New Tool for Selecting Small-Grains Variety



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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

Genotype x Environment Interaction

- 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
 Oats
- Modelling genotype x environment interaction

- Predicting the performance of varieties for that region
 - NORTH DAKOTA MINNESOTA Bismarck WISCONSIN SOUTH DAKOTA St Paul *Pierre MICHIGAN Madison Lansing IOWA OHIO *Des Moines NEBRASKA ILLINOIS INDIANA Lincoln ⁴ Columbus Indianapolis Springfield Jefferson City Topeka KANSAS MISSOURI

Objective

Deploy prediction model in a web-based tool for selecting the topranking 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)

WISCONSIN

Model building: Curating yield data

WISCONSIN-UNIVERSITY OF VISCONSIN-MADISON

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

Genotype x Environment Characterization

- Genetic marker & environmental relationship to borrow information for untested genotypes
- Similar ranking genotypes in one mega-environment

Factor 1 (38.17 %)

Prediction model testing and enrichment

- Prediction model predicted the performance of lines in each megaenvironment
- Enrich the GxE models with environmental covariates to predict 'new' environments

Temperature

7 Mega-Environments in a Map

Use Zip Code to identify top variety

Use Zip Code to identify top variety cont.

Genotype	Location	Zip code	Origin	Released	Ranking
MN-Pearl	Nashua, IA	50658	UMN	2019	1
DEON	Nashua, IA	50658	UMN	2014	2
SADDLE	Nashua, IA	50658	SDS	2019	3

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

Genotype	Rank	ME	BP
X10330.1	1	3	UWM
SD141132	2	3	SDS
SD141133	3	3	SDS
SD140517	4	3	SDS
X9537.4	5	3	UWM
SD150112	6	3	SDS
X10609.1	7	3	UWM
X10204.1	8	3	UWM
X9878.3	9	3	UWM
X10305.6	10	3	UWM

Location in ME3	STATE
URBANA	IL
LAMBERTON	MN
SAINTPAUL	MN
BERESFORD	SD
VOLGA	SD
MADISON	WI

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

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Thank you for listening ©

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for sharing yield data and interested in testing top-performing lines