



**HAL**  
open science

## Genomic prediction of agronomic and malting quality traits in six-rowed winter barley

Gilles Charmet, Pierre Pin, Marc Schmitt, Nathalie Leroy, Bruno Claustres, Christopher Burt, Amélie Genty

► **To cite this version:**

Gilles Charmet, Pierre Pin, Marc Schmitt, Nathalie Leroy, Bruno Claustres, et al.. Genomic prediction of agronomic and malting quality traits in six-rowed winter barley. 6th Conference on Cereal Biotechnology and Breeding, CBB6, EUCARPIA; AKCongress, Nov 2021, Budapest, Hungary. hal-03479442

**HAL Id: hal-03479442**

**<https://hal.inrae.fr/hal-03479442v1>**

Submitted on 14 Dec 2021

**HAL** is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



## 6th Conference on Cereal Biotechnology and Breeding

jointly organized by EUCARPIA Cereals Section  
FULL ONLINE CONFERENCE

3–5 November 2021 / Budapest, Hungary



# Genomic prediction of agronomic and malting quality traits in six-rowed winter barley

Charmet G.\* , Pin P.A., Schmitt M., Leroy N., Claustres B., Burt C., Genty A. \*\*

**Project FSOV 2016T GENOMALT**



INRAE

Genomic prediction of agronomic and malting quality traits in six-rowed winter barley

4 November 2021, CBB6 Budapest



In the beginning there was *Hordeum  
spontaneum*

Now there is ..... *Hordeum vulgare*\*



$2n = 2x = 14$   
5.3 Gbp  
~ 32.000 genes



Nature. 2012 Oct 17. doi: 10.1038/nature11543.

Self-pollinated (hermaphroditic)

\* Technically speaking *spontaneum* and *vulgare* are both  
subspecies of *H. vulgare*



## Inflorescence type

- 2-rowed vs. 6-rowed
- 1 gene/30.000 genes

### Six-rowed barley originated from a mutation in a homeodomain-leucine zipper I-class homeobox gene

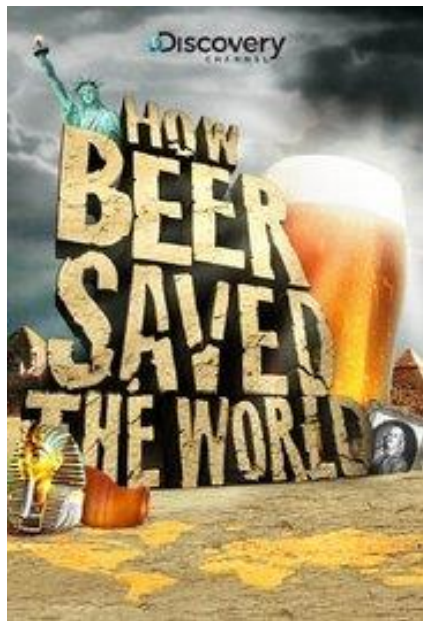
Takao Komatsuda<sup>††</sup>, Mohammad Pourkheirandish<sup>††</sup>, Congfen He<sup>\*</sup>, Perumal Azhaguvel<sup>\*</sup>, Hiroyuki Kanamori<sup>§</sup>, Dragan Perovic<sup>§</sup>, Nils Stein<sup>¶</sup>, Andreas Graner<sup>§</sup>, Thomas Wicker<sup>¶</sup>, Akemi Tagiri<sup>\*</sup>, Udda Lundqvist<sup>\*\*</sup>, Tatsuhito Fujimura<sup>‡</sup>, Makoto Matsuoka<sup>††</sup>, Takashi Matsumoto<sup>\*</sup>, and Masahiro Yano<sup>\*</sup>

<sup>\*</sup>National Institute of Agrobiological Sciences, Tsukuba 305-8602, Japan; <sup>†</sup>Graduate School of Life and Environmental Sciences, University of Tsukuba, Tsukuba 305-8572, Japan; <sup>‡</sup>Institute of Society for Techno-Innovation of Agriculture, Forestry, and Fisheries, Tsukuba 305-0854, Japan; <sup>§</sup>Leibniz Institute of Plant Genetics and Crop Plant Research, D-06466 Gatersleben, Germany; <sup>¶</sup>Institute of Plant Biology, University of Zürich, CH-8008 Zürich, Switzerland; <sup>\*\*</sup>Svalöf Weibull AB, SE-268 81 Svalöv, Sweden; and <sup>††</sup>Bioscience and Biotechnology Center, Nagoya University, Nagoya 464-8601, Japan

# Why barley?

## *Beverage. food. feed*

# 30 %



# 1 %



# 70 %



World annual production  
2016-2021 # 150 Mt

Rank by countries

- 1) EU (# 55 MT)
- 2) Russian Fed # 20 Mt
- 3) Germany # 11 Mt
- 4) France # 10 Mt
- 5) ...

# Malting process

Steeping, Germination, Kilning

Time (~3 – 7 days)

temperature (50o – 350o)

Moisture (10% – 50%)

## Barley malt

The base of beer and spirits

The highest diastasic power (vs wheat and others)

Colour and taste according to Temperature

The economic driver of barley



## Barley malting quality

- Calibration: to achieve fast and homogeneous germination % > 2.5mm  
That's why 2-rowed barley are often preferred for malting
- Proteins: enough to feed yeast, but not in excess (can make beer cloudy)  
9.5 à 11.5%

## Malt quality traits

- Extract rate: yield in malt per barley unit %
- Friability (for grounding)
- Diastatic power ( $\alpha$ -amylases activity) to convert starch into fermentescible sugars
- Bglucans (soluble fibre, healthy component in human diet): Excess causes wort viscosity and filtering problems

**Micro-malting tests are long and seed-demanding**  
**Usefulness of genomic prediction for early selection**

# Genomic selection

More advantages if/when:

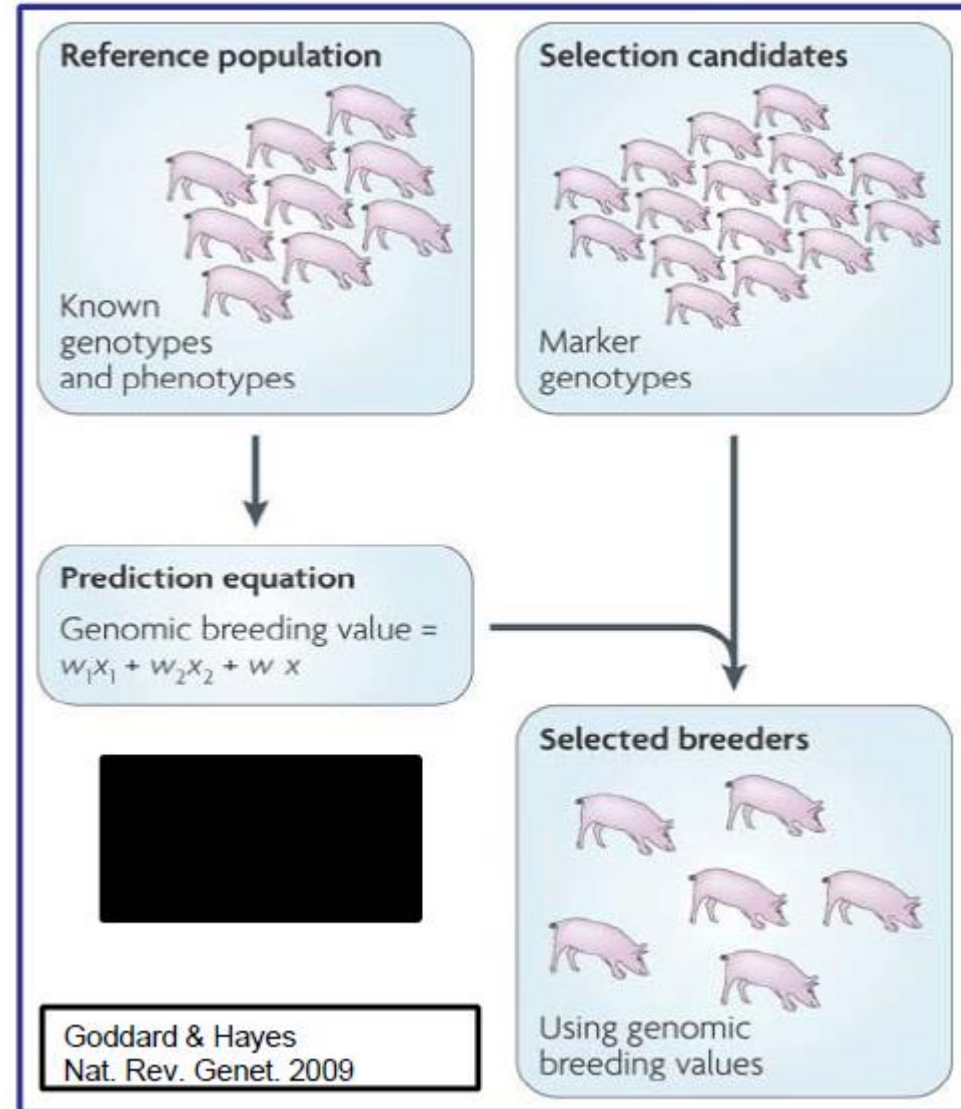
-GEBV for sex-specific traits (e.g. MILK)

-Traits costly to evaluate

-Trait can be measured only after animal death or plant harvest

-Traits expressed late, e.g. longevity

-...





## ➤ Why FSOV GENOMALT

- Winter barley is the second most cultivated small grain cereal in France #1.2 Mha.
- 6-rowed barley for malting purpose is ~specific to France and largely contributes to the competitiveness of the barley-malt-beer food chain in France (80 % of malt is exported).
- Most breeding schemes for 6-rowed barley improvement are based on doubled haploid production (microspores in vitro culture)

## ➤ FSOV GENOMALT : Materials & phenotypes

- **GENOTYPED total 679)**

- 259 breeding lines from Breeder 1
- 315 breeding lines from Breeder 2
- 105 « founder lines », i.e. registered varieties freely available under UPOV agreement

- **PHENOTYPED 2 Years Field trials (2018 & 2019 harvests, treated management)**

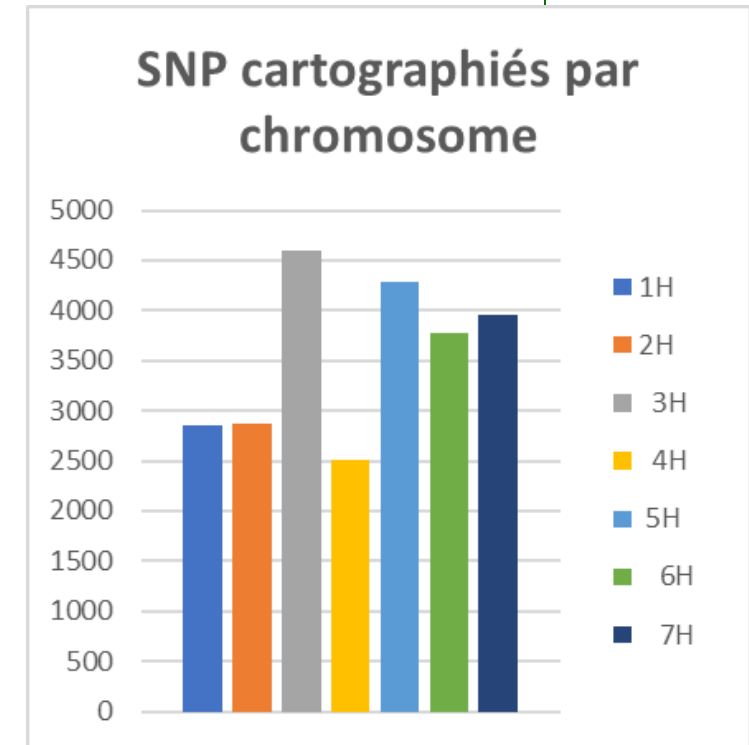
- Breeder 1: 3 locations
- Breeder 2: 2 locations
- Each company evaluated its own material + part of founder lines (88 in common)
- Agronomic variables available in most locations: Yield (dt/ha), protein content (%), thousand grains weight (g), test weight (Kg/hl), Calibrage (%), heading (days from January 1st), plant height (cm)
- Malt-related traits: Only a single location/breeder/year, no replicate: Malt friability, malt extract, wort viscosity and  $\beta$ -Glucan content

## ➤ FSOV GENOMALT : Genotyping

### • Quality control and Cleaning genotype data Infinium HD iSelect (JHI) 50K

- BREEDER 1 44 040 SNP
- BREEDER 2 40 705 SNP (QC)
- In COMMON 38 366 SNP
- Discarding SNP with NA>20% 38 223 SNP
- Discarding SNP with Het > 0.05 36 612 SNP
- Discarding SNP with MAF <0.01 24 945 SNP
- Keeping SNP mapped on chrom 1H-7H **24 101 SNP**
- Fairly even distribution among chromosomes (mapping on barley reference map V2)

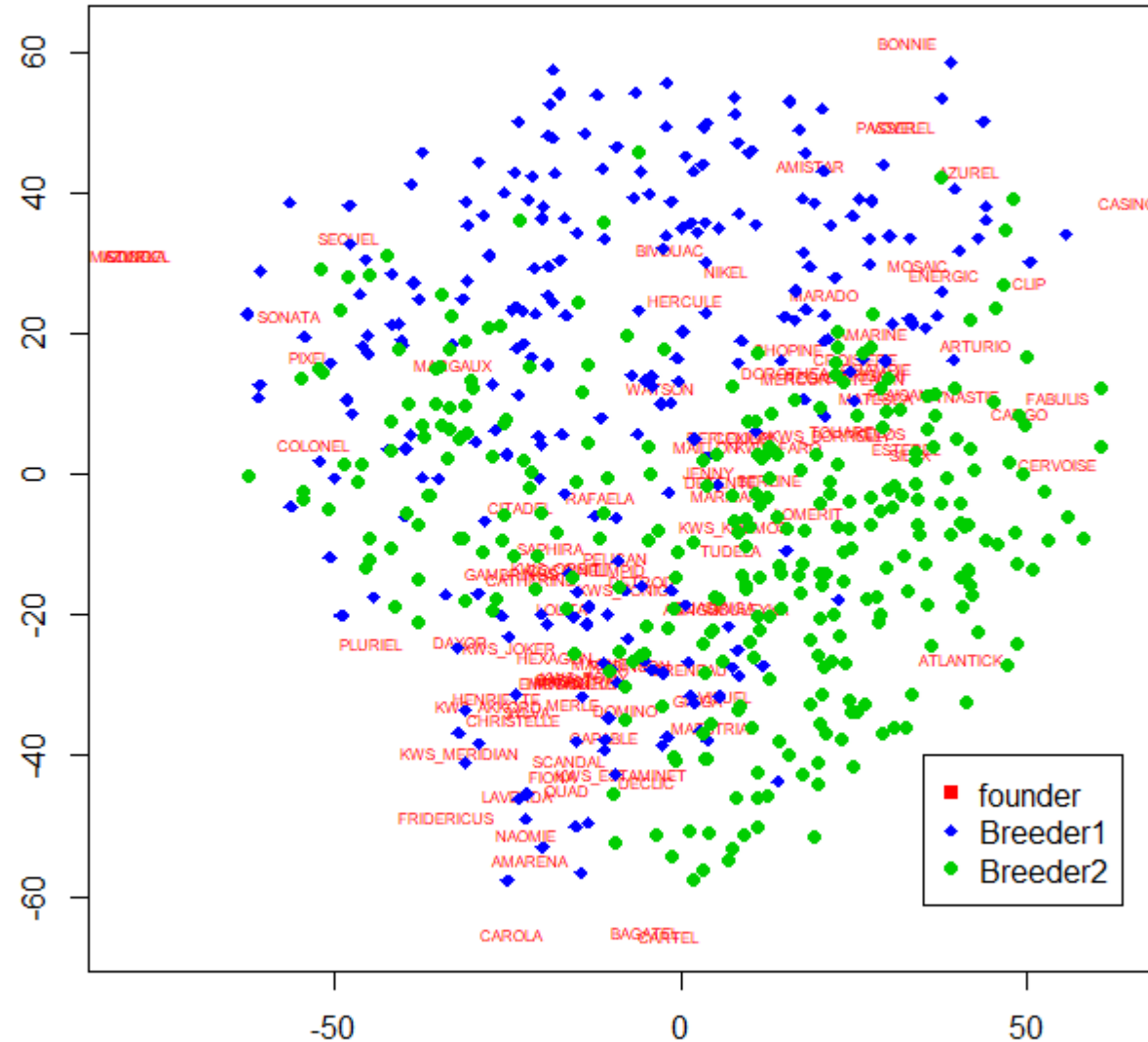
1H	2H	3H	4H	5H	6H	7H
2860	2877	4604	2505	4282	3777	3962



- Homogeneising codes A/A to A:A. C/C to C:C etc
- Recoding minor allele -1. heterozygotes 0. major allele +1 (for rrBLUP package):

# ➤ Graphical display of Principal coordinates analysis

**CMD-SCALE of GENOMALT lines from 24 101 SNP**



## ➤ ANALYSES OF FIELD DATA 2-YEARS 2018-2019

# Data cleaning and pre-treatment

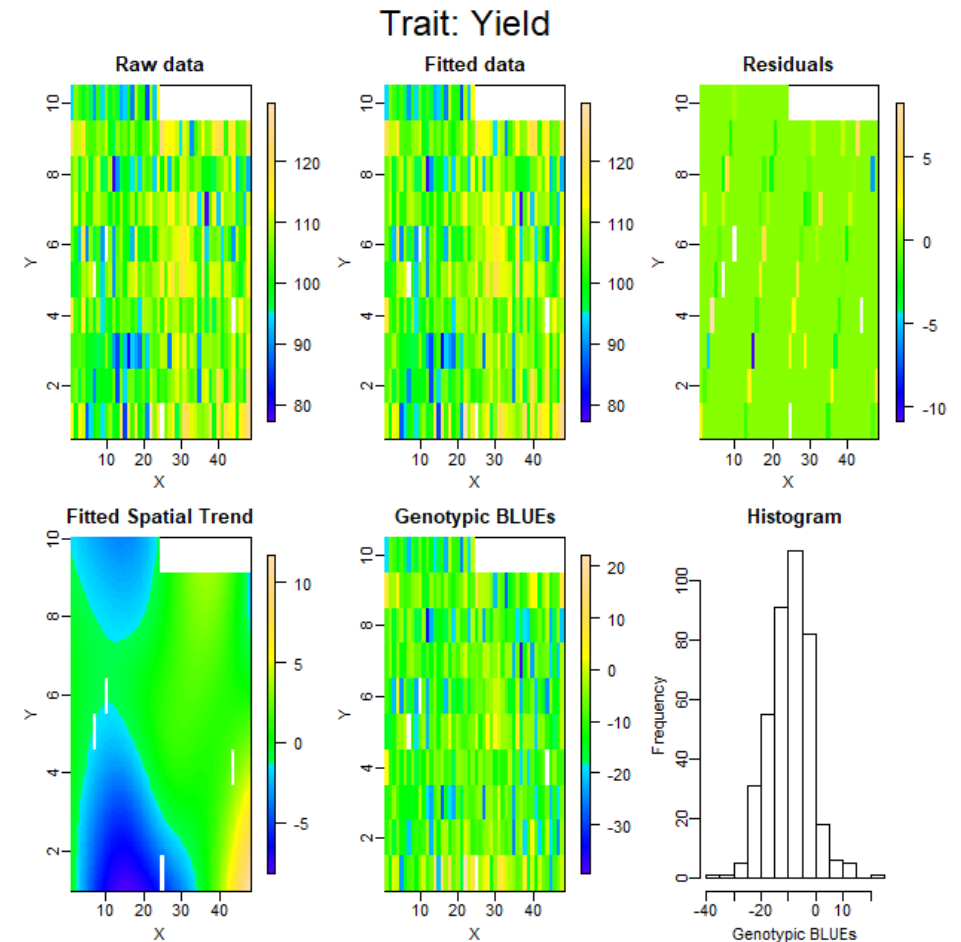
## ➤ Pre-treatment: Spatial adjustment: site by site

```
# e.g. Yield_Breeder2019.M0=
SpATS(response="Yield".spatial=~SAP(X.Y.nseg=c(10.20)).genotype="GENO", data=BRE1_2019.dtf, control=list(tolerance=1e-03))
```

Then assemble spatially adjusted plot data into a dataframe:  
GMALT2YEAR.dtf

Not applicable to malting traits (no replicate)

- Global ANOVA on spatially corrected Data e.g.
  - `Yield2YEAR.LM=lm(Yield~Year + Year:Site + GENO+ GENO*Year + GENO*Site . data=GMALT2YEAR.dtf)`
  - `anova(Yield2YEAR.LM)`



## > ANOVA on spatially corrected Data

F (Res=1148 df)	Yield	Prot	TestW	TGW	Cal	Friability	Extract	Visco	BGlu
Year (1)	12822	274	909	95	118				
<b>GENO (698)</b>	<b>2.97 **</b>	<b>4.78 ***</b>	<b>4.55 ***</b>	<b>7.64 ***</b>	<b>7.74 ***</b>	<b>30 ***</b>	<b>11 ***</b>	<b>20.5 ***</b>	<b>27.8 ***</b>
Site/Env (4)	99	98		716	545	218	67	270	281
Year*Site (4)	845	149	546	309	76				
<b>Y*GENO (664)</b>	<b>1.23 NS</b>	<b>1.14 NS</b>	<b>1.28 *</b>	<b>1.28 *</b>	<b>1.29 *</b>				
<b>Site*GENO (1243)</b>	<b>1.12 NS</b>	<b>1.10 NS</b>	<b>0.95 NS</b>	<b>1.09 NS</b>	<b>1.54 **</b>	<b>2.8 **</b>	<b>1.9 *</b>	<b>4.1 *</b>	<b>3.9 *</b>

Estimation of main GENO effects  
with model

Yield2YEAR.LM=lm(Yield~ Year  
+ Year:Site + GENO .

data=GMALT2YEARS PAT)

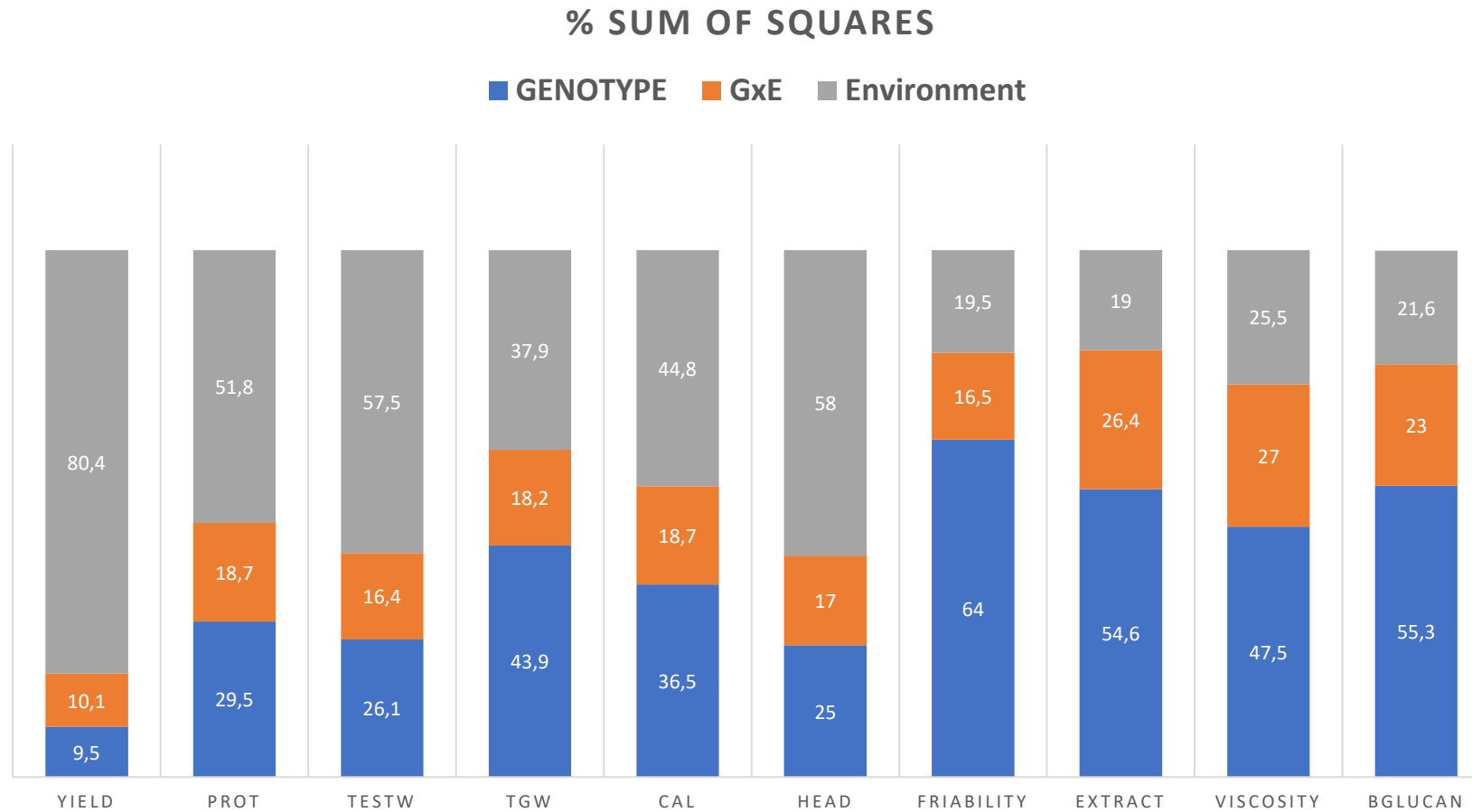
Yield2YEAR.ADJ=Yield2YEAR.L  
M\$coefficients[3:712]

Add Grand Mean  $\mu$  to get  
relevant value

Look at « genetic » correlations

**GENO MAIN EFFECT >> GxE → GS on ADJUSTED MEAN**

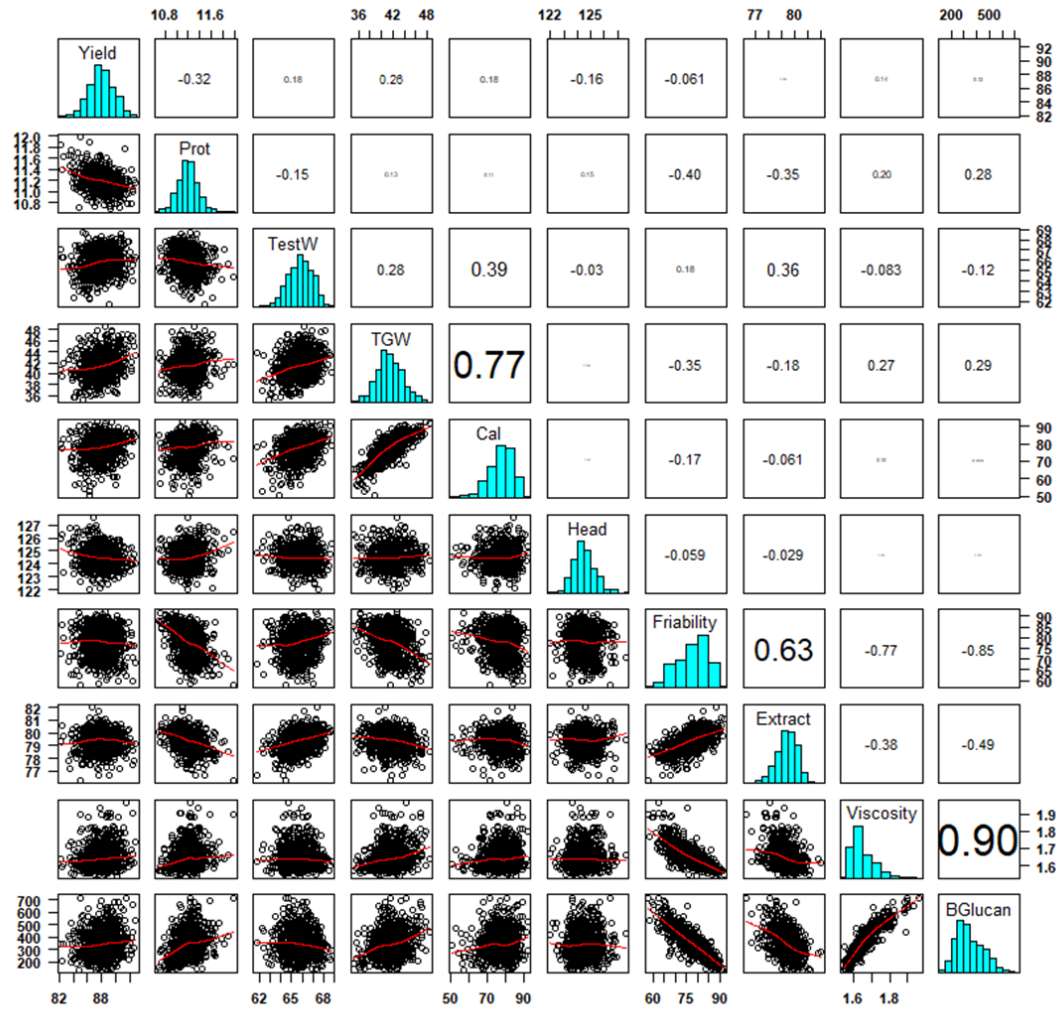
## ➤ ANOVA on spatially corrected Data



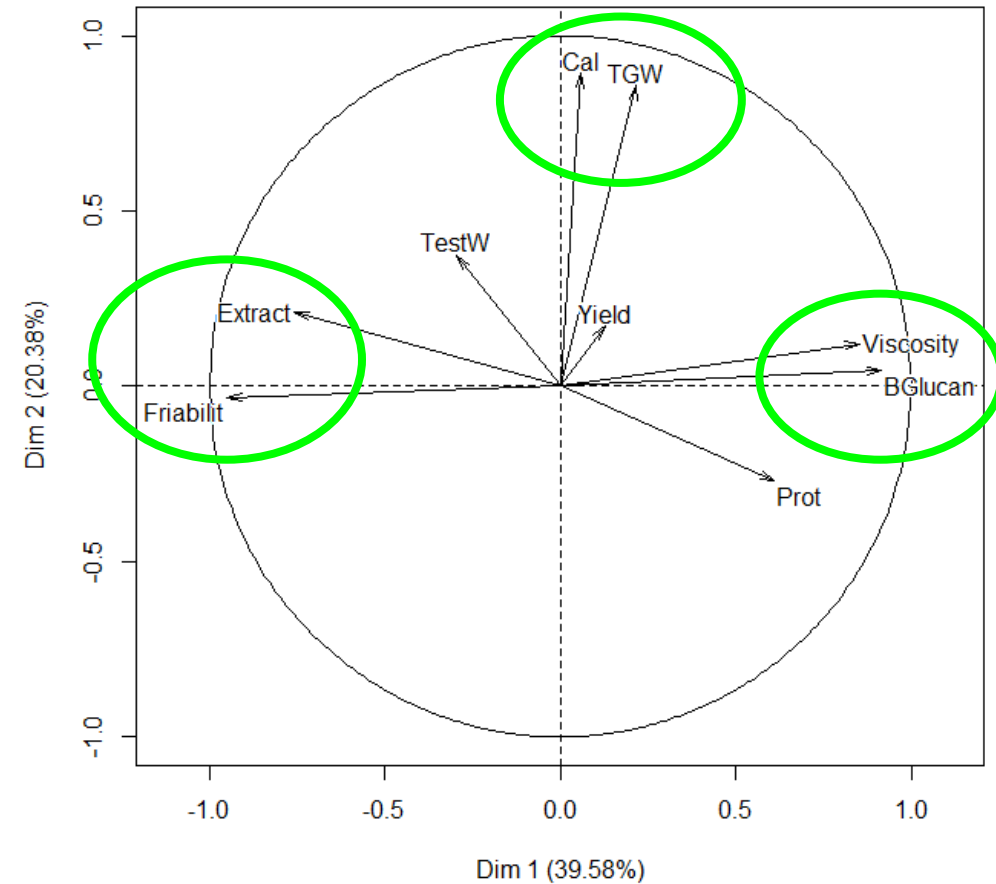


# ➤ Genotypic correlations: favourable or neutral

correlation of genotypic adjusted values



Variables factor map (PCA)



# ➤ GENOMIC PREDICTIONS

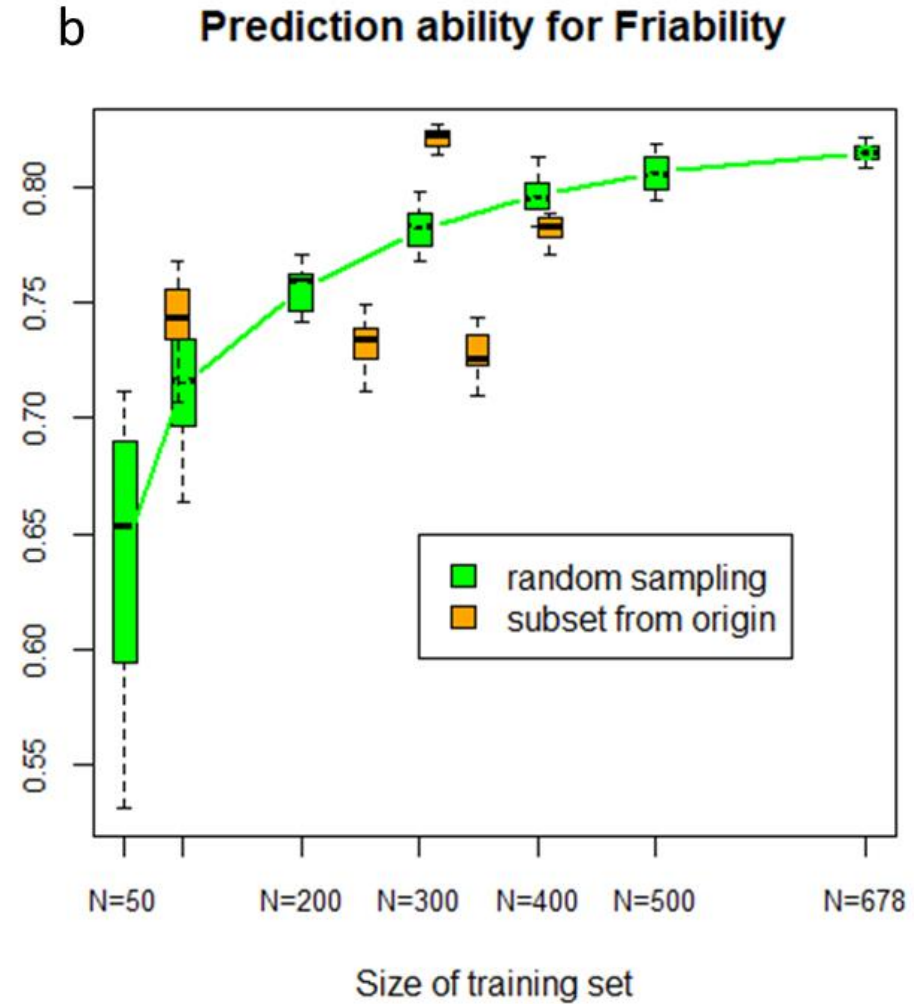
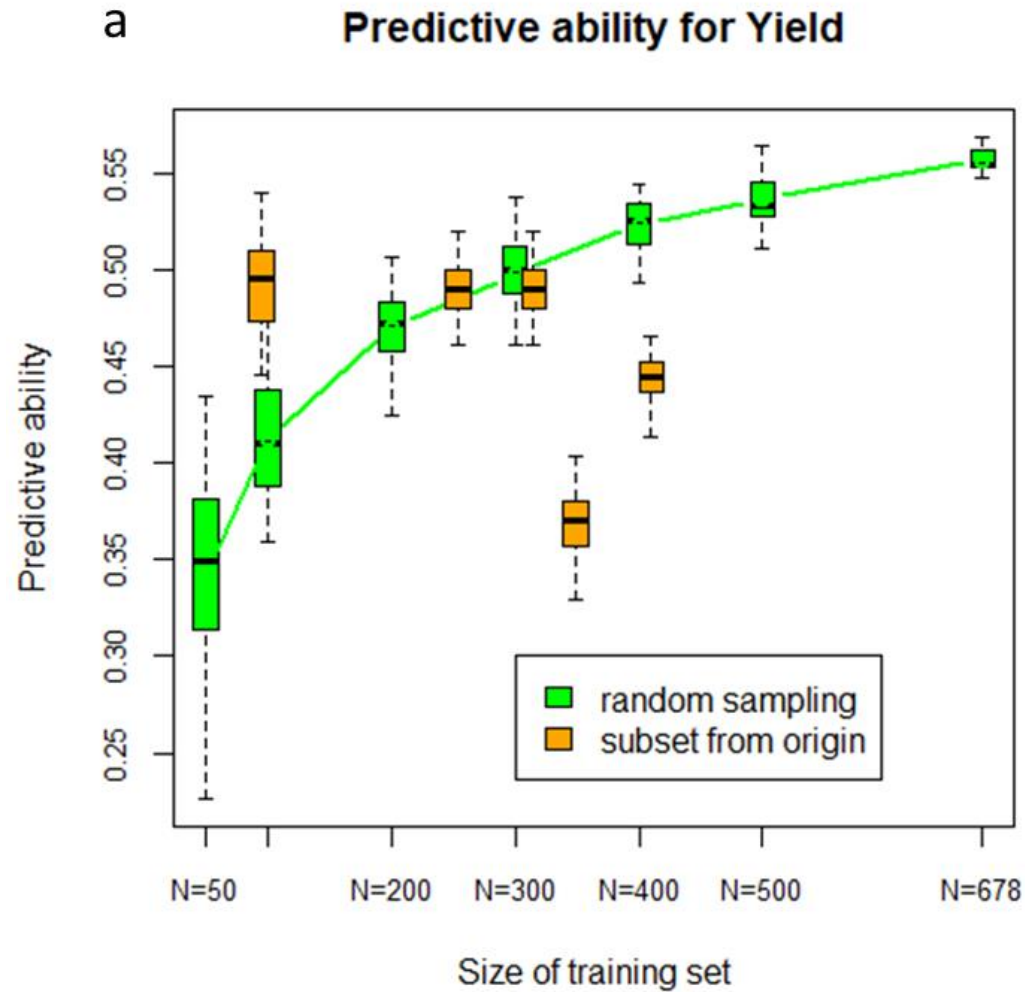
# ➤ GBLUP cross validation

Two vs single breeder

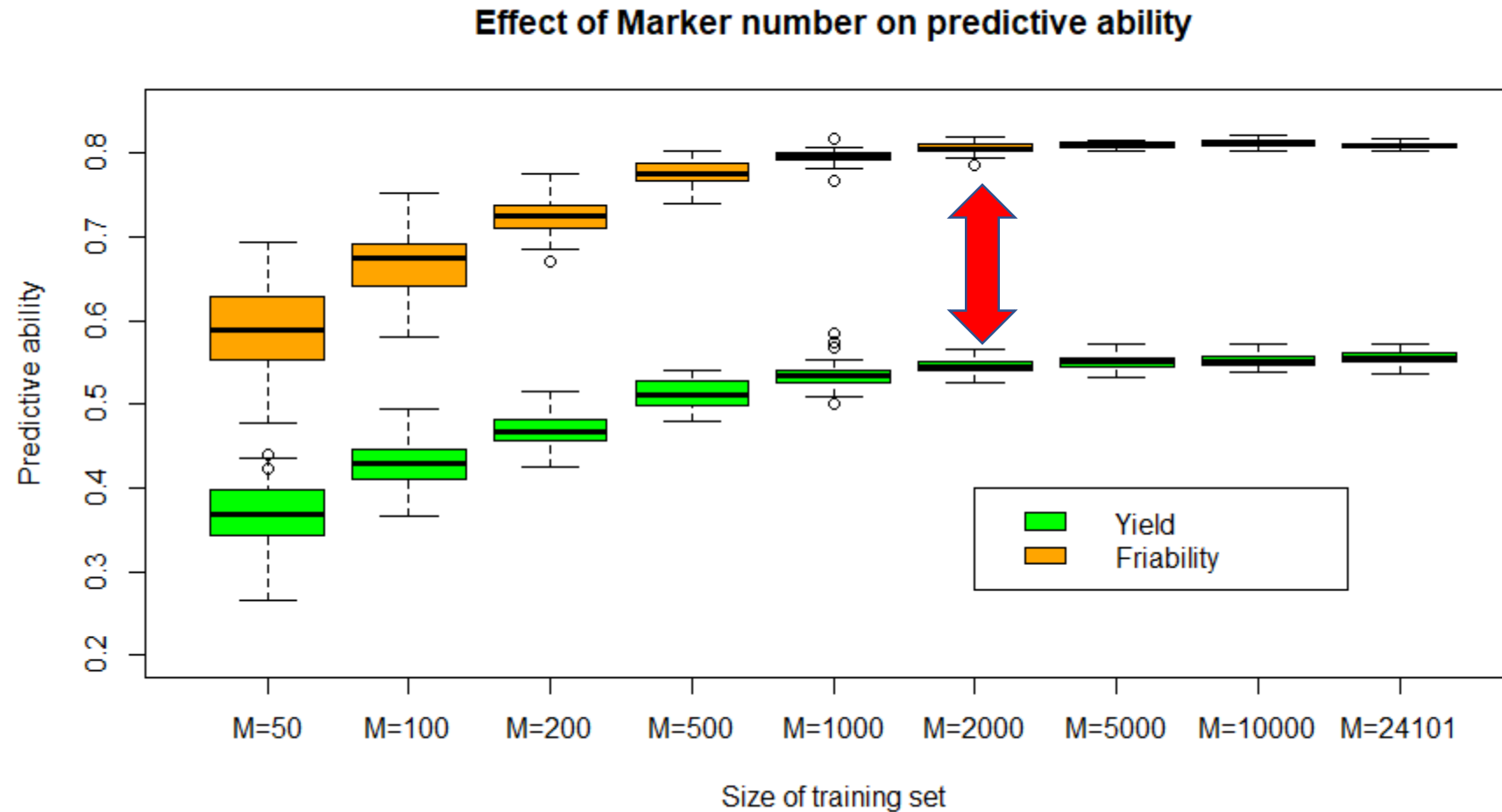
Varieties only

TRAIT	randomCV (N=679)	BRE1+FO.CV (N= 364)	BRE2+FO.CV(N=420)	FounderCV (N=105)
Yield	0.556 / 0.012	0.530 / 0.026	0.431 / 0.023	0.490 / 0.056
Prot	0.515 / 0.014	0.645 / 0.016	0.215 / 0.032	0.379 / 0.064
TGW	0.692 / 0.010	0.763 / 0.014	0.540 / 0.022	0.585 / 0.048
TestW	0.661 / 0.014	0.722 / 0.016	0.578 / 0.016	0.658 / 0.050
Cal	0.714 / 0.012	0.697 / 0.016	0.598 / 0.020	0.350 / 0.072
Head	0.522 / 0.019	0.632 / 0.032	0.676 / 0.034	0.113 / 0.104
Friability	0.814 / 0.006	0.823 / 0.009	0.782 / 0.014	0.745 / 0.032
Extract	0.696 / 0.008	0.766 / 0.027	0.654 / 0.014	0.785 / 0.028
Viscosity	0.698 / 0.011	0.743 / 0.011	0.651 / 0.020	0.706 / 0.036
BGlucan	0.762 / 0.010	0.796 / 0.011	0.725 / 0.017	0.740 / 0.022

# ➤ GBLUP cross validation



# ➤ GBLUP cross validation



## ➤ GBLUP across-population validation

Trait	BRE1+2toFO	BR1+FOtoBR2	BR2+FOtoBR1	BR1toFO	BR2toFO	FOtoBR1	FOtoBR2
Yield	0.451	0.184	0.172	0.338	0.210	0.256	0.125
Prot	0.496	0.163	0.347	0.584	0.240	0.444	0.143
TGW	0.632	0.417	0.585	0.613	0.369	0.595	0.203
TestW	0.693	0.444	0.429	0.580	0.546	0.452	0.325
Cal	0.573	0.477	0.525	0.536	0.404	0.325	0.248
Head	0.630	0.499	0.423	0.485	0.515	0.358	0.243
Friability	0.784	0.666	0.720	0.761	0.683	0.720	0.587
Extract	0.789	0.523	0.532	0.643	0.763	0.500	0.488
Viscosity	0.673	0.465	0.636	0.641	0.545	0.586	0.378
BGlucan	0.770	0.537	0.682	0.756	0.694	0.647	0.475

## ➤ Comparison of 5 prediction methods by random CV

TRAIT	Broad sense $h^2$	h (upper bound)	randomCV GBLUP	RandomCV BC	RandomCV LASSO	RandomCV RKHS	RandomCV RF
Yield	0.595	0.771	0.556	0.557	0.470	0.564	0.542
Prot	0.667	0.817	0.515	0.515	0.499	0.515	0.495
TGW	0.568	0.753	0.692	0.691	0.644	0.698	0.652
TestW	0.798	0.893	0.661	0.666	0.631	0.655	0.619
Cal	0.804	0.897	0.714	0.713	0.671	0.725	0.661
Head	0.603	0.794	0.522	0.523	0.521	0.529	0.515
Friability	0.888	0.942	0.814	0.814	0.795	0.802	0.765
Extract	0.817	0.904	0.696	0.699	0.688	0.677	0.685
Viscosity	0.762	0.872	0.698	0.695	0.653	0.685	0.662
BGlucan	0.851	0.922	0.762	0.764	0.707	0.753	0.713

## ➤ Take-home messages

- Despite a relatively small experimental design, malt-related traits show high repeatability over environments
- Predictive ability of malting traits are high and accurate, either within (CV) or across population
- 2,000 markers seem to be enough to achieve optimal predictive ability (PA)
- Different GS models give similar predictive abilities
- In **this particular case**, there is no obvious gain in PA for malting traits by merging data from two breeders
- High PA can be obtained using a small training set of # 100 varieties
- **These results are very encouraging to successfully use genomic prediction on malt-related traits in 6-rowed barley breeding**



## ➤ Acknowledgements



- A Genty
- P Pin
- G Cresté
- PM Leroux



- B Claustres
- N Leroy
- C Burt (RAGT UK)
- R Dupont
- M Tison



- M Schmitt
- C Colin
- S Shcwebel



Thank you for  
your attention

Ready to answer  
your question