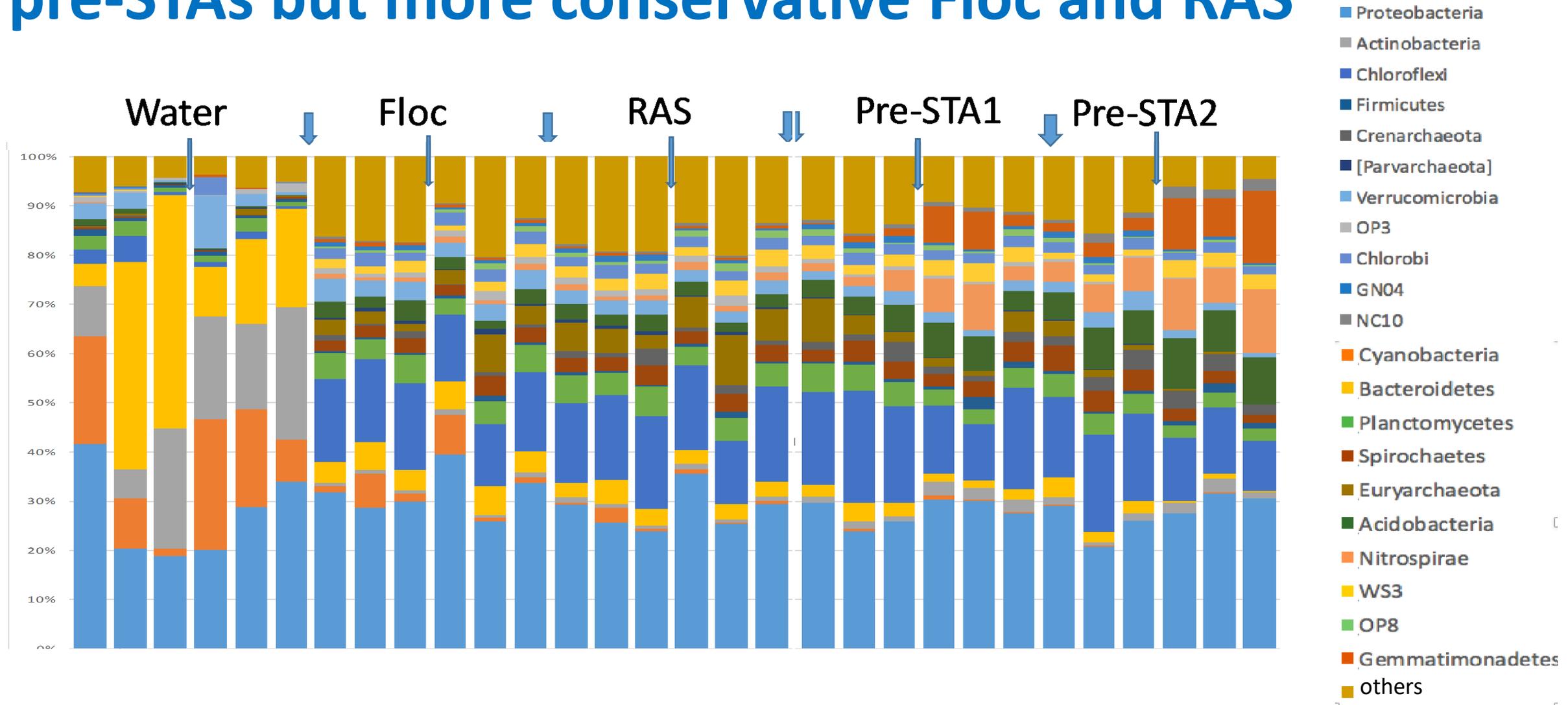
Euryarchaeota was enriched in RAS



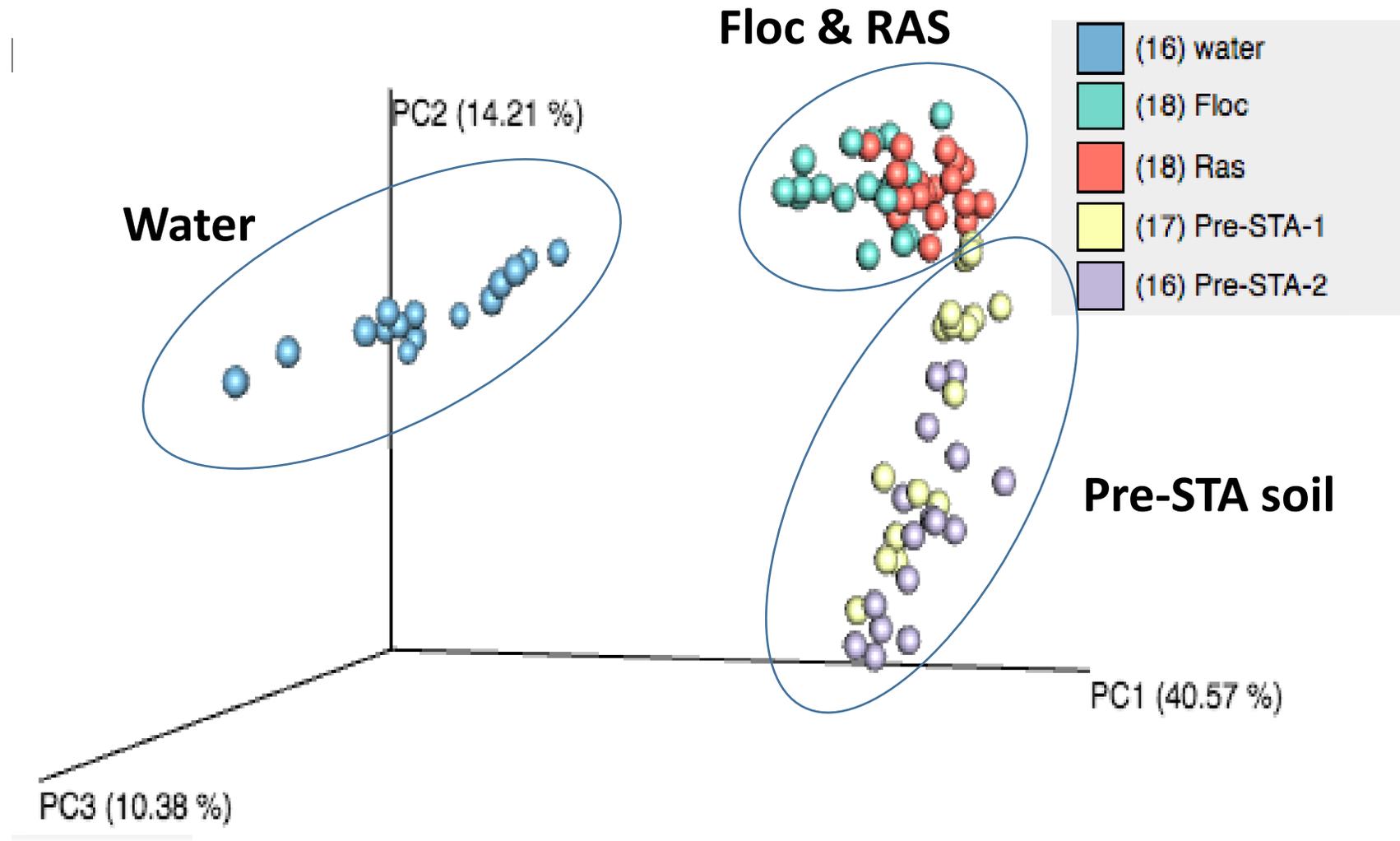
Acidobacteria, Nitrospirae, Gemmatimonadete and NC10 were enriched in pre-STA2 soils



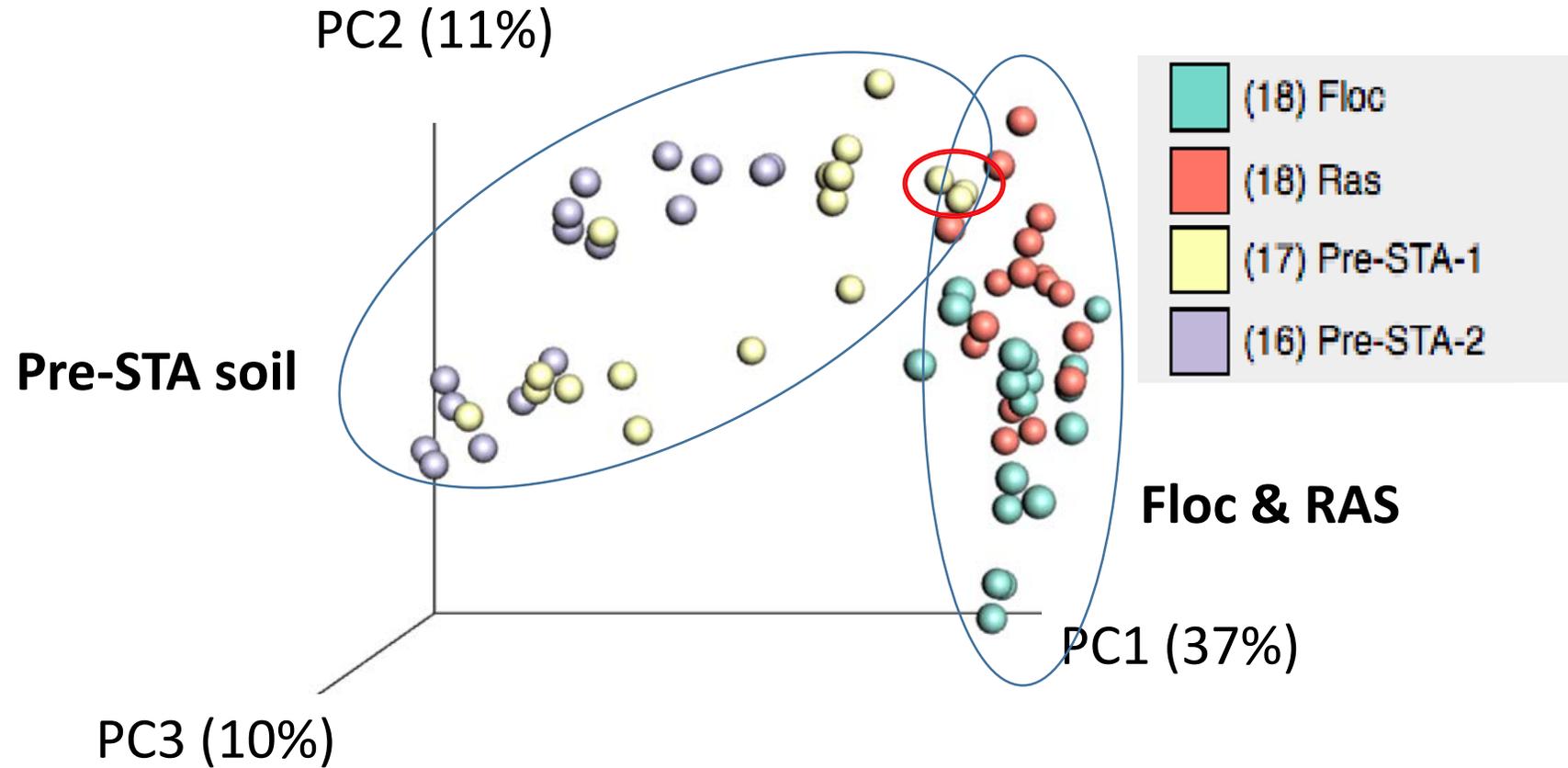
Microbial compositions vary most in water samples > pre-STAs but more conservative Floc and RAS



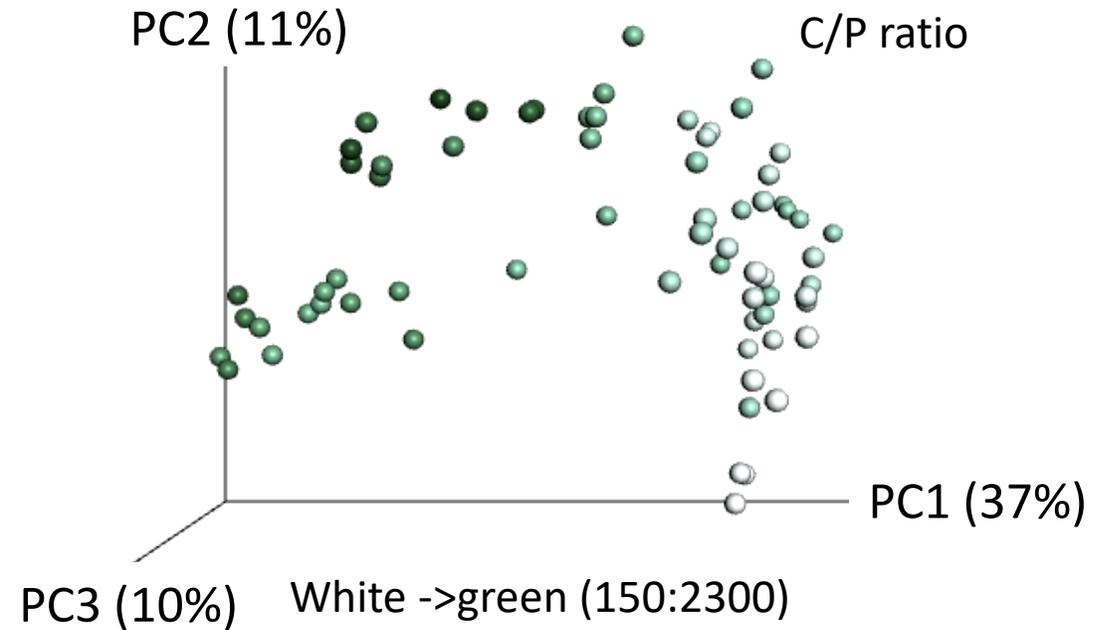
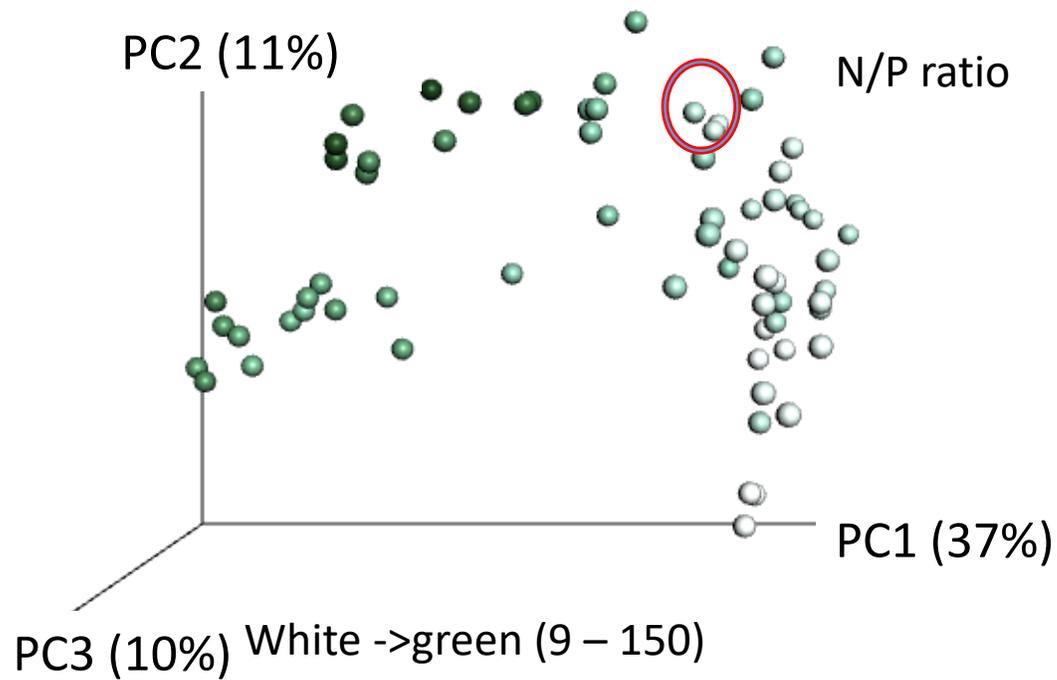
Water samples have distinct microbial structures at OTU level



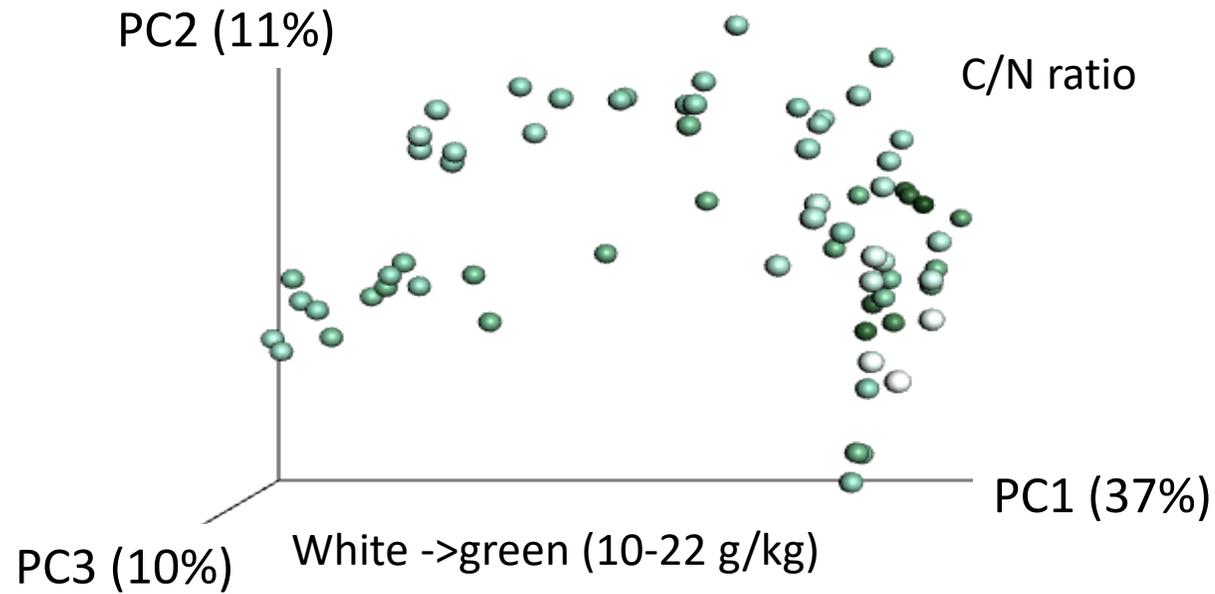
Microbial structures of Floc and RAS are more similar, pre-STA1 is more similar to pre-STA2



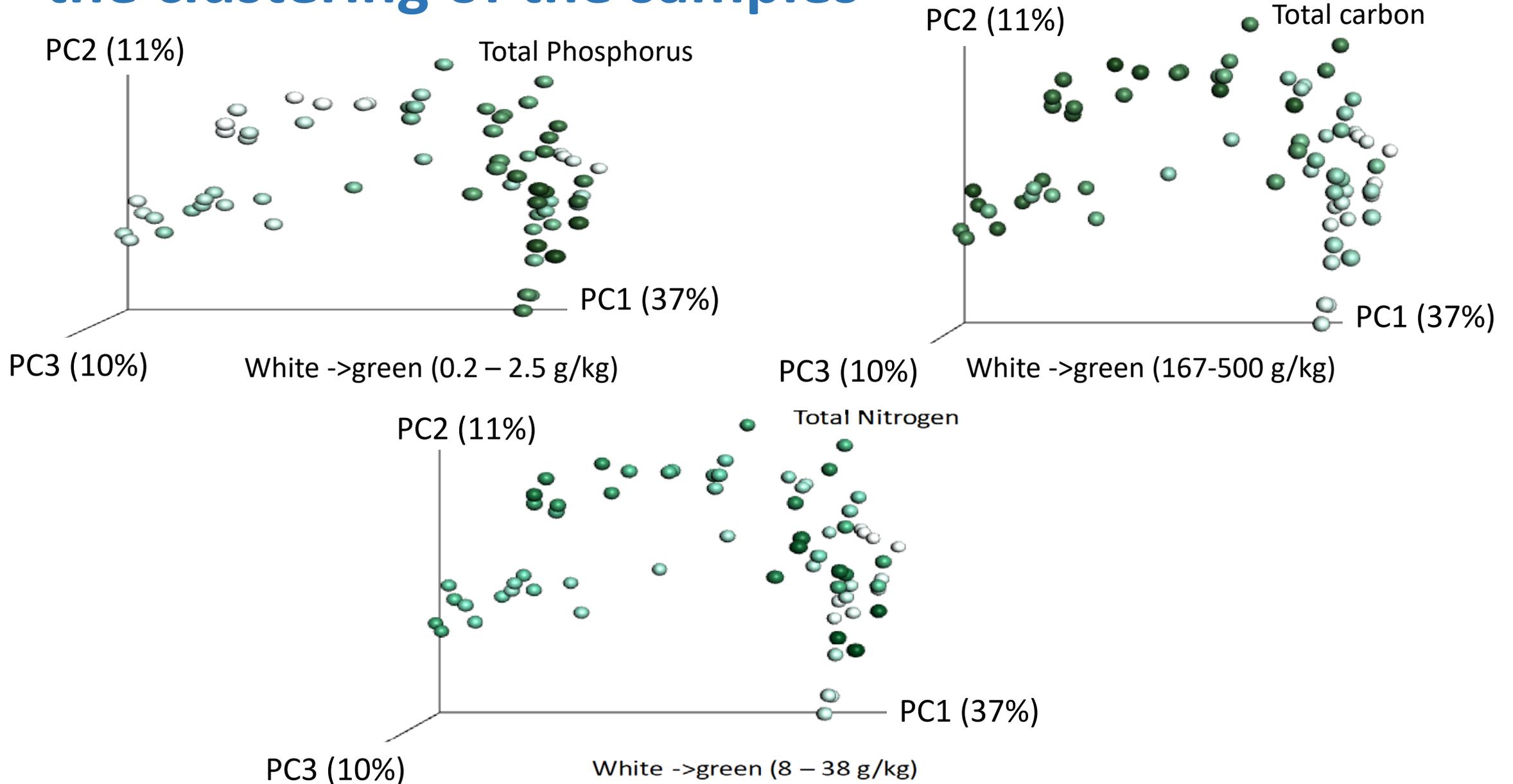
N/P & C/P ratios best explain the patchiness showed in PC1



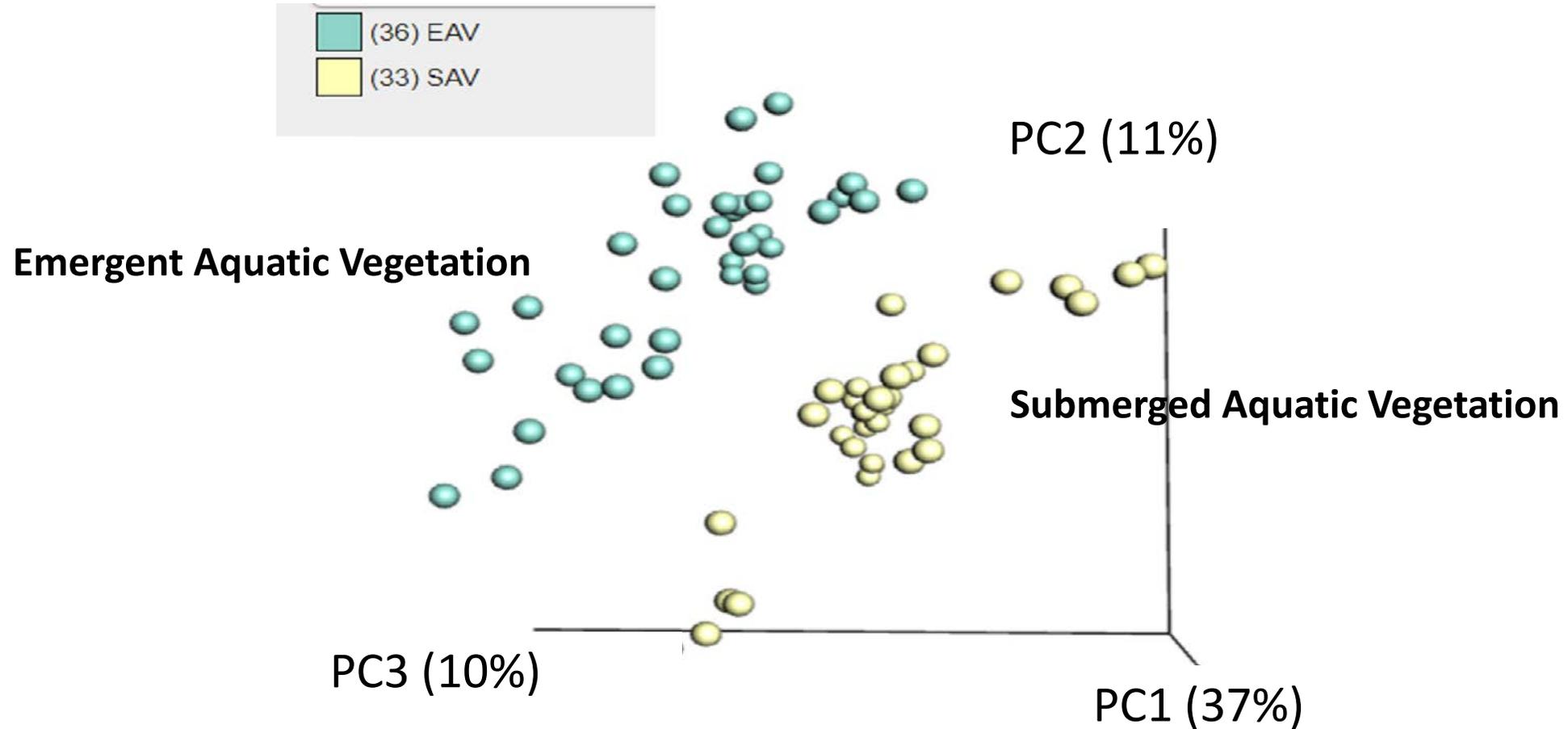
C/N ratios does not explain the patchiness showed in PC1



TP, TC and TN does not explain the patchiness or the clustering of the samples



The samples of same vegetation treatment are grouped together



Take home messages

- **Alpha-diversity: Floc and RAS > pre-STA1 > pre-STA2 > water; EAV > SAV**
- **Beta-diversity: Microbial composition in both cells clustered best by N/P & C/P ratios, vegetation types, depths**
- **Alpha-diversity affected by TP, beta-diversity affected by N/P or C/P ratio.**
- **Future studies need to link microbial compositions to microbial activities**

Acknowledgements

- South Florida Water Management District
- UF-Wetland Biogeochemistry Laboratory
- UF-SWS-Microbial Ecology Laboratory
 - A. Ryan Blaustein
 - M. Nicole Miller

**THANK YOU FOR YOUR
ATTENTION**

???



YESSSS FINALLY OVER!