Multi-scale Ecological Understanding of Cogongrass: Landscape Genetics and Habitat Modeling

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Workshop: Biology and Control of cogongrass (IM): Research and Management Updates
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Overview

- Background
- Research Question(s)
- Habitat Modeling
  - Methodology
  - Results
- Landscape Genetics
  - Methodology
  - Results
- Conclusions
Background
Cogongrass: Documented Introductions

Directly introduced twice, into:

– Mobile Bay, AL in 1912 (accidentally from Japan).

– McNeil, MS in 1921 (purposefully for forage from the Philippines).

(Tabor 1949, 1952)

Map courtesy of the Bugwood Network and cogongrass.org.
Background

Negative Effects of Cogongrass Invasion

– Ecological
  • Displaces native plant and wildlife species
  • Alters fire regimes to more frequent & intense events
  • Creates monotypic stands post-burn

– Economic
  • Management and/or eradication costs
  • Invasion of agricultural crop systems
  • Unusable for forage
  • Silvicultural losses in pine plantations

Ervin 2007
Background

Research Question

Landscape approaches create a picture of historical, current, and predicted invasive plant species distribution.

Allows assessment and management on a landscape scale.

Genetic analysis: Detect historical events

- Infer native range
- Detect genetic patterns

Habitat Modeling:

- Predict future occupation based on current invasion
- Assess threats to conservation/restoration efforts
Research Question

• What do the patterns of extant genetic variation and geographic distribution tell us about invasive plant occurrence and potential spread?

• Can these patterns accurately predict future invasive species distribution (e.g., into new areas or areas of concern/management)?
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• Conclusions
Habitat Modeling
General Approach

Occurrence points
Habitat Modeling
General Approach

Occurrence points

Environmental data
Slope
Vegetation
Soil moisture
Habitat Modeling

General Approach

Occurrence points

Environmental data

- Slope
- Vegetation
- Soil moisture

Predicted habitat
Habitat Modeling
Methods: Environmental Modeling

- Tree canopy cover
- Soil silt content
- CEC
- Organic material
- Soil pH
- Available soil water

+ Locations of *Imperata*
Habitat Modeling

Methods: Maximum Entropy (MaxEnt) Modeling (Phillips et al.)

Maxent software for species habitat modeling

Most current version 3.3.3a (see new feature below).

Use this site to download software based on the maximum-entropy approach for species habitat modeling. This software takes as input a set of layers or environmental variables giving species...

Further description of this approach can be found in:

- **Bjorn H. H wired, Maxent Odds, Robert E. Schapire**
  A maximum entropy approach to species distribution modeling.
  [pdf]

- **Bjorn H. Wired, Robert E. Anderson, Robert E. Schapire**
  Maximum entropy modeling of species geographic distributions.
  (Documents used in this paper are available below)
  [pdf]

**Terms of use:** This software may be freely downloaded and used for all educational and research activities. This software may not be used for any commercial or for further distributed. By clicking on the download button below, you agree to the terms.

Please provide your name, institution and email address prior to downloading.

Name:
Institution:
Email:

Current version (recommended): 3.3.3a

Older, archived versions: 3.3.3 3.3.2 3.3.1 3.3.0-beta 3.2.19 3.2.1 3.1.0 3.0.6-beta 3.0.4-beta 3.0.3-beta 3.0.2-beta 3.0.1-beta

http://www.cs.princeton.edu/~schapire/maxent/
Habitat Modeling
Methods: Mississippi Spatial Data
Habitat Modeling

Results:

- 50% probability
- 70% probability
Habitat Modeling

Results

Receiver Operator Characteristic curve

<table>
<thead>
<tr>
<th>Method</th>
<th>Model</th>
<th>Validation</th>
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</thead>
<tbody>
<tr>
<td>Sensitivity = specificity</td>
<td>26%</td>
<td>27%</td>
</tr>
<tr>
<td>Max sensitivity &amp; specificity</td>
<td>29%</td>
<td>27%</td>
</tr>
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</table>

Area under the curve
Training 79%
Validation 79%

Omission rates

Training data (AUC = 0.794)
Test data (AUC = 0.787)
Random Prediction (AUC = 0.5)
Habitat Modeling

Results

Tree canopy

Contributes 77% of the MaxEnt model variation

Soil silt content

Contributes 10% of the MaxEnt model variation
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Landscape Genetics Application  (Ward et al. 2008)

Test major hypotheses, such as:

- Enemy release
- Evolution of increased competitive ability (EICA)

Plant Species Invasion

- History
- Process and Patterns
- Management
- Evolution
Population Genetic approaches can address:

- Extant levels of genetic diversity within and among populations
- Degree of population subdivision
- Number and potentially, timing of introductions
- Demography of the population
- Bottleneck or population expansion?
- Which genes/genotypes are responsible for spread into new areas.
Landscape Genetics
Methods: Field Sampling

Mississippi: 8-sampled populations (n=150)

Alabama: 10-sampled populations (n=208)

(N=358)
Landscape Genetics
Methods: DNA extraction


- Dried leaf tissue disrupted and homogenized in a bead mill.

- Purified DNA is individually labeled and stored in -20°C freezer.
Landscape Genetics
Methods: AFLPs

Amplified Fragment Length Polymorphisms
Dominant marker based on length (bp)
Presence or Absence (0/1)

- PCR-based
- Genomic DNA undergoes:
  - Digestion with restriction enzymes
  - Ligation with adaptors
  - Pre-selective Amplification
  - Selective Amplification with fluorescent tags (FAM, HEX, NED) and ROX-1000 standard

Selective Primer Combinations

<table>
<thead>
<tr>
<th>Msel-CAT</th>
<th>EcoRI-ACT-FAM</th>
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<tbody>
<tr>
<td>Msel-CTA</td>
<td>EcoRI-AGG-HEX</td>
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<tr>
<td>Msel-CTG</td>
<td>EcoRI-AGC-NED</td>
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<tr>
<td>Msel-CTT</td>
<td>EcoRI-ACT-FAM</td>
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<tr>
<td>Msel-CTC</td>
<td>EcoRI-AGG-HEX</td>
</tr>
<tr>
<td>Msel-CAC</td>
<td>EcoRI-AGC-NED</td>
</tr>
</tbody>
</table>

Meudt & Clarke 2007
Methodology
Methods: Data Development & Management

- Amplified DNA fragments run on ABI 3730 capillary sequencer (Arizona State University)
- Raw data files were analyzed in GeneMarker (SoftGenetics)
- Data matrices were auto-scored and managed in Excel 2007 (Microsoft, Inc.) and PASW v.18.0 (SPSS, Inc.) (Walker & Lucardi).
- Conversions utilized AFLPdat (D. Ehrich) and R v.2.13.0.
- Further genetic analyses were conducted in:
  - GenAlEx v.6.3 (Peakall & Smouse, 2006)
  - Arlequin v.3.5 (Excoffier & Lischer, 2010)
  - STRUCTURE v.2.3.3 (Pritchard et al., 2000a; Falush et al. 2007)
Landscape Genetics
Preliminary results from 2010

- 7-Mississippi populations
- N = 140
- $\phi_{PT} = 0.35$ (P < 0.001)
Results: Genetic Diversity

- 1746 polymorphic loci were found across six selective primer combinations
- Mean heterozygosity ranged from \((0.003 - 0.019)\)
- Nei’s pairwise genetic distance ranged from \((0.001 - 0.016)\)

<table>
<thead>
<tr>
<th>Population</th>
<th>%P</th>
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</thead>
<tbody>
<tr>
<td>Pop1</td>
<td>7.50%</td>
</tr>
<tr>
<td>Pop2</td>
<td>6.41%</td>
</tr>
<tr>
<td>Pop3</td>
<td>6.82%</td>
</tr>
<tr>
<td>Pop4</td>
<td>4.87%</td>
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<tr>
<td>Pop5</td>
<td>12.20%</td>
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<tr>
<td>Pop6</td>
<td>10.19%</td>
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<tr>
<td>Pop7</td>
<td>4.35%</td>
</tr>
<tr>
<td>Pop8</td>
<td>4.01%</td>
</tr>
<tr>
<td>Pop9</td>
<td>6.93%</td>
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<td>Pop11</td>
<td>8.88%</td>
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<tr>
<td>Pop12</td>
<td>15.06%</td>
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<td>Pop13</td>
<td>4.64%</td>
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<td>Pop14</td>
<td>5.67%</td>
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<tr>
<td>Pop15</td>
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<td>Pop16</td>
<td>3.44%</td>
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<tr>
<td>Pop17</td>
<td>3.38%</td>
</tr>
<tr>
<td>Pop18</td>
<td>8.53%</td>
</tr>
<tr>
<td>Mean</td>
<td>7.11%</td>
</tr>
<tr>
<td>SE</td>
<td>0.77%</td>
</tr>
</tbody>
</table>
Landscape Genetics

Results: Frequency of Rare Alleles

![Bar chart showing the frequency of rare alleles for different markers.

- No. Private Bands
- No. LComm Bands (<=25%)]
Landscape Genetics

Results: Partitioning of Molecular Variance ($\Phi_{PT}$)

Partitioning of Molecular Variance within and among sampled populations in MS & AL

$\Phi_{PT} (F_{ST} \text{ analog}) = 0.346$ 
(P < 0.001)

- Among Pops 35%
- Within Pops 65%
Landscape Genetics

Results: AMOVA

**Analysis of Molecular Variance**

- Utilizes F-Statistics (Wright 1931, 1951)
- Measure of population differentiation based on genetic differences (aka, the Fixation Index)

\[ 0 < F_{ST} < 1 \]

- Between *sampled* populations in MS & AL

\[ F_{ST} = 0.444 \quad (P<0.001) \]
Landscape Genetics
Results: STRUCTURE

K=3

Bienville NF, MS
DeSoto NF, MS
West Central AL (Talladega NF)
Mobile Bay, AL
Auburn, AL

Alabama populations

DeSoto NF, MS
Bienville NF, MS
Summary: Mississippi and Alabama

Summary:

- Significant genetic variation within and among populations in Mississippi and Alabama, with majority of genetic variation is significantly partitioned within populations ($\Phi_{PT} = 0.35$, $P<0.001$).

- Evidence of significant population differentiation between MS & AL ($F_{ST} = 0.44$, $P<0.001$).

- Unbiased population structure infers three distinct genetic groups: Bienville NF, DeSoto NF, and Alabama populations, $K=3$).

- Detection of a high number of private bands (or rare alleles, $>100$) suggests recent population expansion in one AL population.
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Conclusions
Summary

• Greater genetic separation between populations in Mississippi than populations in Alabama

• Evidence of asymmetrical introgression of alleles (unequal recombination)

• Influential variables and model performance/fit differed significantly between MS & AL
Conclusions

Future Directions

- We found three genetic groups from STRUCTURE analysis.
- Use genetic information to predict geographic distribution.
- Incorporate genetic information from these groups into a landscape model using MaxEnt.
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Questions?