

Genetically-informed seed transfer zones for *Pleuraphis jamesii*, *Sphaeralcea parvifolia*, and *Sporobolus cryptandrus* 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 appropriate 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 genecological 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.

Genetically-based seed transfer zones are described herein for three priority restoration species on and adjacent to the Colorado Plateau (Massatti 2019). Species include *Pleuraphis jamesii* (synonym includes *Hilaria jamesii*; commonly called James' galleta grass), *Sphaeroclea parvifolia* (commonly called small-leaf globemallow), and *Sporobolus cryptandrus* (commonly called sand dropseed). The seed transfer zones depict both evolutionary lineages (where



applicable) 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 the Bureau of Land Management (BLM)'s Colorado Plateau Native Plant Program, 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 (2019) are described in turn.

Pleuraphis jamesii seed transfer zones

Eight seed transfer zones are reported for *Pleuraphis jamesii* (Fig. 1) (Massatti 2019). 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, *Pleuraphis jamesii* individuals within the orange 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 an orange polygon (either light or dark) with individuals in the green, red, or purple polygons. The saturation of the zones indicates inferred adaptation to the regional environmental variables displayed in Fig. 1B. 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 environmental variables within each of the seed transfer zones. For example, the orange zones 1 and 2 have roughly similar ranges of mean annual temperature, but locations in zone 1 have, on average, lower values of mean diurnal range and higher values of temperature seasonality compared to locations in zone 2 (Fig. 1B). The seed transfer zones cover the majority of the species' distribution with the exception of outlier locations south of zones 6, 8, and 2 at higher elevations in California, Arizona, and New Mexico.



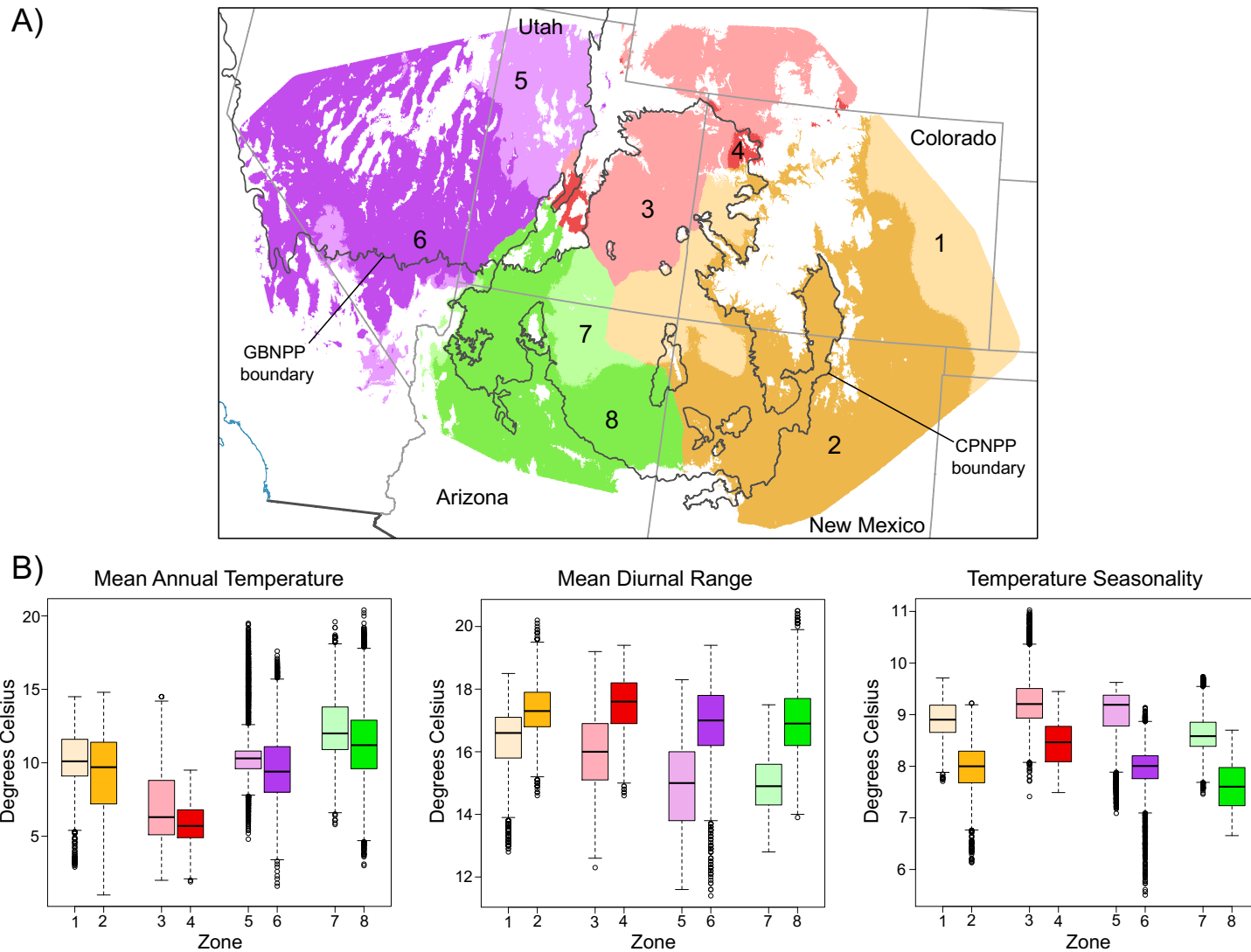


Figure 1. Seed transfer zones (A) and zone statistics for environmental variables influencing adaptation (B) across *Pleuraphis jamesii*'s distribution. Numbers in (A) refer to the zones along the x-axis in (B). Uncolored areas within the seed transfer zones represent locations outside of the species' environmental tolerance. Acronyms refer to Colorado Plateau Native Plant Program (CPNPP) and Great Basin Native Plant Project (GBNPP).

Sphaeralcea parvifolia seed transfer zones

Six seed transfer zones are reported for *Sphaeralcea parvifolia* (Fig. 2) (Massatti 2019). Similar to *Pleuraphis jamesii*, 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, *Sphaeralcea parvifolia* individuals within the green 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 green polygon (either light or dark) with individuals in the red or purple 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., 30,000 random points across the six seed transfer zones). As such, the box and whisker plots represent an estimation of the ranges of the environmental variables within each of the seed transfer zones. For example, the green zones 1 and 2 have roughly similar ranges of temperature of the wettest quarter, but locations in zone 1 have, on average, lower values of mean diurnal range, precipitation seasonality, and mean annual precipitation and higher values of temperature seasonality compared to locations in zone 2 (Fig. 2B). The seed transfer zones cover most of the species' distribution but notably lack a few sites in northern Nevada and Utah. Plants distributed south of zone 6 in Arizona and south/east of zone 2 in Arizona and New Mexico should be scrutinized with respect to their taxonomic identity.



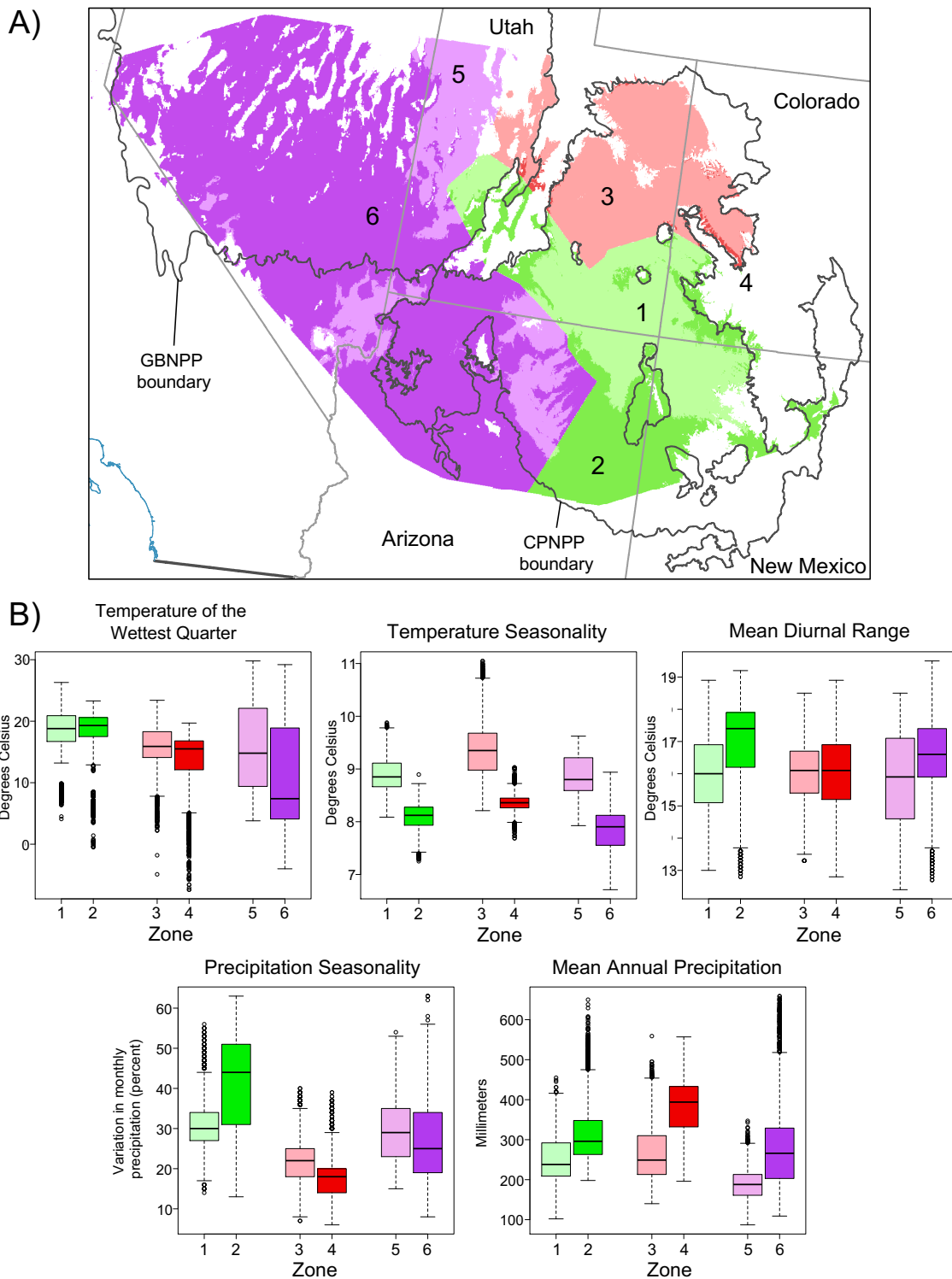


Figure 2. Seed transfer zones (A) and zone statistics for environmental variables influencing adaptation (B) across *Sphaeralcea parvifolia*'s distribution. Numbers in (A) refer to the zones along the x-axis in (B). Uncolored areas within the seed transfer zones represent locations outside of the species' environmental tolerance. Acronyms refer to Colorado Plateau Native Plant Program (CPNPP) and Great Basin Native Plant Project (GBNPP).

Sporobolus cryptandrus seed transfer zones

Three seed transfer zones are reported for *Sporobolus cryptandrus* (Fig. 3) (Massatti 2019). Unlike the other two species, these seed transfer zones account for the species' inferred adaptation to regional climatic gradients only (hue in Fig. 3). Genetic differentiation is very low within the species, likely due to its high dispersibility (Simonin 2000), such that genetic differentiation need not be accounted for across the area of inference. The hue of the zones indicates inferred adaptation to one regional environmental variable displayed in Fig. 3B. Each box and whisker plot is calculated from temperature seasonality values extracted at 5,000 randomly distributed points, or locations, within each seed transfer zone (i.e., 15,000 random points across the three seed transfer zones). As such, the box and whisker plots represent an estimation of the ranges of temperature seasonality within each of the seed transfer zones. The zones are well differentiated with respect to temperature seasonality, which covaries with latitude. *Sporobolus cryptandrus* is broadly distributed across the United States, southern Canada, and northern Mexico and additional research must inform the expansion of seed transfer zones into areas adjacent to the Colorado Plateau.



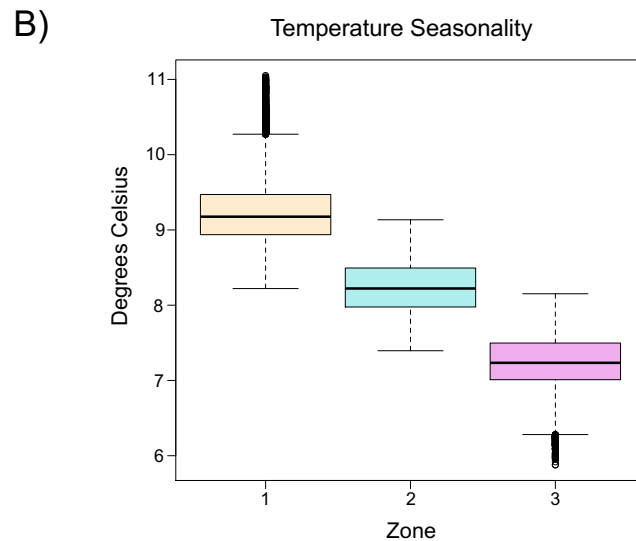
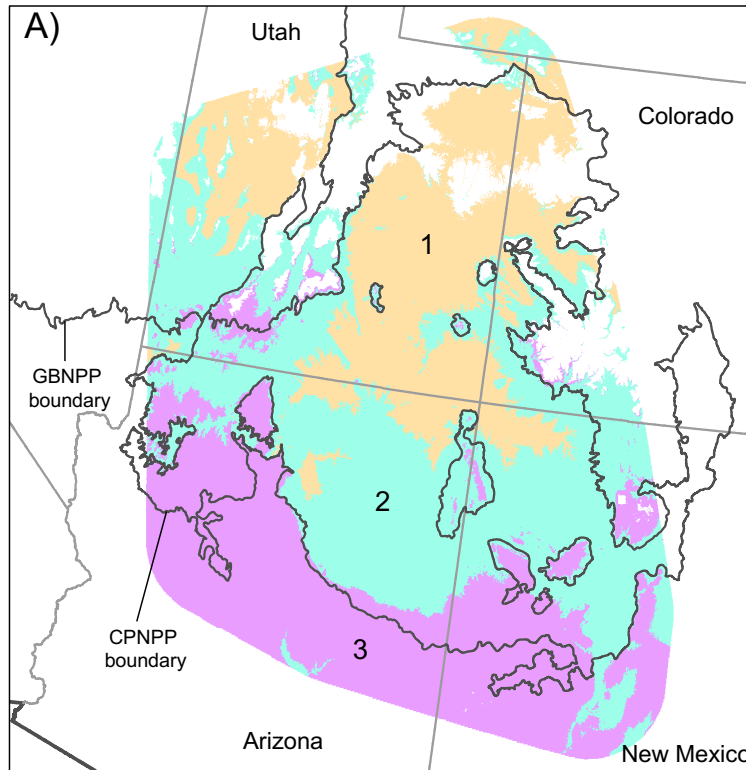


Figure 3. Seed transfer zones (A) and zone statistics for environmental variables influencing adaptation (B) across *Sporobolus cryptandrus*' distribution. Numbers in (A) refer to the zones along the x-axis in (B). Uncolored areas within the seed transfer zones represent locations outside of the species' environmental tolerance. Acronyms refer to Colorado Plateau Native Plant Program (CPNPP) and Great Basin Native Plant Project (GBNPP).

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 2019). 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 would maximize climatic adaptation better than alternatively available information (climate-based provisional seed transfer zones). Any users of these data should review the entire metadata record in Massatti (2019) for each data set in order to have a full understanding of how the data were created.



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