

Is there a difference between the bacterial communities of monogyne and polygyne fire ant colony soils?

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Abstract

North American populations of red imported fire ants (*Solenopsis invicta*) include monogyne and polygyne social variants. We investigated differences in the structure of bacterial communities in soils inhabited by the two social forms. Because monogyne ants are highly territorial and do not share food resources intercolonially, we hypothesized that soils nested by monogyne ant colonies would harbor relatively distinct bacterial communities compared to those of polygyne ants that forage on common resources. Soils were collected, including tumulus and nearby ant-free soils at two depths from monogyne and polygyne fire ant colonies in Raleigh, North Carolina, from which DNA was extracted, and Illumina libraries of 16S amplicons were prepared and sequenced. Alpha and beta diversity analyses of bacterial communities indicated no distinction between monogyne and polygyne fire ant soils, though bacterial communities of soils inhabited by fire ants were distinct from communities in ant-free soils. Bacterial taxa found in soils and differences between fire ant inhabited soils and ant-free soils are reported.

Introduction and Objectives

- **Monogyne** colonies with single queen, highly territorial, aggressive, discriminate and attack non-nestmates
- **Polygyne** colonies with multiple queens, share forging area, less aggressive, fail to attack non-nestmates
- Measure bacterial diversity of microbiome, characterize bacterial community compositions, and test factors

Materials and Methods

- Soil collected from monogyne and polygyne *Solenopsis invicta* colonies and ant-negative soils; collections at 0 cm and 10 cm deep
- 16S rRNA amplicon libraries generated (515F/806R); paired-end sequencing performed on Illumina Mi-Seq platform
- Mock community control to measure PCR bias, sequencing bias, taxonomic assignment accuracy
- Analysis by QIIME 2 (qiime2.org, 2018) using DADA 2 (Callahan et al., 2016) for quality control
- Taxonomy assigned by Greengenes (99%) 16S rRNA database
- Fire ant colonization (colony soil vs. ant-negative soil) and colony social type (monogyne vs. polygyne) tested as factors in bacterial community compositions

Mock bacterial community

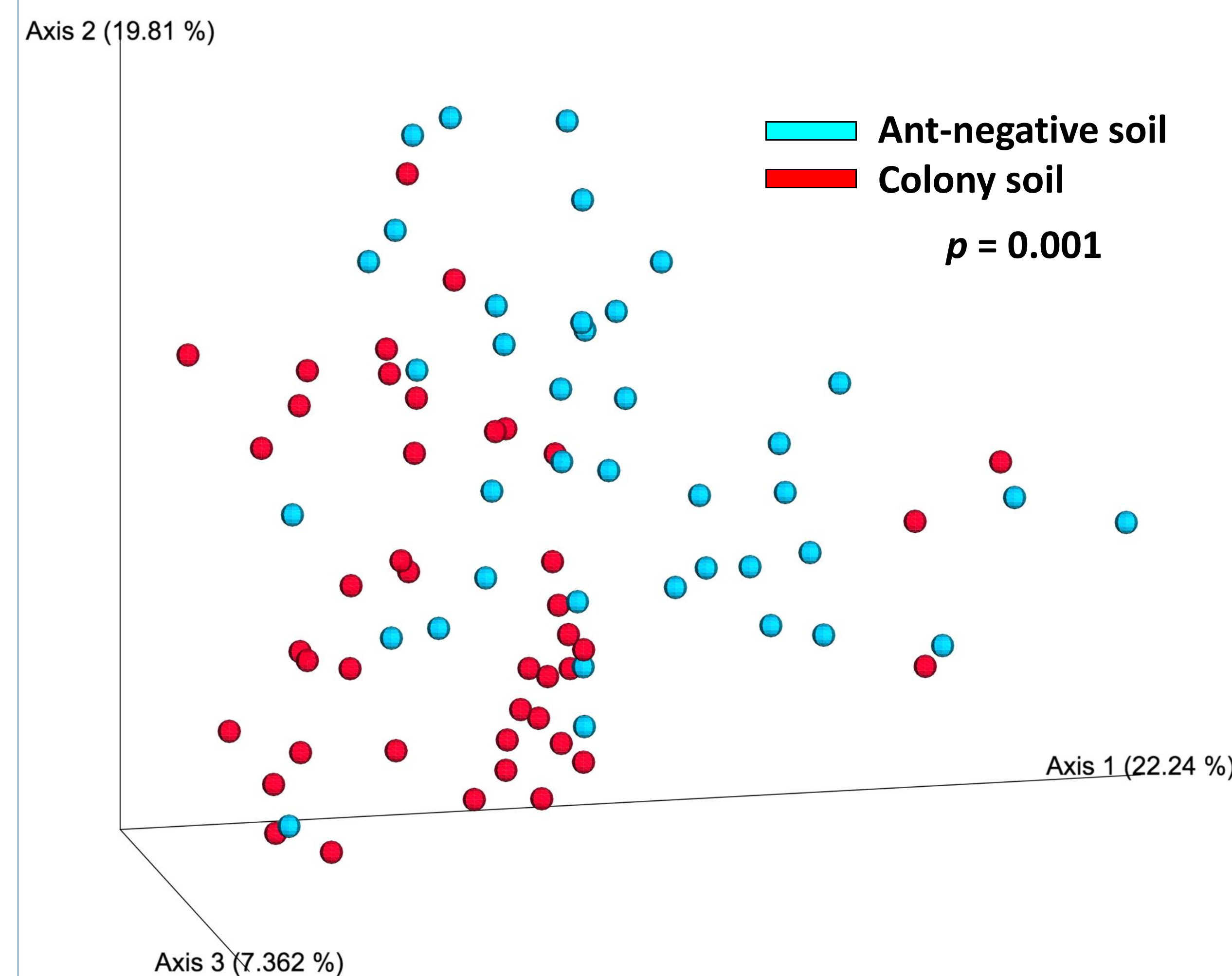
Species	Actual composition (%)	Identified taxa	Measured composition (%)
<i>Pseudomonas auruginosa</i>	4.2	<i>Pseudomonas</i>	14.6
<i>Escherichia coli</i>	10.1	<i>Escherichia coli</i>	7.1
<i>Salmonella enterica</i>	10.4	Enterobacteriaceae	14.4
<i>Lactobacillus fermentum</i>	18.4	<i>Lactobacillus</i>	18.3
<i>Enterococcus faecalis</i>	9.9	<i>Enterococcus</i>	8.6
<i>Staphylococcus aureus</i>	15.5	<i>Staphylococcus</i>	20.4
<i>Listeria monocytogenes</i>	14.1	Listeriaceae	0.0
<i>Bacillus subtilis</i>	17.4	<i>Bacillus</i>	16.6

PCR bias and varying classification resolution detected.

Bacterial community β -diversity

Weighted UNIFRAC analyses

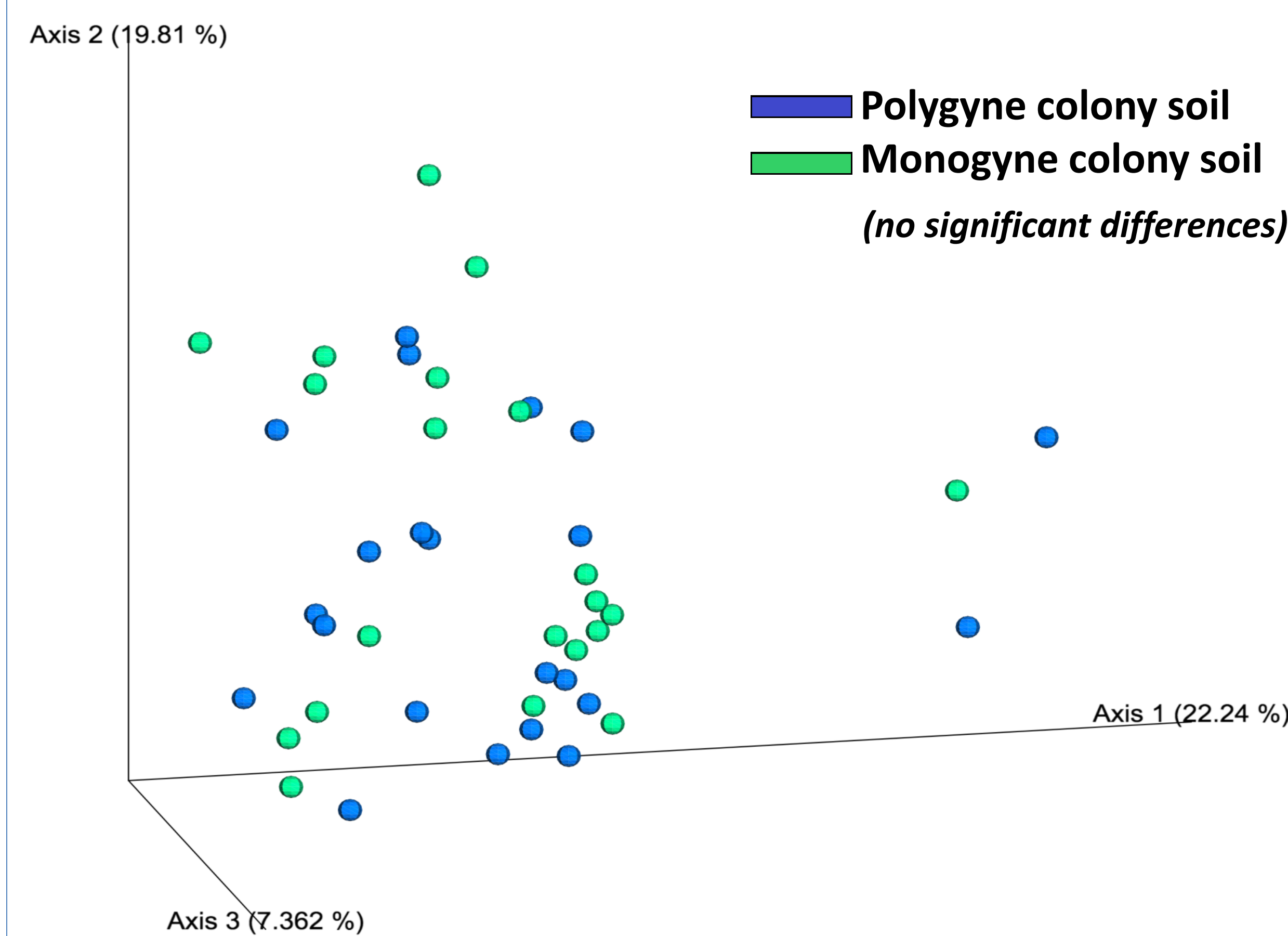
Effects of fire ant colonization



Bacterial communities of colony soils are relatively similar, compared to beta-diversity of ant-negative soils.

Community composition differences are driven by several bacterial tax.

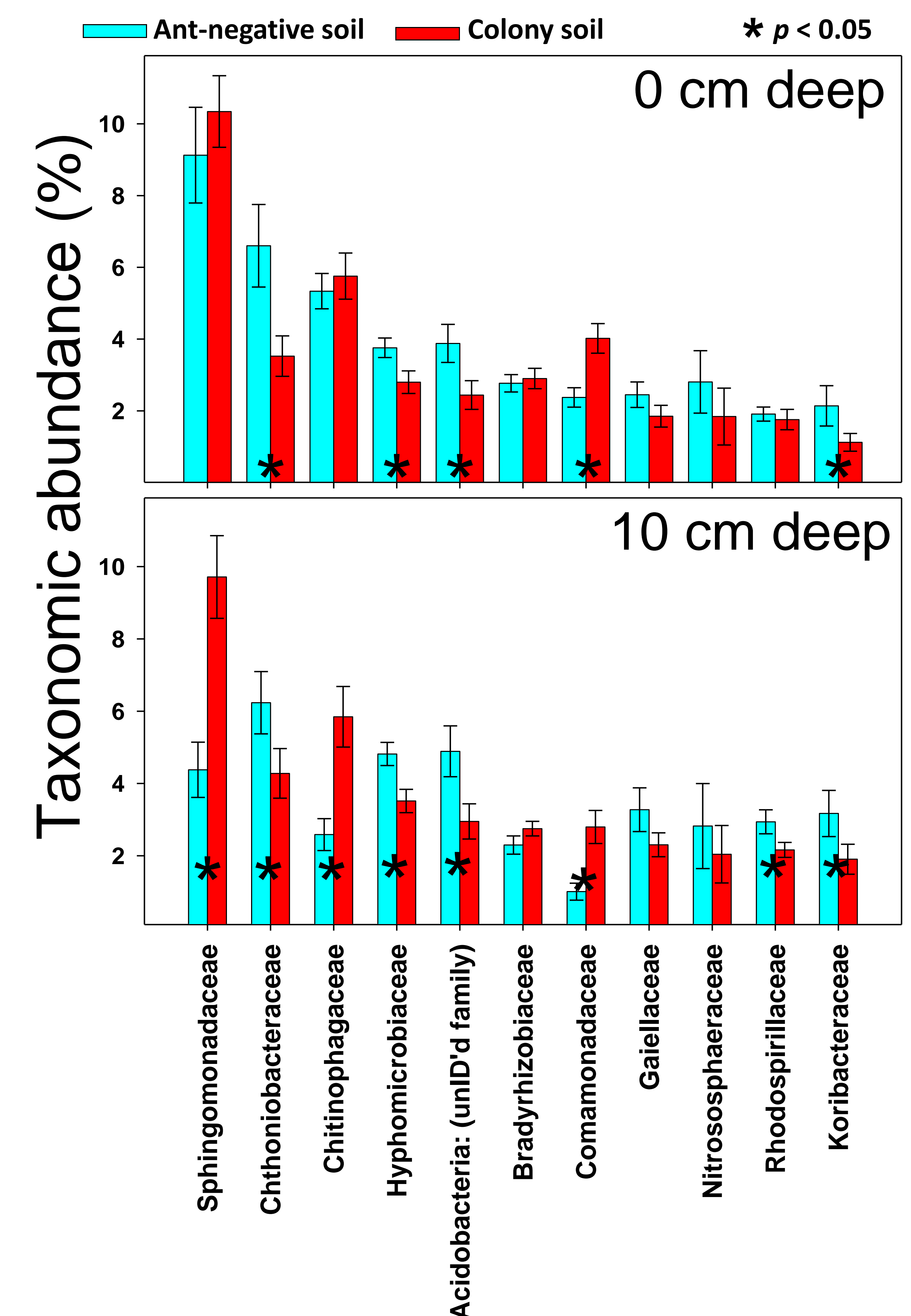
Effects of colony social type



Bacterial communities of monogyne and polygyne colony soils are not distinct.

Taxa dependence on fire ant colonization

Family-level taxa (>2% average abundance)



Conclusions and Summary

No differences were detected between bacterial communities associated with monogyne and polygyne fire ant soils.

Fire ant colonization alters native soil bacterial communities; differences driven by diverse bacterial taxa.

Increased taxa correlate with chitin degrading enzymes and aerobic taxa.

Decreased taxa associated with phenolic compound metabolism.

References

Callahan, B. J., McMurdie, P. J., Rosen, M. J., Han, A. W., Johnson, A. J. A., & Holmes, S. P. (2016). DADA2: high-resolution sample inference from Illumina amplicon data. *Nature methods*, 13(7), 581.

qiime2.org (2018): <https://qiime2.org/>