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Using population genomics to uncover the rapid colonization of Sahara mustard (*Brassica tournefortii*) in the United States

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Overview

Introduction Why study invasion routes? Theoretical and applied needs Sahara mustard and its impacts Objectives

1. Population structure in U.S.

2. Invasion patterns and pathways

Current & Next steps



Why study invasion routes?

- *Invasion routes:* the geographical pathways followed by propagules from their source to the invading populations (Estoup and Gillimaud 2010)
- Approximately 50,000 invasive species in United States. Environmental damage \$120 billion per year (Pimentel et al. 2005)
- Globally, as many as 80% of the endangered species are threatened due to pressures of invasives (Armstrong 1995)



Theoretical needs

- Fundamental questions in biology related to evolutionary selection
- Basic research in population biology
- Natural dispersal events and range expansions of noninvasive species



Applied needs

- Reconstructed invasion routes valuable for land managers
 - designing control programs that effectively reduce spread of invasives (Mack et al. 2000)
 - land managers can monitor geographic areas at high invasion risk to curtail invasive spread (Estoup and Guillemaud 2010)



Sahara mustard (*Brassica tournefortii*) and its impacts

- Capable of self-fertilization
- >10,000 seeds per plant possible
- Broad germination requirements (Bangle et al. 2008)
- Drought tolerant (Pratap and Gupta 2009)
- Promotes fires in deserts (Steers 2008)
- Negatively impacts native plants (Barrows et al. 2009)











Sahara mustard (*Brassica tournefortii*) and its impacts

- First collected in North America February 1927
- Presumed to disperse via roadways (Sanders and Minnich 2000)
- Present distribution: CA, AZ, NV, UT, NM, TX





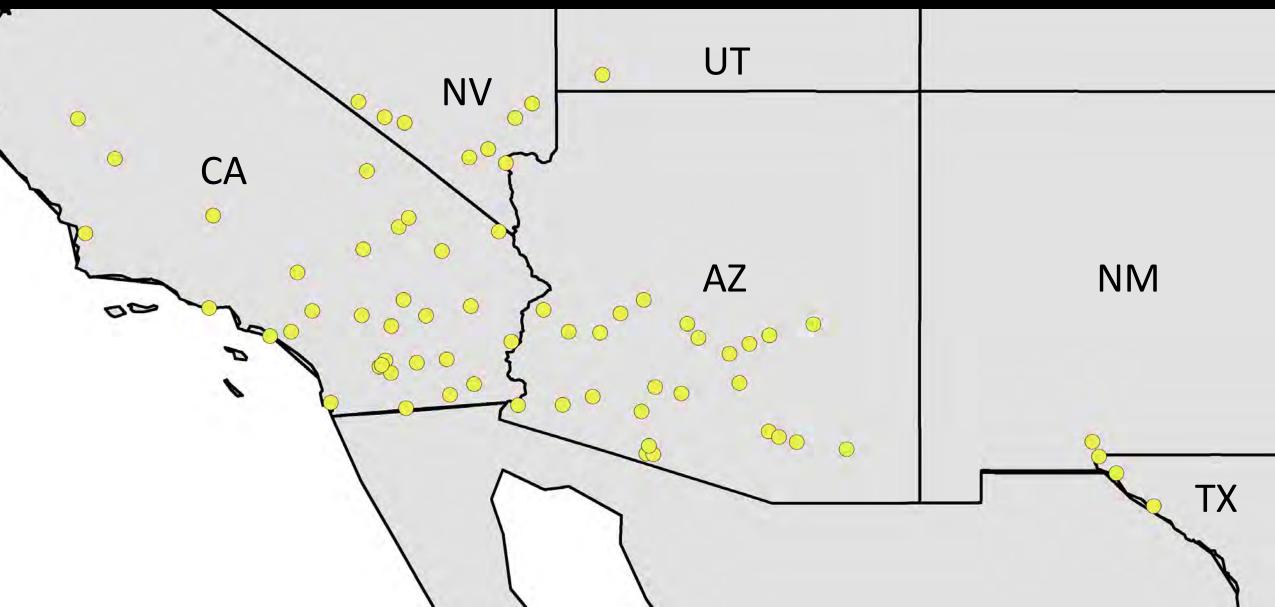


Research objectives

- 1. Identify level of genetic diversity in U.S.
- 2. Determine genetic structure of North American population(s)
- 3. Test models of isolation and association to understand diversity
 - Geographic distance
 - Distance along roadways
 - relatedness



Methods2,061 individuals from 70 unique localities





Methods

- Genotyping-by-Sequencing (nextRAD)
- Sequenced 950 individuals
- 15,000 loci per individual
- 1084 SNPs identified

<u>Population structure</u>: Structure, Structure Harvester, and Distruct 10,000 burnin, 100,000 MCMC runs, 10 iterations, K=1–20

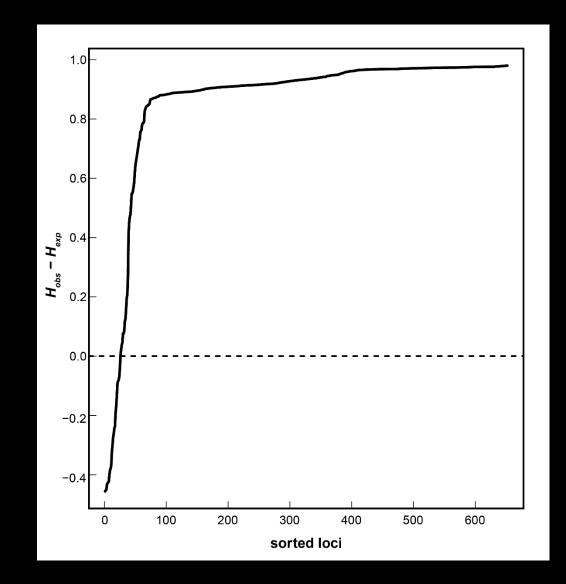
Genetic diversity: adegenet, poppr, fields R packages

H_{obs} – H_{exp}, IBD,
Normalized Index of Association,
Minimum spanning networks



Heterozygosity is higher than expected ~ 95% of loci

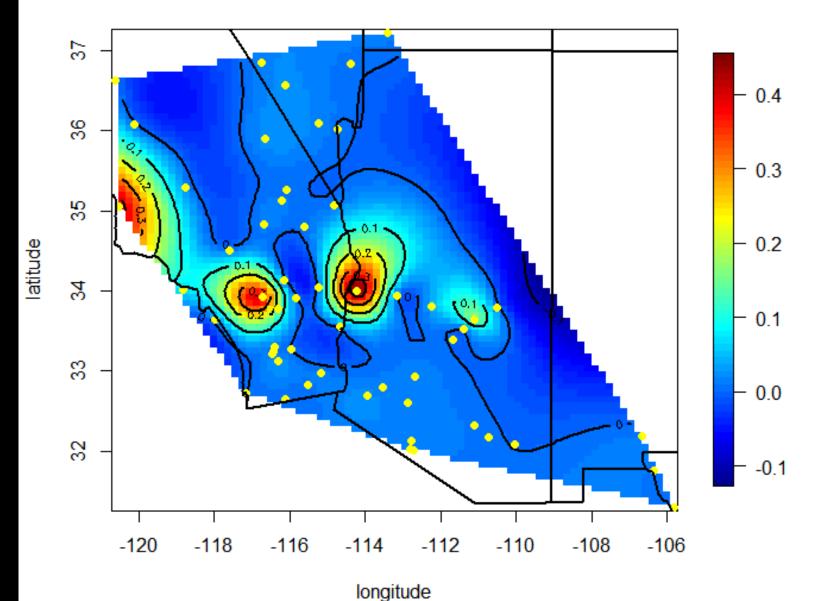
Potential implications: low levels of inbreeding Isolate-breaking effects Differences are rare



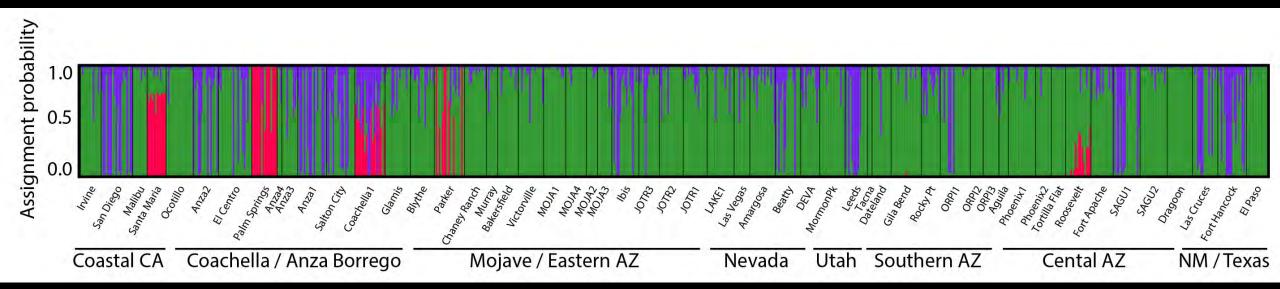
Thin plate spline of Standardized *I_a*

Implies: -selfing is occurring

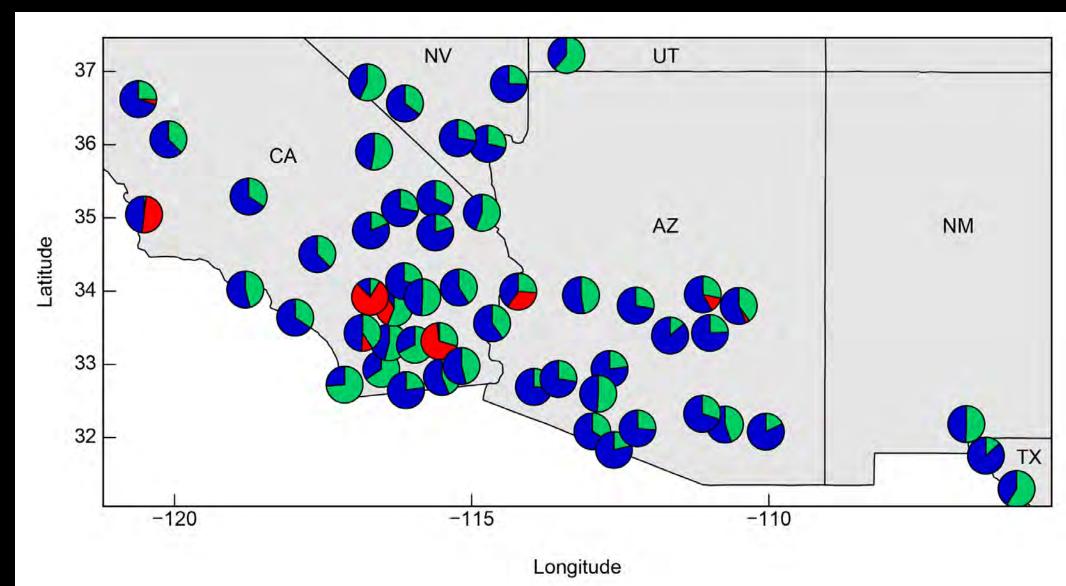
Standardized Index of Association



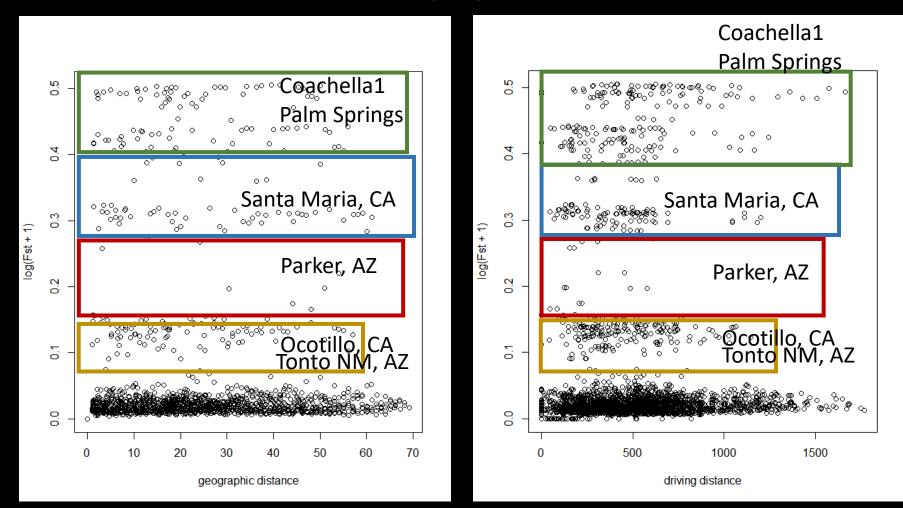
Population structure in US



Haplotype map



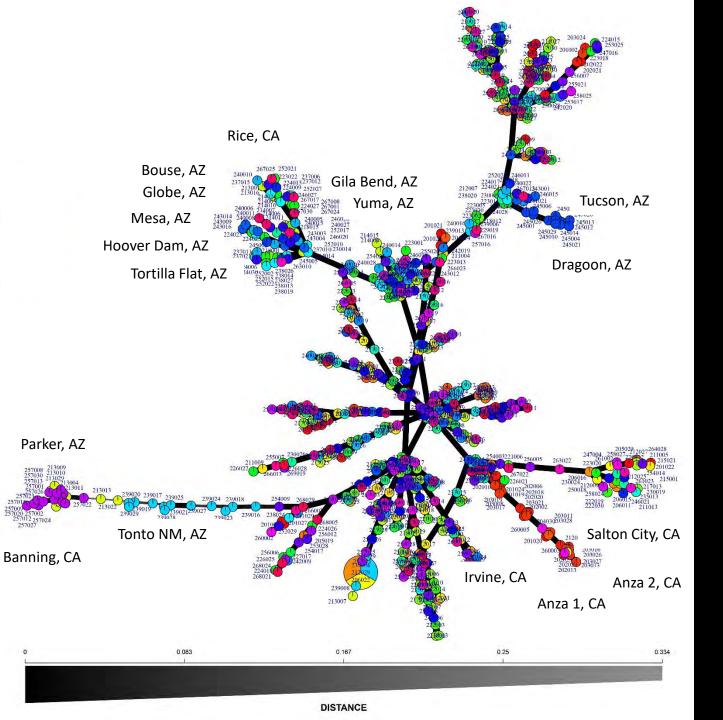
Diversity by distance



IBD Mantel tests not significant

Minimum spanning network

Regional grouping provides evidence for invasion pattern



Conclusions & next steps

3 genetically distinct populations in US

Multiple introductions seem likely

Selfing is prevalent in invaded range



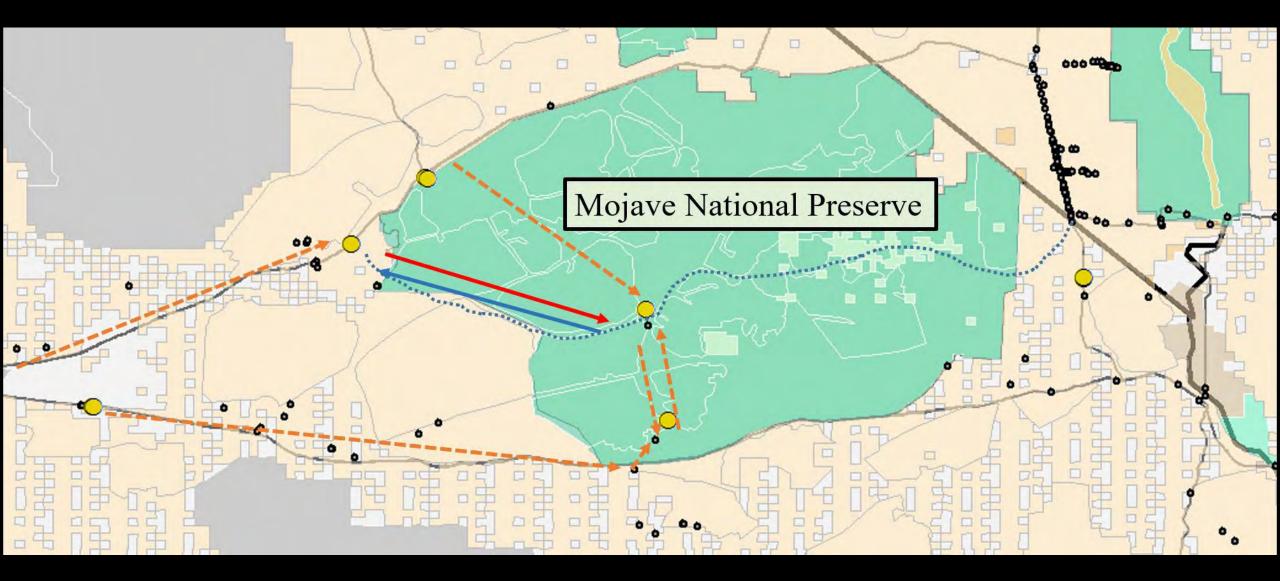
Conclusions & next steps



- Sequence native samples to identify origin(s)
 - Collected thus far: France, Italy, Israel, Turkey, Jordan, Qatar



Applied needs





Germination strategies, maternal investment, phenology, allocation strategies

Thank you

Huxman Lab

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Citizen Scientist Groups/Parks

-Tubb Canyon Desert Conservancy, AmeriCorps

-Death Valley NP weed eradication volunteers

-Park managers and staff



