

GENOMIC SELECTION OF AGRONOMIC IMPORTANT TRAITS IN SPRING BARELY AND WINTER WHEAT

AHMED JAHOOR

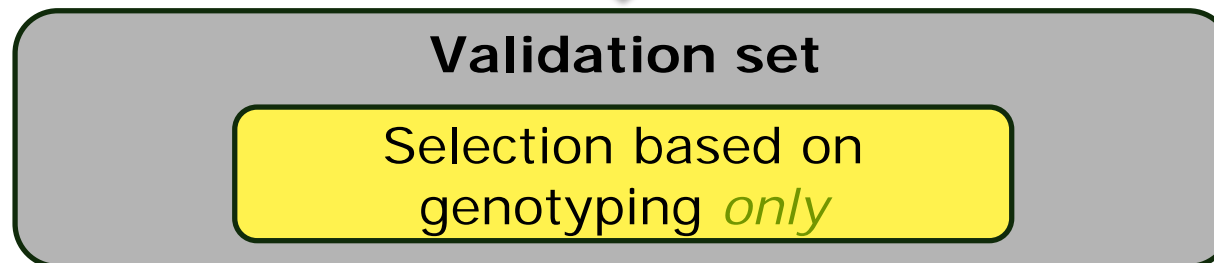
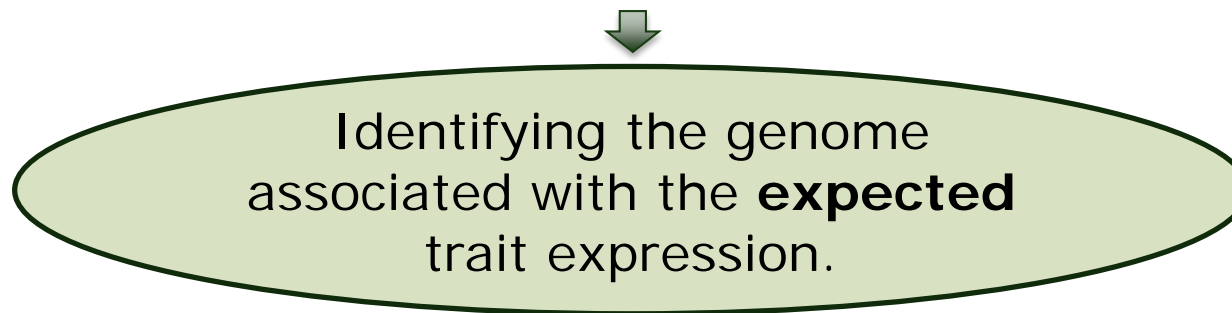
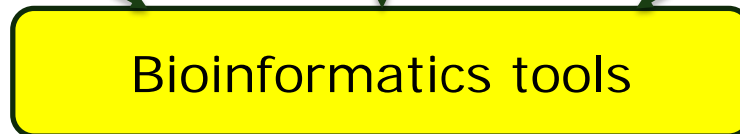
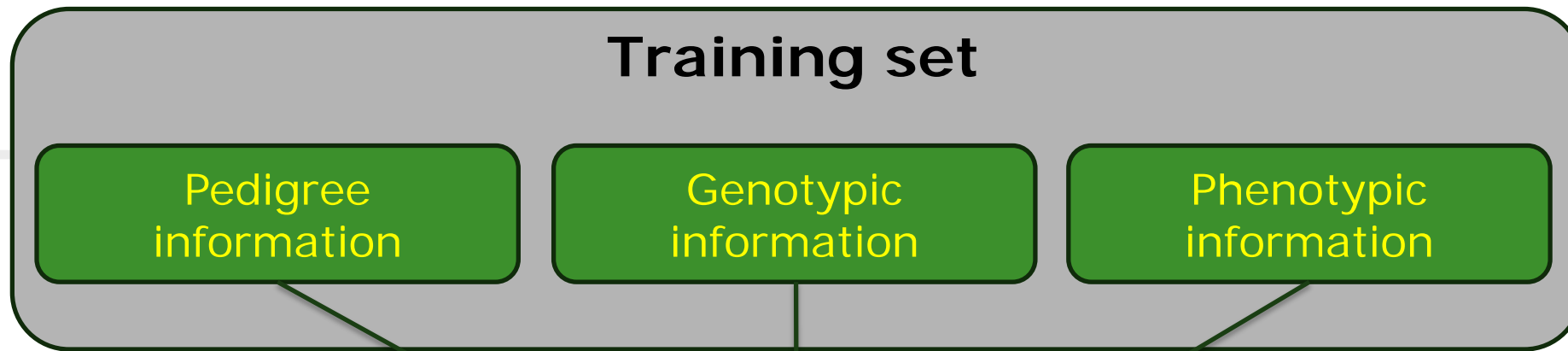


Cultivating Value



AARHUS
UNIVERSITY

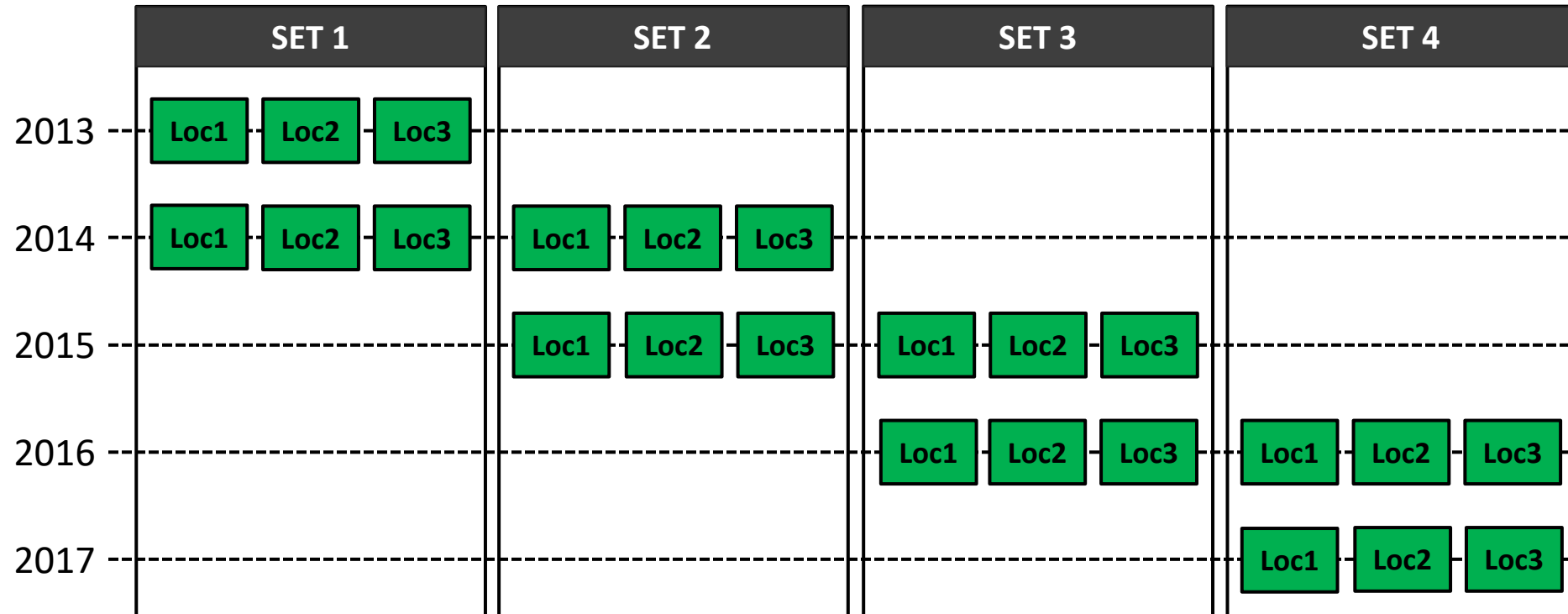
Nordic Seed 



PROJECTS CONCERNING GENOMIC SELECTION AT NORDIC SEED

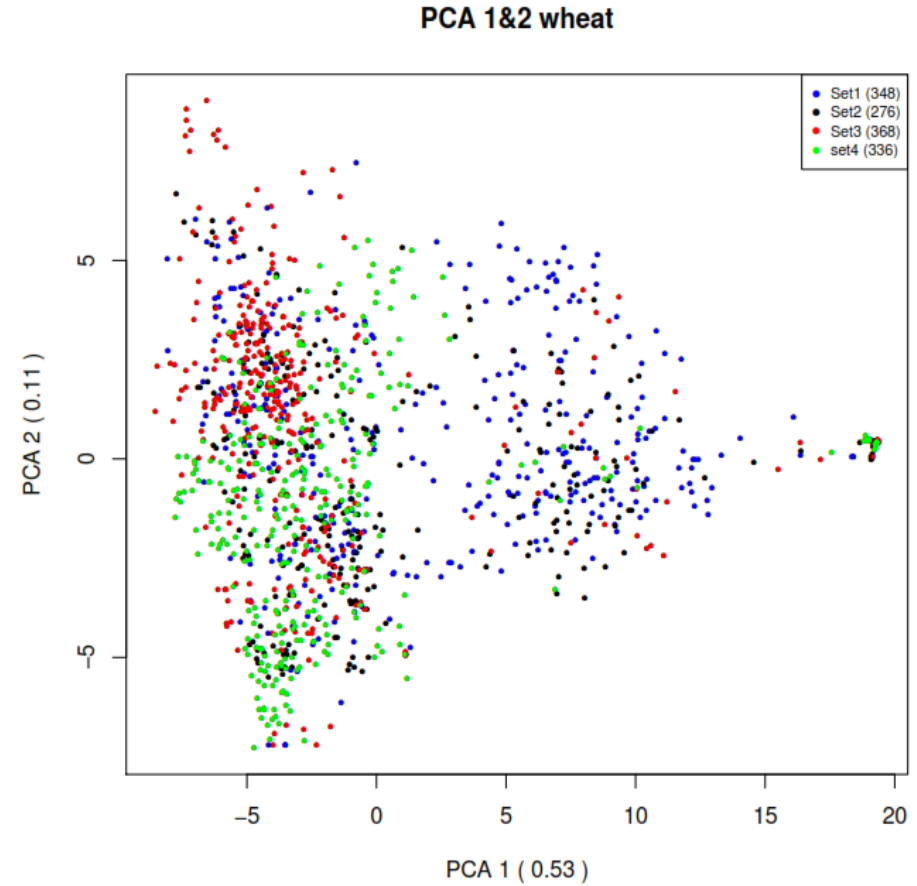
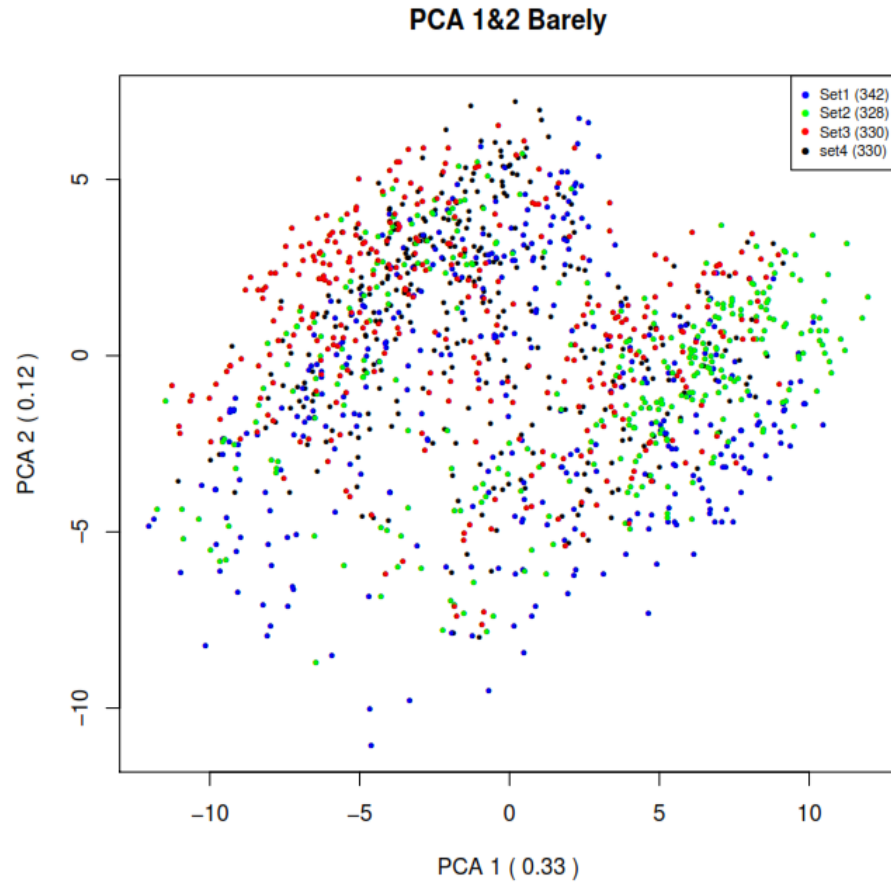
- **Genomic selection in animal and plants (GenSap) (Winter Barley)**
 - Partners: Many Partners
 - Financed: Innovation Foundation Denmark (IFD)
- **Genomic selection for complex traits in barley and wheat breeding**
 - Partners: Nordic Seed and Aarhus University (QGG)
 - Financed: Ministry of Environment and Food (GUDP)
- **Better malting barley by modeling environmental sensitivity, genomics and metabolomics**
 - Partners: Nordic Seed and Aarhus University (QGG and iNANO)
 - Financed: Innovation Foundation Denmark (IFD)
- **Prediction of baking quality in winter wheat by genomic selection**
 - Partners: Nordic Seed and Aarhus University (QGG)
 - Financed: Innovation Foundation Denmark (IFD)

EXPERIMENTAL PLAN

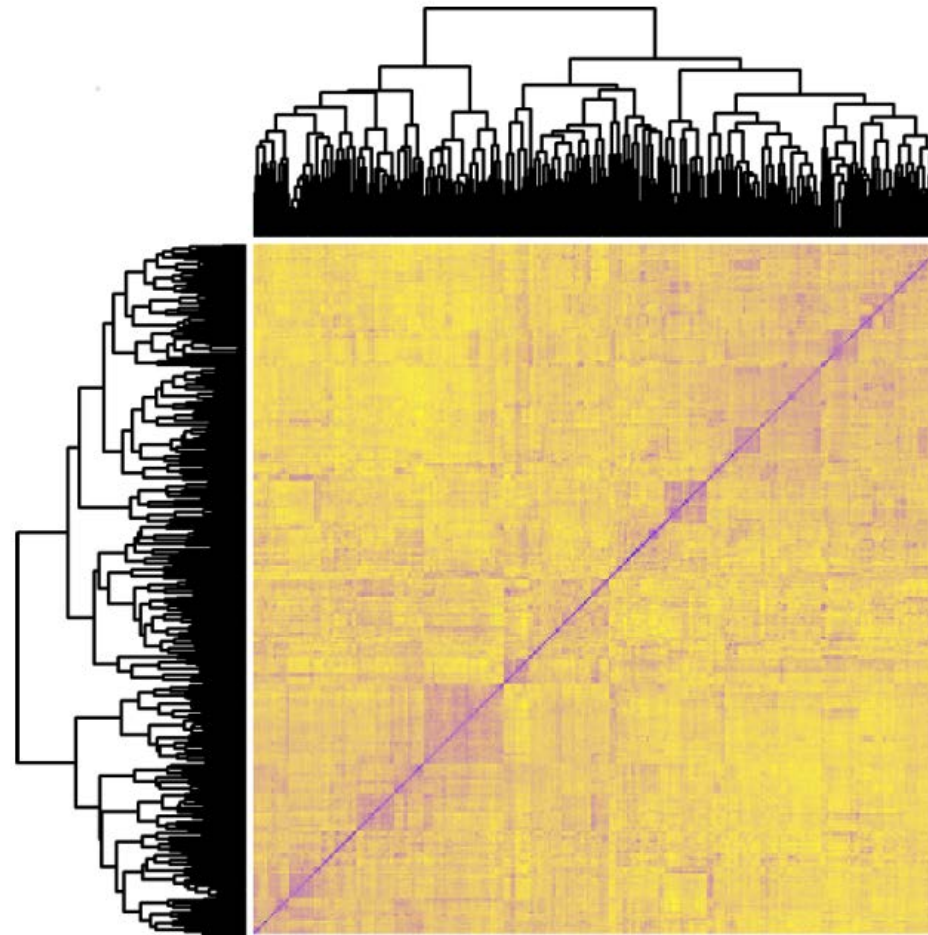


- Four sets of ~330 F6 lines from four different breeding cycles.
- The lines were tested on three different Danish locations for four consecutive years.
Three replicates were planned per each experiment.

POPULATION STRUCTURE



HEATMAP OF BARLEY LINES

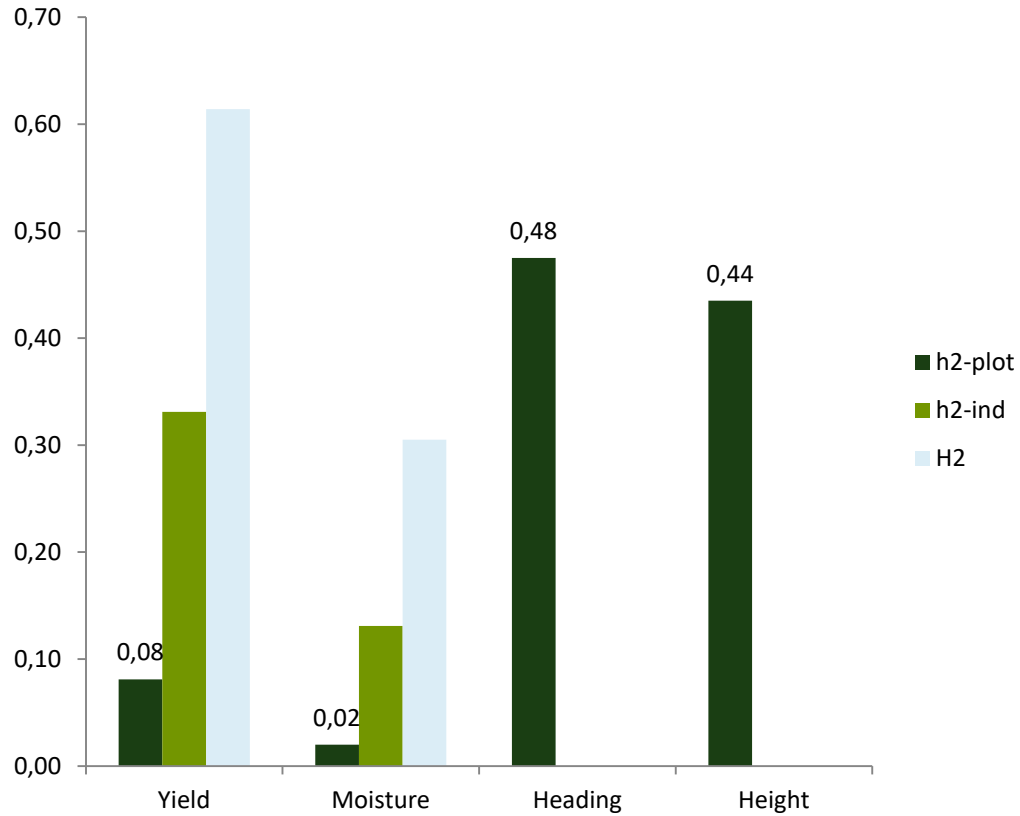


Cultivating Value

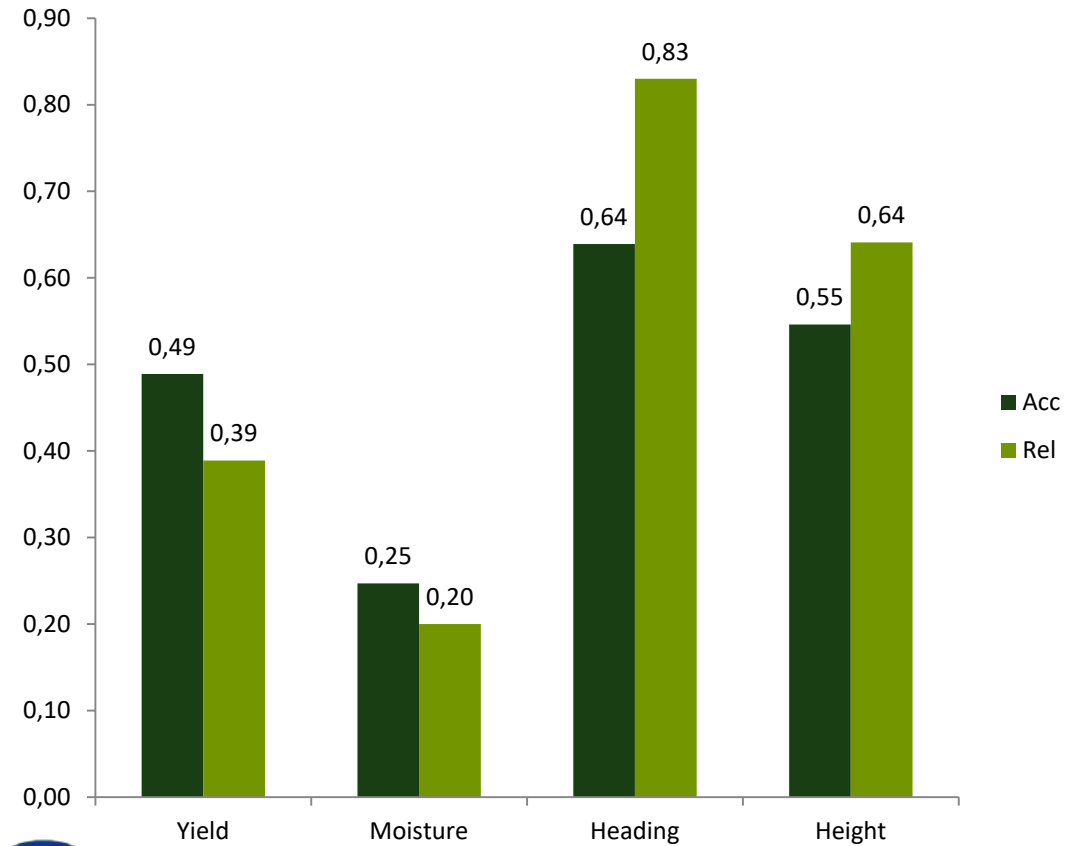


ACCURACIES & HERITABILITY

Heritability



Accuracy and Reliability



PREDICTION ACCURACIES AND HERITABILITIES (LOO)

Traits	Accuracy	Reliability	Heritability
Yield	0.49	0.39	0.33
Height	0.55	0.68	0.43
Heading	0.64	0.86	0.47
Grain 2.5 up	0.67	0.73	0.34
Grain protein %	0.56	0.54	0.31
Grain test weight	0.71	0.60	0.62
Grain Ergosterol	0.78	0.77	0.56
Malting Extract yield	0.45	0.65	0.13
Malting Wort color	0.61	0.53	0.43
Malting β -Glucan	0.33	0.15	0.51
Malting Viscosity	0.34	0.31	0.16
Malting Wort clearness	0.67	0.70	0.37

EFFECTS OF TP SIZE IN BARELY

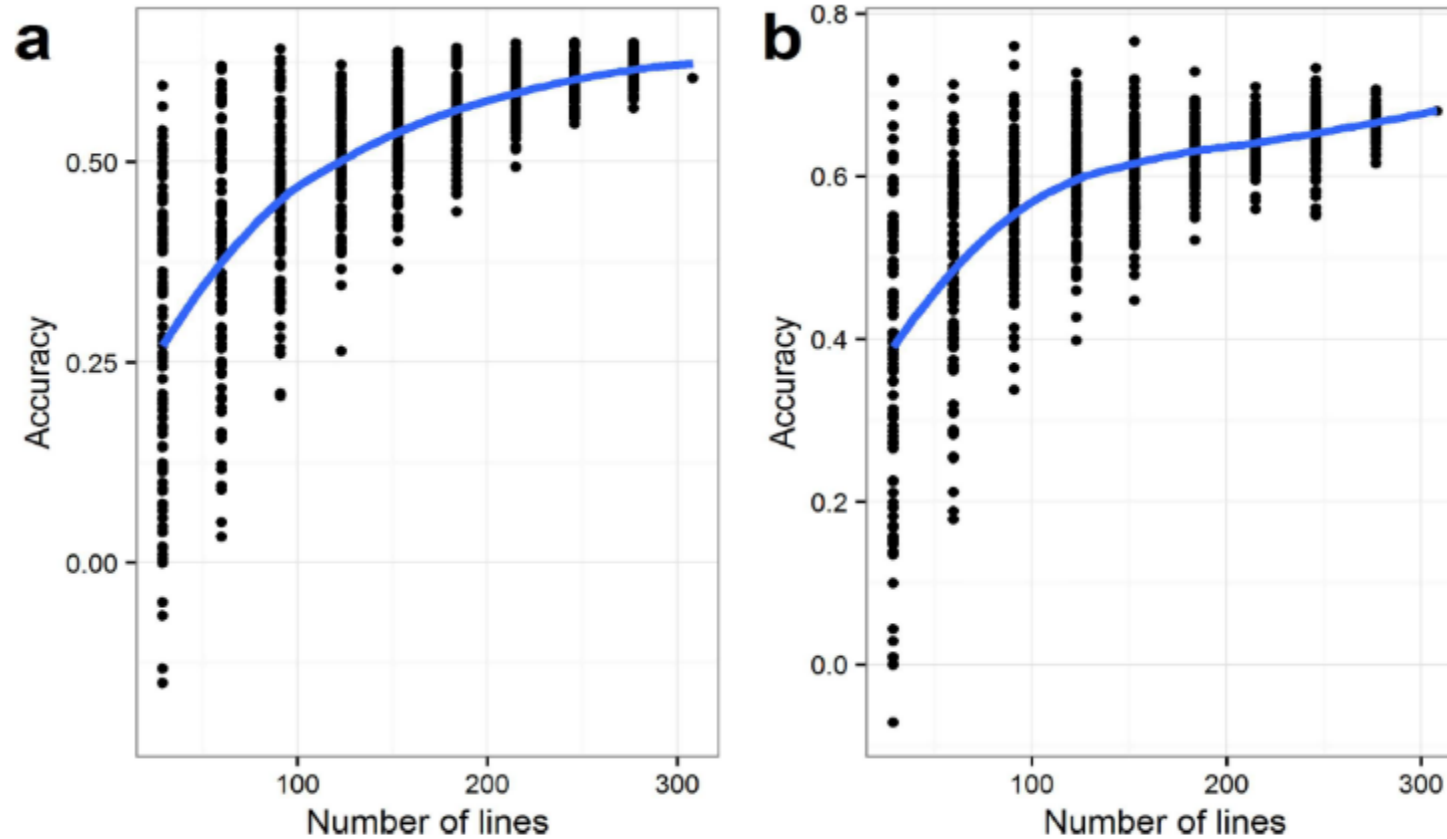
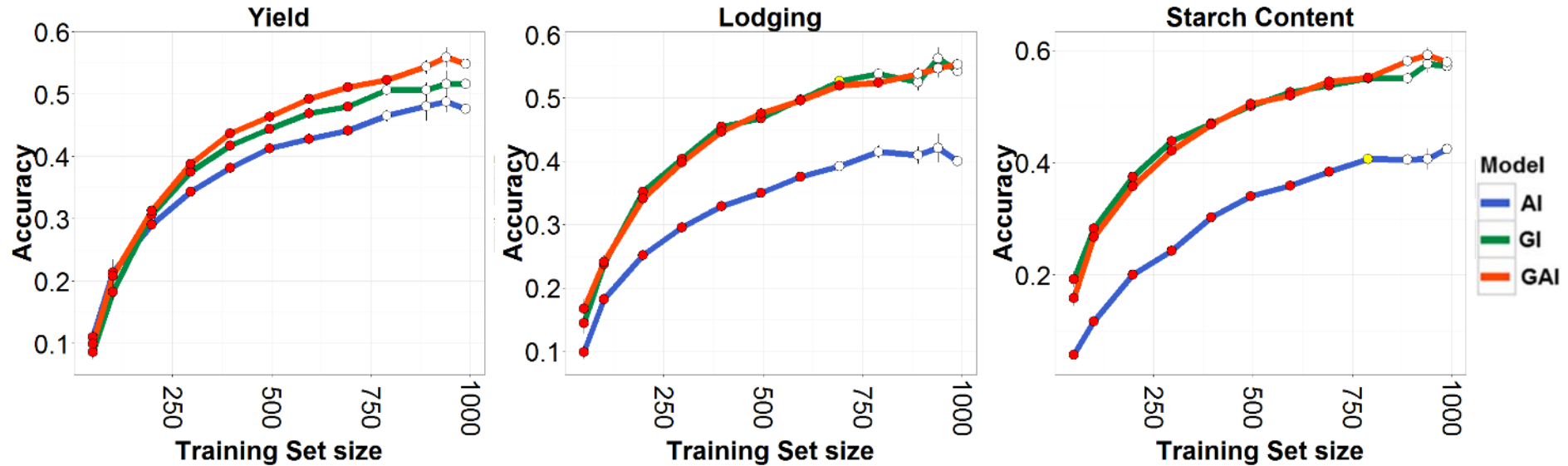


Fig 5. Prediction accuracies with reduced training population size a: Test Weight (TW) ($\text{kg} \cdot \text{hL}^{-1}$) and b: SSW (standardized seed weight). Predictions were done for randomly selected line sets. The analysis was repeated 100 times for each step using a leave-one-out strategy. Curves were fit by loess.

doi:10.1371/journal.pone.0164494.g005

OPTIMIZE TRAINING POPULATION SIZE IN WHEAT

Randomly reduced training population size



1. Models including **G** always outperform the one including only **A**
2. Around 700 lines are enough to maximize the prediction accuracy (~220 per breeding cycles)
3. Phenotyping few hundred of new lines per breeding cycles will allow to predict the others through GP

EFFECTS OF NUMBER OF MARKERS

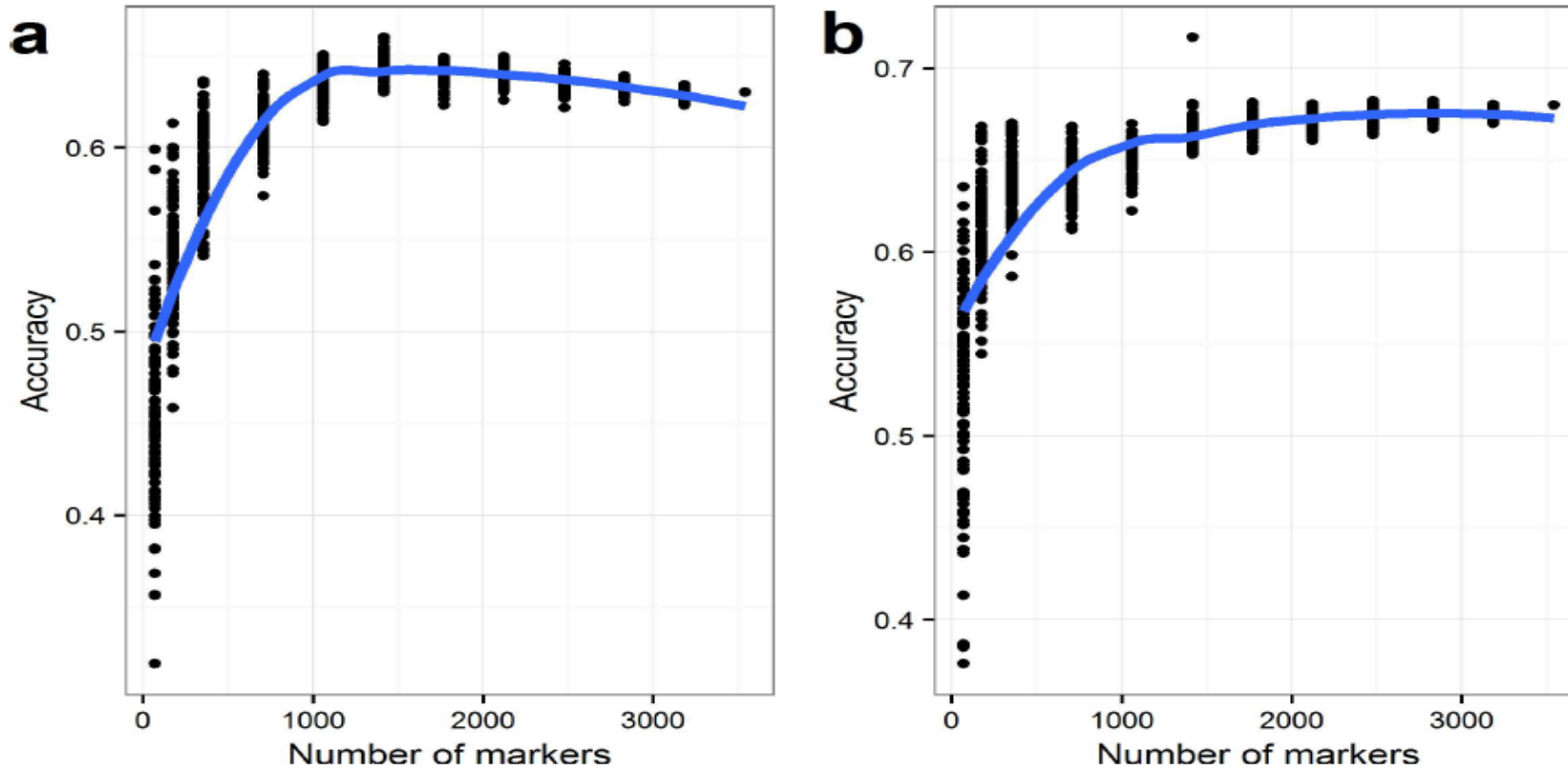


Fig 6. Prediction accuracies with reduced marker numbers. a: Test Weight (TW) ($\text{kg} \cdot \text{hL}^{-1}$) and b: SSW (standardized seed weight). Predictions were done for randomly selected marker sets. The analysis was repeated 100 times for each step using a leave-one-out strategy. Curves were fit by loess.

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PREDICTING FROM FEW MARKERS

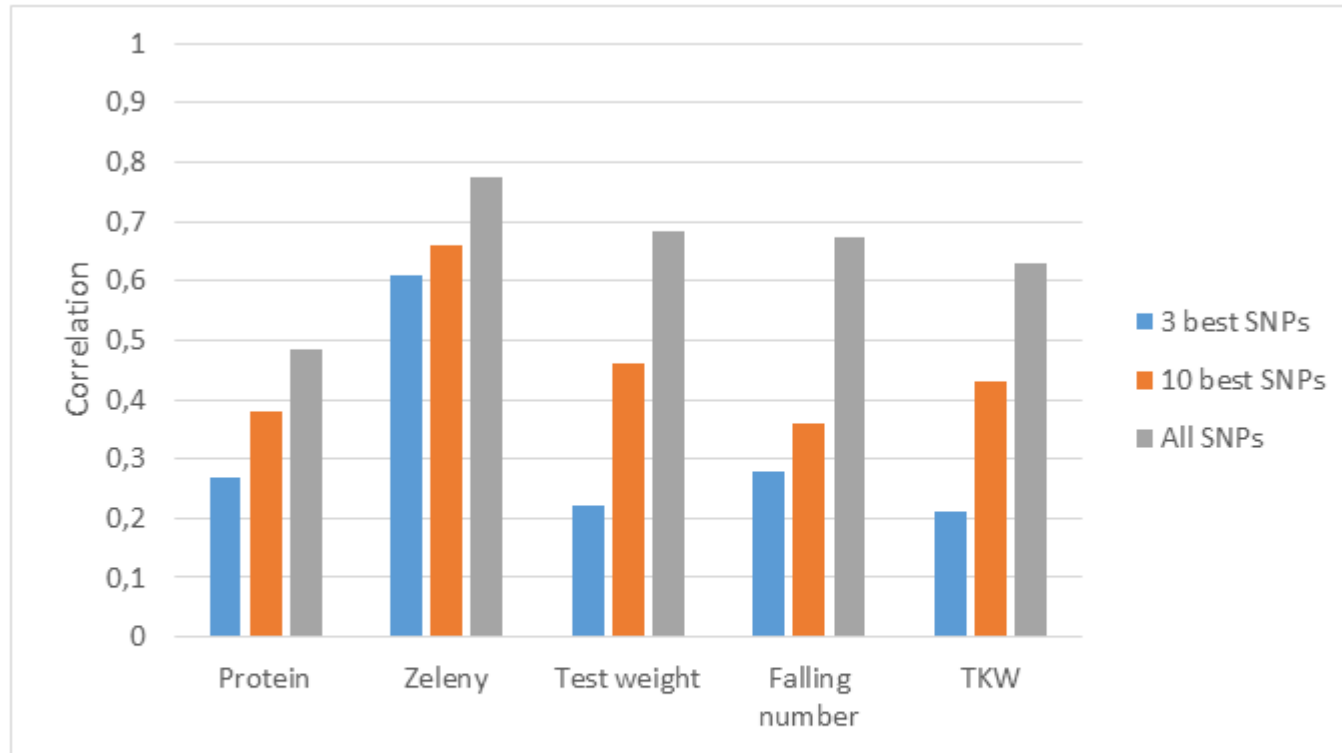
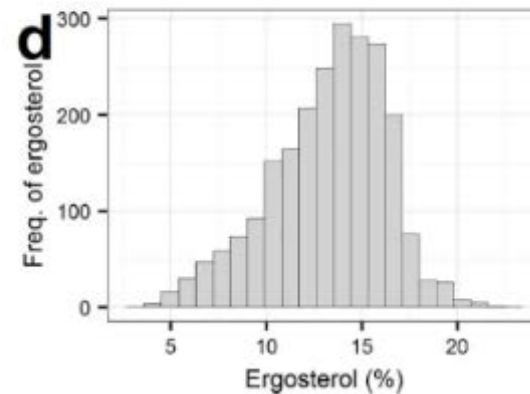
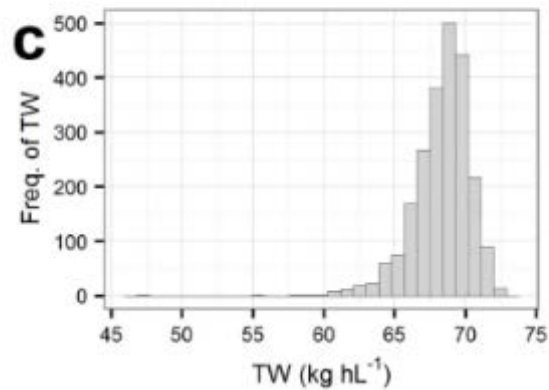
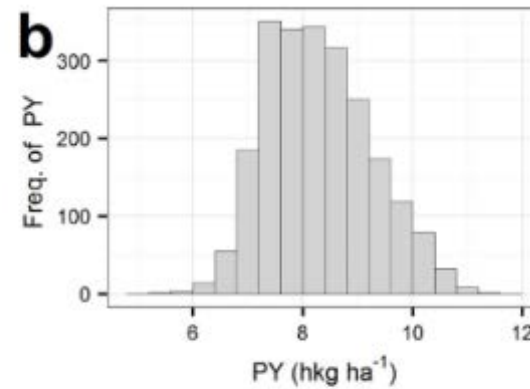
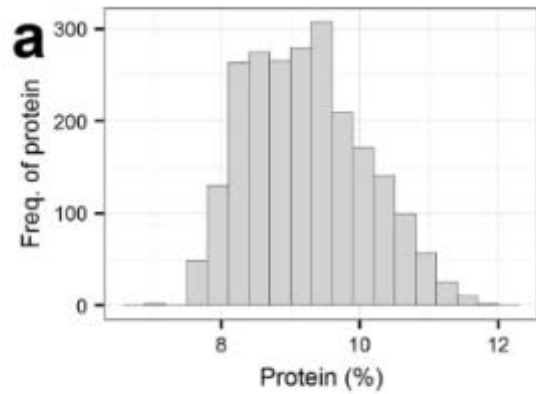


Figure 8. Correlations between observed phenotypes corrected for fixed effects and GEBVs based on 5-fold cross-validations. GEBVs were predicted from the three or ten best SNPs based on single marker regression (effects re-estimated with SNP-BLUP) and from all 10,802 SNPs based on the GBLUP model.

DISTRIBUTION OF NIT-PARAMETERS IN BARLEY



- a: Protein (TS%)
- b: PY = Protein yield (hkg · ha⁻¹)
- c: TW = Test weight (kg · hl⁻¹)
- d: Ergosterol content (%)

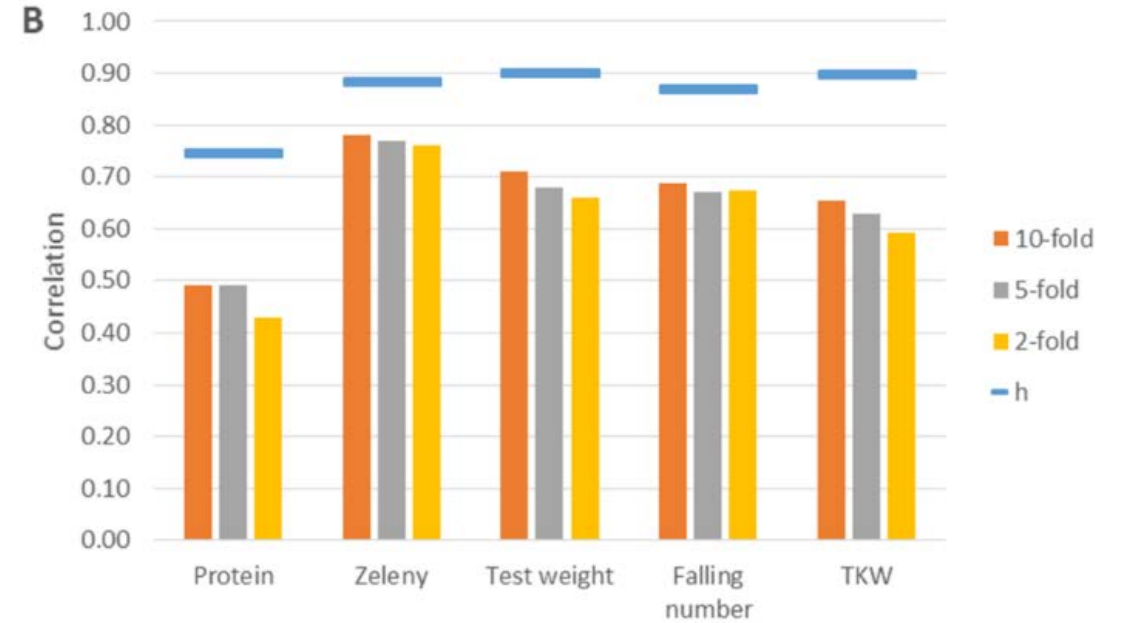
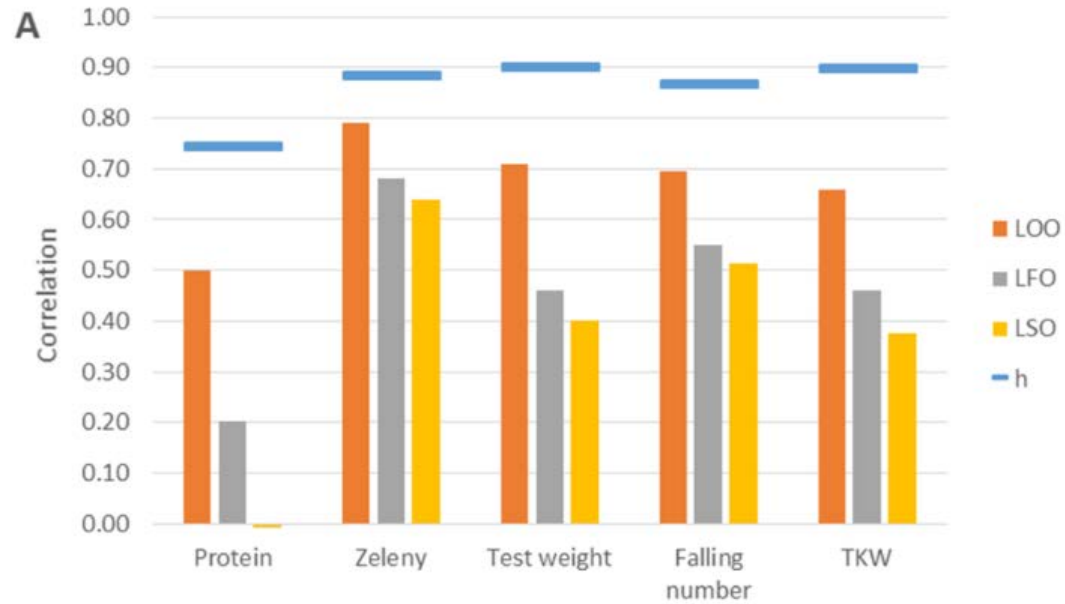
PREDICTION ACCURACIES OF SEED QUALITY IN BARLEY

Phenotype	LOO		LFO	
	Acc.	Bias	Acc.	Bias
SSW	0.68 ± 0.04	0.98 ± 0.06	0.63 ± 0.03	0.98 ± 0.05
Protein	0.40 ± 0.05	0.96 ± 0.12	0.26 ± 0.04	0.68 ± 0.10
PY	0.46 ± 0.05	1.04 ± 0.11	0.33 ± 0.04	0.87 ± 0.10
TKW	0.63 ± 0.04	0.98 ± 0.07	0.56 ± 0.03	0.92 ± 0.06
Ergosterol	0.83 ± 0.03	1.02 ± 0.04	0.79 ± 0.03	1.02 ± 0.03

HERITABILITY AND ACCURACY IN MALTING TRAIT IN BARELY

Traits	Heritability	Accuracy (LOO)	Bias (LOO)	Accuracy (LSO)	Bias (LSO)
Extract yield	0,13	0,43	0,06	0,35	0,16
Filtering speed	0,06	0,35	0,26	0,24	0,04
Wort color	0,30	0,64	0,04	0,53	0,08
Beta glucan	0,22	0,57	0,00	0,44	0,19
Viscosity	0,15	0,45	0,20	0,28	0,17
Wort clearness	0,19	0,67	0,03	0,52	0,04
Free amino nitrogen	0,26	0,48	0,15	0,32	0,19
Protein percentage	0,17	0,42	0,69	0,31	0,37

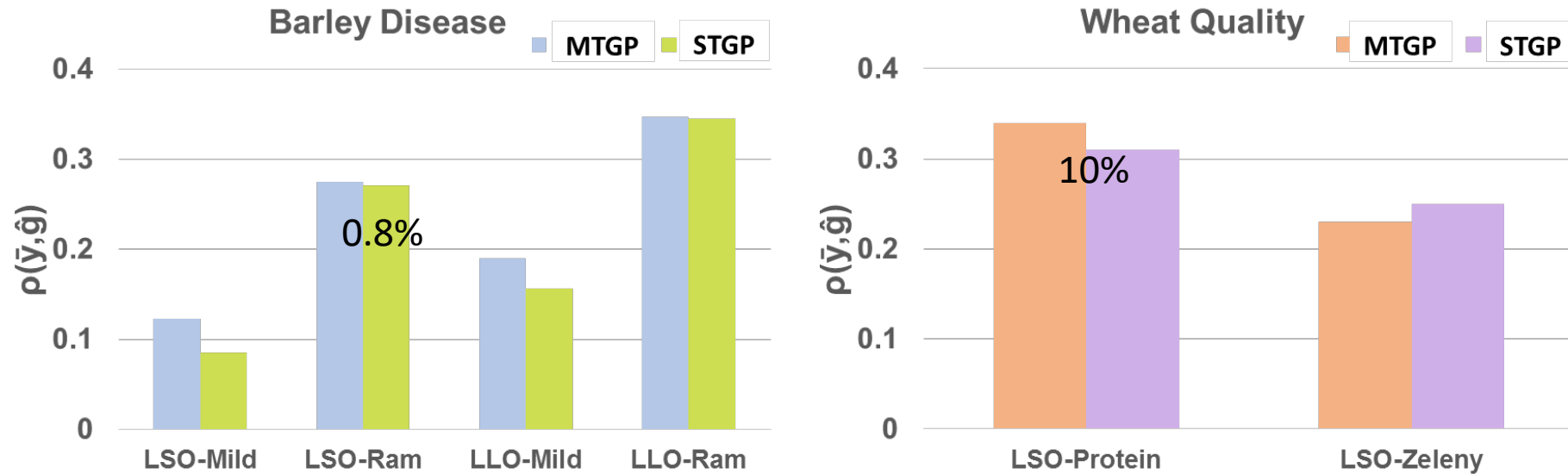
GENOMIC PREDICTION FOR BACKING QUALITY PARAMETRES



MULTIPLE TRAITS

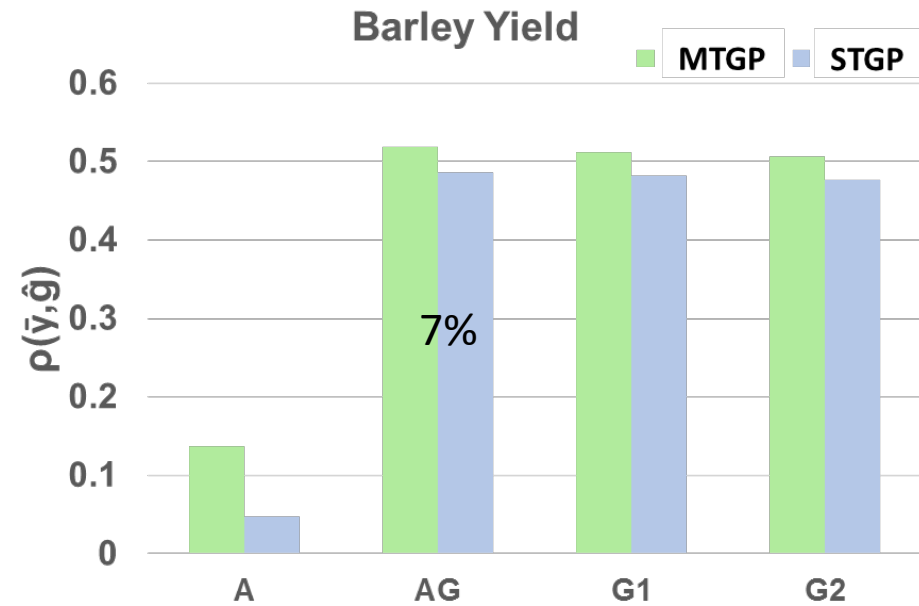
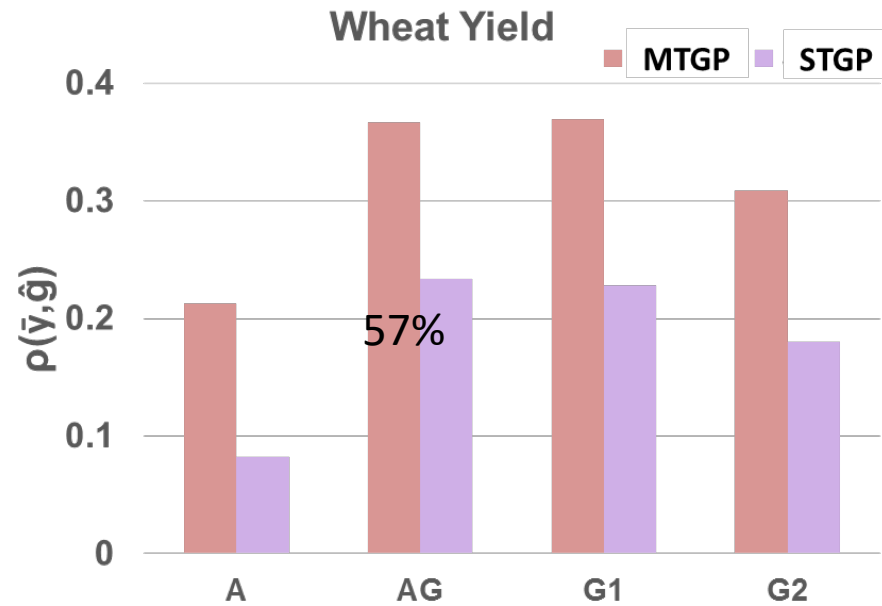
- All breeding programs select for several traits
- Traits are correlated
- Joint analysis of several traits together can increase prediction accuracy
- (Increase in computation and model complexity)

MULTI-TRAIT RESULTS



- g : GRM followed VanRaden (2008) method 1.
- f : GxE effect, including combination of year*location*plotID.
- S : Spatial effect arisen by its surrounding eight plots.
- LSO: Leave-one-set LLO: Leave-one-line

MULTI-TRAIT IN YIELD USING F5 & F6



A: Model fitting pedigree relationship matrix.

AG: Model commonly fitting pedigree plus genomic relationship matrix.

G1: Model with GxE effect and Spatial effect.

G2: Model without GxE effect and Spatial effect.

GENETIC CORRELATION BETWEEN MALTING TRAITS IN BARLEY

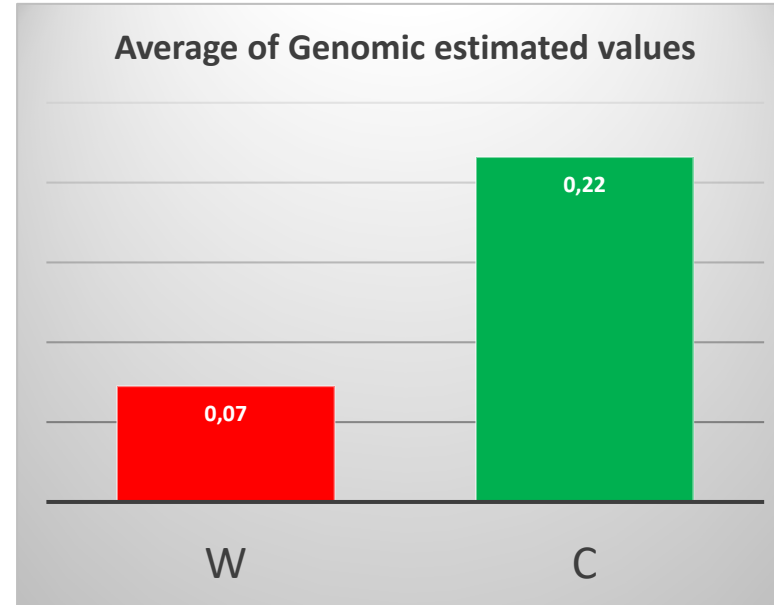
Traits	Extract yield	Filtering speed	Wort color	Beta glucan	Viscosity	Wort clearness
Extract yield	1					
Filtering speed	-0,26	1				
Wort color	0,47	-0,41	1			
Beta glucan	-0,37	0,00	-0,60	1		
Viscosity	-0,26	-0,19	-0,56	0,94	1	
Wort clearness	-0,18	-0,16	-0,13	0,35	0,36	1
Free amino nitrogen	0,53	-0,26	0,83	-0,71	-0,67	-0,35

GENOMIC ESTIMATED BREEDING VALUES

- Lines submitted to official variety testing 2016 in spring barely

Line names	Genomic estimated values	Official result	Yield
NOS 111.026-52	0,35	C	103
NOS 111.036-53	0,25	C	104
NOS 110.352-51	0,18	C	105
NOS 19103-59	0,16	C	99
NOS 19341-55	0,14	C	105
NOS 19103-51	0,11	W	99
NOS 19338-55	0,09	W	98
NOS 111.028-56	0,05	W	101
NOS 111.002-52	0,04	W	98

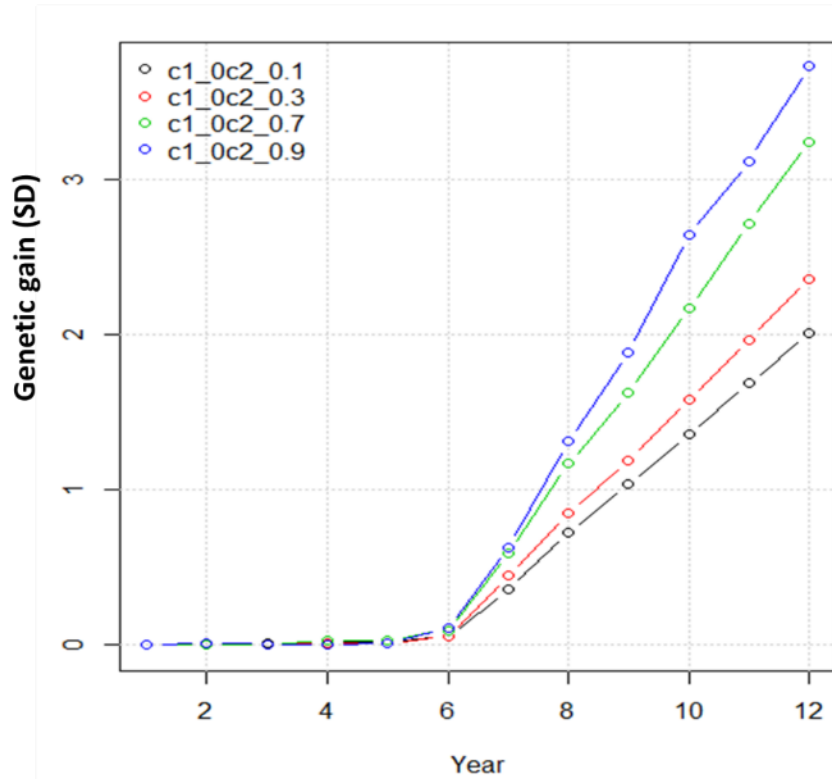
W = withdraw, C = continued



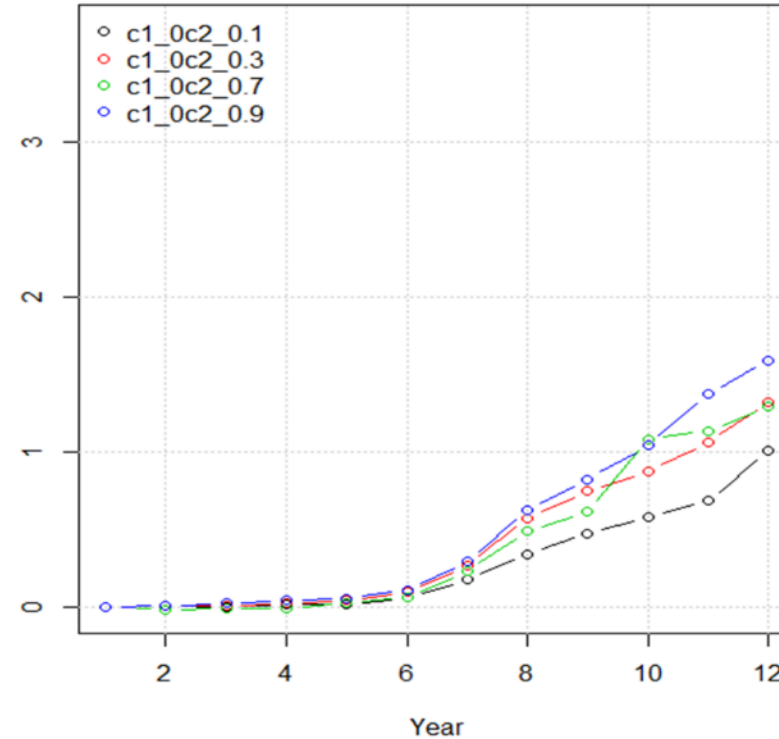
Withdraw lines from official testing also have low gebv values. This indicates for selecting lines to submit to official testing we can get help from gebv values.

PHENOTYPIC VS. GENOMIC SELECTION

Genomic selection



Phenotypic selection



C1= correlation of BVP (F2) with F5&F6 yield
C2= correlation between F5 & F6 yield

GS ADVANTAGE

- Most important advantages are reductions in the selection cycle length and phenotyping cost at the same time increasing genetic gain per year.
- In GS, the underlying genetic control and biological function is not known (the cost of obtaining that knowledge is not needed).
- Genomic information may not be as accurate as real phenotypes, but it is cheaper and faster.
- Genomic selection can improve the complex and costly traits.
- Better protection against copying by competitors (improvement is based on many makers)

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GENETICS AND GENOMICS**



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