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**11<sup>th</sup> INTERNATIONAL  
HERBAGE SEED GROUP  
CONFERENCE**



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# Proceedings & Abstracts



# GENETIC DETERMINISM OF SEED YIELD COMPONENTS IN LUCERNE

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## Abstract

Seed production is a major component of the commercial development of a variety but breeding for seed yield is expensive. A set of 400 cultivated lucerne accessions were phenotyped for seed yield traits in two locations and genotyped with GBS markers. A large diversity was found among accessions but the heritability of the traits was moderate. Quantitative trait loci (QTLs) were found for one seed yield component. Genomic prediction was moderate to high, depending on the traits and the locations. Molecular breeding could be effective to assist lucerne selection for seed yield, in addition to forage-related traits.

## Introduction

Forage legume varieties are commercialized as seeds that are produced in dedicated production fields. When the seed production is low, the cost of production and maintenance of the variety increases. Seed production is affected by management practices but also depends on the variety. Considering the importance of seed yield on the commercial development of a variety, breeding efforts for seed yield of forage crops are generally insufficient. Indeed, scoring seed yield components implies dedicated evaluations that come in addition to forage yield and quality tests, strongly increasing the breeding costs. In these conditions, markers associated to seed yield components and equations of genomic prediction could be useful to select the most promising individuals for the next breeding generation. The experiment aimed at evaluating genetic diversity for seed yield components in a set of 400 cultivated accessions of lucerne, detect quantitative trait loci (QTLs) in a genome-wide association study (GWAS) analysis and test genomic prediction.

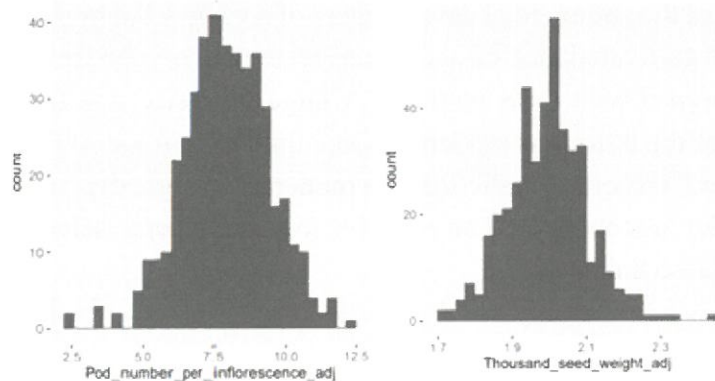
## Materials & Methods

A set of 400 lucerne accessions was studied in field conditions in two locations (France and Serbia) for seed yield components in 2018 in an augmented design. The allele frequency for more than 200K SNPs was available (Pégard et al., 2023). Adjusted values were estimated in each locations and over the two locations, taking into account the spatial effects in the trials. Heritability of traits was estimated. In a GWAS, QTL detection was carried out, taking into account the genetic structure of the material (Pégard et al., 2023). Genomic prediction was tested with a training population of 270 accessions, with a GBLUP option.

## Results

After spatial adjustment, a large genetic variation was evidenced for seed yield and seed yield components (pod number per inflorescence, thousand seed weight) (Figure 1). The heritabilities were moderate in both locations and over the locations (Table 1).

Figure 1 – Distribution of seed yield traits in Lusignan and Novi Sad  
Lusignan:



NOVI SAD:

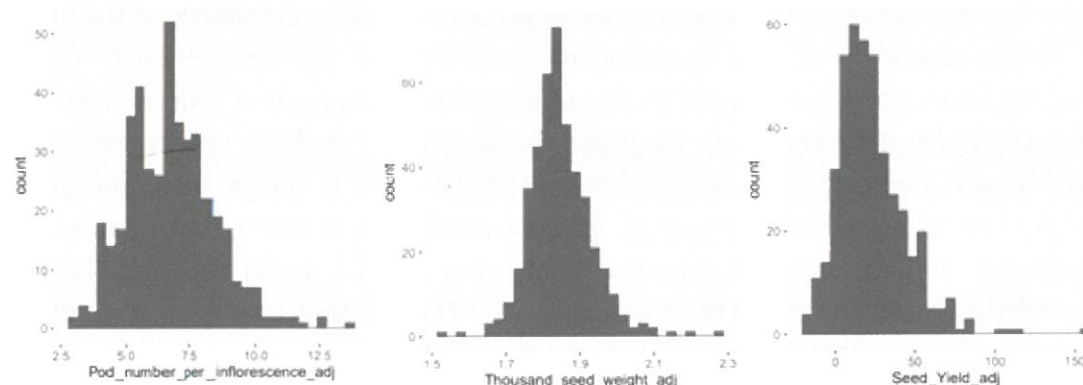


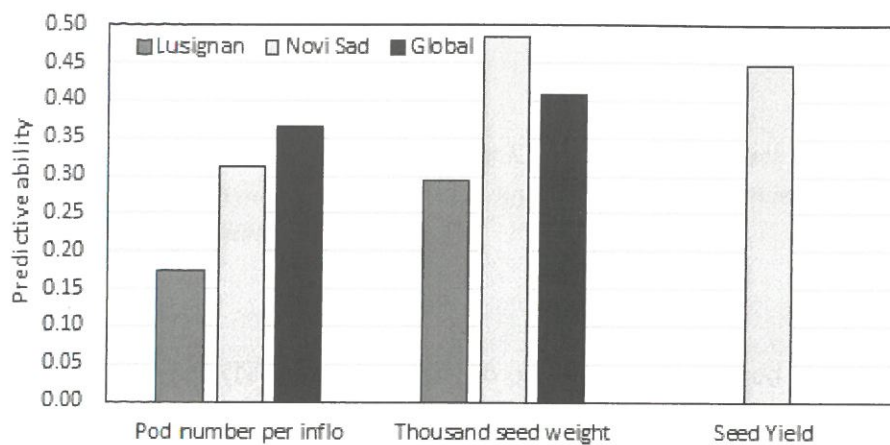
Table 1 – Heritability of seed yield traits in two locations and over the two locations (global)

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

With a GWAS, two QTLs were found for pod number per inflorescence in Lusignan only, explaining 0.086% (on chromosome 3) and 0.074% (on chromosome 7) of the variation.

Genomic prediction showed promising predictive ability (Figure 2).

Figure 2 – Predictive ability (%) for seed yield traits in two locations and over the two locations (global)



### Discussion & perspectives

A large diversity for seed yield traits was evidenced in the set of 400 cultivated accessions. QTLs were found for a single trait, pod number per inflorescence, and the two QTLs explained a total of 16% of the variation. With genomic prediction, a correct predictive ability was obtained. These results suggest that markers could be used to select more intensively for seed yield. Breeding schemes should be revised accordingly.

### References

- Pégard M, Barre P, Delaunay S, *et al.*, 2023. Genome-wide genotyping data renew knowledge on genetic diversity of a worldwide alfalfa collection and give insights on genetic control of phenology traits. *Frontiers in Plant Science* **in press**.