New Tool for Selecting Small-Grains Variety

Madhav Bhatta, Lucia Gutierrez
2020 Small-Grains Conference
Springfield, IL
March 4
What is the Phenotype? \[ P = G + E + GE \]
Environment includes non-genetic factors affecting plant phenotype

**Micro-environment:** Environment of a single plant  
Controlled by good experimental design

**Macro-environment:** Environment associated with location and time  
Defining the target environments and evaluating in multiple-environment is crucial
Genotype x Environment Interaction

*Ranking of genotype changes across environment
1. How should we group locations?

2. What information should we use for choosing varieties?

3. Where should we test the varieties?
Goal of developing variety selector tool

- To build a variety selector tool for wheat, oat, and barley for each geographical region in the Midwest
- Modelling genotype x environment interaction
- Predicting the performance of varieties for that region

Map source: https://uwsslec.libguides.com
Objective

Deploy prediction model in a web-based tool for selecting the top-ranking lines in a specific location using a ZIP code system.
Methodology: Oat Variety Selector Tool

- Historical multi-environment variety testing data from *Triticeae Toolbox* (T3/Oat; https://triticeaetoolbox.org)
Model building: Curating yield data

- Oat genotypes: 2,903
- Midwestern states + New York
- Locations: 70
- Years: 1996-2018 (23 years)
- 1,021 genotypes with 10,077 SNP markers

(fewer missing data)
Genotype x Environment Characterization

- Genetic marker & environmental relationship to borrow information for untested genotypes
- Similar ranking genotypes in one mega-environment
Prediction model testing and enrichment

- Prediction model predicted the performance of lines in each mega-environment
- Enrich the GxE models with environmental covariates to predict ‘new’ environments

Temperature  Precipitation  Soil  Vegetation  Geology
wgnhs.uwex.edu
7 Mega-Environments in a Map
Use Zip Code to identify top variety

Small Grain Selector Tool
A brief explanation of how to use the tool goes here.

Tell us about your project.
Which crop are you interested in?

What is your ZIP Code?

What end market are you targeting?

Food grade
Use Zip Code to identify top variety cont.
Example: List of top cultivars for growers

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Location</th>
<th>Zip code</th>
<th>Origin</th>
<th>Released</th>
<th>Ranking</th>
</tr>
</thead>
<tbody>
<tr>
<td>MN-Pearl</td>
<td>Nashua, IA</td>
<td>50658</td>
<td>UMN</td>
<td>2019</td>
<td>1</td>
</tr>
<tr>
<td>DEON</td>
<td>Nashua, IA</td>
<td>50658</td>
<td>UMN</td>
<td>2014</td>
<td>2</td>
</tr>
<tr>
<td>SADDLE</td>
<td>Nashua, IA</td>
<td>50658</td>
<td>SDS</td>
<td>2019</td>
<td>3</td>
</tr>
</tbody>
</table>

Rank based on predicted yield and mean performance of agronomic and disease resistance traits based on recent data.
Example: List of top cultivars for breeders

Example for Mega-Environment 3

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Rank</th>
<th>ME</th>
<th>BP</th>
</tr>
</thead>
<tbody>
<tr>
<td>X10330.1</td>
<td>1</td>
<td>3</td>
<td>UWM</td>
</tr>
<tr>
<td>SD141132</td>
<td>2</td>
<td>3</td>
<td>SDS</td>
</tr>
<tr>
<td>SD141133</td>
<td>3</td>
<td>3</td>
<td>SDS</td>
</tr>
<tr>
<td>SD140517</td>
<td>4</td>
<td>3</td>
<td>SDS</td>
</tr>
<tr>
<td>X9537.4</td>
<td>5</td>
<td>3</td>
<td>UWM</td>
</tr>
<tr>
<td>SD150112</td>
<td>6</td>
<td>3</td>
<td>SDS</td>
</tr>
<tr>
<td>X10609.1</td>
<td>7</td>
<td>3</td>
<td>UWM</td>
</tr>
<tr>
<td>X10204.1</td>
<td>8</td>
<td>3</td>
<td>UWM</td>
</tr>
<tr>
<td>X9878.3</td>
<td>9</td>
<td>3</td>
<td>UWM</td>
</tr>
<tr>
<td>X10305.6</td>
<td>10</td>
<td>3</td>
<td>UWM</td>
</tr>
</tbody>
</table>

Location in ME3

<table>
<thead>
<tr>
<th>STATE</th>
</tr>
</thead>
<tbody>
<tr>
<td>URBANA IL</td>
</tr>
<tr>
<td>LAMBERTON MN</td>
</tr>
<tr>
<td>SAINTPAUL MN</td>
</tr>
<tr>
<td>BERESFORD SD</td>
</tr>
<tr>
<td>VOLGA SD</td>
</tr>
<tr>
<td>MADISON WI</td>
</tr>
</tbody>
</table>
Selector Tool: Status

• PFI have developed a beta version of the web-interface tool to provide farmers with access to best predictions using the zip-codes (releasing soon)

• Prediction model is in the process of refinement and will be deployed at large scale

• Growers will have access to zip-code predictions
Next Steps

- PFI have selected farmers for conducting on-farm experiments
- We are recruiting farmers in Wisconsin
- Testing top-performing experimental lines in public breeding programs
- Genotype and/or phenotype more lines to leverage existing data
- Enriching farmers data
- Use farmers result to improve the GxE models by increasing location coverage even at lower depth
- Tool be extended to wheat and barley
Take home message!!

• The variety selector tool will help growers and scientist in identifying best ranking genotypes
• This study will help in developing breeding strategy in the Mid-west region
• Provide further insights on utilizing large historical datasets
Acknowledgments

Cereal Breeding and Quantitative Genetics Lab

PFI
Alisha Bower
Sarah Carlson
Rebecca Clay

UIL
Jessica E. Rutkoski
Jean-Luc Jannink
Clay Birkett
David James Waring

Cornell University
Melanie Caffe
Jonathan Kelinjan

SDSU
Kevin Smith
Jochum Wiersma

UMN
Joel Ransom
Michael McMullen

NDSU
Thank you for listening 😊

Contact PFI, Alisha or Madhav (mbhatta@wisc.edu) for sharing yield data and interested in testing top-performing lines