Factors Controlling Diversity and Composition of Soil Microbial Communities in Mangroves

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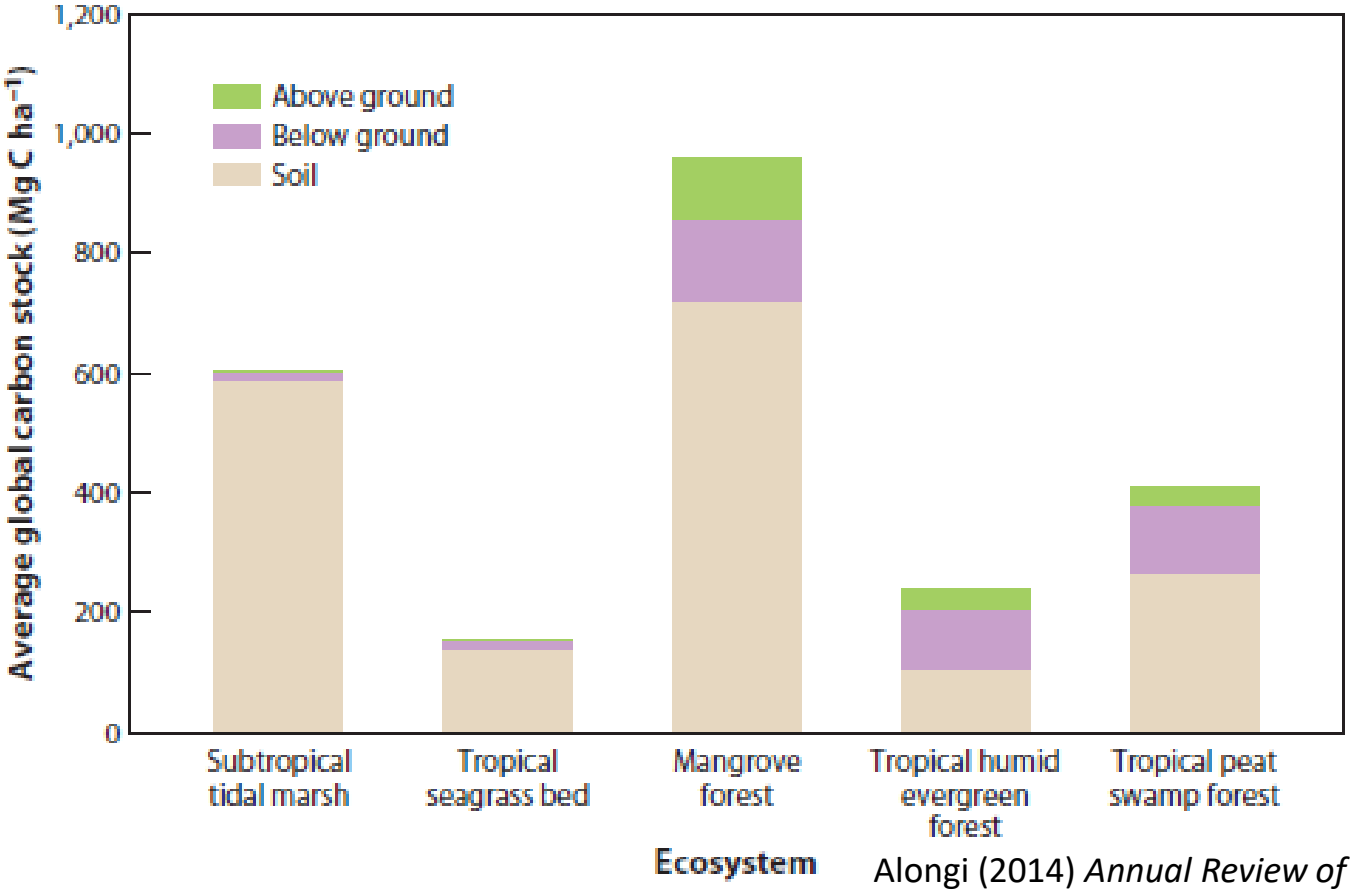
Study aims

- Find out more about what microbes are present in mangroves and how diverse they are
- Is microbial community composition affected by:
  - plant species identity
  - plant genetic diversity
  - tidal/vegetation zone
  - other environmental factors

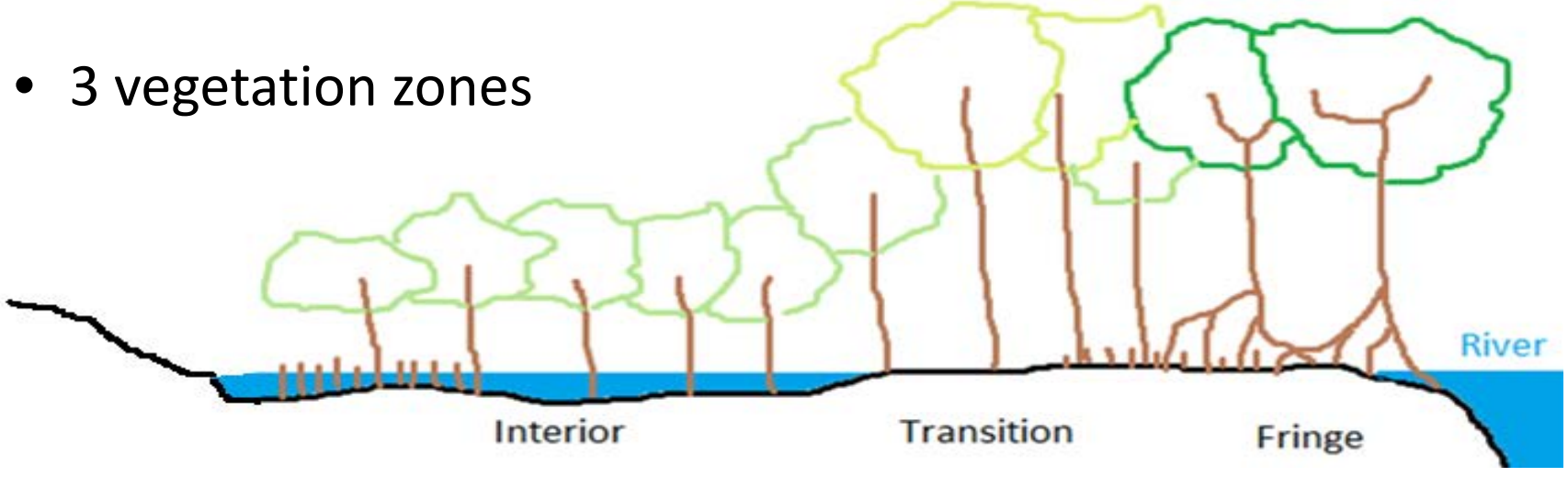
Why are mangrove microbes important?



Alongi (2014) *Annual Review of Marine Science*

Study

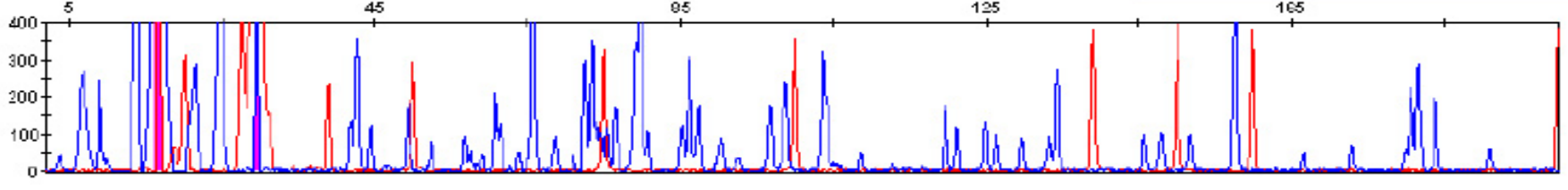
- Field study - 2 sites on Florida's east coast
- 2 plant species – *Rhizophora mangle & Avicennia germinans*
- Soil bacteria and fungi
- 3 vegetation zones



Methods

Techniques:

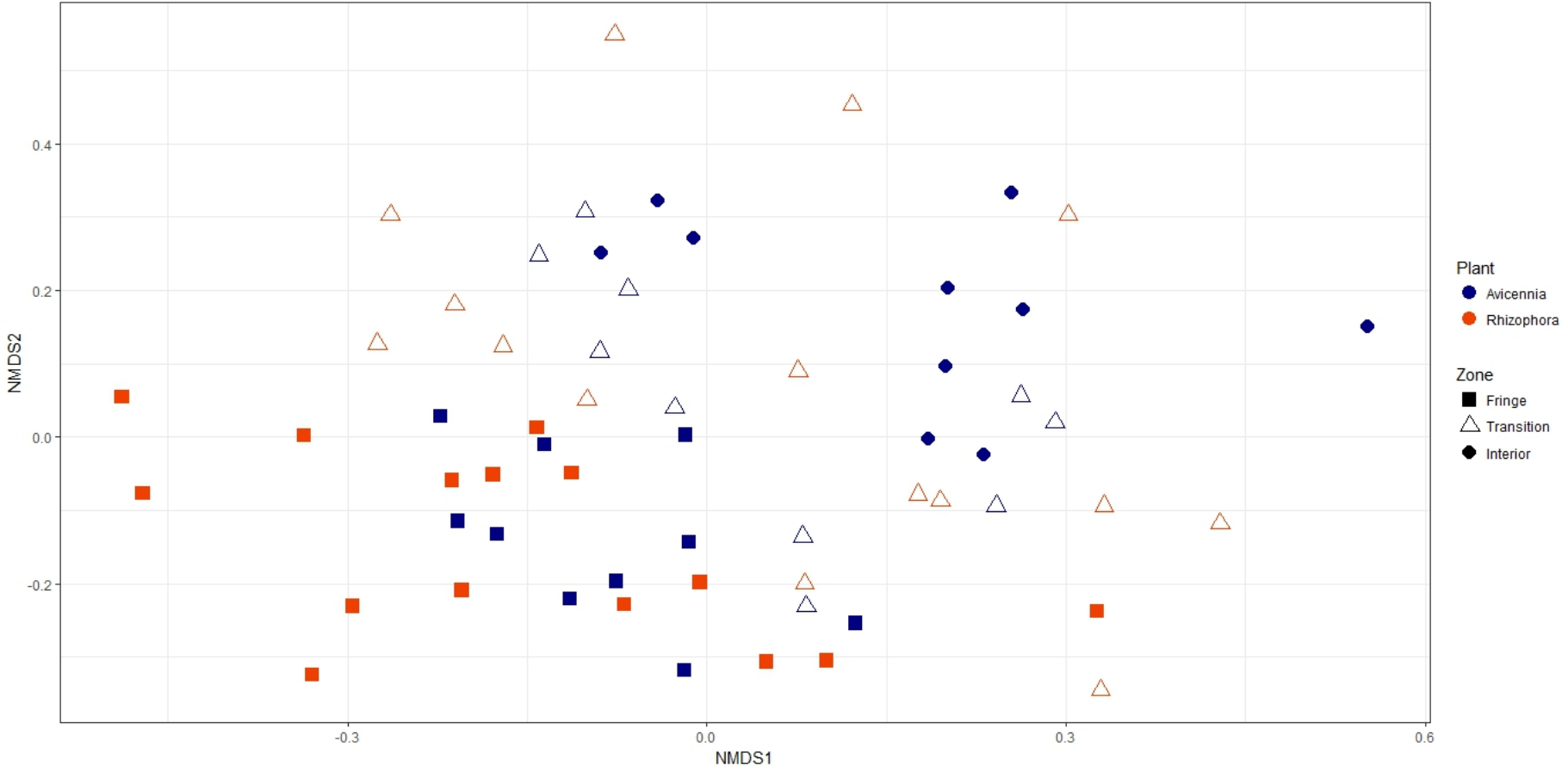
- Microsatellite markers for plant population genetics
- T-RFLP for microbial community genetics
- Next generation sequencing – Illumina MiSeq



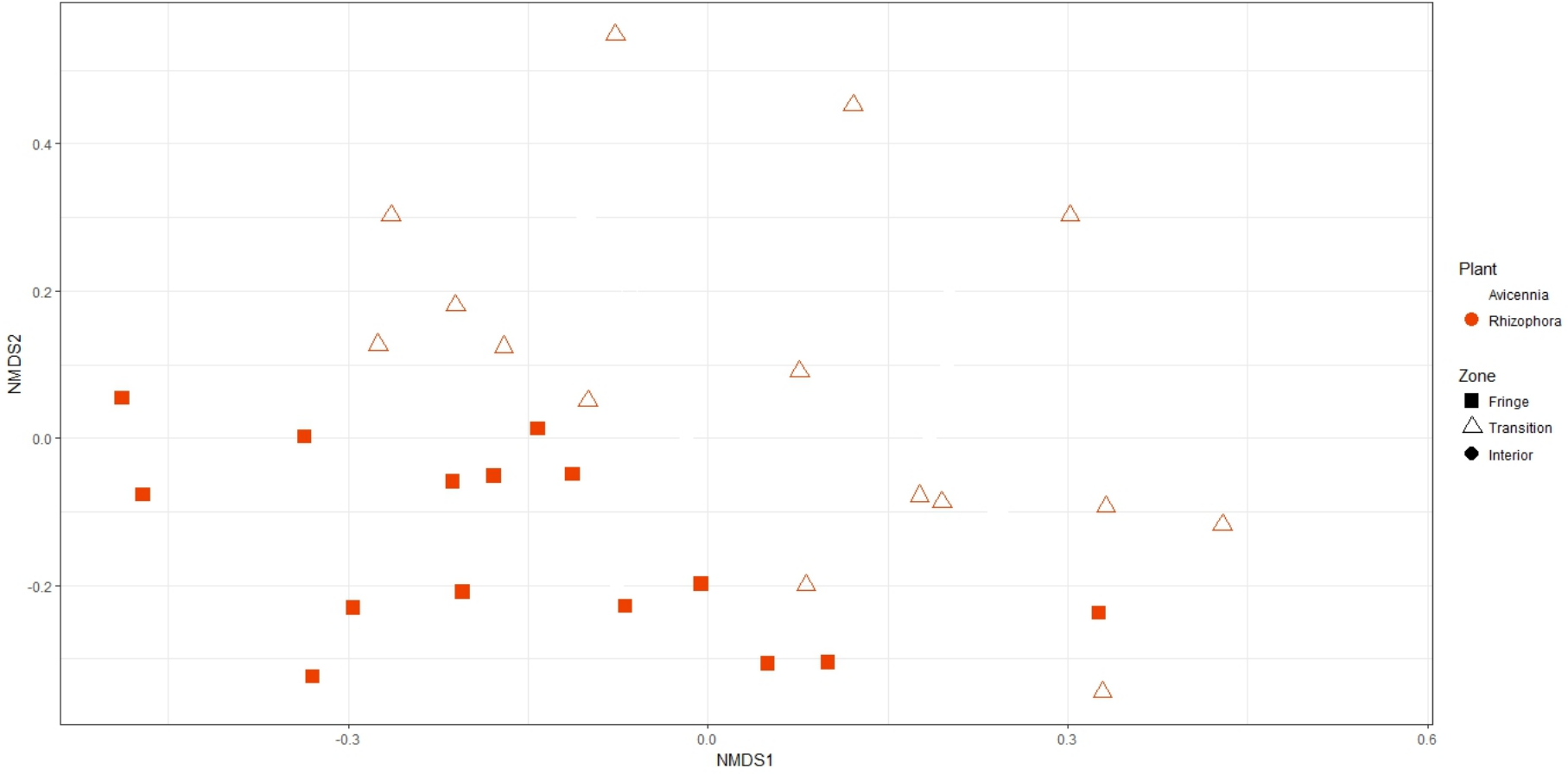
16S results

- Bacterial community composition affected by:
  - vegetation zone
  - plant species
  - total % soil carbon
  - pore water pH
  - salinity (marginal)

16S results


NMDS2
0.4
0.2
0.0
-0.2
-0.3
0.0
0.3
0.6
NMDS1
Plant
Avicennia
Rhizophora
Zone
Fringe
Transition
Interior

16S results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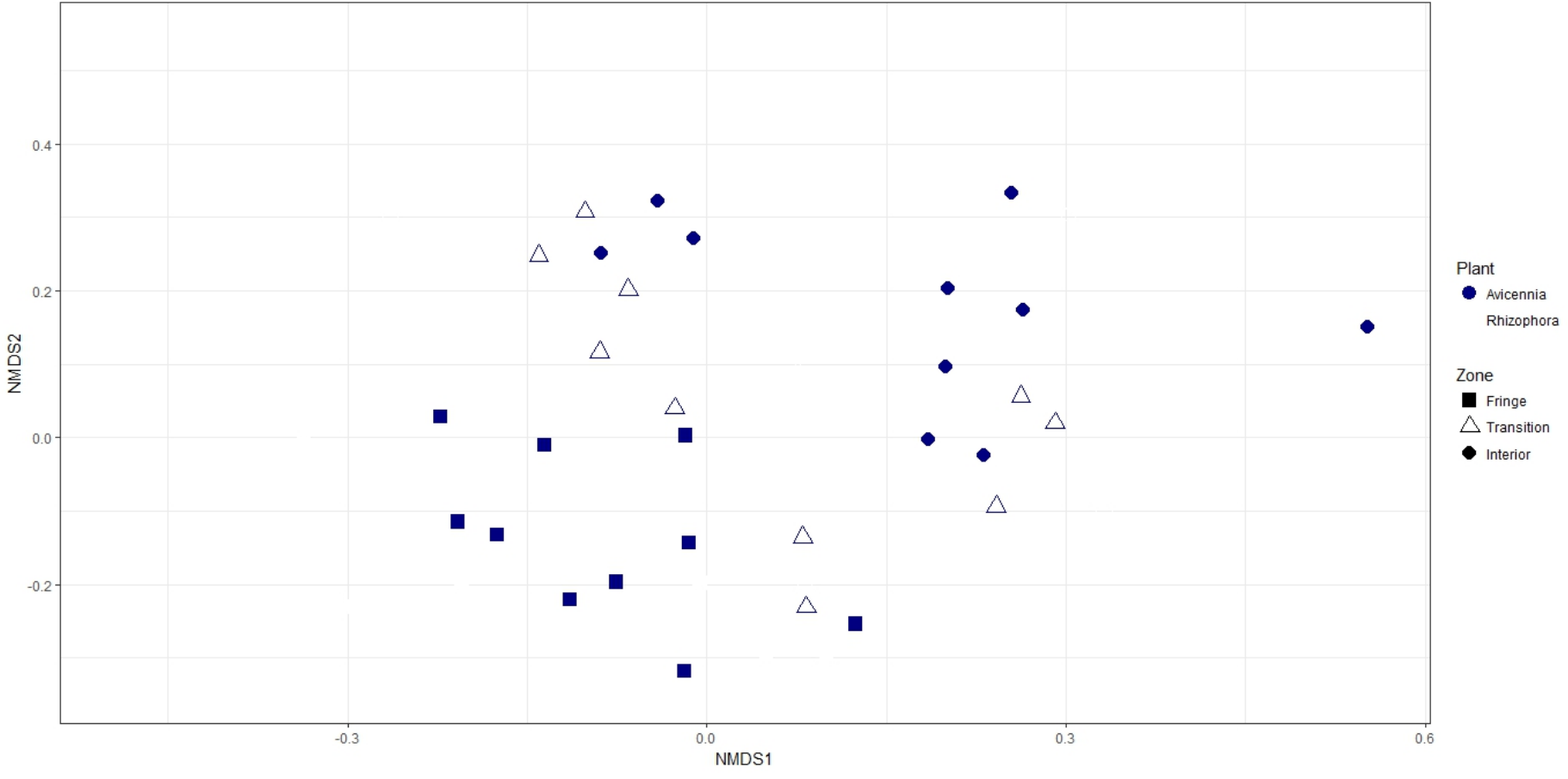
Plant
Avicennia
Rhizophora
Zone
Fringe
Transition
Interior

16S Results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NMDS2
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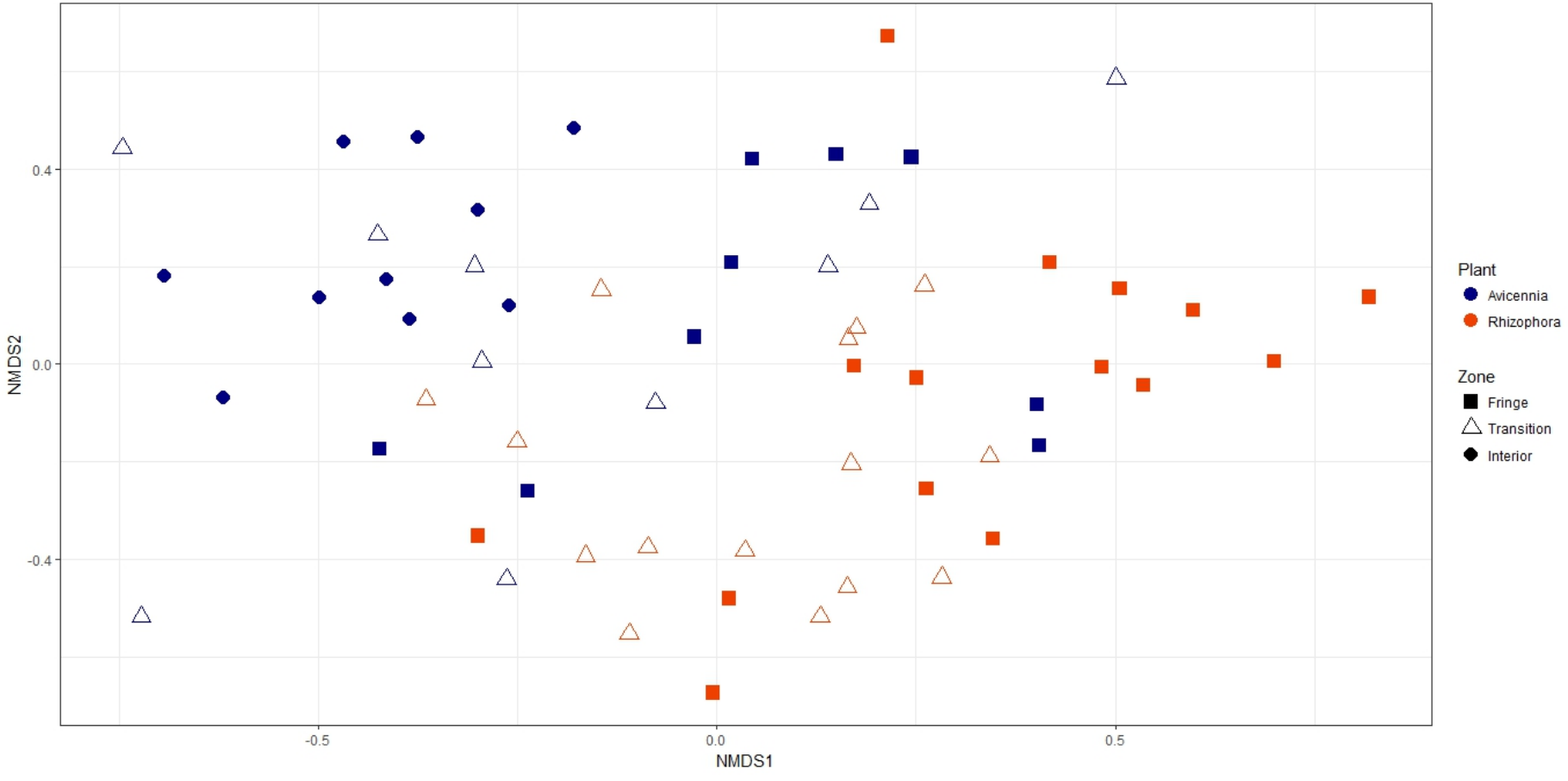
NMDS1
Plant
Avicennia
Rhizophora
Zone
Fringe
Transition
Interior

ITS results

- Fungal community composition affected by:
  - vegetation zone
  - plant species
- Pore water pH and salinity, total soil carbon and nitrogen had no significant effect

ITS results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NMDS2
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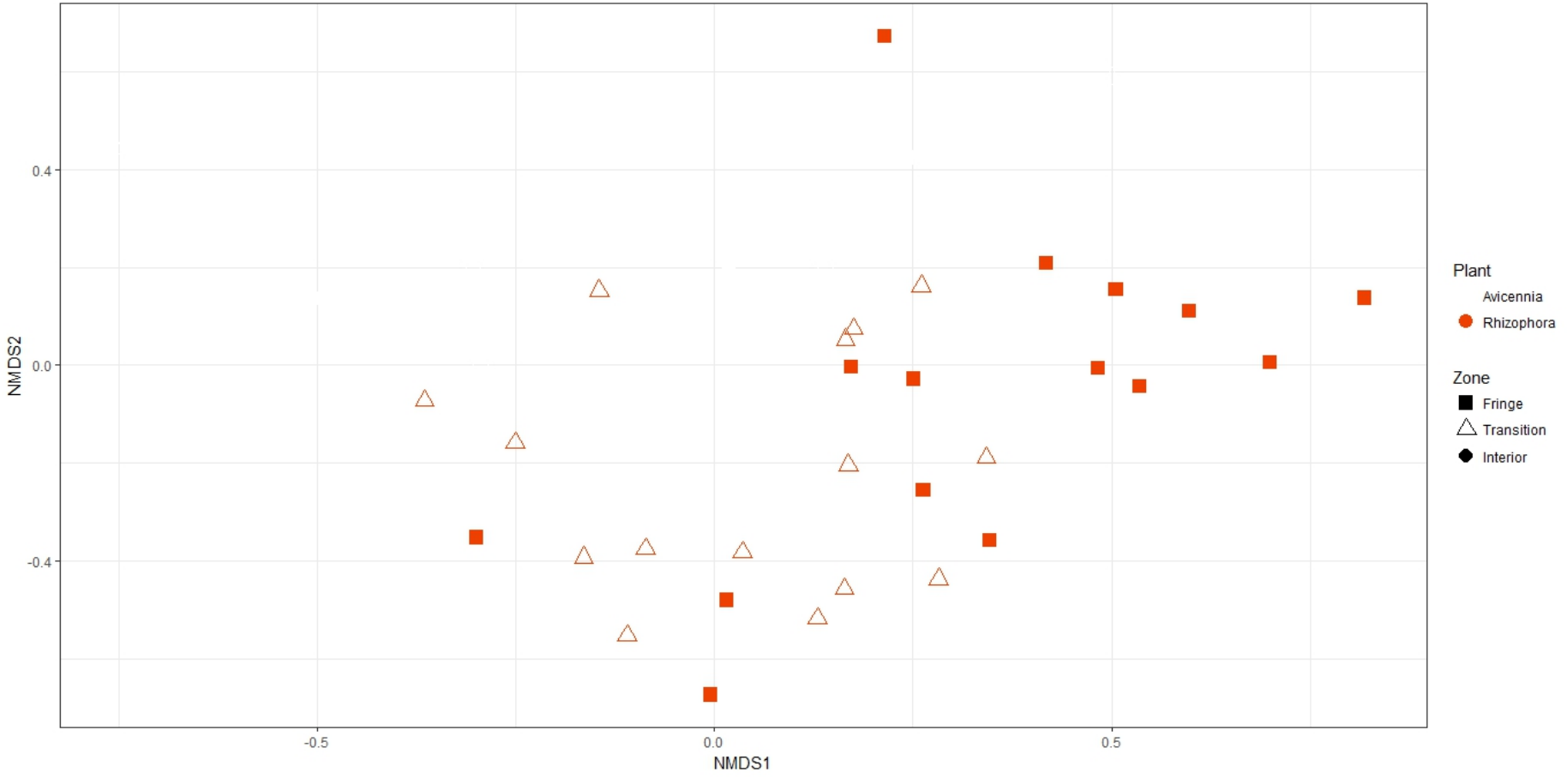
NMDS1
Plant
Avicennia
Rhizophora
Zone
Fringe
Transition
Interior

ITS results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NMDS2
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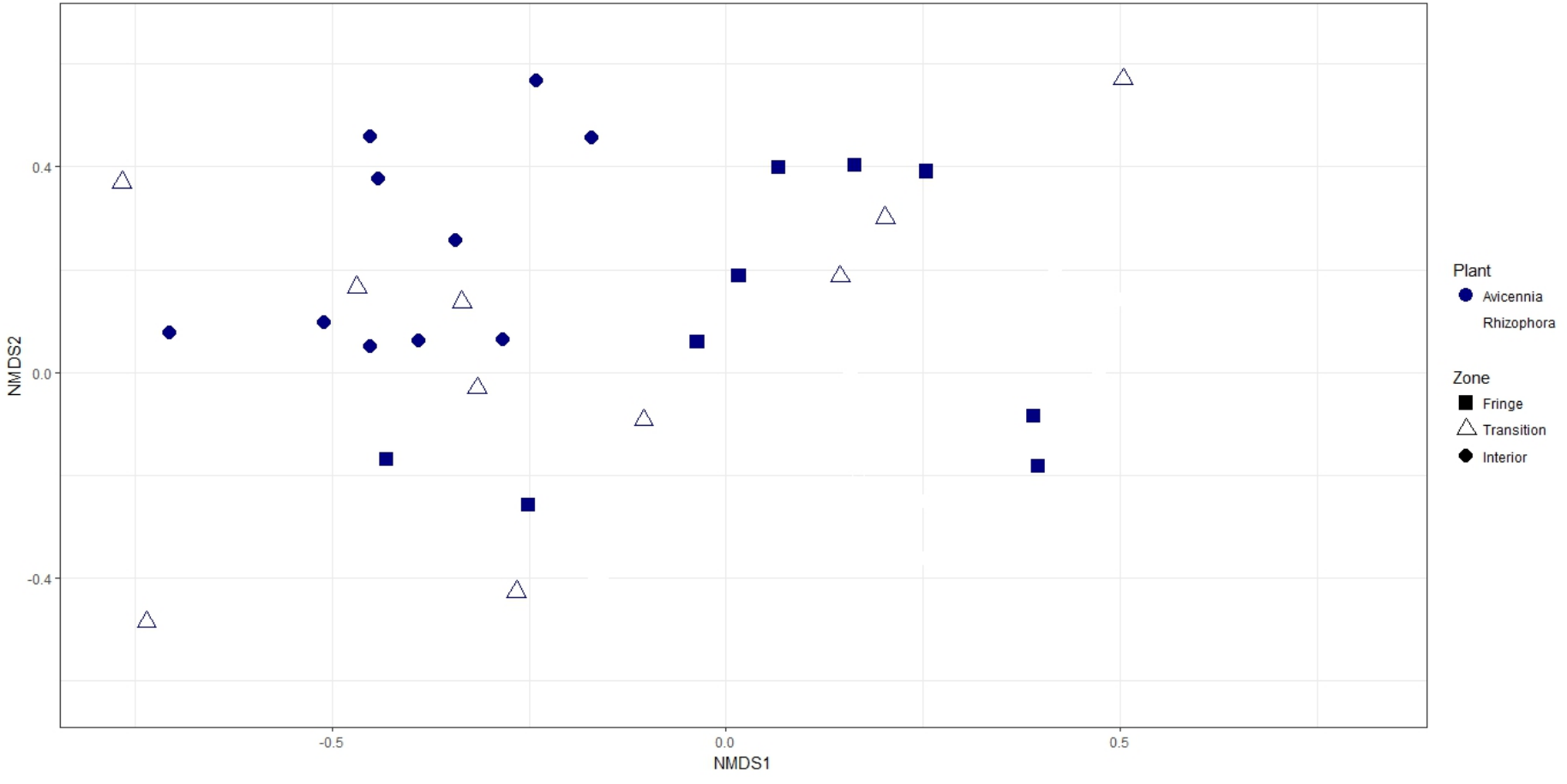
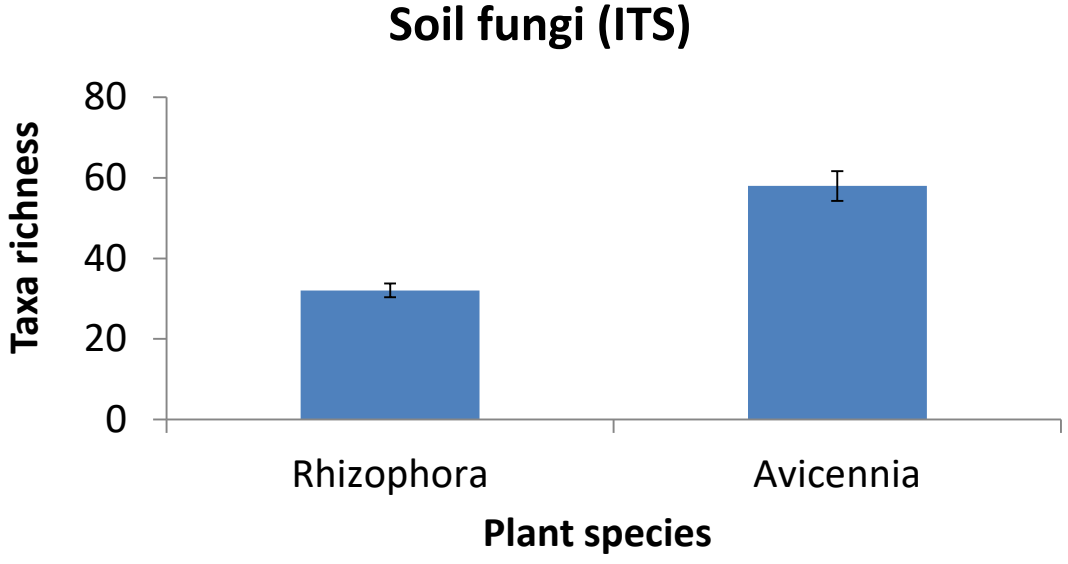
0.5
NMDS1
Plant
Avicennia
Rhizophora
Zone
Fringe
Transition
Interior

ITS results


0.4
0.0
-0.4
NMDS2
-0.5
0.0
0.5
NMDS1
Plant
Avicennia
Rhizophora
Zone
Fringe
Transition
Interior

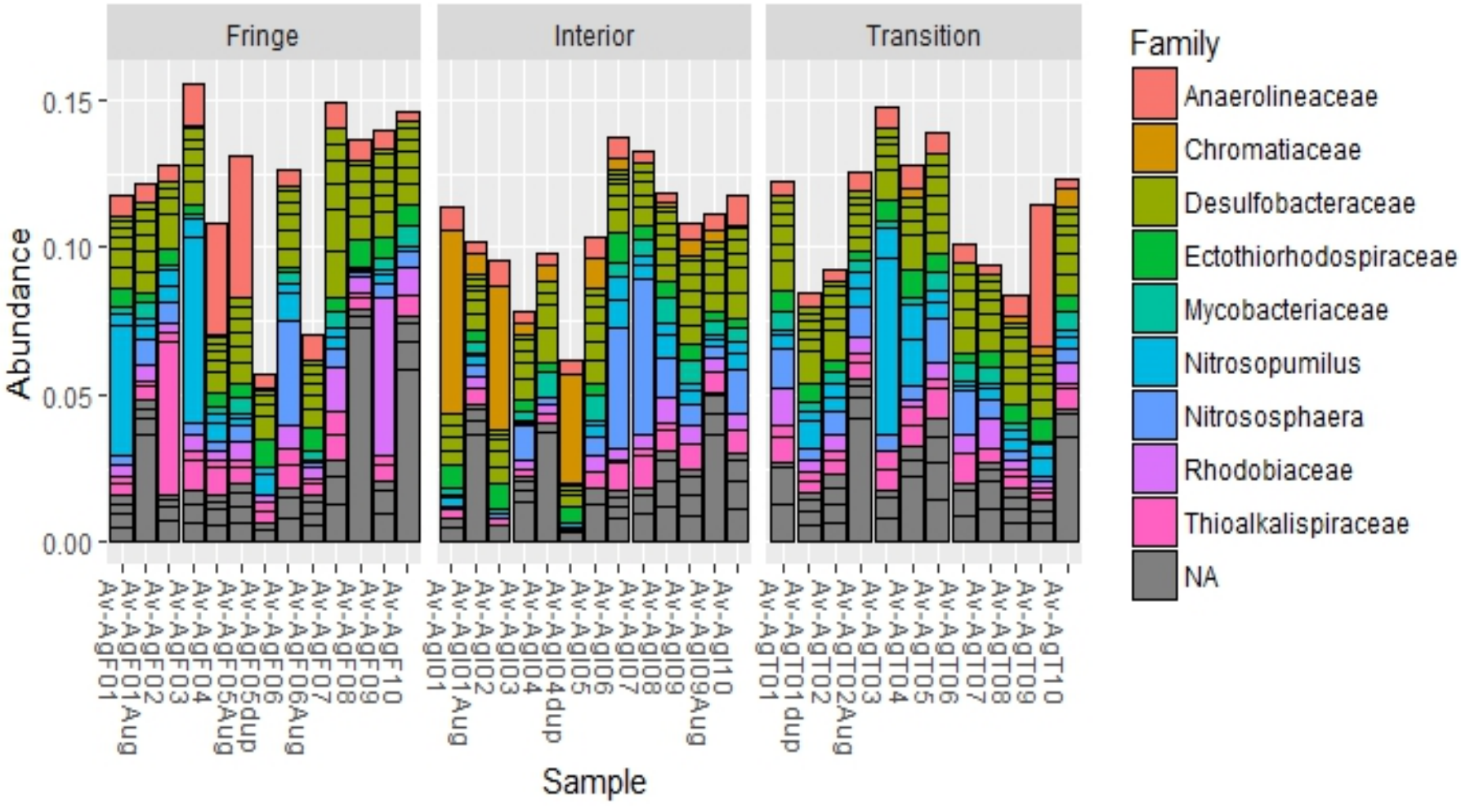
Microbial richness results

- Taxa richness higher in interior zone for bacteria & fungi
- Higher fungal taxa richness in *Avicennia germinans* soil



More results

- No relationship between plant genetic similarity and bacterial or fungal community similarity
- Significant relationship between 16S and ITS communities - more similar bacterial communities had more similar fungal communities


Fringe
Interior
Transition
Abundance
0.15
0.10
0.05
0.00
Sample
Aw-AgF01
Aw-AgF01Aug
Aw-AgF02
Aw-AgF03
Aw-AgF04
Aw-AgF05Aug
Aw-AgF05dup
Aw-AgF06
Aw-AgF06Aug
Aw-AgF07
Aw-AgF08
Aw-AgF09
Aw-AgF10
Aw-Agl01
Aw-Agl01Aug
Aw-Agl02
Aw-Agl03
Aw-Agl04
Aw-Agl04dup
Aw-Agl05
Aw-Agl06
Aw-Agl07
Aw-Agl08
Aw-Agl09
Aw-Agl09Aug
Aw-Agl10
Aw-AgT01
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Aw-AgT02Aug
Aw-AgT03
Aw-AgT04
Aw-AgT05
Aw-AgT06
Aw-AgT07
Aw-AgT08
Aw-AgT09
Aw-AgT10
Family
Anaerolineaceae
Chromatiaceae
Desulfobacteraceae
Ectothiorhodospiraceae
Mycobacteriaceae
Nitrosopumilus
Nitrososphaera
Rhodobiaceae
Thioalkalispiraceae
NA

Summary

- Microbial community composition in mangroves is affected by plant species and tidal/vegetation zone
- Richness of soil microbial taxa varies by zone & plant species
- No significant relationship between plant genetic similarity and microbial community similarity
- More similar bacterial communities have more similar fungal communities

Acknowledgements

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