

Seed dispersal among *Lasthenia californica* (and *Achyrachaena mollis*) patches in a Southern Oregon prairie



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Upland Prairie Project: Collaboration among PSU, UO, Duke, UC Boulder

- Experimental plots (manipulated temperature and precipitation)
- Demography (growth, reproduction, survival) in natural populations
- Landscape genetics to understand seed dispersal ability, barriers to dispersal



Using these data to model species' probabilities of persistence and extinction as climate gets warmer and drier

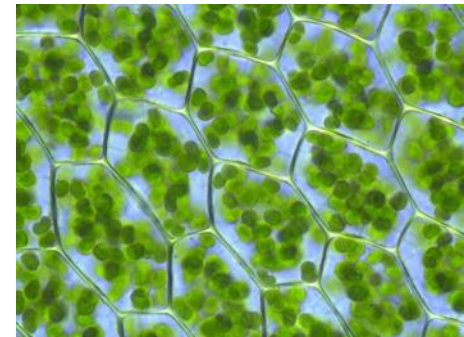
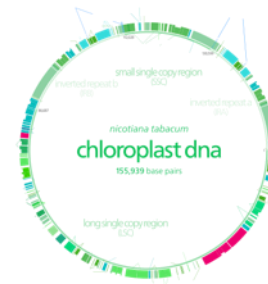
Seed dispersal: Critical process, difficult to observe



- Seed dispersal = colonization of new populations
- Mediated by dispersal agent behavior, or abiotic forces

Chloroplast

- Maternally inherited = seed dispersal
- Haplotypes, because loci are linked
- Low variation; whole cp genome sequencing is helpful



Assessing plant dispersal: Landscape genetics

Isolation by Distance

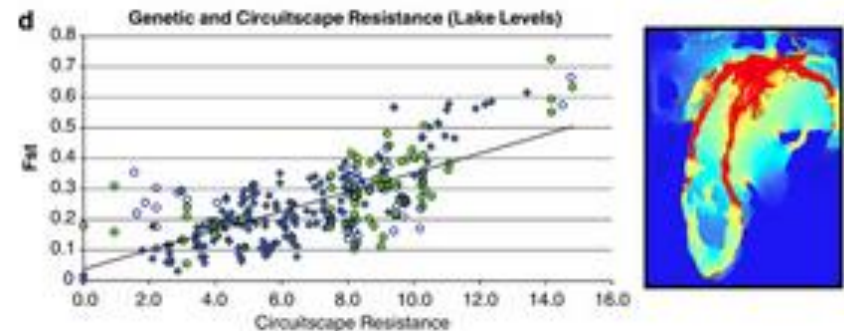
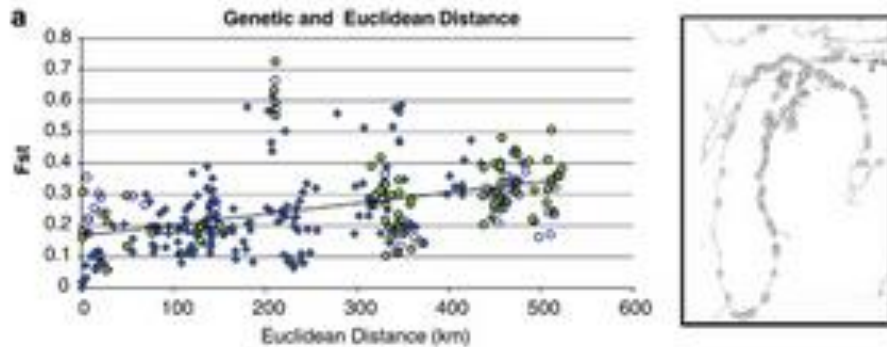
Common null model.

Euclidean distance shapes gene flow.

vs.

Isolation by Resistance

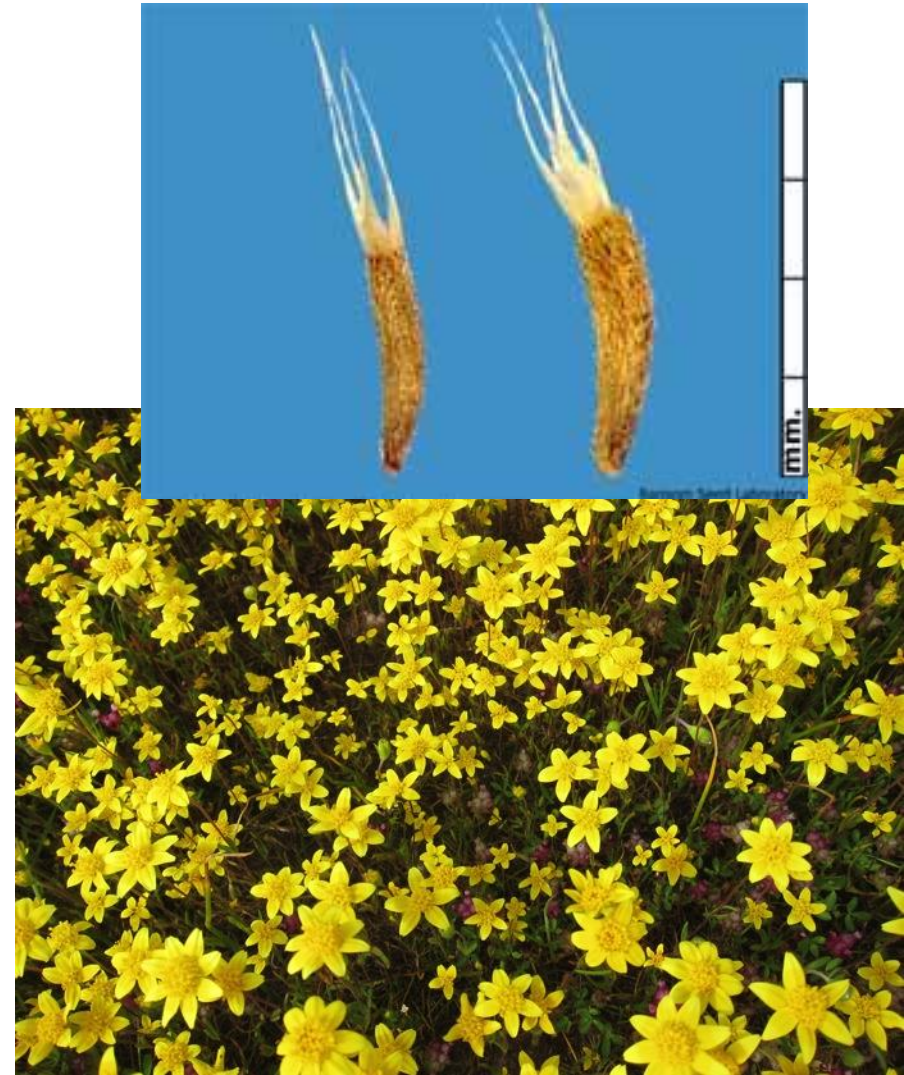
Different landscape features have different influences on gene flow. Circuit theory used to create resistance surfaces.



Figures from Fant et al. 2014, Heredity

Fine scale seed dispersal in a single prairie: *Lasthenia californica* (California goldfields) at Whetstone

- Self-incompatible, annual forb that forms large patches
- Prefers edges of vernal pools in Southern OR
- Specialist bee pollinators (Andrenids)
- Seeds have small pappus, possibly wind or gravity dispersed



Study system: Whetstone Savannah Preserve

Ceanothus cuneatus bushes

hummocks

vernal pools/swales

Lasthenia californica flowers



Vole Runways

California vole

(Microtus californicus)

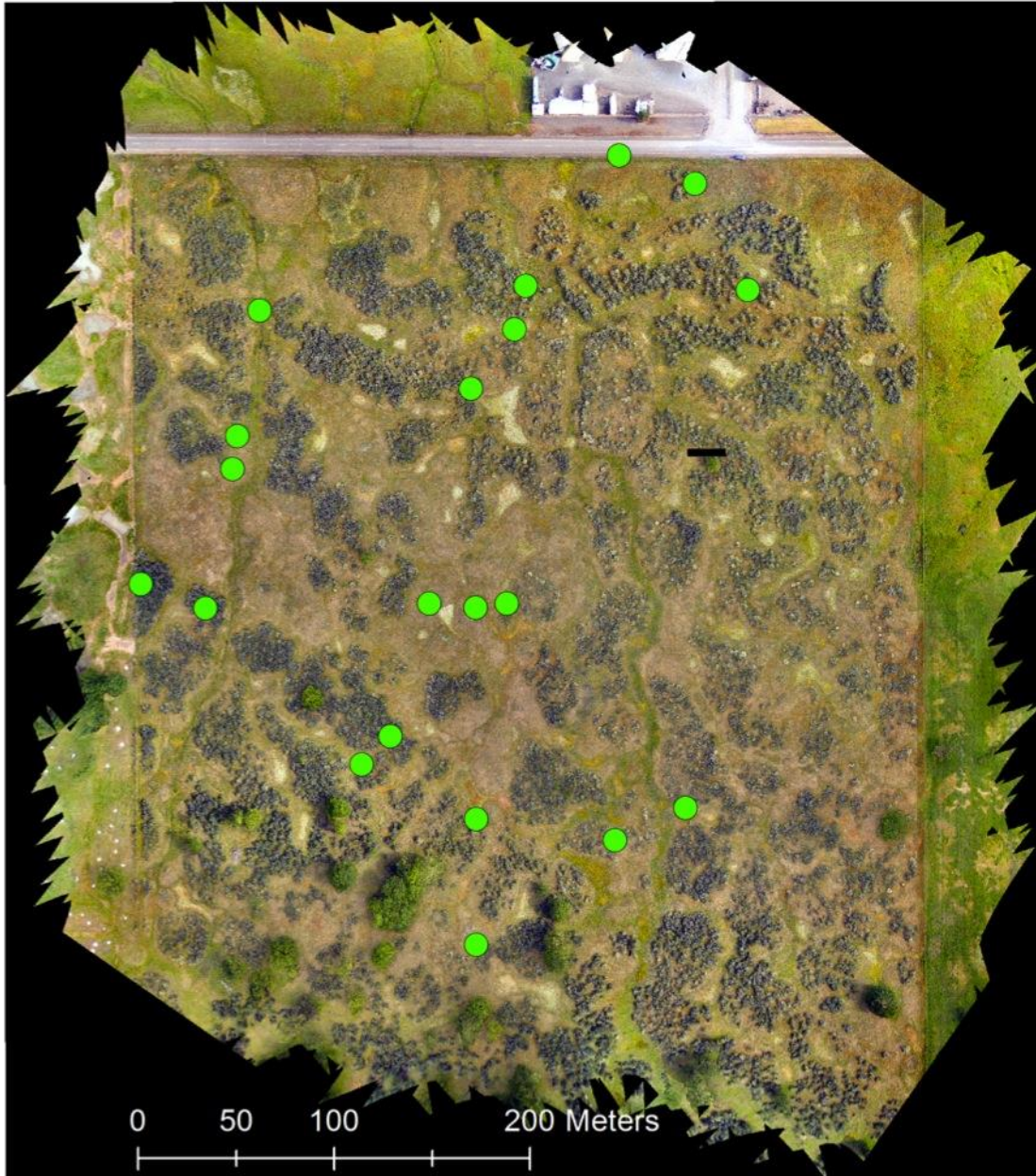


What landscape features influence seed movement in *Lasthenia californica*, on a fine-scale?

Predictions:

- *L. californica* will have limited seed dispersal, demonstrated by high genetic structure in the cpDNA
- Bushes will shape seed dispersal, if primarily wind-dispersed; vole trails may act as secondary dispersal conduits

Mapping the prairie with a drone

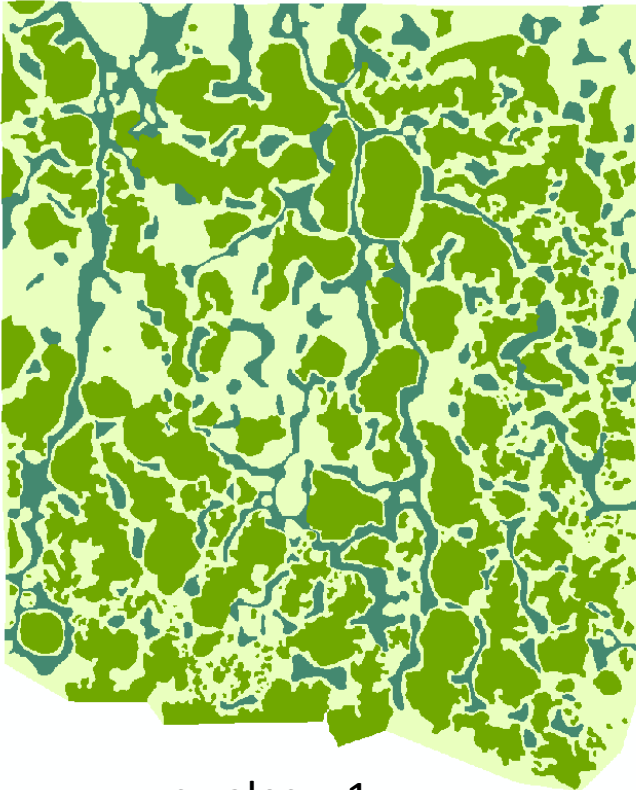


Cruzan et al. 2016, Applications in Plant Sciences

Sampling for *L. californica*:
20 pops, 20 individuals;
Sequenced 1 individual and a
pool of 20 for each population

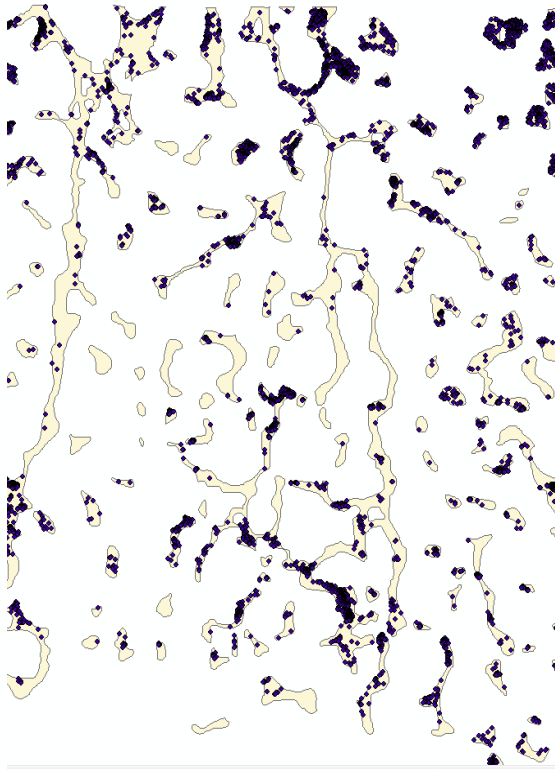
Landscape variables of interest

habitat type



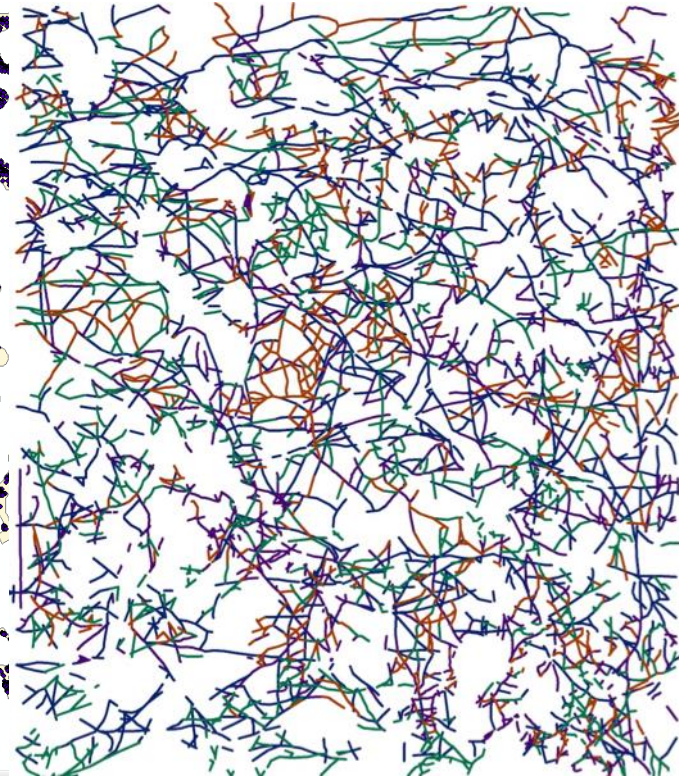
swales = 1
hummocks = 5
bushes = 10

flower presence



flower pixel = 1
no flower pixel = 10

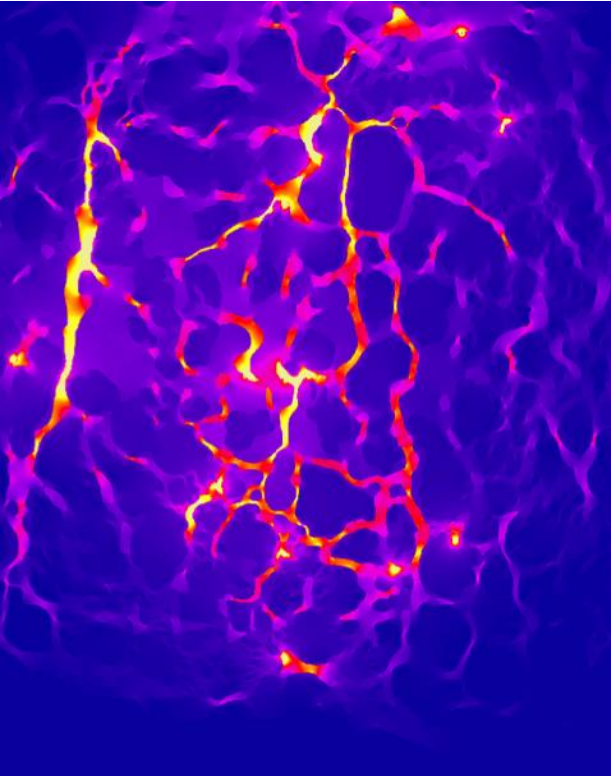
vole trails



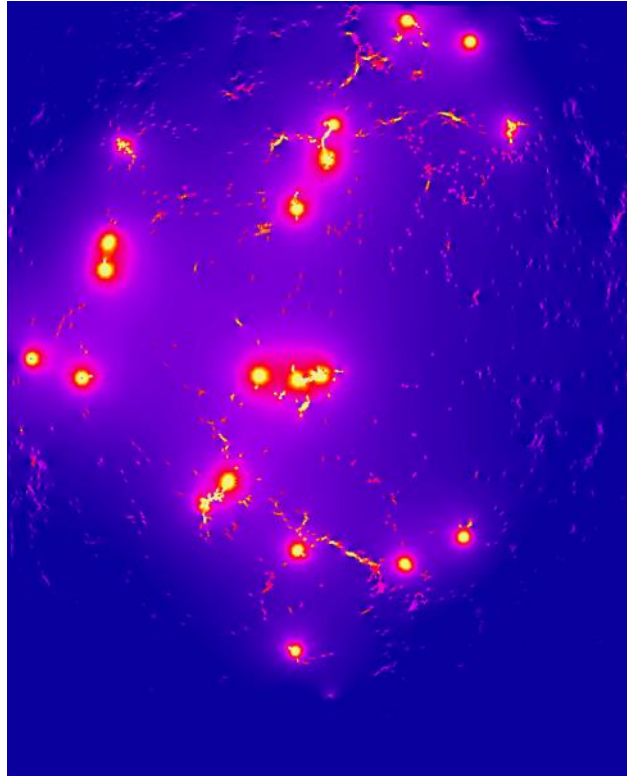
vole trails = 1
non-vole trails = 10

Circuitscape: Current surfaces

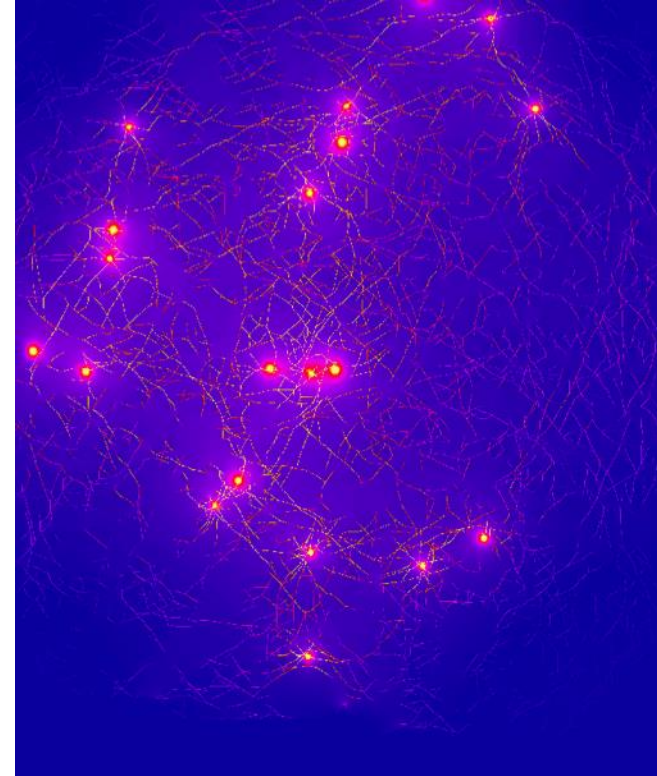
habitat type



flower presence



vole trails



Resistance values between pairwise populations are given as output

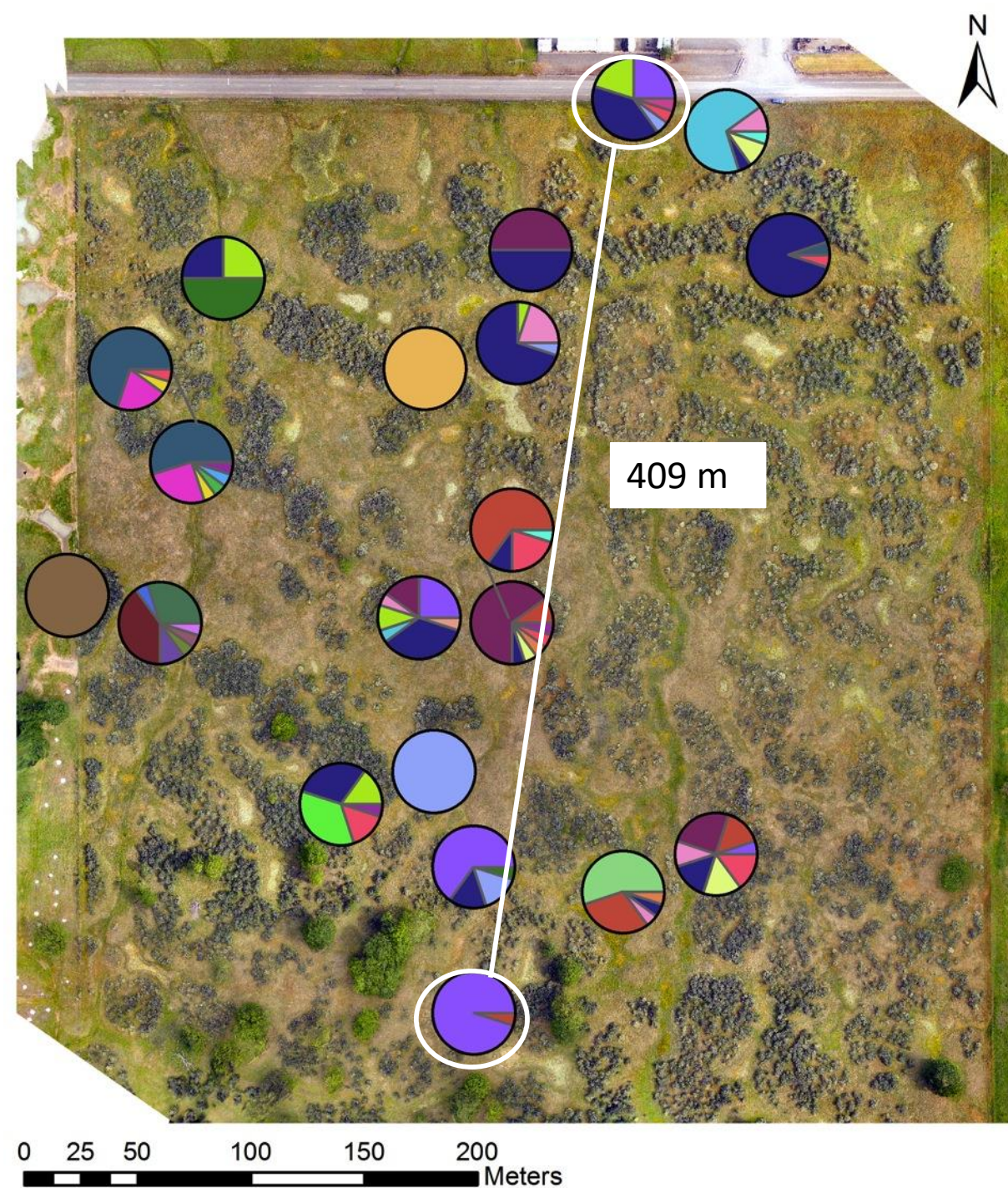
Results for cpDNA of *L. californica*:

Custom script
reassembles the
haplotypes from pooled
data (CallHap)

Kohn et al. 2017

-40 SNPs,
32 haplotypes

-Multiple populations
with no shared
haplotypes = Limited
dispersal



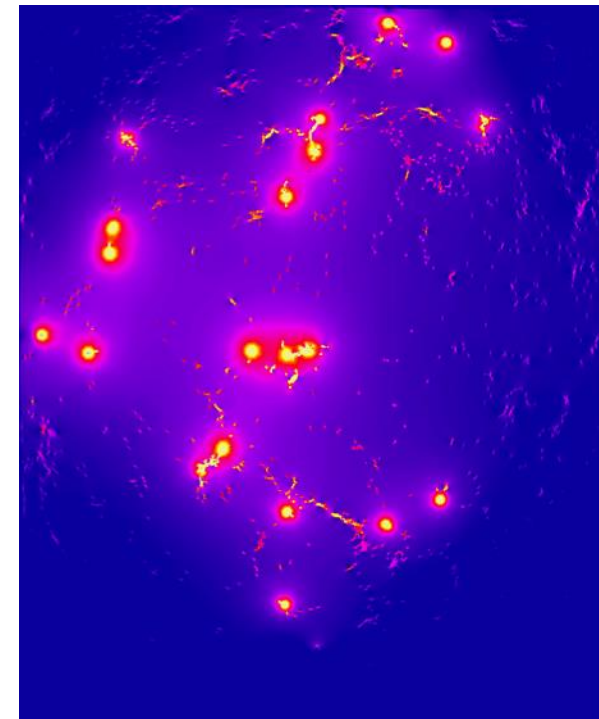
Regression of landscape variables on cpDNA genetic distance for *L. californica*

Predictor	Step 1			Step 2			Step 3			Step 4		
	Coeff	P-value	vif	Coeff	P-value	vif	Coeff	P-value	vif	Coeff	P-value	vif
flower presence	0.038	0.046	2.30	0.0369	0.0411	2.3777	0.031	0.041	1.723	0.023	0.030	---
vole trail	-0.011	0.659	2.09	-0.013	0.5138	1.821	-0.016	0.407	1.723	---	---	---
habitat	-0.015	0.576	2.54	-0.015	0.5582	2.0808	---	---	---	---	---	---
geodist	0.000	0.770	2.43	---	---	---	---	---	---	---	---	---

Flower presence significantly explains
Edwards genetic distance (cpDNA) ($R^2=0.092$,
 $p=0.027$)

This may be a result of the flower presence
defining the habitat in a more precise manner
than we are able to (micro-habitat)

Also, dispersal is limited, may be gravity
dispersed



Meso-scale gene flow: Seed dispersal among prairies near Medford, OR

Achyrochaena mollis



Ranunculus occidentalis



Eriophyllum lanatum



Plectritis congesta



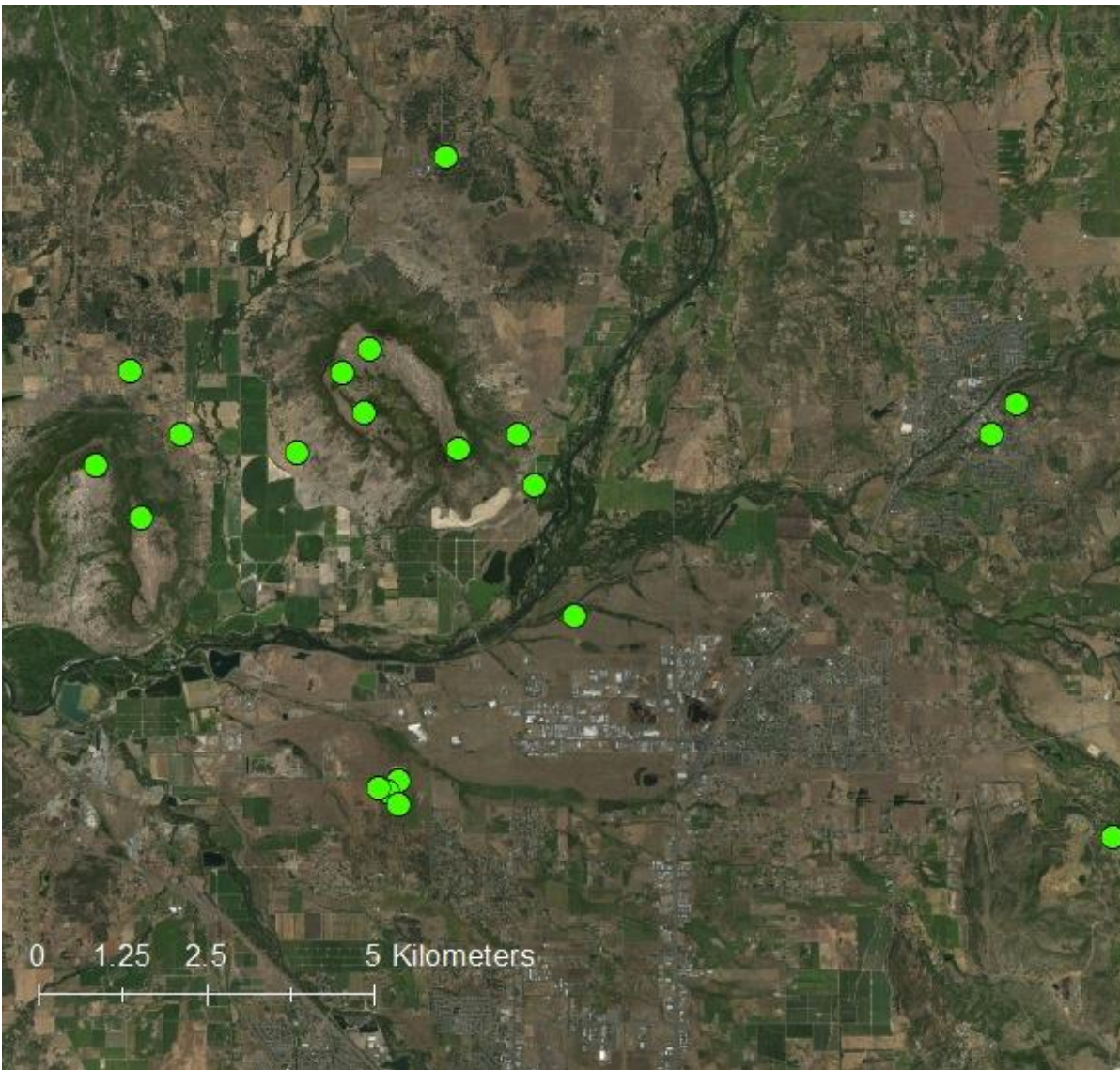
Ranunculus austro-oreganus



Cynoglossum grande



Achyrrachaena mollis

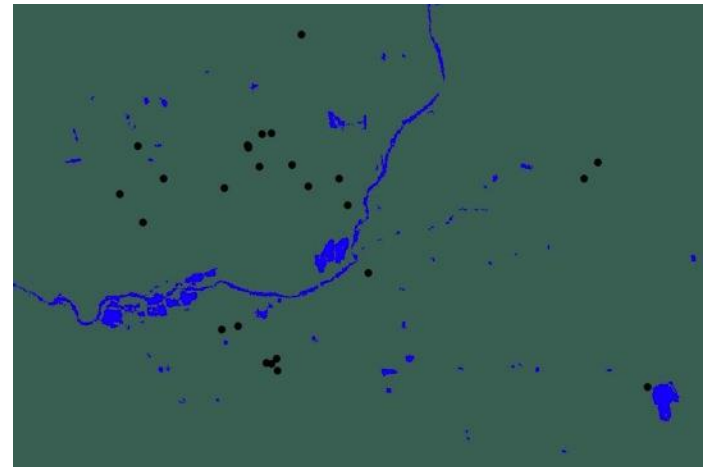
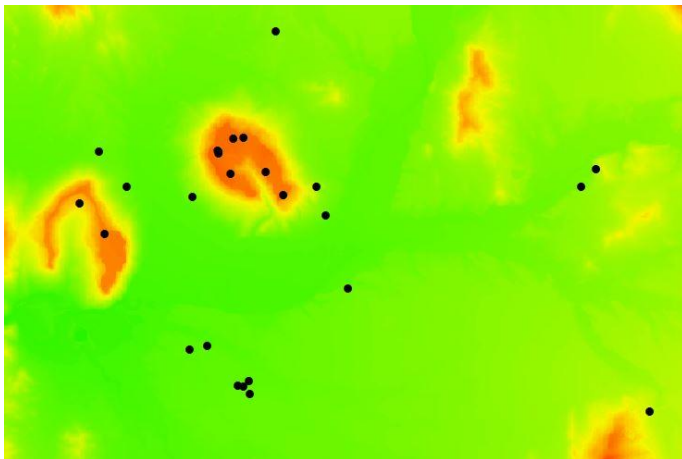
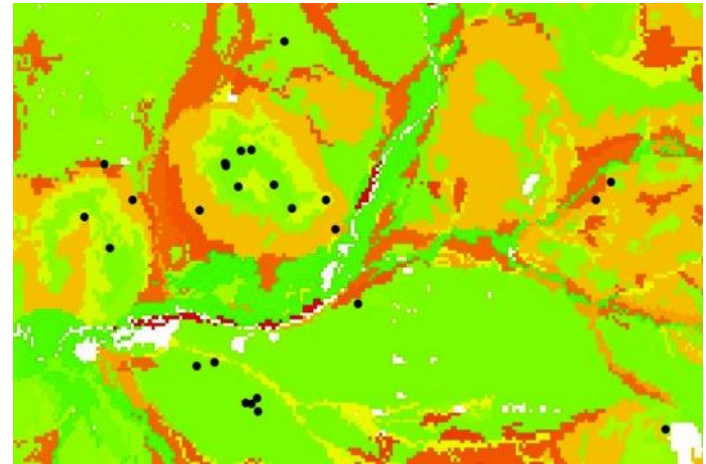
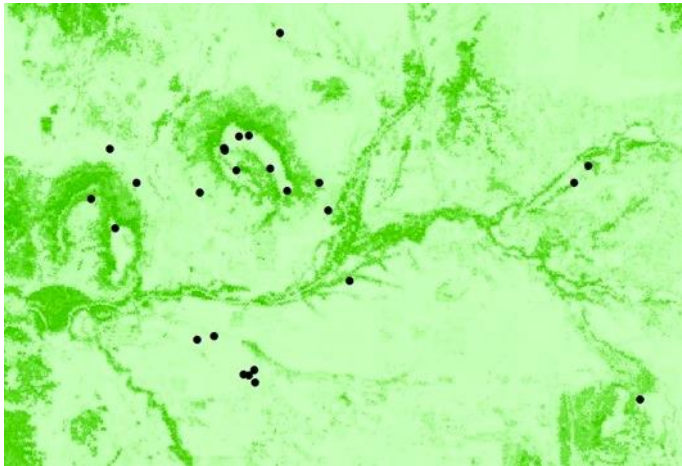


Sampling

20 pops, 20 individuals

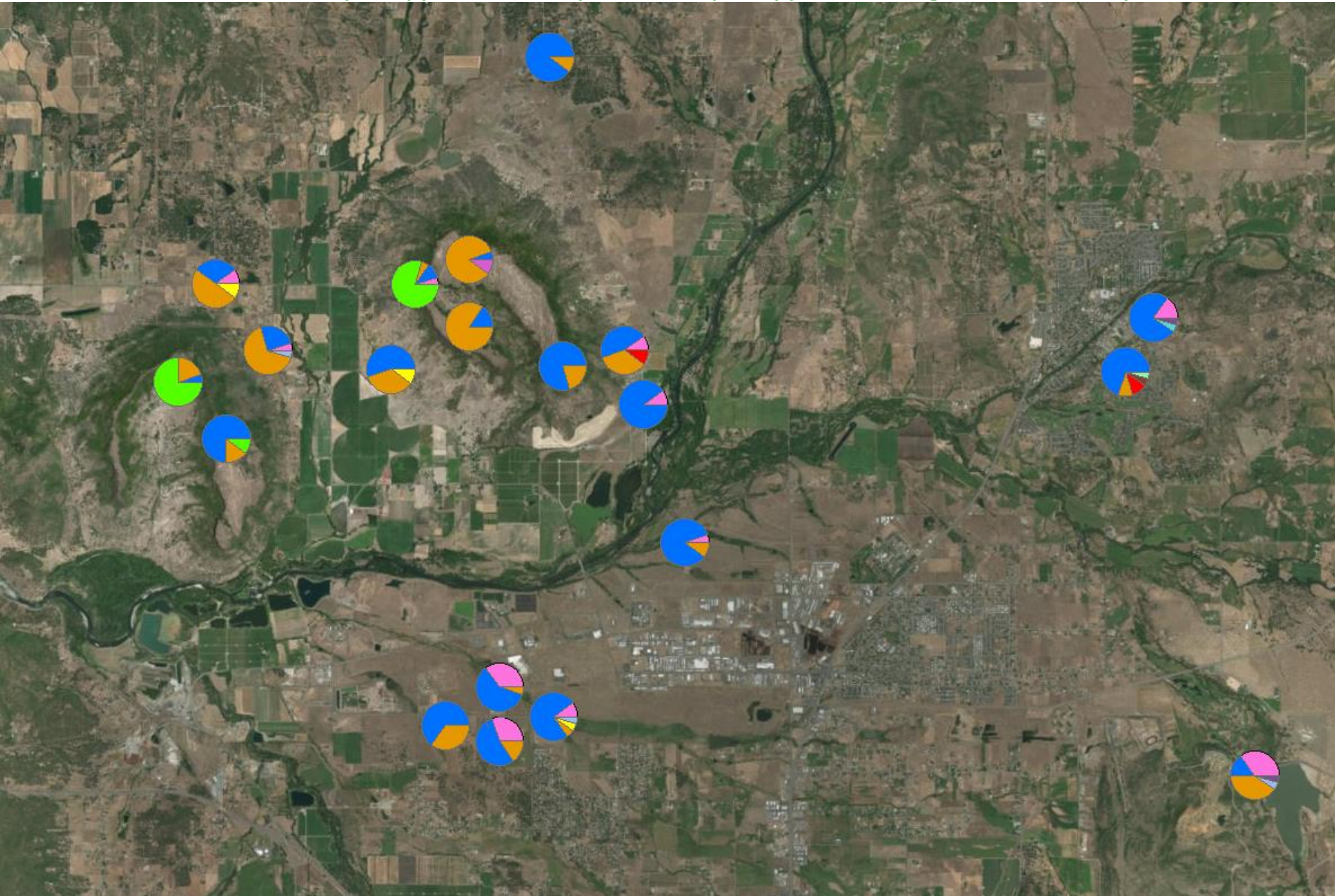
Sequencing per population:
cpDNA: 1 individual, 1 pool
of 20 individuals, capture

Landscape features evaluated: canopy cover, elevation, soil type (sand), rivers/open water



Results for cpDNA of *A. mollis*:

14 SNPs, 12 haplotypes, widespread haplotype sharing across study sites

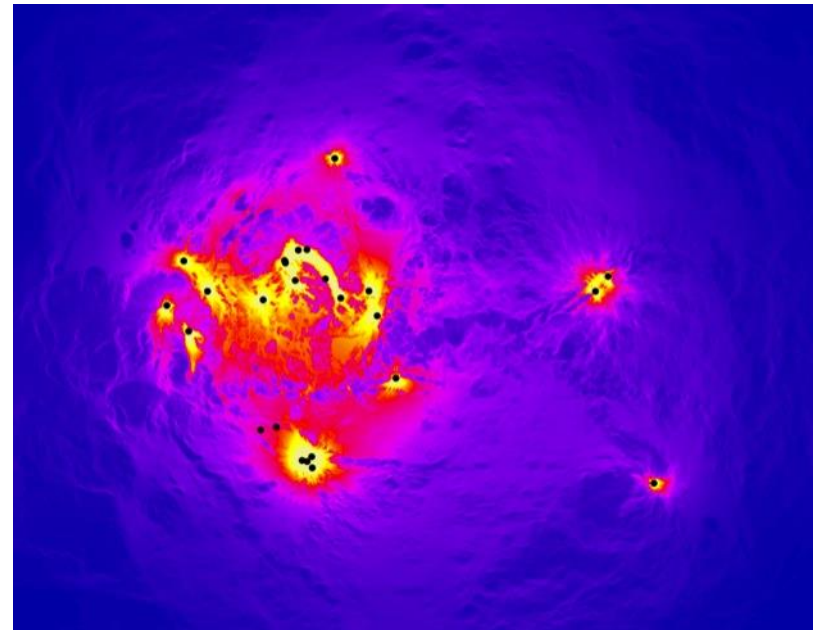


Regression of landscape variables on genetic distance for *A. mollis*

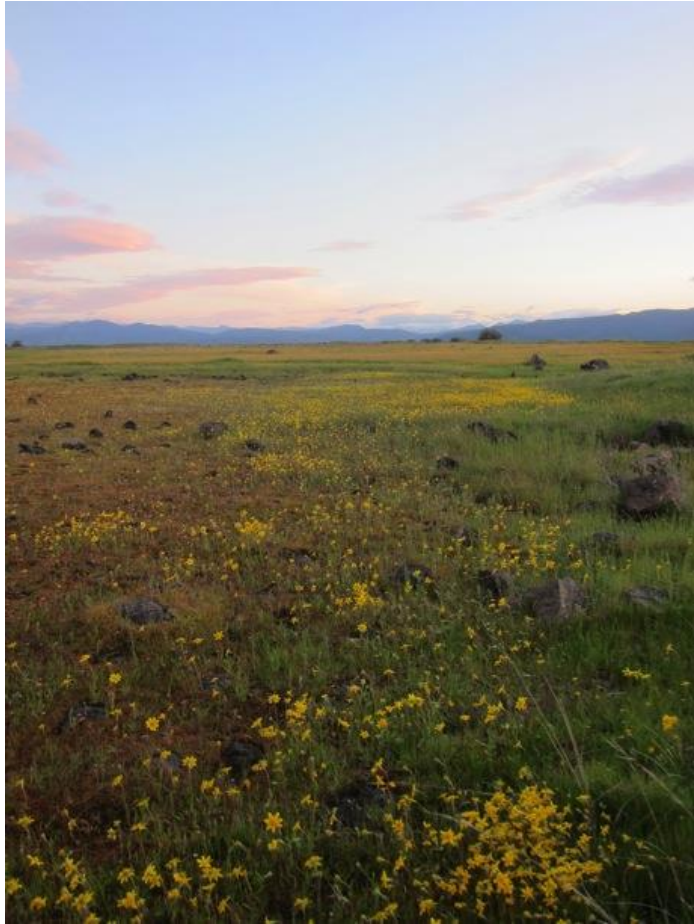
	Step 1: All			Step 2: Remove elevation because it is highly correlated to water			Step 3: Remove geographic distance			Step 4: Remove water			Step 5: Remove sand	
Predictor	Coeff	P-value	vif	Coeff	P-value	vif	Coeff	P-value	vif	Coeff	P-value	vif	Coeff	P-value
canopy	0.237	0.016	2.2	0.251	0.010	2.1	0.252	0.008	2.1	0.247	0.009	2.0	0.159	0.011
sand	-0.105	0.314	3.2	-0.096	0.356	3.2	-0.093	0.359	3.1	-0.110	0.155	2.0	---	---
water	-1.881	0.434	160.4	-0.232	0.508	8.2	-0.096	0.726	2.6	---	---	---		
geodist	0.000	0.785	7.9	0.000	0.668	7.7	---	---	---					
elevation	1.876	0.465	174.3	---	---	---								

Canopy cover significantly explains Edward's genetic distance ($R^2= 0.160$, $p=0.011$)

Because *A. mollis* is wind-dispersed, high canopy cover likely is a barrier to wind dispersal



Prairie Project: Preliminary Conclusions



Fine-scale:

- *L. californica* had limited seed dispersal, and this was influenced by flower presence; likely gravity dispersed

Meso-scale:

- *A. mollis* seed dispersal more widespread than the fine scale species, probably due to wind dispersal
- Seed dispersal shaped by canopy cover

Prairie Project: Next steps

More species:

- Sequence data ready for *R. occidentalis* and *R. austro-oreganus*, *E. lanatum*, *P. congesta*
- Complications and Opportunities: *R. occidentalis* and *R. austro-oreganus* hybridization (Jessica Persinger)
- Complications and Opportunities: *E. lanatum* ploidy variation (Nic Diaz)



Multi-year sampling for migration:

- For 2 annual species (*A. mollis* and *P. congesta*), sampled the same sites across 2 years to estimate allele frequency changes
- Can calculate N_m from F_{ST} , and N_e (effective population size) from allele frequency changes
- Using N_m and N_e , can get number of individuals arriving per year (M)
- From that, relative estimates of dispersal, range of M for different distance classes



Thank you!



Cruzan Lab at PSU

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