In ecological restoration, germination of wide variety native species is the threshold. More specifically, most native seeds are dormant and need environmental triggers prior to germination. Only limited species and environmental triggers have been studied, which are far less than the species are needed in ecological restoration. Instead of testing germination on each species, if we can draw some connection between seed germination and easily measured seed traits, it will help predict germination of native seeds mixture and directly benefit the ecological restoration.

Seed contain and express genetic information to maintain specie’s feature, such as seed germination and seed morphology. Seed germination varies by species, which is largely influenced by genetic factors, dormancy, and epigenetic factors, environmental signals (Citation). Further, long persistent epic factors will drive species evolution, leading species to develop environmentally related traits and break dormancy after sense environmental signals. For instance, if a species establishes and survives in a fire dominated region, the species may develop heritable fire related traits, responding to heat, smoke or sunlight exposure (Citation). Resolving dormancy breaking traits will help identify the genetic factors of seed germination. Germination experiments are needed to understand seed dormancy as a species trait. However, if we can discover other easy measured heritable traits associate with seed dormancy, a practical measurement may develop to estimate seed dormancy and predict seed germination of each ingredient of seed mix.

Seed morphology is related with seed germination and hazard tolerance (Westoby et al. 2002) and may be good an indicator for seed germination as well. Seed mass and seed shape are two major heritable seed indexes. Seed mass represents three fourths of energy allocated by plants to reproduction, supporting the initial growth of a plant. Seed shape will influence the seed dispersal which may lead to potential hazard by wind, water or animals and delay seed germination. Strong evidence supports (Leishman et al. 2000) that large seeds can stay dormant longer and produce stronger seedlings after germination, benefiting from nutrient stored in seed under “larger-seed-later-deployment” interpretation or “cotyledon functional morphology hypothesis”. In general, large seed can be preserved longer and germinate better than small seed under hazard. 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. Since seed morphology is related to seed germination, it has potential to predict seed germination. Further, seed mass and seed shape are easy to be measured, it would be a good practical tool for restoration practice to understand germination variety of restoration seed mix. However, while seed morphological traits are heritable to maintain species’ character, the heritable information also largely shares with common ancestor and closely related species. This biological relation may lead to statistical violation for independent observation, which needs phylogenetic comparative methods help.

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 relation and diversification. A phylogenetic tree alone may only contain structure information of branch length, tips, and nodes, but analysis of relative position of species can reveal how traits evolve across species. Typically, on phylogenetic trees, large portion of species with similar traits are positioned closely meaning under similar environmental stress their ancestor evolved similar traits and passed them to descendants. In trait evolution, the relative position of species on trees represents the trait development path. Evolutionarily closely related species are likely to inherit trait information from their common ancestor. If so, trait measurements can’t be analyzed 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 trait 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 measured seed mass, seed shape (length, height, shape) and the ratio of embryo and seed, and concluded that seed shape best predicted germination response.

In this paper, we tested phylogenetic signal in seed morphological traits of shortgrass prairie species (seed mass and seed surface area). We also test the relationship between seed morphological traits and seed germination response with phylogenetic comparative method.