Evaluating the *Chenopodium* microbiome: How do rhizosphere microbial interactions affect plant growth and stress tolerance?

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Introduction

Quinoa (*Chenopodium quinoa*) has gained popularity worldwide due to its **high nutritive properties** and **tolerance to stresses** such as soil salinity, acidity, and drought (1). **Quinoa has great potential for cultivation in North America, specifically in New England** (NE), where up to 11 native/naturalized Chenopodium species have been documented (2). Quinoa cultivation faces many obstacles in NE (Fig 1 and 2). How do we grow a crop in a place where it has never been grown before?

The **rhizosphere microbiomes of NE native *Chenopodium* species can provide insight to whether microbial interactions are a key factor in the success of native *Chenopodium* spp**. in the region and can be used to identify microbial taxa with the potential to provide beneficial services to quinoa.

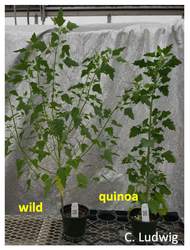

Figure 1. Phenotypic diversity among *Chenopodium* spp. Wild *C. berlandieri* var. *macrocalycium* plant compared to quinoa

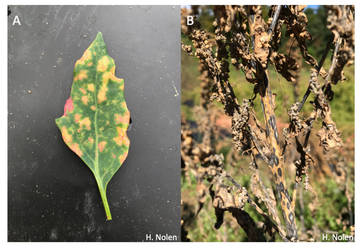

Figure 2. Downy mildew (A) and stem lesion (B) diseases on quinoa in New Hampshire

Methods

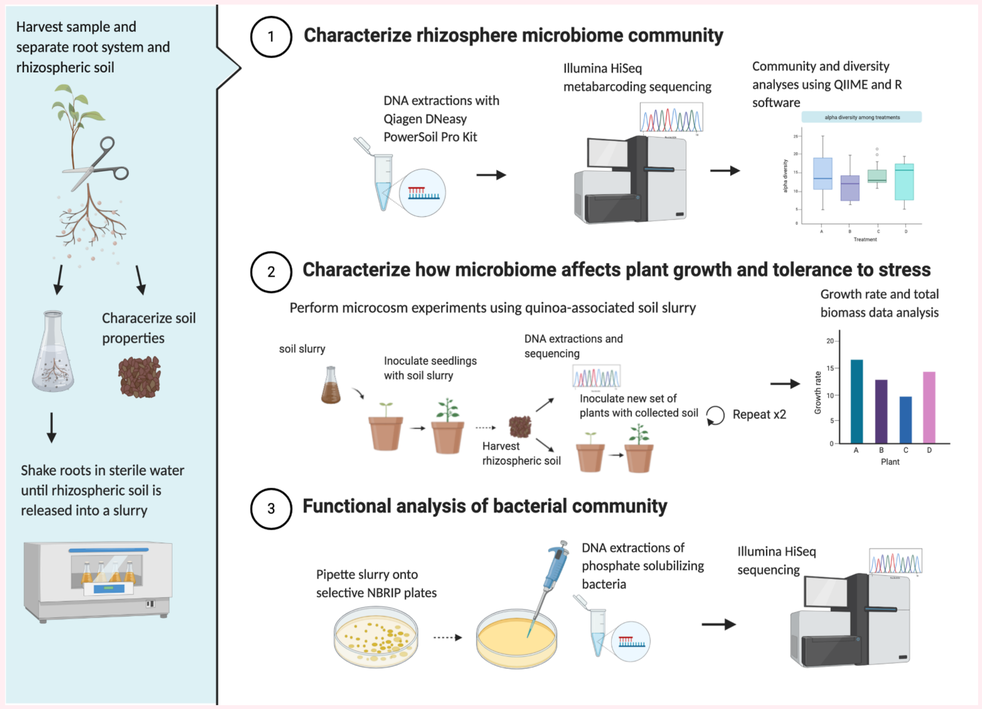

Figure 3. Overall project methodology and objectives. Left side panel describes preparation of soil slurries used in each objective. Created with Biorender.com

Objective 1: Soils were collected from *Chenopodium* spp. in agricultural and wild sites in New Hampshire, Vermont, Utah, Colorado, and Idaho. DNA was extracted from soils and bacterial (16s rRNA) and fungal (ITS rRNA) communities were sequenced by the Hubbard Center for Genome Studies.

Objectives 2a and 2b: Soil slurries were applied to plants under controlled conditions. Plant growth and leaf production were measured once per week for 4 weeks after inoculation. After 4 weeks, soil was collected from each experimental unit to create a new slurry to apply to the next generation of plants. This process was repeated twice for 3 total microbial generations (Fig 3).

Objective 3: Selective media is currently being used to isolate nitrogen fixing and phosphate solubilizing bacteria from soils.

Project objectives

1) Determine if different *Chenopodium* species harbor unique rhizosphere communities.

2a) Investigate generational changes in microbial communities of different origins and host selection under stress.

2b) Investigate how these changes in the microbial community affect plant growth under stress.

3) Identify *Chenopodium*-associated beneficial microbes that enhance plant growth and tolerance to stress.

Long-term goal

Redomesticate quinoa for North American agriculture by domesticating a New England native *Chenopodium* relative with agriculturally favorable traits using quinoa as a model.

Results

- Microbial community **composition** (bacterial and fungal) **and diversity** (bacterial) **were more affected by whether a site was agricultural or wild** compared to host species (Fig 4)
- **Fungal communities display more variation** compared to bacterial communities in community composition in both wild and agricultural sites (Fig 4)
- **The presence of a host-adapted microbial community does not enhance *Chenopodium* spp. growth** under drought or non-stress conditions (data not shown)
- **There are significant differences in *Chenopodium* spp. ability to handle drought stress,** with *C. berlandieri* var. *macrocalycium* having greater biomass and leaf production compared to quinoa (data not shown)

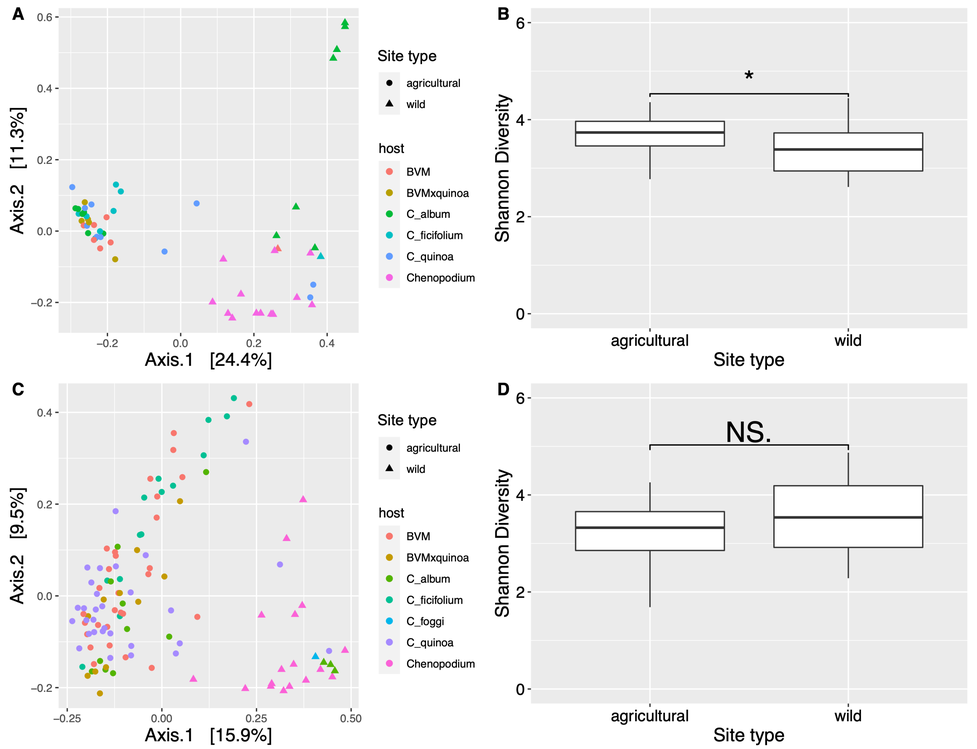

Figure 4. Principle coordinates analysis (PCoA) and Shannon Diversity of 2019 bacterial (A, B) and fungal (C, D) composition among *Chenopodium* species grown in agricultural and wild environments. Samples are colored by species and the shape of each symbol indicates site type.

Acknowledgments: This work was supported by the New Hampshire Agricultural Experiment Station Project and the New Hampshire Space Grant. We also thank Evan Ford and the Woodman Farm staff.

References:
1) Testen et al. 2014. Molecular Detection of *Peronospora variabilis* in Quinoa Seed and Phylogeny of the Quinoa Downy Mildew Pathogen in South America and the United States. The American Phytopathological Society 104: 379-386.
2) Neff, E. 2017. Developing a molecular pipeline to identify *Chenopodium* species in New England. Thesis, University of New Hampshire.

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