Identification of QTLs controlling biological nitrogen fixation in soybean

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Effort de develop soybeans for Southern Africa

- Food system highly reliant on white maize
  - Nutrient deficiencies
  - Depletion of soils (particularly for N)
- IITA leading efforts to develop alternative crops for this region
  - Includes soybeans

IITA-Laval collaboration

- Funded by International Development Research Corporation (IDRC) of Canada
- Focused on:
  - Genetic characterization of breeding materials from the IITA soybean program
  - Analysis of selected traits
    - Nodulation and nitrogen fixation
    - Asian soybean rust resistance

SNP genotyping via GBS

- 297 soybean lines
- Genotyping by Sequencing (GBS)
- 50K high quality SNPs
- Imputation

Phenotyping

- Two treatments: *Bradyrhizobium japonicum* (race 532C)
- Nitrogen fertilizer
- Temperature: 26 °C
- Relative humidity: ~60%

Population structure

(a) Dendrogram
(b) PCA
(c) Structure

Two treatments:
- Shoot Dry Weight (SDW)
- Number of Nodules (NN)
- Root Dry Weight (RDW)
- Nodule Dry Weight (NDW)
- NDW/SDW ratio
- normalized NDW (nNDW)
- NDW/RDW ratio
- SDW inoculated/SDW fertilized
- RDW inoculated/RDW fertilized
Overview of GWAS analysis

- A total of 35K tag SNPs were selected for GWAS with a MAF of >5%
- 50 highly significant SNPs were identified ($q < 0.01$)
- These markers defined 14 QTL regions

GWAS analysis

- Two treatments: *Bradyrhizobium japonicum* (race 532C)
  - Nitrogen fertilizer

Nine traits:

- Shoot Dry Weight (SDW)
- Number of Nodules (NN)
- Root Dry Weight (RDW)
- Nodule Dry Weight (NDW)
- NDW/SDW ratio
- normalized NDW (nNDW)
- NDW/RDW ratio
- SDW_{inoculated}/SDW_{fertilized}
- RDW_{inoculated}/RDW_{fertilized}

No significant associations with NN

- Ample variation (0 to hundreds of nodules)
- Too much intra-line variation

Highly significant associations with SDW

- Shoot Dry Weight (SDW)

Phenotyping

- Two treatments: *Bradyrhizobium japonicum* (race 532C)
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Nine traits:

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Distribution of SDW_{inoculated}/fertilized
Significant associations with ratios

Looking for candidates in QTL regions

Candidate gene enrichment

Conclusion

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