Why Malting Barley in New York?

- Farm brewery bill Passed in 2012
  - “New York State labeled beer”, permit not required to serve by glass, branch offices, tax incentive
  - Until end of 2018, at least 20% of ingredients have to be grown in NY, increasing to 60% in 2019
  - Jumps to 90% minimum by end of 2024

- How much barley is NY producing now?
  - ~1600 acres in 2015, ~2000 in 2016

- What has the Cornell Small Grains program done so far?

- Why are we implementing a NY malting barley breeding program?
Spring Two Row Malting Barley Breeding for the Northeastern U.S.

• Spring 2-row: avoid winterkill risk, short generation time, preferred by brewers & maltsters

• Dependent on excellent collaboration in the barley community – Oregon State Univ, Univ of Minnesota, Canadian and European programs et al.

• Opportunity to test approaches to rapidly and efficiently start a small breeding program from scratch
  • Integration of high-throughput phenotyping methods and genomic selection to speed up development of a spring two row malting variety adapted to New York

• Base population - 7 biparentals linked by common female parent
Traits of interest

• Fusarium head blight (*Fusarium graminearum*)
• Spot blotch (*Cochliobolus sativus*)
• Pre-harvest sprouting
• Malt quality
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| Mean  | 1085  | 1982  | 1721  | 765  | 1852  | 65.1  |

| CV    | 27.9  | 13.3  | 11.8  | 31.8  | 19.9  | 6.1   |
The primary reason for implementing a spring 2-row malting barley program for the Northeast is because the environments in the northeast pose constraints that are unique to this region – FHB, foliar pathogens, preharvest sprouting.
Near Infrared Spectroscopy: Plant Breeding Applications

• NIR spectroscopy for non-destructive measurement of chemical composition of grain
• Non-destructive prediction of grain chemistry traits - moisture, oil, protein, mycotoxins
• Can we build single kernel calibration models for barley grain protein and β-glucan for selection of single kernels in F₂ generation?
• How does early selection for quality traits in F₂ and F₃ seeds affect training population performance and selection for disease resistance?
**Single Seed Analyzer**

- Designed and built by Paul Armstrong, USDA Kansas State University
- Load seed into 48 well microtiter plate
- Single seed NIR spectroscopy
- Seed weight
- 3-D photography
- Returns seed to same well in microtiter plate
- Runs 4-48-well plates in 1 to 1.5 hrs
Calibration Samples

• Single kernels are small samples so separate calibrations for protein & β-glucan
• Each seed was run through SSA twice and absorbance values averaged
• Seed weight recorded for all samples
• Spectrophotometer wavelengths 957-1635nm used for model calibration
• Partial least squares regression models fit with ParLes chemometrics software
• Seed from replicated regional yield trials in 2014 and 2015
Calibration sets

- **Protein**: 132 seeds (12 varieties, 11 seeds each variety)
  - Destructively phenotyped on a LECO TrueMac N combustion analyzer
  - Single kernel protein values ranged from 2.9 – 19.6%
- **β-glucan**: 192 seeds (8 varieties, 12 seeds each variety)
  - Destructively phenotyped with modified Megazyme mixed linkage β-glucan enzymatic assay kit, scaled to 1/10 for microtiter plate
  - β-glucan values ranged from 0.7 - 6.3 % w/w
Calibration results:
Percent Protein

$R^2 = 0.77$ (r = 0.88)
Root Mean Sq. Error = 1.24
Mean = 10.3% protein
Calibration result: β-glucan

$R^2 = 0.51$  $(r = 0.71)$
Root Mean Sq. Error = 0.94
Mean = 3.6% β-Glucan
Selection using a single kernel protein model

Protein model adequate for selection
β-glucan model may be useful for negative selection

- 1000 F₂ seeds from each of 7 biparental populations
- Selected seeds w/ protein values between 10 & 8.5%
- Corrected for F₁ plant and spike within plant
- Selection index = protein/10 +10*(seed weight)

Selected best 10% (100) per biparental & planted in GH
Included tails of each population selected for comparison
Spring Two Row Malting Barley Breeding for the Northeastern U.S.

2016
- April: Initial crosses in
- June: 25 $F_1$ seeds from each biparental cross planted, harvested late August
- September: SSA selections made, $F_2$ seed planted early October
- December: $F_2$ harvest, select again in January

2017
- January: Plant $F_3$
- April: Harvest and field plant $F_4$, phenotype and increase seed for 2018
Experimental Plans

- Crosses
  - F1
  - Random selections
  - Single Seed Analyzer selection
    - F2 September ‘16
    - F3 January ‘17
    - F4 April ‘17 (field evaluation)

Evaluate in State-wide Trials and/or implement Recurrent Selection 2018

Planting date
- February ‘16
- June ‘16
- June ‘16
Next Steps

- Phenotype F₃:₄ selections, divergent selections, and random lines at two locations in the field summer 2017
- Evaluate potential for genomic selection for traits measured in 2017
- Explore integrating environmental or genetic covariates into model
- Seed increase for state-wide evaluation in 2018
Acknowledgements

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- **USDA National Institute of Food and Agriculture**, NRI Triticeae  Coordinated Agricultural Project 2011-68002-30029 Improving Barley and Wheat Germplasm for Changing Environments

- **Bill & Melinda Gates Foundation** grant to Cornell University for Borlaug Global Rust Initiative Durable Rust Resistance in Wheat

- **Cornell Small Grains Breeding Project Team**: David Benscher, Amy Fox, Jesse Chavez

- **Cornell Cooperative Extension Team**: Gary Bergstrom, Mike Stanyard, Kevin Ganoe et al.
Questions?
Biparental crosses

Training population summer 2017
- Two cohorts randomized together
- 2 environments + FHB nursery
- 100 lines each BP (1400 total)
- Genotype all lines
- Agronomic, disease, and malt quality phenotypes

Validation population summer 2019
Other projects

- Link between barley lipoxygenases (LOX) and FHB/DON susceptibility or resistance
  - LOX enzymes in malt lead to accumulation of compounds that contribute to stale “cardboard” taste in old beer
  - LOX also implicated in resistance and susceptibility to different pathogens in maize and wheat; complex relationships still being unraveled
  - Is a LOX locus co-localizing with FHB resistance QTL from mapping studies and GWAS?
  - Screen JIC panel and UMN population with KASP assay