Population phylogenetics with the highly clonal desert moss, *Syntrichia caninervis*

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Outline

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System

Mojave Desert moss *Syntrichia caninervis*

- Small, nonvascular plant
- Extremely desiccation tolerant
- The dominant plant in some parts of the Mojave
- Also occurs in arid climates around the world

System

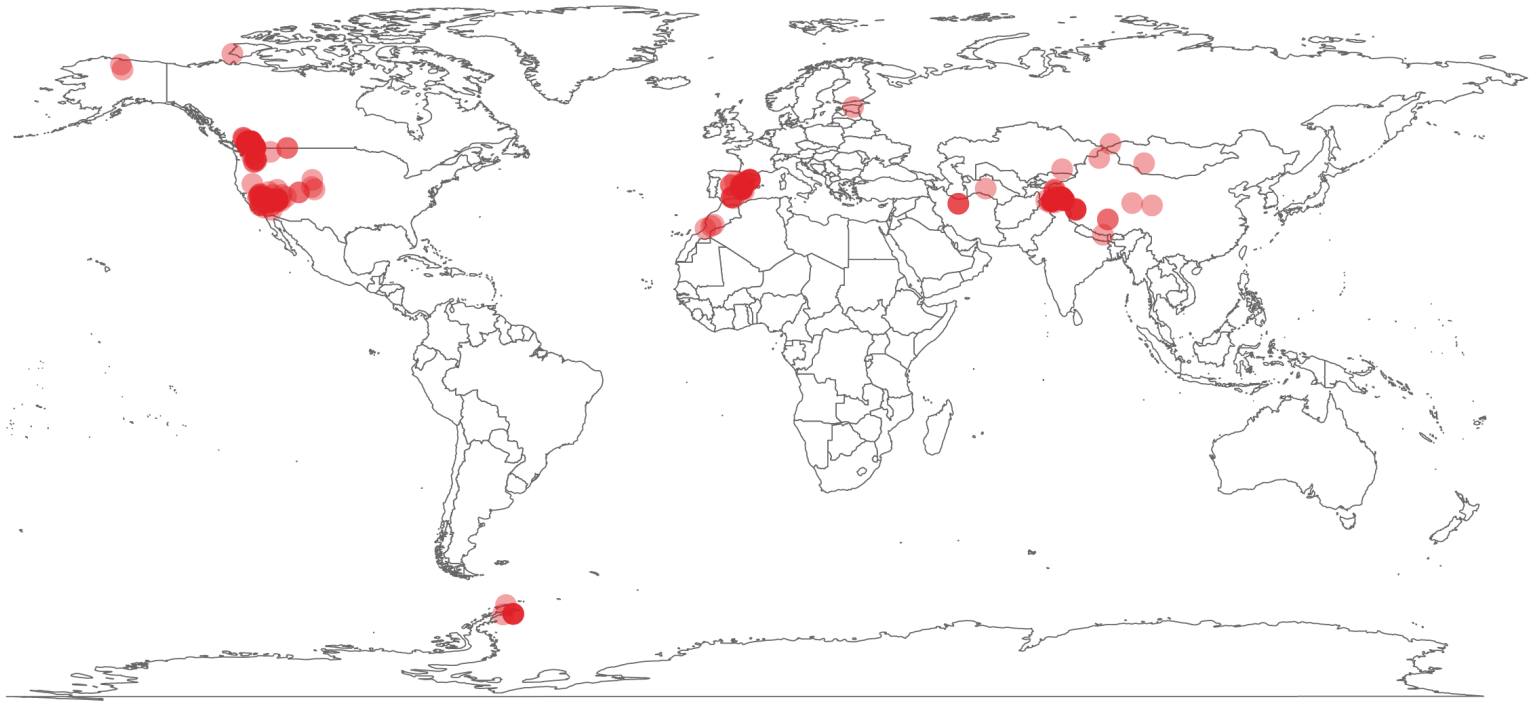


Figure 1: *S. caninervis* GBIF distribution

Research Question

Can phylogenetic methods be used with populations of a clonal organism?

Which population is "older"?

Hypotheses

- Relationships among individuals within populations will have good support values in a bifurcating tree, suggesting clonal reproduction and accumulation of mutations.
  - Low support may indicate:
    - Insufficient data
    - Past sexual reproduction and recombination
    - Gene flow
- The higher elevation population will be younger than and nested within the lower elevation population.

Sequence Data

- 131 sterile samples
  - Double-digest restriction site-associated DNA sequencing (ddRADseq); Illumina HiSeq platform
- Outgroup: *Syntrichia caninervis* transcriptome from a population in China
  - *in silico* ddRADseq

in silico ddRADseq

- Mirrored wet lab ddRADseq
  - "Digested" transcriptome with:
    - EcoRI (cuts G|AATTC)
    - MseI (cuts T|TAA)
  - Size selection; keep only fragments 250-500 bp long
  - "Sequence" (keep) only fragments that start with "AATTC"
  - Remove enzyme cut site and trim to 80 bp
- Want both strands so reverse-complement transcriptome and repeat!

Methods: Modified `Biopieces` scripts for digestion, size selection, and cut site removal. `FASTX-Toolkit` script for trimming. `BioPython` used for data cleaning and preparation. `SequenceMatrix` used to concatenate sequences.

Character Matrix

Item	Quantity
OTUs	132
Characters	136160
Informative SNPs	2492
Uninformative SNPs	133

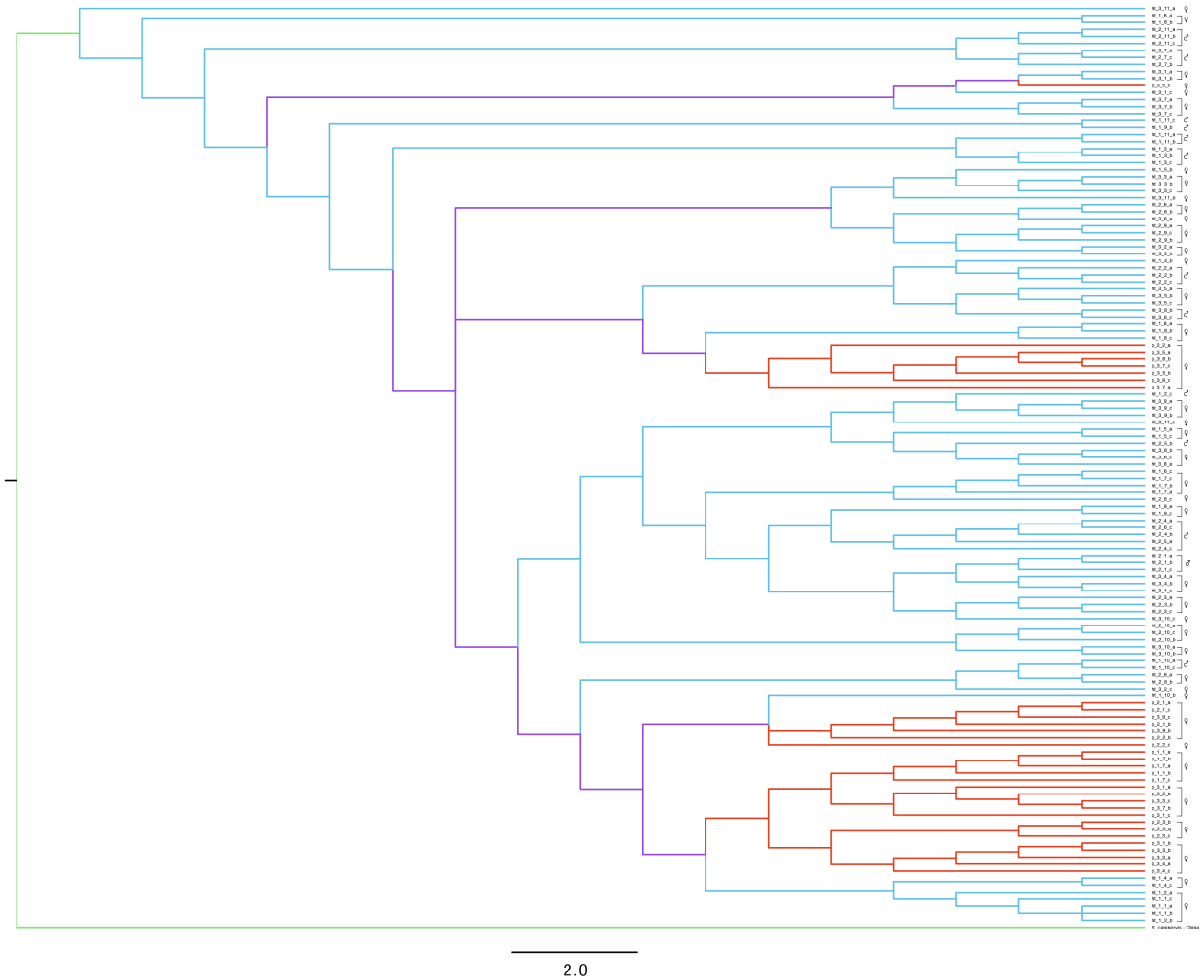
- 1702 80 bp RAD loci with 1-3 SNPs (variable nucleotides) each
  - 60 shared with *S. caninervis* transcriptome outgroup

Tree-Building

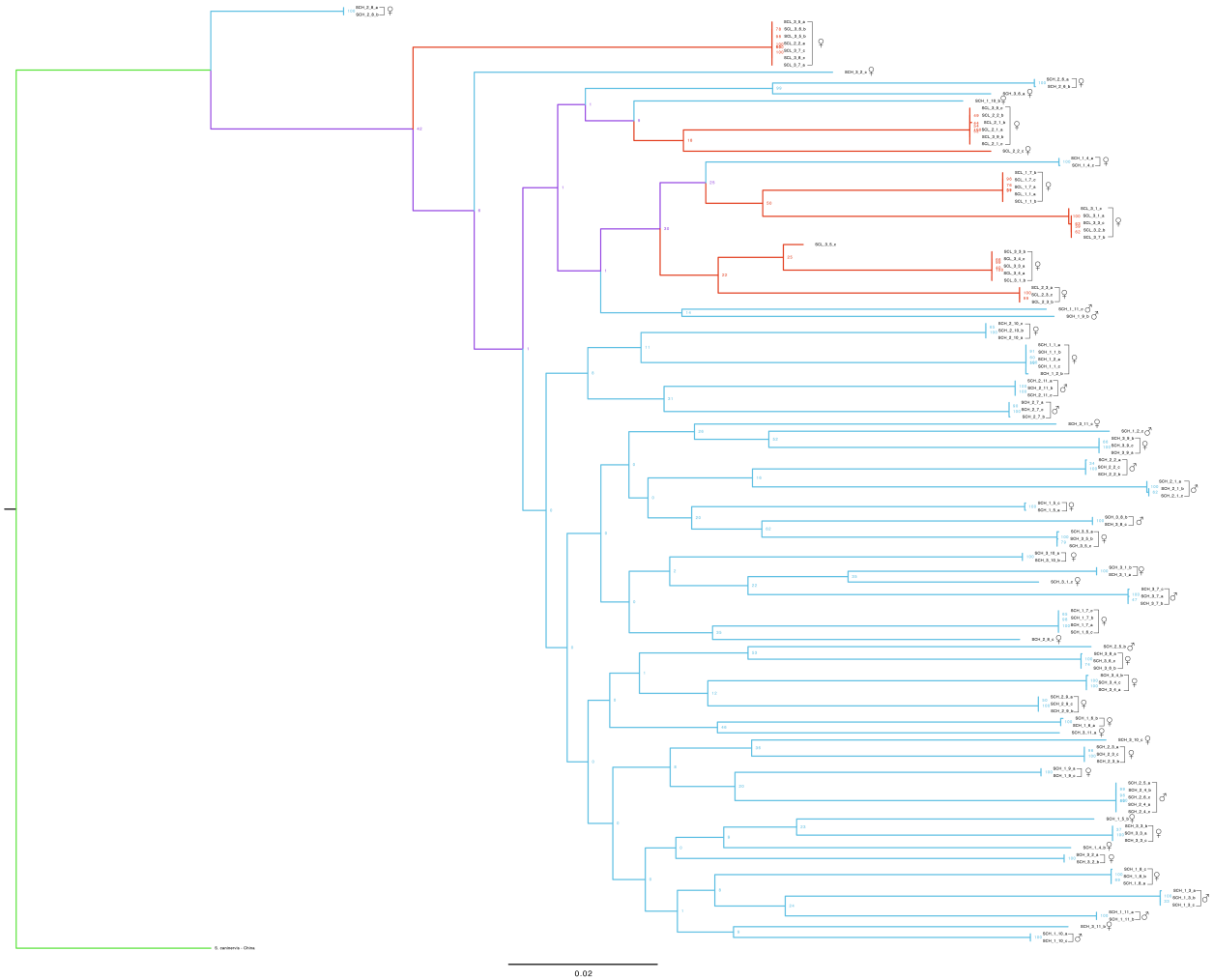
- Parsimony tree-building using Paup on Cipres Science Gateway
  - Strict consensus tree built with Paup*
- Maximum likelihood tree built with RAxML on Cipres
  - 1000 bootstraps
  - GTR GAMMA nucleotide substitution model

Parsimony Strict Consensus Tree

149 equally parsimonious trees



Maximum Likelihood Tree



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Conclusions

- High support for clades at tips; likely clones
- Lower support for relationships deeper in tree
  - May be due to past sexual reproduction
- This approach may be more suitable for more distantly related clonal populations

Next Steps

- Find out what genes the 60 expressed loci are within.
  - Are the SNPs "silent" mutations?
- `Structure`: a population genetics analysis to determine structure among populations
- `TreeMix`: a phylogenetics approach to determine the historical relationships among populations
- `Migrate`: a coalescence model to determine presence and direction of gene flow between populations

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References


THE UNIVERSITY OF CALIFORNIA BERKELEY
LET THERE BE LIGHT
1868