INTRODUCTION

- Losses of milkweeds in monarch butterfly (Danaus plexippus) breeding habitats and migratory corridors are hypothesized to be a chief contributor to widespread declines in monarch populations across North America (Pрасас и Oberhauser 2013; Flockhart et al. 2015).
- Successful habitat restoration requires germplasm that is adapted to target restoration environments.
- Genealogy evaluates variation in putative traits related to survival among populations in relation to source environments and local selection pressures (St. Clair et al. 2013).
- Previous approaches suggest local seeds are best, but may not be available in suitable quantities, or may not be adapted to projected climate change scenarios (Kilkenny 2015).
- We evaluated phenotypic variation in growth form traits among 36 populations of showy milkweed (Asclepias speciosa) to evaluate genetically appropriate adaptive traits among local climates to aid in identifying seed sources for monarch habitat restoration.

METHODS

Plant Propagation and Transplanting
- Precipitated seeds from 36 populations (Fig. 1).
- BLM, USFS germplasm accessions.
- Citizen scientist collections.
- Seeds were sown in February in plug trays. Seedlings were transplanted to pots in April and transplanted in the common garden in late May.
- Prior to planting, the site was treated with herbicide and covered in weed barrier and crushed gravel to reduce weed competition and heat loads.
- After planting, the garden received supplemental irrigation and was weeded on a weekly basis.
- Among the 360 experimental plants (ten per a population), we used 158 non-experimental units as buffer rows and columns, and to spaces in the experimental layout.

Data Collection
- Weekly collection of morphological measurements and plant growth data (Table 1).
- Remotely sensed climate data retrieved from ClimateWNA V5.3 (Wang et al. 2012).

Analysis
- Principal components analysis: Conducted in program R version 3.5.1 using prcomp () function in package (stats)
- We used single factor ANOVAs to determine which measured traits significantly varied among populations.
- Tukey’s HSD was used to determine where the variance was among populations at a significance level of α = 0.05.
- Relationships between collections site characteristics and measured traits were analyzed with a simple linear regression models (Table 1).

RESULTS

- 79% of variation among populations is explained by two Principal Components (Fig. 2).
- P<0.05 for both principal components.
- Some populations from common seed zones across both PCs show similar traits (Fig. 3).
- ANOVAs revealed significant (α = 0.05, df=35) effect of populations on all measured traits.
- Statistical differences driven mostly by 3-4 populations with significantly different growth characteristics.
- Significant positive relationships with plant height (Fig. 4a, 4b).

DISCUSSION

- Preliminary support that Showy milkweed exhibits geoeiological differences across western US.
- Patterns do not clearly correspond to provisional seed zones, suggesting that species specific seed zones should be constructed for showy milkweed.
- Predominate divisions among populations due to differences in growth form and leaf characteristics (Fig. 2).
- Regressions across individuals nested within populations (not shown) indicate that the bulk of variation in traits exists among individuals.
- Phenotypic plasticity may play an important role in showy milkweed responses to annual weather conditions (Sultan 2000).
- Environmental maternal effects may also serve as a source of variation in evaluating trait recurred between generations (Coleman 2005, Donohue 2009).
- Regression analyses indicate that plant height may be adaptive.
- Higher MWM (°C) and MAT (°C) correlated with increased height (less size often correlates to competitive ability (Wesolfsky 1998).
- Cool, wet spring in 2018 may be responsible for large differences in growth form.
- Variation among principal components does not strongly correspond to provisional seed zones.
- Closely clustered populations suggest some populations from common seed zones may have similar characteristics (Fig. 3).

FUTURE WORK

- Multi-year study (≥ three years).
- Incorporate measures of phenology, above ground biomass, precise leaf surface area, surface, emergence and flowering phentology.
- Explore correlations with additional climate variables in ClimateWNA.
- Examine population genetics.
- Explore variations in cardenolide toxins with respect to ecotypes and stress.

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Michaela Sonnen, Daison Weedop, Sacha Wells, Leslie Blackburn, Dusty Perkins
College of Western Idaho