Trait variation and plant species invasion/colonization
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**Rationale**

*What makes a community more or less likely to be invaded?*

1. Propagule pressure; often
2. Disturbance: often
3. Diversity? Mixed results
4. Resource availability?
We explored the potential for plots with greater functional variation to predict invasion.

We also measured several other common predictors of invasion.
Methods

- In 2005, 50 1x1 m plots were randomly located in a field at the Queen’s University Biology Station (field ~300 m² in size)
- Field is abandoned farm land, untilled for 40 years
- All plant species in each plot were identified
- Seeds of six invaders were added to each plot in Oct. 2005
Methods

Plots were monitored through summer 2006:

a) light penetration
b) soil moisture, nitrate, ammonia
c) Number of ramets flowering in each plot
d) Number of ramets belonging to clonal species
e) Ramet density of resident species
f) Seed mass, max. height, SLA for all resident species
g) All new colonizers of plots
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A measure of multivariate trait volume

Seed mass, maximum height, and SLA were collected for each species

These traits have been found to play a role in community assembly (Weiher et al. 1998, Franzen 2004, Stubbs & Wilson 2004, Schamp & Aarssen 2009, Long et al. 2011)

From Cornwell et al. 2006
Methods

- Traits were collected from 20-25 plants per species
- Means or maxima were used as species-level traits
- Traits were transformed as necessary and standardized to zero mean with unit variance (Stubbs & Wilson 2004)
### Trait variation and plant species invasion/colonization

**Results (natural colonists):**

<table>
<thead>
<tr>
<th>Independent variable</th>
<th>Coefficient</th>
<th>P-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Plot density (ramets)</td>
<td>0.00004</td>
<td>0.486</td>
</tr>
<tr>
<td>Biomass</td>
<td>0.0002</td>
<td>0.770</td>
</tr>
<tr>
<td>% light not captured</td>
<td>0.785</td>
<td>0.436</td>
</tr>
<tr>
<td>Ave. soil moisture</td>
<td>-1.270</td>
<td>0.413</td>
</tr>
<tr>
<td>No. ramets flowering</td>
<td>-0.0005</td>
<td>0.411</td>
</tr>
<tr>
<td>Nitrate + ammonia</td>
<td>-533.91</td>
<td>0.076</td>
</tr>
<tr>
<td>No. of clonal species</td>
<td>0.0943</td>
<td><strong>0.003</strong></td>
</tr>
<tr>
<td>Species richness</td>
<td>-0.0825</td>
<td><strong>0.021</strong></td>
</tr>
</tbody>
</table>

R²=0.32; P=0.059; Multiple Regression

Convex Hull volume for the three study traits was not a significant predictor*
Conclusions: natural colonists

- Multivariate trait space was not a significant predictor of invasion in this study system
- Clonal species appear to play a role; initial species richness appears to play a marginal role, although negative
- Several other factors that have been important in other studies were not important in this particular study
Trait variation and plant species invasion/colonization

**Results: seeded invaders**

<table>
<thead>
<tr>
<th>Independent variable</th>
<th>Coefficient</th>
<th>P-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Biomass</td>
<td>-0.0034</td>
<td>0.328</td>
</tr>
<tr>
<td>Ave. soil moisture</td>
<td>-4.627</td>
<td>0.600</td>
</tr>
<tr>
<td>No. ramets flowering</td>
<td>-0.0076</td>
<td>0.082</td>
</tr>
<tr>
<td>No. of clonal species</td>
<td>0.107</td>
<td>0.546</td>
</tr>
<tr>
<td>Species richness</td>
<td>0.319</td>
<td>0.134</td>
</tr>
<tr>
<td>% Light not captured</td>
<td>13.562</td>
<td>0.054</td>
</tr>
<tr>
<td>Nitrate + ammonia</td>
<td>-4422.8</td>
<td>0.030</td>
</tr>
<tr>
<td>Plot density (ramets)</td>
<td>0.0012</td>
<td>0.026</td>
</tr>
<tr>
<td>Convex hull volume</td>
<td>0.613</td>
<td>0.043</td>
</tr>
</tbody>
</table>

Multiple Logistic Regression; $P=0.002$ (Likelihood Ratio Test Statistic)
Conclusions: seeded invaders

- Soil nitrogen, resident plant density, and resident functional trait volume are significant predictors of invasion.
- Invasion by community members is influenced by different factors than invasion by non-community members seeded in.
- This may reflect the relative contribution of the seed bank to the natural colonization process.
Success in the prediction of invasion using functional diversity may depend on the traits considered.

Prediction may be more successful when measured traits contribute evidence of limiting similarity.

We ran null model tests for the traits used here and found no evidence that trait volume in plots is significantly greater than expected by under the null model (CHV: $P=0.116$).

In fact, trait volume tended towards being lower than expected if trait suits are assigned randomly to species.

Some species may successfully invade plots by being similar to resident species while others succeed by being different.
More recently

We’ve carried out a different invasion study

- **Treatments included:**
  - a) Control plots
  - b) All flowers cut
  - c) Seed from resident species added

- **We’ve also collected trait data for all resident plant species**
More recently...

- We’ve focused on collecting a larger number of traits that have contributed to evidence of limiting similarity in other studies:

- Plant height, support fraction, leaf succulence, SLA, Leaf area, leaf angle, leaf lobation, leaf shape, number of leaves on the terminal shoot, leaf nitrogen...

(Stubbs & Wilson 2004; Wilson & Sttubs 2011)
Many thanks to...