

Understanding The Bacterial Community And Its Response To Nutrients And Carbon Functional Groups In The Little Washita River Experimental Watershed Reservoirs, Oklahoma, USA.

Walker Marechal & Lucy Ngatia

Presented by:

Walker Marechal, Ph.D.

Florida A&M University

Overview

- ❖ Background and Objectives
- ❖ Material and Methods
- ❖ Results and Discussion
- ❖ Conclusion

Background

- ❖ Reservoirs play a crucial role in the development of human society
- ❖ Annual capacity of the world's reservoirs is declining at a rate of 0.5-0.1% due to sedimentation
- ❖ Half of the world's reservoir storage capacity will disappear by 2050 (Sumi 2018)
- ❖ Sediments accumulate in reservoirs can lead to a wide variety of problems



Background Cont...

- ❖ Excess of nutrients in reservoirs can cause eutrophication
- ❖ Microbiota play a vital role in the biogeochemical transformations of nutrients
- ❖ Understand how bacterial communities respond to nutrients and C functional groups impact the Little Washita River Experimental Watershed Reservoirs (LWREW), Oklahoma, USA

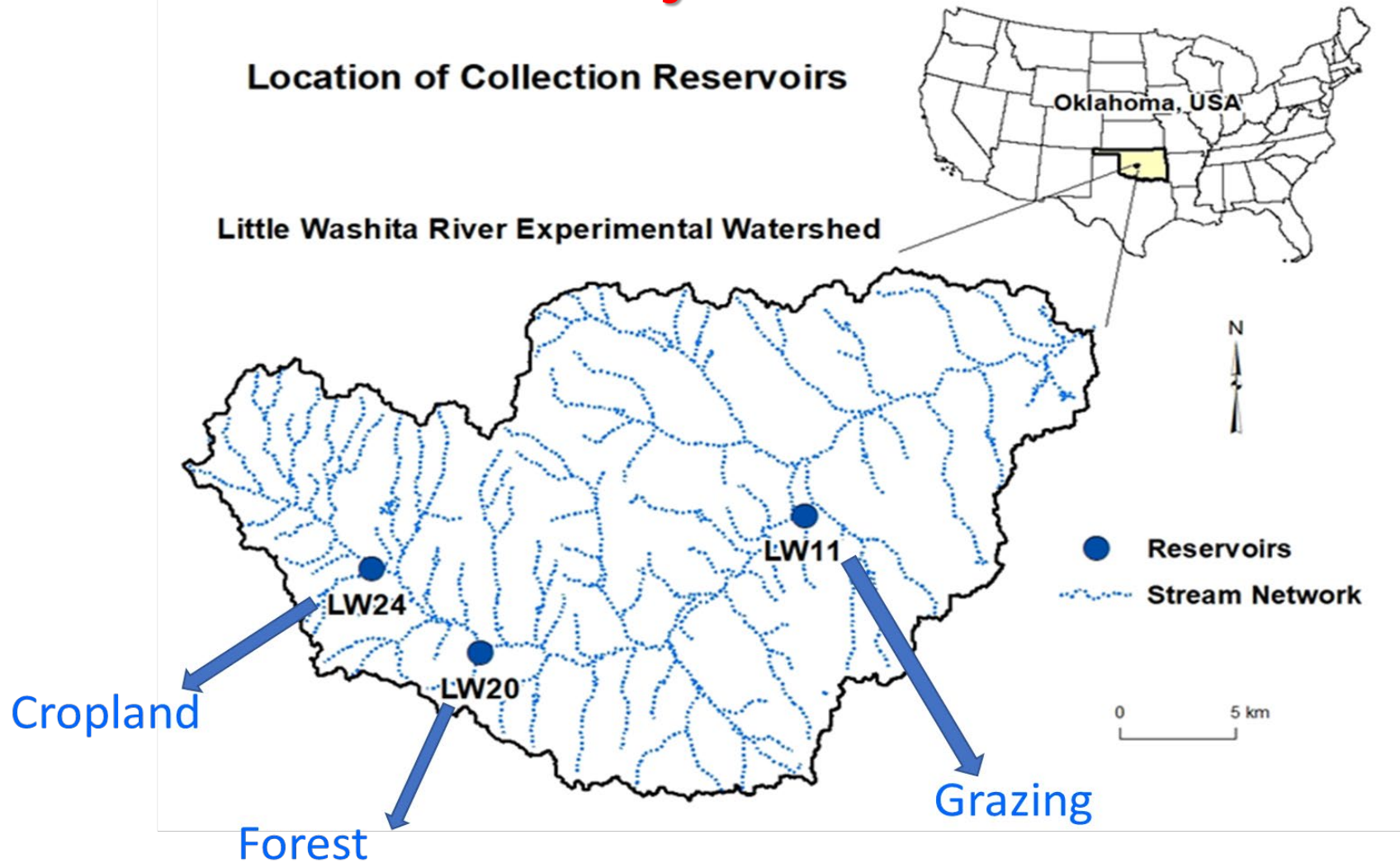
Materials And Methods

Study area

- ❖ Little Washita River Experimental Watershed (LWREW) (Area:610 km²)
- ❖ Southwestern Oklahoma between Chickasha and Lawton
- ❖ 300 to 500 m above mean sea level
- ❖ Grazing (65 %), Cropland (16%), and Forest (13%) from 1994 to 2008 (Starks et al. 2014)
- ❖ Grazing: 34°53'37" N, 97°59'47" W; Forest: 34°50'2" N, 98°8'56" and Cropland: 34°52'3" N, 98°12'9" W.

Materials And Methods Cont...

Study Site



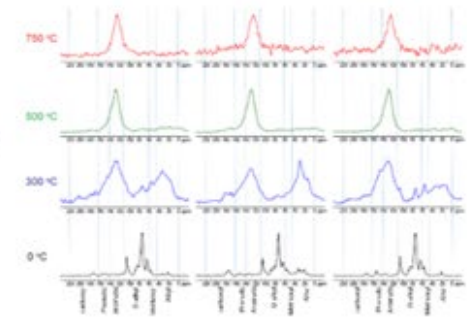
Materials And Methods Cont...

Chemical Analysis

Sediment sample



^{13}C NMR



**Carbon and Nitrogen
Elemental analyzer**

Carbon, Nitrogen



ICP

Macro and micronutrient

Nutrients

Materials And Methods Cont...

DNA Extraction and 16s rRNA Sequencing

- ❖ DNA isolated from 1g fresh soil samples using Ultraclean Soil DNA kit (Qiagen, Germantown, Maryland)
- ❖ Archaeal 16s rRNA gene amplified with 515F (GTGCCAGCMGCCGCGGTAA) and 926R (CCGYCAATTYMTTTRAGTTT)
- ❖ Filtering and trimming conducted by DNAS core facility
- ❖ QIIME v1.8 pipeline used to prepare sequence files (FASTA, sequences.zip)

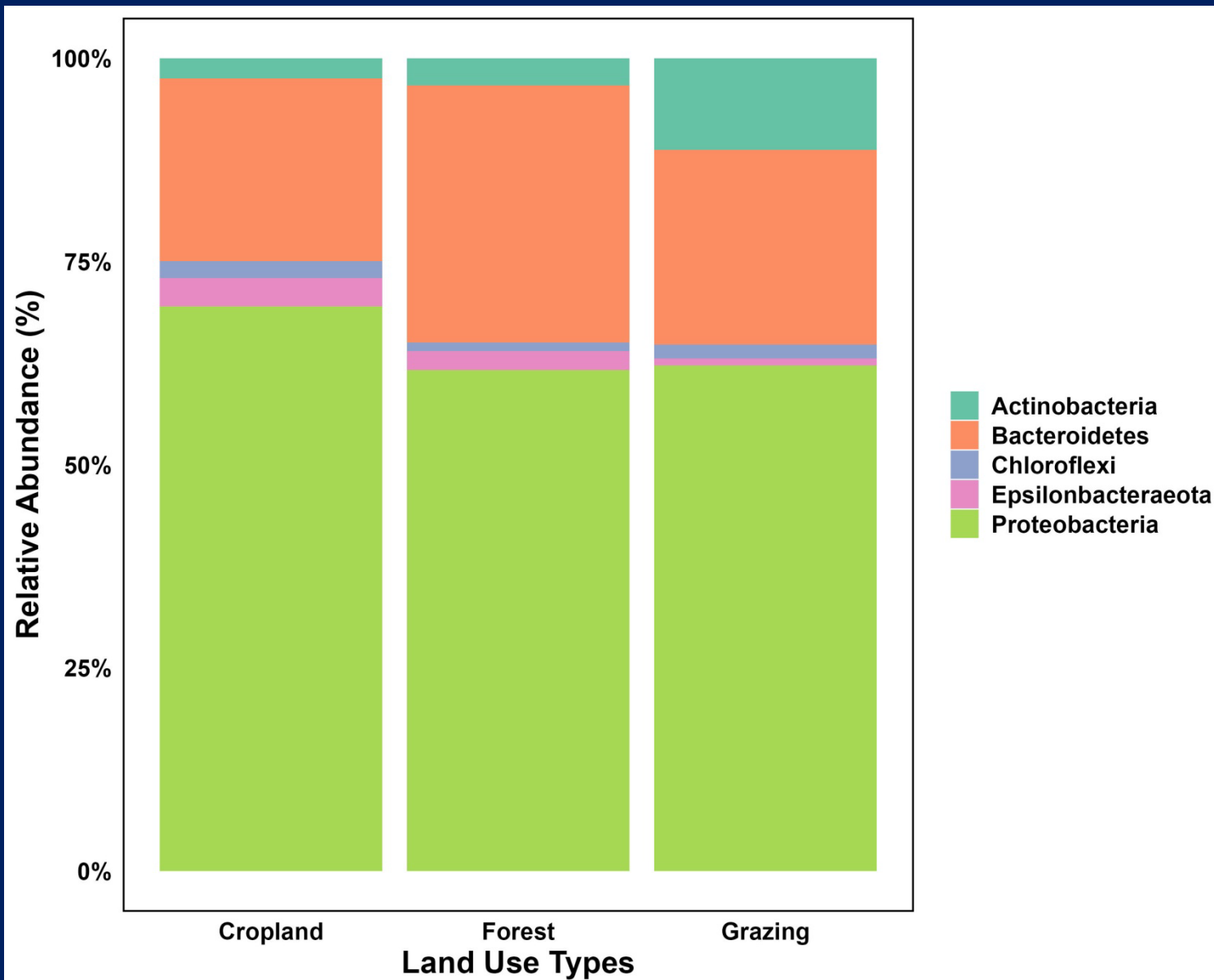
Materials And Methods Cont...

Data Analysis

- ❖ Statistical analysis performed using RStudio version 2024.04.2+764
- ❖ PCoA plot was built using the ggplot2 package
- ❖ Bioinformatics analysis of raw sequence data performed using QIIME v1.8 (Caporaso 2010)

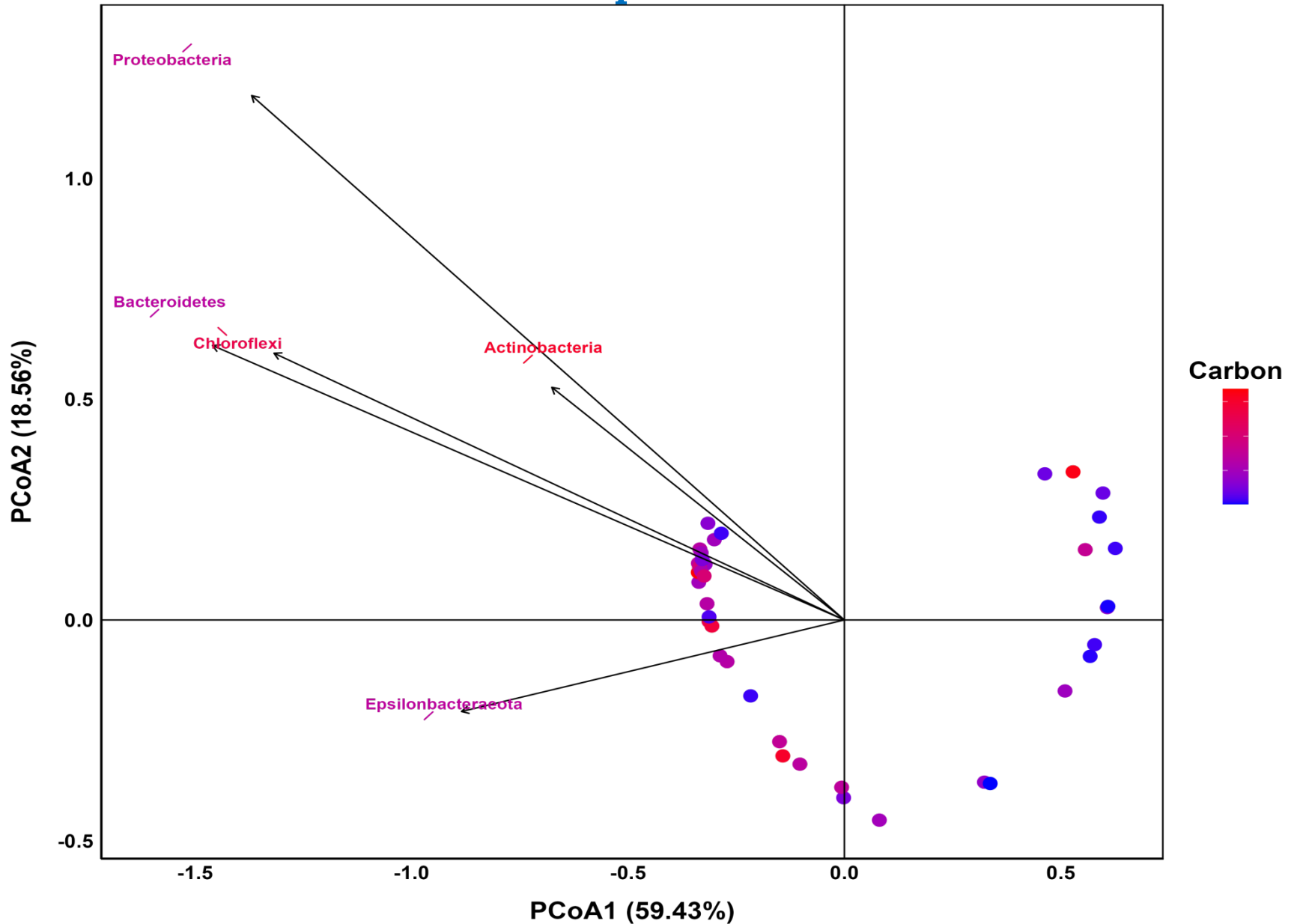
Results and Discussion

Microbial Community Composition



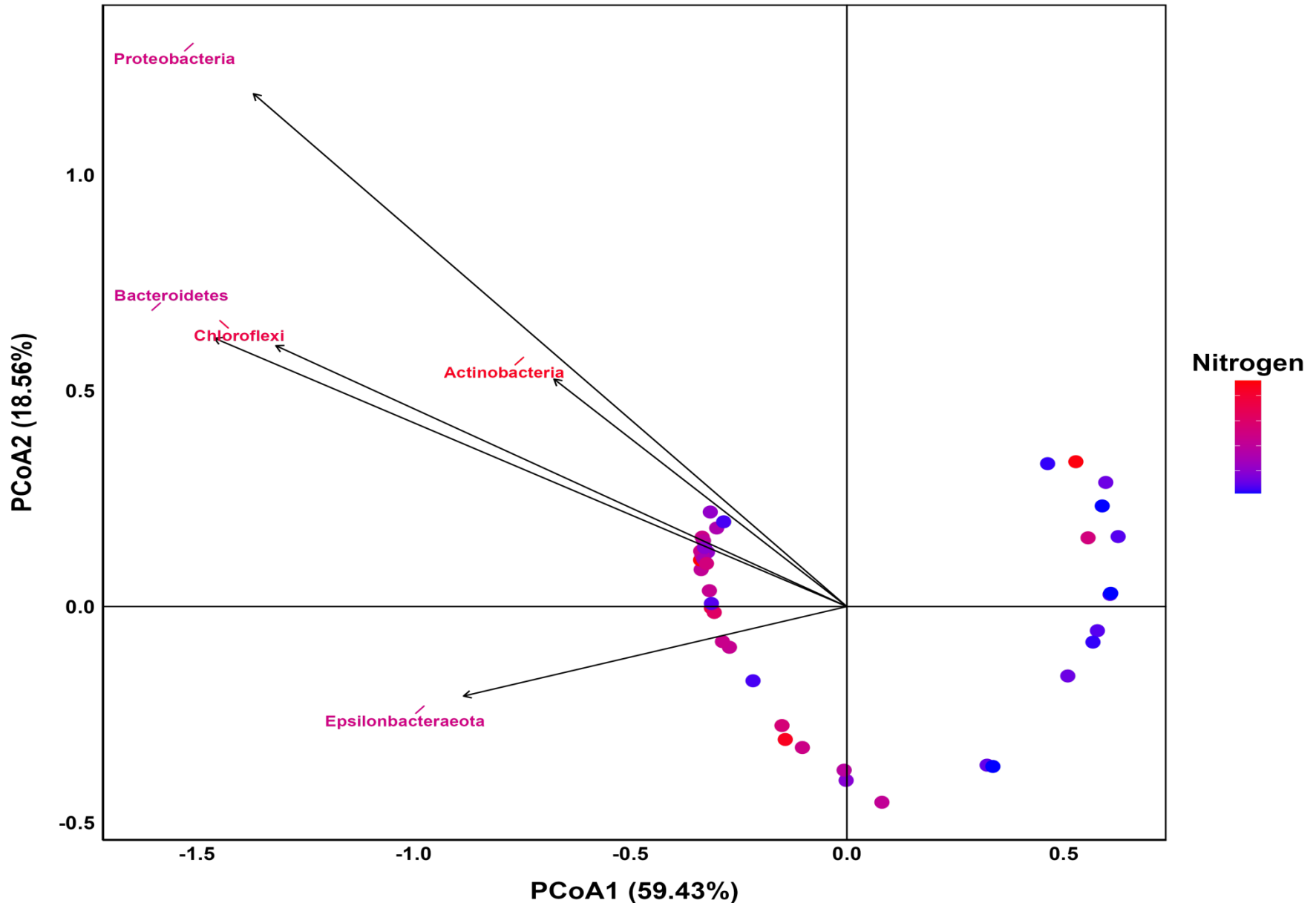
Results and Discussion

Microbial Response to Carbon



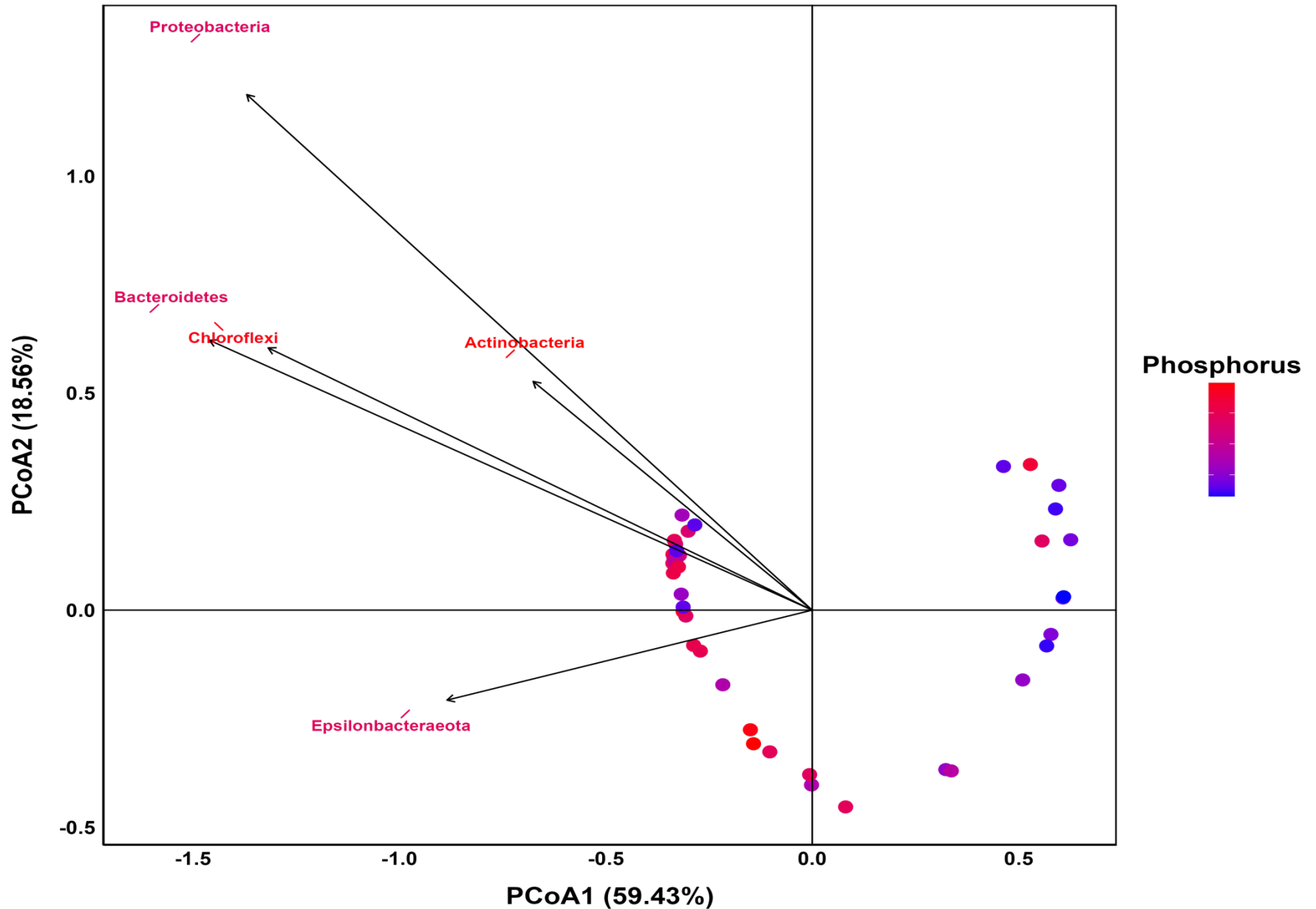
Results and Discussion Cont...

Microbial Response to Nitrogen



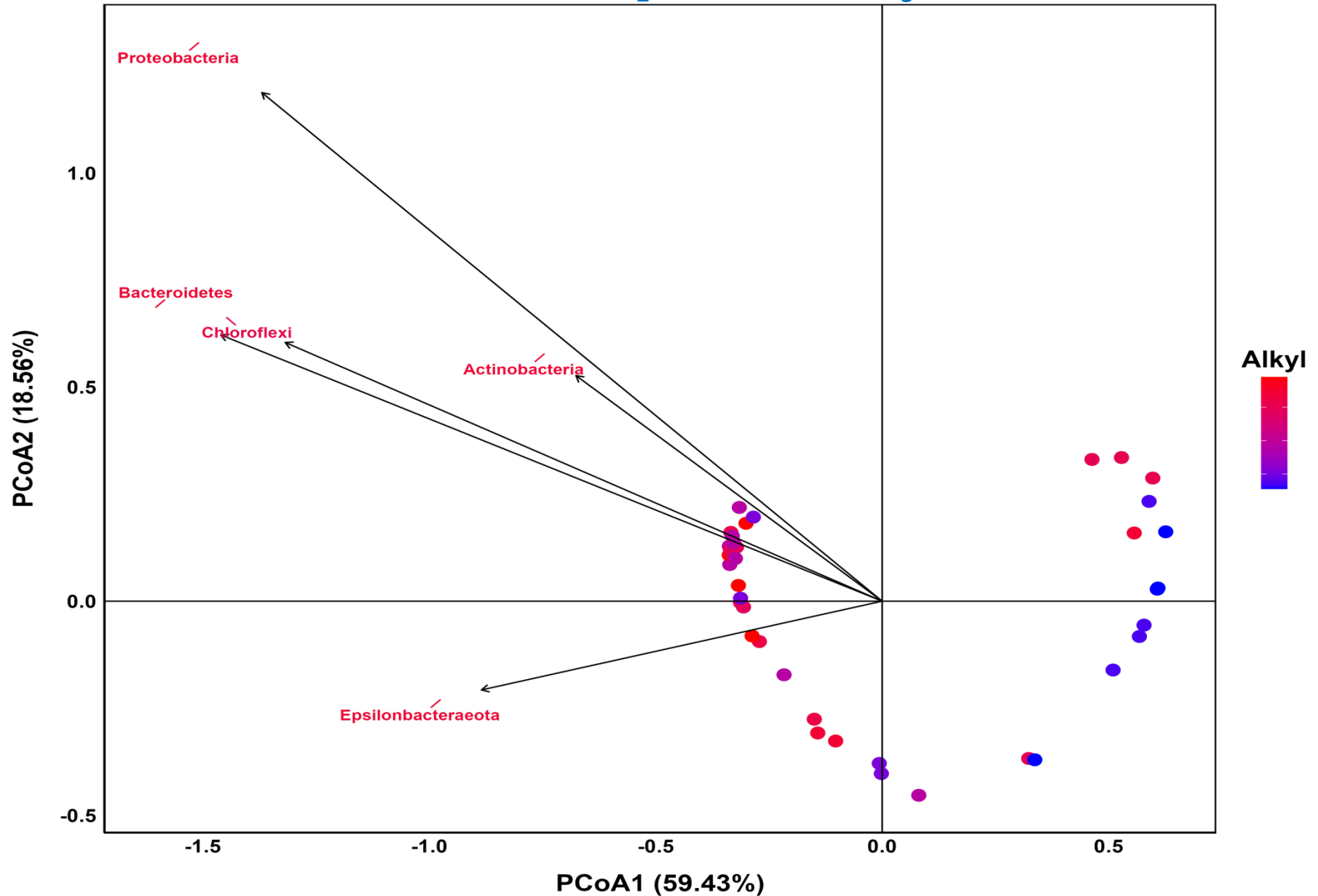
Results and Discussion Cont...

Microbial Response to Phosphorus



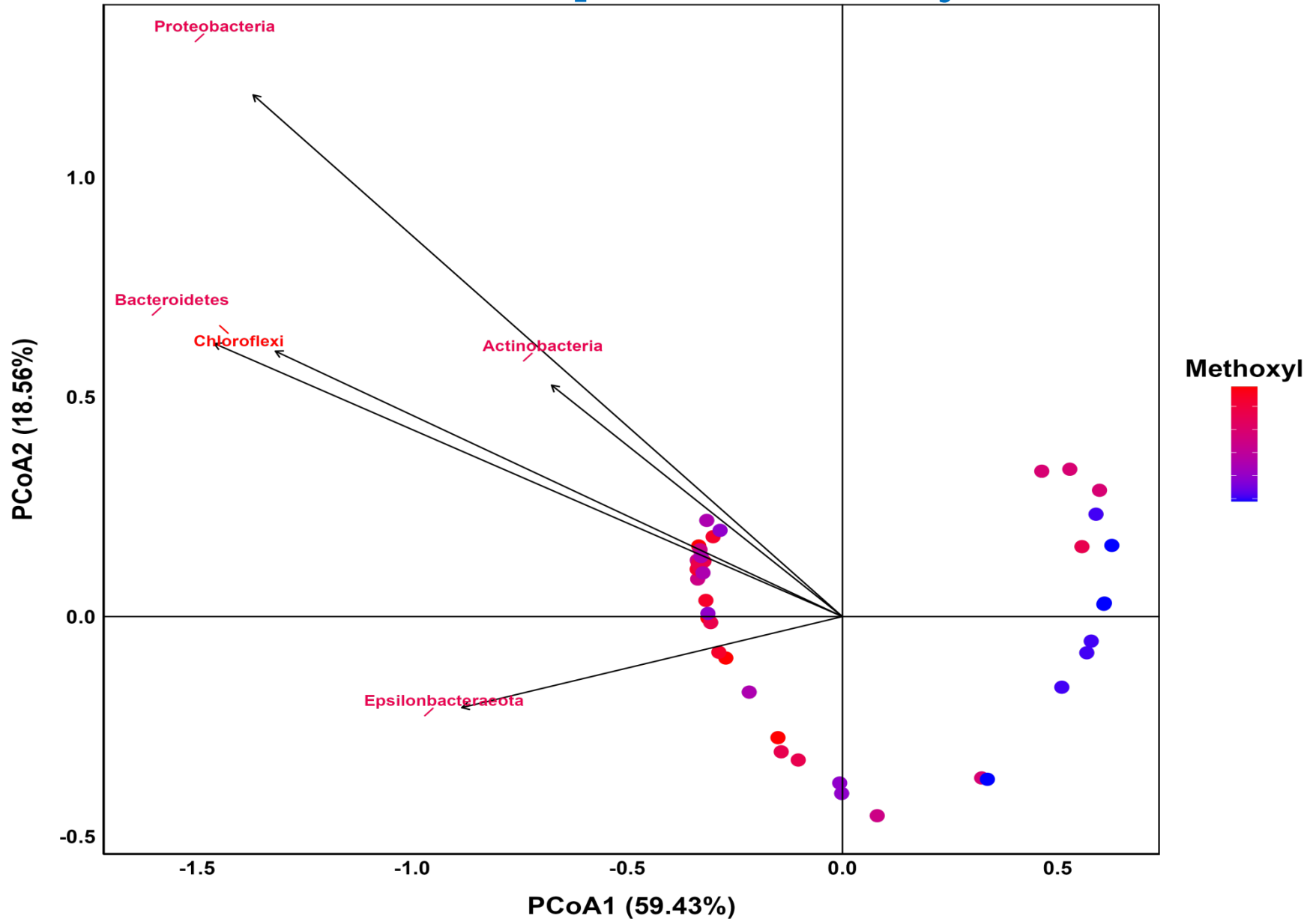
Results and Discussion Cont...

Microbial Response to Alkyl



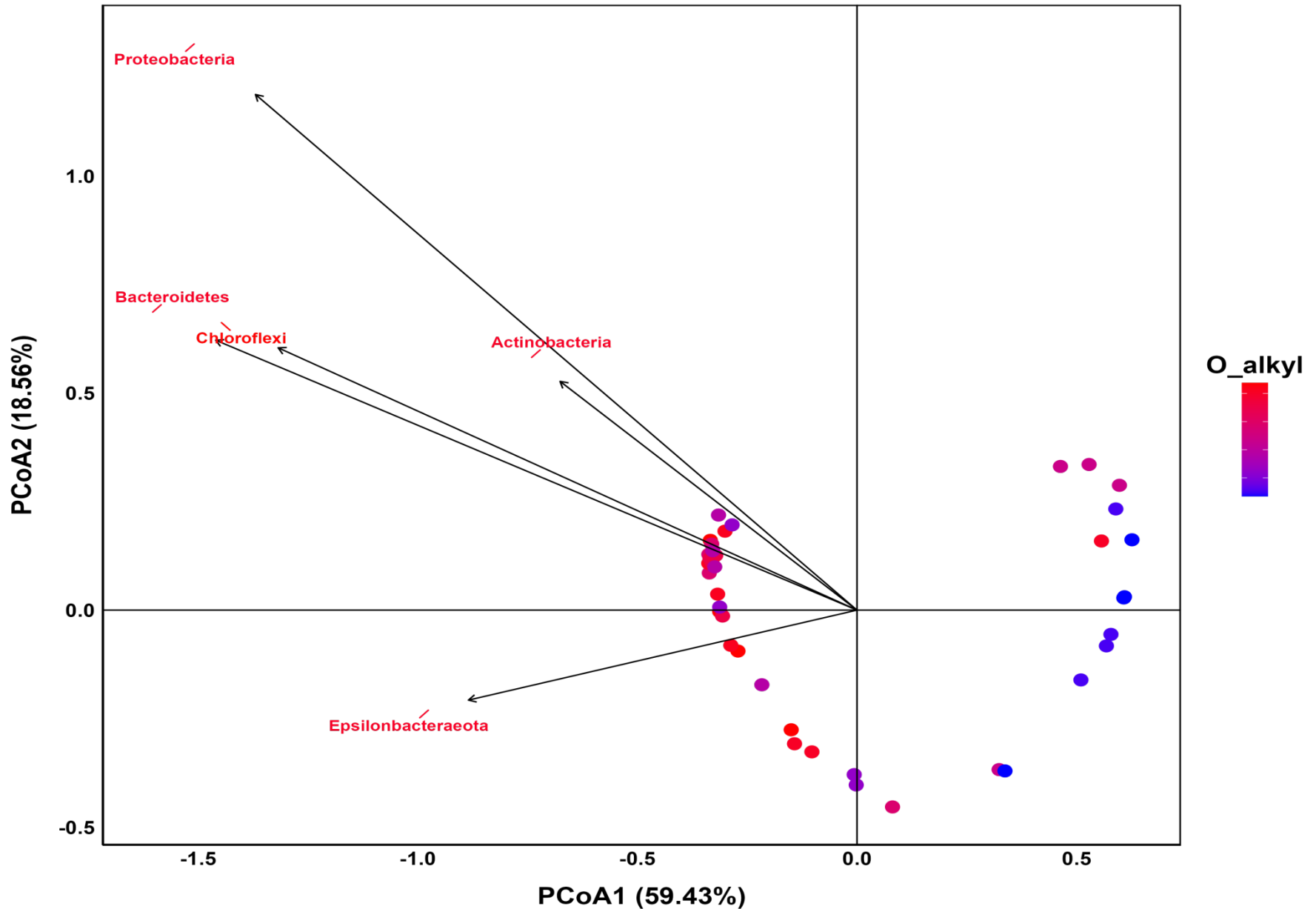
Results and Discussion Cont...

Microbial Response to Methoxyl



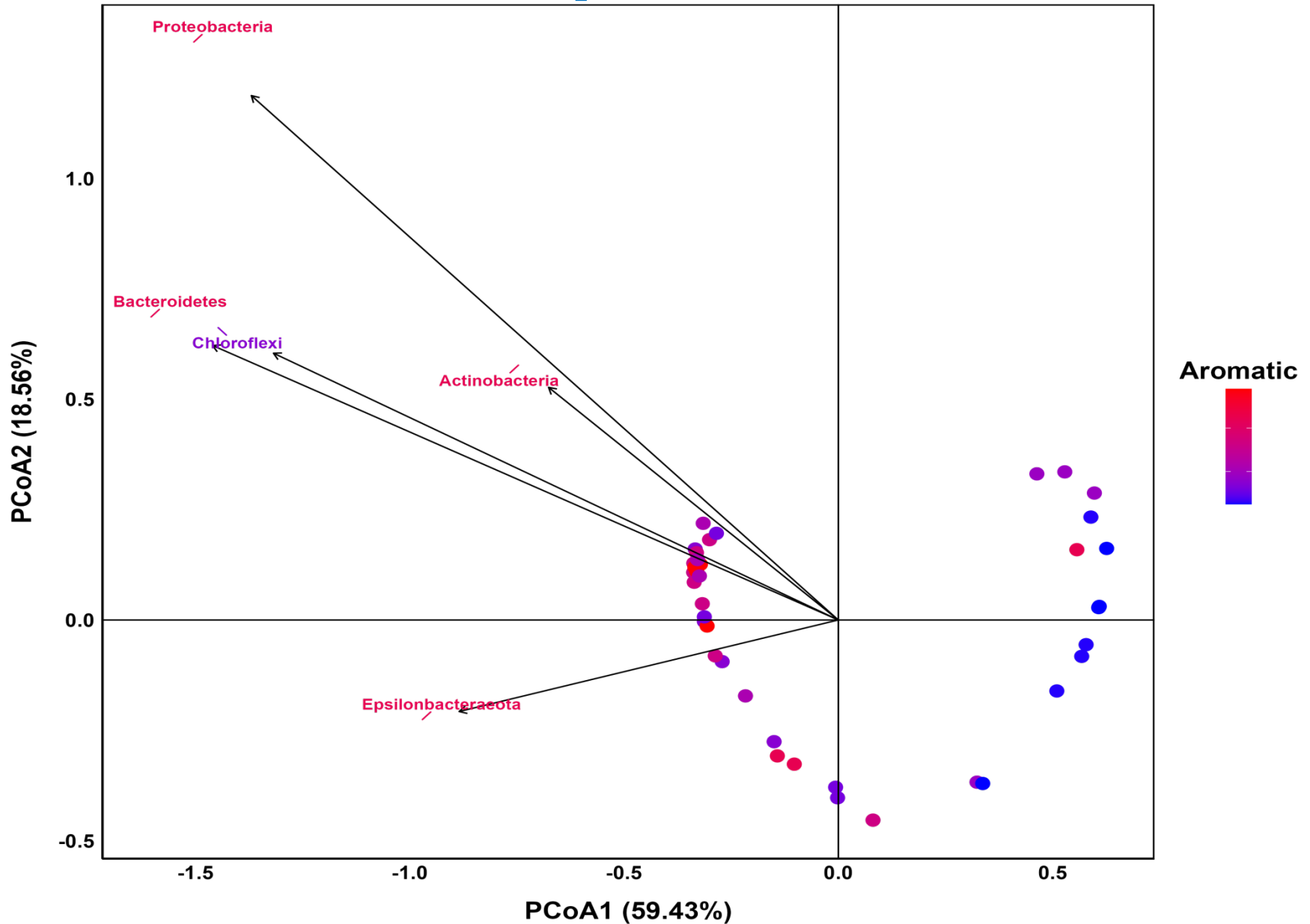
Results and Discussion Cont...

Microbial Response to O-Alkyl



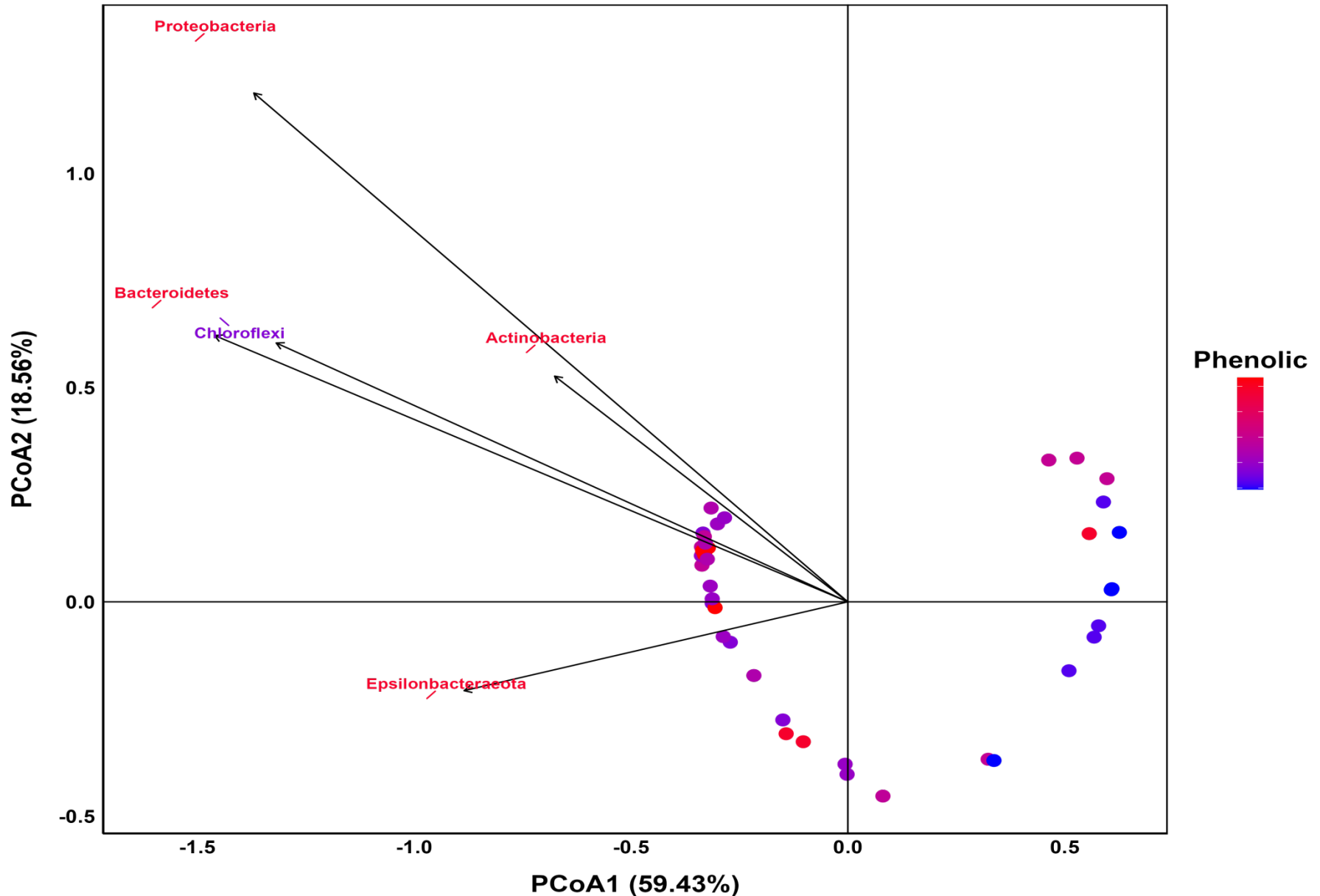
Results and Discussion Cont...

Microbial Response to Aromatic



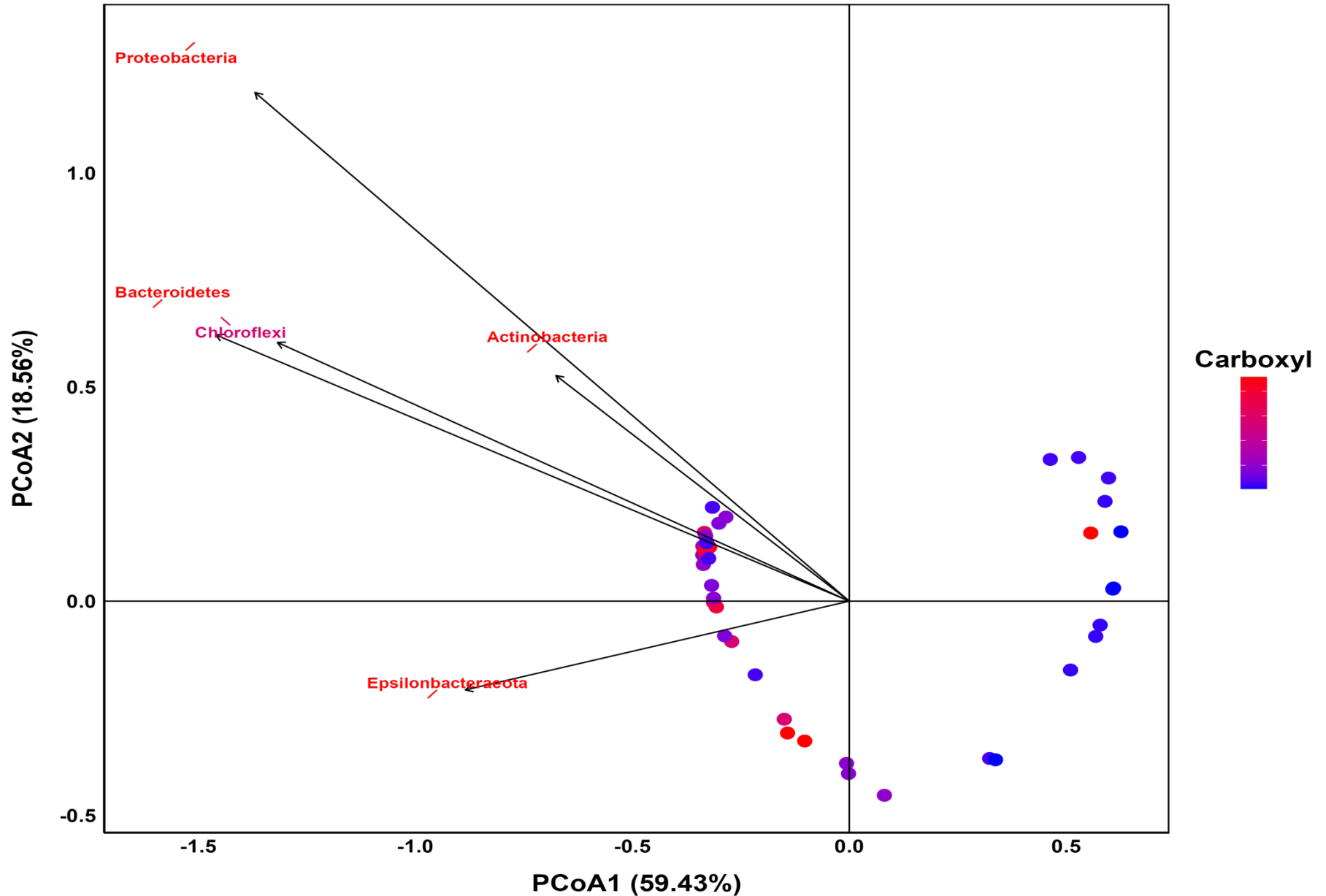
Results and Discussion Cont...

Microbial Response to Phenolic



Results and Discussion Cont...

Microbial Response to Carboxyl



Conclusion

- ❖ **Proteobacteria is dominant across all land use types**
- ❖ **Chloroflexi is less dominant, but consistent**
- ❖ **Proteobacteria and Bacteroidetes often dominate in environments rich in C, N, P and C functional groups**
- ❖ **Epsilonbacteria appear in the negative space of both PCoA1 and PCoA2**

Acknowledgement

- ❖ **NMR experiments were performed at the National High Magnetic Field Laboratory (NHMFL) supported by the NSF Cooperative Agreement No. DMR-1644779/DMR-2128556 and the State of Florida**
- ❖ **USDA-ARS - Agreement no. 58-3070-009**

Thanks

Any Questions?