

Genetic information and avoiding pitfalls in wildland plant propagation and restoration

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Introduction and problem

- Shift toward diverse native seed mixes and nursery stock
 - Good... however, limited information exists on many of the native plants
 - Information mainly limited to morphological descriptions
- Risk failure by naively pushing ahead on restoration programs before understanding the biology
 - Example of misguided efforts: Ribes eradication program
 - Ribes seed bank
 - Other alternate hosts

Information needs for restoration species

1. Taxonomic boundaries

- Taxonomy based on morphology may or may not reflect reality

2. Species niche

- Straightforward until climate change is factored

3. Population structure and adaptation

- How far can plants be moved within a species boundary before maladaptation (loss of fitness)?

Taxonomic boundaries/polyploidy



Developing knowledge base on native forbs

- Emphasis on developing native seed mixes/nursery stock that have a diverse array of species (sage grouse and pollinator forage)
 - Forb list: *Chaenactis douglasii*, *Crepis accumulata*, *Erigeron speciosus*, *Macranthera canescens*, etc
- Taxonomic 'issues':
 - *Erigeron*: variation in characters
 - *Chaenactis*: polyploidy = reproductive incapability and adaptation
 - *Crepis*: polyploidy, apomictic populations

Getting it wrong

- Unrecognized taxonomic differences:
 - Failed establishment due to maladaptation
 - Low or no seed increase due to genetic incompatibility
 - Outbreeding depression
 - create nursery stock that has lower fitness due to mixing of genetically distinct taxa or populations
 - Inbreeding depression
 - Create nursery stock that has lost genetic diversity important to its fitness

Genetics approaches

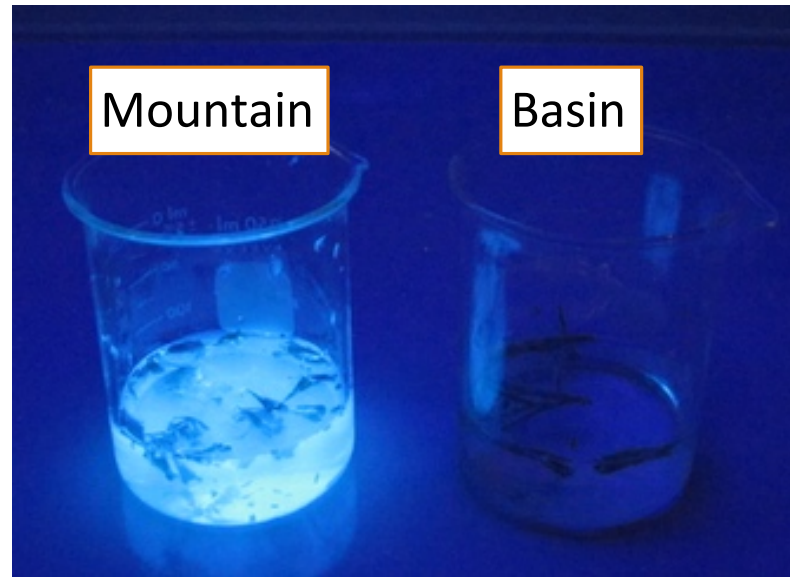
- Two techniques to help resolve taxonomic uncertainties:
 - DNA sequencing approaches: resolve taxonomic boundaries and population structure within species
 - Flow cytometry: detect variation in genome (polyploidy)
- Examples:
 - Discern subspecies and evaluate traits in big sagebrush



Diagnostics for sagebrush subspecies

Using genetic techniques to define taxonomic boundaries help evaluate diagnostic tests

UV fluorescence- mtn big sagebrush



Importance of polyploidy

- Sagebrush:
 - Changes the physiological and phenotypic characters:
 - Doubling lowers the growth rate
 - Diagnostic in determining subspecies (Wyoming big sagebrush)



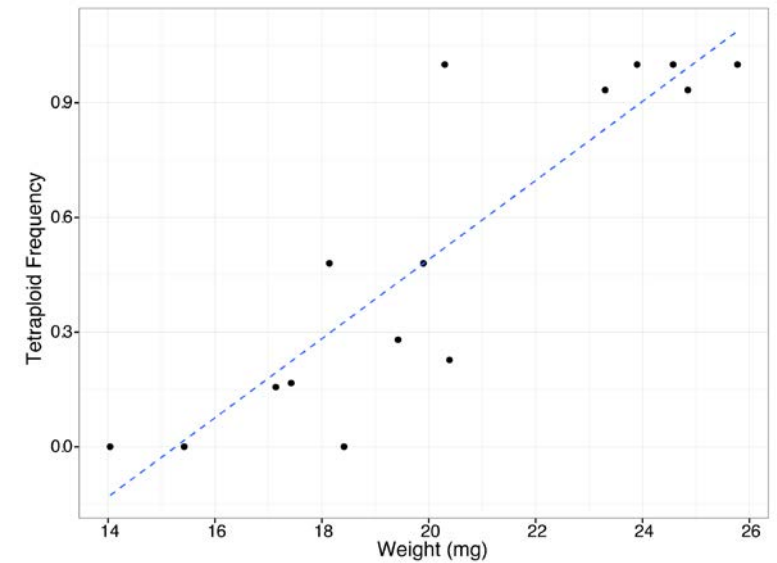
vaseyana(2X)

4X

4X

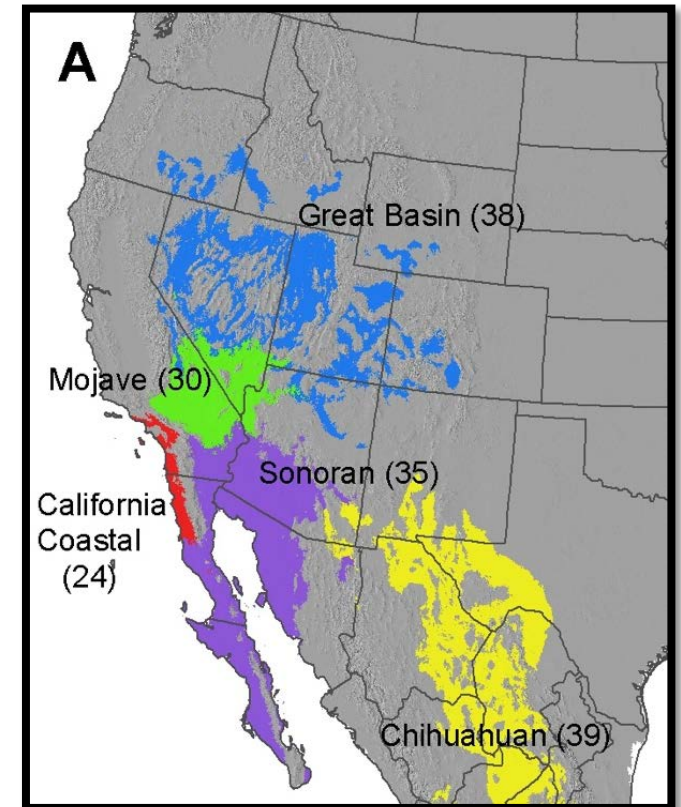
tridentata(2X)

Seed weight- Wyoming/basin big sagebrush



Species/biotic community boundaries (climatic niche)

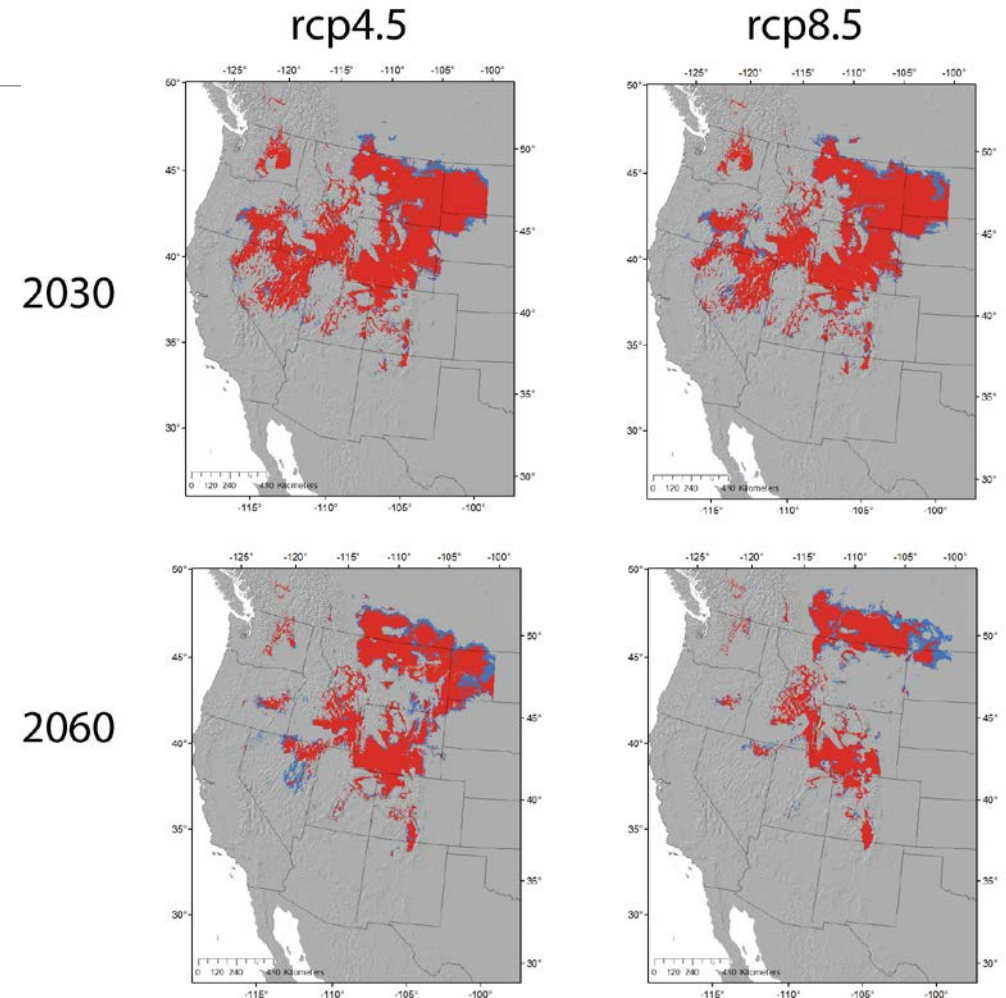
- Many biotic communities and individual species boundaries are shifting from climate change.
- Predicting of areas of contraction, stability and expansion of a species distribution will aid in plant material deployment.



Rehfeldt et al 2012

WY Sagebrush futures

- Methods present/absence points
- Emissions make a difference
 - Lower emission (rcp 4.5) = much greater assemblage of Wyoming sagebrush in Great Basin and elsewhere
- 1/3rd of the subspecies niche is lost by mid-century
- Restoration efforts to establish sagebrush ecosystems in the warmest regions may be misguided

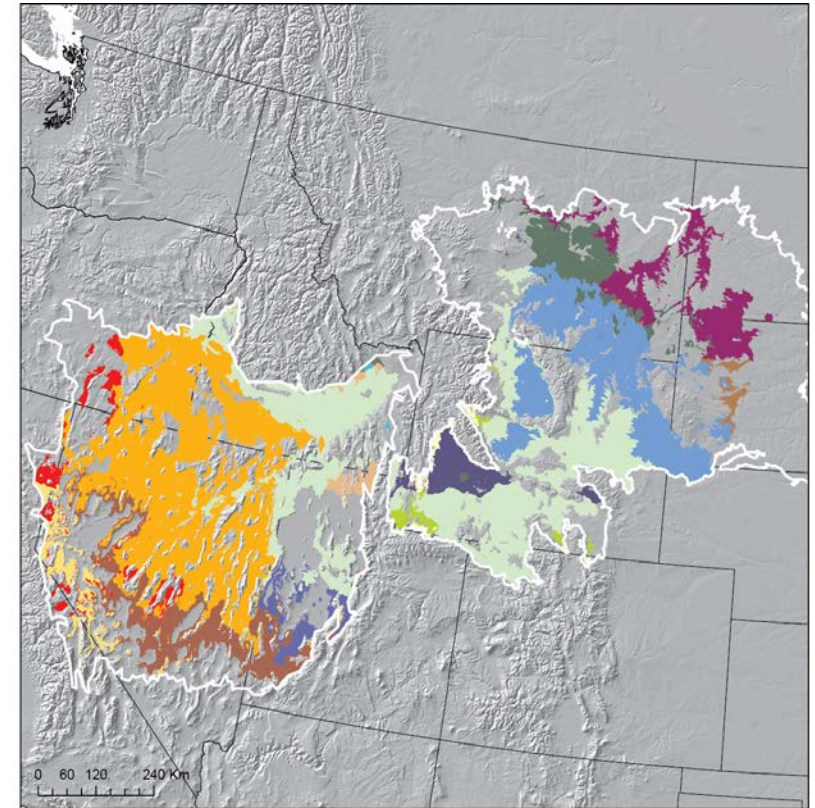


Population genetic structure and adaptation

Two distinct approaches:

- Molecular (DNA) approaches: address gene flow and isolation
- Quantitative approaches: Use phenotypes in a common environment to address adaptive patterns (clines)

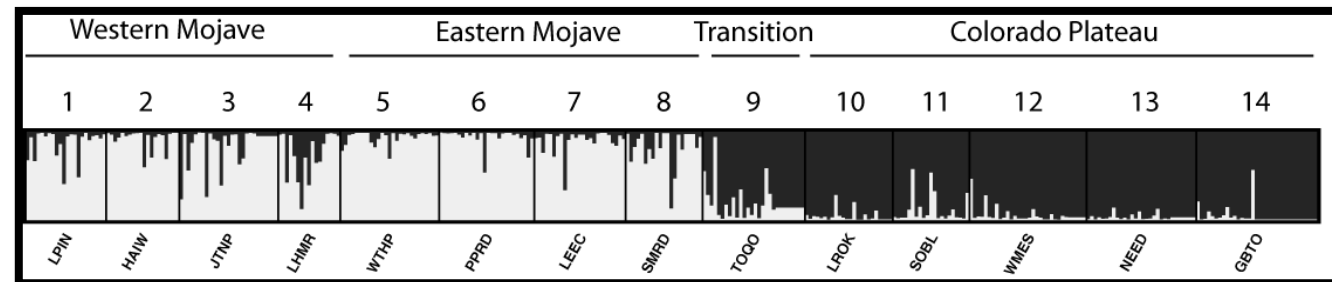
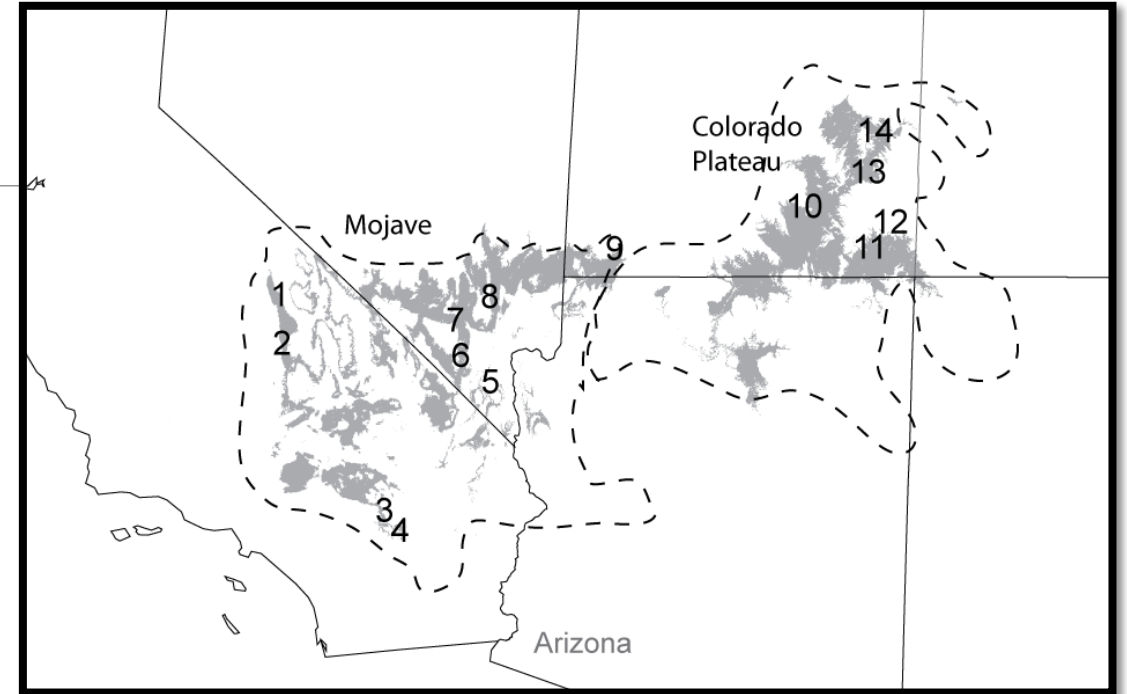
Examples: Blackbrush, Big sagebrush



Blackbrush population genetics

Distinct populations in the Mojave and Colorado Plateau

Overlap with patterns of cold hardiness



(Richardson and Meyer, in press)

Populations (variation within subspecies)



Phenotypic variation:

- What environmental factors affect trait variation
- Why is it important

Populations

Triangles = *ssp tridentata* (n=25)

Circles = *ssp wyomingensis* (n=14)

ssp vaseyana not included in this analysis

Gray = bioclimatic niche of *ssp wyomingensis* (1981 to 2010)



Populations – Surviving the cold

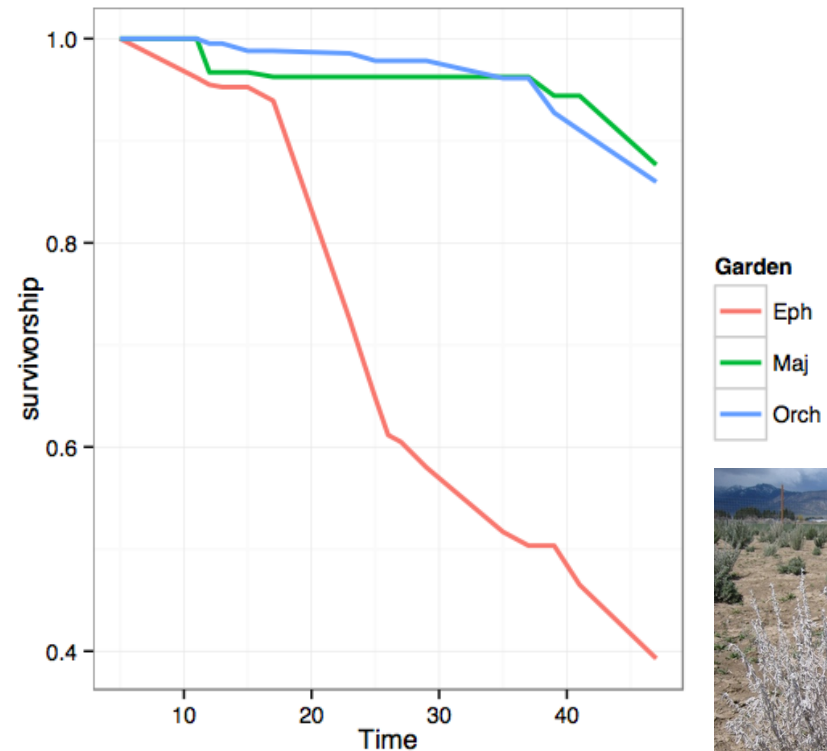
Subspecies ranges are large = face very different climates

Ephraim kills plants from warmer climates:

< 40% surviving after 5 years

Causes?

- Winter inversions / cold air drainage
- Winter minimums > 10°C colder
- Late spring frosts

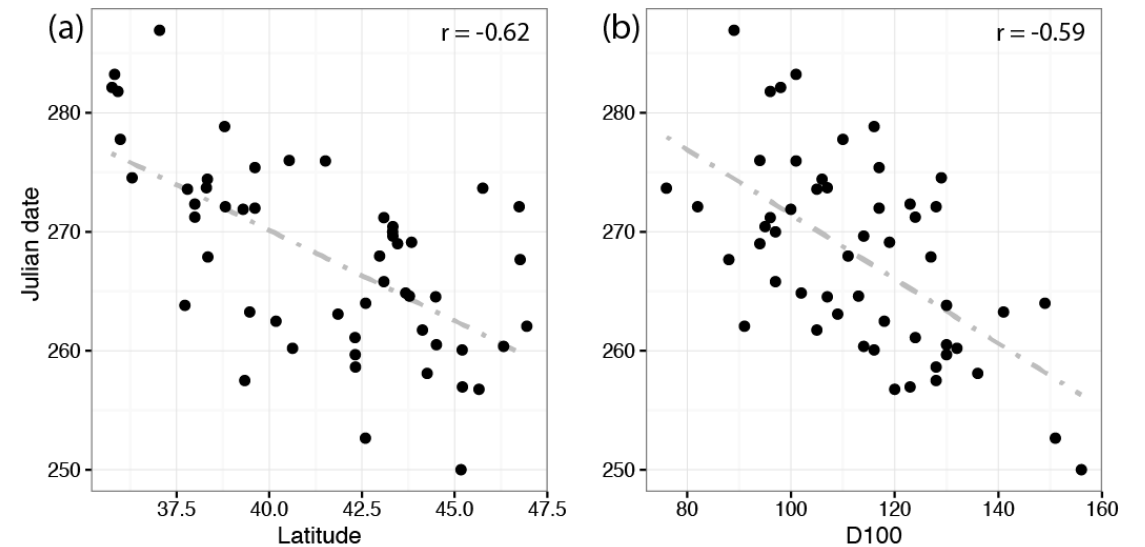


Populations – Phenology

Changes in flowering time have been observed in many species and correlation with rising temperatures

Flowering from August to November

For temperate plants: flowering is affected by photoperiod and vernalization (chilling)



Traits

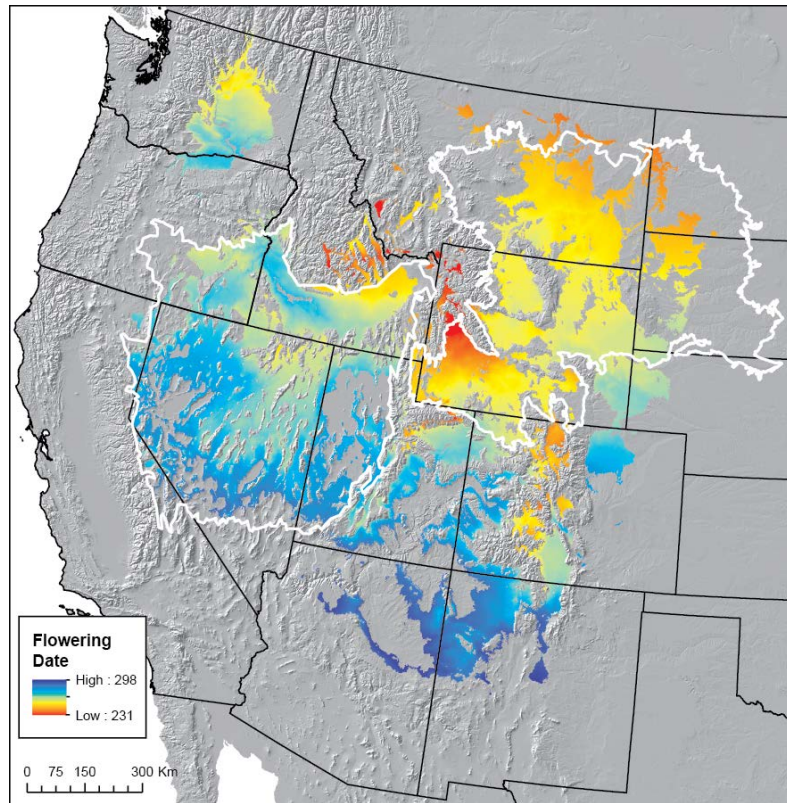
Trait	Explanatory variables (Climate)	R^2c (total)	R^2m (genetic)
Flower Phenology	Photoperiod(lat), DD<18°C	0.8	0.31
Survival	TD(MTWM-MTCM), PPTsm	0.51	0.11

Growth and seed yield also measured:

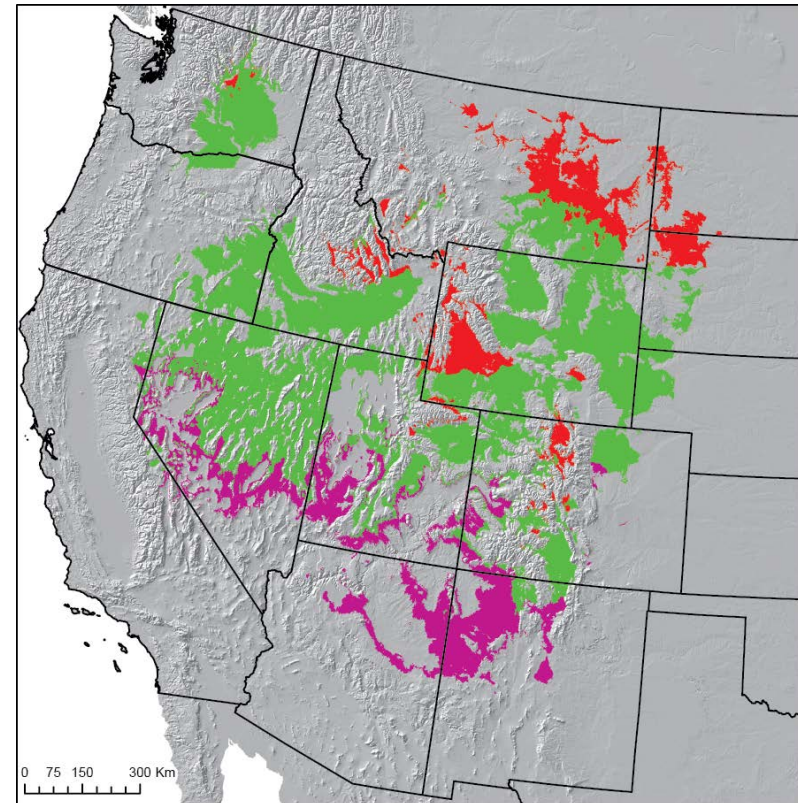
- Higher plasticity and lower genetic contributions (3%)
- Correlated with survival or flowering

Genecological models and climatypes: flower phenology

MODELED GENETIC VARIATION

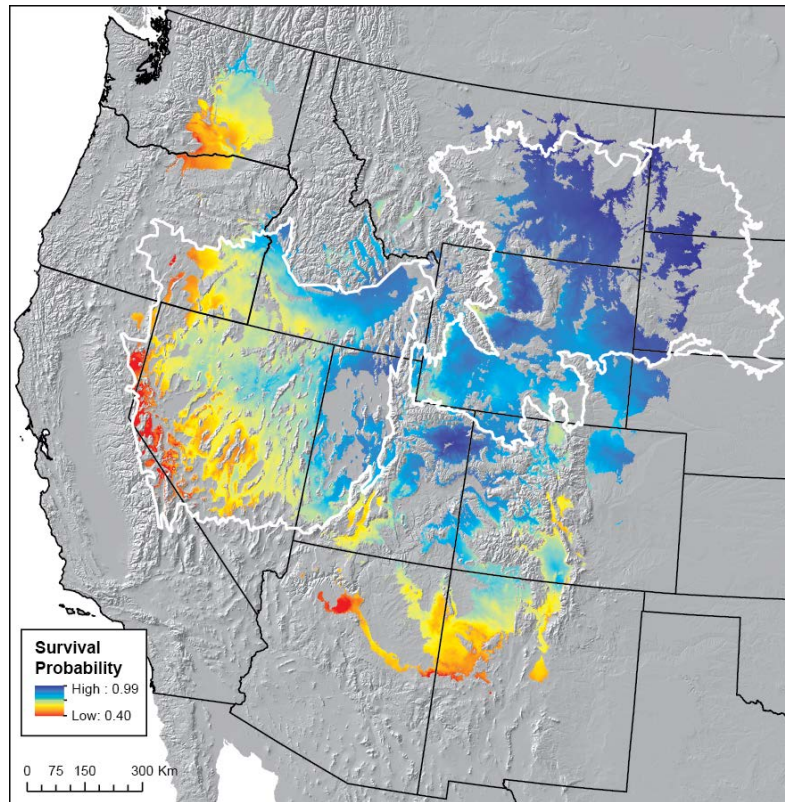


CLIMATYPES USING CONFIDENCE INT.

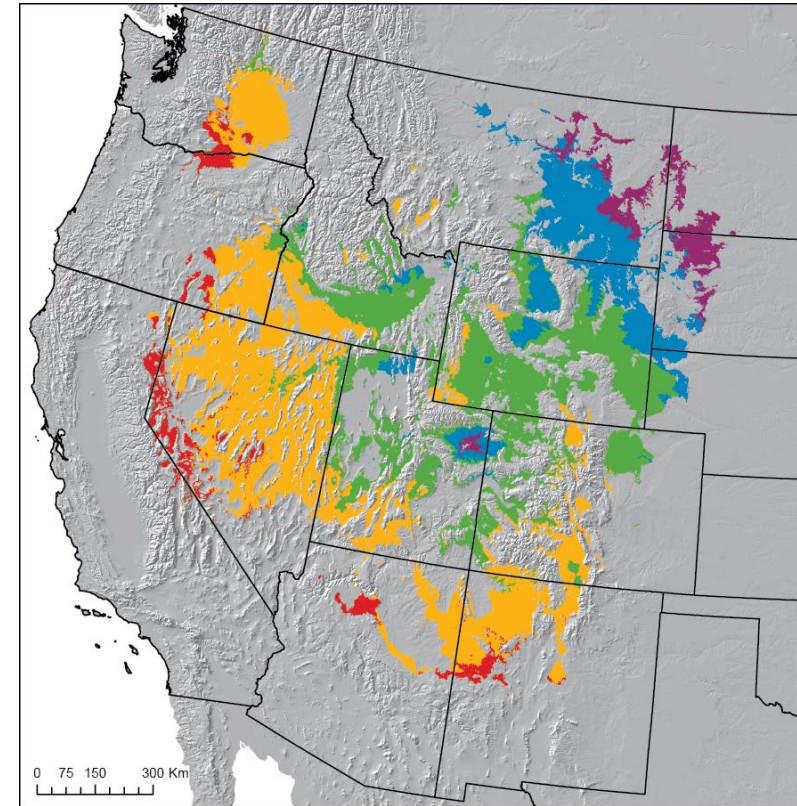


Genecological models and climatypes: survival

Modeled Genetic variation



Climatypes using Confidence Int.



Focal point seed zones

Climate variables derived from grids
using lat and long

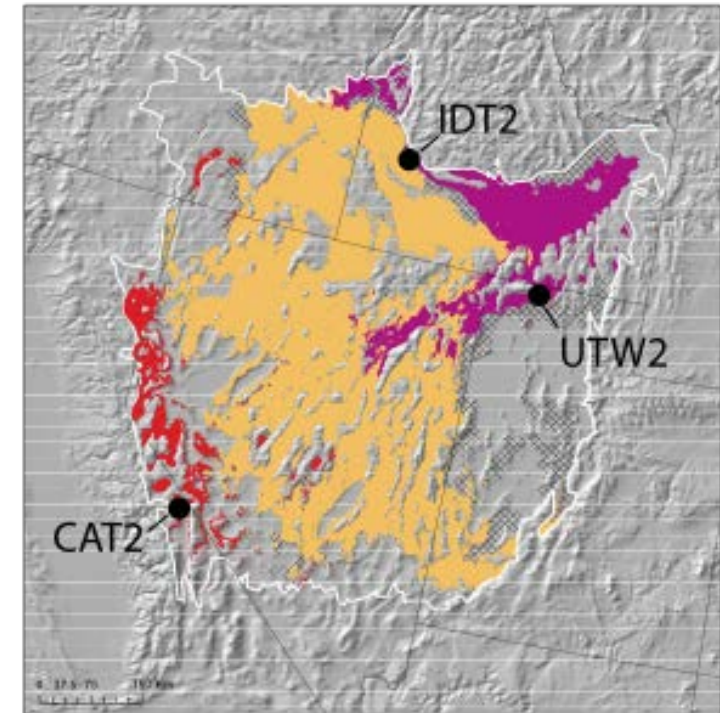
Survival

Site	Upper limit	Lower limit
IDT2	0.423	-0.553
UTW2	2.313	1.689

Flowering date

Site	Upper limit	Lower limit
IDT2	280	260
UTW2	288	267

Contemporary



Seed transfer limits for two populations
30-yr climate for 1981 to 2010

Winners and losers

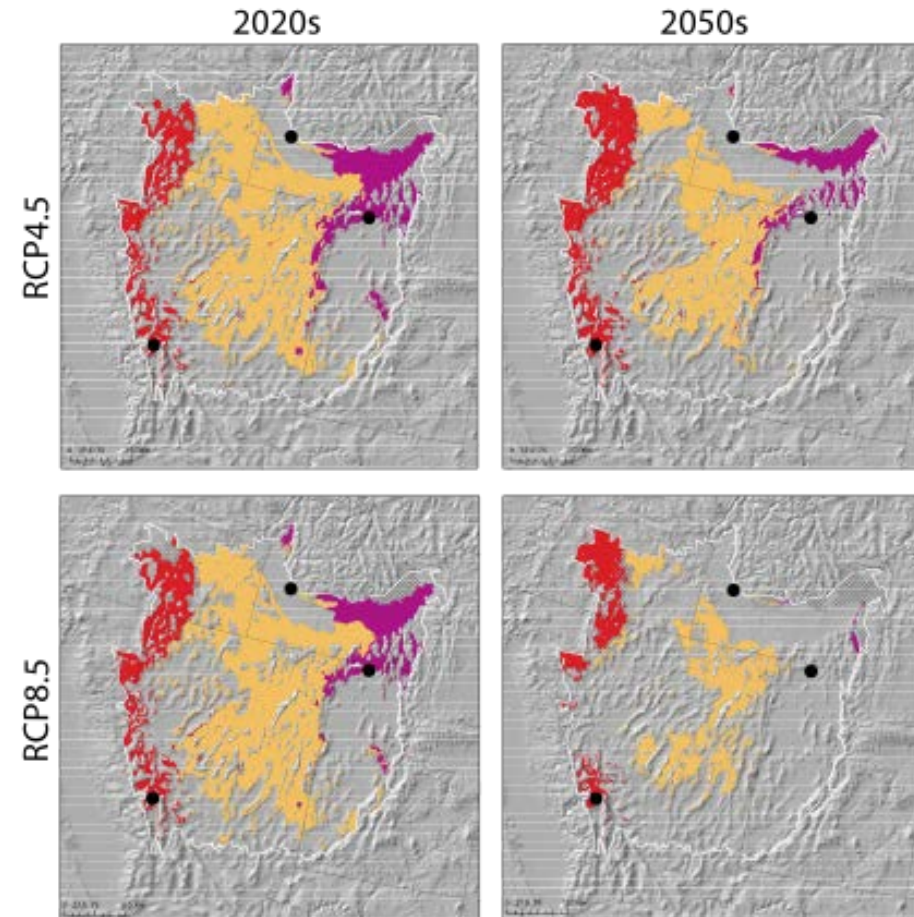
Winners:

Warm-adapted trailing edge populations win or colder populations in the Great Basin

Warm populations: California and Idaho

Loser:

Cold populations: Utah



Climate-smart restoration tool

Operation would be similar to SST, but specific to *A. tridentata*

Input: latitude and longitude

Select constraint:

Subspecies, GCM/decade

Climate variables already selected.

The screenshot displays the 'Seedlot Selection Tool' interface. The left panel contains configuration options:

- Select climate scenarios:** 'Which climate are the seedlots adapted to?' and 'When should trees be best adapted to the planting site?' both set to '1981 - 2010'.
- Select transfer limit method:** 'Custom' is selected over 'Zone'.
- Select climate variables:** 'Metric' units are selected. A table lists selected variables: TD (26.1 °C, 3.00 °C) and DD_0 (416 dd, 50 dd).
- Apply constraints:** An 'Add a constraint...' button is visible.
- Map your Results:** A 'Run Tool' button is at the bottom.

The right panel shows a map of the western United States with a heatmap overlay. A blue location pin is placed in the Great Basin region. A legend in the bottom right corner indicates 'Match' levels from Low (yellow) to High (red). The map includes labels for various geographical features and cities across Washington, Oregon, Idaho, Utah, Nevada, and California.

Summary

- Prior to propagating species for restoration:
 - Species boundaries
 - Polyploidy?
 - Population structure
- For widespread foundational species:
 - Climate niche, climate impacts
 - Adaptive variation, seed transfer guidelines

Thank you.

Acknowledgements

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