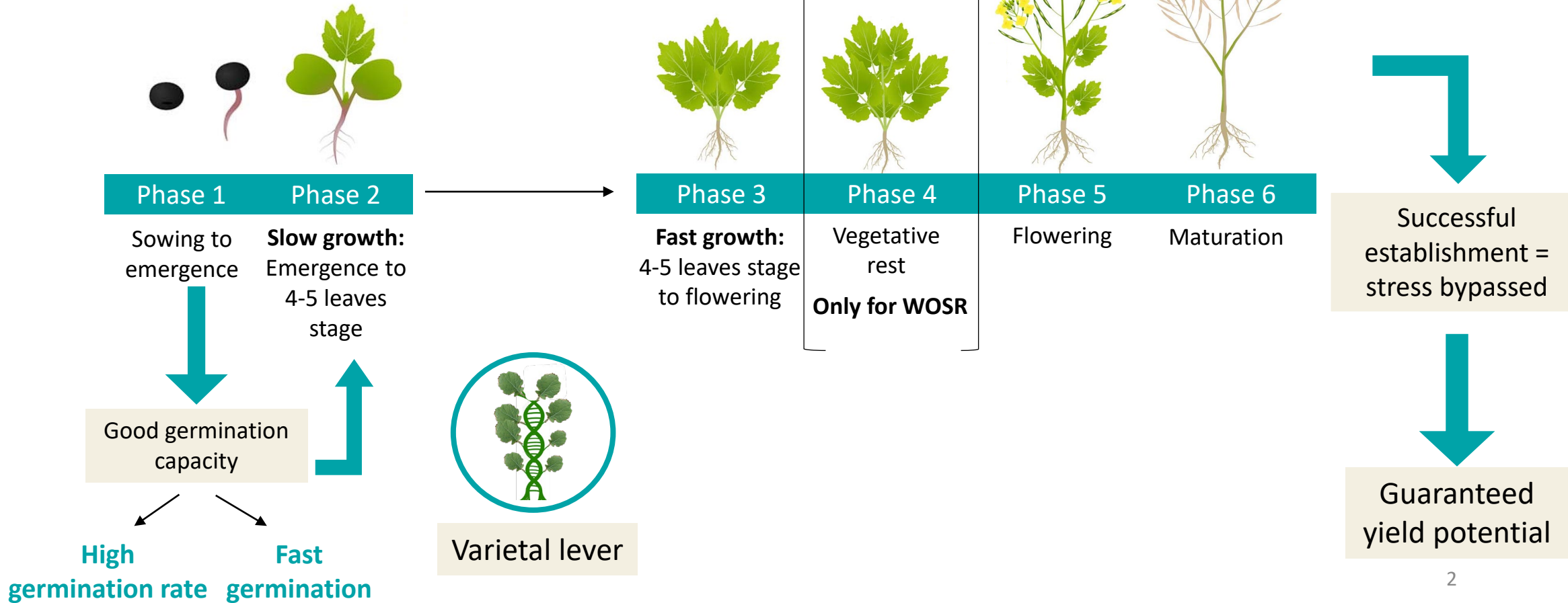


Genetic control of germination-related traits in rapeseed and the potential of genomic and phenomic selection to predict fast germinating ability

Marianne Laurençon, Julie Legrix, Marie-Hélène Wagner, Didier Demilly, Cécile Baron, Sylvie Ducournau, Anne Laperche, Nathalie Nesi

Agronomic challenges: establishment, a decisive stage



Agronomic challenges: establishment, a decisive stage



What is the genetic determinism of germination-related traits?

→ GWAS approach with large genetic diversity germplasm

Which predictors are best suited to predicting these traits ?

→ Genomic vs Phenomic predictions

→ Impact of population structure on the predictive ability

Good germination capacity

High

germination rate

Fast

germination



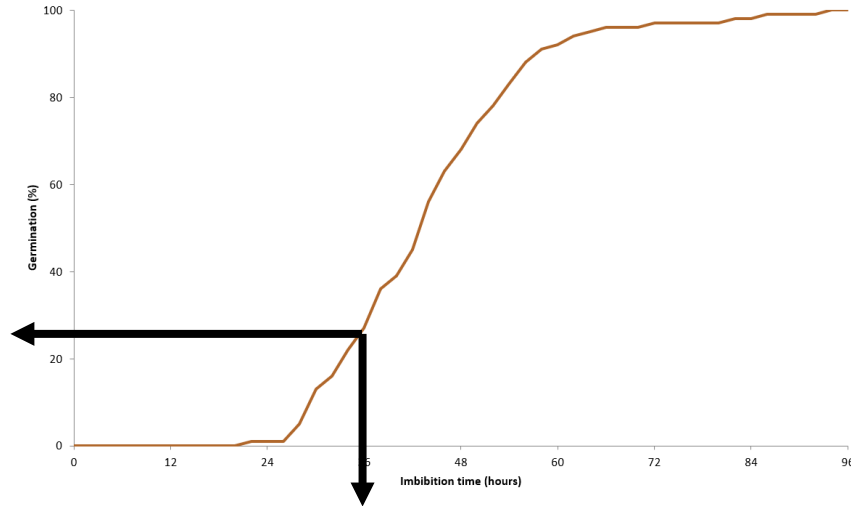
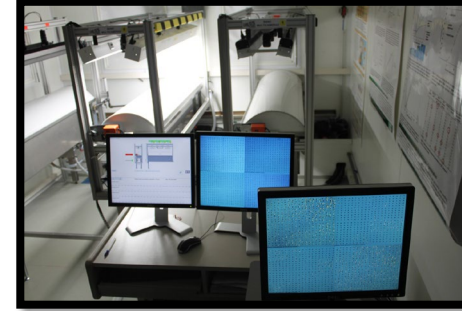
Varietal lever

Successful establishment = stress bypassed

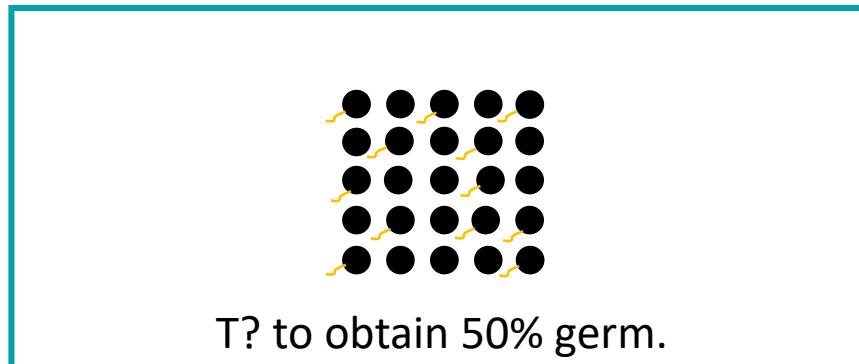
Guaranteed yield potential

Traits phenotyped for seed germination using a high throughput phenotyping platform

Seeds germination dynamics monitored during 96 h after imbibition
Pictures taken every 2 h
Repetitions: 25 seeds*4 repetitions per genotype



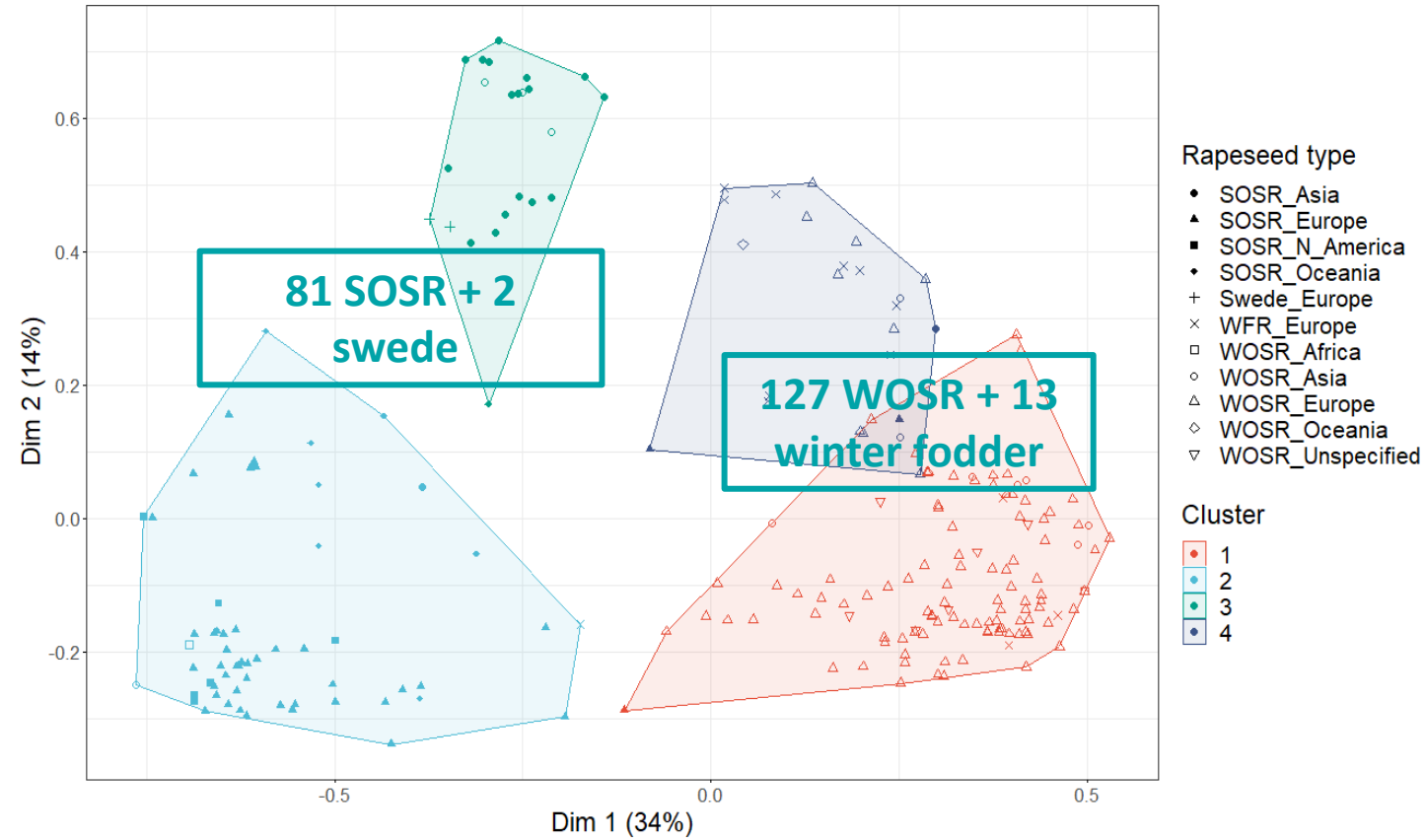
GR36



- Deduced from germination dynamics :
- Time to reach 20% of germination (T20)
 - Time to reach 50% of germination (T50)
 - Time to reach 80% of germination (T80)
 - Germination rate at 36 h (GR36)**
 - Uniformity (UNI) ~ Germination speed (T80-T20)
 - Area under the curve (AUC)

- Other traits:
- Time of the first germination (FG)
 - Mean germination time (MGT)**
 - Final germination rate at 96h (GR)

Genetic structure
33 151 SNP from *Brassica*
60K Infinium SNP array



Mean $\pi=7.69e^{-05}$

=> Important genetic diversity

What are the relationships between germination-related traits ?

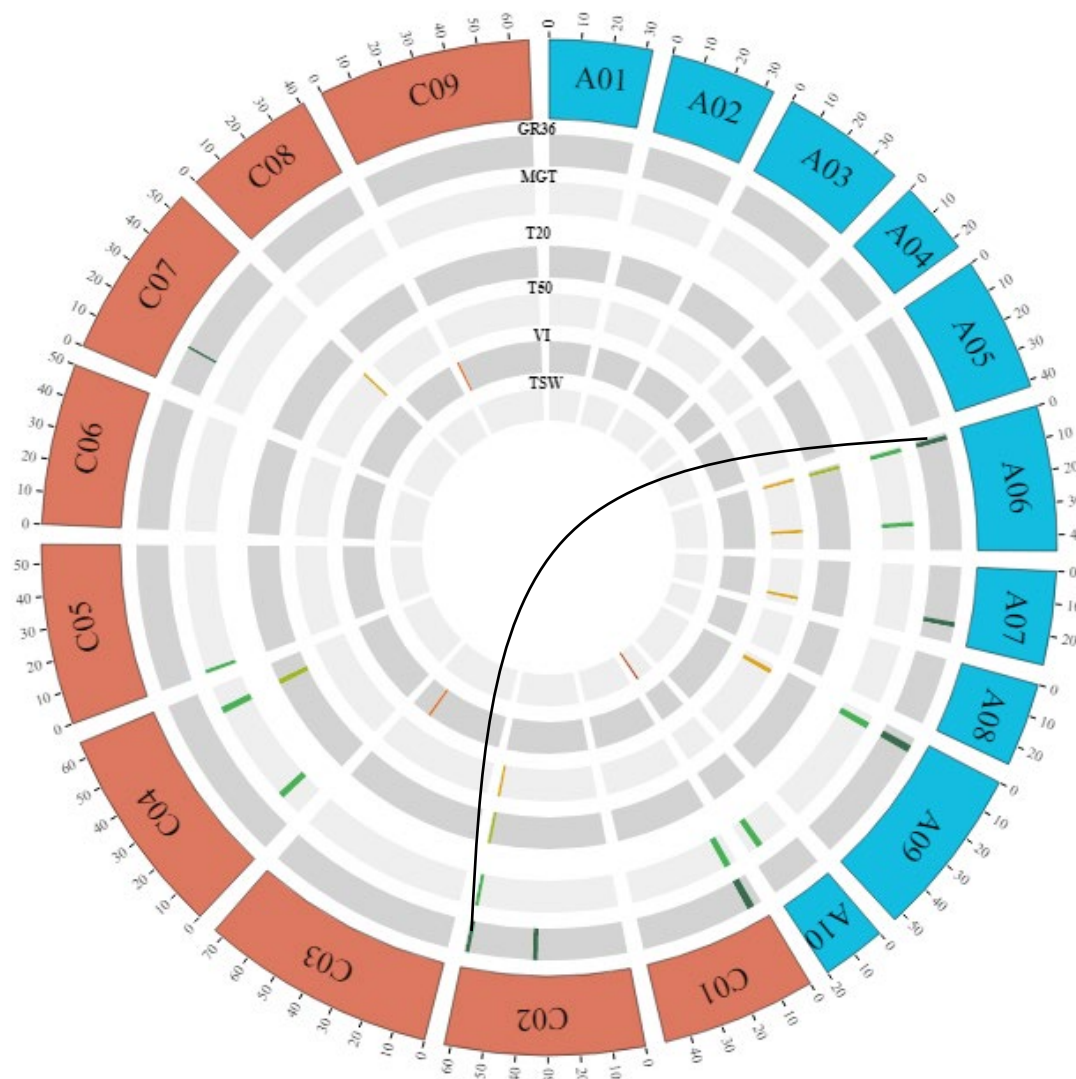
	FG	T20	T50	T80	MGT	UNI	AUC	GR36	GR
H ²	0.51	0.69	0.65	0.61	0.68	0.43	/	0.69	0.46

Moderate to high heritability for seed germination traits

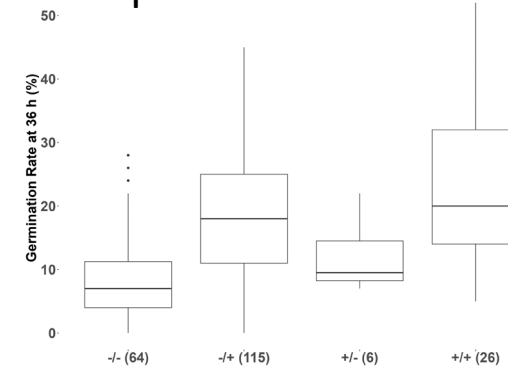
What are their genetic determinants ?

What are the genetic determinants of these traits ?

14 associations with $6.30\% < R^2 < 8.78\%$
identified by GWAS
1 pair of markers in epistasis for GR36

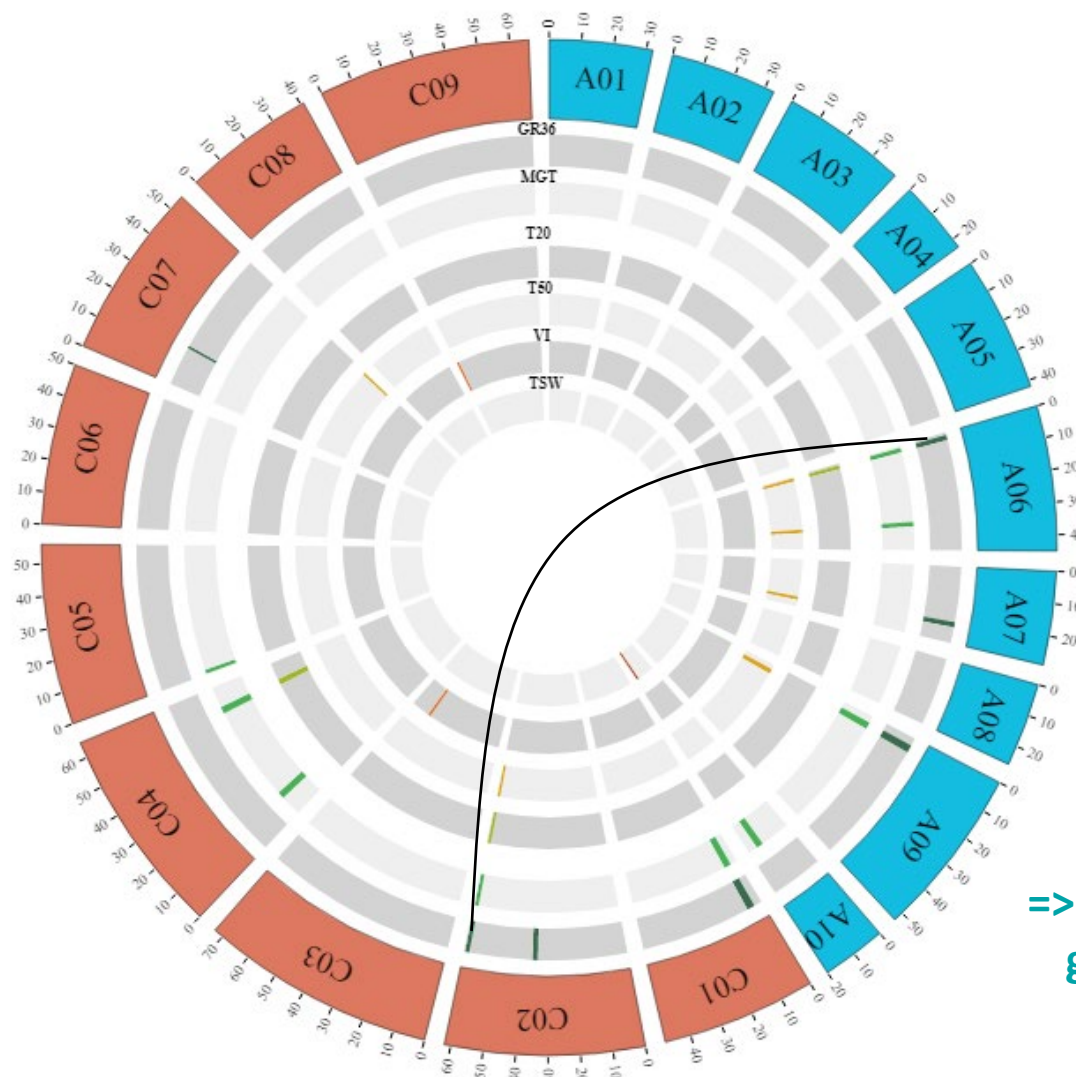


Epistasis for GR36

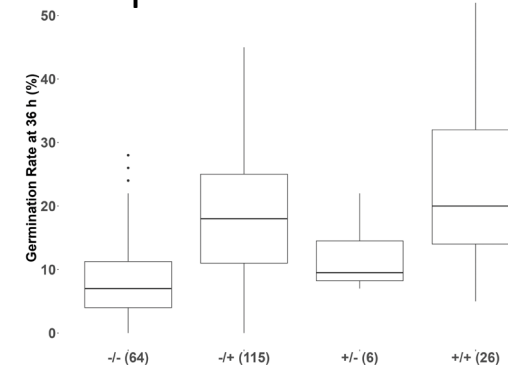


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Epistasis for GR36

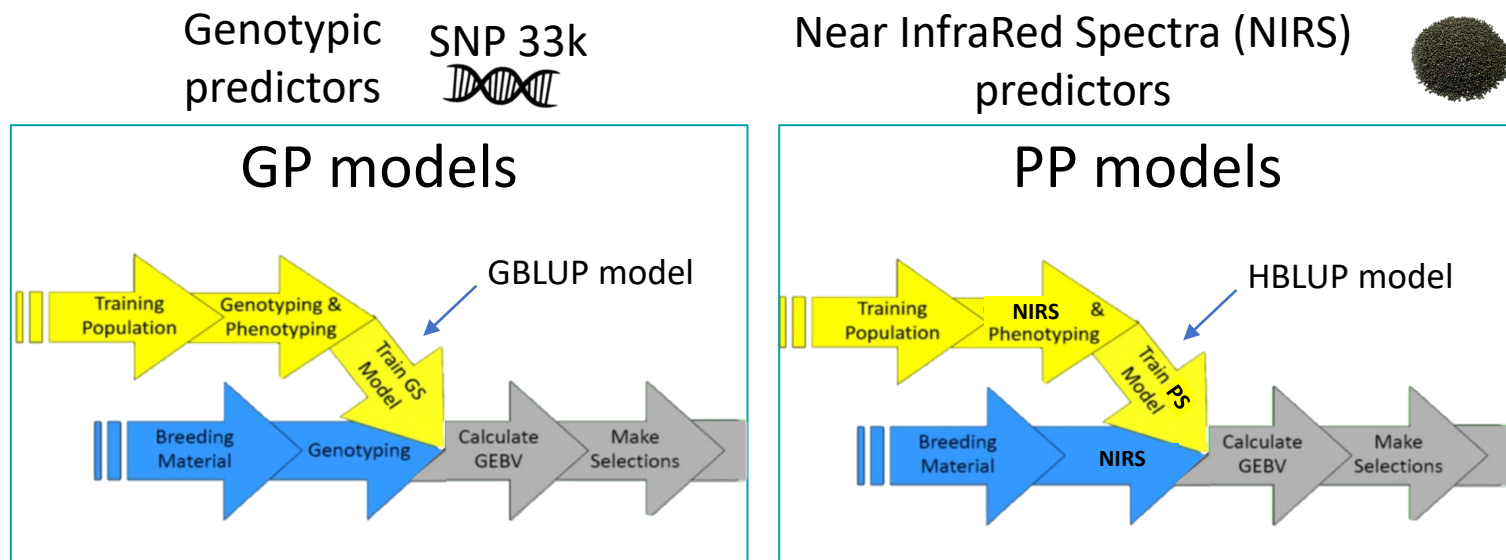


Genetic determinism is more complex and cannot be approximate using only few additive effects

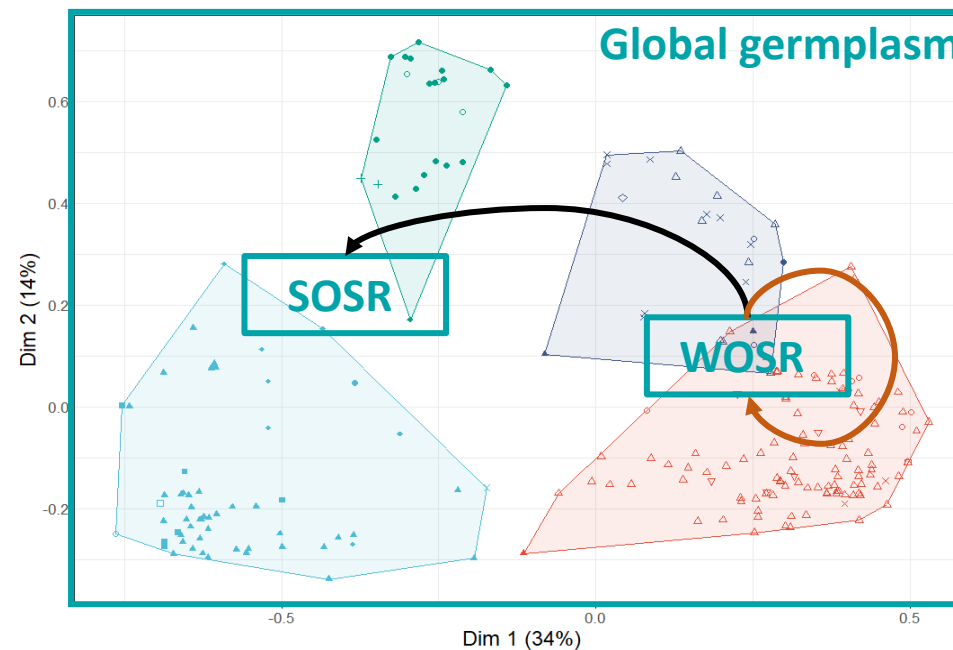
=> Possible to predict these traits using genomic and phenomic prediction?

Is it possible to predict GR36 and MGT with genomic (GP) and phenomic prediction (PP)?

Which predictor is the best ?

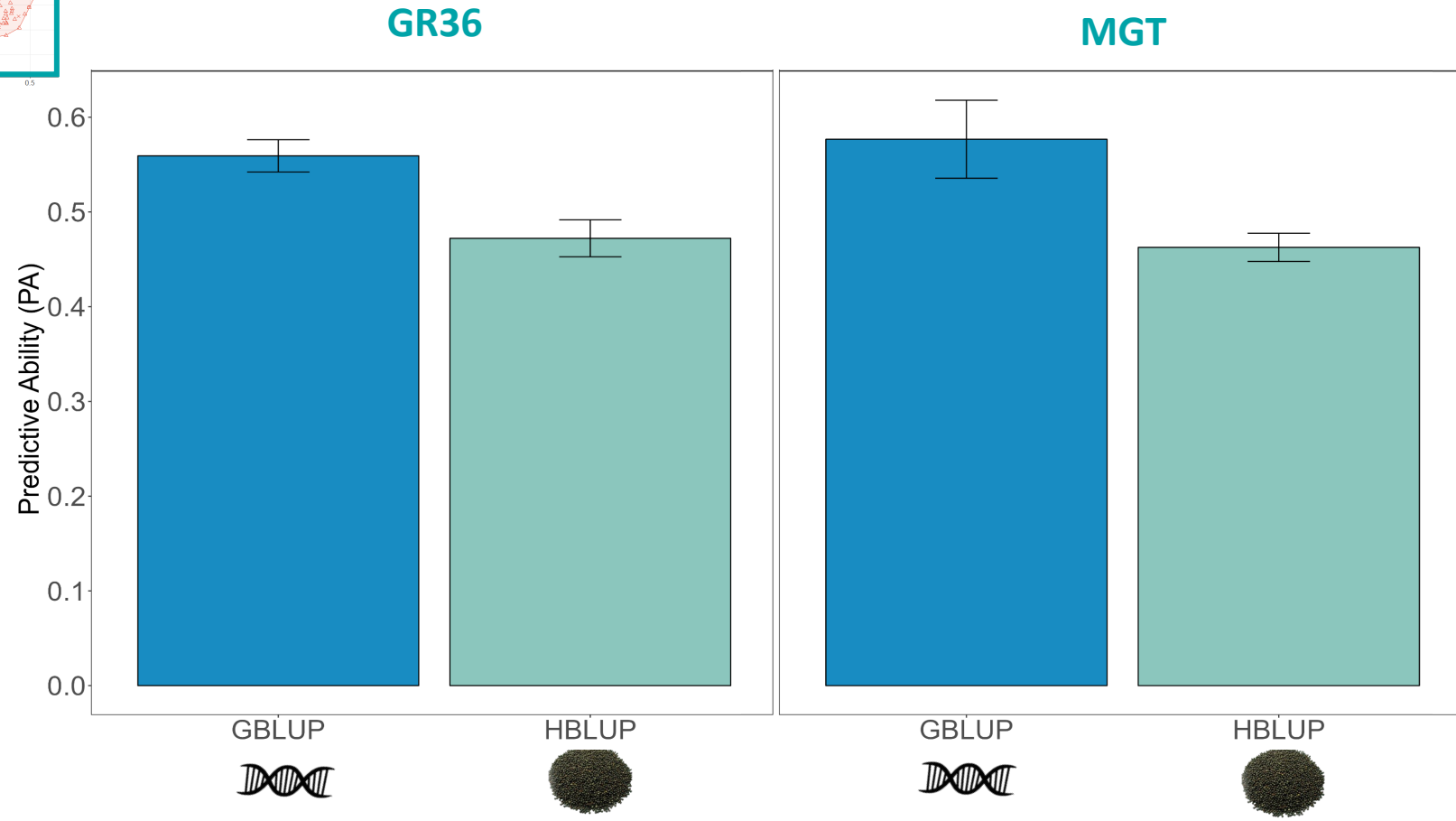
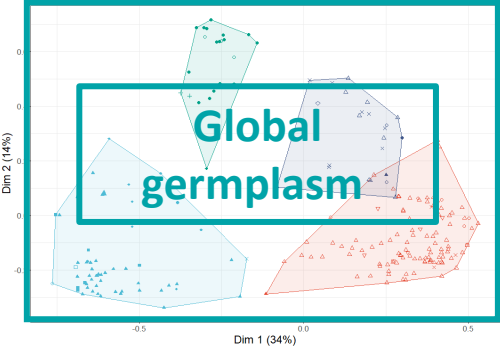


How does population structure impact the prediction ability ?



Is it possible to predict GR36 and MGT with genomic (GBLUP) and phenomic prediction (HBLUP)?

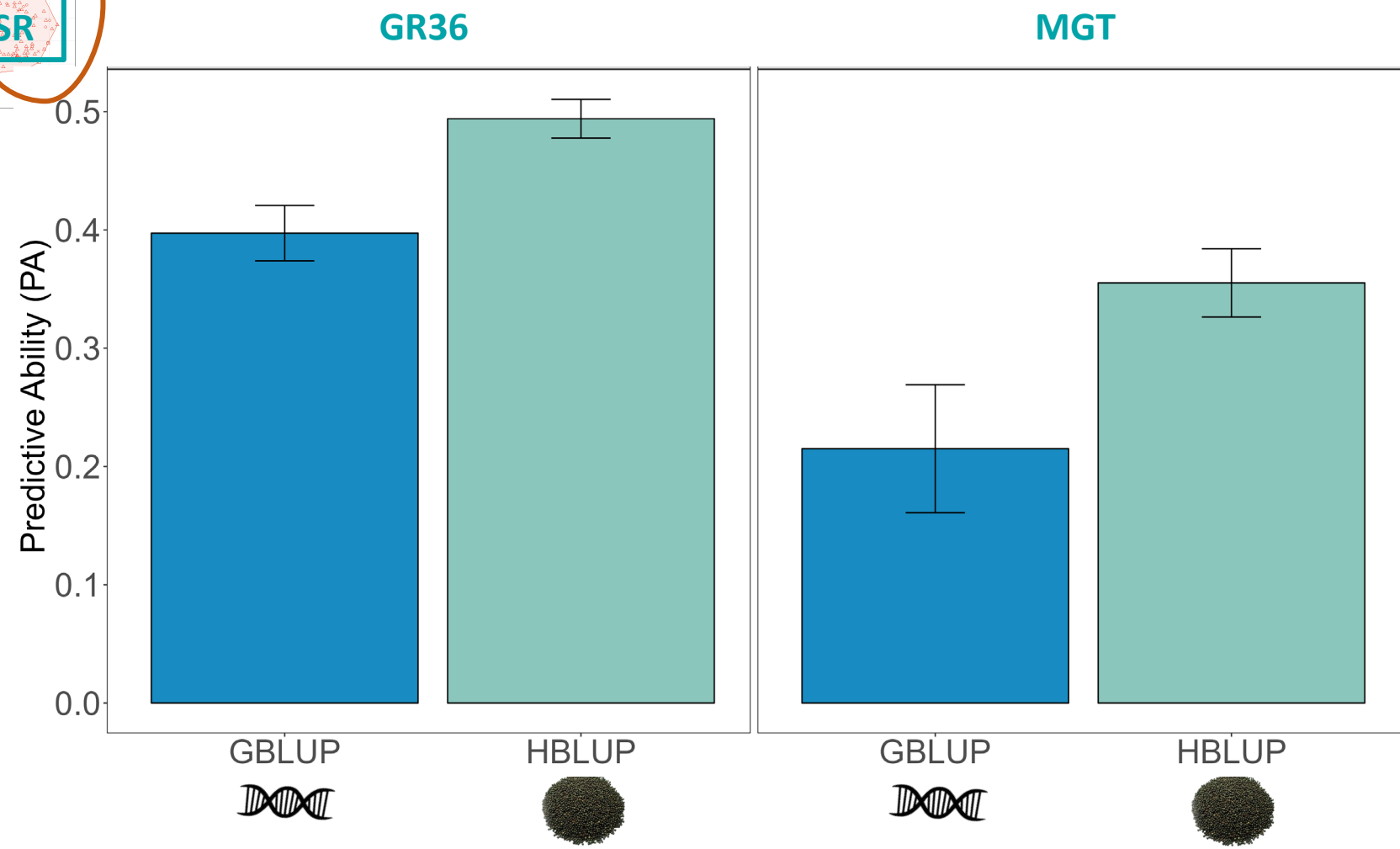
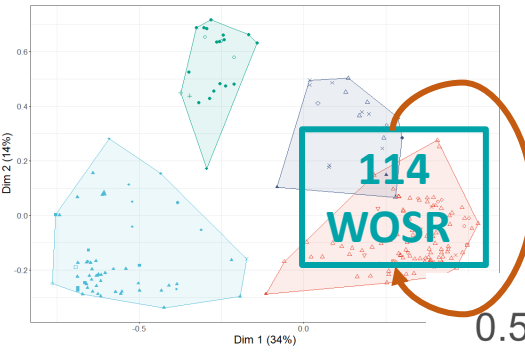
CV: 4/5pop
100 repetitions
30K SNP
2k NIRS



High predictive ability for GR36 and MGT
GP outperforms PP: overestimation due to high genetic structure ?

Is it possible to predict GR36 and MGT with genomic (GBLUP) and phenomic prediction (HBLUP)?

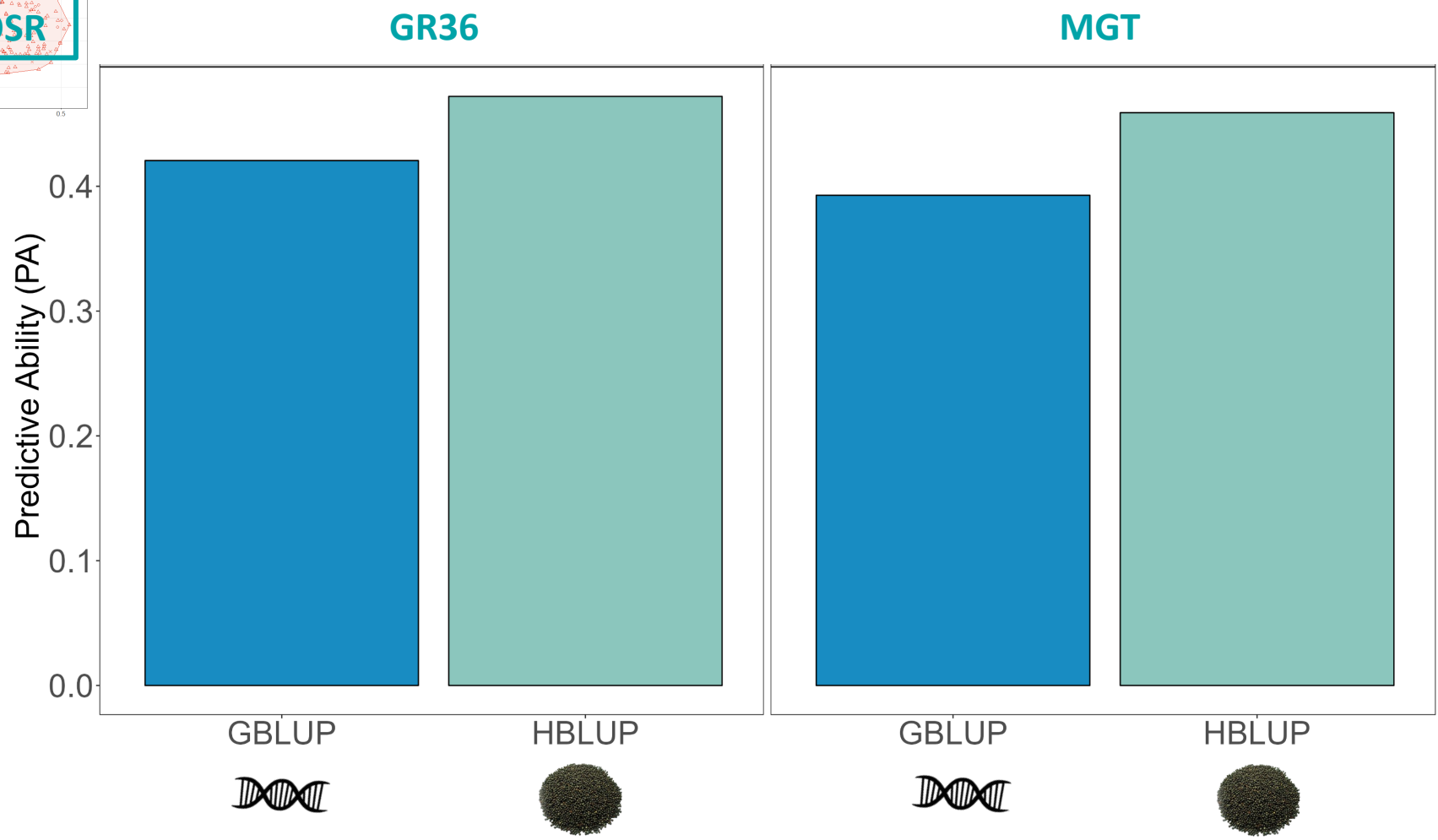
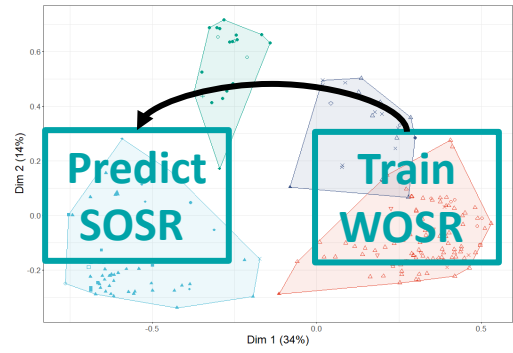
CV: 4/5pop
100 repetitions
30K SNP
2k NIRS



Decrease of PA for both traits compared to before
PP outperform GP: population structure

Is it possible to predict GR36 and MGT with genomic (GBLUP) and phenomic prediction (HBLUP)?

30K SNP
2k NIRS



PP outperform GP and stable across germplasms

Conclusion

- High heritability
 - => Selection of these traits in breeding
- 14 QTL identified
- Determinism of seed germination is definitely complex and QTL identification is not enough to improve these traits
- Both GP and PP can be used to predict for germination ability
- In case of population structure: PP seems more adapted

Perspectives

- Integration of QTL in GBLUP models
- Linking seed germination capacity under controlled conditions to:
 - Seed germination under stresses: germinative vigor
 - Seed germination in field conditions
 - Early development/early vigor



M. H. Wagner



D. Demilly



S. Ducournau



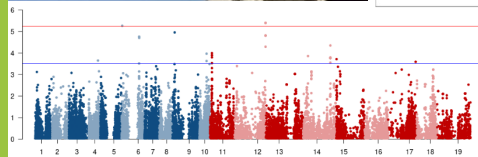
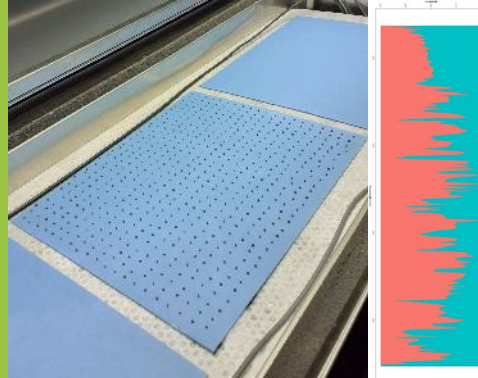
M. Rousseau-Gueutin



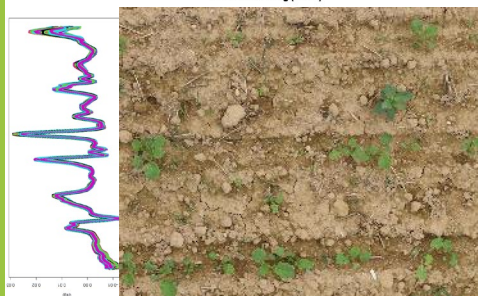
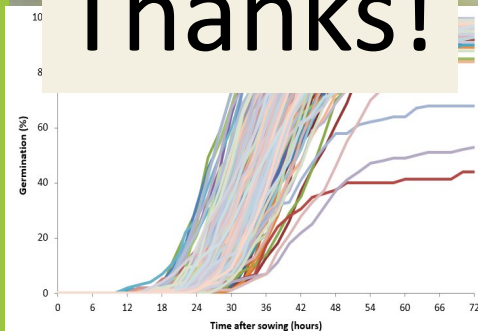
R. Rincet



C. Sauvage



Thanks!



N. Nesi



A. Laperche



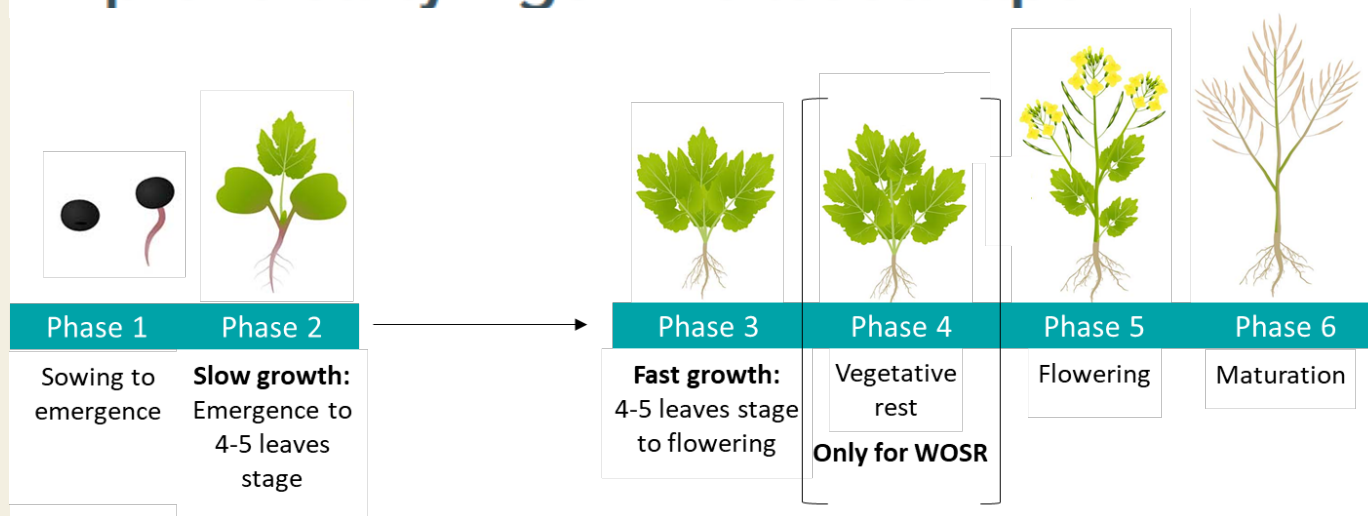
J. Legrix



C. Baron

N°73

Leaf cover dynamics highlighted old spring germplasm as promising resources to improve early vigor in oilseed rape



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Leaf cover dynamics highlighted old spring germplasm as promising resources to improve early vigor in oilseed rape

Context

Early vigor is: - a main component of plant establishment
 - comprised from plant emergence to the 4-5 leaf stage
 - commonly approximated by leaf area or total biomass

Our aim is to unveil the genetic diversity for early vigor by phenotyping plant development dynamics until the 5-leaf stage.

Material and Methods

Germplasm genetic diversity
 217 OSR genotypes
 ++ and 00 quality from 1946 to 2010

Early vigor phenotyping
 - 2 repetitions
 - 9 plants replicates per genotype and per rep.
 - Photos taken every two days
 - Harvest at 5/6 leaves

Traits at harvest

Category	Trait	Heritability
Biomass production	Shoot biomass (SBW)	0.91
	Root biomass (RBW)	0.94
	Total biomass (TBW)	0.91
	Shoot:Root ratio (SR)	0.93
	Specific carbon assimilation (SCA)	0.89
Plant development	Shoot:Nitrogen ratio (SN)	0.95
	Leaf Area (LA)	0.80
	Shoot nitrogen content (SNC)	0.84
	Leaf surface to shoot nitrogen ratio (LSA/SN)	/
	Leaf Area Ratio (LAR)	0.95
	Specific Leaf Area (SLA)	0.95

Traits in dynamics

Table 1 Description of traits obtained at harvest and associated heritabilities. Main traits are represented in blue.

Fig. 3 Evolution of leaf cover regarding growing degree days (GDD). The evolution of leaf cover allowed to obtain a set of dynamic traits, represented in black.

Results

1. SOSR genotypes develop faster than WOSR

2. Seed quality (++)/00) does not impact early vigor

Fig. 4 PCA (A) and clustering (B) realized on phenotypic traits using 217 OSR genotypes. Strong effect of the germplasm structure on early development

Fig. 5 Mean phenotypic value of each trait for SOSR ++ (—), SOSR 00 (—) and WOSR 00 (—) types.

3. Old SOSR germplasm is a promising genetic resource for improving early vigor

Fig. 6 Mean phenotypic values of the top SOSR 25% (—) and the bottom SOSR 25% (—) and the top WOSR 25% (—) and bottom WOSR 25% (—) and composition according their breeding periods: 1946-1979, 1980-1989, 1990-1999, 2000-2010, missing information for TDW (A) and LA (B).

Conclusion and perspectives

AUC dynamic analysis is critical to understand early vigor and to discriminate genotype behaviors. Leaf cover dynamics revealed that some SOSR genetic resources developed faster than SOSR 00 and WOSR 00. These results need to be confirmed with current elite germplasm (hybrids and lines, under progress). Genetic control of these traits need are under investigation.