Demography at different scales in the widespread tropical species Symphonia globulifera (Clusiaceae)

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Introduction

Non-random distribution of genotypes: spatial genetic structure (SGS)

Demographic processes and divergence in populations

Main drivers:
- Local genetic drift
- Gene dispersal abilities
- Local selective processes
- Barriers to gene flow
- Distance
- Adaptation

Fine-scale SGS within populations

Wide-range SGS among populations
The species *Symphonia globulifera* (Clusiaceae)

- Widespread late-successional rainforest tree → Afro- and Neotropics
- “Living fossil”: pollen fossils of 45 Ma in the Niger delta, fossils of at least 15-18 Ma in Mesoamerica, 15 Ma in South America
- High ecological amplitude: rainfall of 650–2100 mm, 0 - 2600 m a.s.l.
- Hermaphroditic, fleshy drupes → animal pollination and seed dispersal
- Different morphotypes in several regions
The within-population SGS

Markers:
- 6 Nuclear SSR: SG03, SG10, SG18, SG19, SGC4, SG06
- Plastid DNA-Sequences (cpDNA intergenic spacer: psbA-trnH)
**Hypothesis**

1. **Is within-population SGS significant?**
   
   - **Drift-dispersal equilibrium?** (genetic similarity decreases with distance, IBD theory)

   ![basic expected pattern](image)

   - **mutual influence**

2. **Are there any similarities in the strength and patterns of SGS in groups of populations due to common drivers?**

   - **Within-population spatial discontinuities in allele frequencies?**

   ![different gene pools](image)

   - **assortative mating**
   - **Topographic features**
   - **secondary contact**
   - **isolation by environment**
   - **behaviour of dispersers**
**SGS assessment**

- **Markers:**
  - SGS maternally inherited >> SGS biparentally inherited

- **Continents:**
  - Higher SGS in Africa: gene flow is more restricted
  - Weaker SGS in America

**Sp** statistic quantifies the SGS strength (Vekemans & Hardy 2004)

- America SSR Sp = 0.0116***
- Africa SSR Sp = 0.0223***

**Markers:**

- BCI
- Yasuní
- Paracouda
- Ituberá
- São Tomé
- Mbikiliki
- Nkong Mekak

**Continents:**

- America
- Africa
Similarities in groups of populations

**America**
- **Topography:**
  altitudinal sampling range = 25-72 m
- **Communities of dispersers:**

<table>
<thead>
<tr>
<th>Visitors</th>
<th>Function</th>
</tr>
</thead>
<tbody>
<tr>
<td>hummingbirds</td>
<td>pollinator</td>
</tr>
<tr>
<td>perching birds</td>
<td>pollinator</td>
</tr>
<tr>
<td>lepidoptera</td>
<td>pollinator</td>
</tr>
<tr>
<td>bees</td>
<td>pollinator</td>
</tr>
<tr>
<td>scatter-hoarding rodents</td>
<td>Seed disp.</td>
</tr>
<tr>
<td>nocturnal arboreal mammals</td>
<td>Seed disp.</td>
</tr>
<tr>
<td>monkeys</td>
<td>Seed disp.</td>
</tr>
<tr>
<td><strong>tapirs</strong></td>
<td>Seed disp.</td>
</tr>
<tr>
<td><strong>bats</strong></td>
<td>Seed disp.</td>
</tr>
</tbody>
</table>

**Africa**
- **Topography:**
  altitudinal sampling range = 365-1225 m
  complex relief
- **Communities of dispersers:**

<table>
<thead>
<tr>
<th>Visitors</th>
<th>Function</th>
</tr>
</thead>
<tbody>
<tr>
<td>sunbirds</td>
<td>pollinator</td>
</tr>
<tr>
<td>monkeys</td>
<td>Seed d.</td>
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<tr>
<td>ruminants</td>
<td>Seed d.</td>
</tr>
<tr>
<td>hornbills</td>
<td>Seed d.</td>
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</tbody>
</table>

**A wider-ranging seed dispersal in America:**
flat topography & long-range dispersers (bats, tapirs)
Bayesian clustering analysis

**Mbikiliki**

**Nkong Mekak**

**Cytonuclear disequilibrium**

*GP* + *H*

*GP* + *H*

**secondary contact**

**STRUCTURE:**

%-pure ind (q>87%) when K>1:

- >50% in Africa
- <8% in America

$F_{ST}(q\geq0.5)$ among GP:

- America <0.08
- Africa >0.08
Distribution of ancestry coefficients suggests continuous admixture.

Absence of gene pools.

No cytonuclear disequilibrium.
## The wide-range genetic structure between continents

<table>
<thead>
<tr>
<th>Country</th>
<th>Population</th>
<th>Sample Size</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cameroon</td>
<td>Mbikiliki</td>
<td>66</td>
</tr>
<tr>
<td></td>
<td>Nkong Mekak</td>
<td>65</td>
</tr>
<tr>
<td></td>
<td>Korup</td>
<td>20</td>
</tr>
<tr>
<td>Benin</td>
<td>Porto Novo</td>
<td>20</td>
</tr>
<tr>
<td>Gabon</td>
<td>Ngounié</td>
<td>20</td>
</tr>
<tr>
<td>São Tomé Island</td>
<td>Ngounié</td>
<td>42</td>
</tr>
<tr>
<td>Brazil</td>
<td>Ituberá</td>
<td>65</td>
</tr>
<tr>
<td>French Guiana</td>
<td>Paracou</td>
<td>66</td>
</tr>
<tr>
<td></td>
<td>Regina</td>
<td>20</td>
</tr>
</tbody>
</table>

- **Genotype probabilities:**
  - Number of reads
  - Presence of both alleles

- **Two morphotypes**

- **Genotyping by sequencing**
  - Protocol in Parchman et al. (2012)
  - The “ novo assembly “
  - Assembly with the reference (5-base mismatch)
  - 1 SNP per contig

- **4921 SNPs in 367 individuals**
  - huge divergence among gene pools

- **Colonization history?**
ENTROPY plots: similar to STRUCTURE

**Benin & Sao Tomé:**
GP influence from both continents

Dispersal between continents?

**Mbikiliki & Nkong Mekak**
(Cameroon, 48 km dist): the same GP

**Gabon:** admixture of GPs

**French Guiana:**
Genetic differentiation between morphotypes

- Paracou _S. globulifera_
- Regina _S. globulifera_
- Alternative morphotype
Genetic distance increases with geographic distance

Neighbour-joining tree: genetic distance of Neis’s D
American lineages → more recent

The alternative morphotype (French Guiana) Ituberá → more related

Treemix: Tree representing drift among populations from a root based on population allele frequencies

SNAPP: Species tree based on SNPs 3 ind. / population

Coalescence model
Detection of loci under selection:

**Preliminary results:**
- Bayescan → 277 loci
- Bayescenv → 164 loci (161 already in Bayescan)

Next: LFMM software

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**Environmental variables**
- 19 Climate variables + lat/long/alt (4 PC): Worldclim data
- 15 Soil variables (4 PC): FAO data
- Climate+soil variables (5 PC)

**Significant loci: q-value <0.05**

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![Graph showing the distribution of significant loci across different environmental variables.](image-url)
Conclusions

**SGS at fine scale:**
wide diversity of SGS patterns within *S. globulifera* populations

**NO generalization** of genetic structure patterns at fine scales from a limited number of populations in widespread species

**SGS at wide scale:**
deep insight into the macroevolutionary process promoting the current wide distribution of *S. globulifera*
Thank you!

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• YOU for your attention

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