Population Genetics of Polygala lewtonii: high self-fertilization rate and fine-scale structuring of genetic variation

Joel Swift, University of Central Missouri
Refugia in Florida

• 11 major glaciations occurred during the Pleistocene.

• As glaciers advanced and receded the sea level globally decreased and rose accordingly.

• This rising of sea levels caused plants and animals to move to higher elevations such as Lake Wales Ridge.
The Lake Wales Ridge acted as a refuge for plant and animal species.

20 plant species endemic to the ridge are classified as federally endangered.

Since the colonization of Florida the ridge’s ecosystems have been degraded and fragmented by human development. (Only 15% remains)

“Sculpted by the sea and maintained by fire”
Polygala lewtonii

- Perennial herb.
- Multiple stems with a bushy appearance.
- Found only on yellow sandy soils on the ridges of Florida.
- Adapted to frequent burning of its habitat.
- Federally endangered.
• *P. lewtonii* possesses three types of flowers:

1. Above-ground, open, cross pollinated (chasmogamous)
2. Above-ground, closed, self pollinated (cleistogamous)
3. Below-ground, closed, self pollinated (cleistogamous)
Amphicarpy

• Plant that produce two types of offspring with different ecological roles.

1. Dispersal
2. Recovery from stochastic disturbance

• *P. lewtonii* uses two types of seeds to fit these ecologic roles.

1. Above-ground seeds, available to be dispersed.
2. Below-ground seeds, remain viable in seed bank.

Aboveground seeds, *Polygala lewtonii*
Research Goal

• To investigate the primary mode of reproduction in *Polygala lewtonii* and its effects on fine-scale and rangewide patterns of genetic structure.

**Hypotheses**

1. If *P. lewtonii* is reproducing primarily via self-fertilization then we should see tight clusters of highly similar individuals with most genetic variation among populations.

2. If *P. lewtonii* is primarily reproducing via outcrossing then, we should see greater genetic variation across the landscape.
Sampling

- Fine scale genetic structure was assessed with 4 blocks with 72 individuals each, broken down into 8 plots.

- Rangewide genetic structure was assessed with an additional 3 Blocks with 24 individuals each.

- In total 360 tissue samples were collected.
DNA was extracted using a CTAB extraction method.

Utilized 12 microsatellite loci to look for variation among individuals.
Fragment analysis and scoring was carried out to call the alleles (Bp size repeats) with the program Genemarker.
Analysis

• Summary analyses of the data looked at diversity within populations and patterns of genetic structure among populations.
• Low heterozygosity expected (0.016 to 0.474) and even lower heterozygosity observed (0.006 to 0.108).

• Very high $F_{IS}$ values (0.572 to 0.885), average of 70% of reproduction through inbreeding.
Results

High genetic differentiation among populations (0.251 to 0.671).

These values are extremely large, higher than what is normally seen between different species.

<table>
<thead>
<tr>
<th></th>
<th>Block 1</th>
<th>Block 2</th>
<th>Block 3</th>
<th>Block 4</th>
<th>ONF</th>
<th>LWR</th>
<th>SPP</th>
</tr>
</thead>
<tbody>
<tr>
<td>Block 1</td>
<td>-</td>
<td>0.634</td>
<td>0.604</td>
<td>0.436</td>
<td>0.692</td>
<td>0.511</td>
<td>0.506</td>
</tr>
<tr>
<td>Block 2</td>
<td>0.634</td>
<td>-</td>
<td>0.251</td>
<td>0.548</td>
<td>0.582</td>
<td>0.462</td>
<td>0.671</td>
</tr>
<tr>
<td>Block 3</td>
<td>0.604</td>
<td>0.251</td>
<td>-</td>
<td>0.498</td>
<td>0.498</td>
<td>0.417</td>
<td>0.621</td>
</tr>
<tr>
<td>Block 4</td>
<td>0.436</td>
<td>0.548</td>
<td>0.498</td>
<td>-</td>
<td>0.570</td>
<td>0.397</td>
<td>0.481</td>
</tr>
<tr>
<td>ONF</td>
<td>0.692</td>
<td>0.582</td>
<td>0.498</td>
<td>0.570</td>
<td>-</td>
<td>0.361</td>
<td>0.637</td>
</tr>
<tr>
<td>LWR</td>
<td>0.511</td>
<td>0.462</td>
<td>0.417</td>
<td>0.397</td>
<td>0.361</td>
<td>-</td>
<td>0.480</td>
</tr>
<tr>
<td>SPP</td>
<td>0.506</td>
<td>0.671</td>
<td>0.621</td>
<td>0.481</td>
<td>0.637</td>
<td>0.480</td>
<td>-</td>
</tr>
</tbody>
</table>
Pairwise Genetic Distance Tree

Sampling Map
Conclusions

- *P. lewtonii* relies primarily on self-fertilization for its reproduction.

- Very fine scale structuring of genetic variation.

- The majority of the genetic variation of the species is among populations.

- Each population has a group of individuals that are very highly similar to one another and extremely different from geographically close neighbors.
To protect the full range of genetic variation we have to protect every population.

More efficient conservation efforts should focus on seed banking populations that are on unprotected land.

Habitat loss remains the biggest threat to *P. lewtonii* as the ridge is developed for human use.
Thank you to everyone that helped make this project a success.

Dr. Christine E. Edwards
Dr. Burgund Bassüner

Archbold Biological Station:
Eric Menges
Stacy Smith
Carl Weekly

MBG staff
Dr. David Bogler
REU students

Funding:
MBG
NSF
FDACS
Thank you