INSIGHTS INTO THE ROLE OF MOUNTAIN RANGE LOCATION ON GENETIC STRUCTURE OF *PENSTEMON PACHYPHYLLUS.*

Emily Orr[1], Katie Kucera[2], Andrea Kramer[2,3], and Jeremie Fant[2,3]

[1]University of Missouri - Kansas City, Kansas City, MO [2]Northwestern University, Evanston, IL [3]Chicago Botanic Garden, Glencoe, IL

Introduction

Conservation of native species has turned a new page: from conserving extant habitats to actively restoring degraded habitat. The challenge arises in with what source of plant material to bring in to a restoration site. Identifying species- and landscape-specific genetic structure can aid land managers in sourcing the most genetically appropriate plant material for restorations [2].

- *Penstemon pachyphyllus* is a species of restoration concern in the Intermountain West.
- Previous studies have identified population genetic structure in *P. pachyphyllus* to be delineated by mountain range location and pollinator syndrome [1].
- *P pachyphyllus* seed is currently being collected and increased for restoration efforts, thus insights to genetic diversity and gene flow are paramount.
- Our study aims to refine understanding of genetic structure of *P. pachyphyllus* to inform restoration management decisions with regard to seed souring and reseeding efforts.

Penstemon pachyphyllus

Objectives

- **To characterize population genetic structure of six wild populations of *Penstemon pachyphyllus* across two mountain ranges**
- **To explore spatial relationships among populations**

Hypothesis

Populations among the same mountain range will have more similar genetic structure than populations located on other ranges.

Methods

Leaf Tissue Collection & DNA Extraction
- Dried leaf tissue was collected from 35 individuals from a range of life stages from six wild populations
- Extracted via modified CTAB protocol

PCR & Capillary Electrophoresis
- Ran extracted DNA on Fnlxt48, Fnlxt49, Pen0245L PCR programs
- Used primers Pen04, Pen18, Pen23, Pen24 and PS032

Analysis
- Statistical analysis in GenAlEx in Microsoft Excel
- Inferred population clusters visualized in STRUCTURE
- Visualized population locations in ArcMap
- Isolation by distance analysis in Genepop

Contact: emilyroseorr@outlook.com
katherinekucera2019@u.northwestern.edu

Results

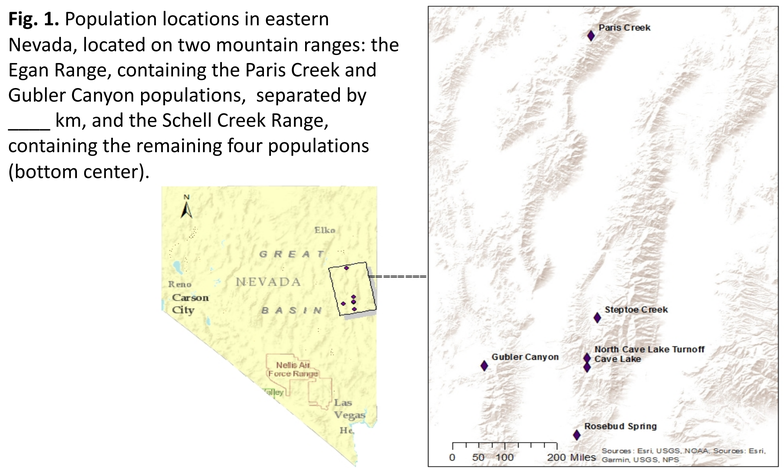

Fig. 1. Population locations in eastern Nevada, located on two mountain ranges: the Egan Range, containing the Paris Creek and Gubler Canyon populations, separated by ____ km, and the Schell Creek Range, containing the remaining four populations (bottom center).

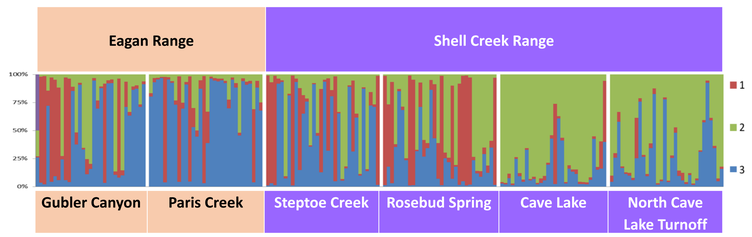

Fig. 2. STRUCTURE analysis identified 3 genetic clusters, 1-3, on right of the figure (K= 3). Each vertical line represents an individual sample within a population, populations separated by a vertical white line. Mountain Ranges are labeled above figure and population names below.

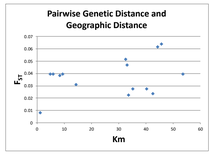

Fig. 3. Pairwise genetic distance (F_{ST}) and geographic distance (km), p-value 0.1.

Discussion

- STRUCTURE analysis did not identify genetic clusters to be represented by mountain range.
  - Cave Lake and North Cave Lake Turnoff were most closely related. (Cluster 2)
  - Clusters 1, 2 and 3 were found on both mountain ranges, indicating possible gene flow.
- Isolation by distance could not explain limits to gene flow.
  - Study area is possibly too fine scale.

Future Research

There is possible evidence for gene flow among mountain ranges, thus other factors, including habitat connectivity and pollinator movement, should be examined to determine what influences of gene flow.

Acknowledgments:

Special thanks to Scott Jensen, Botanist for the US Forest Service in Provo, Utah for kindly touring us to the wild populations and the seed increase beds in Nevada and Utah. Another special thanks to Hilary Noble for her leadership and help in the genetics lab.
We'd like to thank NSF-REU grant DBI-1757800 for support.

References

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