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

# Introduction

Establishing the territory

* + Seed germination is critical for species survival and colonize new territory, which is threshold for reseeding restoration practice.
    - Seed germination capacity variate by species, which is decided by internal and external factors.
    - Along with species evolution, consistent preserved external factors (abiotic and biotic pressure) also shape the species.

Identifying the niche (the Problem)

* + Publications try to detect seed germination patterns
    - Seed germination response to hormones;
    - Seed germination response to environmental factors (fire, flood, cold et al.);
  + However, without phylogenetic information of species may have a mislead conclusion.
    - If species are closely related, the measurement of species may be influenced by their heritable traits, such the germination rate of closed related species may be influenced by heritable dormancy traits. Including Using the comparative phylogenetic method to analyze seed germination could exclude the heritable information and ensure the statistical analysis fulfill the assumption of independence.
    - Phylogenetic analysis for species will be a systematic way to understand species traits. The results will not only benefit the tested species, but conclusion is expandable to tested phylogenetic system.
    - Publications tried to detect the correlation between seed morphology and seed germinations without phylogenetic information.

Occupying the niche

* Hypothesis:
  + Seed traits (mass and surface area) contains phylogenetic signal.
  + If applying comparative phylogenetic method to analyze patterns between seed traits and seed germination, then the seed traits could build a predict model to predict seed germination.
* Approach:
  + Test phylogenetic signal in seed morphological measurements
    - Pagel’s lambda
    - Blomberg’s K
  + Build phylogenetic general linear model for seed morphology and seed germination.
* Prediction:
  + Seed morphology in shortgrass prairie species contains phylogenetic signal
  + Seed morphology is weakly correlated with seed germination

Seed is the bridge of genetic information pass along generation within species. Seed stores genetic information from current generation to maintain species traits. Then after germination, the genetic information is activated, transferred and translated into different material to control and manage plant growth and reproduce in new generation.

Seed germination capacity varies by species, which is decided by the interaction between species and environments. The environment factors can influence seed germination, such as cold, flood, drought. If certain environmental consistently stress species, species will develop adapted traits to response to specialize climate, such as fire prone environment develop fire traits, response to heat, smoke, and open canopy.

In open area restoration, human tend to maximum the reseeding restore outcome through improve the germination of target species. One of the best approaches is understanding the germination patterns across species.

Previous researches have tried to explore seed germination response to hormones;

others summarized seed germination response to environmental factors.

However, most of the analyzed traits are physiology traits. in comparison for morphological traits is relative hard to collect the data for field practices. More importantly, most of the previous study didn’t include phylogenetic information while analyzing the correlation between seed traits and seed germination rate.

Phylogenetic analysis for species will be a systematic way to understand species traits. If species are closely related, the measurement of species may be influenced by their heritable traits, such the germination rate of closed related species may be influenced by heritable dormancy traits. Including Using the comparative phylogenetic method to analyze seed germination could exclude the heritable information and ensure the statistical analysis fulfill the assumption of independence. The results will not only benefit the tested species, but conclusion is expandable to tested phylogenetic system.

In this study, I tried to detect relation between seed morphological traits (seed mass and seed surface area) and seed surface area. In order to exclude the phylogenetic influences between species, I first test the phylogenetic signals in seed traits, using Pagel’s lambda and Blomberg’s K. Further I applied phylogenetic least square to evaluate the relationship between seed traits and seed germination rate.

# Methods

## Material

## Data Analysis

# Results

# Discussion

# Citation