

*FROM PROJECT TO PRACTICE, SUCCESSFUL IMPLEMENTATION
OF GS IN A COMMERCIAL BARLEY BREEDING PROGRAM*



GENSAP 6th annual meeting – Barley breeder Jens Due Jensen

Cultivating Value

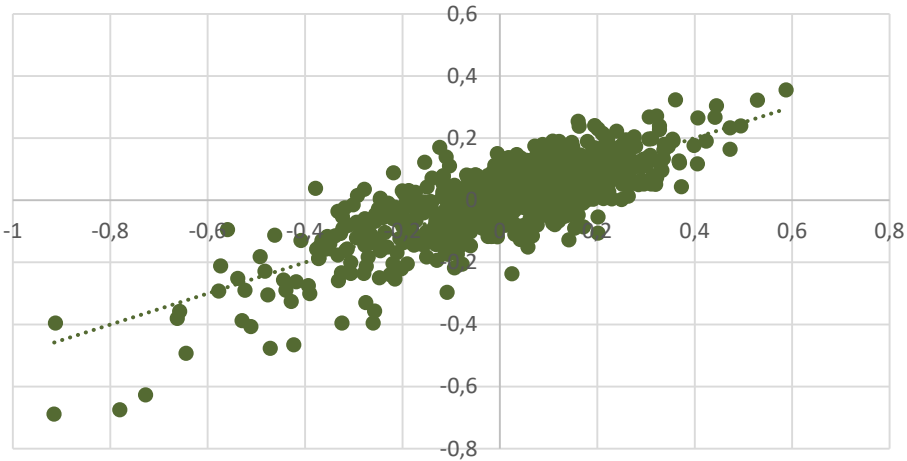
Nordic Seed 

INVOLVEMENT IN GENSAP

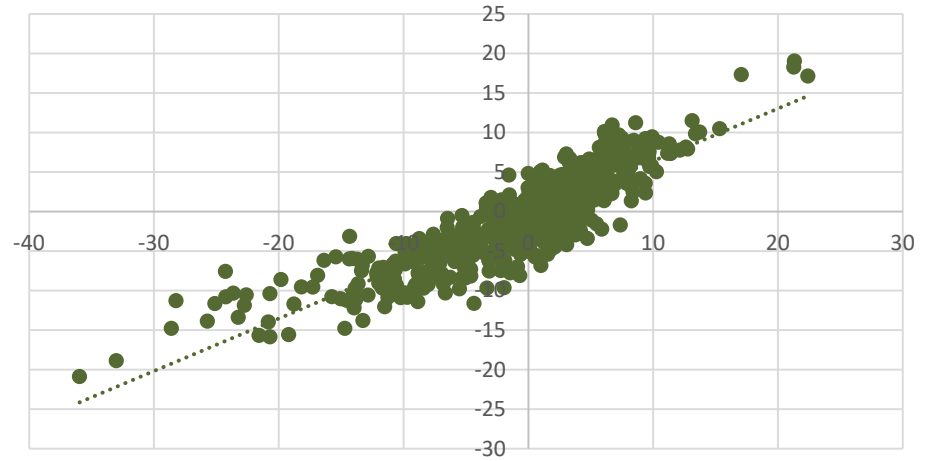
- Provided by breeding companies (Sejet and Nordic Seed):
 - 550 Lines from NOS commercial winter barley breeding program
 - 9K SNP genomic information (for some 50K)
 - Phenotypic data for specific seed quality traits + cereal grain sample
 - Seed size distribution
 - Specific weight (density)
 - Protein content
- To be provided by university partner (University of Copenhagen):
 - Mineral content profiling by ICP-MS
 - Amino acid profiling
 - Phytic acid, Pi, and starch profiling
 - Models (QGG – Luc Janss)

GENSAP – ACCURACY ON SELECTED TRAITS

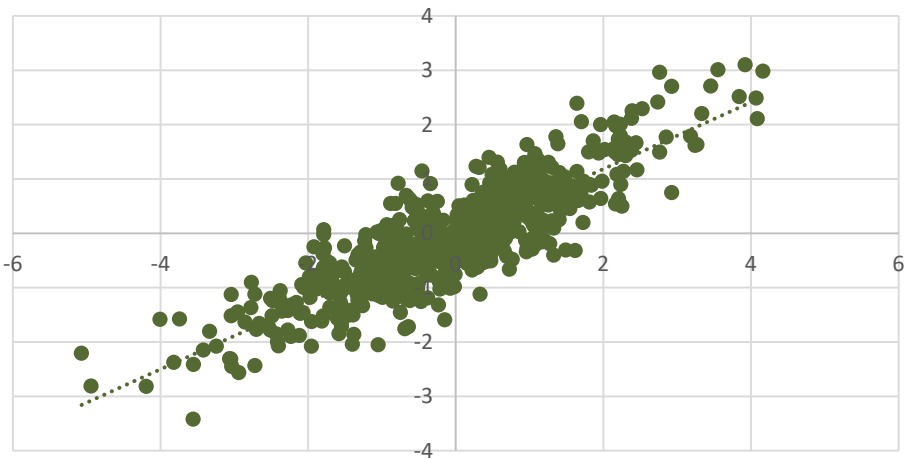
Grain yield $R^2 = 0,6426$



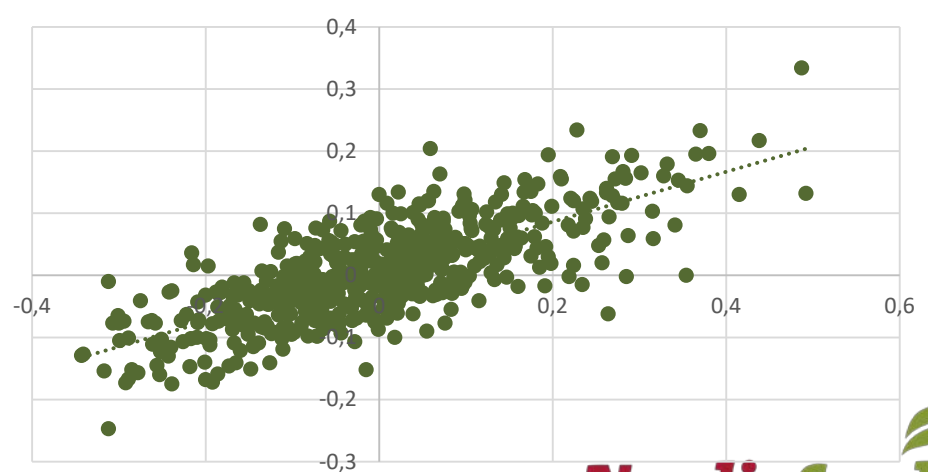
Seed size distribution $R^2 = 0,7652$



Specific weight (density) $R^2 = 0,7474$



Protein content $R^2 = 0,5675$



Cultivating Value

X axis = EBV, Y axis = GEBV

GENOMIC SELECTION PROJECTS AT NORDIC SEED

🌿 Genomic selection for complex traits in barley and wheat breeding

- GUDP project - 2013-2017
- Partner QGG Foulum – Just Jensen



🌿 Better malting barley by modeling environmental sensitivity, genomics and metabolomics

- Innovationsfonden financed project - 2015-2017
- Partners QGG Foulum – Just Jensen and I-nano Aarhus – Frans Mulder

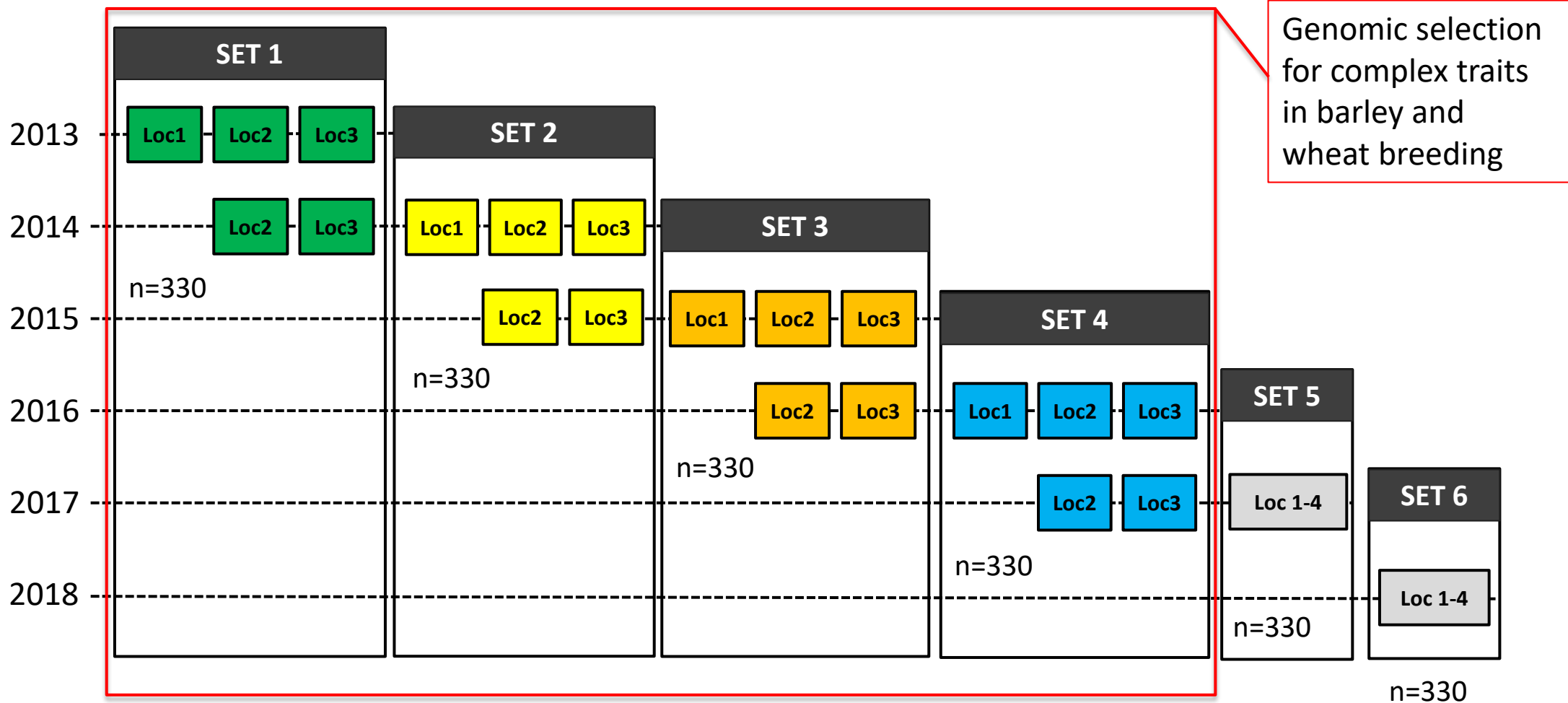


🌿 Økosort II – Genomic selection for traits related to organic farming

- GUDP financed project – 2018-2021
- Partners Økologisk Landsforening and Agrologica



DEVELOPMENT OF TRAINING POPULATION

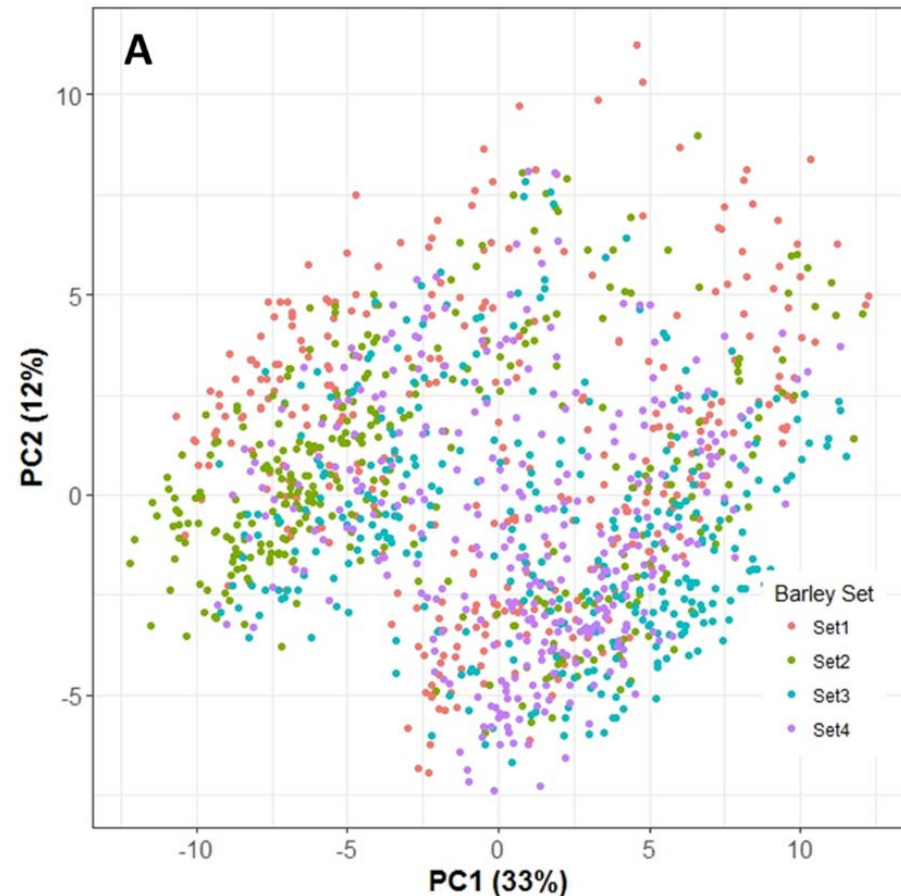


TRAITS & POPULATION STRUCTURE

🌿 All important agronomic and quality related traits was recorded, i.e.,

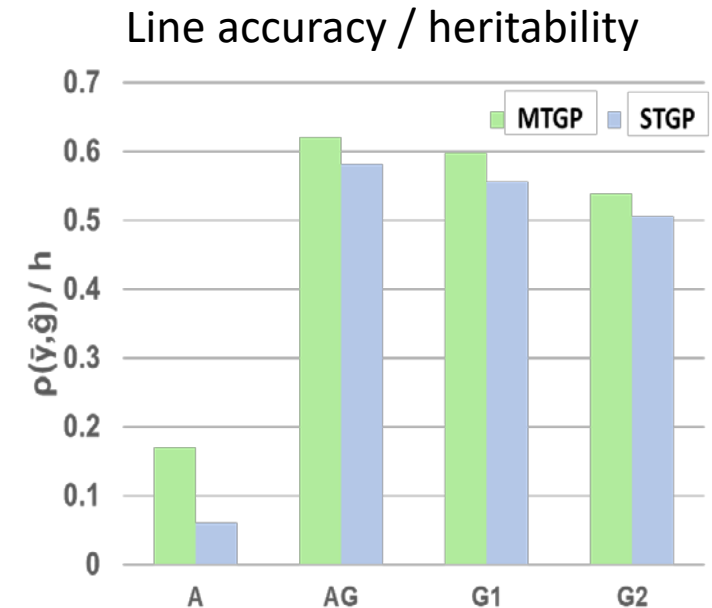
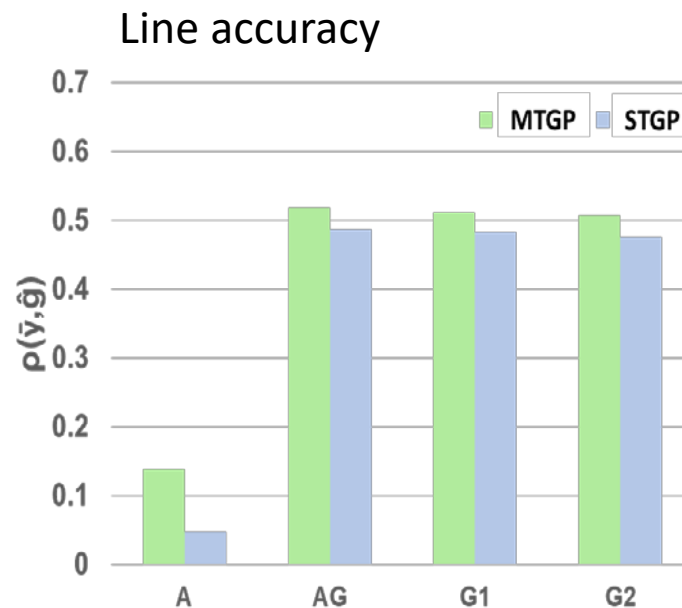
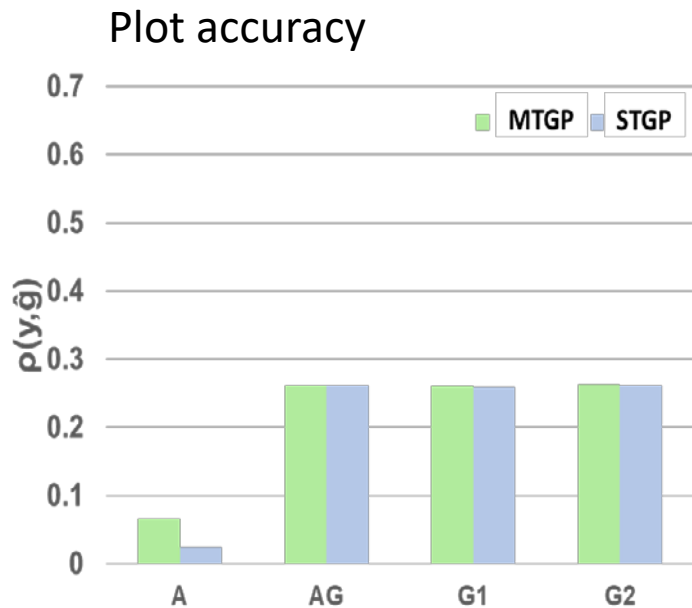
- Grain yield (kg/plot), Protein
- Heading, Height, Lodging etc.
- All major diseases
- Seed size distribution, Density
- Malting/brewing quality

In total 30 traits



SINGLE TRAIT GP & MULTI TRAIT GP APPROACHES FOR PREDICTING YIELD IN F6 BARLEY

Barley



A: Pedigree matrix / spatial effects
 G1: Genomic matrix / spatial effects

AG: Pedigree & Genomic matrix / spatial effects
 G2: Genomic matrix

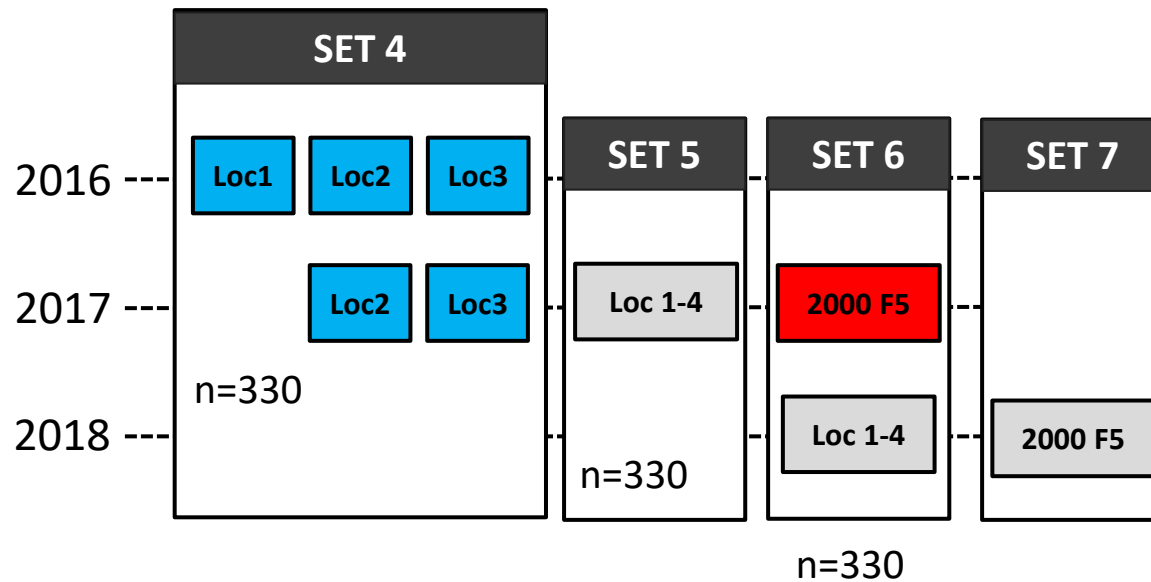
Cultivating Value

SPRING BARLEY BREEDING PROGRAM

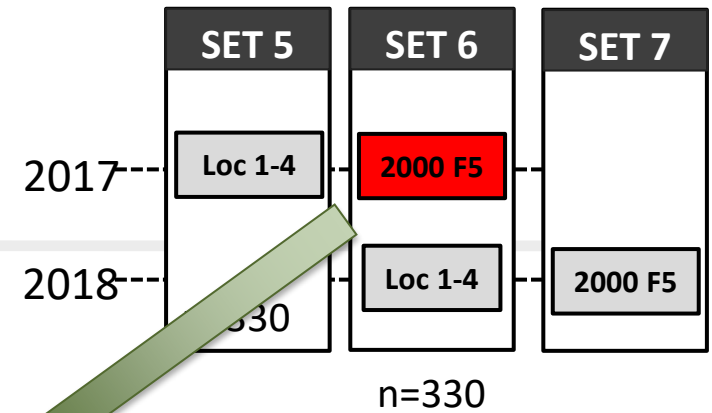
Generation	Details
Crossing	
F1	Greenhouse
F2-F4	Selection for disease resistance (F4 = 150.000 individuals)
F5 (NL-3)	One Yield plot – seed coming from one plant (2000 individuals)
F6 (NL-2)	Multi-location replicated yield trials (330 individuals)
F7 (NL-1)	Multi-location replicated yield trials (30 individuals)

VALIDATIONS STRATEGIES

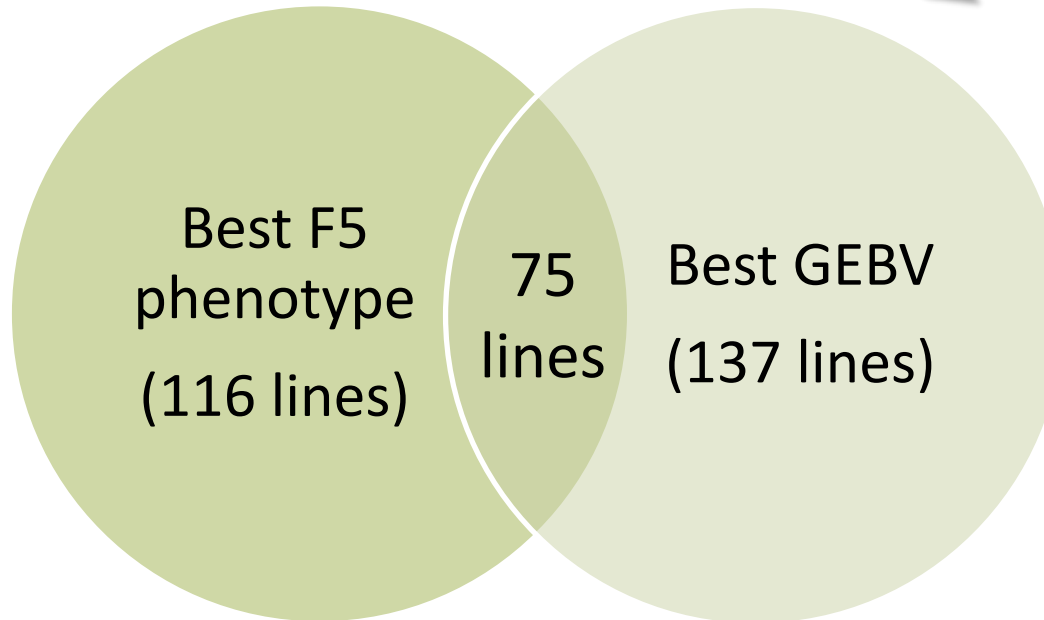
- 🌿 In the first years TP < 900
 - Leave one out / Leave family out
- 🌿 TP > 900 lines
 - Leave set out



VALIDATION AND IMPLEMENTATION

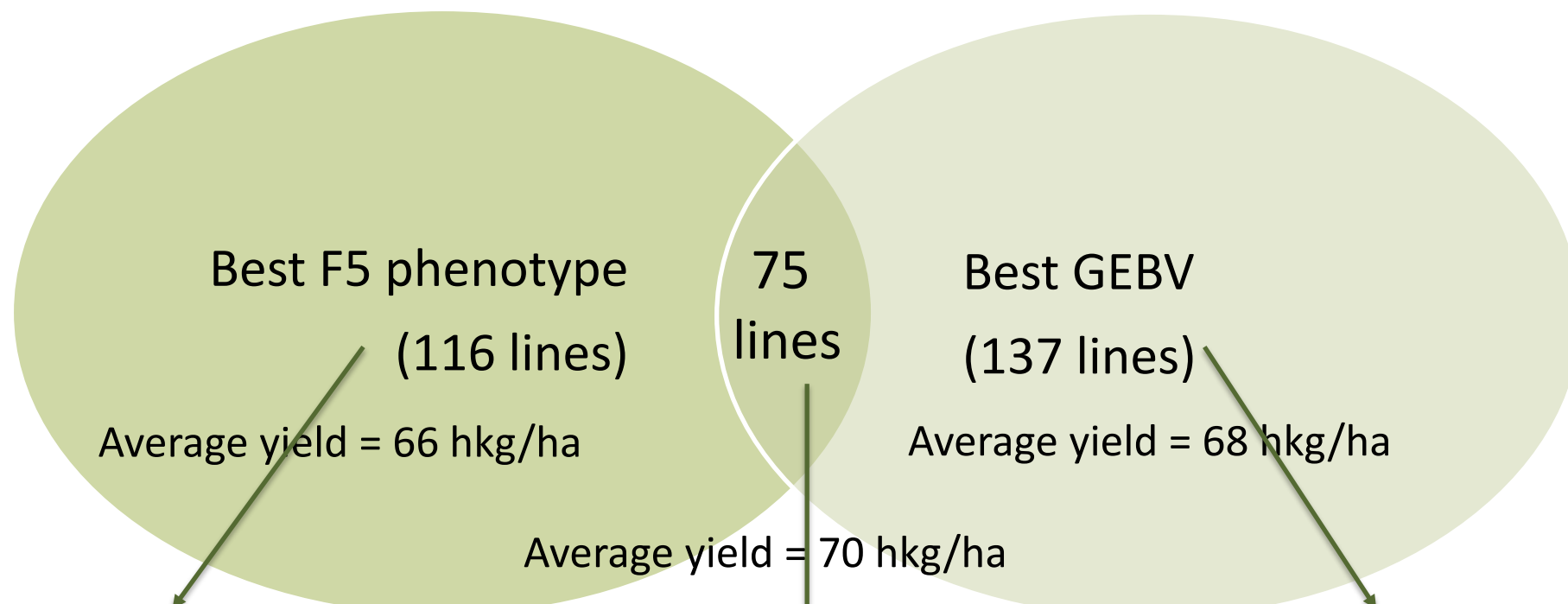


Selection in F5 Spring Barely 2017



Based on F6 line performance (2018) the selection pressure on each group will be determined

SELECTION OF THE 30 BEST LINES FROM F6 BASED ON 12 PLOT AVERAGE FROM 4 LOCATIONS (YIELD)

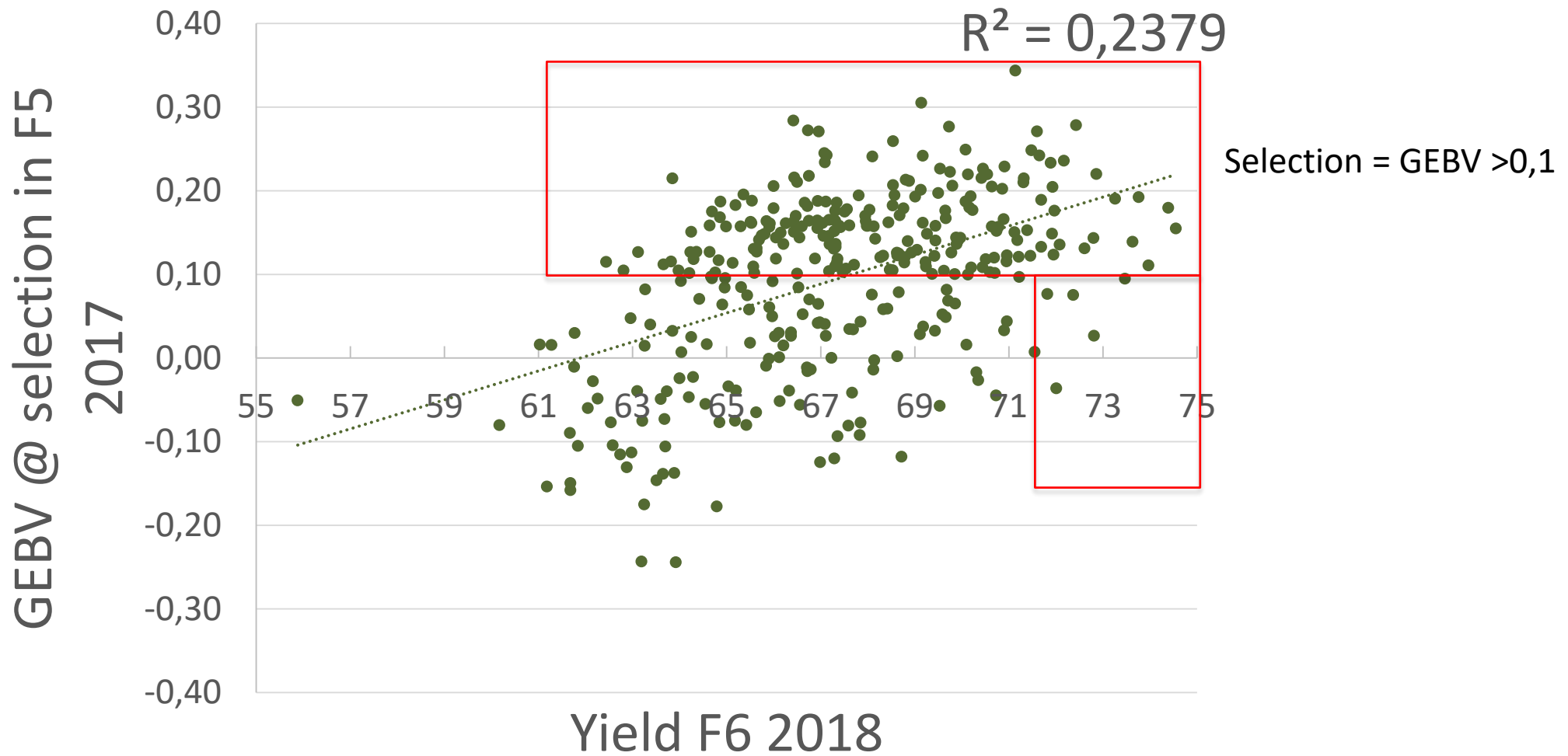


Selected 5 of 30 lines (17%)
Average yield = 72,1 hkg/ha
Selection intensity 4%

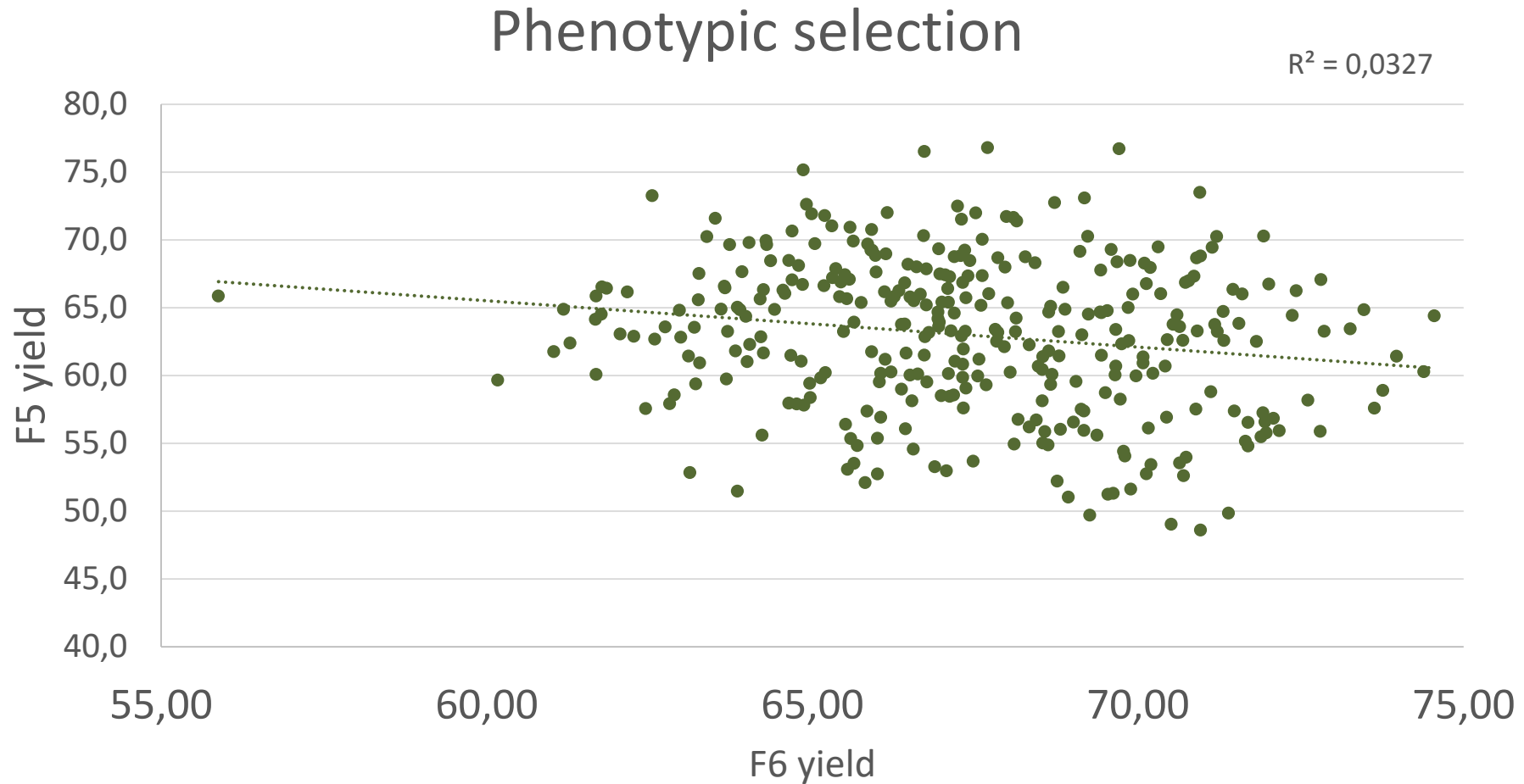
Selected 18 of 30 lines (60%)
Average yield = 72,5 hkg/ha
Selection intensity 13%

Selected 7 of 30 lines (23%)
Average yield = 72,6 hkg/ha
Selection intensity 9%

CORRELATION BETWEEN F5 GEBV (YIELD) AND F6 YIELD OBS



CORRELATION BETWEEN F5 YIELD (1 PLOT) AND F6 YIELD 12 (PLOTS)



THE ANSWER IS GENOMIC SELECTION!!

SORRY WHAT WAS THE QUESTION?



Gen	Before implementation of GS	After
Crossing		
F1	Greenhouse	
F2-F4	Selection for disease resistance (F4 = 150.000 individuals)	
F5 (NL-3)	One Yield plot – seed coming from one plant (2000 individuals)	
F6 (NL-2)	Multi-location replicated yield trials (330 individuals)	30 % less plot
F7 (NL-1)	Multi-location replicated yield trials (40 individuals)	30 % less plot



PUBLICATIONS AND ACKNOWLEDGEMENT

- 2-3 peer reviewed paper + several conference abstracts and posters



RESEARCH ARTICLE

Genomic Prediction of Seed Quality Traits Using Advanced Barley Breeding Lines

Nanna Hellum Nielsen^{1*}, Ahmed Jahoor^{1,3}, Jens Due Jensen¹, Jihad Orabi¹, Fabio Cericola², Vahid Edriss¹, Just Jensen²

RESEARCH ARTICLE

Optimizing Training Population Size and Genotyping Strategy for Genomic Prediction Using Association Study Results and Pedigree Information. A Case of Study in Advanced Wheat Breeding Lines

Fabio Cericola^{1*}, Ahmed Jahoor^{2,3}, Jihad Orabi³, Jeppe R. Andersen³, Luc L. Janss¹, Just Jensen¹

Under review in **Frontiers in Plant Science**

Multiple trait genomic prediction improves the prediction accuracy in spring barley and winter wheat breeding programs.

Hsin-Yuan Tsai^{1*}, Fabio Cericola¹, Vahid Edriss², Jeppe R. Andersen², Jihad Orabi², Jens D. Jensen², Ahmed Jahoor^{2,3}, Luc L. Janss¹, Just Jensen¹

THANK YOU FOR LISTENING

