Origins of Invasive French Broom

Annabelle Kleist PhD Candidate, UC-Davis







Spatio-Temporal Stages of the Invasion Process

Transport	Colonization	Establishment	Landscape Spread
Species whose propagules are transported over long distances may become "casual" in a new region	Abiotic factors determine whether propagules survive in the new habitat and affect growth rates	Several processes create "biotic resistance" to establishment, suppressing non- native species' reproductive rates	Spread rates depend on establishment, dispersal ability, habitat connectivity, etc
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Hybridization and Invasion



Zebra + Donkey = Zeedonk (sterile)



Tamarix chinensis + *T. ramosissima* = invasive *Tamarix* in the States (not sterile)

Hybridization and Invasion



T. chinensis + *T. ramosissima* = invasive *Tamarix*







French Broom

Evolutionary relationships among invasive brooms

French broom characteristics





French Broom Distribution



Horticulture Connection: Sweet Broom

- Putative close relative of French broom
 - Evolutionary relationships unclear because it is sold under a variety of scientific names
- Common scientific names:
 - Cytisus spachianus, Teline stenopetala ssp spachiana, G. spachiana, and T. canariensis







French broom identity: Hypotheses



Genista monspessulana



Genista stenopetala



Phylogenetic Approach



Objectives:

- 1. Identify sources of invasive broom populations in CA
- 2. Determine whether hybridization between ornamental cultivars and invasive populations has occurred

Rationale:

- Species identity of invasive French broom is unknown
- Species identity of ornamental sweet broom is unclear
- Contribution of currently available ornamental brooms to invasive populations is unknown

Experimental Design



Sampling:

- >20 invasive populations throughout CA
- Collect sweet broom from >10 nurseries and landscape plantings

Data Collection:

- DNA extracted from each individual
- Sequence 4 DNA regions from each plant
 - 2 nuclear: ETS and ITS (+ 8 sequences per invasive or ornamental individual)
 - 2 chloroplast: *trnL-F* and tRNA-leu

Data Analysis:

 Reconstruct relationships among organisms using Maximum parsimony and Bayesian analyses





California Sampling

Populations Sampled



Total # of Invasive Populations: 23 Total # of Landscape Plantings: 7 Total # of Nursery Plants: 5

Methods: Molecular Phylogenetics

Phylogenetic trees show evolutionary relationships



Hypotheses and Expected Results



Ornamental sweet broom

Invasive French broom

Ornamental sweet broom does contribute to invasive broom populations

Alternatively

Invasive French broom Invasive French broom Ornamental sweet broom Ornamental sweet broom

2.

Ornamental sweet broom may not be contributing to invasive broom populations



Chloroplast Results

Sweet broom

- All ornamental and landscape sweet broom
- Some invasive brooms from urban invasions
- G. canariensis
- G. stenopetala

Invasive "French Broom" Group

- Invasive "French Broom"
- Genista monspessulana
- Genista canariensis



ITS Results (nuclear region)

Sweet broom Group

- Ornamental and landscape clones
- ¹/₂ of the sequences from 5 invasive broom individuals
- Genista stenapetala and Genista canariensis

Invasive "French broom" Group

- Invasive "French broom" sequences
- Genista monspessulana

Conclusions

Ornamental Brooms:

- Ornamental sweet broom most likely contributes via hybridization to invasive broom populations
- At least 2 different things are sold as Sweet Broom:
 - 1. G. stenopetala
 - 2. G. stenopetala and G. canariensis hybrid

Invasive French broom:

Most of the invasive French broom in CA is G. monspessulana



Next Steps

 What are the cultivated sources and introduction history of invasive French broom populations in natural and urban areas of California?

Trace the origins and spread of invasive populations by characterizing genetic structure in the native and introduced range

2. Do French broom populations have similar patterns of genetic diversity, introduction, and structure in California and Australia?

Trace the origins and spread of invasive populations by characterizing genetic structure in the native and 2 introduced ranges

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