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
Methods

2,061 individuals from 70 unique localities
Methods

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

Population structure: 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
Results

Heterozygosity is higher than expected
~ 95% of loci

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

Thin plate spline of Standardized $I_a$

Implies:

- selfing is occurring
Results

Population structure in US
Results

Haplotype map
Results

Diversity by distance

IBD Mantel tests not significant
Results

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

Mojave National Preserve
Germination strategies, maternal investment, phenology, allocation strategies
Thank you

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Results