# Phylogenetic Information in Seed Morphology and Seed Germination for Shortgrass Prairie Species

# Introduction

Seed germination model is needed for ecological restoration

Phylogenetic information in seeds can help

In ecological restoration, while we try to simulate previous stage of plant community and maximum the portion of native species, the seed germination become a threshold. More specific, the variety of understudy species are needed in ecological restoration, with limited knowledge of seed germination of each specie, there is a difficulty in plant community restoration. If there is a formula to predict seed germination of different species, it will definitely benefit ecological restoration.

Seed stores genetic information and pass them to next generation. Seed germination capacity varies by species, which is decided by genetic and epigenetic factors. Further, long persistent epigenetic factors will drive the species evolution, and lead species develop environmental related species traits. For instance, if a species establishes and survives in fire active region, the species may develop and heritage fire related traits, such as responding to heat, smoke, or sunlight exposure. Unpuzzle the germination related traits will help understand the genetic factors of seed germination.

Seed morphology is related with seedling establishment and hazard tolerance (Westoby et al. 2002). Seed mass represents three fourths energy allocating to reproduction, which needs be counterbalanced between development of current generation and reproduction for next generation. Seed shape can be represented by the surface area, volume, circumference, height, width, and length. The seed shape will influence the seed dispersal by wind, water and animals.

Strong evidence supports (In review, Leishman et al. 2000) that large seeds produce stronger seedlings, benefiting from nutrient stored in seed under “larger-seed-later-deployment” interpretation or “cotyledon functional morphology hypothesis”. In general, large seed performs better than small seed under hazard condition during seed establishment. Exceptions happen in some hazard condition may explain by larger seed size might initially evolve in one type of advantage, but also associate with other hazards later. A predict model combining seed mass and seed shape may be a good for predict seed germination for restoration practice. However, simply draw correlation between seed morphology and seed germination rate of closed related species bias by phylogenetic information.

Phylogeny is the systematic analysis of living organism, which represents evolution of species over time. Phylogenetic information uses tree shape (phylogenetic tree) to express species the relation and diversification. A phylogenetic tree alone may only contain structure information of branch length, tips, and nodes, but analyzing of relative position of species also can reveal traits evolve across species. On phylogenetic trees, large portion of species with similar functions are positioned closely. In trait evolution, the relative position of species on trees represents the trait development path. Traits of evolutionary closely relative species are sharing a common ancestor; it is highly possible they heritage traits information from their common ancestor. If it is true, the traits measurement can’t not analyze in common statistical model, since it violates the foundation assumption of independence. In 1985, Felsenstein (1985) proposed independent contrast to solve the non-independent observation for analysis on traditional traits regression. Under the assumption of random walk process, i.e. Brown motion, the observed individual represent independent evolution pathway, therefore differences between closely related species are independent. However, there are circumstances the phylogeny will be over-correctly by phylogenetic independent contrast, since sometimes the closely related species may not be similar. In such condition, traditional trait analysis without phylogeny may be more suitable. Some have tried to explore the relation between single seed trait and phylogenetic information, such as seed dormancy (Willis et al. 2014, Dayrell et al. 2016), dispersal (Razafindrastsima et al. 2016), seed bank composition (Griffiths et al. 2014), germination (Carta et al. 2016). Others try to combine phylogeny with other scientific models and reveal how one trait evolves and how different traits interact with each other (Gallagher et al. 2014, Paquette et al. 2015). In 2018, Dr. Barak and her colleagues (Barak et al. 2018) have attempts to explore relationship between seed traits and seed germination with phylogenetic information in tallgrass prairie restoration preferred species. Their work shot lights seed shape predict germination response.

In this paper, we tested phylogenetic signal in seed morphological traits (seed mass and seed surface area). We also explored the relationship between seed morphological traits and seed germination response with and without phylogenetic information.

# Methods

## Material

## Data Analysis

# Results

# Discussion

# Citation