

Progress Report: Genetic Considerations for Wildland Forb and Shrub Restoration Plantings



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Are native or restored populations more variable?

Taxon	Populations		Polymorphic loci		Alleles/locus	
	N	R	N	R	N	R
Artemisia	3	2	43%	28%	1.53	1.43
Atriplex	9	3	55%	63%	1.59	1.57
Ericameria	6	2	56%	62%	1.63	1.63
Krascheninnikovia	2	1	44%	53%	1.53	1.67
Purshia	4	3	33%	40%	1.57	1.60

N = Native

R = Restored

No consistent pattern.

Genetics of Restored Populations of Intermountain Shrubs

Results for complete sets:

Usually seed source was

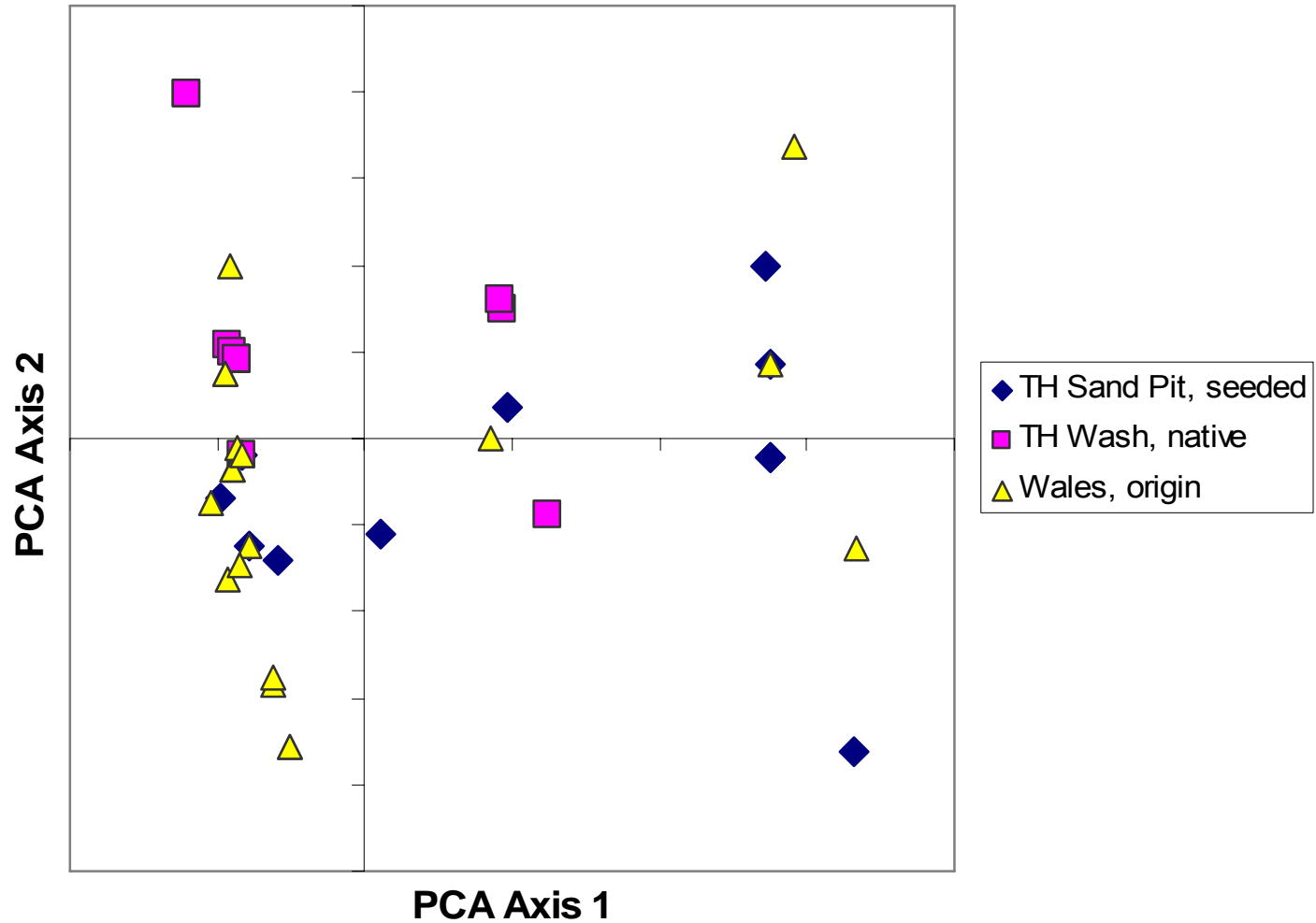
“genetically appropriate”

= similar to natives

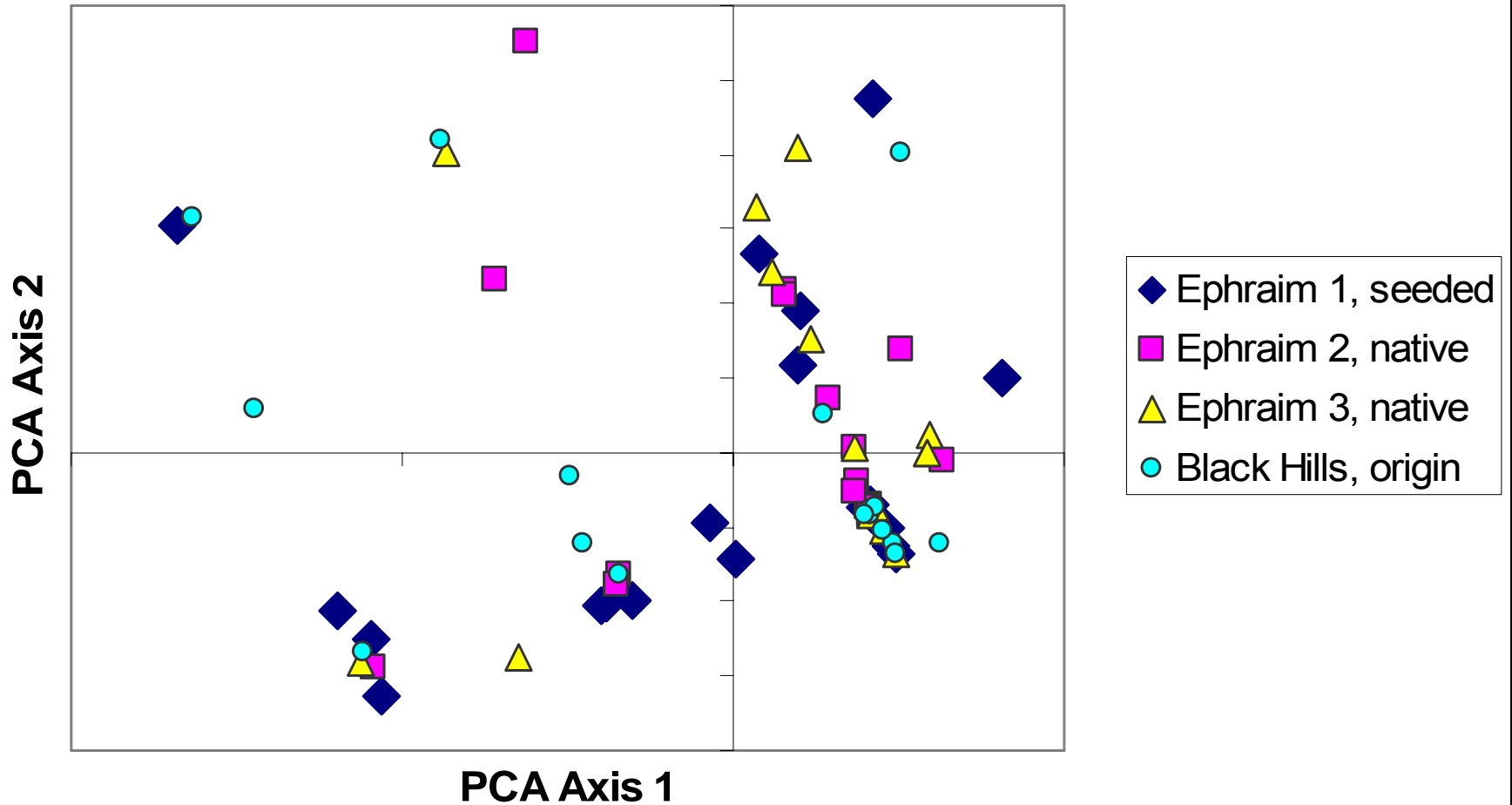
near restoration site

and the restored population was similar, too.

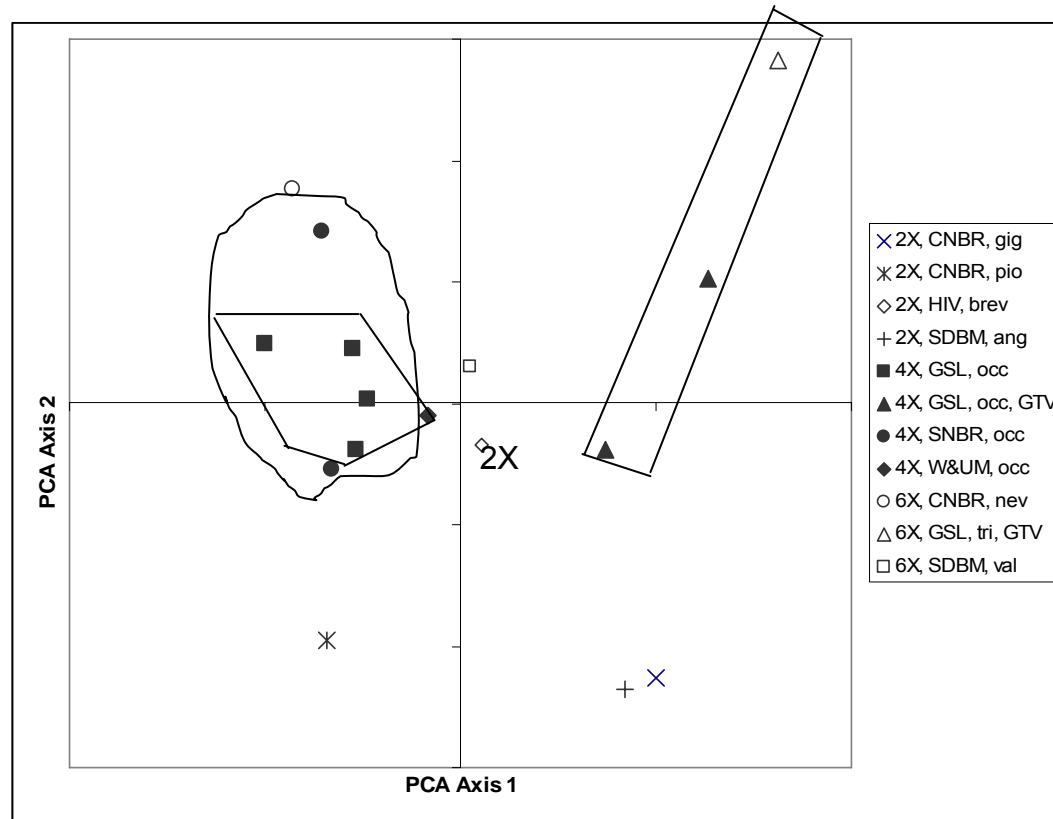
**PCA of Isozyme Alleles, *Atriplex canescens* occidentalis
restored population at Twist Hollow**



**PCA of Isozyme Alleles, *Atriplex canescens* occidentalis
restored population at Ephraim**



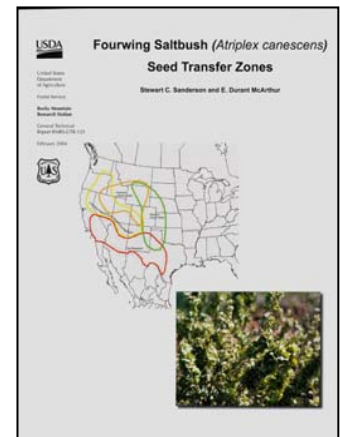
Principal Components Analysis of Genetic Distances Based on Isozymes of *Atriplex canescens* and *A. tridentata*



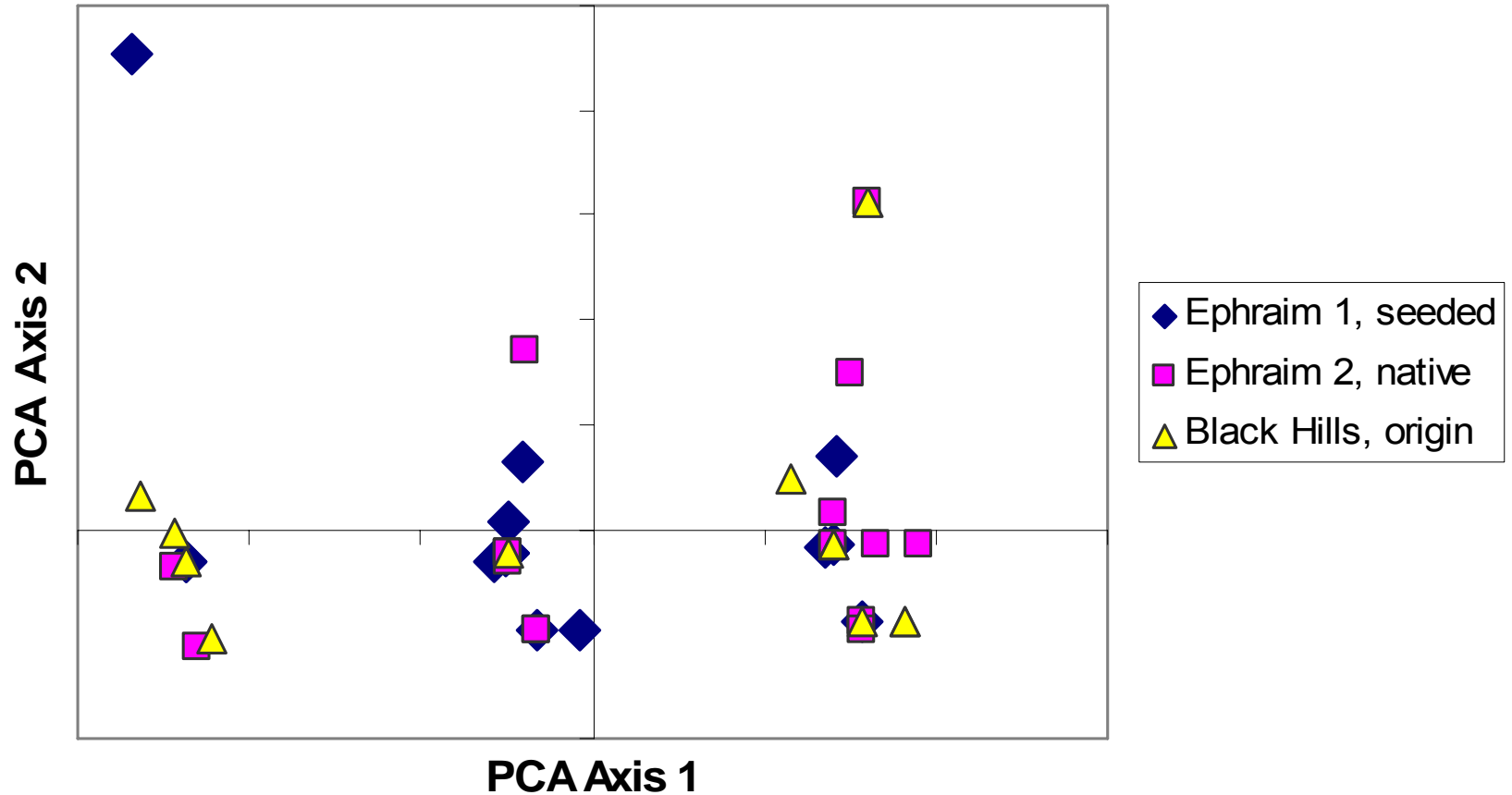
16 Populations
272 Individuals
12 Loci

Influences of PCs
Axis 1 = 57%
(Isoenzyme Frequency)
Axis 2 = 26%
(Ploidy)

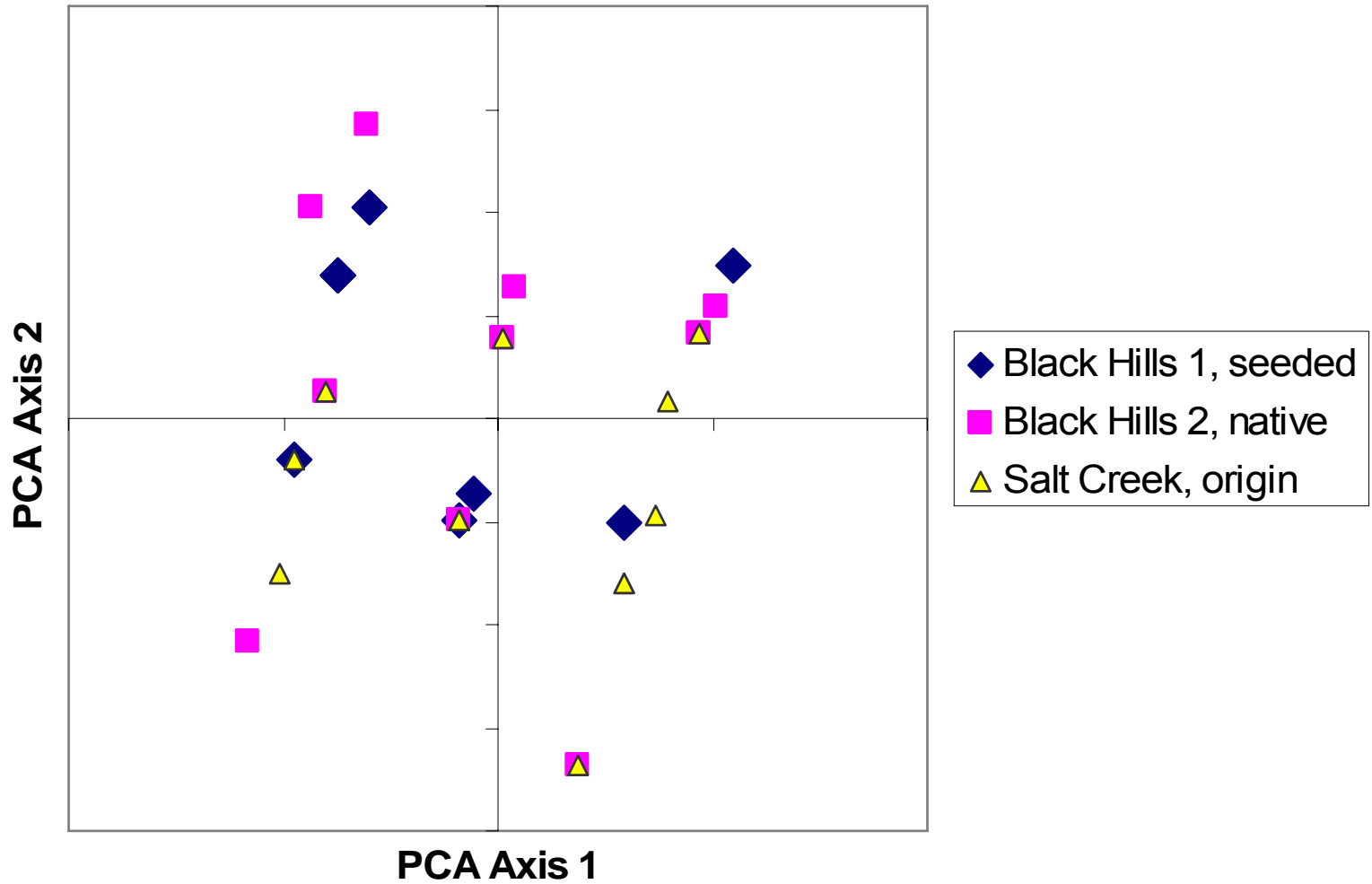
Supports Sanderson
& McArthur (2004)



PCA of Genetic Distances among individuals, *Ceratoides lanata*, restored population at Ephraim



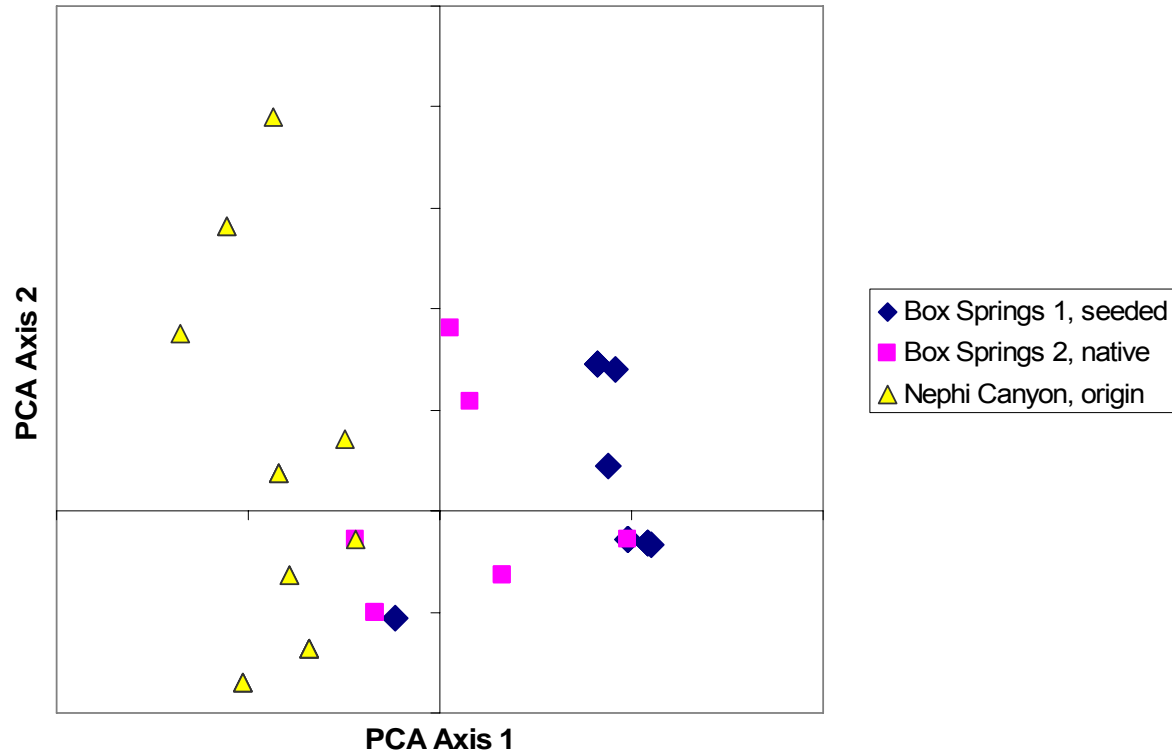
PCA of Isozyme Alleles, *Ericameria nauseosa* restored population at Black Hill



Genetics of Restored Populations of Intermountain Shrubs

Sometimes results were unexpected.

PCA of Isozyme Alleles, *Ericameria nauseosa*
restored population at Box Springs

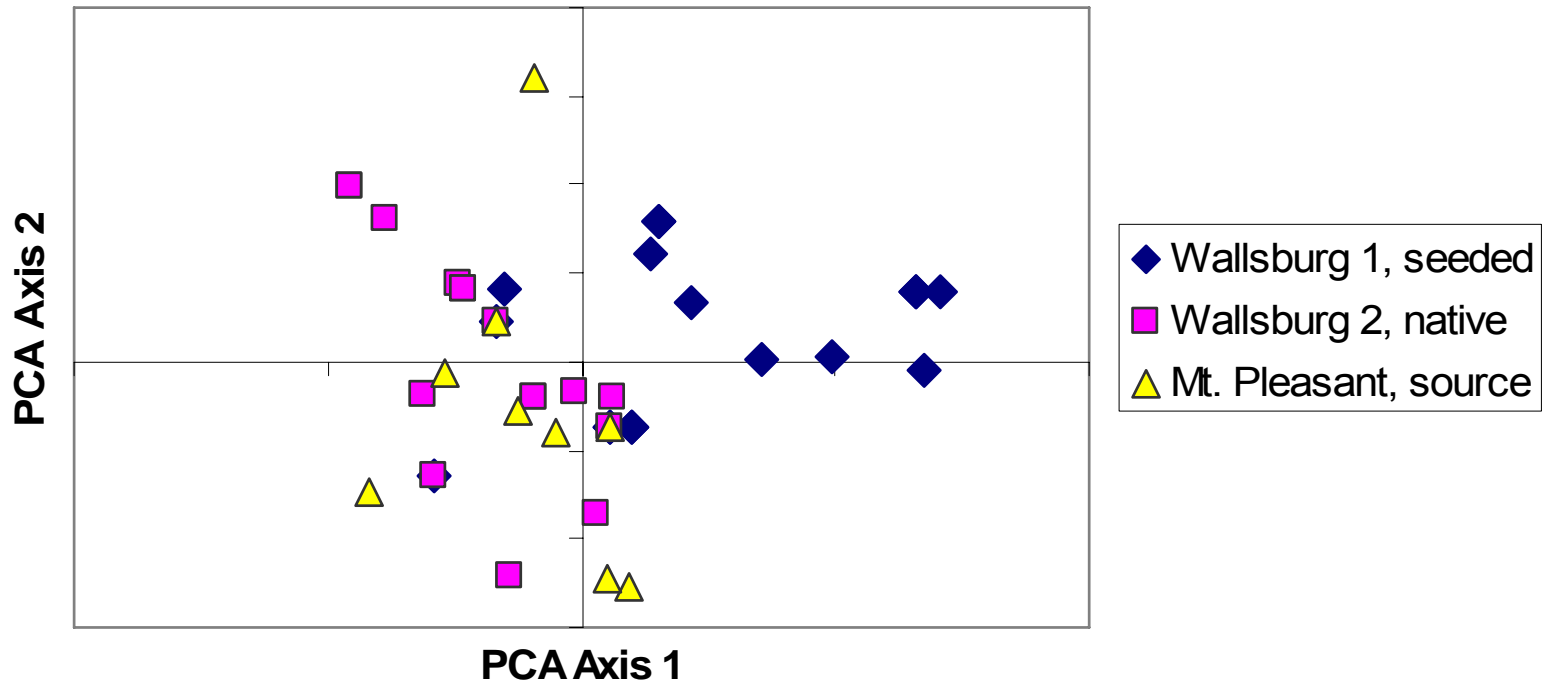


Did seeded population fail?

Was the area reseeded naturally from nearby populations?

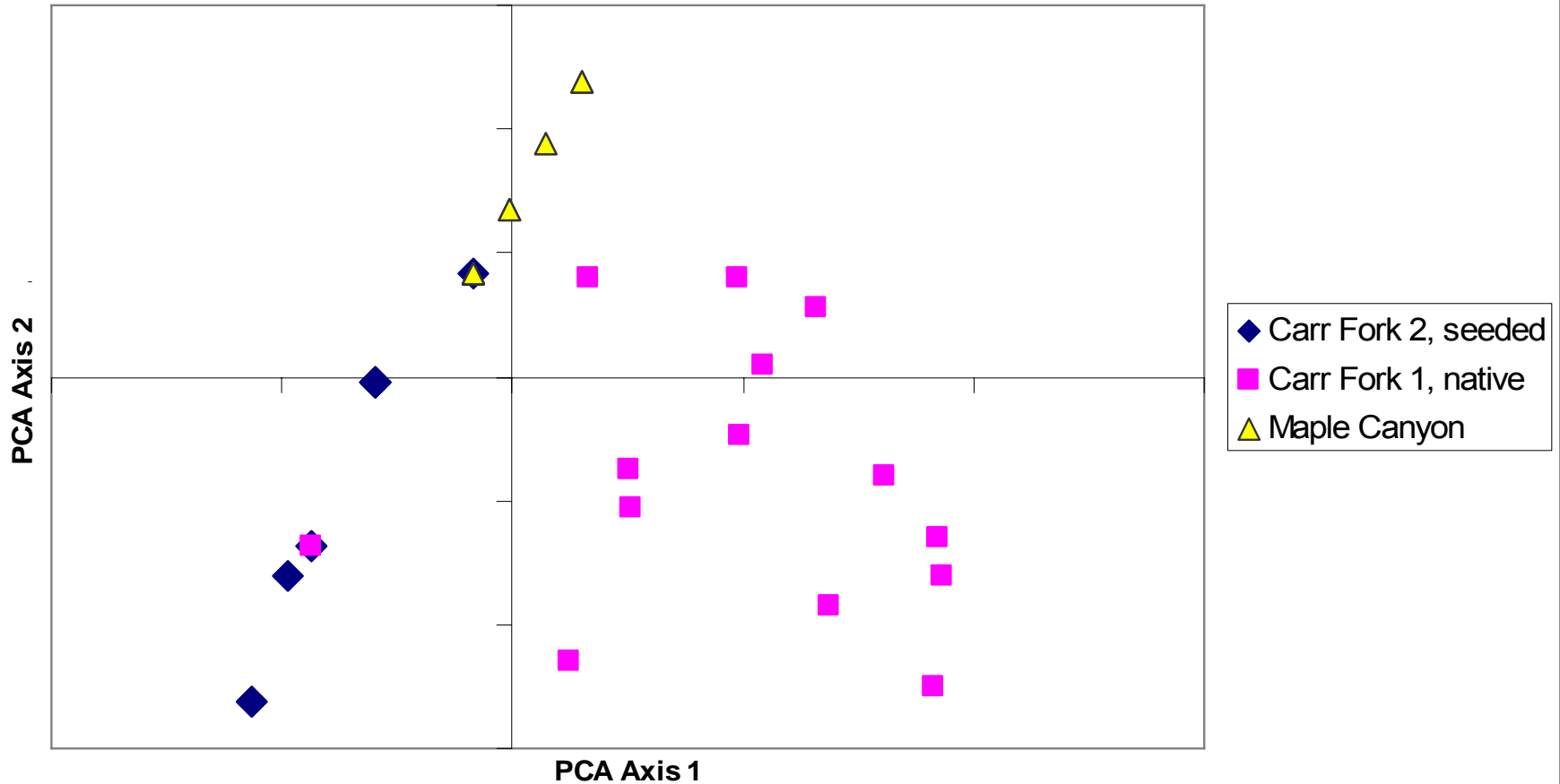
Was the area reseeded from a soil seed bank? Most likely explanation.

PCA of Genetic Distances, *Purshia tridentata*, restored population at Wallsburg Burn



Why the seeded population is so different, when the parents are similar, is unknown but it appears that that a mistake was made in the identity of the seeded population.

**PCA of Genetic Distances (Isozymes), *Artemisia tridentata*
restored population at Carr Fork**



Both Carr Fork 2 and Maple Canyon are seriously lacking in genetic variation. Inappropriate transfer? More analysis is needed.

Do Ecoregions Explain Genetic Results?

Taxon	Set	Location	Ecoregion		MLRA	
			from	to	from	to
“Genetically appropriate”			from	to	from	to
<i>Artemisia tridentata</i>	B	Carr Fork	19f	13c	GSL	GSL
<i>Atriplex canescens</i>	A	Twist Hollow	14a	14a	GSL	SNBR
<i>Atriplex canescens</i>	C	Ephraim	19d	19g	GSL	GSL
<i>Ericameria nauseosa</i>	B	Black Hills	19f	19g	GSL	GSL
<i>Krascheninnikovia lanata</i>	A	Ephraim	19d	19d	GSL	GSL
“Genetically appropriate,” but outcome questionable						
<i>Purshia tridentata</i>	A	Wallsburg Burn	19g	19g	GSL	GSL
Genetically inappropriate						
<i>Ericameria nauseosa</i>	A	Box Springs	19f	19f	GSL	CP

Species	Populations	Isozymes	AFLPs	cpDNA	Form	Family
<i>Astragalus utahensis</i>	5	5	4	5	forb	Fabaceae
<i>Balsamorhiza sagittata</i>	4	4	*	0	forb	Asteraceae
<i>Crepis acuminata</i>	5	5	2	5	forb	Asteraceae
<i>Crepis occidentalis</i>	1	1	1	1	forb	Asteraceae
<i>Erigeron pumilus</i>	8	7	5	7**	forb	Asteraceae
<i>Eriogonum umbellatum</i>	7	4	4	7	forb	Polygonaceae
<i>Eriogonum heracleoides</i>	1	1	1	1	forb	Polygonaceae
<i>Eriogonum ovalifolium</i>	2	2	1	2	forb	Polygonaceae
<i>Heliomeris multiflora</i>	6	6	2	0	forb	Asteraceae
<i>Lathyrus brachycalyx</i>	2	2	2	2	forb	Fabaceae
<i>Lomatium dissectum</i>	3	3	*	*	forb	Apiaceae
<i>Lomatium grayii</i>	2	2	*	*	forb	Apiaceae
<i>Lupinus argenteus/sericeus</i>	8	8	4	8	forb	Fabaceae
<i>Penstemon acuminatus</i>	1	1	*	*	forb	Scrophulariaceae
<i>Penstemon deustus</i>	2	0	*	*	forb	Scrophulariaceae
<i>Penstemon speciosus</i>	2	2	*	*	forb	Scrophulariaceae
<i>Phlox longifolia</i>	3	3	*	*	forb	Polemoniaceae
<i>Tragopogon dubius</i>	3	3	*	*	forb	Asteraceae
<i>Vicia americana</i>	6	6	6	6	forb	Fabaceae

Long-styled 'Appar"
Linum perenne



Short-styled 'Appar"
Linum perenne

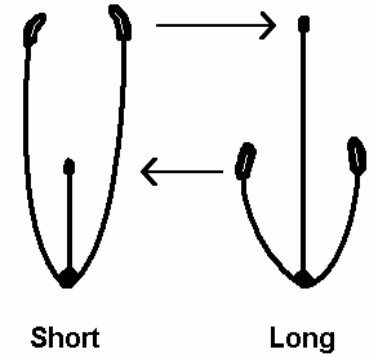


Long-styled Native
Linum lewisii

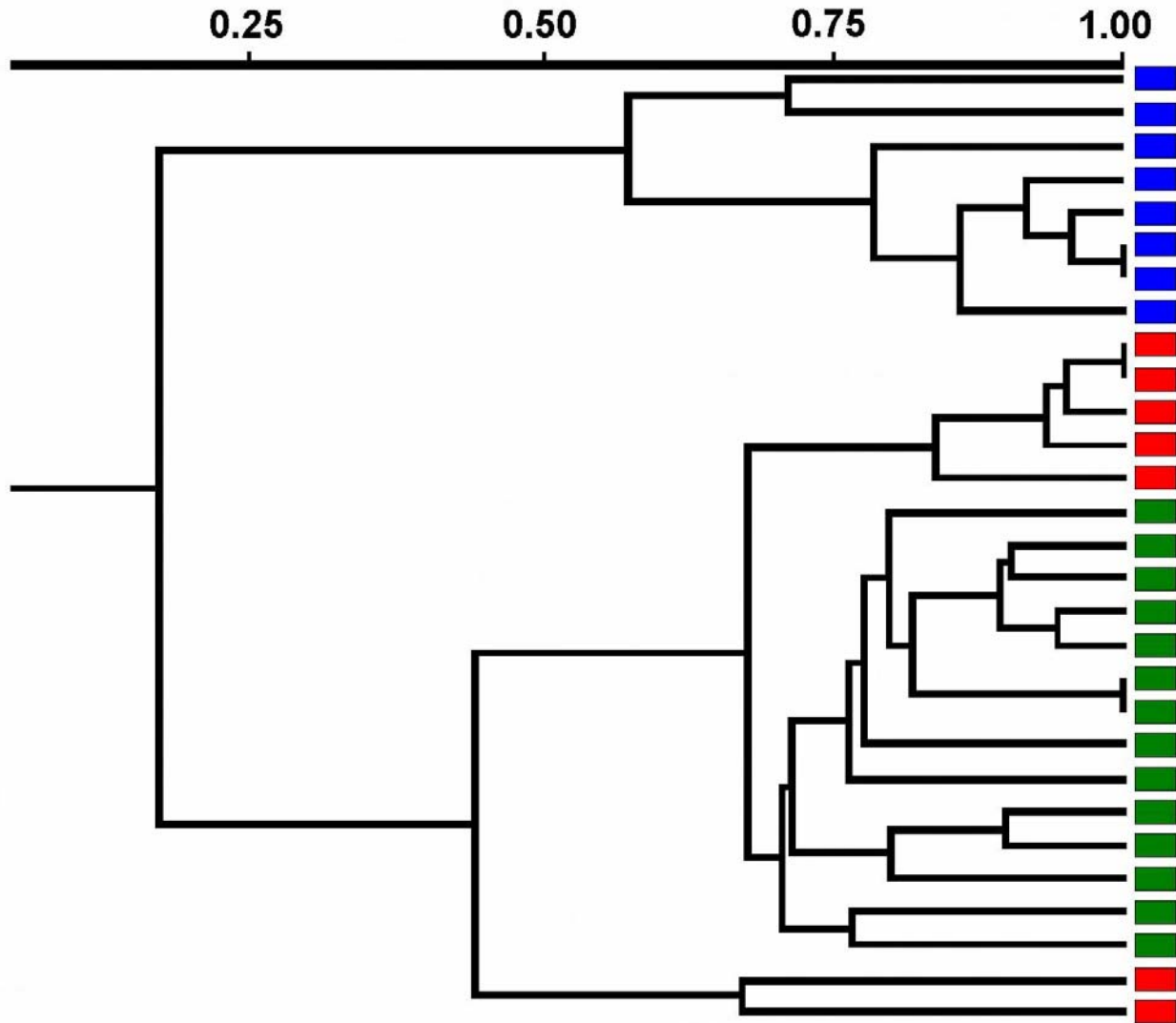


Perennial
Blue Flax
Flowers

Dystyly



Phenogram of Perennial Blue Flax Populations Based on Bulked RAPD Samples



Population Key:

Blue = North American

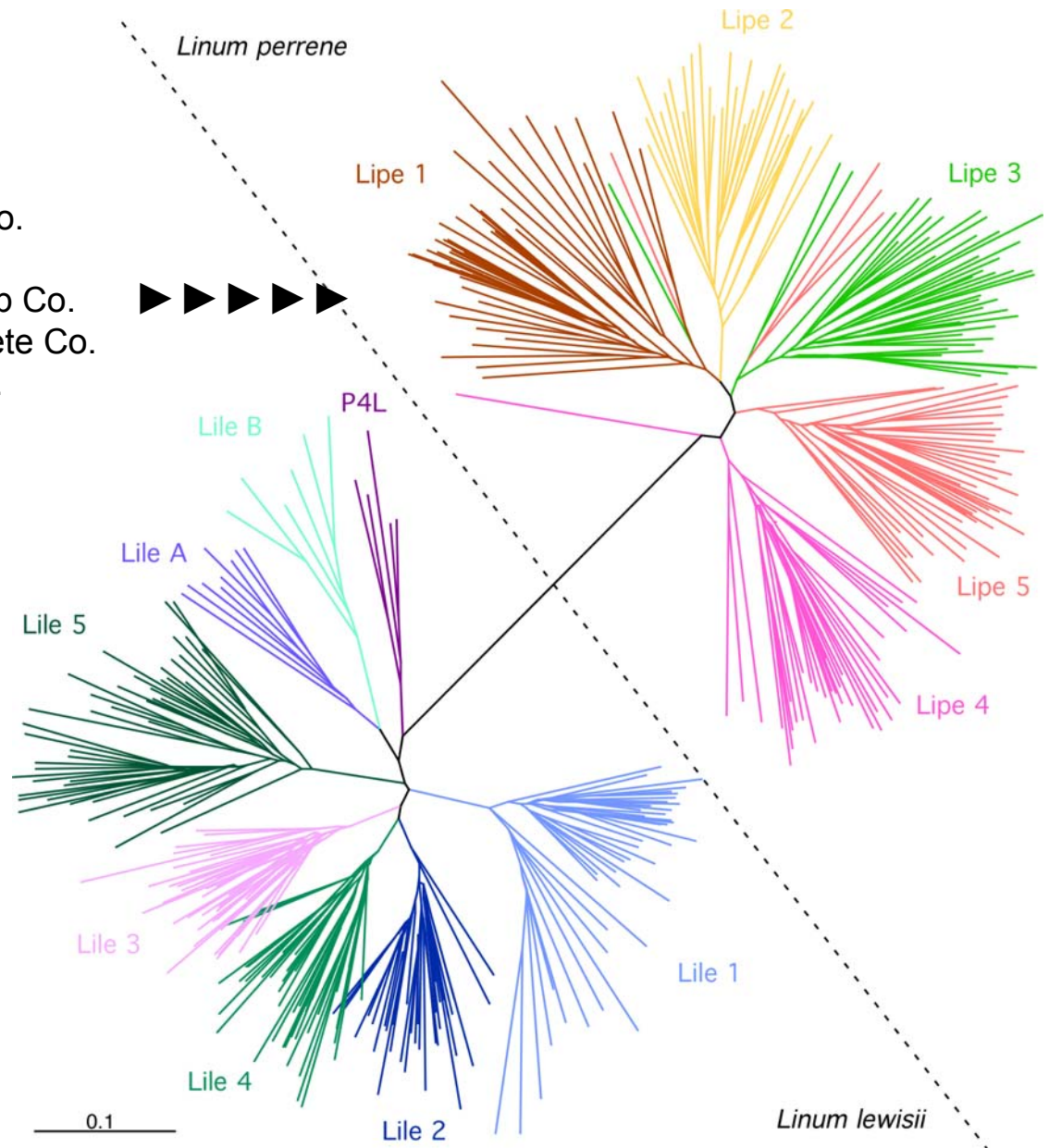
Red = European

Green = 'Appar'

Neighbor Joining Phenogram of Genetic Similarity Based on 470 Loci from 8 ISSR Primers

- 1 = Eagle Mountain, Utah Co.
- 2 = Holden, Millard Co.
- 3 = Salt Creek Canyon, Juab Co.
- 4 = Ephraim Canyon, Sanpete Co.
- 5 = Provo Canyon, Utah Co.

- 1 = Eureka, Tooele Co.
- 2 = Holden, Millard Co.
- 3 = Cove Fort, Millard Co.
- 4 = Maple Grove, Millard Co.
- 5 = Ibapah, Tooele Co.
- A = Pony Express, Tooele Co.
- B = Richmond, Cache Co.
- PL4 = Native in 'Appar' planting





Flax Seed

Character	n	North American accessions	n	European accessions	n	'Appar' accessions	Attained significance
Seed length (mm)	9	4.0 a	9	3.5 b	3	3.3 b	0.010
Seed width (mm)	9	2.1 a	9	2.0 a	3	1.9 a	0.128
Seed width/length ratio	9	0.52 a	9	0.58 b	3	0.57 ab	0.011
Weight of 25 seeds (mg)	9	49 a	9	42 ab	3	34 b	0.047

Means and attained significance values for 4 seed characters from 21 accessions of *Linum*. Significant model effects are in bold. Letters following means denote significant differences among source groups at $p = 0.05$.

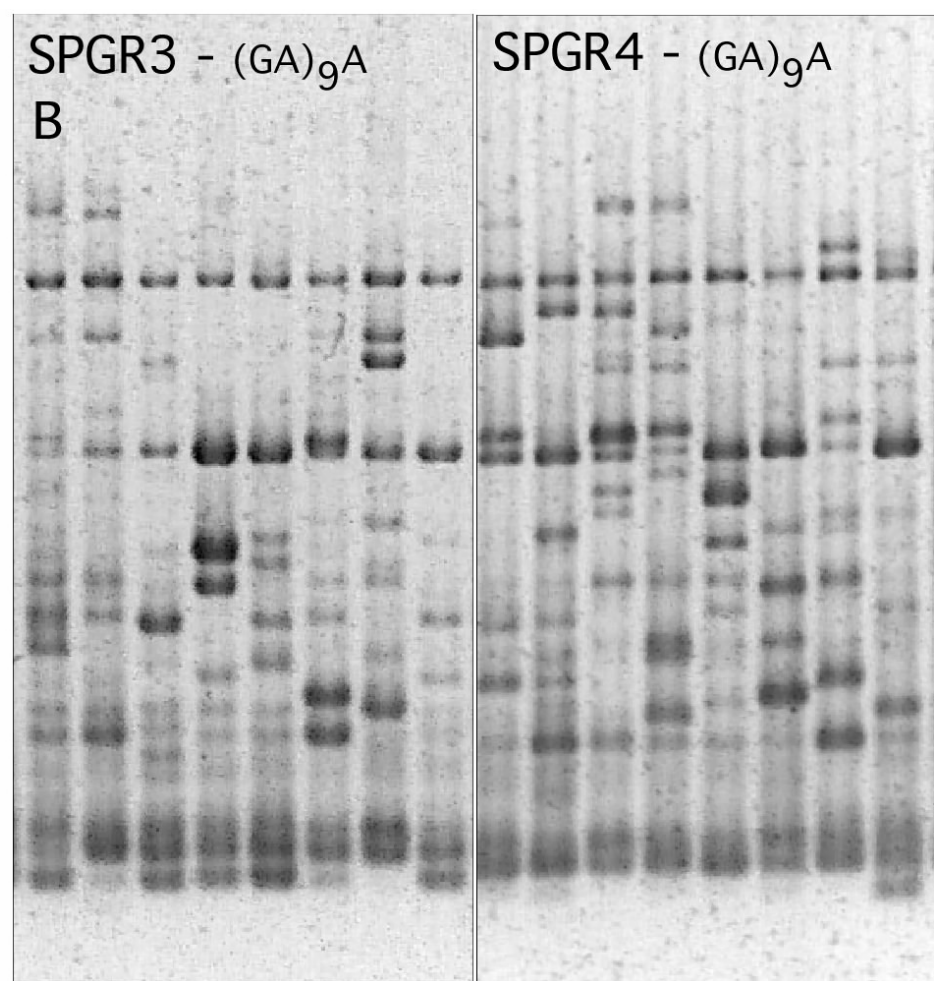
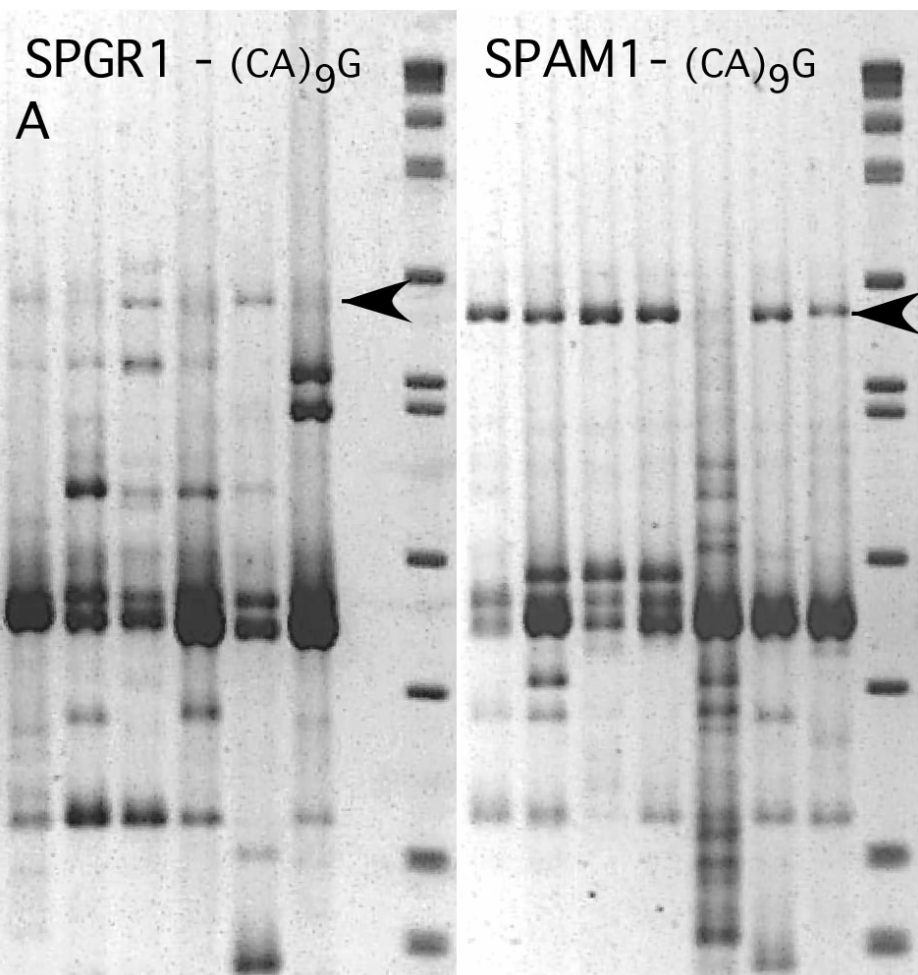
Means and attained significance values for 16 morphological characters from *Linum*.

Character	n	North American accessions	n	European accessions	n	'Appar' accessions	Attained significance
Plant height (cm)	81	47.7 a	87	43.5 a	30	39.2 b	< 0.0001
Leaf angle (rank 1-5)	83	3.6 a	87	2.0 b	30	1.6 b	< 0.0001
Leaf length (mm)	81	16.2 a	87	14.4 b	30	12.3 c	< 0.0001
Leaf width (mm)	81	1.6 a	87	1.6 a	30	1.3 b	0.0002
Longest internode length (mm)	81	6.7 a	87	4.7 b	30	5.2 b	< 0.0001
Number nodes per 3 cm	79	8.6 a	87	10.8 b	30	10.2 ab	0.0005
Basal stem color(y,g,r)	82	Green a	87	Green/Red b	30	Red c	0.0052
Stem diameter (mm)	79	1.5 a	87	1.3 b	30	1.1 c	< 0.0001
Number flowering stems	79	11.2 a	87	17.6 b	30	16.7 b	< 0.0001
Number of days to first flowering	77	23.6 a	87	24.1 a	30	23.6 a	0.6041
Flower diameter (mm)	77	29.6 ab	87	31.1 a	30	29.4 b	0.0007
Petal color(b,l,w)	76	Lavender a	87	Blue/Lavender b	30	Blue c	< 0.0001
Pistil length of long-styled (mm)	76	10.9 a	40	8.3 b	16	7.5 b	0.0029
Stamen length of long-styled (mm)	76	7.1 a	40	4.7 b	16	4.5 b	< 0.0001
Pistil length of short-styled (mm)	--	--	47	4.9 a	14	4.8 a	0.2531
Stamen length of short-styled (mm)	--	--	47	7.4 a	14	7.1 a	0.5054



Sphaeralcea appears to have high levels of genetic diversity in both seeded and native stands.

Sphaeralcea parvifolia
along Colorado River
In Utah





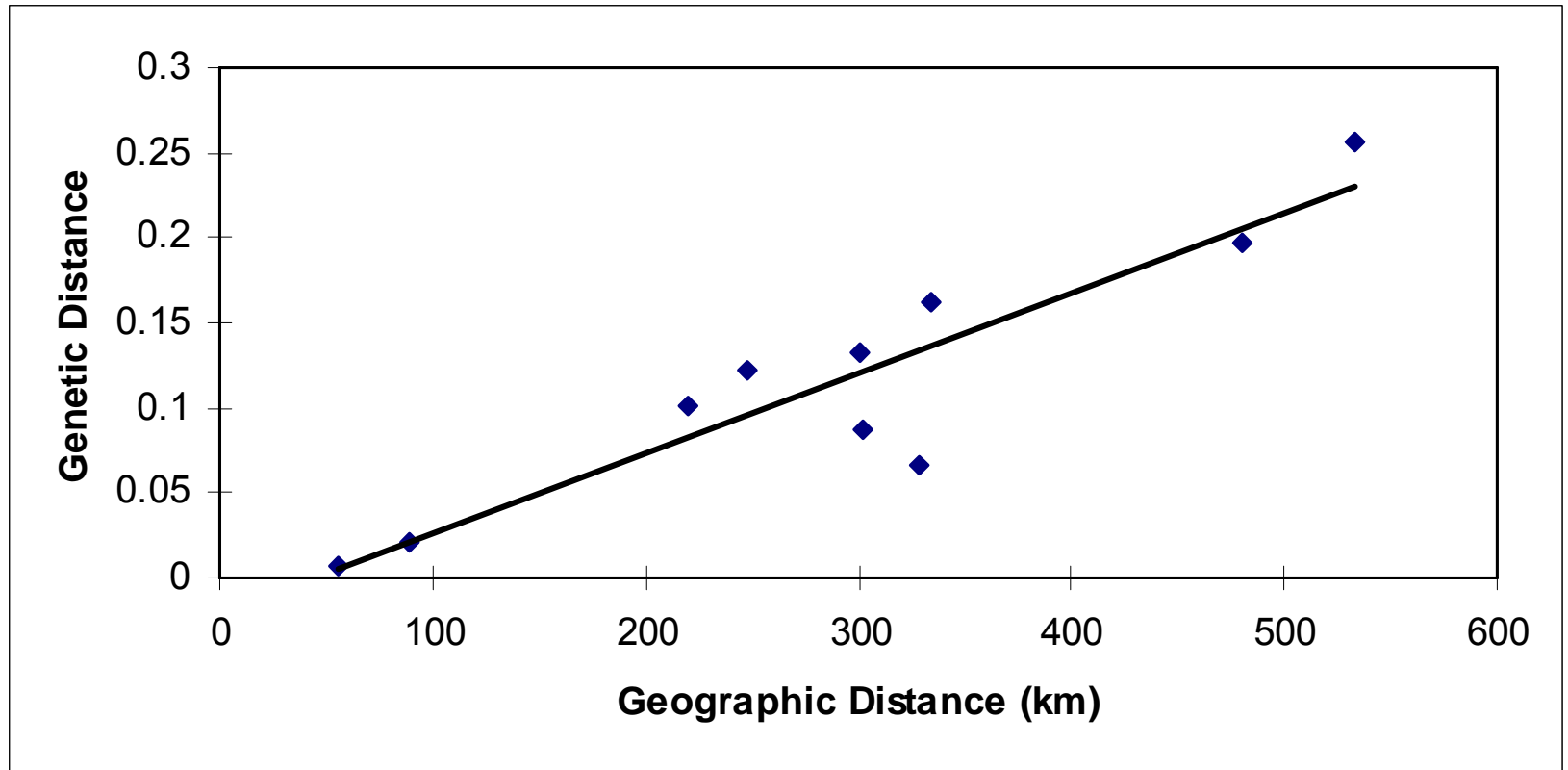
Penstemon speciosus

Penstemons have been used widely in revegetation plantings; penstemons are known to hybridize. Our studies with Palmer's penstemon, however, showed no introgression with sympatric indigenous penstemons.

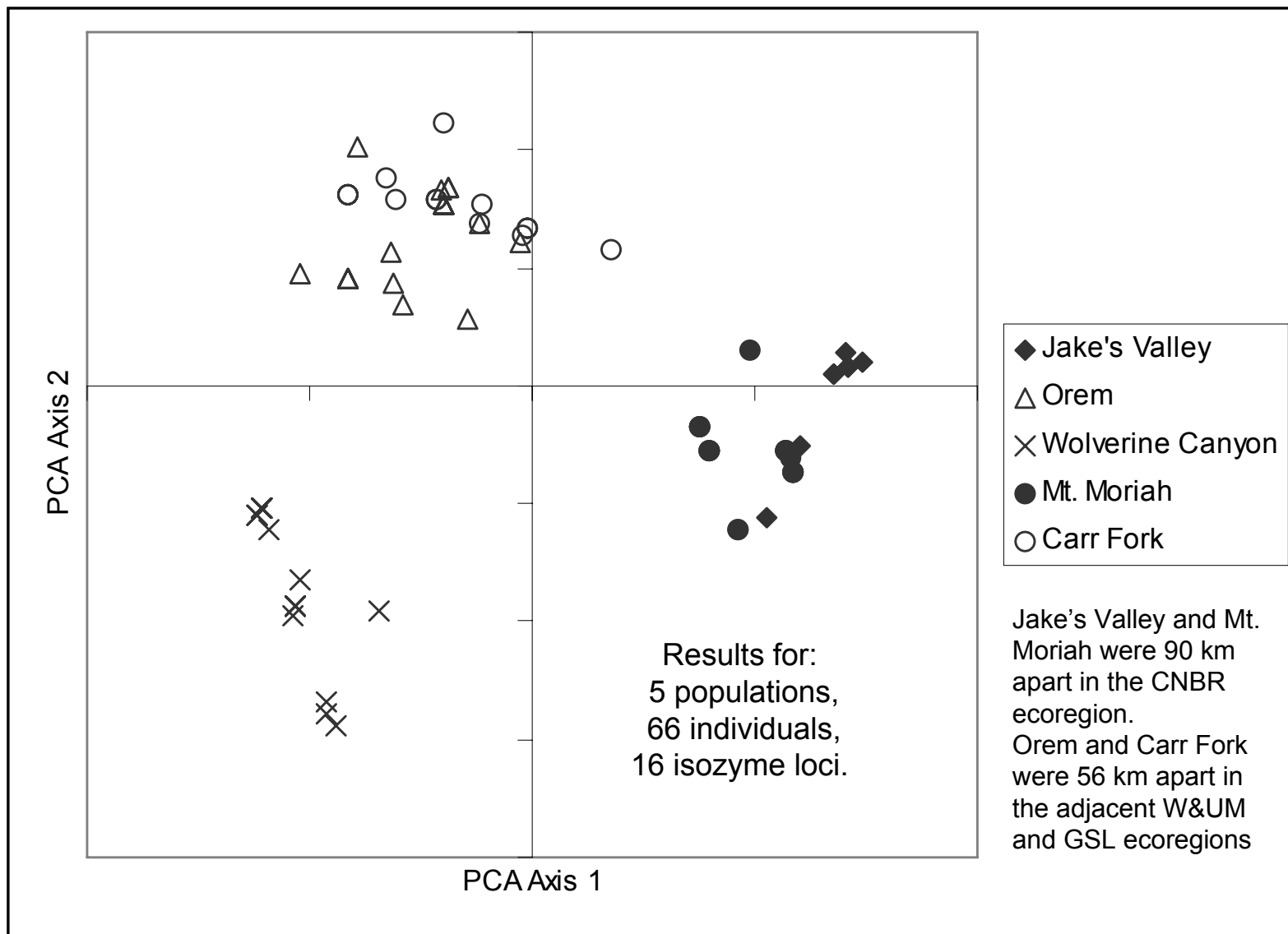


Penstemon palmeri

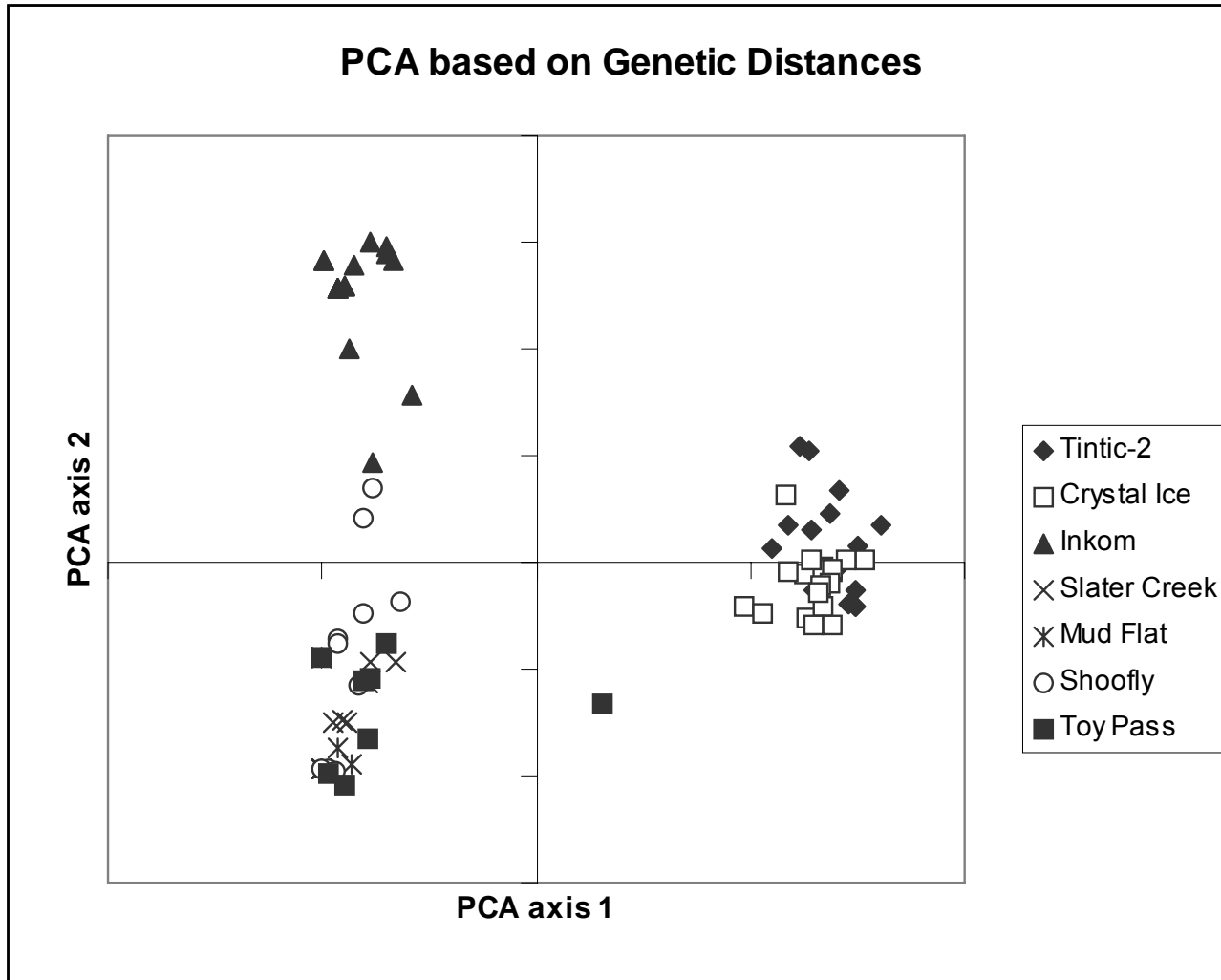
Genetic distance as a function of geographic distance, for *Astragalus utahensis*.

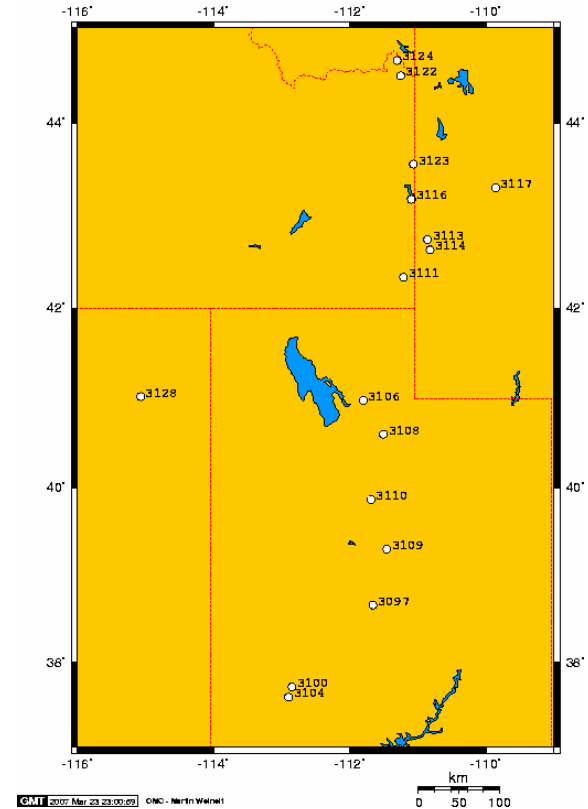
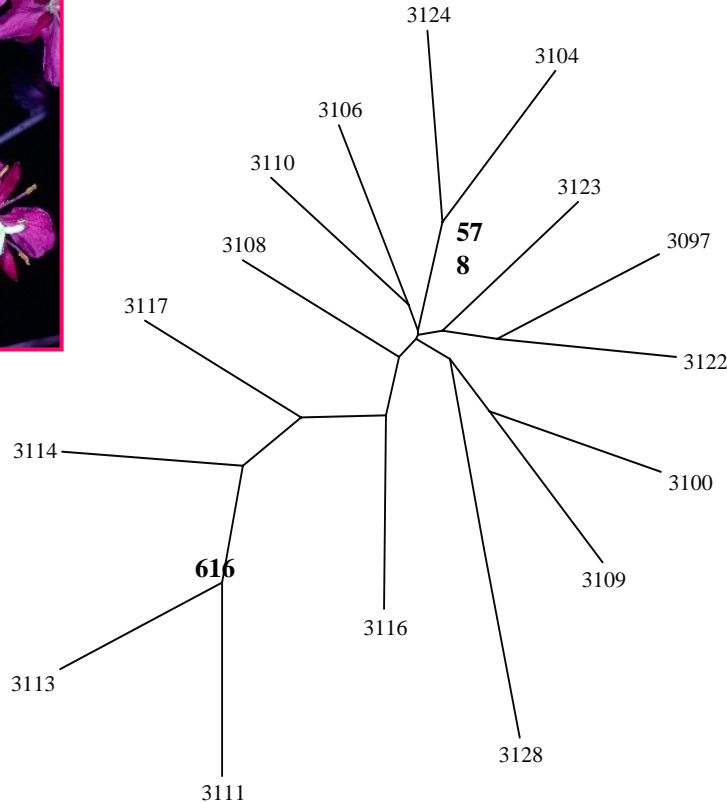


Principal Components Analysis of Genetic Distances Among Individuals of *Astragalus utahensis*.

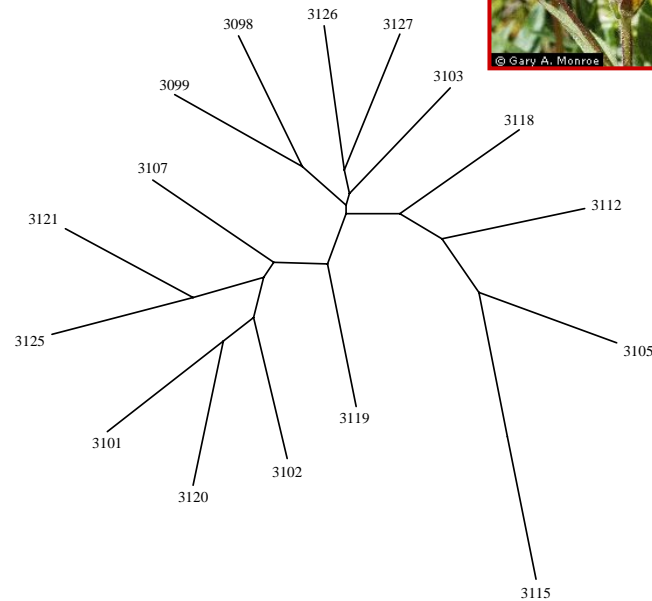
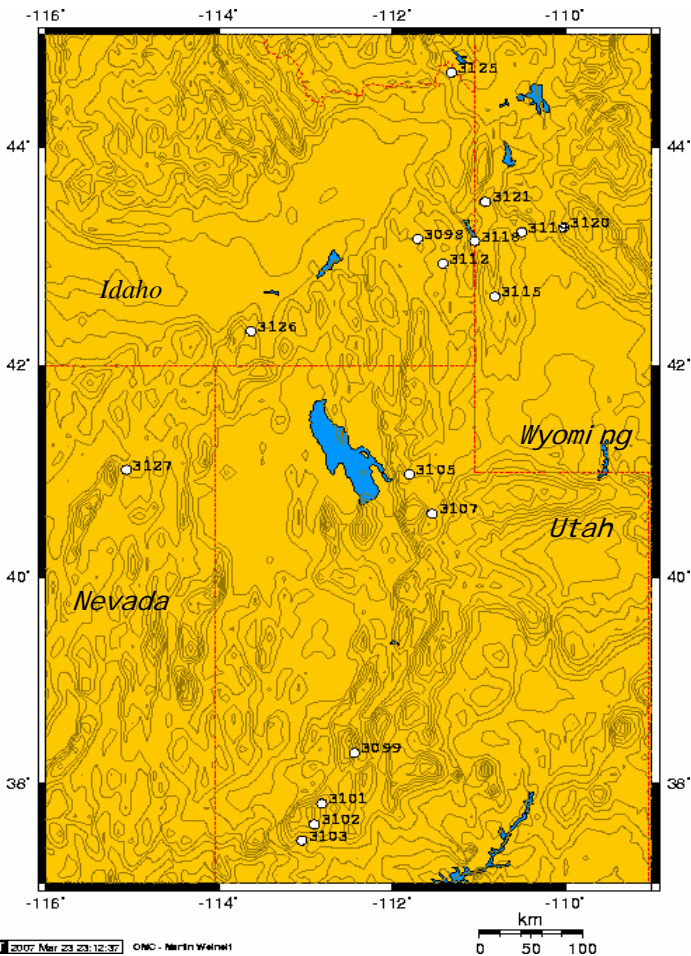


Principal Components Analysis Based on Genetic Distances Among
87 Individuals of 7 *Eriogonum umbellatum* Populations, Generated
Using Eight Loci



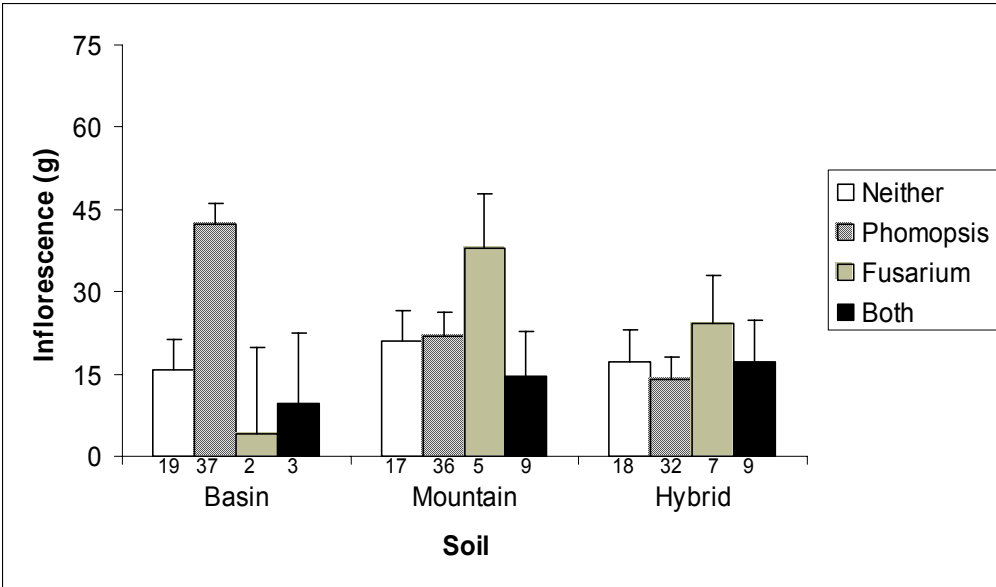


Significant allele frequency variation was observed among populations ($\theta = 0.184$, 95% C.I. 0.125 to 0.251), but no evidence of isolation by distance was observed among all populations ($R^2 = 0.003$, $P = 0.56$), indicating that differentiation is likely due to restricted gene flow even at small scales. Population assignment tests indicate a single population, EDM 3111, to be distinct from the other collections.



Populations were significantly differentiated ($\theta = 0.205$, 95% C.I. 0.128 to 0.301), indicating that 20% of the observed variation is partitioned among populations. Pairwise measures of differentiation indicated most pairs of populations to be significantly differentiated, but no evidence was found for isolation by distance, indicating neighboring populations are no more likely to be genetically similar than geographically separated pairs. Bayesian clustering analyses indicate 7 genetic groups to be present in the combined data set, and individual assignment tests indicate these groups do not follow a geographic pattern.

Salt Creek Canyon Big Sagebrush Hybrid Zone





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