

Investigating the Distribution and Diversity of Bacterial ACC-d to Promote Plant Growth During Abiotic Stress Jamell Dacon¹, Patrick Kearns², and Ashley Shade³ ¹Department of Mathematics, Medgar Evers College CUNY, Brooklyn, NY 11225



Research Experience for Students

²Department of Microbiology and Genetics, Michigan State University, East Lansing, MI 48825

Introduction

When plants are stressed, they produce ethylene, which limits their growth and development. Our objectives were to improve understanding of the biogeographic distribution and diversity of the bacterial gene

1-aminocyclopropane-1-carboxylate deaminase (ACC-d). ACC-d is an enzyme that degrades ethylene. Therefore, bacteria that carry ACC-d are capable of promoting plant growth in spite of external stress that the plant experiences. Bacteria that contain ACC-d are of interest for improving plant productivity and yield during times of stress, such as drought.

Objectives

- To understand the biogeographic distribution of ACC-d genes across different ecosystems and its diversity among microbial lineages.
- To compare the diversity of ACC-d genes between soil and plant communities, which are relevant to agricultural applications.

Methods

Mined the Joint Genome Institute Integrated Microbial Genomes database for ACC-d genes

- Retrieved nearly 150,000 full length ACC-d sequences from ~3200 samples
- Collated metadata for each sample
- Gathered ACC-d abundance and *rplB* abundance for each sample

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- Operational Taxonomic Unit (OTU) clustering \bullet at 85% identity
- Calculate OTU richness
- Calculate beta diversity based on Bray-Curtis similarity



Figure 1. Map of the distributions of studies examined for the presence of ACC-d. Note: The key is applicable to **Figure 1** and **Figure 2**.



Data visualization



Figure 2. Box and whisker plots of normalized ACC-d Abundance (A) and OTUs observed. ACC-d abundance is normalized to the single copy bacterial gene rplB. The black line in the box is the media, the edges of the boxes are the 25th and 75th quartiles, and dots are outliers.





Results Cont.



Figure 3. Principle coordinates analysis based on Bray-Curtis similarity. (PERMANOVA, F=134.51, p<0.001, R²=0.18).

Conclusions

- ACC-d is a widespread gene across many ecosystems (Fig. 1).
- ACC-d is the most abundant and diverse in soil and plant-associated environments (soil, rhizosphere, rhizoplane, Fig. 2).
- Outside of soils, freshwater environments are also hot spots for ACC-d abundance and diversity (Fig. 2).
- Despite large geographical distances, soil and plant have different ACC-d diversity and representation (Fig. 3).

References

- Glick, B.R. *Microbiol Res* 169: 30-39 (2014).
- Caporaso, J. G. et al. Nat Meth 7: 335-336 (2010).
- Team, R. Core. Vienna, Austria: R foundation for statistical computing (2000).

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