Identifying Loci and Genomic Prediction Models for PHS Tolerance in Northeast Soft Wheat Breeding Programs

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Cornell University

Soft Wheat Quality Meeting
April 23rd, 2019
Physiological Maturity (PM)

Grain Development

Highest Dormancy

After-ripening

Sprout

Combine Harvest

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We are not alone - 2018 Preharvest Sprouting

England

Tobias Barber
I guess this is what you'd call pre-harvest sprouting #Harvest18

2:21 PM - 25 Aug 2018

Think rain has stopped play #wheatHarvest18 @AllpressF @LumleySean @coostiebarreyc @chrisbettinson2

2:15 PM - 27 Jul 2018

Kansas

Kyler Millershaski
I'm always happy to have rain, but not the view I want during #WheatHarvest18 #kswx

5:16 PM - 22 Jun 2018

On the edge. #wheatHarvest18

3:16 PM - 22 Jun 2018

Nebraska

Chris Cu11an
Should have brought the combines to the field 3 months ago. Just need 1 more day #Harvest18

5:06 PM - 12 Jul 2018

Farms.com

Canada

Farmers Chauffin Farms Ltd
#wheatHarvest18 started here at fermeschauvinfarms.com in StoneyPoint. Decent yields for no rain ... #OntAg #AgMoreThanEver #goodineverygrain

4:51 PM - 5 Jul 2018
Physiological Maturity (PM) after ripening leads to highest dormancy. Combine harvest methods to screen for PHS.

Methods to Screen for PHS:
1. Falling Number
   - LOW FN: "watery" grain, more starch damage
   - HIGH FN: "gravy" grain, little starch damage

2. Spike Wetting Test
   - Physiological Maturity (PM) after ripening
   - 5-7d harvest, 4d mist, score
Visible Sprout Scored

PHS Tolerant  

0 1 2 3 4 5 6 7 8 9

Roots
Germination

Coleoptile
Seedling Growth

1st Leaf

PHS Susceptible
<table>
<thead>
<tr>
<th>Both</th>
<th>Red KC</th>
<th>White KC</th>
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</table>

**GWAS**
- rrBLUP
- 4PC
- MAF > 0.05

Y ~ GID+Loc+Yr+HarvD+HD

**Sprouting Score (BLUP)**

- Both
- Red
- White

rrBLUP | 4PC | MAF > 0.05
Both Red KC White KC

QTN Across All Environments

5% Bonferroni Threshold
Do We See Different QTN Within a Single Year?

GWAS: rrBLUP | 4PC | MAF > 0.05
QTN Across Single Year

- □ Both
- ■ Red KC
- ▲ White KC

Chrm Pos

- 2008
- 2009
- 2010
- 2011
- 2012
- 2013
- 2014
- 2015
- 2016
TaVP-1A 158.4 Mbp
TaVP-1B 200.5 Mbp
TaVP-1D 710.2 Mbp
TaVP-1B 659.5 Mbp
R-A1 703.9
TaMFT-3A 7.2
TaDOG1 67.1
TaDOG1 91.1
TaA (Qsd1) 432.4
TaB (Qsd1) 693.3
TaB (Qsd1) 757.9
TaD (Qsd1) 570.7
TaD (Qsd1) 525.4
TaMKK3-A 605.0 Mbp
*estimate

TaSdr-B1 142.6 Mbp
TaSdr-D1 142.6 Mbp
TaSdr-B1 200.5 Mbp
TaSdr-D1 142.6 Mbp
TaSdr-B1 200.5 Mbp
TaSdr-D1 142.6 Mbp

TaA (Qsd1) 387.7
TaD (Qsd1) 332.0
TaMKK3-B 710.2
TaMKK3-D 556.5

PHS and Dormancy Genes
RefSeqv1.0
Positions

IWGSC, 2018
Genes in the Neighborhood

3A
- TaMFT-3A
- TaDOG1
- TaVP-1A
- R-A1

3B
- TaDOG1
- TaVP-1B
- R-B1

3D
- TaDOG1
- TaVP-1D

Red
- 627,269,712
- 737,861,720

Both
- 714,436,047
- 703,906,112

Red & Both
- 50,022,042
- 461,745,627

Red & Both
- 5,61

Both
- 665,255,992
- 755,250,882
- 757,917,663
- 566,131,654

Red
- 665,255,992
- 755,250,882

Red
- 627,269,712
- 665,255,992

Red & Both
- 5,61

Both
- 5,61

Both
- 566,131,654
- 570,799,694

KCs group sig marker position
Not found in the Both dataset…
Could the R genes be masking a 4A QTL when red and white kernels are analyzed together?
Genomic Prediction: Another Tool in the Toolbox

- **G**: Genetic Matrix (11604 GBS x 1287)
- **y**: Sprout observed phenotypes 1287
- **K**: Relationship Matrix (1287 x 1287)
- **X**: Design Matrix for fixed effects (Yr Loc etc)
- **u**: Breeding Values (GEBV)
Genomic Prediction

<table>
<thead>
<tr>
<th>All Env</th>
<th>total n</th>
<th>Five-fold CV</th>
<th>Prediction Model</th>
<th>Prediction Accuracy (PA)</th>
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<tbody>
<tr>
<td>Both</td>
<td>1287</td>
<td>Train</td>
<td>RKHS</td>
<td>cor ( \text{Pheno}<em>{\text{obs}}, \text{GEBVs}</em>{\text{model}} )</td>
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<tr>
<td>Red</td>
<td>369</td>
<td>Test</td>
<td>Ridge regression</td>
<td>cor ( y_{\text{test}}, \text{GEBVs}_{\text{train}} )</td>
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<tr>
<td>White</td>
<td>904</td>
<td></td>
<td>Bayesian LASSO</td>
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- Prediction Accuracy (PA):
  - Perfect Prediction: 1.0
  - Inaccurate: 0.0
The RKHS Model Appears to Predict Better

Prediction Accuracy

RKHS
Ridge Regression
Bayesian LASSO

1287  369  904

Combined  Red  White
### Five-fold CV

#### All Env
- **Both**: Total $n = 1287$, Train $n = 369$, Test $n = 904$
- **Red**: Total $n = 369$, Train $n = 189$, Test $n = 183$
- **White**: Total $n = 904$, Train $n = 189$, Test $n = 183$

#### Prediction Model
- **RKHS**: Colored purple
- **Ridge regression**: Colored teal
- **Bayesian LASSO**: Colored green
It’s Not as Obvious: “The RKHS Model Appears to Predict Better”

The RKHS model appears to predict better accuracy in the data compared to other models. The chart shows the prediction accuracy over different years and environments for Helfer, Ketola, McGowen, and Snyder.
Next Steps: Will Known Genes Improve Prediction?

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Mixed Model

- $Y \sim \text{GiD} + \text{Loc} + \text{Yr} + \text{HarvD} + R$
- $Y \sim \text{GiD} + \text{Loc} + \text{Yr} + \text{HarvD} + \text{MKK3}$
- $Y \sim \text{GiD} + \text{Loc} + \text{Yr} + \text{HarvD} + 2\text{BL}$
- $Y \sim \text{GiD} + \text{Loc} + \text{Yr} + \text{HarvD} + 2\text{AL}$
- $Y \sim \text{GiD} + \text{Loc} + \text{Yr} + \text{HarvD} + \text{all4}$

Fixed Marker Effects
When Implementing Spike-Wetting Tests in a Breeding Program: The Germplasm / Environment Could Affect the Variance

WA Breeding Program

NY Breeding Program

Sprouting Score

0 0.5 1 1.5 2 2.5 3 3.5 4 4.5

Standard Deviation

0 0.5 1 1.5 2 2.5 3 3.5 4 4.5

Number of Lines

n = 7.3%

n = 32.2%

Above 1.5% Deviation
Genomic Prediction: Why

What is the best model Mark Sorrells (et al) can use to predict sprouting susceptibility and tolerance if he only had the resources to genotype a line(s) and no spike wetting test

Early generations prediction?: sprouting response to a 50%-75% accuracy
Breeding for PHS

MAS known PHS genes, (MKK3, MFT, etc)

2018: 828 wheat and 414 barley plots
S.Martinez & D.Sweeney PHS genomic prediction

D.Sweeney is on track to release CNL Barley

Fine mapping Cayuga's 2B dormancy gene
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