

# Genetically-informed seed transfer zones for *Cleome lutea* and *Machaeranthera canescens* across the Colorado Plateau and adjacent regions

Cooperator Report for the Bureau of Land Management's  
Colorado Plateau Native Plant Program

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## Introduction

The majority of native plant materials (NPMs) utilized for restoration purposes are developed for widely distributed species that provide a variety of ecosystem services (Wood et al. 2015; Butterfield et al. 2017). Disturbed ecosystems benefit from the use of appropriate NPMs, which are those that display ecological fitness at the restoration site, are compatible with conspecifics and other members of the plant community, and that do not demonstrate invasive tendencies (Jones 2013). Furthermore, the use of appropriate NPMs can help address specific environmental challenges, rejuvenate ecosystem function, and improve the delivery of ecosystem services (Hughes 2008). While many NPMs have been developed for restoration (e.g., Aubry et al. 2005), there is interest in broadening the diversity of species available and the geographic representation of sources to provide suitable choices in relation to the characteristics of any restoration site. In addition, researchers are providing guidance to managers and practitioners regarding how best to transfer NPMs across the landscape. For example, guidance on seed transfer has been derived from genealogical studies, which utilize common gardens to correlate phenotypic variation with environmental gradients (summarized in Kilkenny 2015); molecular studies, which identify putative adaptive genetic loci and infer environmental drivers of variation (Shryock et al. 2017); and climate modeling studies, which can provide guidance when species-specific data are unavailable (Bower et al. 2014; Doherty et al. 2017). All of these approaches intend to improve the long-term viability of NPMs at restoration sites, thereby improving outcomes and stretching limiting restoration resources (e.g., time and money).

Genetic data (which hereafter refers to molecular/sequencing data) have broad, often unrealized utility when considering the use of existing NPMs or development of new NPMs. A well-designed landscape genetic analysis can resolve patterns of neutral genetic diversity across a species' distribution and delineate the geographic distribution of evolutionary lineages, which can have impacts on restoration outcomes (Hufford and Mazer 2003; McKay et al. 2005; Frankham et al. 2011). For example, determining how long evolutionary lineages have been separated and their rate of gene flow can help practitioners identify regions across a species' range where individuals should not be mixed, even if those individuals occupy similar environmental space (Massatti et al. 2018a). In addition, neutral genetic diversity is well suited to determine taxonomic relationships in instances where morphology tends to be unreliable (Fujita et al. 2012). Landscape genetics can also identify adaptive genetic variation, or variation that may provide a benefit to the survival (and therefore reproductive capacity) of a species (Holderegger et al. 2006). Genetic variation that correlates with environmental gradients suggests adaptively significant environmental conditions that can inform the development of seed transfer zones (as introduced above, Shryock et al. 2017; Massatti et al. 2018b). Furthermore, the inclusion of existing NPMs in genetic analyses permits the assessment of how they represent the known neutral and adaptive genetic diversity of a species. As such, genetic analyses can guide the appropriate deployment of existing NPMs, as well as suggest what additional NPMs may be important to develop. For most of the important Colorado Plateau restoration species, knowledge on adaptive differentiation, genetic diversity, and spatial variation in standing genetic diversity is lacking. The Bureau of Land Management (BLM)'s Colorado Plateau Native Plant Program (CPNPP) is strategically supporting research to fill these gaps (e.g., Massatti 2019).

Genetically-based seed transfer zones are described herein for two priority restoration species on and adjacent to the Colorado Plateau (Massatti 2020). Species include *Cleome lutea*



Hook. (Capparaceae; commonly called yellow spiderflower or yellow beeplant; synonym *Peritoma lutea* (Hook.) Raf.) and *Machaeranthera canescens* (Pursh) A. Gray (Asteraceae; commonly called hoary tansyaster; synonym *Dieteria canescens* (Pursh) Nutt.). The seed transfer zones depict both evolutionary lineages and inferences of adaptation as discerned from molecular investigations. These shapefile data may support successful restoration outcomes if, for example, seed transfer follows seed transfer zones depicted herein and/or composite seed strategies for native plant materials development utilize seed transfer zones when determining which seed accessions may be combined. The ultimate goal of these seed transfer zones is to protect species' natural patterns of genetic variation – genetic diversity is increasingly recognized a unit of conservation concern (Hoban et al. 2013) – and to understand species' adaptations to regional environmental gradients. Development of these seed transfer zones was funded by CPNPP, which was established, in part, to evaluate and develop native plant materials for important grass and forb species adapted to the unique ecological conditions of the Colorado Plateau (Wood et al. 2015). Each species' shapefile data available in Massatti (2020) are described in turn.

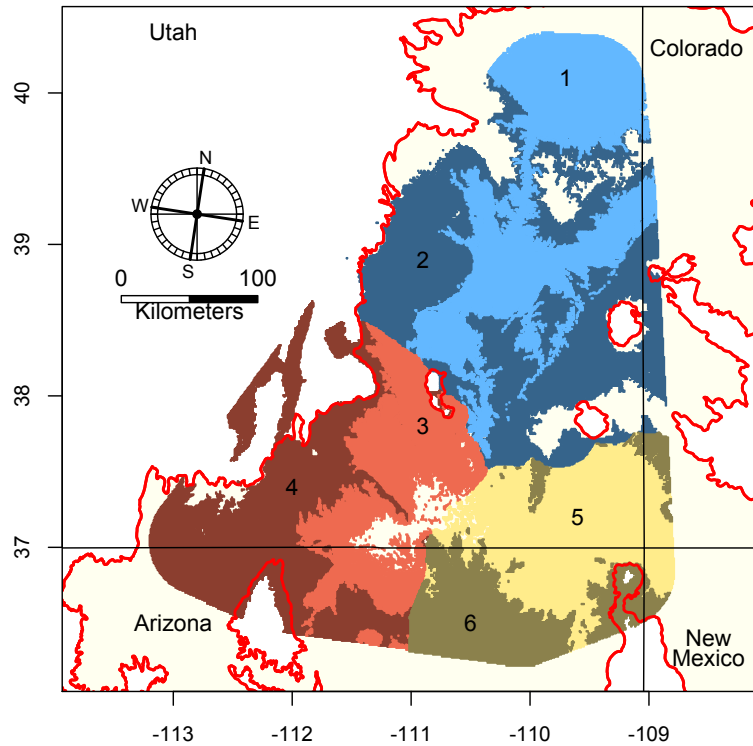
## Seed Transfer Zones

### *Cleome lutea* seed transfer zones

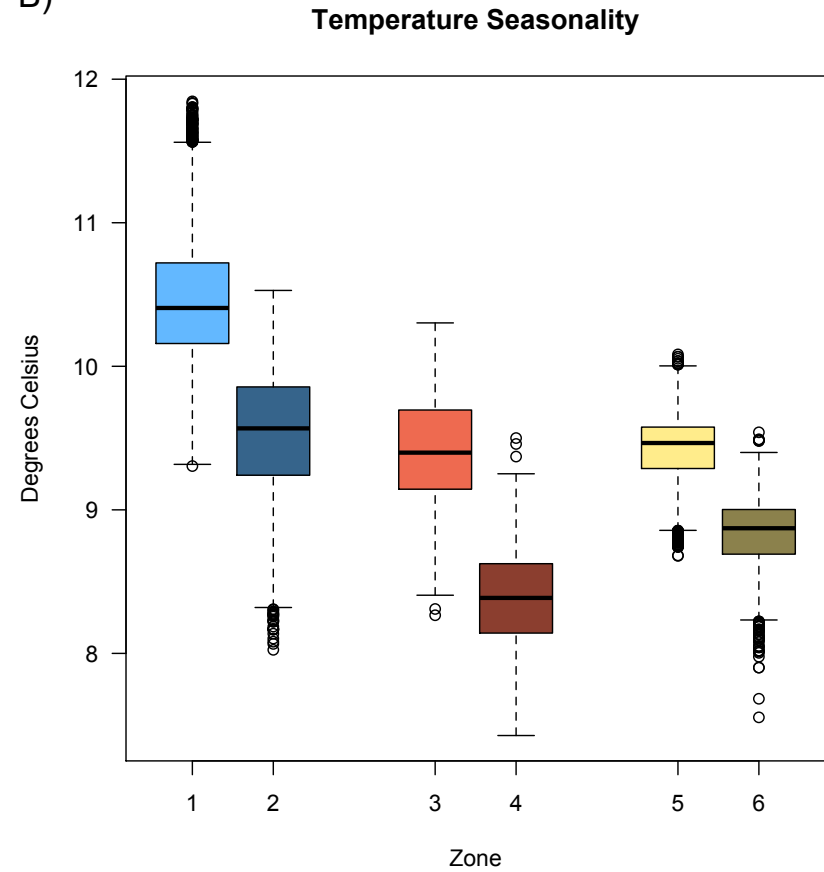
Six seed transfer zones are reported for *Cleome lutea* (Fig. 1) (Massatti 2020). These seed transfer zones account for both genetic differentiation and the species' inferred adaptation to regional climatic gradients (hue and saturation in Fig. 1, respectively). For example, *Cleome lutea* individuals within the blue polygons (i.e., zones 1 and 2) in Fig. 1A are all most closely related to one another, which means that genetic differentiation among individuals is minimized as opposed to comparing individuals in a blue polygon (either light or dark) with individuals in the red or yellow polygons. The saturation of the zones indicates inferred adaptation to the environmental variable displayed in Fig. 1B. Each box and whisker plot is calculated from values of temperature seasonality extracted at 5,000 randomly distributed points, or locations, within each seed transfer zone (i.e., 30,000 random points across the six seed transfer zones). As such, the box and whisker plots represent an estimation of the range of temperature seasonality within each of the seed transfer zones. For example, locations in zone 1 have, on average, higher values of temperature seasonality compared to locations in zone 2 (Fig. 1B). The seed transfer zones cover only the Colorado Plateau portion of the species' distribution.



A)



B)

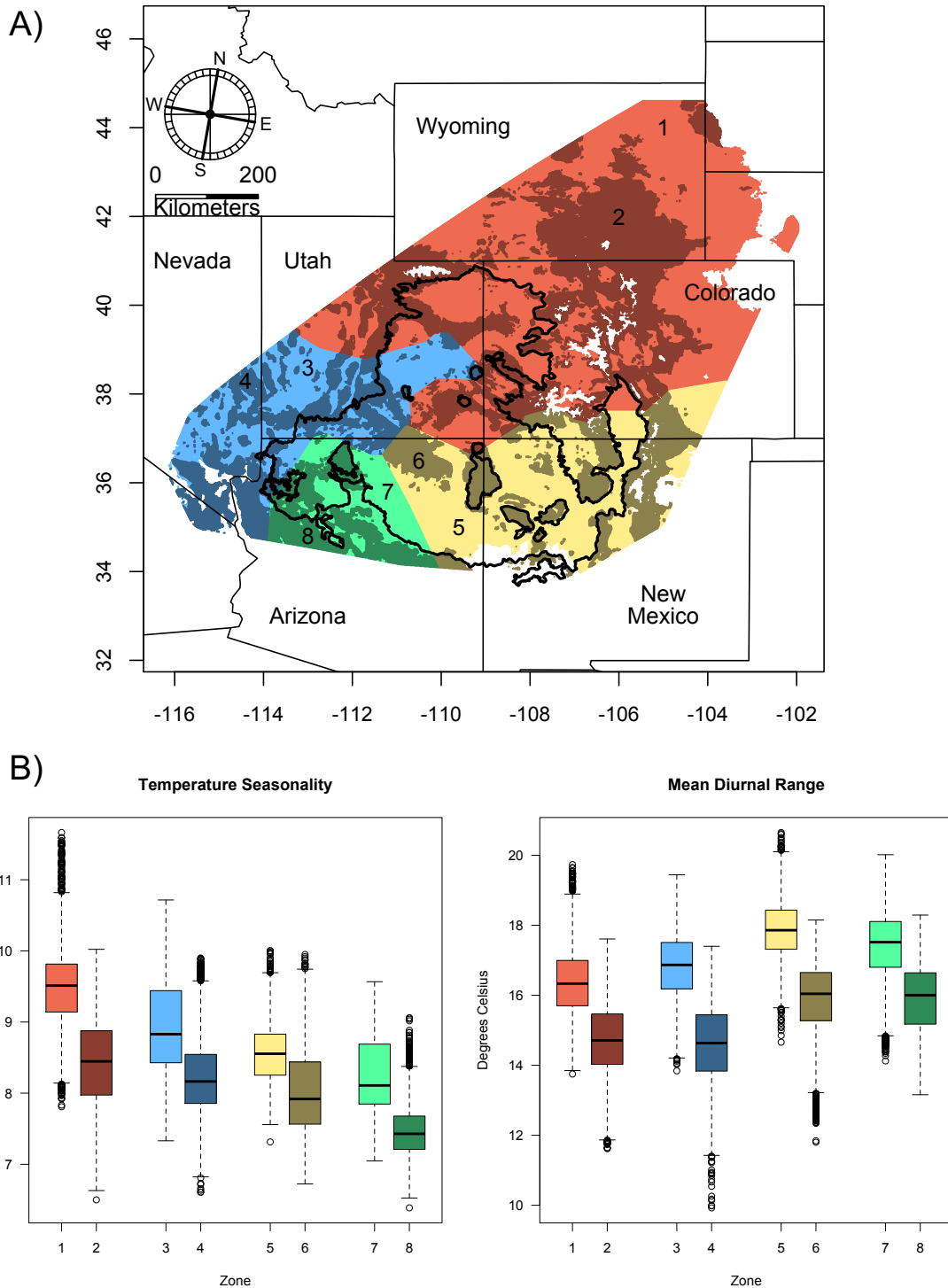


**Figure 1.** Seed transfer zones (A) and zone statistics for temperature seasonality (B), the environmental variable influencing adaptation across *Cleome lutea*'s Colorado Plateau distribution. Numbers in (A) refer to the zones along the x-axis in (B). Uncolored areas (either white or ivory) within the seed transfer zones represent locations outside of the species' environmental tolerance. The red polygon with ivory background represents the Colorado Plateau boundary.

### *Machaeranthera canescens* seed transfer zones

Eight seed transfer zones are reported for *Machaeranthera canescens* (Fig. 2) (Massatti 2020). Similar to *Cleome lutea*, these seed transfer zones account for both genetic differentiation and the species' inferred adaptation to regional climatic gradients (hue and saturation in Fig. 2, respectively). For example, *Machaeranthera canescens* individuals within the red polygons (i.e., zones 1 and 2) in Fig. 2A are all most closely related to one another, which means that genetic differentiation among individuals is minimized as opposed to comparing individuals in a red polygon (either light or dark) with individuals in the green, blue, or yellow polygons. The saturation of zones indicates inferred adaptation to the regional environmental variables displayed in Fig. 2B. Each box and whisker plot is calculated from values of the environmental variables extracted at 5,000 randomly distributed points, or locations, within each seed transfer zone (i.e., 40,000 random points across the eight seed transfer zones). As such, the box and whisker plots represent an estimation of the ranges of the important environmental variables within each of the seed transfer zones. For example, locations in zone 1 have, on average, higher values of mean diurnal range and temperature seasonality compared to locations in zone 2 (Fig. 2B). *Machaeranthera canescens* is a widely distributed species across the western United States, and these seed transfer zones represent only a portion of the species' distribution.





**Figure 2.** Seed transfer zones (A) and zone statistics for temperature seasonality and mean diurnal range (B), the environmental variables influencing adaptation across *Machaeranthera canescens*' regional distribution. Numbers in (A) refer to the zones along the x-axis in (B). Uncolored areas within the seed transfer zones represent locations outside of the species' environmental tolerance. The black polygon represents the Colorado Plateau boundary.

### **Further considerations**

The seed transfer zones represented herein are based upon the best available evidence of geographic patterns of genetic differentiation and putative adaptive loci (Massatti 2020). Additional empirical genetic data may shift seed transfer zone boundaries. Furthermore, the inference of adaptation should be confirmed using field-based experiments (e.g., common gardens or reciprocal transplants). Nonetheless, use of the seed transfer zones reported herein would protect the species' natural patterns of genetic variation and maximize climatic adaptation better than alternatively available information (e.g., climate-based provisional seed transfer zones). Any users of these data should review the entire metadata record in Massatti (2020) for each data set in order to have a full understanding of how the data were created.



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