



## ➤ Genetic determinism of seed yield components in lucerne

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## ➤ Breeding: a lever to improve seed yield

- Seed yield : a component of the commercial success of a variety
- Seed yield progress mostly due to agricultural practices, so far
- How and when apply a selection pressure for seed yield?
  - Seed yield evaluation is not time-compatible with forage trait evaluation (cut at budding stage)



# ➤ Breeding scheme in forage crops

A 10-15 year process

Introduction of new origins

Nursery of spaced plants:  
choice of individual plants  
3 years

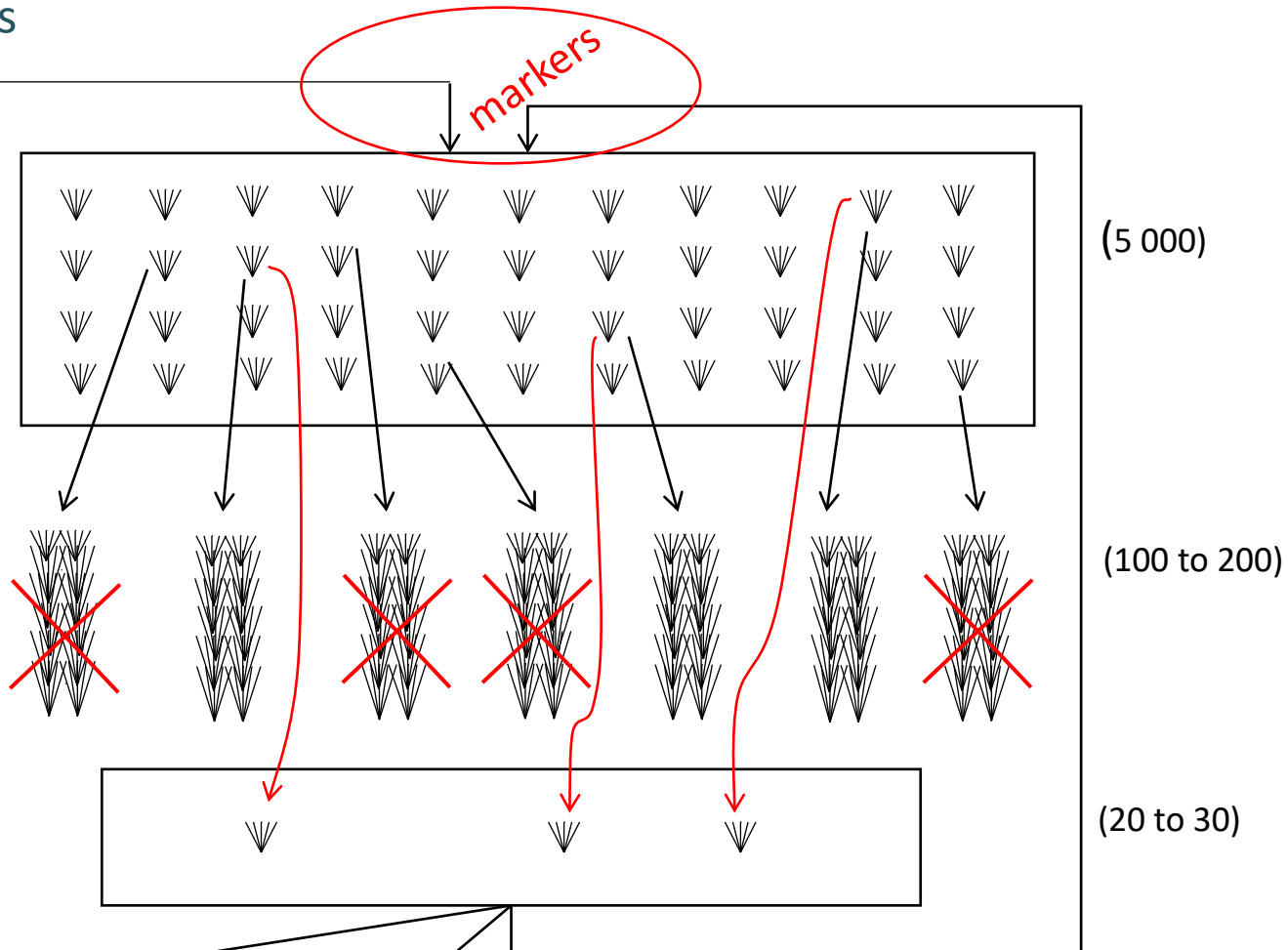
Harvest of seeds on mother plants

Test of progeny in microplots  
3 years

Polycross of the best plants  
1 year

Evaluation in multi-site trials  
3 years

Varieties



Genetic gain  $\Delta G$ :

$$\Delta G = \frac{i h^2 \sigma_P}{T}$$

$i$ : selection intensity

$h^2$ : heritability

$\sigma_P$ : phenotypic variation

$T$ : time

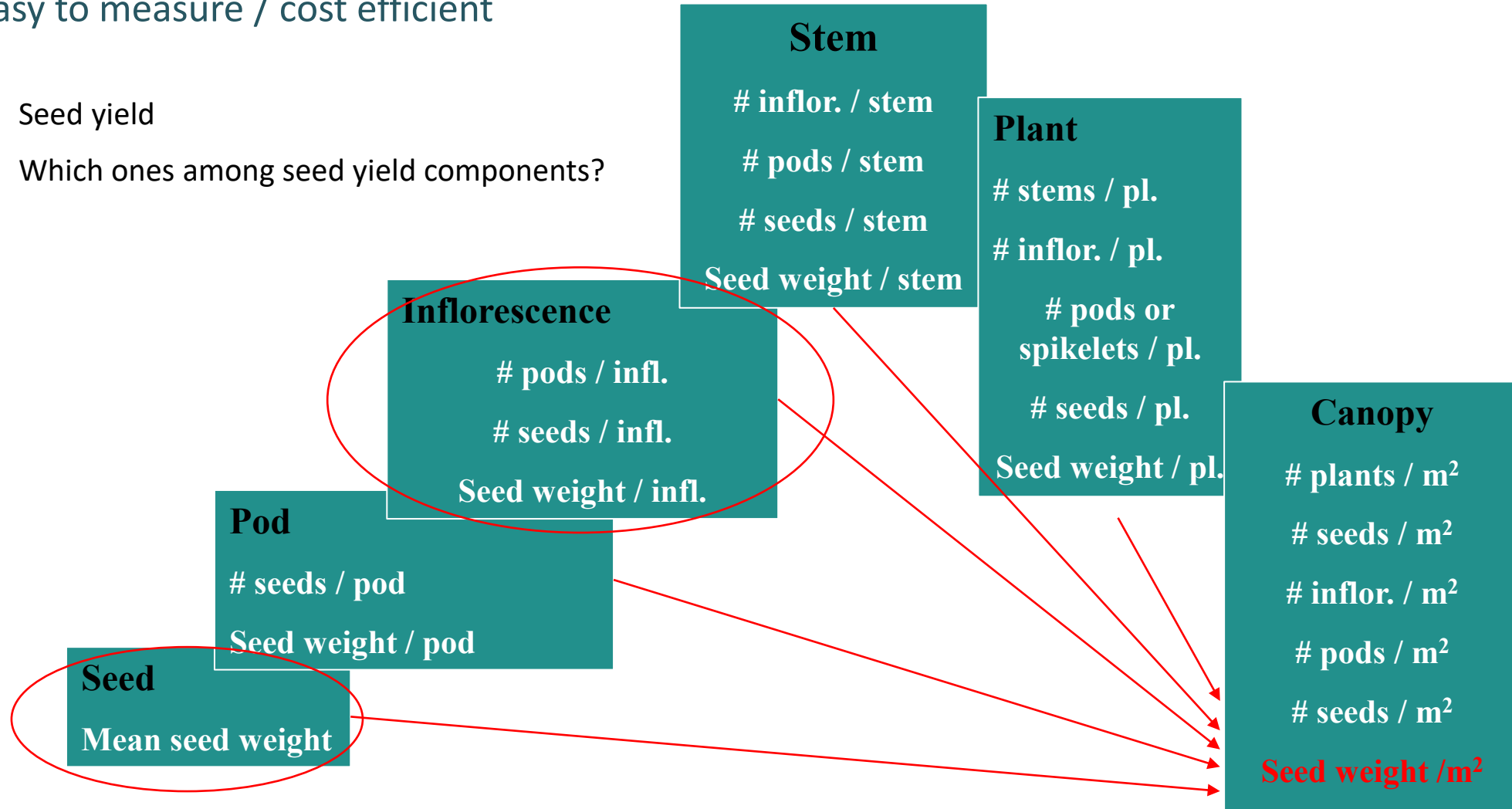
phenotypes



# ➤ Seed yield components

Easy to measure / cost efficient

- Seed yield
- Which ones among seed yield components?

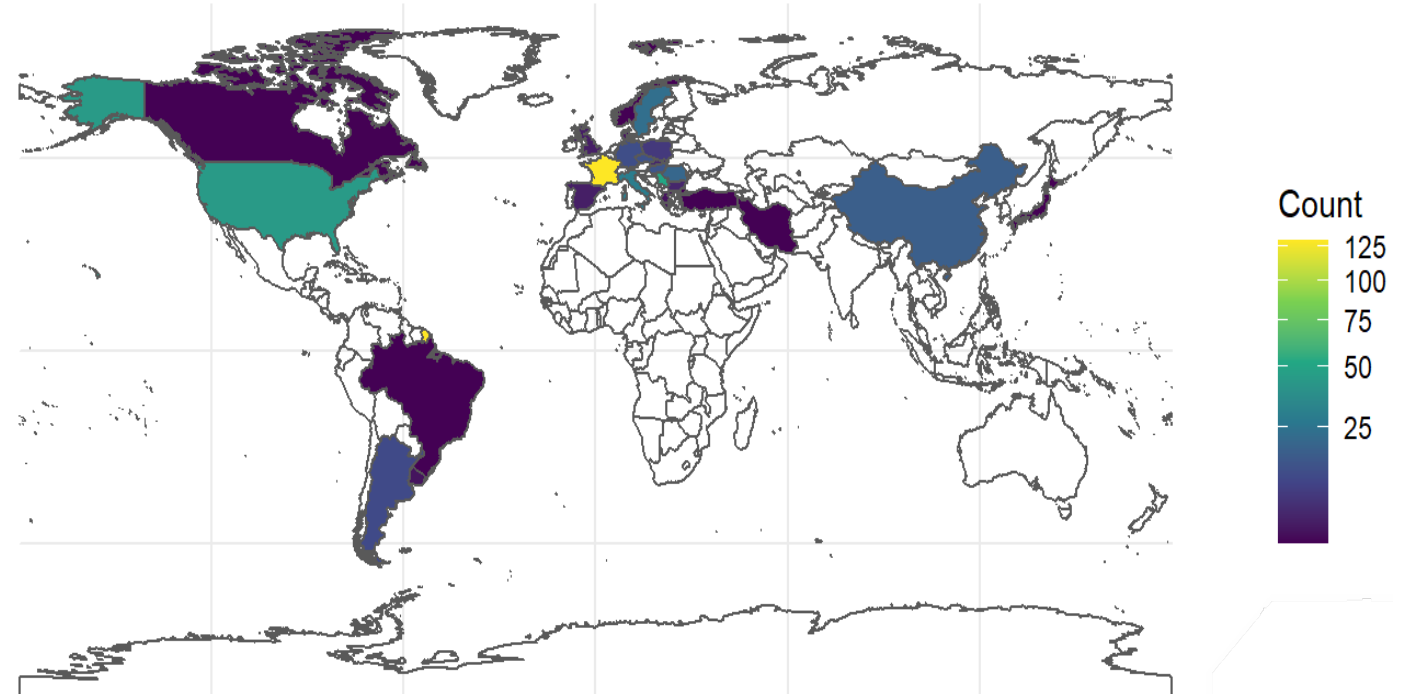


## ➤ Genetic study of seed yield traits

in a set of 400 cultivated accessions of lucerne

Origins:

- Europe : 313
- North America : 45
- South America : 16
- China : 17
- Middle East : 3
- Japan : 1



# ➤ Genetic study of seed yield traits

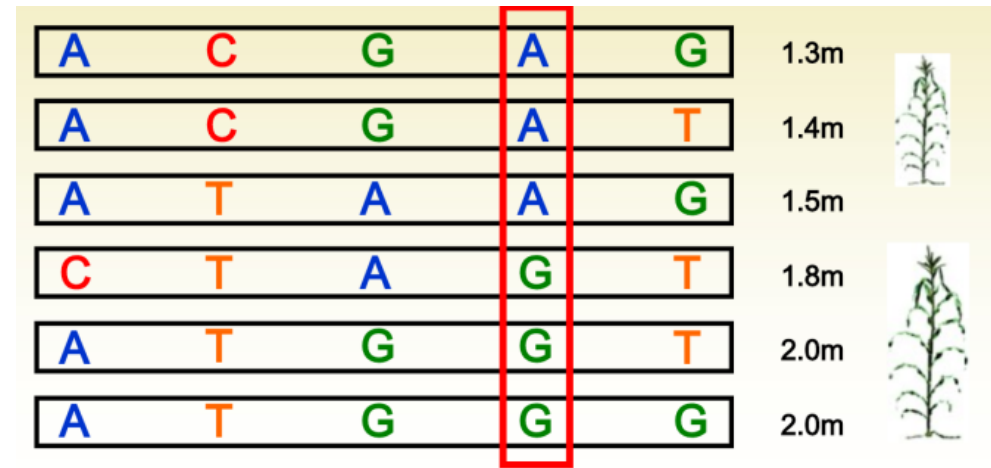
in a set of 400 cultivated accessions of lucerne

Genetic diversity for seed yield components

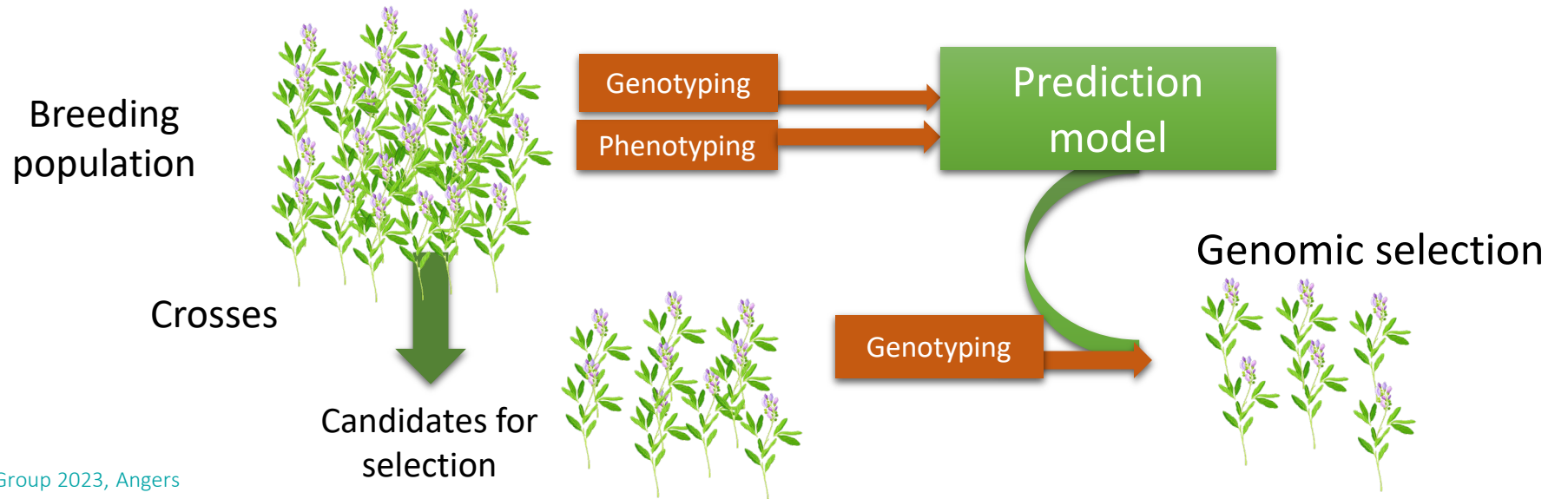
QTL detection in a genome-wide association study (GWAS)

Test of genomic prediction

GWAS: to find the markers associated to traits



Genomic prediction (genomic selection): to predict the traits with a large number of markers



# Experimental design



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## > Experimental design

2 locations : Lusignan (France), Novi Sad (Serbia)

**Phenotyping** of 400 accessions in an augmented design with 4 blocks, 440 plots / location

- Seed yield (Novi Sad)
- Pod number, seed number, pod weight, seed weight **per inflorescence**
- Seed number **per pod**
- Thousand seed weight

**Genotyping** with GBS markers: 228 k SNP

### **Statistical study**

- Heritability, correlations
- GWAS, with mlmm method
- Genomic prediction, with GBLUP method





# Results



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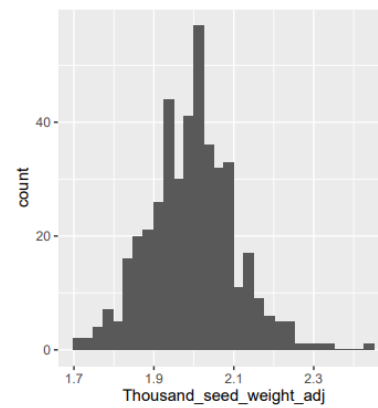
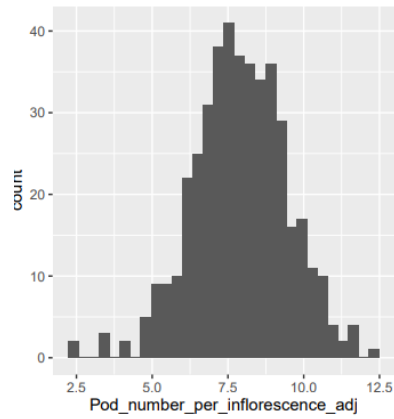
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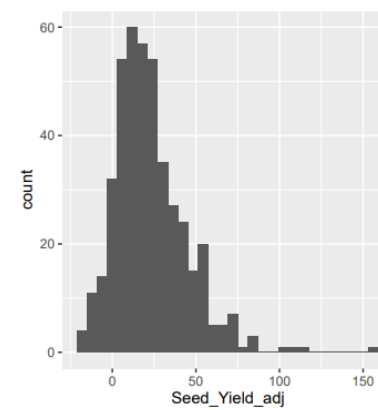
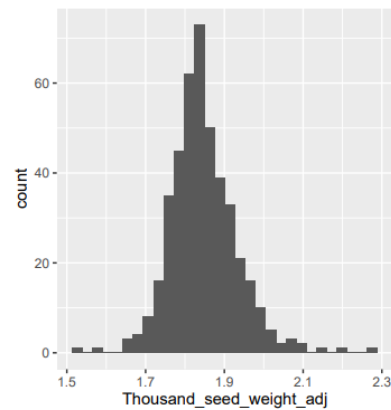
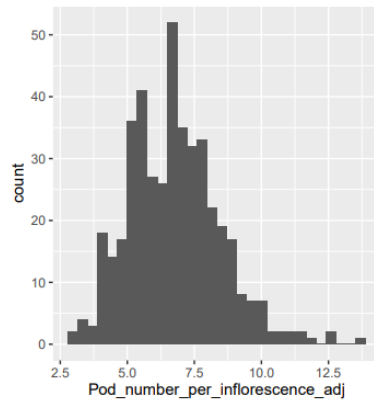
# ➤ Genetic diversity

A large diversity

Lusignan



Novi Sad



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## > Genetic diversity

### Genetic correlations

Novi Sad	Pod Weight / Inflo	Pod # / Inflo	Seed # / Inflo	Seed weight / Inflo	Seed # / Pod	1000 Seed Weight
Seed yield	0.269	0.682	0.825	0.805	0.677	-0.394

Correlations	Pod Weight / Inflo	Pod # / Inflo	Seed # / Inflo	Seed weight / Inflo	Seed # / Pod	
Pod Weight / Inflo		0.917	0.871	0.937	0.687	Lusignan
Pod # / Inflo	0.388		0.764	0.945	0.764	
Seed # / Inflo	0.302	0.203		0.970	0.874	
Seed weight / Inflo	0.541	0.917	0.959		0.855	
Seed # / Pod	0.015	0.878	0.675	0.562		

Novi Sad

## > Genetic diversity

### Heritability

Traits	Location	Heritability
Pod Number per Inflorescence	Lusignan	0.274
	Novi Sad	0.224
	2 locations	0.153
Thousand Seed Weight	Lusignan	0.321
	Novi Sad	0.685
	2 locations	0.206
Seed Yield	Novi Sad	0.349



## > GWAS

Pod number per inflorescence in Lusignan: 2 QTL only

- Chromosome 3 (SNP chr3\_64501447):  $R^2 = 8.6\%$
- Chromosome 7 (SNP chr7\_19532571):  $R^2 = 7.4\%$

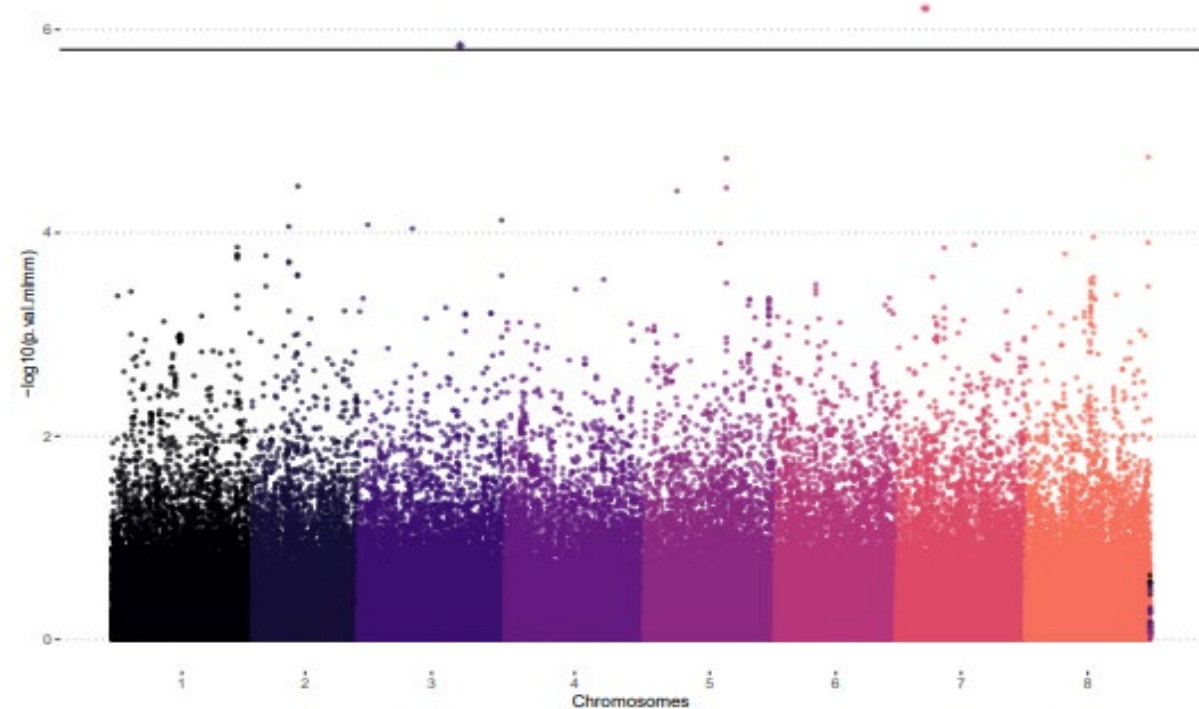
Total  $R^2 = 15.6\%$

Other QTL for some other traits

Quantitative traits

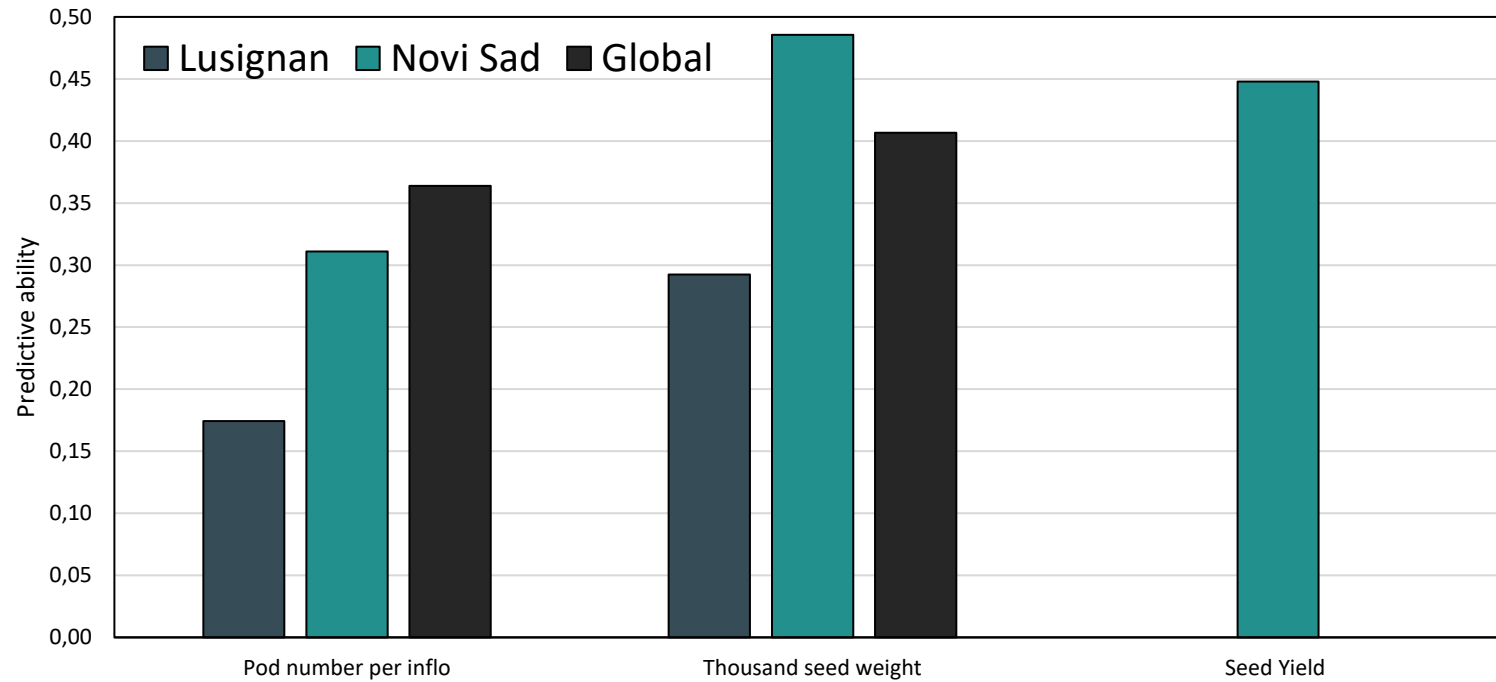
Size of the population

Non permissive statistic threshold



## ➤ Genomic prediction

Low to moderate predictive ability



# Conclusion



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## > Conclusion

Seed yield traits are quantitative traits

Breeding is not easier for seed yield than for forage traits: moderate heritability

The inflorescence level is accurate: pod number, seed number, pod number, pod weight / inflorescence

Thousand seed yield is negatively correlated to other seed yield components

A few QTL were detected: to be selected for

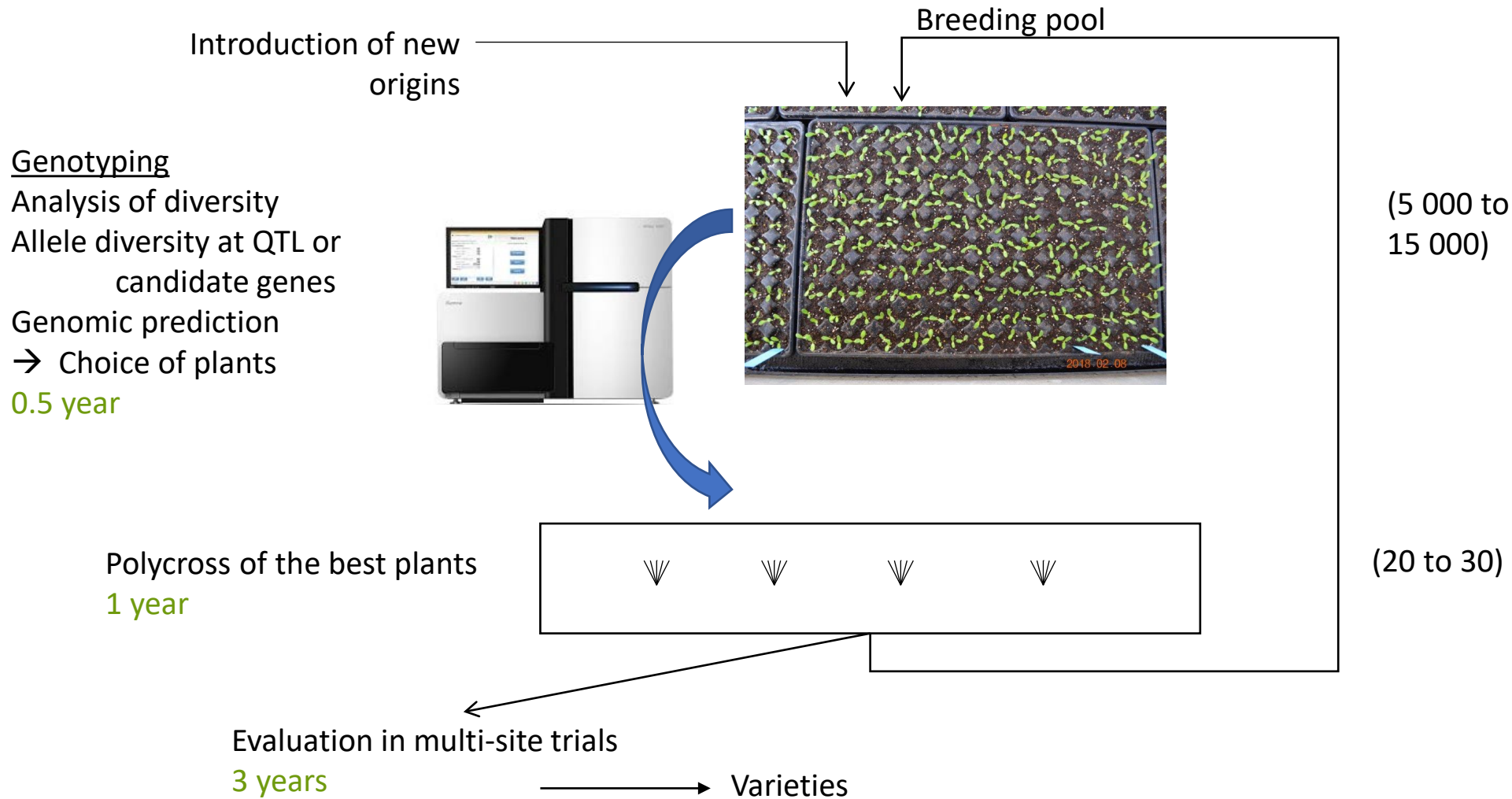
Genomic prediction is promising

→ To be pursued





# ➤ A revision of alfalfa breeding schemes



» Thanks !



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