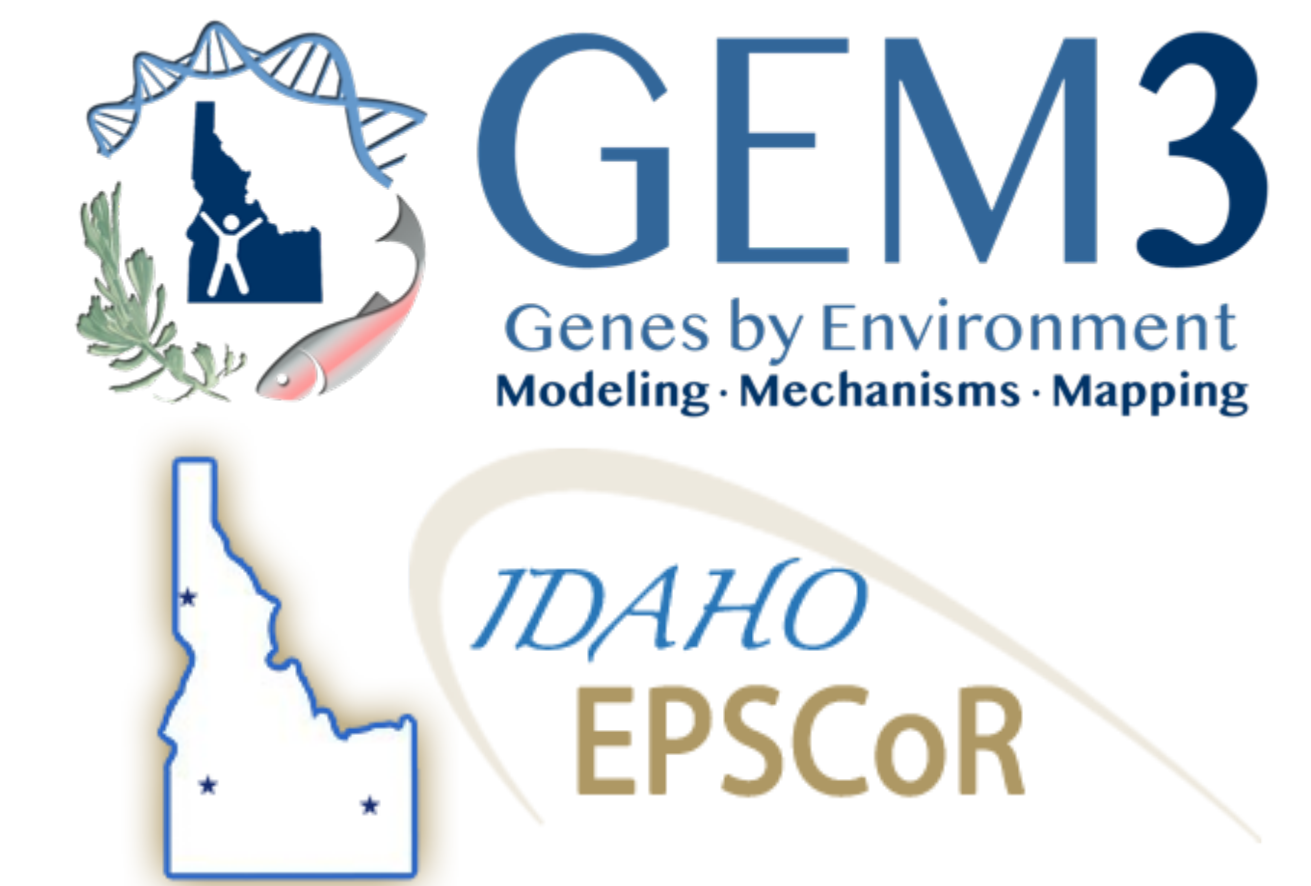


# Genome Size Variation in the Big Sagebrush (*Artemisia tridentata*) Polyploid Complex

Jonas Frankel-Bricker<sup>1</sup>, Bryce A. Richardson<sup>2</sup>, Matthew J. Germino<sup>3</sup>, Stephen Novak<sup>1</sup>, Peggy Martinez<sup>1</sup>, Kara Navock<sup>1</sup>, Kevin Degan<sup>2</sup>, and Sven Buerki<sup>1</sup>



<sup>1</sup>Department of Biological Sciences, Boise State University, Boise, ID, 83725  
<sup>2</sup>USDA Forest Service, Rocky Mountain Research Station, Moscow, ID, 83843  
<sup>3</sup>USGS Geological Survey, Forest and Rangeland Ecosystem Science Center, Boise, ID, 83706



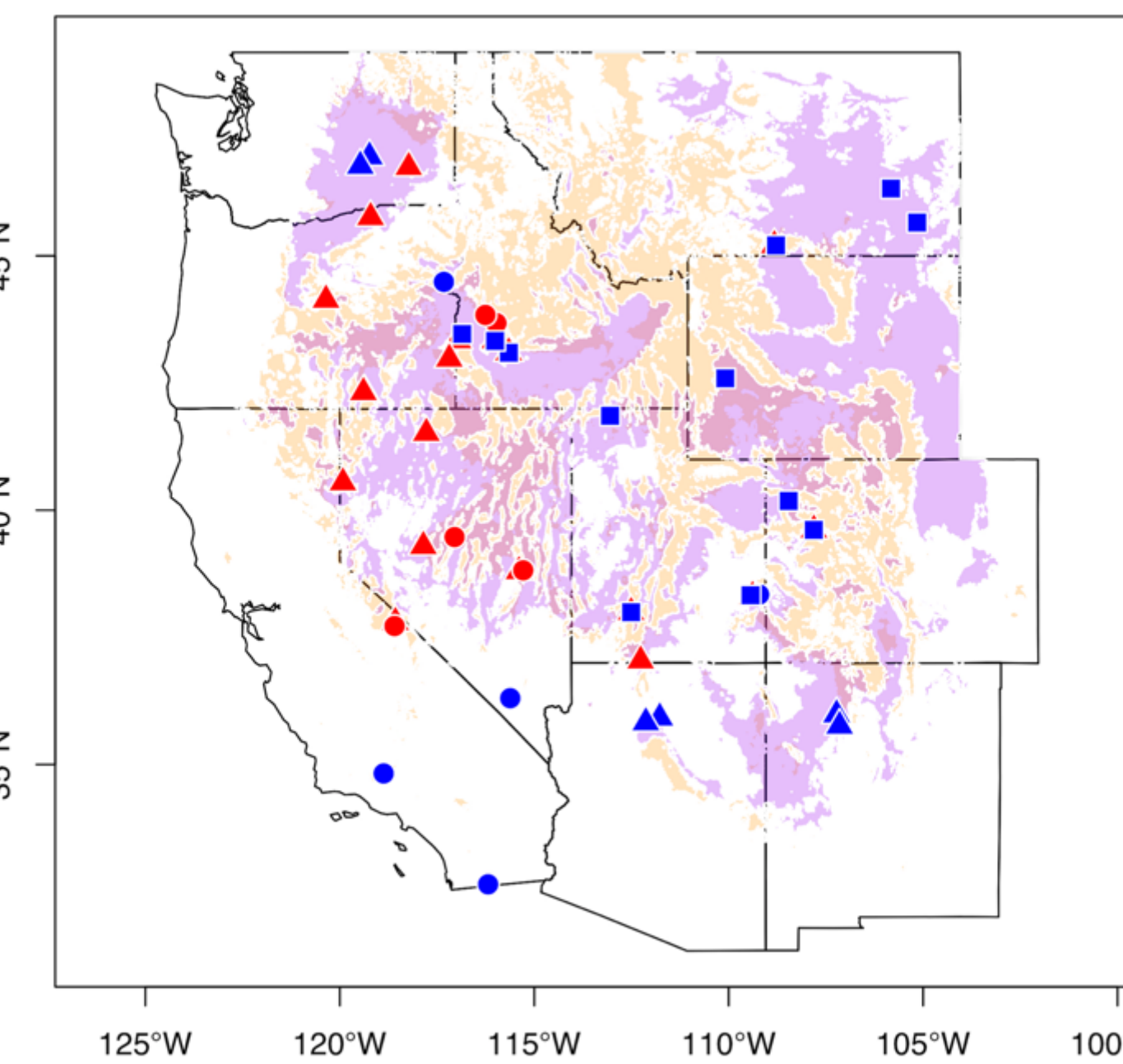
## Abstract

The size of an organism's genome is known to affect the duration of the essential life process of cell division [1,2]. This relationship promotes the coupling of a species' genome size (GS) with its growth rate and other phenotypic traits. Understanding how genomic processes other than gene expression influence an organism's biology is a target for research, motivating studies of GS dynamics. Here, we investigate the distribution of GS across the landscape in the widespread polyploid complex *Artemisia tridentata* (big sagebrush, Asteraceae).

## Methods

- 1) Conduct flow cytometry to calculate 2C DNA content for individuals descended from 48 wild populations, three subspecies, and two cytotypes across the big sagebrush's range.
- 2) Coalesce GS data with previously recorded environmental variables from the locations of wild populations.
- 3) Assess patterns of GS variation and test for environmental selection.

**Right:** Seed source locations of experimental populations of the three subspecies (circle: *vaseyana*, triangle: *tridentata*, square: *wyomingensis*) and cytotypes (red: 2x, blue: 4x) in relation to predicted distributions of *tridentata/wyomingensis* (purple), and *vaseyana* (orange) [9].



## Conclusions

- 1) Genome size is not a fixed trait in big sagebrush.
- 2) Extensive variation was found across and within populations, subspecies, and cytotypes.
- 3) No evidence was detected for environmental selection on GS.

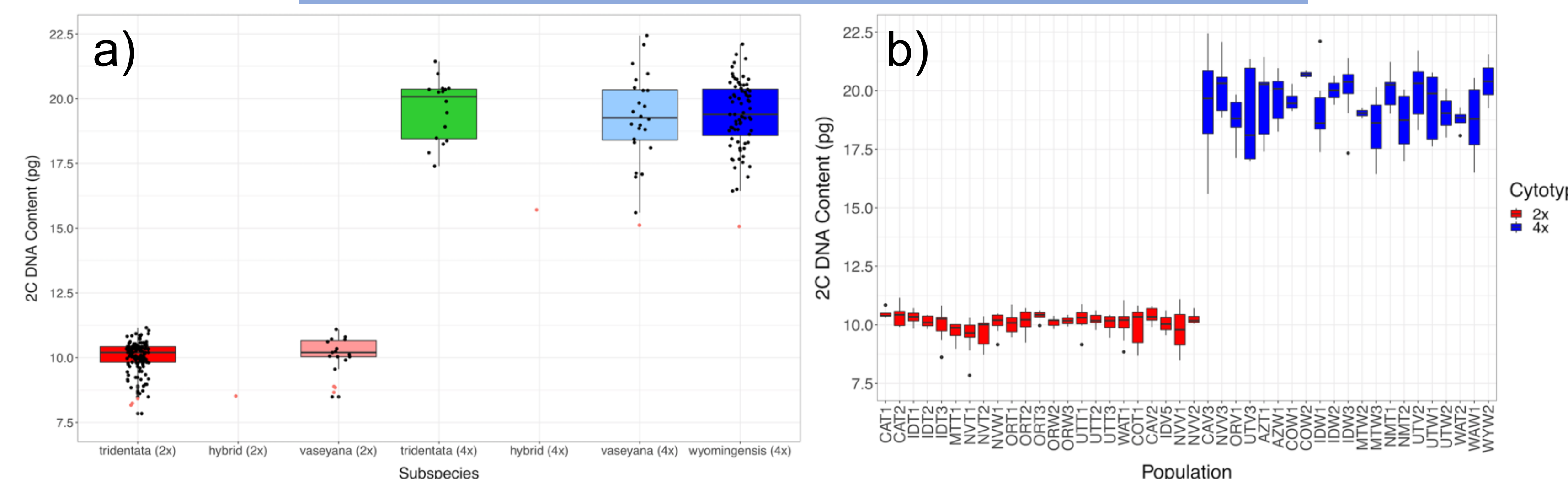
## Future Directions

Future laboratory-based studies could grow seedlings with variable GS and manipulate different environmental variables to further investigate impacts of GS on big sagebrush fitness. Genome size could also be quantified from additional natural populations as well as reintroduced populations to assess whether GS correlates with persistence in the landscape and reintroduction success. Finally, mechanisms maintaining GS variation could be investigated by evaluating hybridization processes between populations, cytotypes, and subspecies.

## Background

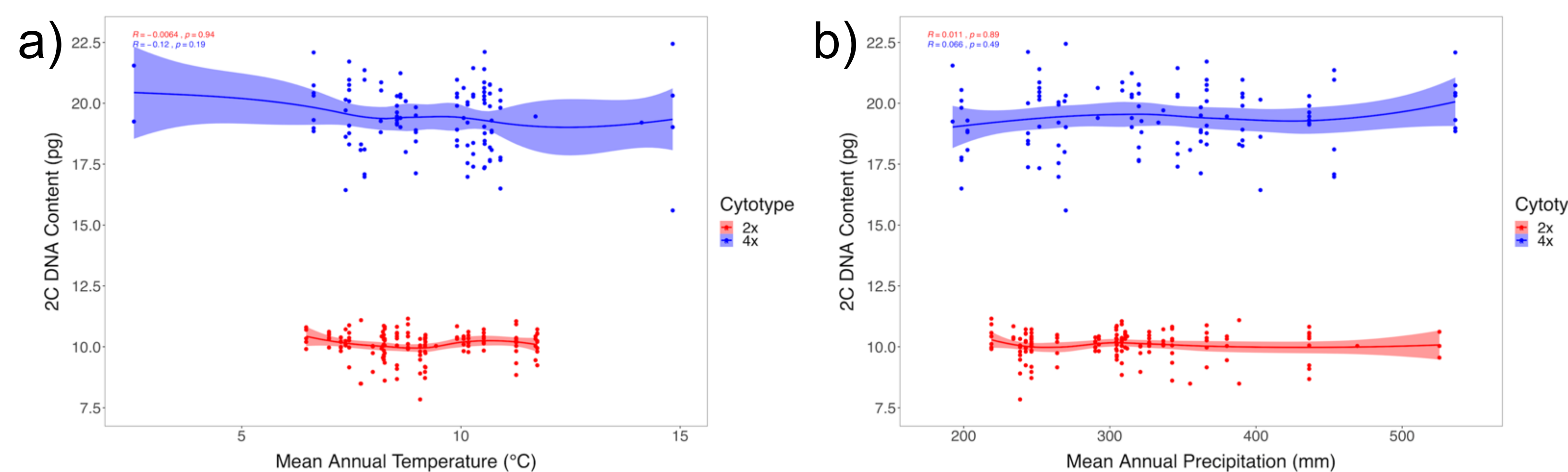
Big sagebrush is a widely distributed shrub species of substantial ecological importance in western North America [3,4]. The species is a polyploid complex, composed of diploid (2x) and tetraploid (4x) cytotypes. Although GS is known to impact phenotypic traits, little research has investigated GS variation in big sagebrush. Several studies estimated GS for some individuals from certain populations [5-7]; however, the full extent of GS variation across subspecies, populations, cytotypes, and environmental gradients across its range is largely unknown. Millions of dollars in governmental funds are invested into restoration efforts of big sagebrush in regions ravaged by wildfires [8]. Understanding GS dynamics in big sagebrush could be crucial in unraveling evolutionary histories of wild populations and providing contextual genomic information to conservation efforts.

## Results



### Extensive GS Variation

Summary of GS across and within *A. tridentata* subspecies and cytotypes. a) Box plots of GS of subspecies and hybrids (black points = GS of experimental plants, pink points = GS previously calculated [5-7]). b) Box plots representing GS of populations within cytotypes. Diploids had a mean GS of 10.08 picograms (pg) with a range of 3.32 pg. Tetraploids had a mean GS of 19.42 pg with a range of 6.84 pg.



### No Signal of Environmental Selection on GS

Genome sizes of individuals within cytotypes and Spearman correlation coefficients for a) Mean annual temperature (°C), and b) Mean annual precipitation (mm), of the geographic locations of source populations. No significant correlation was detected for any of the environmental variables tested (including elevation and mean July temperature (not shown); results in top left of each panel).

## Research Questions

- 1) Is GS a conserved trait in big sagebrush?
- 2) Does GS vary across subspecies, populations, and cytotypes?
- 3) Is there evidence for environmental selection on GS?

## Acknowledgements

This publication was made possible by the NSF Idaho EPSCoR Program, National Science Foundation under award number OIA-1757324, the Bureau of Land Management, and the Great Basin Native Plant Program. We thank Diedre Jaeger and the late Stewart Sanderson for conducting flow cytometry measurements. Any use of trade, firm, or product names is for descriptive purposes only and does not imply endorsement by the U.S. Government.

## Literature Cited

- [1] Hof J V., AH Sparrow 1963 A relationship between DNA content, nuclear volume, and minimum mitotic cycle time. Proc Natl Acad Sci 49:897.
- [2] Hesse DO, J Persson 2009 Genome size as a determinant of growth and life-history traits in crustaceans. Biol J Linn Soc 98:393-399.
- [3] Prevý J S, M J Germino, N J Huntly 2010 Loss of foundation species increases population growth of exotic forbs in sagebrush steppe. Ecol Appl 20:1890-1902.
- [4] Miller RF, ST Knick, DA Pyke, CW Menke, SE Hanser, MJ Wisdom, AL Hild 2011 Characteristics of sagebrush habitats and limitations to long-term conservation. Studies in Avian Biology 38:145-185.
- [5] Torrell M, N Garcia-Jacas, A Susanna, J Vallés 1999 Phylogeny in *Artemisia* (Asteraceae, Anthemideae) inferred from nuclear ribosomal DNA (ITS) sequences. Taxon 48:721-736.
- [6] Garcia S, M Sanz, T Garnatje, A Kreitschitz, ED McArthur, J Vallés 2004 Variation of DNA amount in 47 populations of the subtribe Artemisiinae and related taxa (Asteraceae, Anthemideae): Karyological, ecological, and systematic implications. Genome 47:1004-1014.
- [7] Garcia S, M A Canela, T Garnatje, ED McArthur, J Pellicer, SC Sanderson, J Vallés 2008 Evolutionary and ecological implications of genome size in the North American endemic sagebrushes and allies (*Artemisia*, Asteraceae). Biol J Linn Soc 94:631-649.
- [8] Shriver RK, CM Andrews, RS Arkle, DM Barnard, MC Duniway, MJ Germino, DS Pilliod, DA Pyke, JL Welty, JB Bradford 2019 Transient population dynamics impede restoration and may promote ecosystem transformation after disturbance. Ecol Lett 22:1357-1366.
- [9] Still SM, BA Richardson 2015 Projections of contemporary and future climate niche for Wyoming big sagebrush (*Artemisia tridentata* subsp. *wyomingensis*): A guide for restoration. Nat Areas J 35:30-43.