Evaluating the Taxonomic Relationships of Different *Phlox pungens* Population Centers Utilizing Genetic Characteristics

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Introduction

Phlox pungens is a Wyoming state endemic, it is part of the morphological group of *Phlox* species characterized by bearing glandular inflorescence trichomes and is also known as granite prickly-phlox.
Phlox pungens is endemic to two areas in west-central Wyoming (Figure 3) and was first discovered in the Wind River Basin (Waselkov et al. 2020, Figure 1) and later documented in the Green River Basin (Waselkov et al. 2020, Figure 2).

Figure 1 - An image of a *Phlox pungens* plant from the Wind River Basin of Wyoming from the Beaver Rim area (Waselkov et al. 2020).

Figure 2 - An image of a *Phlox pungens* plant from the Green River Basin of Wyoming (Waselkov et al. 2020).

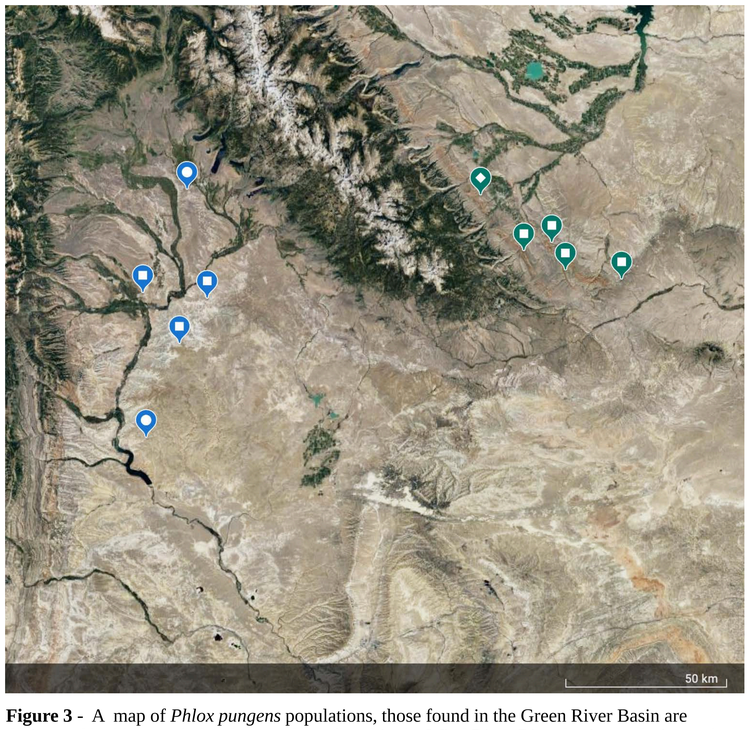

Figure 3 - A map of *Phlox pungens* populations, those found in the Green River Basin are designated by blue symbols whereas, those found in the Wind River River basin are designated by green symbols. The ploidy level of each population is represented by different shape within the symbols: circle =2x, square = 4x, and diamond =10x.

Objective

Noting these morphological differences between these two population centers, my objective is to find whether the morphological forms are taxonomically distinct and if they warrant ranking as subspecies or species.

Methods

I will extract DNA from ~ 6 *Phlox pungens* samples per each of the 10 populations. This process includes the use of a modified hexadecyltrimethylammonium bromide (CTAB) method (Figure 4) in conjunction with liquid nitrogen (LN_2) tissue grinding. (Figure 5).

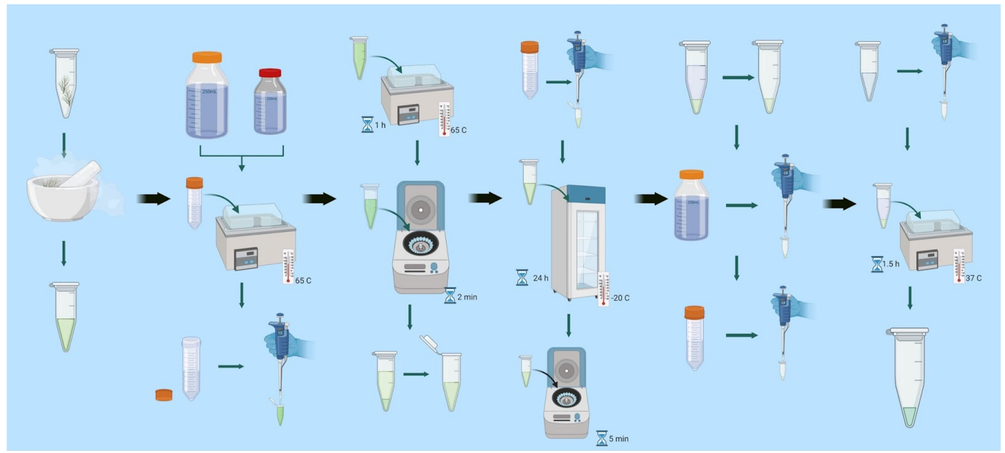

Figure 4 - A diagram depicting the 17-step process to complete a CTAB-based DNA extraction.

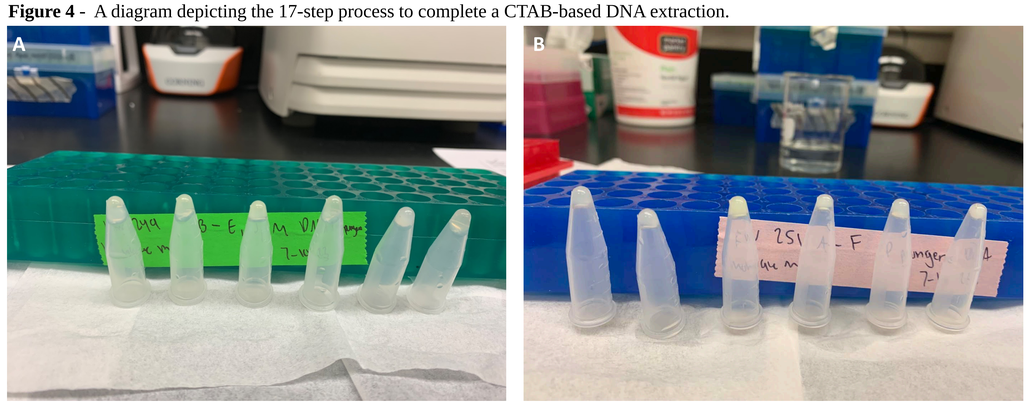

Figure 5 - *Phlox Pungens* DNA in the form of a gel-like pellet that forms at the bottom of a 1.5 mL tube for populations KW 249 (A) and KW 251 (B).

I will then perform a Polymerase Chain Reaction (PCR) test based on amplifying a chloroplast marker *(rbcL)* to ensure high DNA quality. (Figure 6).

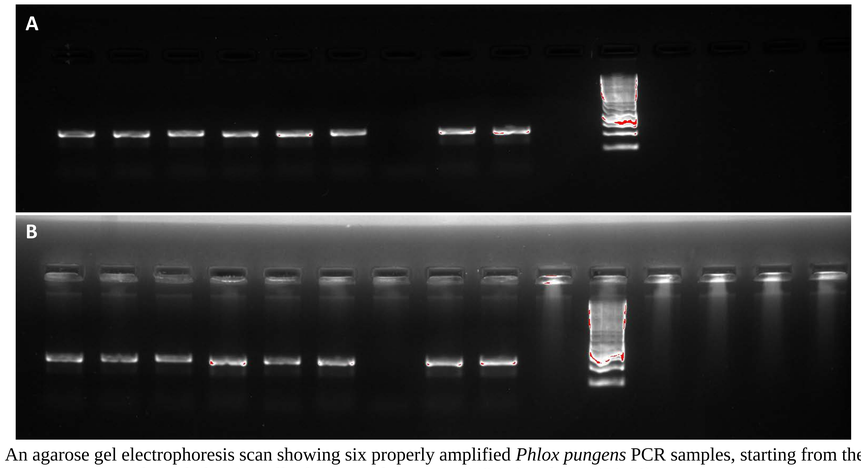

Figure 6 - An agarose gel electrophoresis scan showing six properly amplified *Phlox pungens* PCR samples, starting from the very left of the image scanning to the right by six wells, from population KW 249 (A) and KW 251 (B).

I will complete microsatellite genotyping using prescreened microsatellite markers that have successfully amplified in other *Phlox* species.

Preliminary Results

- At the time this poster was printed, I was still performing DNA extractions on the remaining populations.
- I found that when analyzing the agarose gels there was successful DNA amplification of 5 populations.
- I conducted microsatellite genotyping where I tested one prescreened marker.

Discussion

- The findings of this project will help in furthering the understanding of population genetics in this particular group of Wyoming endemic wildflowers.
- This work also has conservation implications, these two different morphological forms merely lack the taxonomic variation needed if the results warrant them as such.

Ongoing and Future Work

- I am currently conducting research that will yield more successful DNA extractions and microsatellite genotyping.
- I plan to participate in further efforts during the Spring and Summer of 2024 to include other cespitose *Phlox* species from Wyoming for future analysis.

References

Waselkov, K., Santiago, M., Heidel, B., Mayfield, M. H., & Ferguson, C. J. (2020). Population genetics of the Wyoming endemic Phlox Pungens Dorn (Polemoniaceae). *Western North American Naturalist*, *80*(3), 369–380. https://doi.org/10.3398/064.080.0309

Acknowledgements

I would like to acknowledge the work of Dr. Katherine Waselkov, Mercedes Santiago, Bonnie Heidel, Dr. Mark H. Mayfield, and Dr. Carolyn J. Ferguson whose field research and efforts in DNA extraction, preliminary microsatellite genotyping, and data quantification, contributed to the continuing success of this project. I would also like to acknowledge Dr. Kate Ostevik and Dr. Katherine Waselkov for their assistance in reviewing and feedback for this project. This work is supported by the Building Bridges to Professoriate Program.