

California Botanic Garden, Molecular Systematics Laboratory:

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Resolving long-standing plant species taxonomic, conservation, and management problems using genomic data

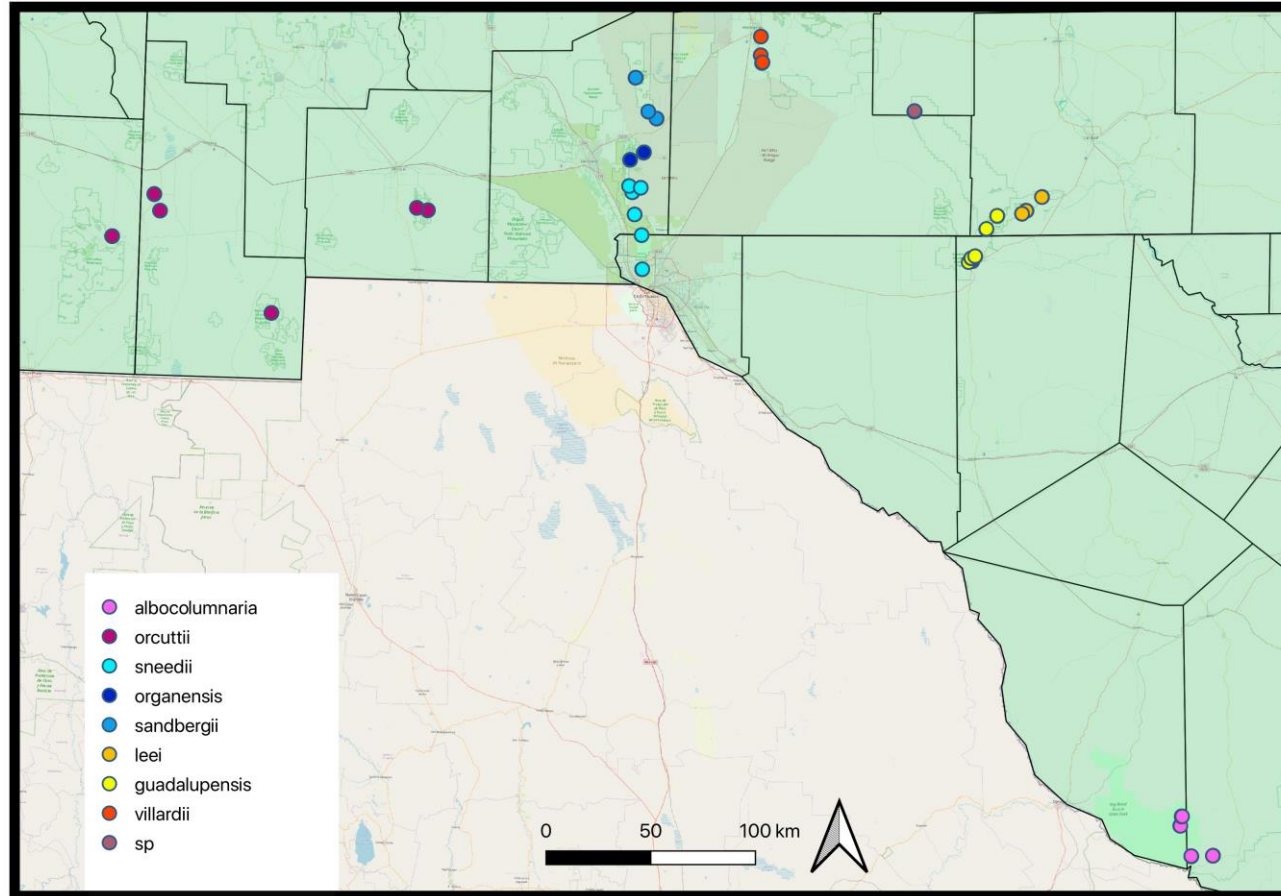
Systems under study

- *Coryphantha (Pelecyphora) sneedii* complex
- *Coryphantha robustispina*
- *Cylindropuntia x viridiflora*
- *Eriogonum gypsophyllum*
- *Eriogonum lachnogynum*

Methods

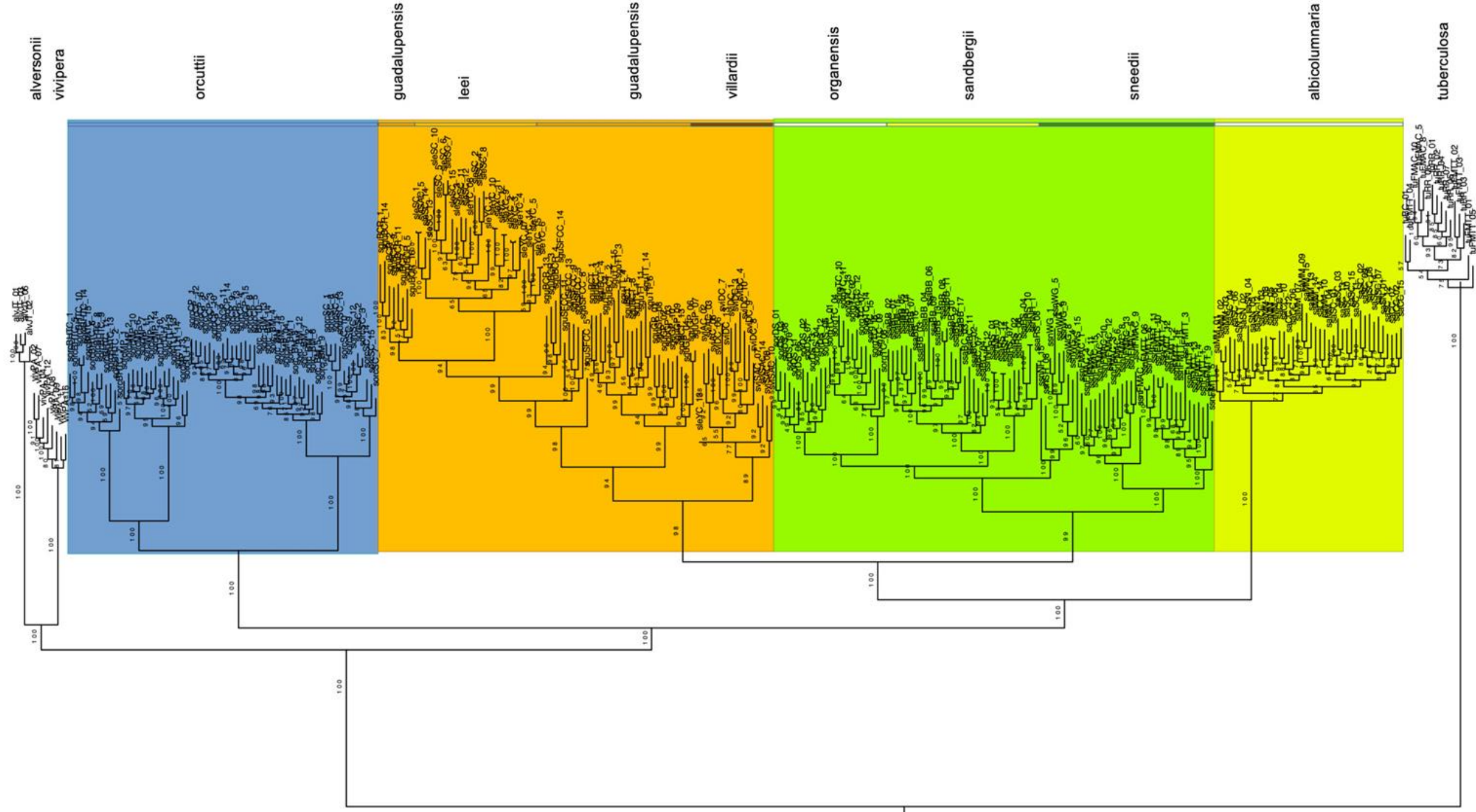
- Range-wide sampling (exclusive of Mexico)
- Double-digest restriction site associated sequencing (Miller et al. 2007)
- Assembly using iPyrad (Eaton 2014) and STACKS (Catchen et al. 2011) pipelines
- Phylogenetic and genetic analyses
 - Maximum likelihood phylogeny estimation: IQtree (Nguyen et al. 2015)
 - Ordination: discriminate analysis of principle components (dapc) (Jombart 2015)
 - Population genetic parameters, structure, AMOVA, isolation by distance

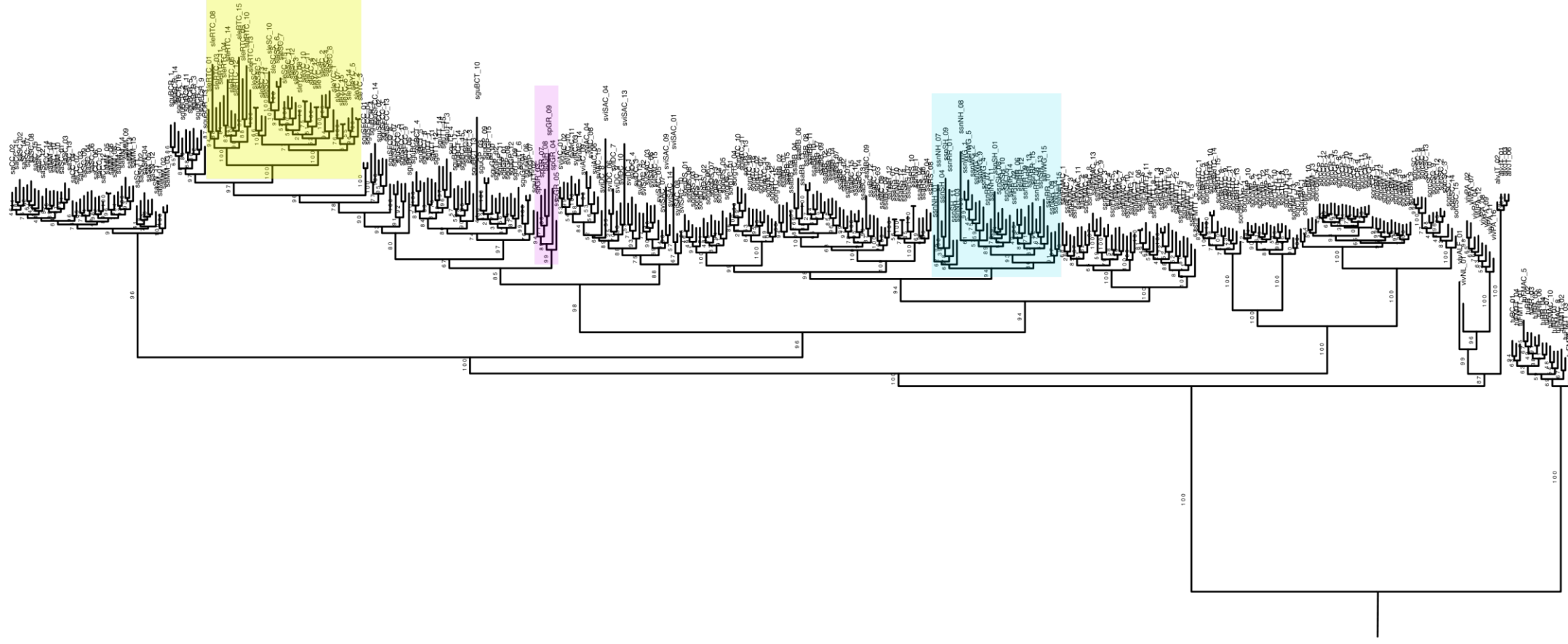
Coryphantha (Pelecyphora) sneedii complex



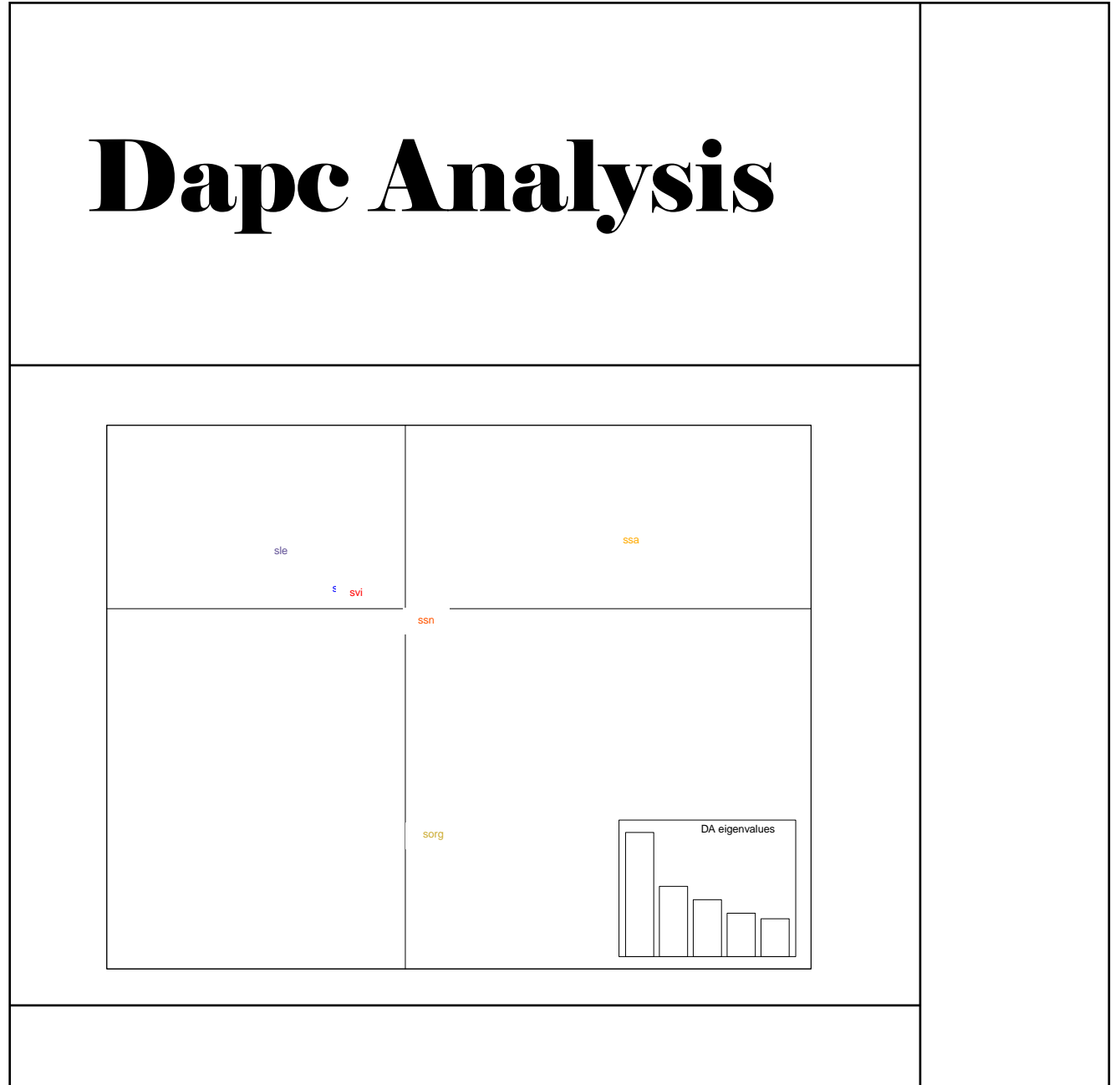
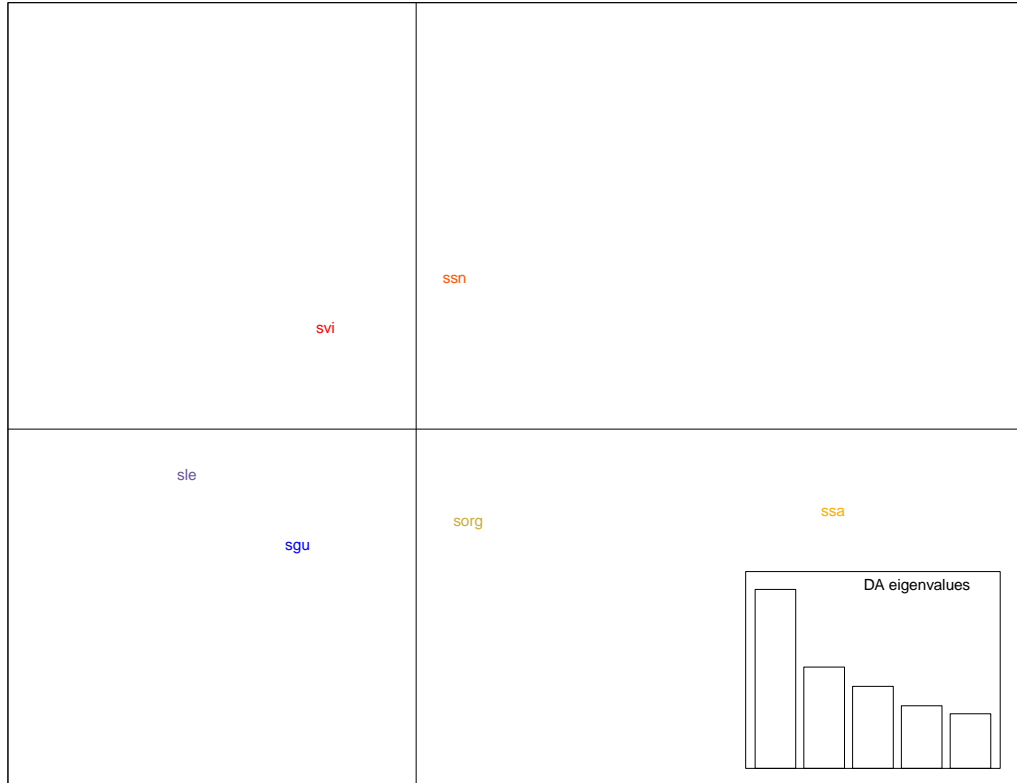
Coryphantha (Pelecyphora) *sneedii* complex: Assembly and Data Sets

- 413 individuals; 33 ingroup populations; 8 outgroup populations
- 1,588,411 loci
 - Filtered to 2,869 loci (87% of individuals possess loci) (iPyrad)
 - Filtered to 20,527 loci (50% of individuals possess loci)





Dapc Analysis



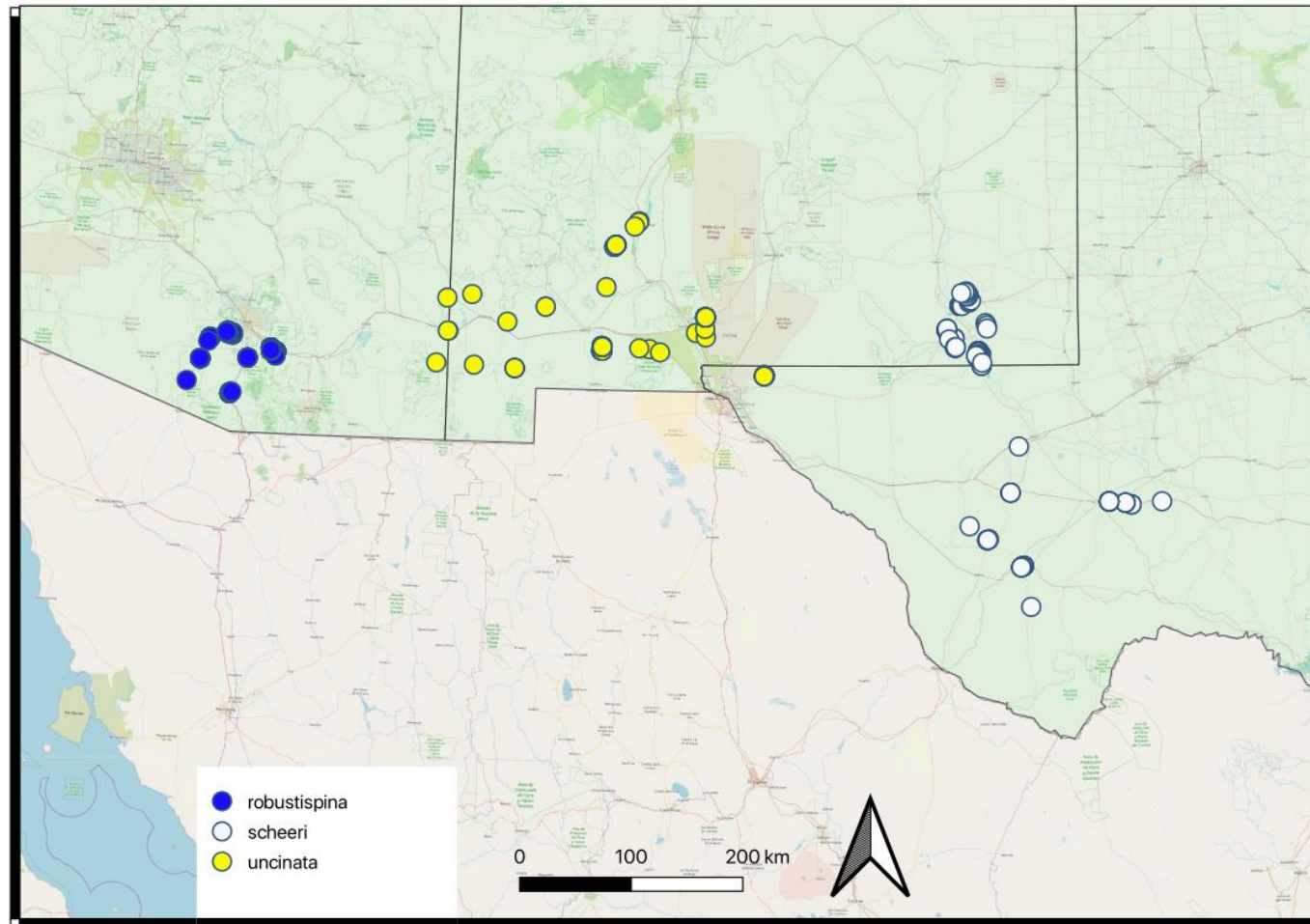
Mean population divergences (F_{ST} , Nei 1987)

	viv	alv	sa	sgu	sle	svi	sorc	ssn	sorg	ssa
alv	0.12565	NA								
sa	0.20088	0.21759	0.03166							
sgu	0.13308	0.11183	0.14995	0.05154						
sle	0.20661	0.21322	0.19082	0.09261	0.05985					
svi	0.17859	0.17543	0.19846	0.07088	0.16876	0.10753				
sorc	0.22702	0.24332	0.25265	0.18748	0.25372	0.21864	0.16601			
ssn	0.15731	0.13532	0.22695	0.10137	0.16209	0.16955	0.20535	0.13650		
sorg	0.17299	0.19872	0.19703	0.24002	0.18167	0.15170	0.23114	0.15047	0.10978	
ssa	0.20969	0.25959	0.18947	0.18531	0.18876	0.19328	0.25808	0.20782	0.07747	0.06098

Conclusions

- Our sample of the *C. sneedii* complex is composed of four geographically and phylogenetically defined lineages: Franklin-Organ-San Andreas Mtns. Lineage, Guadalupe-Sacramento Mtns. Lineage, *C. orcuttii*, and *C. albicolumnaria*.
- All of the U.S. varieties characterized by Zimmermann (1985) show significant genetic divergences and should be taxonomically recognized (contra Zimmerman and Parfitt 2003)
- There may be evidence of hybridization between *C. sneedii* var. *guadalupensis* and *C. vivipera* (currently under investigation)

Coryphantha robustispina



Genetic divergences in *C. robustispina*

F _{st}			
	COROR(13)	COROU(19)	COROS(16)
COROR(13)	0.1930839	0.37167669	0.43770114
COROU(19)		0.26683367	0.37781143
COROS(16)			0.29475701
Phi _{st}			
	COROR(13)	COROU(19)	COROS(16)
COROR(13)	0.03803297	0.35034481	0.45423949
COROU(19)		0.06252684	0.33450404
COROS(16)			0.12365971

Taxon(number of populations)

COROR= *Coryphantha robustispina* subsp *robustispina*

COROS= *Coryphantha robustispina* subsp *scheeri*

COROU= *Coryphantha robustispina* subsp *uncinata*

COROR displays the the least genetic divergence among populations.

COROU has the second lowest genetic divergence among populations.

COROS has the highest interpopulational divergence measures, much greater than the other two.

In all cases, divergences between taxa are greater that divergences within taxa