A preview of the Climate Smart Restoration Tool (CSRT) using big sagebrush ecological genetics

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MOSCOW, IDAHO

Collaborators and acknowledgements

Sagebrush genetics team:

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CSRT Team:

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Outline

- Importance of genetic information
- Overview of the biology of big sagebrush
- Adaptation to climate
- Merits of different approaches to seed transfer
- Development and use of the web-tool: Climate Smart Restoration Tool (CSRT)


Nancy Shaw

More details…

Chaney, L., Richardson, B. A., & Germino, M. J. (2017). Climate drives adaptive genetic responses associated with survival in big sagebrush (Artemisia tridentata). *Evolutionary Applications*, *10*(4), 313–322. http://doi.org/10.1111/eva.12440

Richardson, B. A., Chaney, L., Shaw, N. L., & Still, S. M. (2017). Will phenotypic plasticity affecting flowering phenology keep pace with climate change? *Global Change Biology*, *23*(6), 2499–2508. http://doi.org/10.1111/gcb.13532

Richardson, B.A., & Chaney, L. (2018). Climate-based seed transfer of a widespread shrub: populations shifts, restoration strategies and the trailing edge. Ecological Applications (Early Online) https://doi.org/10.1002/eap.1804

Why genetic information is important for restoration:

1. Identify taxonomic boundaries and polyploidy. Traditional taxonomy has it limitations.
2. Understand demographic history. How has the species been shaped by past events and landforms.
3. Understand breeding system. Selfing? Outcrossing?
4. **Identify adaptive variation: clines and ecotypes. Develop empirical seed transfer approaches**

What could go wrong?

Seed increase:

- Low to no seed yield due to genetic incapability
- Narrow genetic diversity resulting in inbreeding and low fitness

Seed transfer:

- No establishment
- Mortality caused by climate events, insects, diseases
- Low fitness → low resiliency

Seed transfer: Lessons learned from forestry

- Plants are adapted to local climate
- Seed transfer guidelines were established for trees to ensure improved growth and fitness

Big sagebrush

Background:

- Part of the subgenus Tridentatae: woody *Artemisia* unique to North America, 12 species
- Most widespread species in the western US
- Large adaptive breadth (300 ft to 10,000 ft)
- Critical habitat to numerous wildlife species.

Genetics/taxonomic review of big sagebrush

- Three predominate subspecies: *tridentata* (Basin), *vaseyana* (mountain) and *wyomingensis* (Wyoming)
- Subspecies *tridentata* and *vaseyana* predominately diploid, and to lesser extent tetraploid
- Subspecies *wyomingensis* exclusively tetraploid
- Subspecies can be distinguished by: morphology, chemistry, and DNA
- BUT… individuals don't always fall neatly into bins. Some plants can have a mixture traits due to introgression.
- Hybrid plants generally occur along ecotones (McArthur et al. 1981, 1988, Wang et al. 1997)

How are subspecies arrayed on the landscape?

Basin ecosystems:

Increasing soil depth / moisture favors basin big sagebrush

Decreasing soil depth / moisture favors Wyoming

Montane ecosystems:

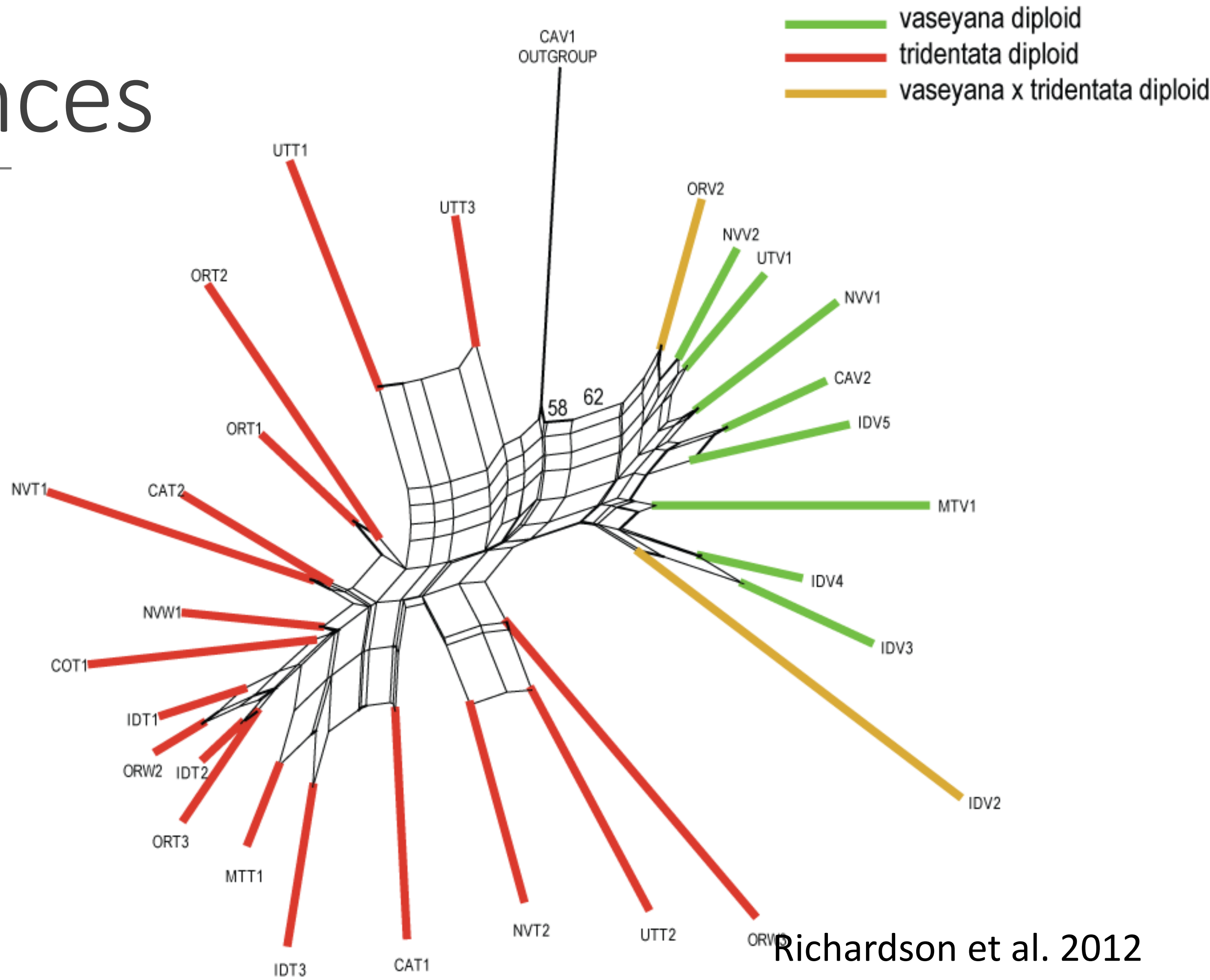
Support mountain

Ecotones:

Hybridization between basin and mountain.

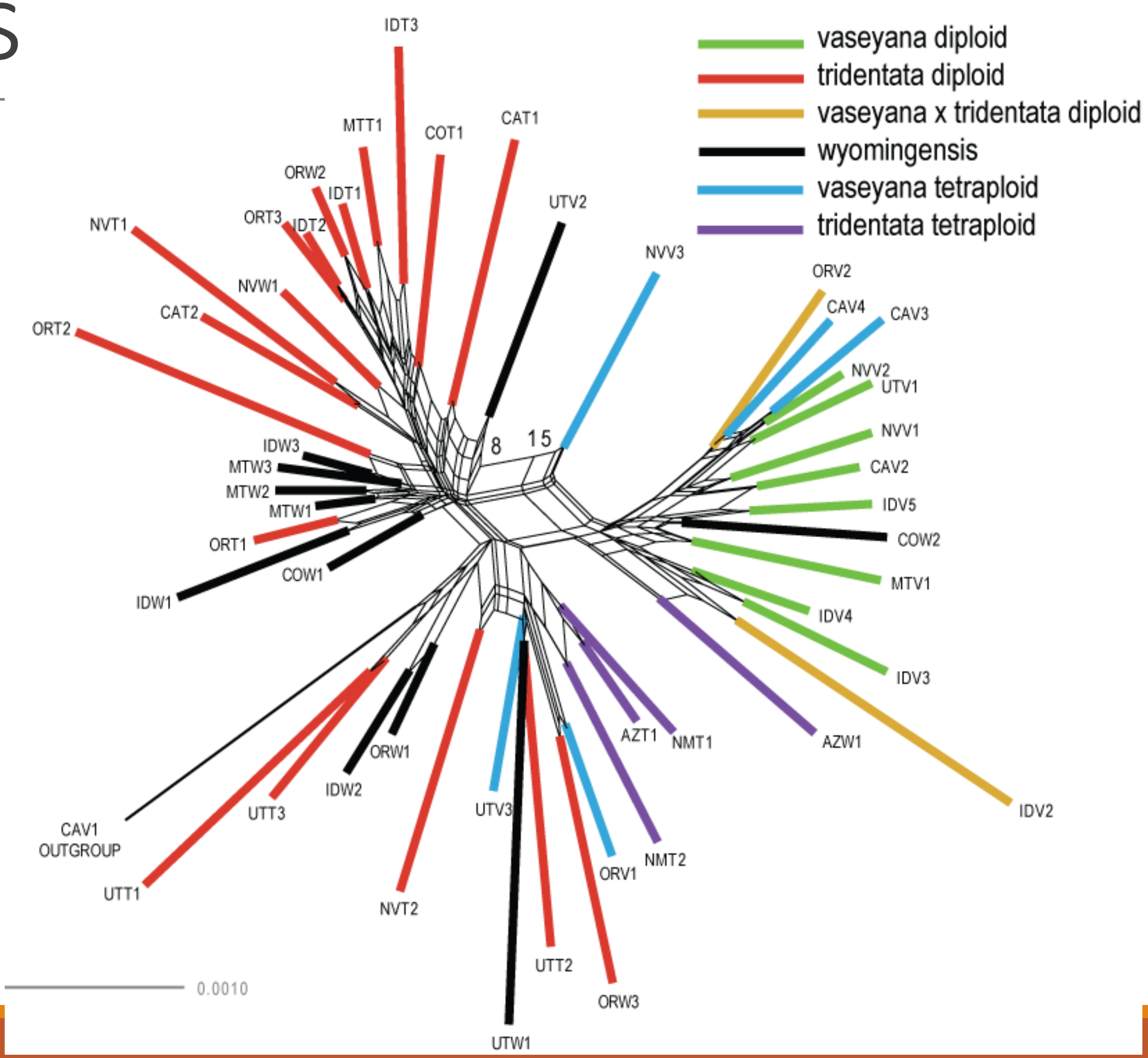
Overlap between basin and mountain are common.

DNA-level differences



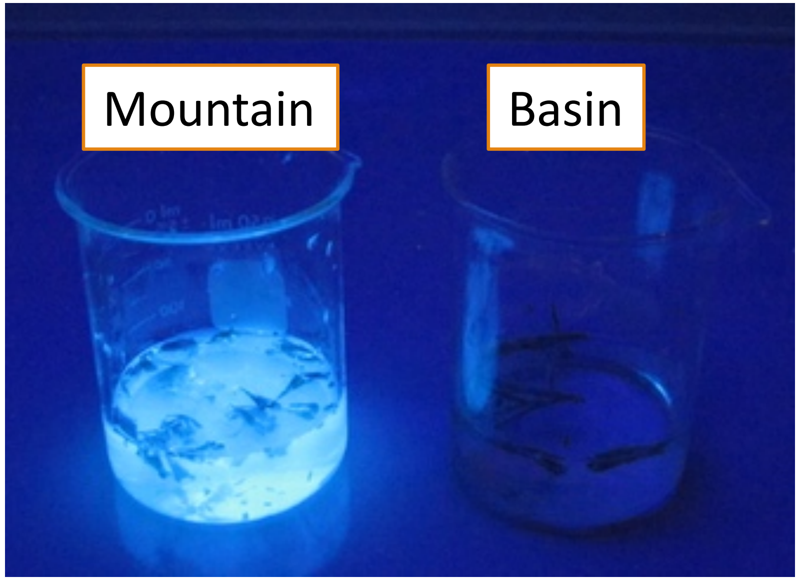
Richardson et al. 2012

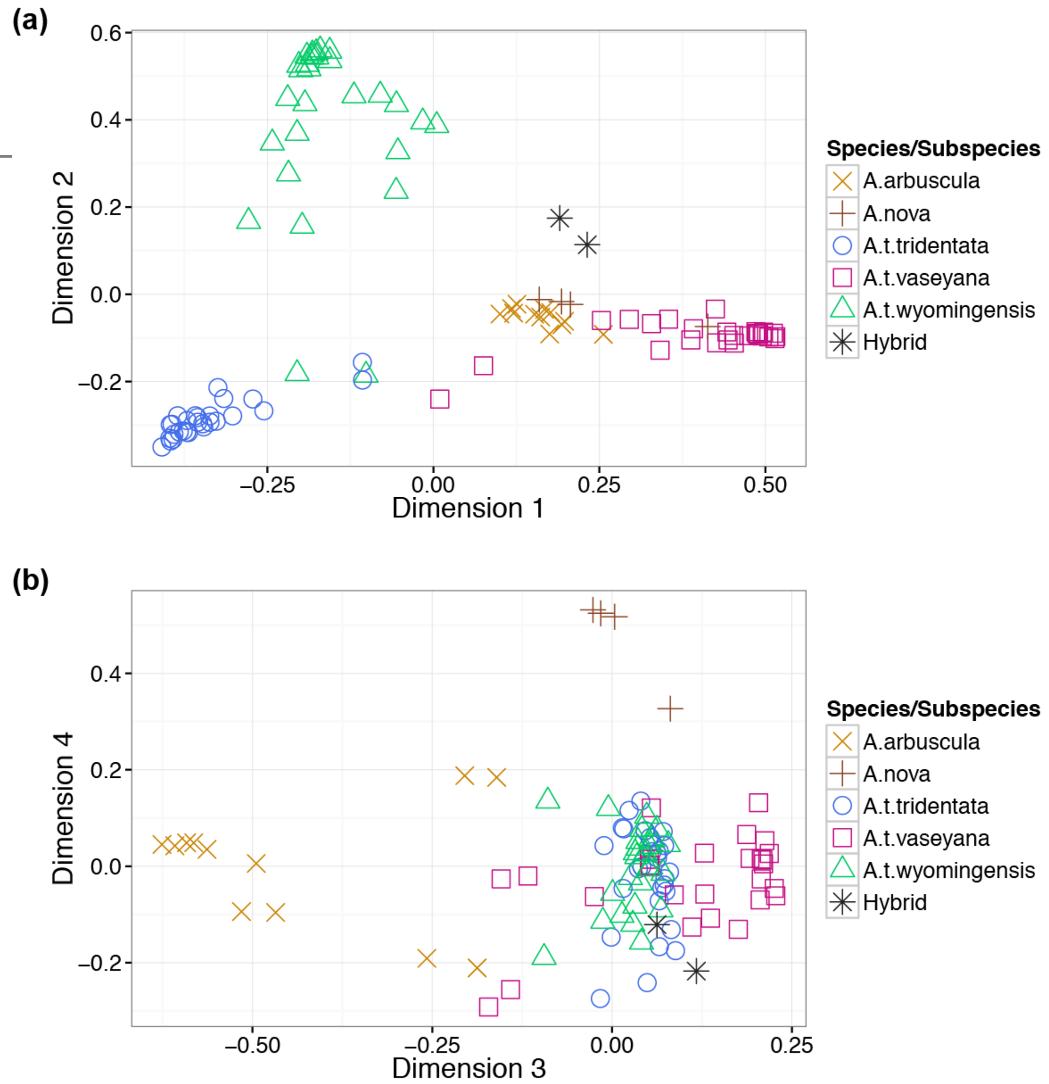
DNA-level differences



Chemistry

Chemistry is one of the best means to distinguish subspecies, but some methods are not very practical.





Sagebrush restoration failures

- Environment: Weather/timing
- Competition: weeds, non-natives
- Wrong species/subspecies - Genetic
- **Adaptation (move seed outside of its adaptive niche) - Genetic**
- **Climate change? – Genetic: seed transfer, assisted migration**

Common gardens

Ephraim, UT
Cool - dry

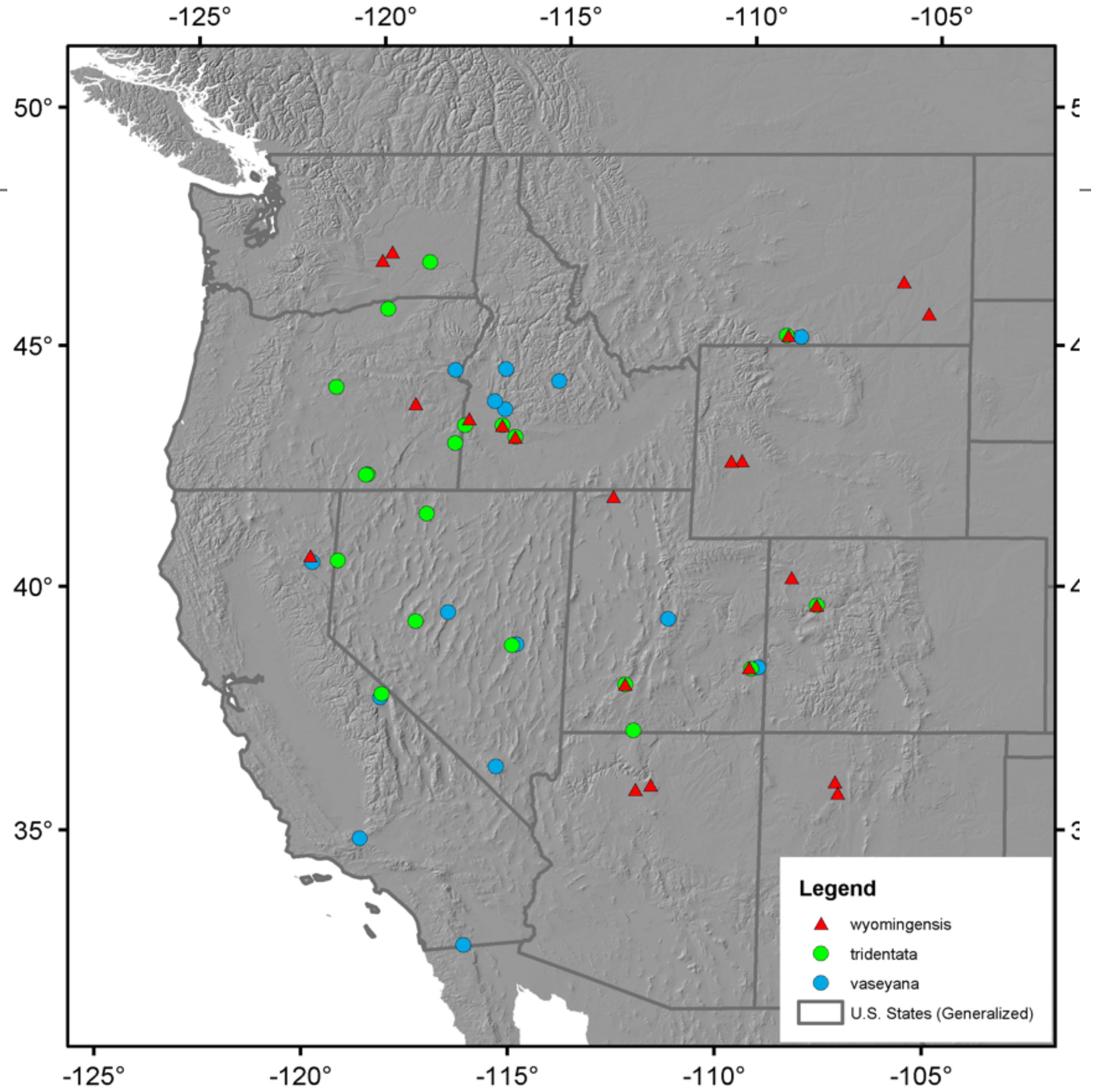
Majors Flat, UT
Cool - wet

Orchard, ID
Warm - dry

Why common gardens?

Minimize environmental variation to assess genetic attributes. Multiple garden provide a means to assess phenotypic plasticity (a traits ability to change with the environment)

Seed sources of big sagebrush



Phenotypic variation

Four traits examined:

- Growth, seed yield, flower phenology and survival
- Flower phenology and survival had the strongest association with climate and are used in developing seed transfer
- Basin and Wyoming subspecieswill be the focus.

Analysis

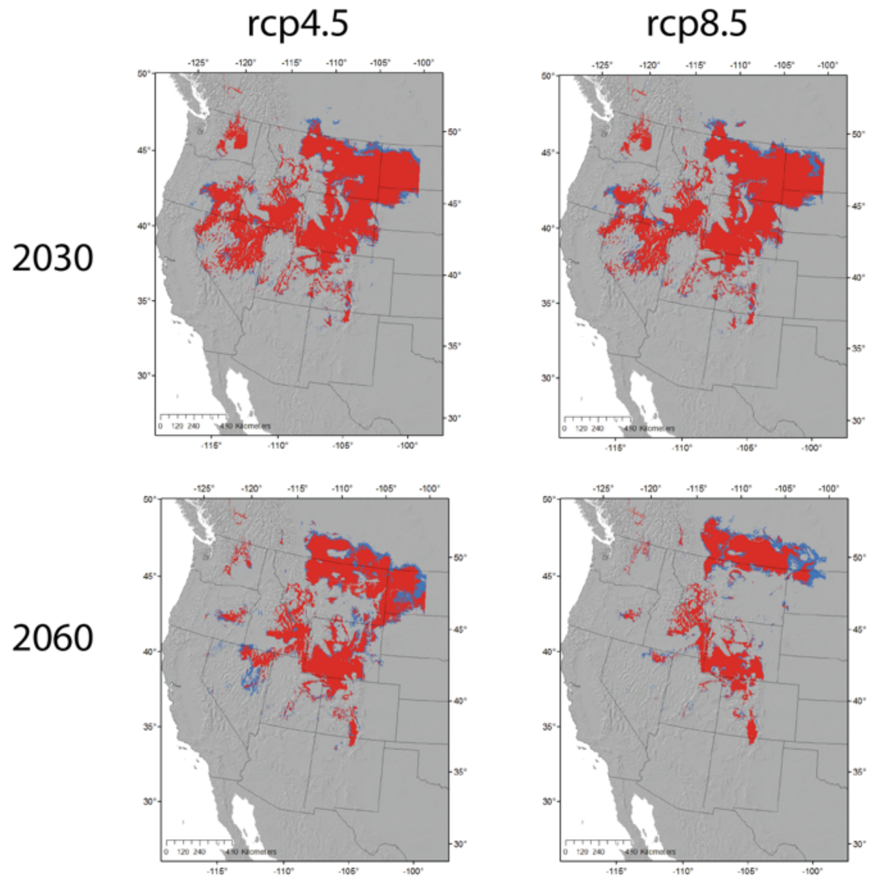
Mixed effects models:

- Fixed effects = pertain to genetics (association between a trait and the climate of origin)
- Random effects = variables associated with experimental design (gardens, populations, subspecies)
- Confidence intervals were calculated from fixed effects for each trait and used as seed transfer limits for population means.

Models are driven by climate, therefore predictions of change can be made using GCMs

WY Sagebrush SDM

- Subspecies *wyomingensis* SDM based on present/absence points
- Used as a constraint for genetic models (adapted from Still and Richardson 2015)
- Contemporary and GH gas emission scenarios (RCP8.5 and RCP 4.5) to assess variation in predictions for decades 2020 and 2060

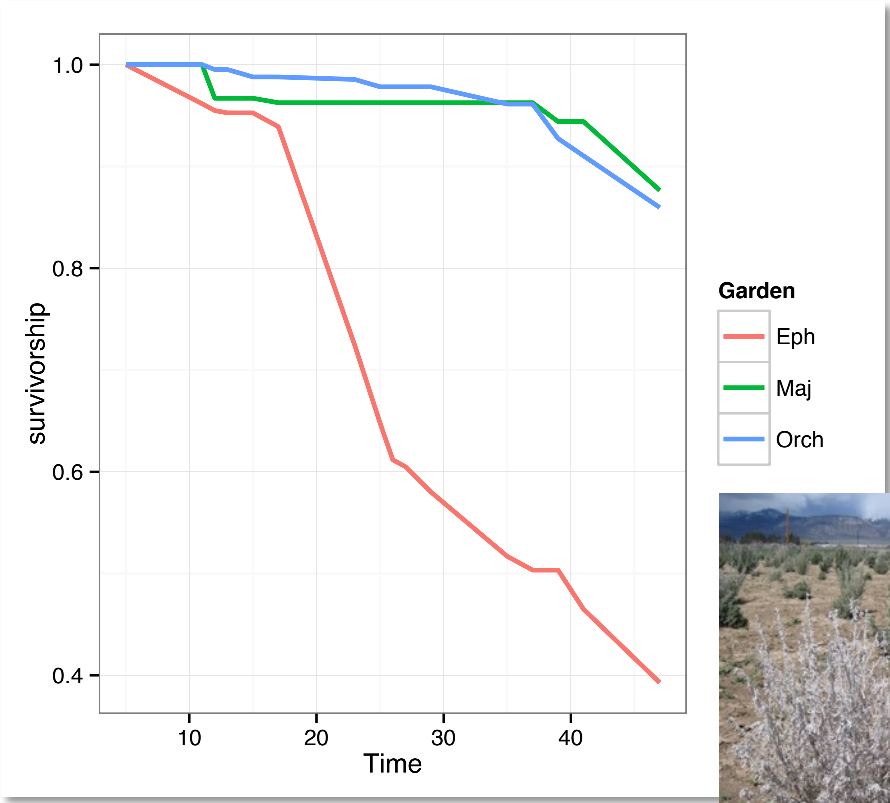


Traits: Survival

Sagebrush occupies wide-ranging climates

Ephraim kills plants from warmer climates:

- < 40% surviving after 5 years
- Population survival ranged from 100% to 0%



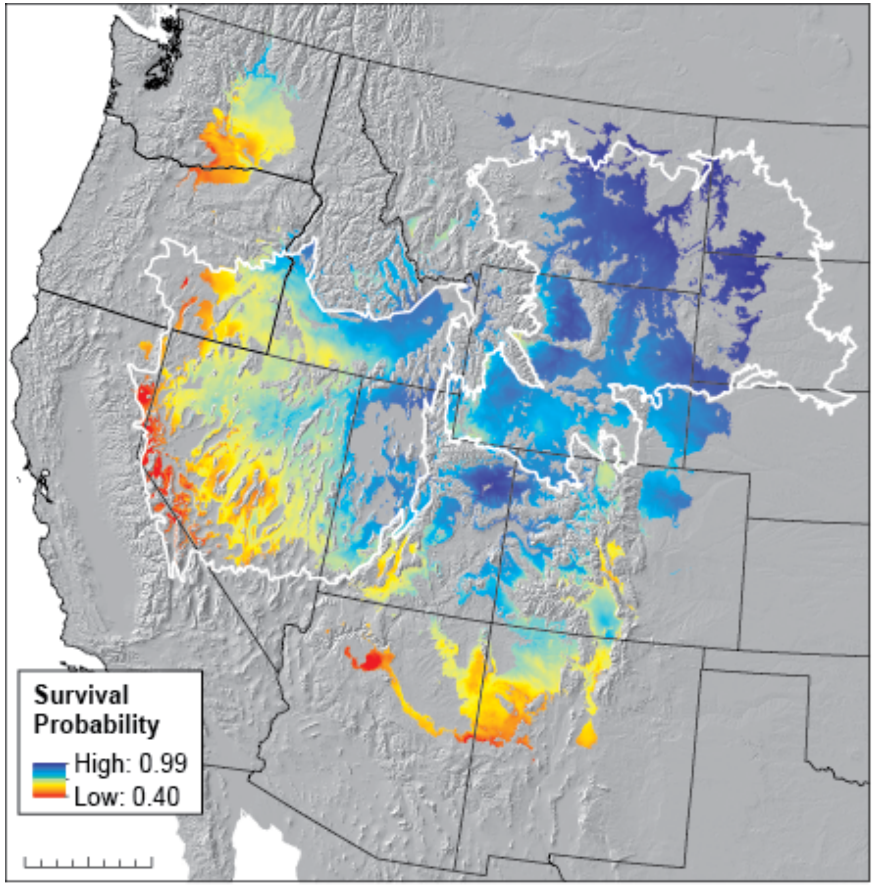
Survival cline

Predicted survival

This pattern is best explained by:

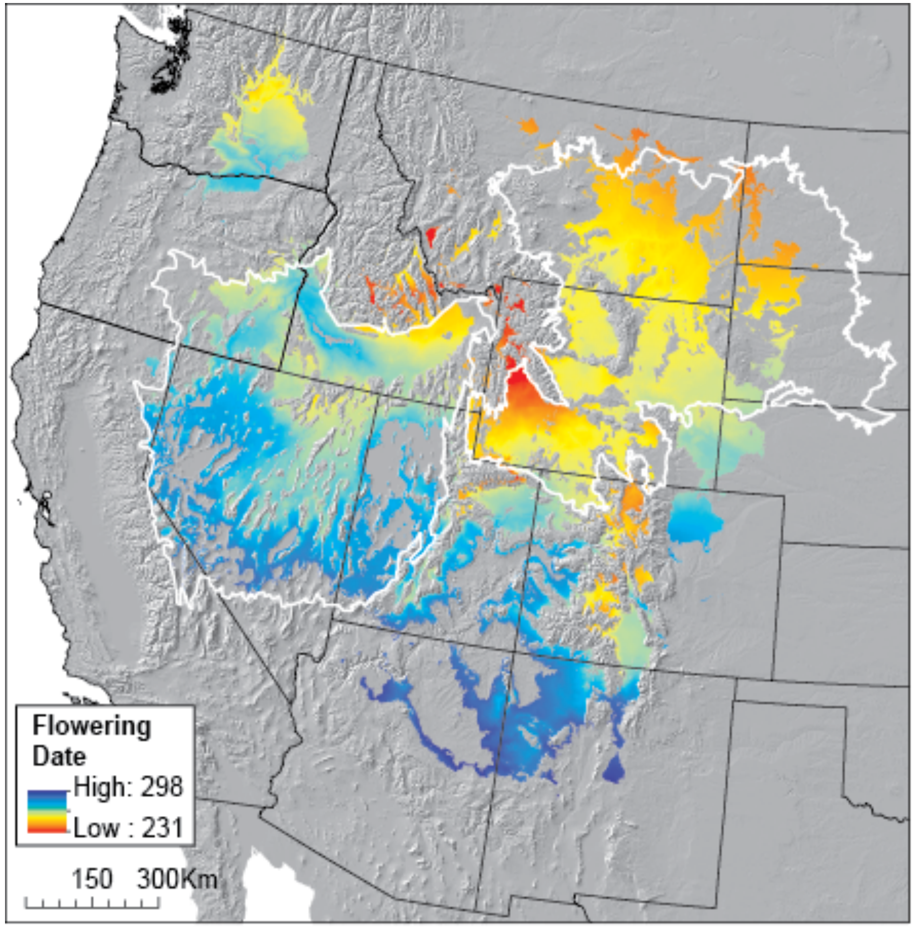
- Continentality: mtwm – mtcm
- summer precip

- Patterns support variation in cold hardiness
- The ecophysiological data also support these patterns: Lazarus et al. (in review)



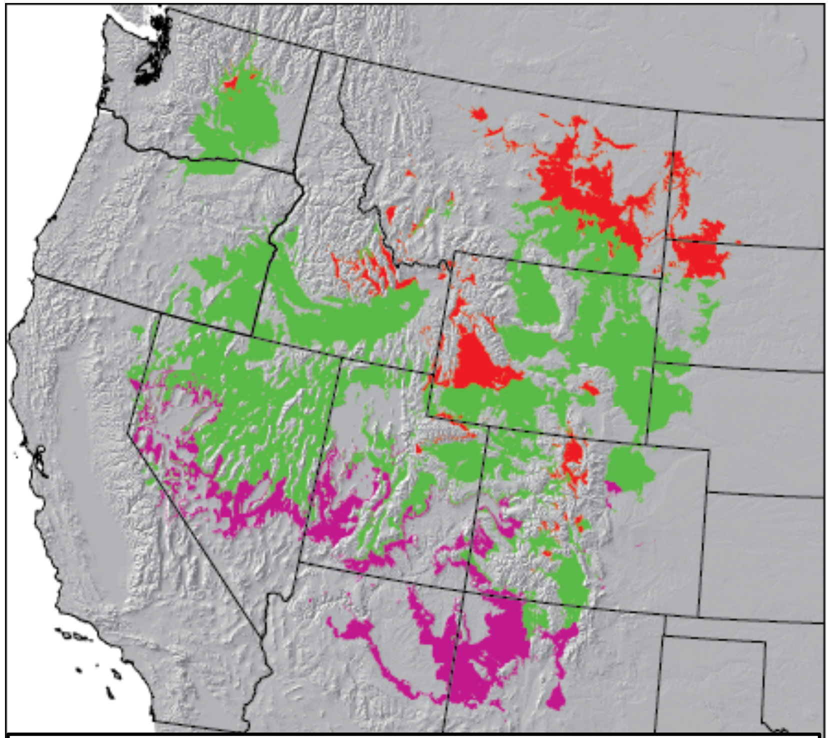
Traits: Flower phenology

- Observed flowering from July to November.
- Flower date later at lower latitudes.
- Flower date later for population with less chilling days.

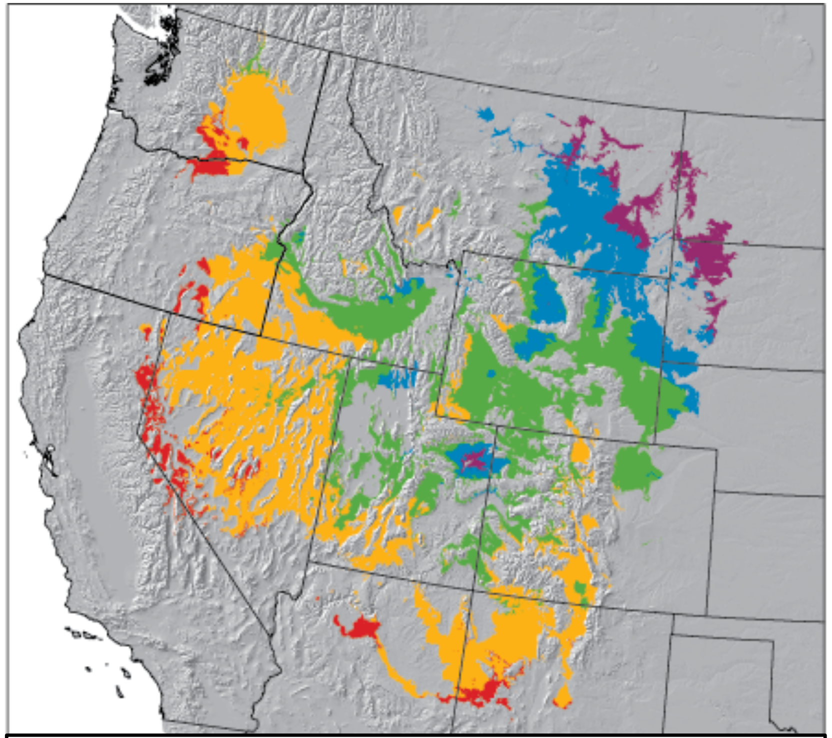


Richardson et al. 2016, Global Chang Biol.

Climatypes (climatically defined populations based on a trait)



Flower phenology, CI = +/- 10.5 days

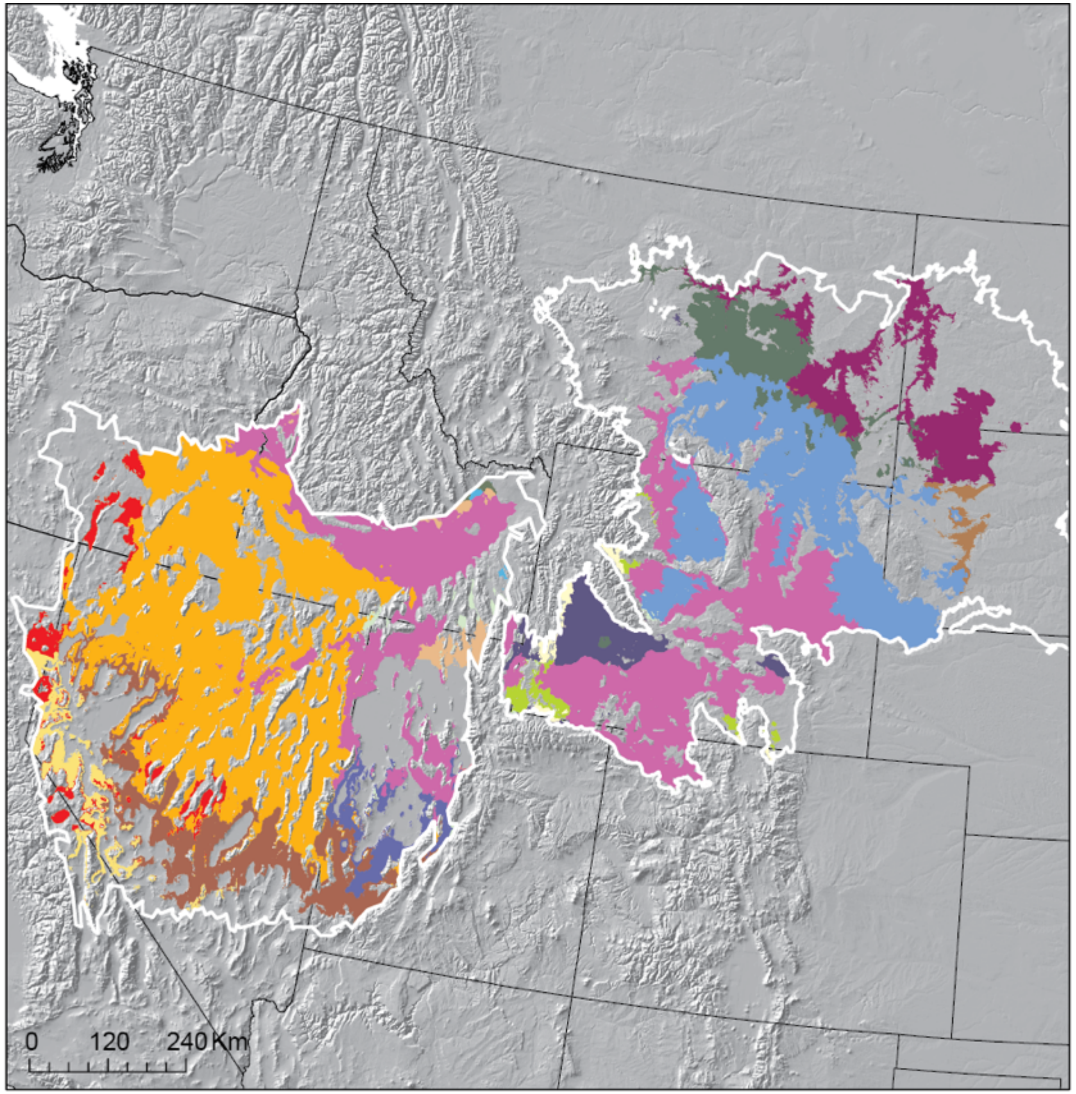


Survival, CI = +/-0.09 change

Seed transfer:
Fixed seed zones

The two trait climatypes are combined to map contemporary (1981-2010) seed zones.

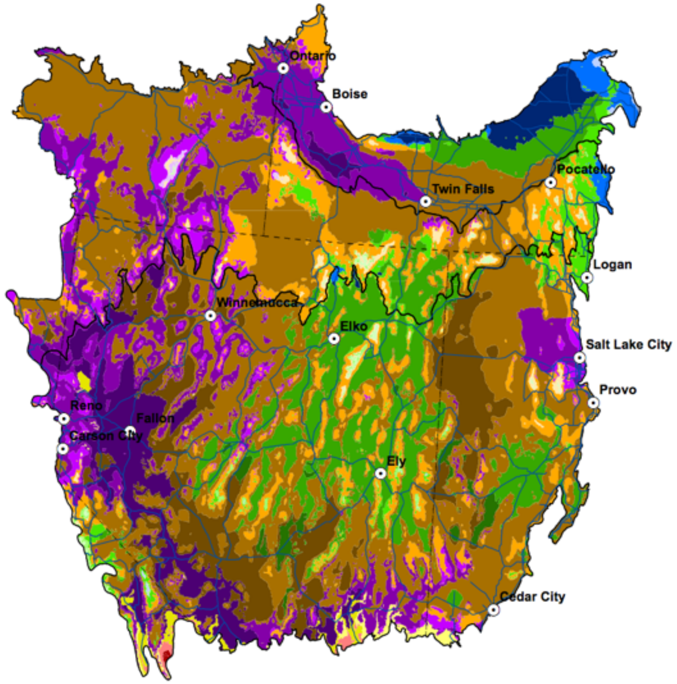
12 fixed seed zones across Great and Wyoming Basins



Richardson and Chaney 2018, Ecol. Apps.

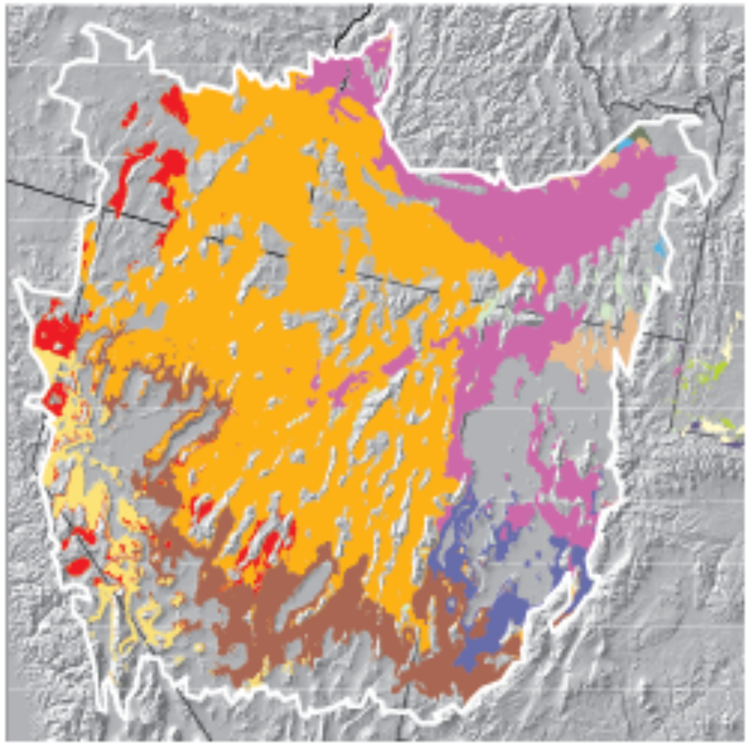
Comparison with provisional seed zones

18 PROVISIONAL SEED ZONES



MCMT x AHM

7 EMPIRICAL SEED ZONES



Focal point seed transfer

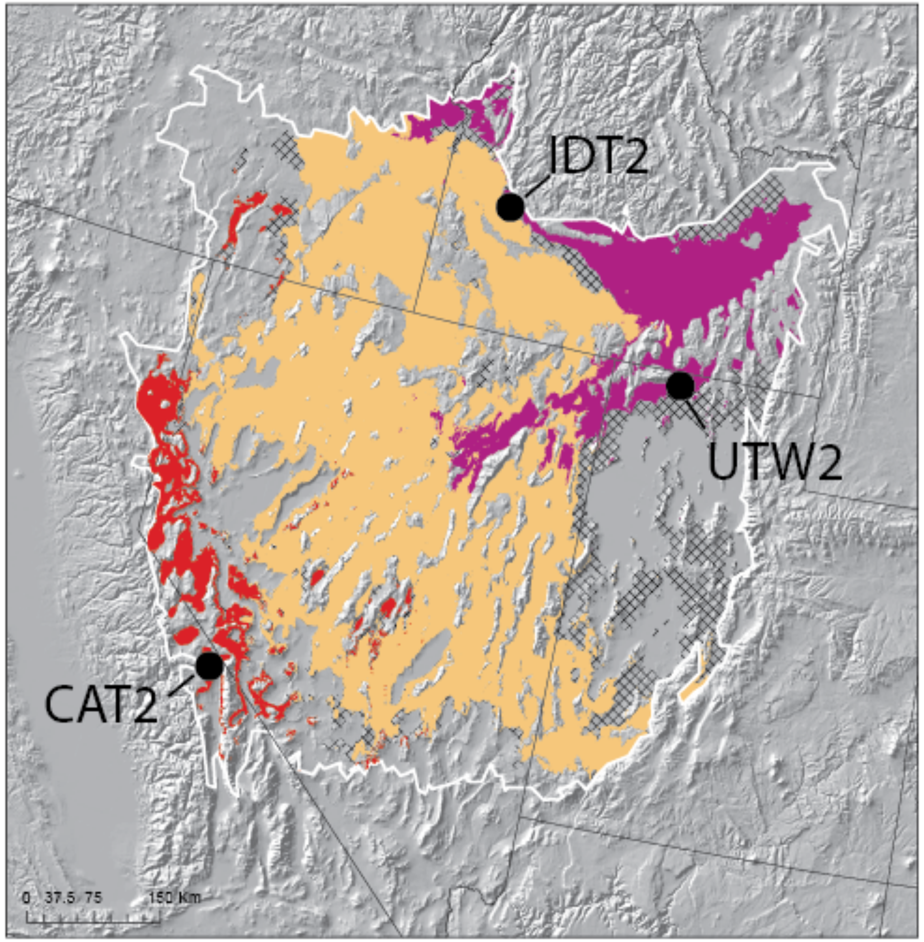
Seed transfer distances are mapped for 3 focal points (sites).

CAT2 = red

UTW2 = purple

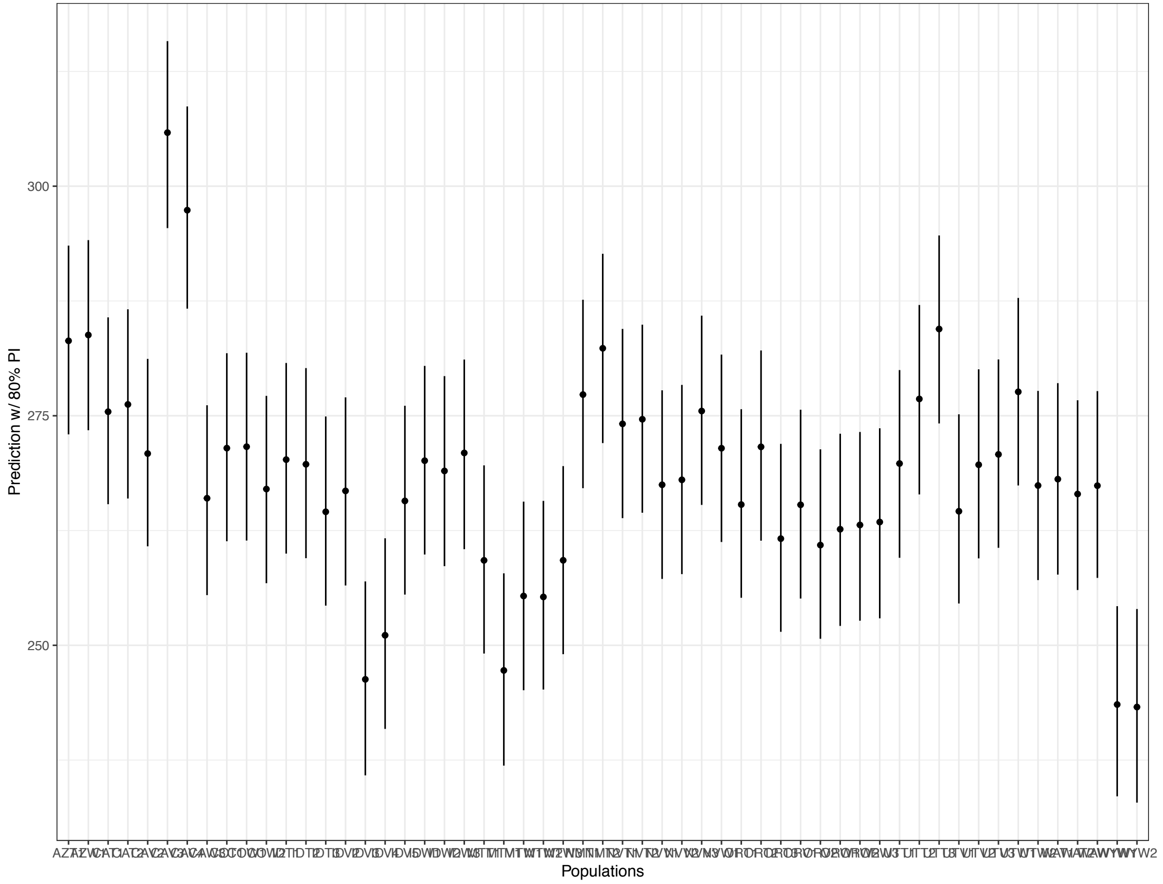
IDT2 = beige

Crosshatching = within the subspecies niche, but outside seed transfer limits.



Calculating focal point seed transfer limits in sagebrush

1. Determine the climatic value and confidence intervals for a particular site for each trait using the genecological function.
2. Map the intervals and combine the two maps to show the transfer distance.



Fixed vs. Focal Point Transfer

Fixed

Divides zones across the range of variation

Pros: Simple to use.

Cons: Not as accurate since zones are based on areas and not sites.

Complicated with climate change.

Focal

Defines seed transfer around each location

Pros: More accurate since it is mapped to the desired site.

More adaptable to climate change.

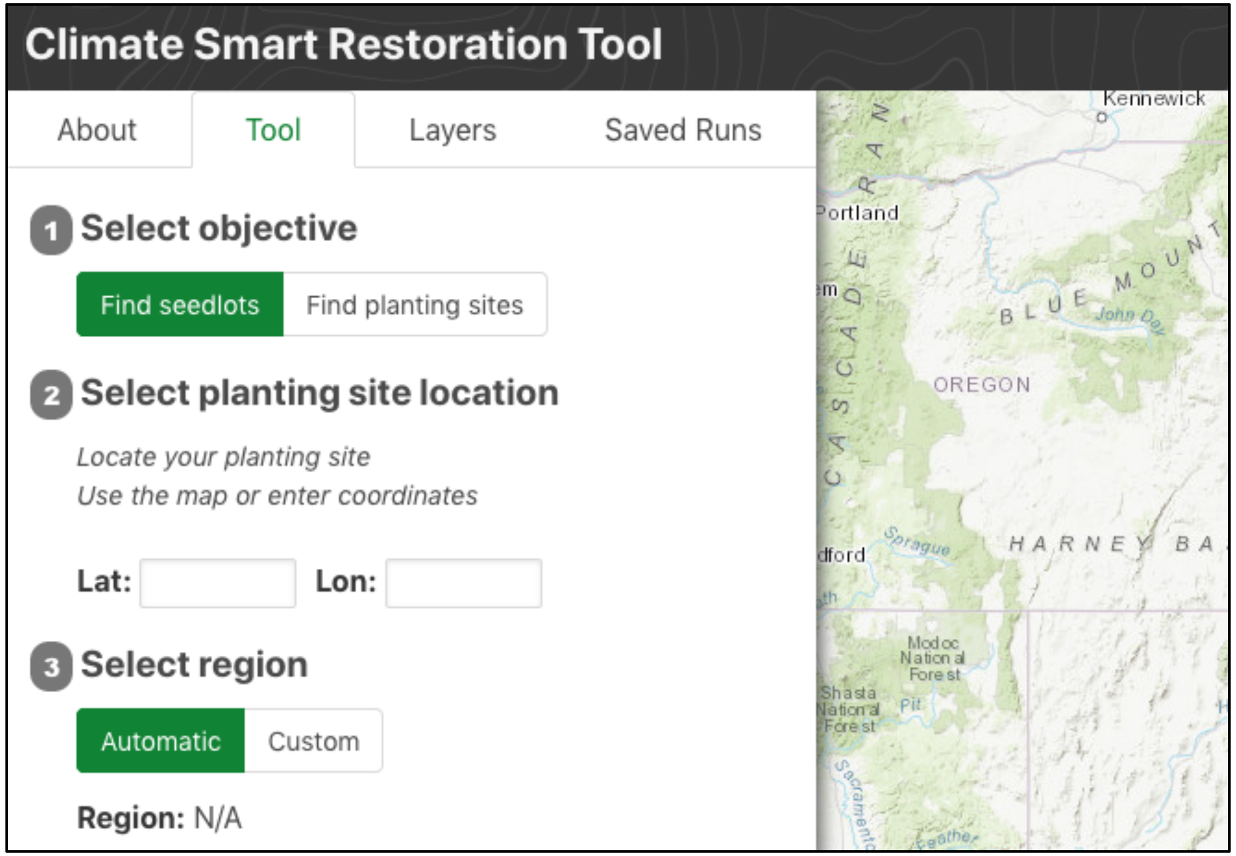
Cons: More complex to develop and map custom seed transfer limits (unless you have web program)

Climate Smart Restoration Tool (under development)

Uses the Seedlot Selection Tool framework and offers similar tools. CSRT differs in its ability to use genecological functions.

Workflow: Steps 1 to 3

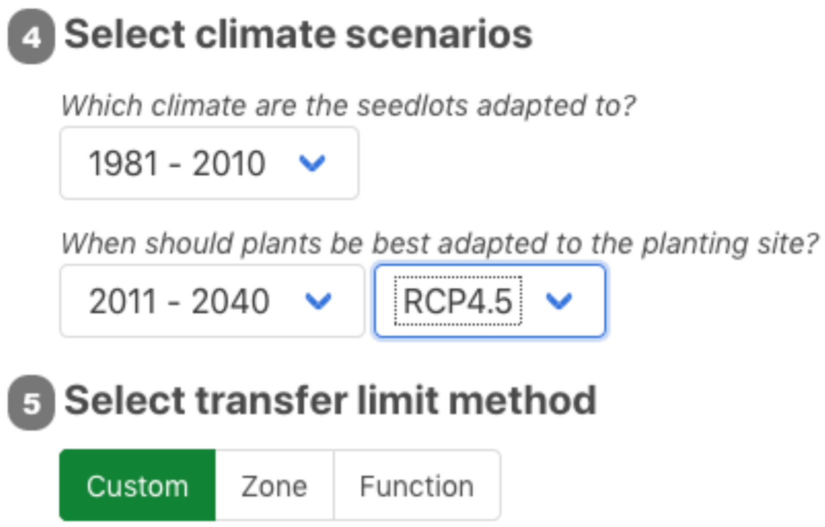
1. Select Objective
   - Seedlots or planting sites
   - Planting sites offers ability to project future climate scenarios
2. Select site
3. Select Region



CSRT

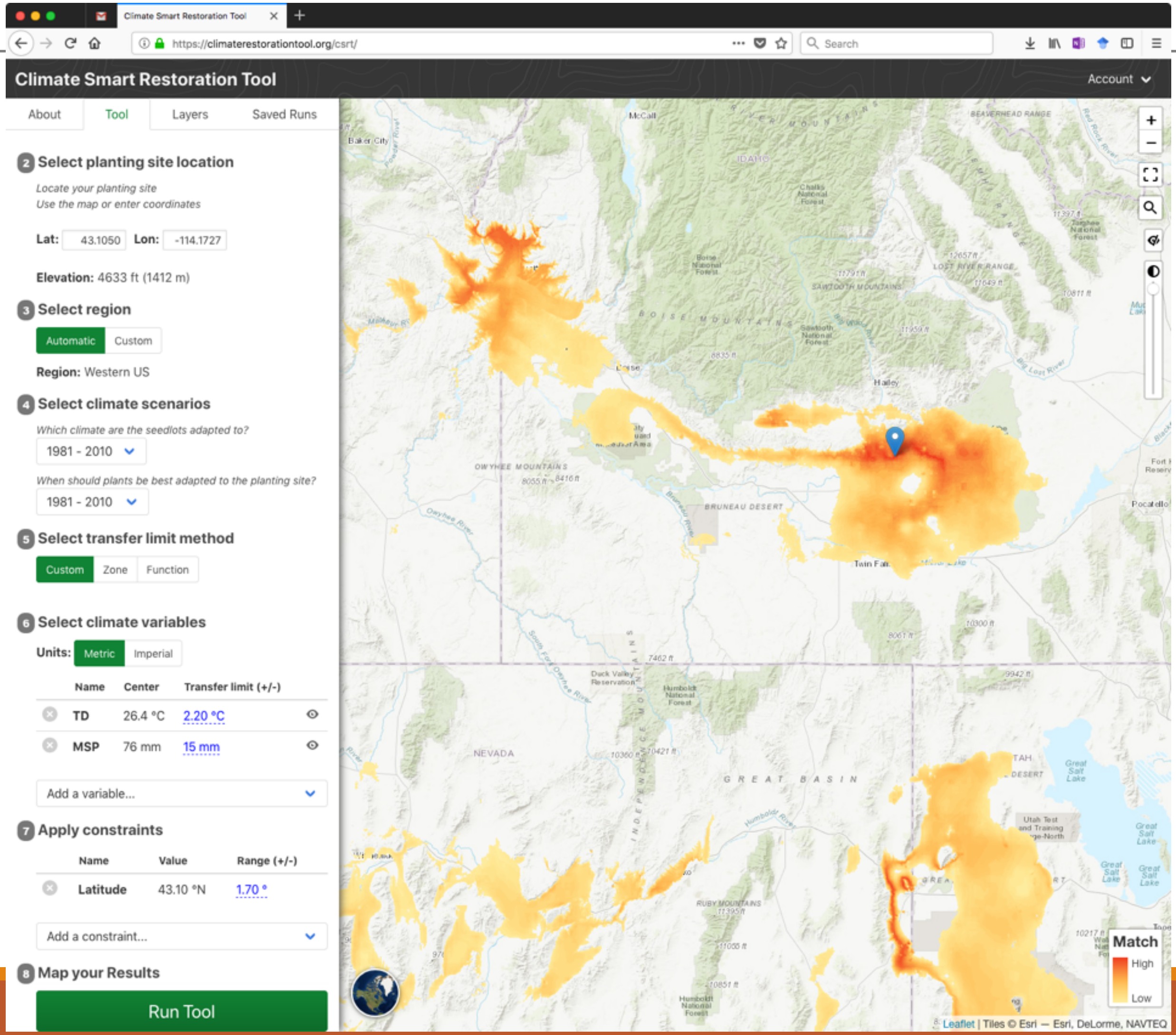
Steps 4 and 5

4. Select climate scenarios for seed collection (past, current or future)
5. Select transfer limit method:
   - Custom
   - Zone
   - Function



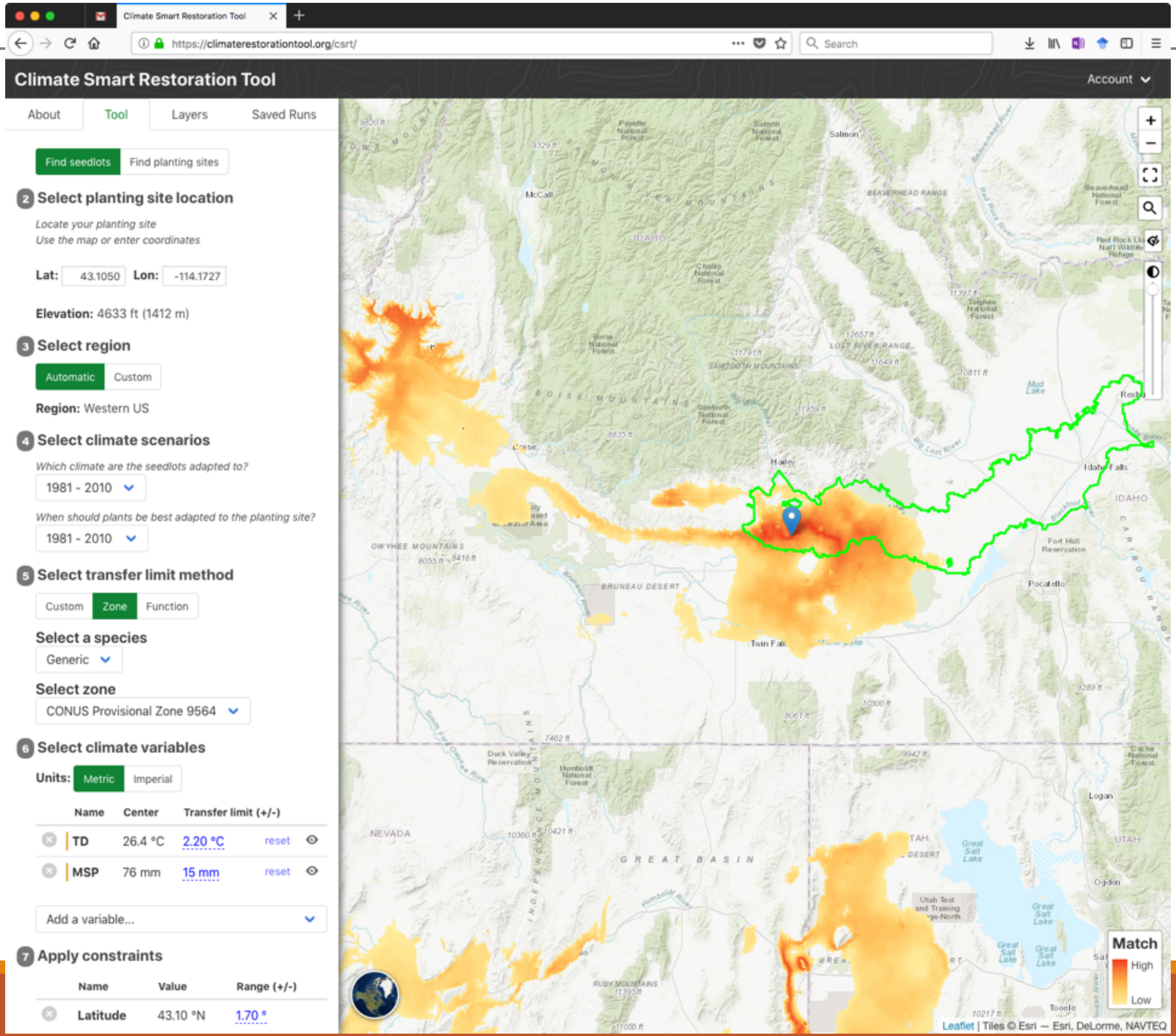
CSRT: species with no empirical data (custom)

- **Custom**: select climate variable and build your own contraints
- Zone
- Function



CSRT: species with no empirical data (custom)

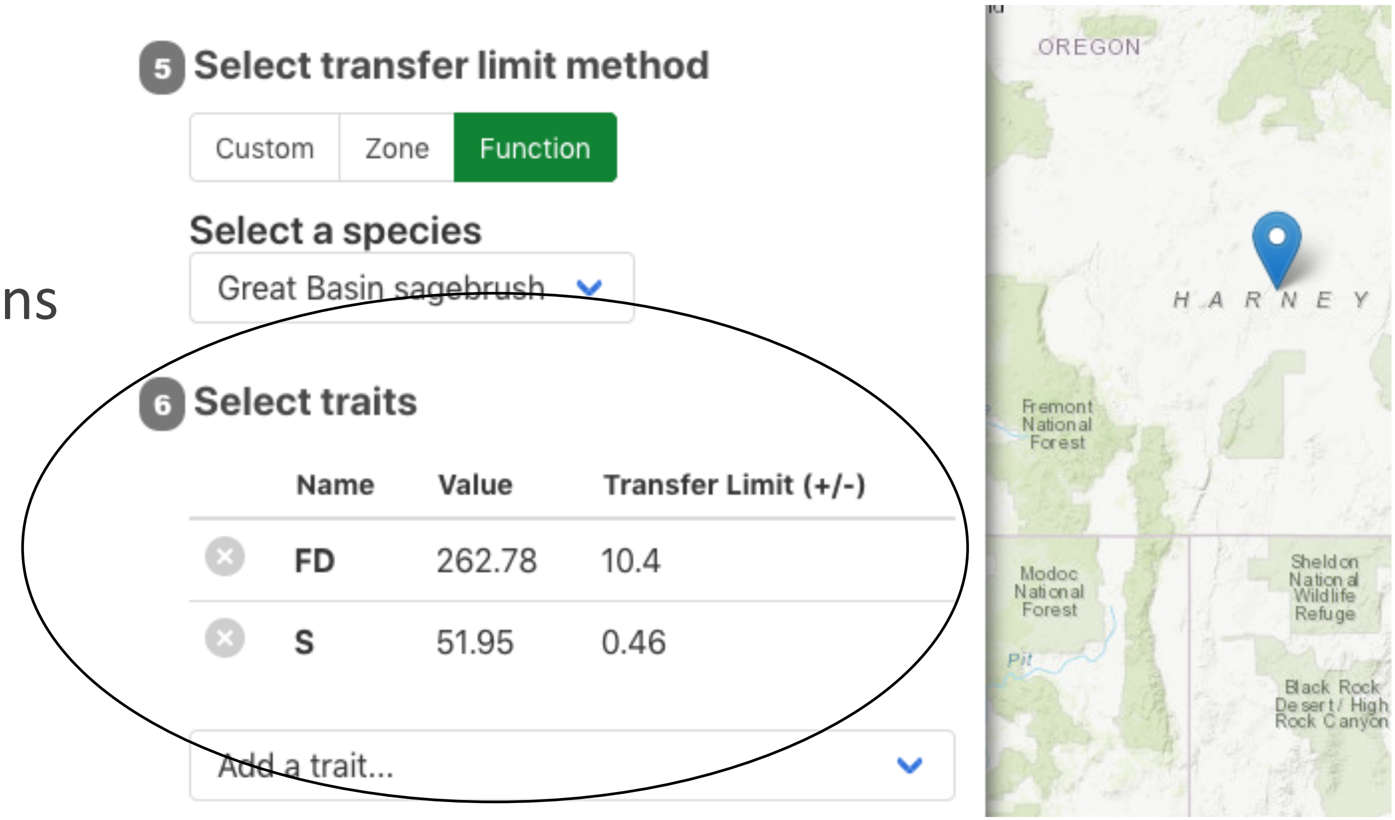
- Custom
- **Zone**: predefined constraints based on provisional seed zones
- Function



CSRT: function option for sagebrush

- Custom
- Zone
- **Function**: allows user to select predefined genecological functions

6. **Select traits**
7. Apply constraints (SDM automatically applied)
8. Map…



CSRT: function option for sagebrush

6. Select traits

7. **Apply constraints (SDM automatically applied)**

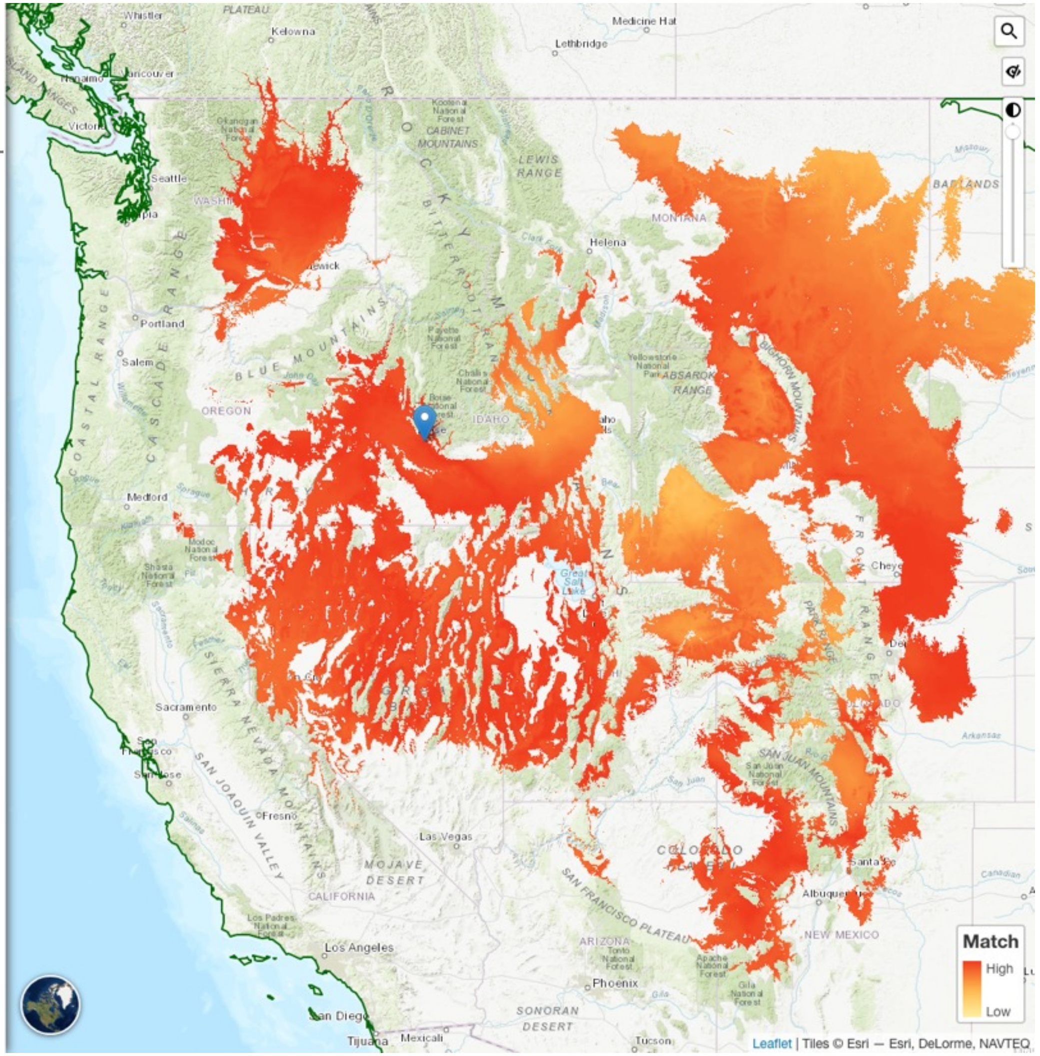
7 Apply constraints

Name	Value	Range (+/-)
Wyoming big sagebrush	1981 - 2010	

Select...

8 Map your Results

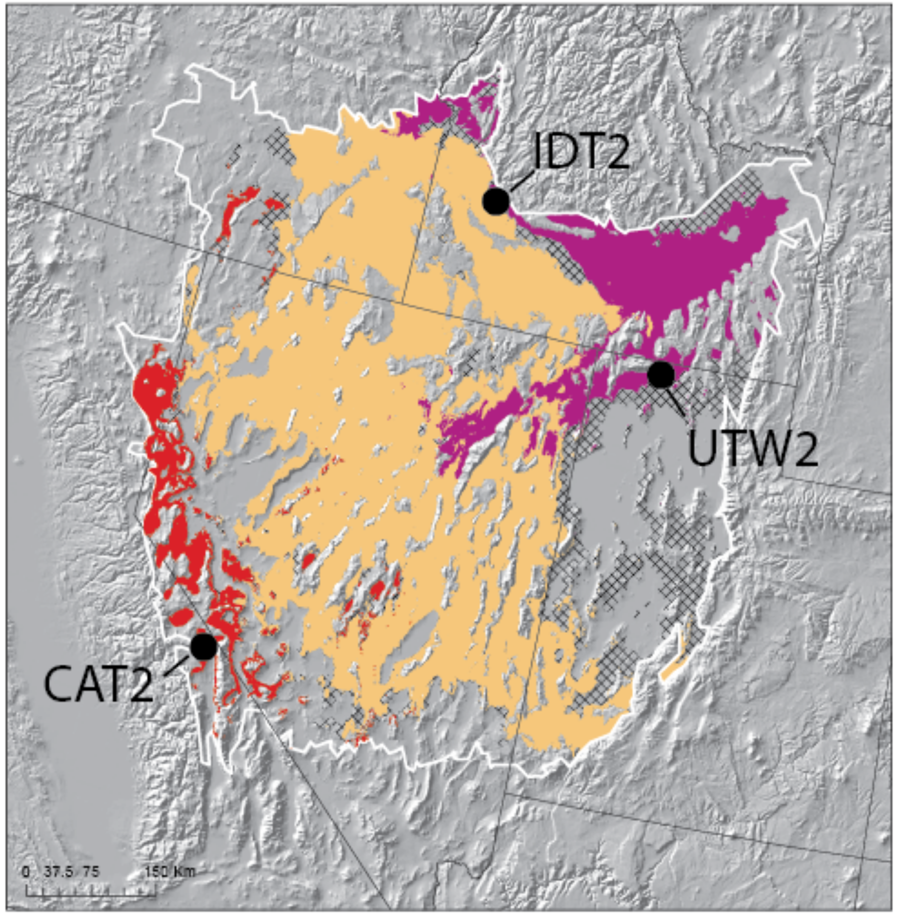
Run Tool



Focal point seed transfer: examples of use

Notify seed coordinator or vendors of where seed collection is needed based on specific sites.

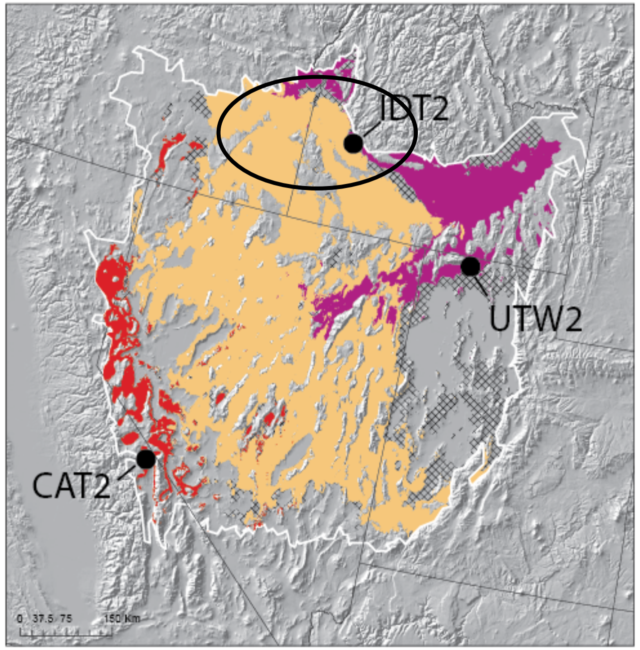
CSRT will also map a gradient related to the climatic similarity within the seed transfer area, providing more precision



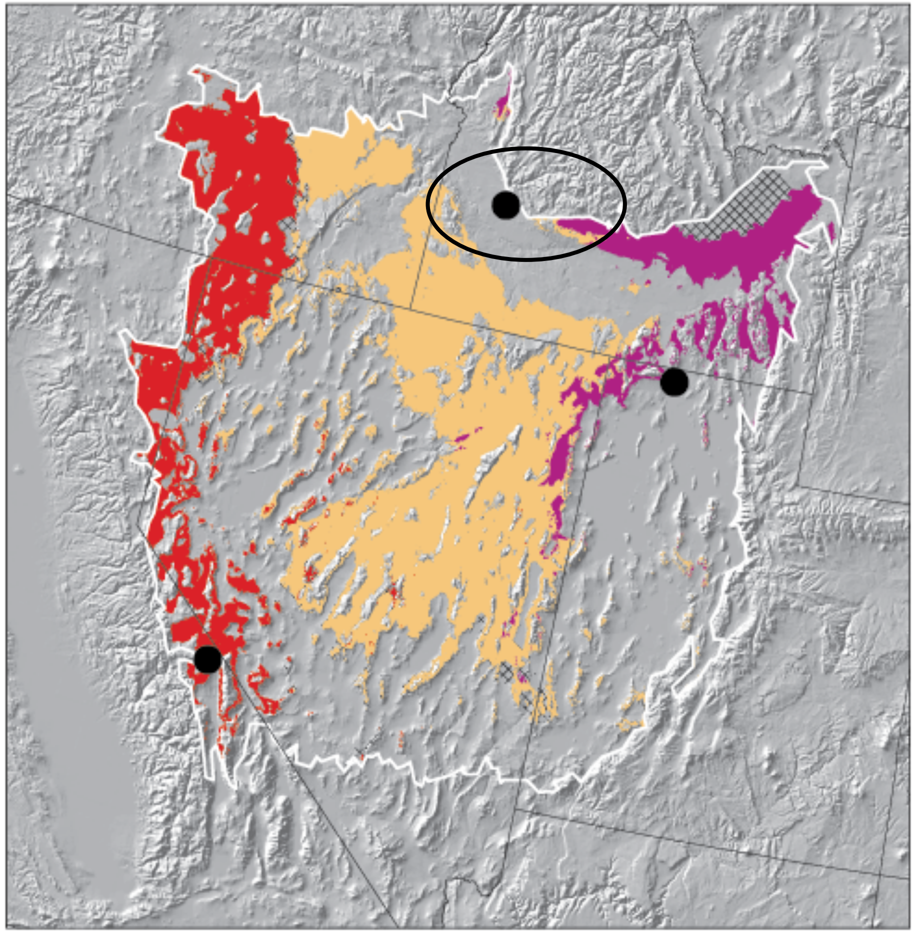
Use of change projections

Long-term strategies: look for warmer adapted spp? Rescue existing seed for elsewhere?

contemporary



2020s



Caveats

Mapping seed transfer limits work only from geographic coordinates within the SDM (Basin and Wyoming big sagebrush niche). Sites outside the SDM will be inaccurate, unless the subspecies constraint is removed.

Mountain big sagebrush: genecological functions are similar to basin and Wyoming. Working on niche model.

Other sagebrush species? Use the provisional seed zones.

Summary

It is our goal to develop a webtool that is:

- User friendly, requires minimal user input.
- Flexible, map species with empirical data (genecological functions) or species without, like the SST.
- Forward looking, having functionality to project future SDMs and seed transfer limits to mitigate climate change.

The website url: https://climaterestorationtool.org

Under development.