

Comparative analysis of selection responses using genomic prediction approaches and phenotypic selection on a barley elite population



Maximiliano Verocai¹, Bettina Lado¹, Silvina Baraibar², Lorena Cammarota³, Lucía Gutiérrez⁴, Fernanda Pardo⁵, Ariel Castro¹

1 Facultad de Agronomía, Universidad de la República, Uruguay. 2 Instituto Nacional de Investigación Agropecuaria, 3 Maltería Uruguay S.A., 4 University of Wisconsin-Madison, 5 Maltería Oriental S.A.

Takeaways

Genomic selection performed similarly to breeder and phenotypic selection.
GEBV-selected lines consistently ranked among the top 10 across all environments.
GEBV lines exhibited the lowest genetic similarity to other groups, while Wgmat showed the highest genetic similarity.

Introduction

Phenotypic selection faces significant challenges improving complex traits. In contrast, genomic prediction offers a valuable approach, allowing for the prediction of untested genotypes. However, few studies have compared conventional breeding methods with more modern strategies.

Our objectives are to empirically compare phenotypic and genomic selection for grain yield improvement and to estimate genetic similarity among groups

Materials and methods

We used an elite nested association mapping population representative of local breeding to compare selection strategies.

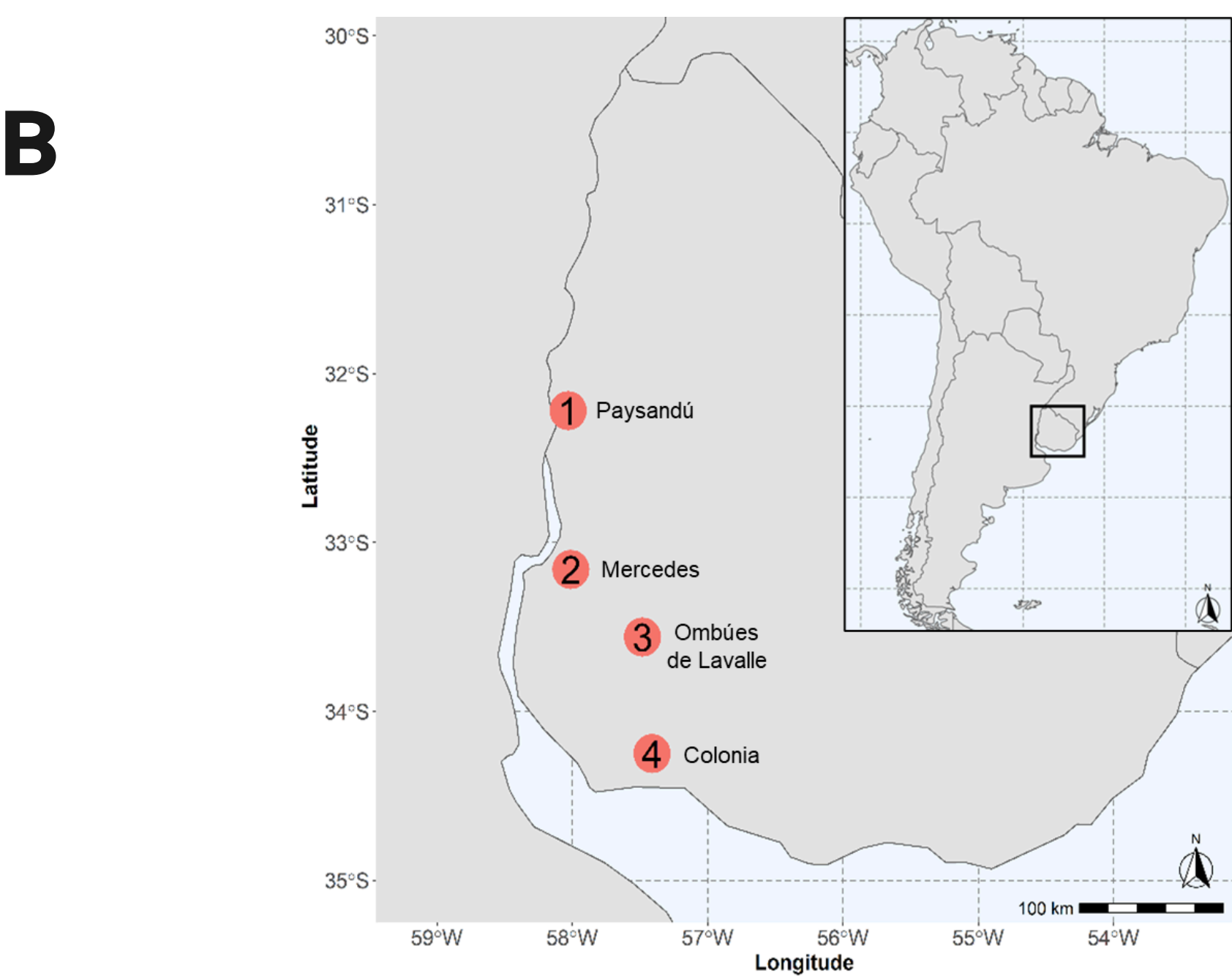
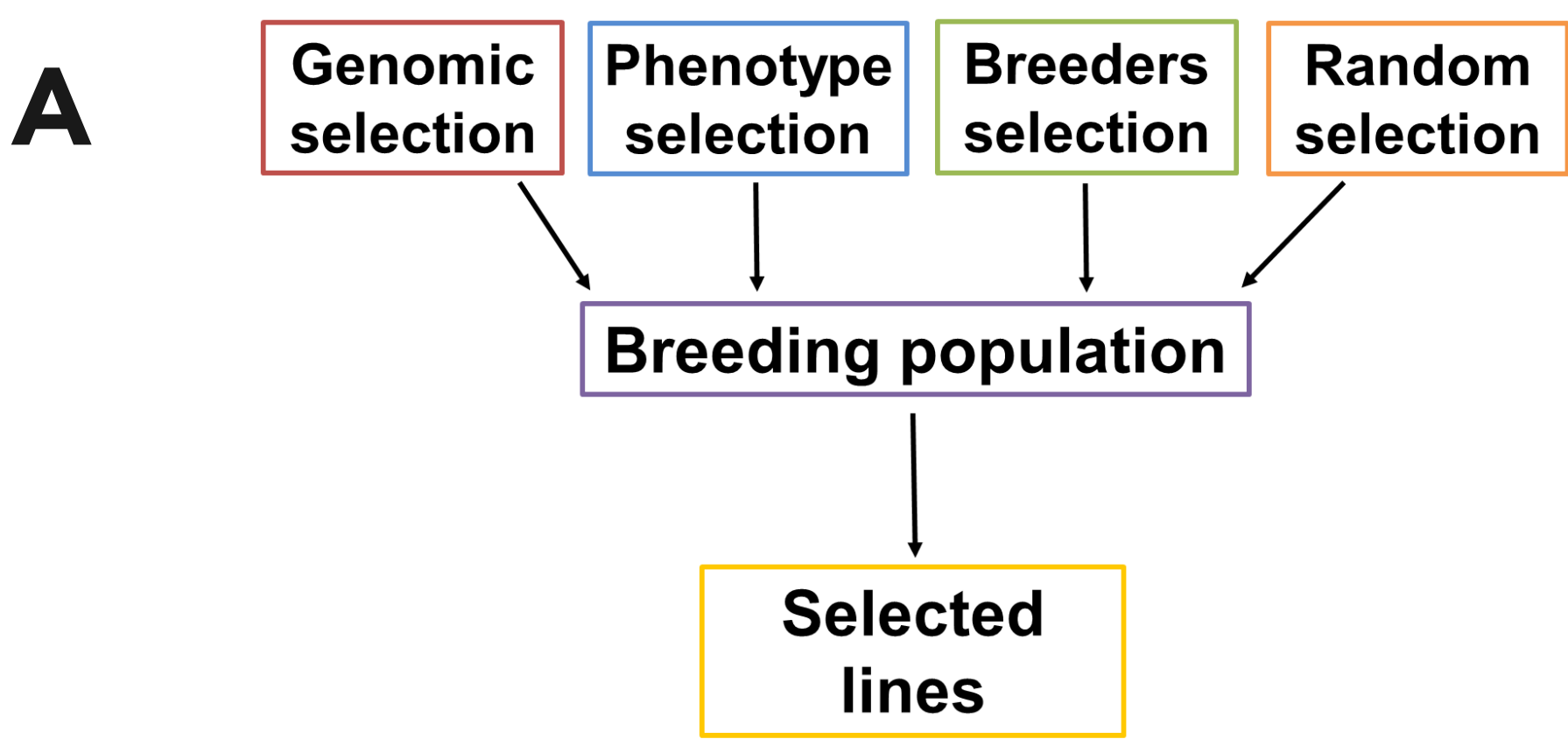


Figure 1. A) schematic overview of population design, B) Geographical locations of experimental sites and the years in which the experiments were conducted.

Results

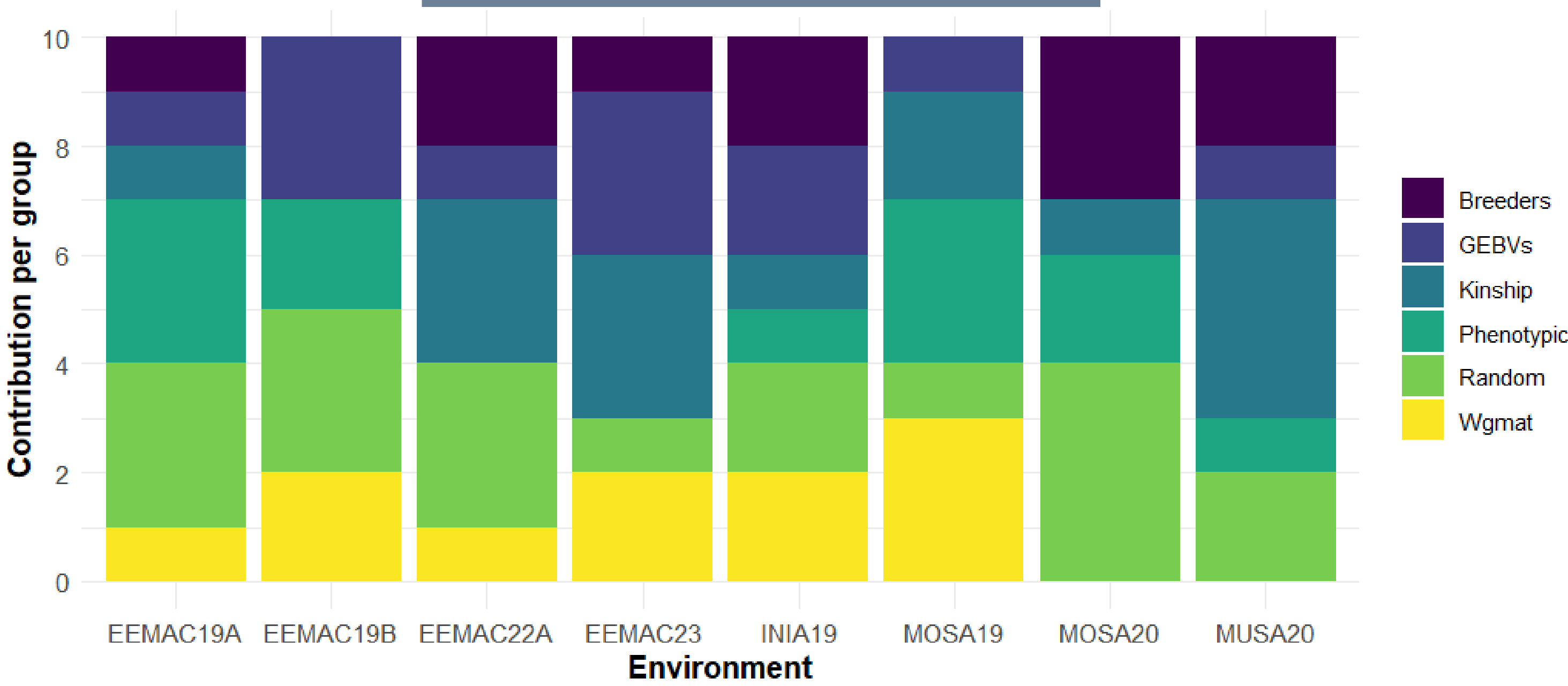


Figure 2. Contribution of each group to the top 10 highest-performing lines

Surprisingly, randomly selected lines ranked among the top 10 best lines across all evaluated environments.

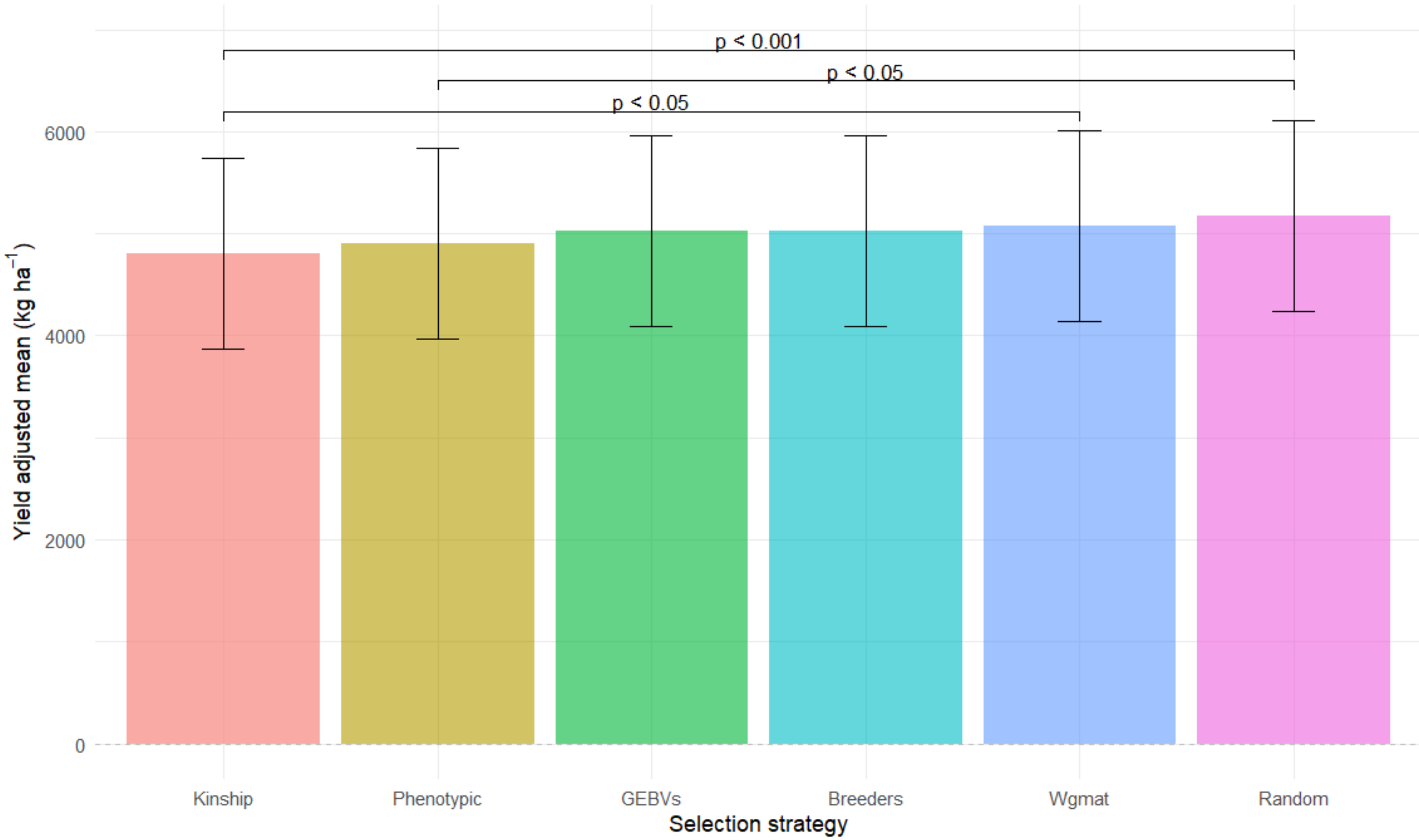


Figure 3. Grain yield and standard error for different selection strategies.

Breeder-selected lines showed similar grain yield to those selected through random sampling and genomic selection.

Table 1. Average genetic distance among groups

	GEBVs (1)	Kinship	Phenotypic	Breeders	Wgmat (2)
Random	0.400	0.375	0.364	0.305	0.342
GEBVs		0.388	0.392	0.395	0.368
Kinship			0.365	0.364	0.315
Phenotypic				0.348	0.321
Breeders					0.320

High genetic similarity observed across groups

References

[1] Bhatta, M., et al. (2020). Multi-trait genomic prediction model increased the predictive ability for agronomic and malting quality traits in barley (*Hordeum vulgare* L.). *G3 Genes| Genomes| Genetics* 10: 1113-1124.
[2] Berro, I., et al. "Training population optimization for genomic selection." *The Plant Genome* 12.3 (2019).



View poster online