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

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Preharvest Sprouting



The Northeast U.S. is not alone

England

Tobias Barber @ekte_Toby

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



Jim Thompson @jimt_farmer

Think rain has stopped play #wheatharvest18 @AllpressF @LumleySean @coostiebarrey @chrisbettinson2

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Kansas



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



3:36 PM - 22 Jun 2018



Pacific Northwest



Nebraska

Chris Cu11an @ChrisCullan1

On the edge. #wheatharvest18







Farms.com



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#wheatharvest18 started here at fermeschauvinfarms.com in StoneyPoint. Decent yields for no rain ... #OntAg #AgMoreThanEver #goodineverygrain





Twitter





Wheat has quite a bit of genetic variation

Year	Location	White	Red	Total (Comb)
2008	Ketola	109	11	120
	Snyder	109	11	120
2009	McGowen	109	11	120
2010	Helfer	149	59	208
	Ketola	157	59	216
	Snyder	153	59	212
2011	Helfer	198	76	274
	Ketola	206	69	275
	McGowen	208	66	274
2012	Helfer	183	80	263
	Ketola	194	78	272
	Snyder	187	74	261
2013	Helfer	52	29	81
	Ketola	56	25	81
	McGowen	106	23	129
2014	Helfer	128	85	213
	Ketola	128	85	213
	Snyder	128	85	213
2015	Helfer	218	160	378
	Ketola	192	138	330
	McGowen	195	136	331
2016	Helfer	181	192	373
	Ketola	154	185	339
	Snyder	175	184	359
2017	Ketola	199	139	338
	Snyder	199	139	338



R, GAPIT, dplyr



Genomic Prediction

random fixed effects effects **Observations/Phenotype**

u is the vector of breeding values with estimated relationship matrix K

 $\mathbf{u} \sim \mathbf{N}(0, \mathbf{K}\sigma_{g}^{2})$

Models can calculate K differently:

Ridge Regression Gaussian Kernel

```
y = X\beta + WZu + \varepsilon
```

e: experimental error

u: GEBV

design matrix

design matrix

+ (1|variety)

Genomic Prediction



0.0 Inaccurate

Genomic Prediction



Both $y_{obs_both} \sim Loc + Yr + HarvDate + KColor + (1|variety)$

Red $y_{obs} \sim Loc + Yr + HarvDate + (1|variety)$

White $y_{obs} \sim Loc + Yr + HarvDate + (1|variety)$

A comparison of Ridge Regression and Gaussian kernel models across seed coat colors



What does an accuracy of 0.6 even mean?

Accuracy of an phenotypic estimate (without genetic data)

```
PA = cor(Obs_EnvA, Obs_EnvB)
```

cor(Obs2008, Obs2009)

cor(Obs2015, Obs2017)



PA

pheno

The correlation (PA) from one environment to another environment is comparable, to genomic prediction accuracies.



rrBLUP

White kernel GWAS found multiple significant loci





Zanetti et al., 2000; Munkvold et al. 2009; Fofana et al. 2009; Zhang et al. 2013; Kumar et al. 2015; Martinez et al. 2018; Zuo et al., 2019

Will associated QTL improve prediction?

Observed phenotype mixed model

y ~ Loc+Yr+HarvD+(1|variety)

Five-fold CV



 $PA = cor (y_{obs_test}, GEBVs_{test})$

Adding significant QTL as fixed effects seems to improve accuracy for Gaussian kernel model



GAUSSadditive + non-additiveRRonly additive

GAUSS vs RR

The real question is, what do you want to use it for?

Want additive RR for selection Want +non-add for prediction

Need to investigate if adding significant QTL markers as a fixed effect is overfitting the model?

How many years between phenotyping can a breeding program skip without losing substantial PA?



How many years between phenotyping can a breeding program skip without losing substantial PA?



It may be possible to phenotype for PHS tolerance every couple of years, without effecting accuracy

Something to consider:

Increased genetic diversity year to year will reduce ability to accurately calculated GEBVs
Year to year GEBV calculations tend to have lower PA than GEBV calculated from hundreds of individuals over multiple environments

> Ridge Regression White KC only



Why use genomic prediction for this trait?

Phenotyping occurs at the end of the growth cycle

No "mid-cycle" selections before harvest



Precise sampling



Very labor intensive

Breeding for PHS tolerance

GEBVs can help guide selection; less

likely to throw out PHS Tolerant lines

when applying selection pressure

Still need to confirm selected lines with phenotyping in later generations

Assist in predicting PHS tolerance for variety selection, if unable to apply high frequency phenotypic pressure



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Munkvold et al., 2009; Kulwal et al., 2012; Martinez et al., 2018; FRANCE, CCSU, SD

FarmCPU

PHS_Blup_Red



Rasul et al 2009