A Synthesis of Genome-Wide Methods for Improvement of Oat Beta-Glucan

Mark Newell – The Samuel Roberts Noble Foundation
Franco Asoro – Monsanto
Paul Scott – USDA-ARS
William Beavis – Iowa State University
Jean-Luc Jannink – USDA-ARS

Outline

- LD/Population Structure
- GWAS – World Collection, North American Elite
- Accuracy/Training Population for GS
- Comparison of Selection Methods
  - Methods
  - Results
  - Conclusions

LD/Population Structure

- Material
  - 1,200 lines, 400 DArT markers
- Results
  - $r^2 = 0.2$ at 1 cM
  - Need marker density for oat on the order of 10,000

GWAS

- World Collection
  - ~430 lines, ~800 markers
  - 3 significant markers (0.24-0.36), 1 adjacent to rice CslF gene family
- North American Elite
  - ~450 lines, ~1000 markers
  - 6 (OPN)-15 (Ames) (single marker) and 24-37 (LASSO) markers significant
  - 4 within 4 cM of previous QTL, 2 adjacent to rice candidates

Accuracy/Training Population

- Accuracy increased with:
  - Number of markers
  - Training population size
- Including older material increased or maintained accuracy
- Accuracy was greater when training population and selection candidates were more closely related
- No difference between BayesCπ and RR-BLUP

Comparison of Selection Methods

- Comparison of GS, MAS, and Pedigree-BLUP selection methods
- 2 cycles of selection, 2 replicates/selection method
- C0 Base Population
  - 446 lines
  - evaluated in UOPN, QUON, and others
Methods

- **GS**
  - \[ y = Xb + E_i + Z u_i + e \]
  - \[ \text{Var}(u) = K_V A \]
- **MS** – two stage
  - \[ y = Xb + Mo + P_i + Z u_i + e \]
  - 6 at FDR 0.33
  - Analyzed jointly
  - Index of M, P, y*
- **PS**
  - Pedigree based coancestry
- **Cluster Analysis of top 40**

Genetic Variance and Coancestry

- Significant reduction between C1 and C2 for P5
- For C2, GS and PS significantly different

Progeny Performance

- NPGS Submitted Germplasm

Conclusions

- Advantage of GS would be due to conducting at least 2 selection cycles per year
- Breeding resulted in a decrease in genetic variance and increase in genetic coancestry
- GS and MAS resulted in top-performing progenies, superiority for cultivar development
Presented Manuscripts


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