Mycorrhizal Fungi Association and Population Genetics of *Comandra umbellata*

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Introduction

Plant diversity enhances overall ecosystem stability in prairies (Tilman & Downing, 1994; McGrady et al., 1997; Naeem & Li, 1997) and both species richness and functional diversity tend to be higher in remnant prairies compared to restored prairies (Polley et al., 2005). *Comandra umbellata* is a hemiparasitic species common to remnants and desirable in prairie restorations due to a high C-value and reputed association with increased overall plant species diversity. However, *C. umbellata* has been difficult to reintroduce in restorations and has primarily been achieved by transplanting (Buchholz, unpublished).

Arbuscular mycorrhizal fungi (AMF) is also associated with increased species diversity and can even have a regulatory effect on species composition in tallgrass prairies (Koziol & Bever, 2017). However, little is known about the relationship between AMF and hemiparasitic plants, *C. umbellata* in particular. It is also not known what conditions foster germination of *C. umbellata* and seed recruitment has not been regularly observed in the field. This study seeks to identify if there is an association between the presence of *C. umbellata* and AMF communities as well as to better understand the role of seedling establishment versus clonal expansion in the persistence of populations at Nachusa Grasslands.

AMF Association Question

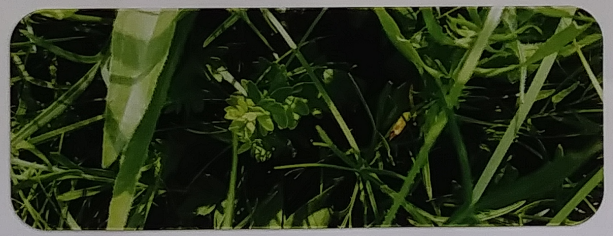
Is there an association between a specific community diversity, composition, and/or abundance of AMF and the establishment and persistence of *C. umbellata*?

Population Genetics Question

What is the genetic diversity of *C. umbellata* at Nachusa Grasslands and what are the spatial dynamics of that diversity?

AMF Association Hypothesis

There is an association between AMF community diversity, composition, and/or abundance and establishment and persistence of *C. umbellata*.



Population Genetics Hypothesis

Comandra umbellata stands are persisting/expanding primarily by clonal growth and are most closely related to their nearest neighboring stand.

AMF Association Methods

Six soil samples were collected from 10 *C. umbellata* stands in remnants and 10 stands in restorations, each using a 10 x 15cm bulb planter. Each *C. umbellata* site was paired with a location within 100 yards that was comparable in obvious features but lacking *C. umbellata*. Six soil samples were taken from each of the paired locations using the same method. Root samples were taken from *C. umbellata* where present and from *Schizachyrium scoparium* at the paired locations. DNA will be extracted from the AMF in soil and root samples.

DNA extraction will be done using DNeasy PowerSoil Kit from Qiagen. Extracted DNA will be amplified using Polymerase Chain Reaction (PCR) with DreamTaq™ Hot Start PCR Master Mix following the manufacturer's protocol. DNA will be marked using AMF specific primers and sequenced on Illumina MiSeq. Sequences will be grouped into OTUs using USEARCH and UPARSE-OUT. OTU sequences will be compared with known sequences to identify mycorrhizal species and QIIME 2 (Quantitative Insights Into Microbial Ecology) will be used for taxonomic assignment. Soils will also be analyzed for nutrients, organic matter, pH, and microbial biomass.

Population Genetics Methods

Three leaves of *C. umbellata* were be taken from 5 stems at 20 *C. umbellata* sites. Half of those stands are spontaneous populations within remnants. The other half are stands transplanted into restorations. Microsatellites are currently being tested for amplifying *C. umbellata* DNA. Successful primers will be used to identify individuals within the sampled population to determine what portion of the sampled population is clonal. To interpret population structure, data will be analyzed and visualized in Structure to infer distinct populations, gene migration, and admixed individuals.

Acknowledgements

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Literature Cited

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