PHENOTYPIC VARIATION, MAPPING AND QTL ANALYSIS OF ADVENTITIOUS ROOTING UNDER LOW PHOSPHORUS STRESS IN COMMON BEAN (Phaseolus vulgaris L.)

Ivan Ochoa1, Matthew W. Blair2, Kathleen M. Brown1, Jonathan P. Lynch3
1 Department of Horticulture, The Pennsylvania State University, University Park, PA 16802 USA
2CIAT, Cali, AA 6713, Colombia

Problem

- Over half of global bean production occurs on extremely P-deficient soils.
- Phosphorus distribution is highly heterogeneous in most soils, generally being greater in surface horizons and decreasing with depth.
- P efficiency is a typical quantitative trait that is subject to great environmental variability.
- Evaluations of root traits associated to mechanisms of tolerance are laborious and time consuming.

Approach

- Adventitious roots are the shallownest portion of bean root system and might explore topsoil horizons more efficiently than other root types (Lynch and Brown 2001).
- Genotypic variation was observed for both inherent ability to produce adventitious roots as well as the plasticity of adventitious rooting in response to phosphorus stress (Miller, Ochoa et al. 2002).
- Recombinant Inbred Lines (RILs) from contrasting parents for adventitious rooting will permit the genetic mapping of this trait, which will be important in understanding its genetic basis, and will enable the generation of DNA markers to assist breeding programs.

Objectives

- To characterize the phenotypic variation and genetic regulation of adventitious rooting in phosphorus limiting environments
- To develop a genetic linkage map and identify putative QTLs for adventitious root traits under low and high P conditions

Materials and Methods

- Locations:
  - Field (F): Darien, Colombia (8-week-old plants, 3 reps)
  - Greenhouse (G): PSU, PA, USA (2-week-old plants, 3 reps)
- Phosphorus treatments:
  - High P: 45 kg P2O5 (F) or 100 µM buffered Alumina-P (G).
  - Low P: 7.5 kg P2O5 (F) or 1.5 µM buffered Alumina-P (G).
- Plan Material:
  - Parents:
    - G2333: small seeded, race M from Massacassian gene pool.
    - G19839: large seeded, race N from Andean gene pool.
- Mapping population: 84 F2 Recombinant Inbred Lines (RILs).
- Root image analyses: Adventitious roots for the whole RIL population were quantified scanned with WinPhizo software program for getting root length, and oven-dried for biomass determination.
- Map construction: A genetic linkage map based on 149 genetic markers including 76 SSR, 60 RAPD, 8 SCAR, 3 STS, 1 morphological (flower color), and 1 biochemical marker (phenol) was constructed using MAPMAKER/EXP 3.0 (Lander et al., 1987) and MAPMASTOR (Loreixo, 2000) computer programs software to assign markers to the linkage groups.
- QTL identification: Putative QTLs for the traits were identified by employing interval mapping analyses and QTL Cartographer software (Basten et al., 1999).

Results and Discussion

- Table 1. Mean values, probabilities between parents and among RILs, and heritability values ($h^2$).

<table>
<thead>
<tr>
<th>Trait</th>
<th>Mean F</th>
<th>Mean G</th>
<th>Mean Difference</th>
<th>Probability</th>
<th>Heritability ($h^2$)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Adventitious root number</td>
<td>5.24</td>
<td>3.52</td>
<td>1.72</td>
<td>&lt;0.001</td>
<td>0.99</td>
</tr>
<tr>
<td>Length (mm)</td>
<td>20.4</td>
<td>10.2</td>
<td>10.2</td>
<td>&lt;0.001</td>
<td>0.99</td>
</tr>
<tr>
<td>Weight (mg)</td>
<td>9.2</td>
<td>4.5</td>
<td>4.7</td>
<td>&lt;0.001</td>
<td>0.99</td>
</tr>
</tbody>
</table>

- Table 2. Genotypic location, percentage of phenotypic variation, and genetic effect of QTLs for adventitious root traits grown under low and high P conditions in the field (F) and greenhouse (G).

<table>
<thead>
<tr>
<th>Trait</th>
<th>Location</th>
<th>Percentage</th>
<th>Genetic Effect</th>
</tr>
</thead>
<tbody>
<tr>
<td>Adventitious root number</td>
<td>F</td>
<td>30.2</td>
<td>0.80</td>
</tr>
<tr>
<td>Length (mm)</td>
<td>F</td>
<td>20.4</td>
<td>0.70</td>
</tr>
<tr>
<td>Weight (mg)</td>
<td>F</td>
<td>9.2</td>
<td>0.60</td>
</tr>
</tbody>
</table>

- Figure 1. Frequency distribution of number of adventitious roots

- Figure 2. Molecular Markers and map location of putative QTLs for several adventitious root traits in G2333/G19839 RIL population under low and high P conditions in the field and greenhouse.

- Conclusions

- There is genetic variation and transgressive segregation for adventitious rooting that could be useful for dissecting its physiological function under low phosphorus conditions.

Acknowledgments

This research was supported by bean crop CRIP and USDA-NRI grant 660207-22-90, and NM and USDA funding to MB. We acknowledge Dr. Steve Baxley from CIAT for developing the RL population used in this study and Oscar Chica for his collaboration in analyzing RAPD and SCARs markers. Also the technical assistance and collaboration of the molecular marker lab team and field team from CAT is gratefully acknowledged.

References