



UNIVERSITY OF
**NORTHERN
COLORADO**

Using Genomics to Investigate Rare Plant Taxonomy

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Genetics and Resource Management



Rare Plants

- Examine evidence of hybridization
- Population Structure
- Measure genetic variation, diversity, population connectivity..... Etc



Address taxonomic concerns

- Species status
- Species boundaries and relationships to other species
- Eligibility for the ESA



Inexpensive

- Do not need and prior genetic knowledge

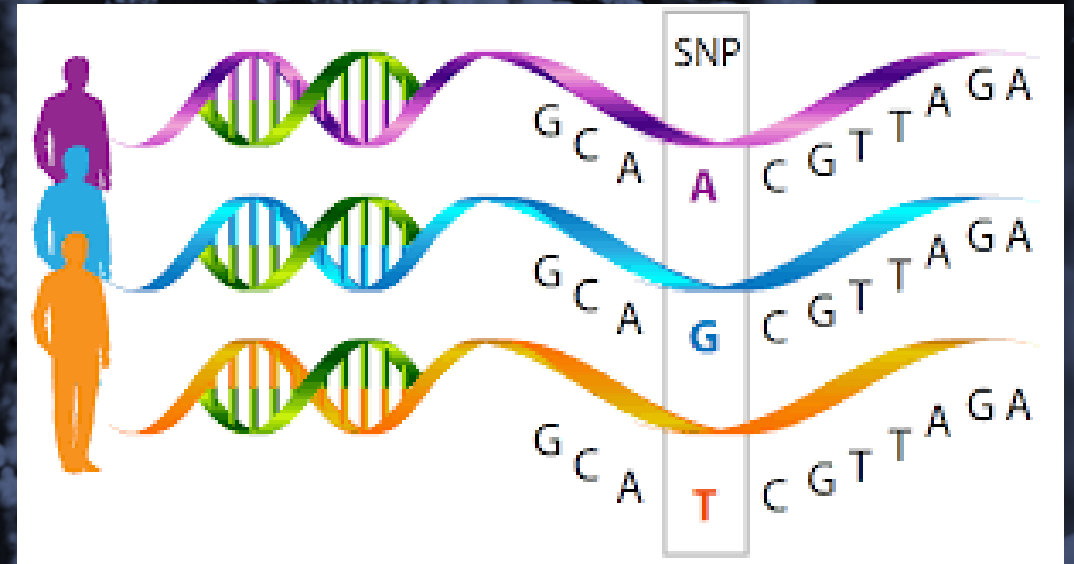


Conservation

- Helps land managers know where conservation \$\$\$ will be best used
- Maintain geneflow and genetic variation

Genetic methods

- ddRAD – genome skimming technique
 - Modern
- Fine-Scale observations between:
 - Individuals
 - Populations
 - Closely related species
- 1000's of unique genetic regions
 - Whole genome
 - Single Nucleotide Polymorphisms (SNP's)



Versus 10 -20 microsatellite regions on unknown regions of the genome

- Relatively inexpensive
- No prior genetic information



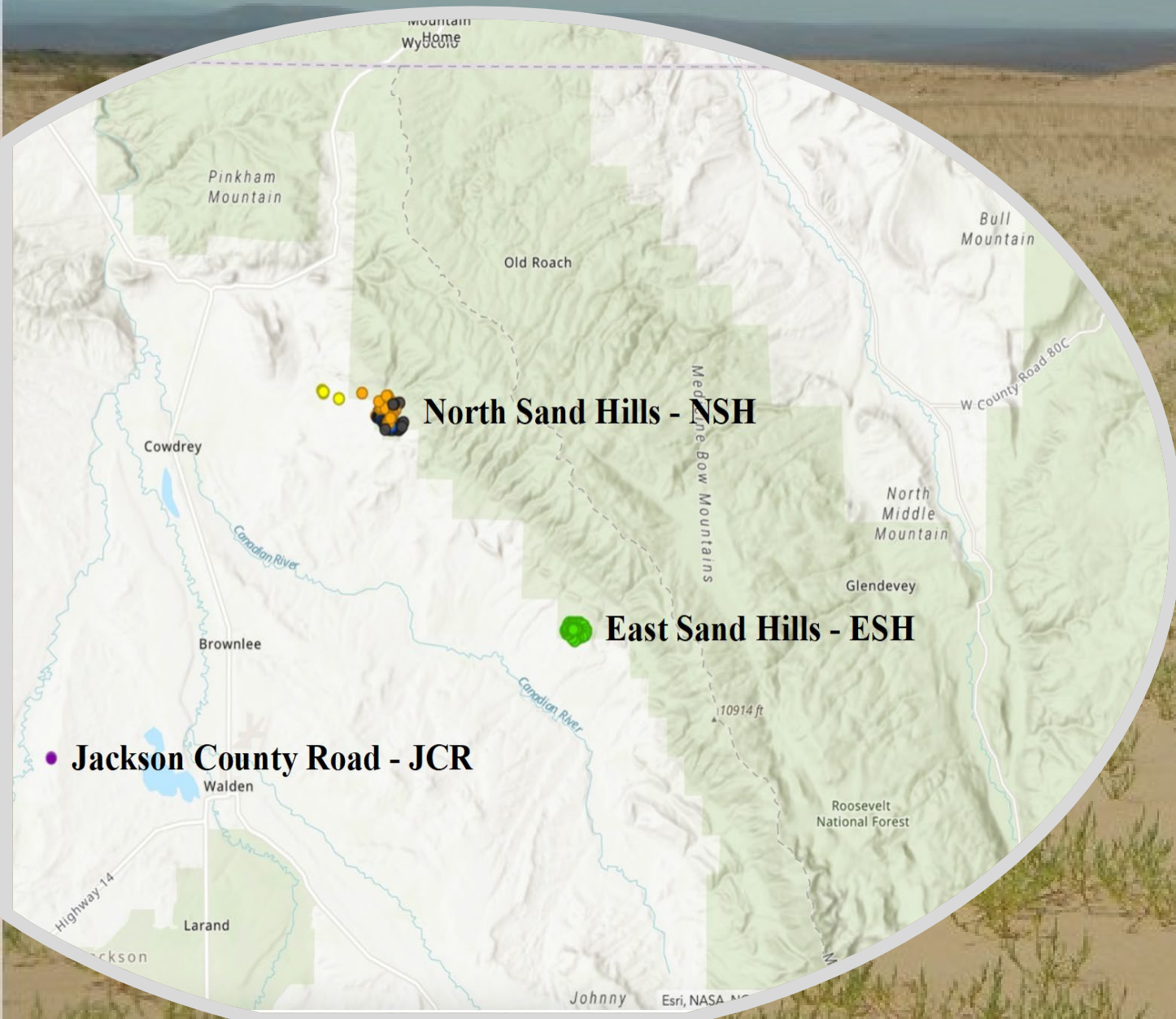
Exploration of species boundaries and genetic structure of *Draba weberi* Price & Rollins (Brassicaceae)

Final Report – August 30, 2022



Molecular Characters of the Colorado Endemic, *Corispermum navicula* Mosyakin (Amaranthaceae): Species Delimitation and Implications for Management

Final Report – May 31, 2022



Corispermum navicula

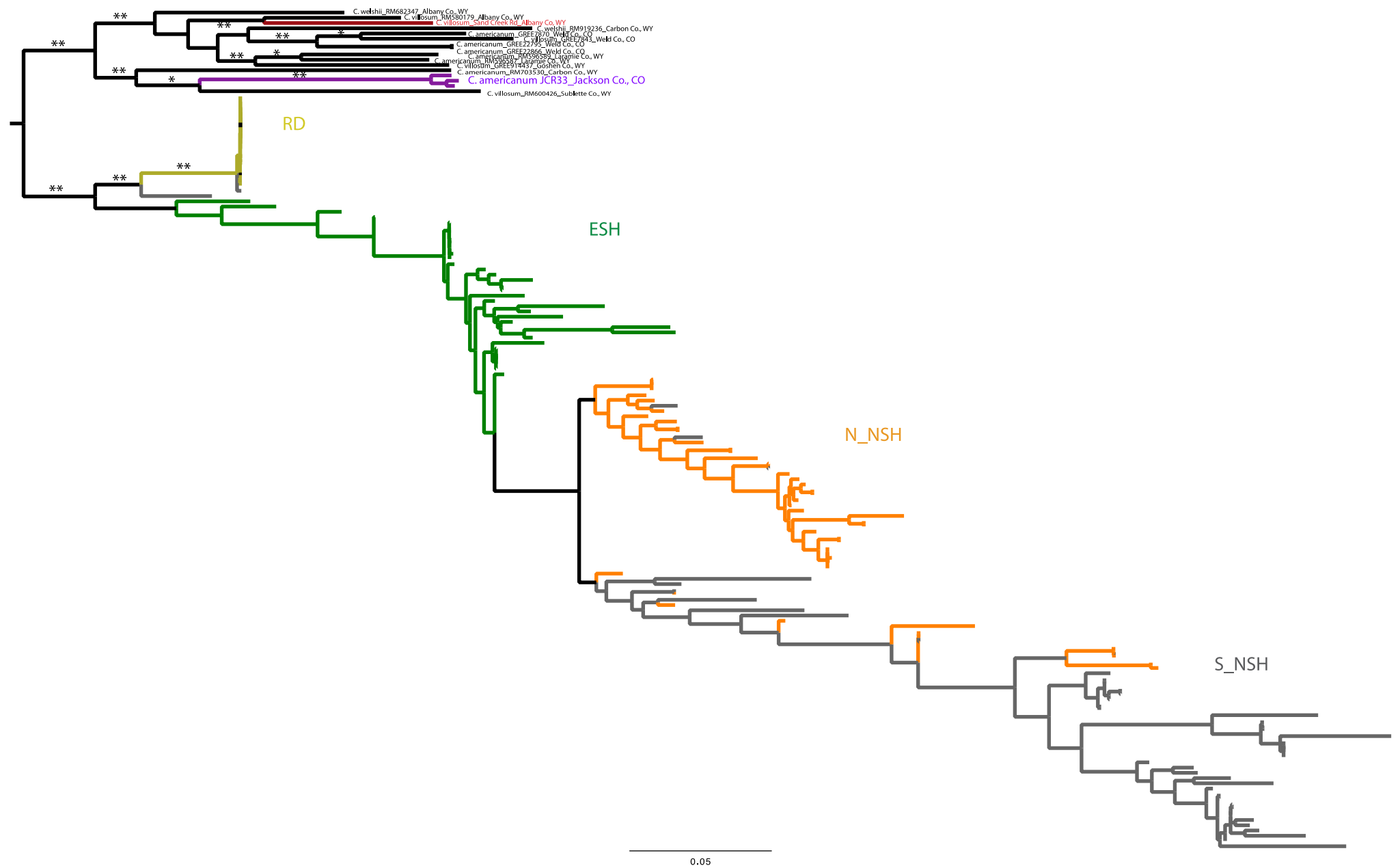


Figure 4. Maximum Likelihood phylogenetic tree with rapid bootstrap support values. Bootstrap values greater than 95% are depicted with *, while bootstrap values of 100% are depicted with **. This tree supports the distinction of plants collected from the Northern Sand Dune System and outgroups. Substructuring between The Northern Sand Dune System and the access road (RD) is significantly supported, but some plants collected on S_NSH are also located in this group. Genetic distinction between ESH (green) and NSH (N_NSH:orange, S_NSH:grey) are not supported.

Inbreeding Coefficients - G_{IS}

- Ranges from -1 to 1
 - Negative values are associated with outbreeding
 - 0 = no inbreeding
 - 1 = completely inbred
 - > 0.4 = high levels of inbreeding

Population	N	A	Ho	He	G_{IS}
COVI	5	1.303	0.012	0.140	0.918
COWE	2	1.149	0.013	0.137	0.904
COAM	9	1.370	0.012	0.133	0.907
RD	22	1.087	0.010	0.009	-0.160
ESH	40	1.312	0.011	0.037	0.694
N_NSH	45	1.426	0.013	0.067	0.811
S_NSH	51	1.358	0.010	0.080	0.881

Table 3. The mean number of alleles (A), observed heterozygosity (Ho), expected heterozygosity (He), and Inbreeding Coefficient (G_{IS}) is shown for all species and populations.

Kinship Coefficients

- Range from 0 – 1
 - 0 = complete strangers
 - 0.25 = half – siblings
 - 0.50 = full siblings / parent – child
 - 1 = clone/identical twin
- 14 clones

Population	# Comparisons	# > 0.5	Range	mean	s.d.
COVI	10	6	0.24 - 0.85	0.49	0.20
COWE	1	1	0.51	-	-
COAM	36	13	0.29 - 1.0	0.54	0.27
RD	231	231	0.79 - 0.87	0.83	0.01
ESH	780	111	0.01 - 0.60	0.36	0.14
N_NSH	990	45	0.00 - 0.79	0.20	0.17
S_NSH	1,200	316	0.00 - 1.00	0.29	0.28
All Samples	14,790	803	0.00 - 1.00	0.11	0.18

Table 5. Kinship Coefficients measured for all individuals sampled within each population and outgroups. The range of coefficients is shown (low - high) and the mean and standard deviation of each population was calculated.

PCoA

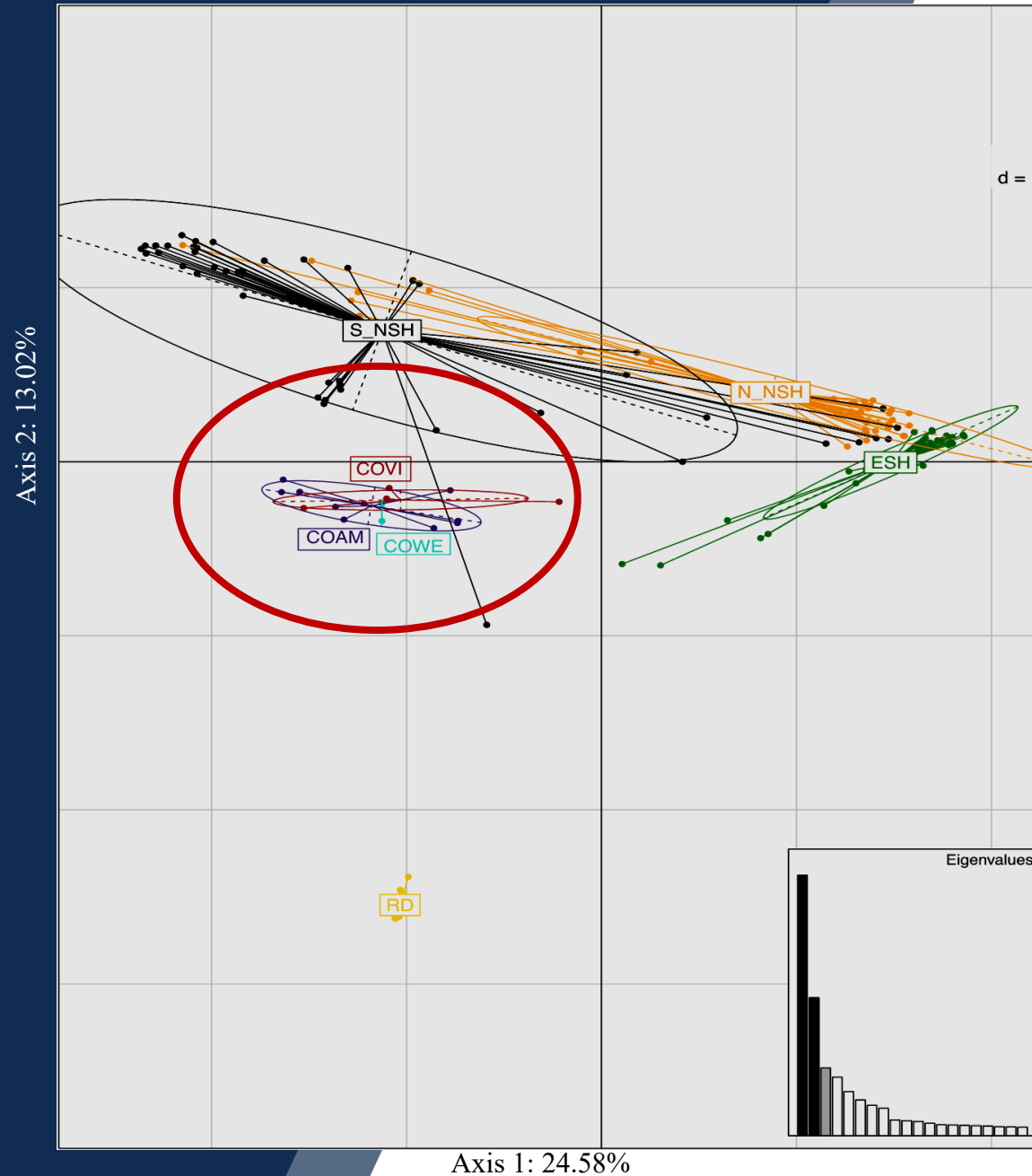


Figure 6. Principle Component Analysis plot of Axis 1 (24.58%) and Axis 2 (13.02%) based on a genome-wide SNP dataset. Bar graphs with eigen values for each axis are shown in the inset figure. 95% confidence intervals for each group are included. The seven collection groups are identified with various colors, but do not correspond to any cohesive genetic grouping. ESH (green), S_NSH (black), N_NSH (orange), RD (yellow), JCR33/COAM (purple), and outgroups COVI (red) and COWE (turquoise).

Conclusions

- *Corispermum navicula* does not warrant treatment as a distinct species
- “Existing structure does not correspond to previous descriptions of *C. navicula*’s distribution (Mauz & Dawson 2007, Neale et al. 2013), existing herbarium records, or general morphologies (Naibauer and McGlaughlin 2021).
- *Corispermum* Bering Land Bridge Colonization ~38,000 years ago
 - Explains the lack of genetic variation seen among Rocky Mountain *Corispermum*
 - Wind pollinated – wide dispersal ability
 - *Model species for phenotypic plasticity





Draba weberi

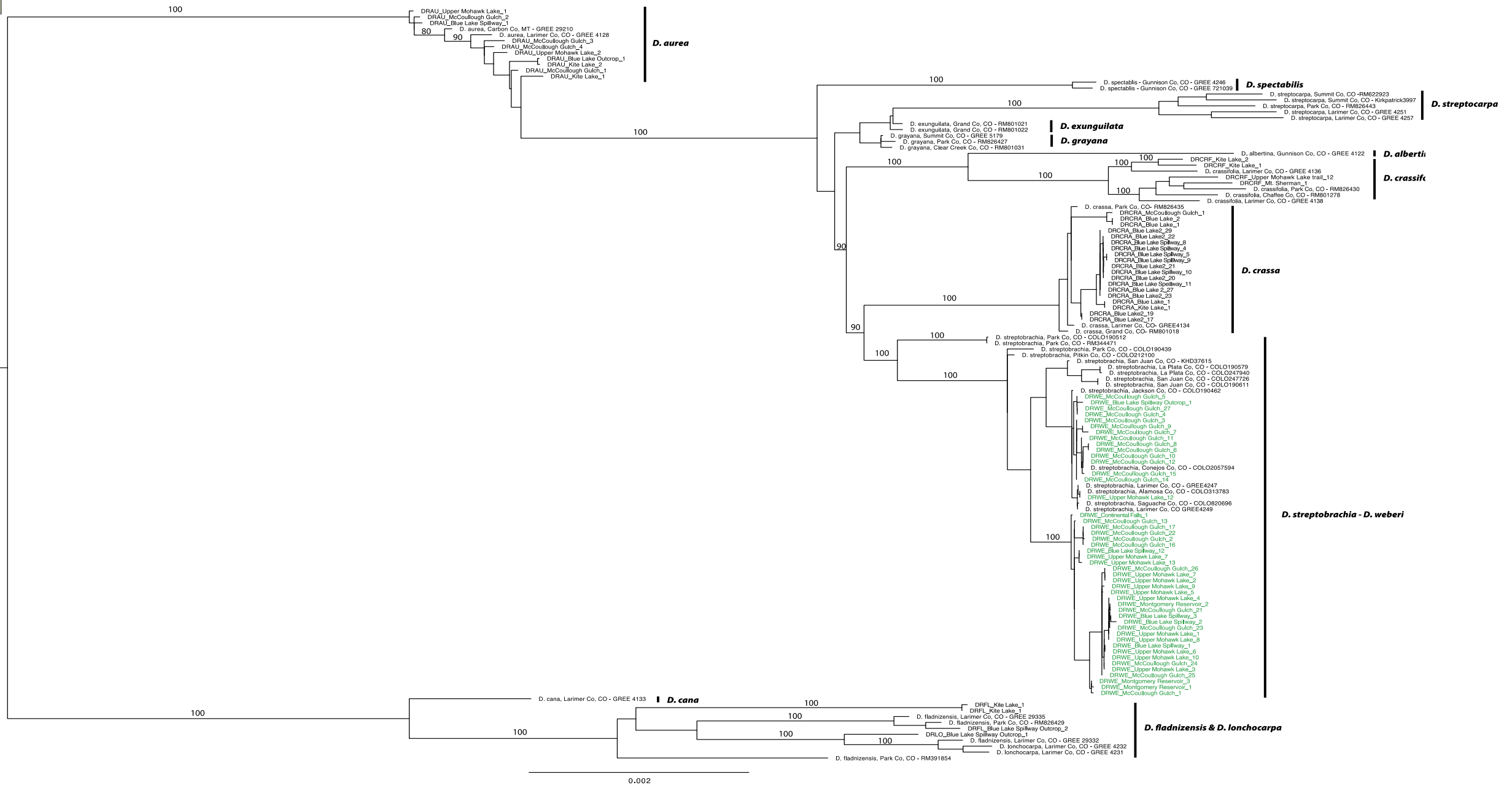


Figure 3. A ML phylogenetic tree with rapid bootstrap support values. Results are based on a dataset consisting of 15,286 SNP's shared among 127 individuals. Samples collected in from the Tenmile-Mosquito Range are labeled with specific abbreviations, population name, and unique identifier. Samples collected from herbaria are labeled by their specific name, county and state where they were collected, and accession number. *Draba weberi* samples are highlighted in green. Refer to Tables 1 and 2 for more sample details.

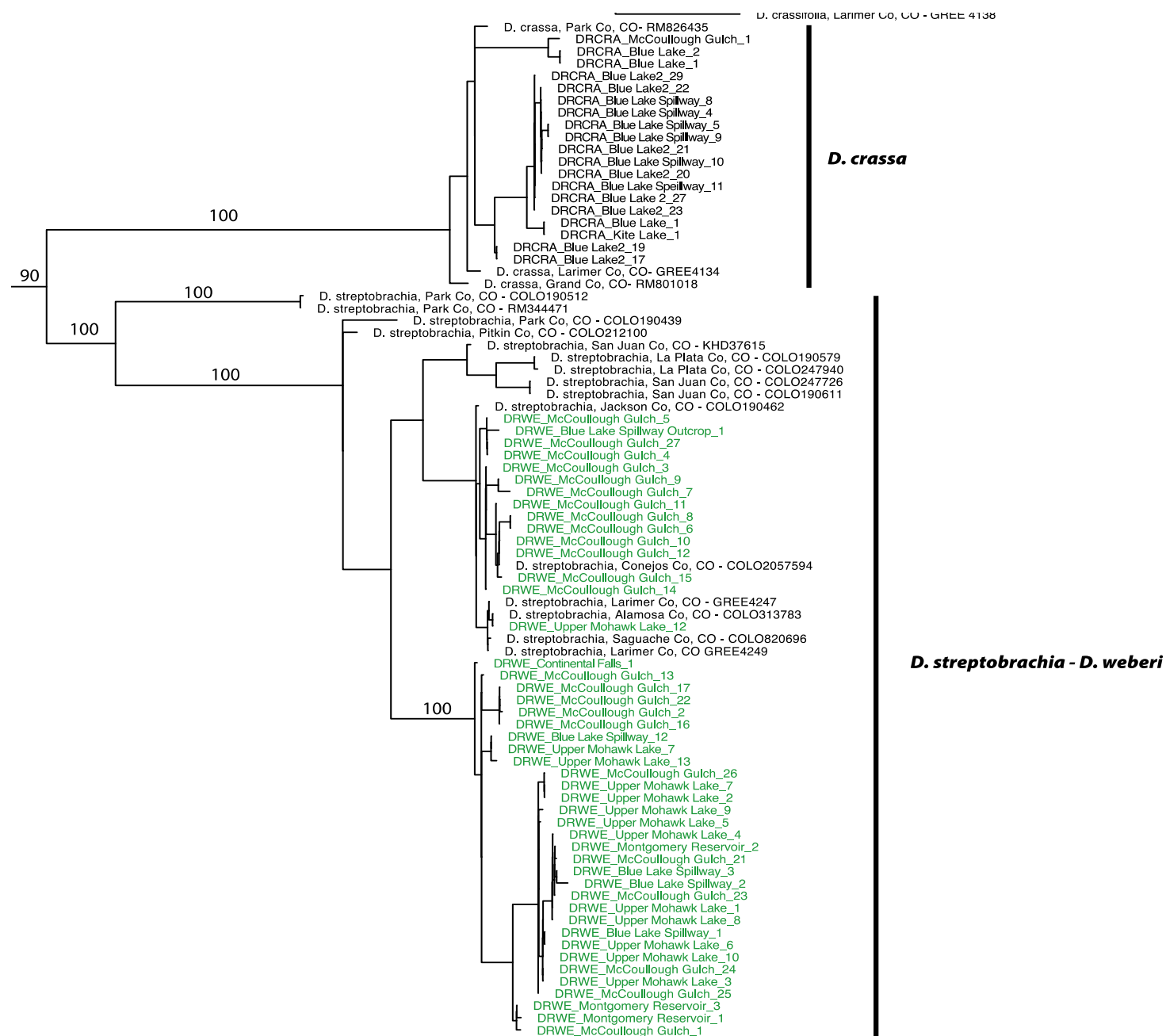
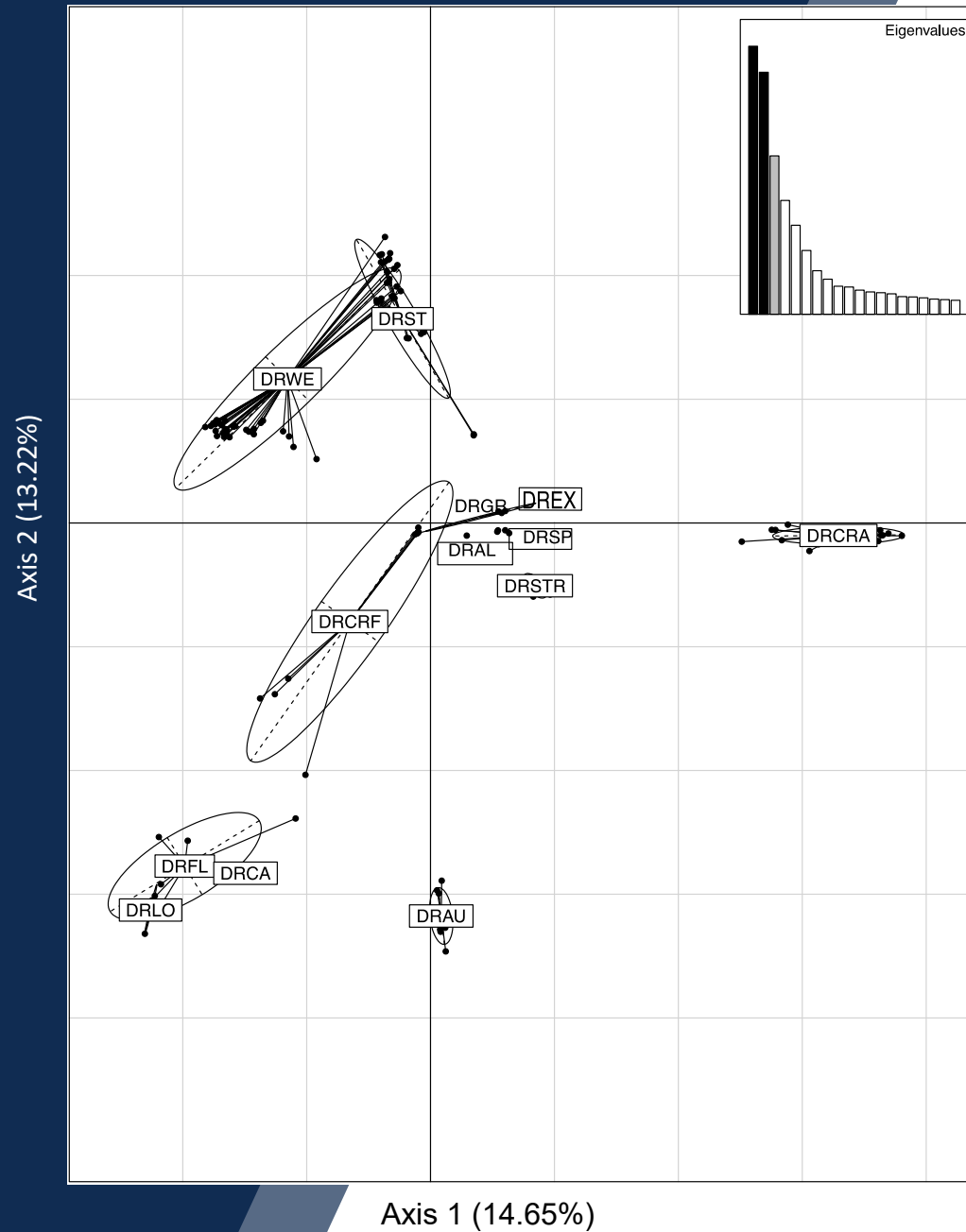


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PCoA

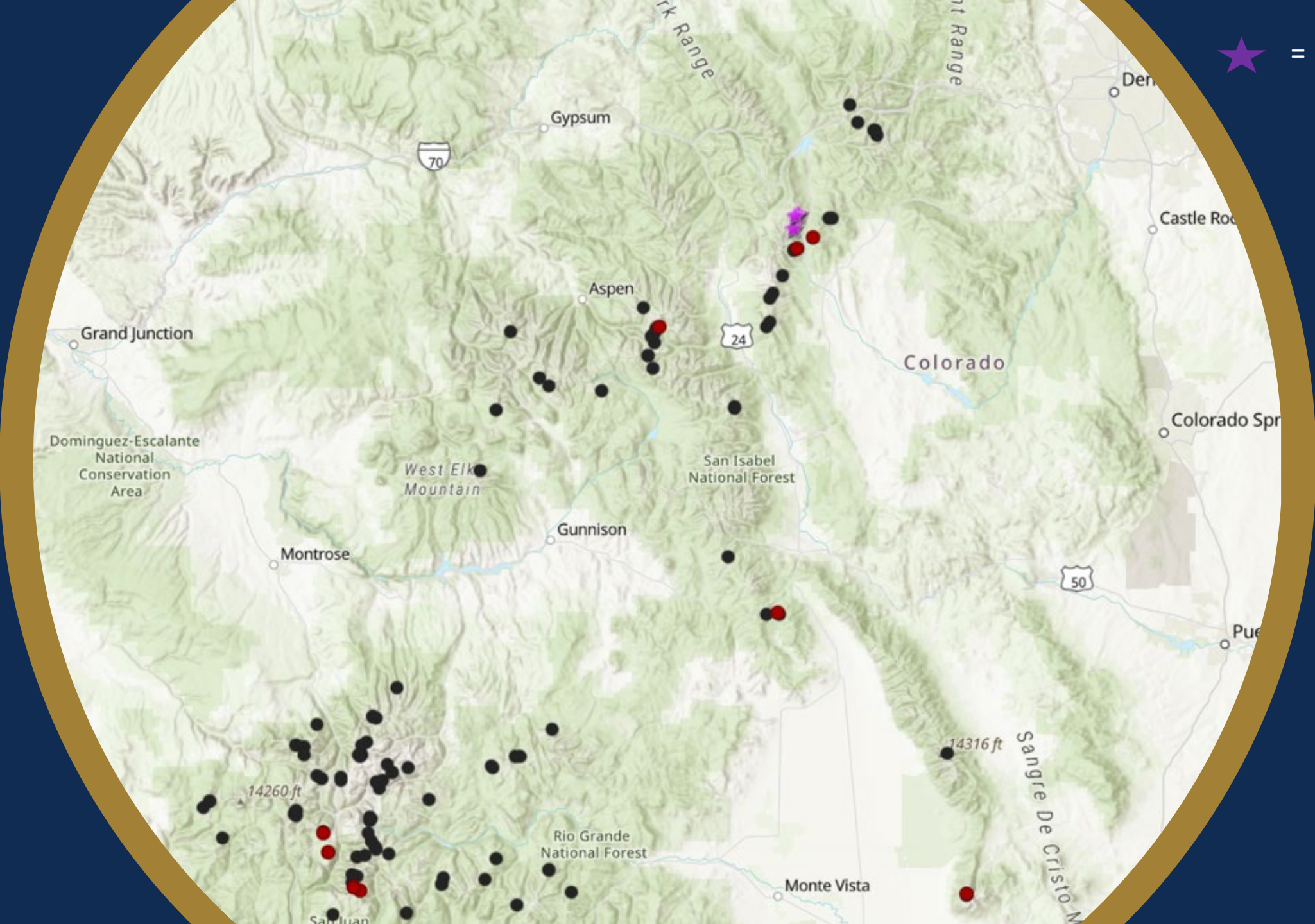


Legend

- DRAL* = *D. albertina*
- DRAU* = *D. aurea*
- DRCA* = *D. cana*
- DRCRF* = *D. crassifolia*
- DRCRA* = *D. crassa*
- DREX* = *D. exunguilata*
- DRGR* = *D. grayana*
- DRFL* = *D. fladnizensis*
- DRLO* = *D. lonchocarpa*
- DRSP* = *D. stectobilis*
- DRST* = *D. streptobrachia*
- DRSTR* = *D. streptocarpa*
- DRWE* = *D. weberi*

Figure 4. Principle Component Analysis (PCA) plot of Axis 1 (14.65%) and Axis 2 (13.22%) based on a genome-wide SNP dataset consisting of 15,286 SNP's shared among 127 individuals. Bar graphs with eigen values for each axis are shown in the inset figure.

★ = *D. weberi*





Conclusions

- “The results shown in this final report demonstrate that *D. weberi* is not a distinct taxonomic entity as described by Price (1991) and should be subsumed as *D. streptobrachia* “
 - In the original description of *D. weberi* (Price 1991) it is noted that *D. streptobrachia* is likely a close relative
 - *D. streptobrachia* is the older named taxon

Wrap it up

- *Corispermum navicula*
 - Under consideration for ESA
 - Taxonomic issues
 - Annual plant
 - Incredibly difficult to manage
- *Draba weberi*
 - Under consideration for ESA
 - Microspecies?
 - Unstable population trends

Using resources to conserve the species that need it



Other Projects

- Completed
 - *Eriogonum brandegeei*
 - *Eriogonum pelinophilum*
 - *Sclerocactus glaucus*
 - *Sclerocactus dawsonii*
 - *Corispermum navicula*
 - *Draba weberi*
- *Sclerocactus* phylogenetics of the West
 - *Sclerocactus mesa-verdeae*
 - *Sclerocactus cloverii*
- Ongoing
 - *Phacelia formosula* – coming soon
 - *Lygodesmia dolorensis*
 - *Oenothera acutissima*
 - *Penstemon penlandii*
 - *Penstemon scariosus* var. *albifluvis*
 - *Penstemon grahamii*
 - *Astragalus osterhoutii* – coming soon
 - *Eutrema penlandii* – coming soon
 - *Mimulus gemmiparus* – coming soon
 - *Penstemon yampahensis* – coming soon
 - *Penstemon acaulis* – coming soon
 - *Physaria X1*

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Questions