

Enhancing Multi-Trait Genetic Gains in Durum Wheat (*Triticum durum* Desf.) Using Ideotype-Based Selection Indices

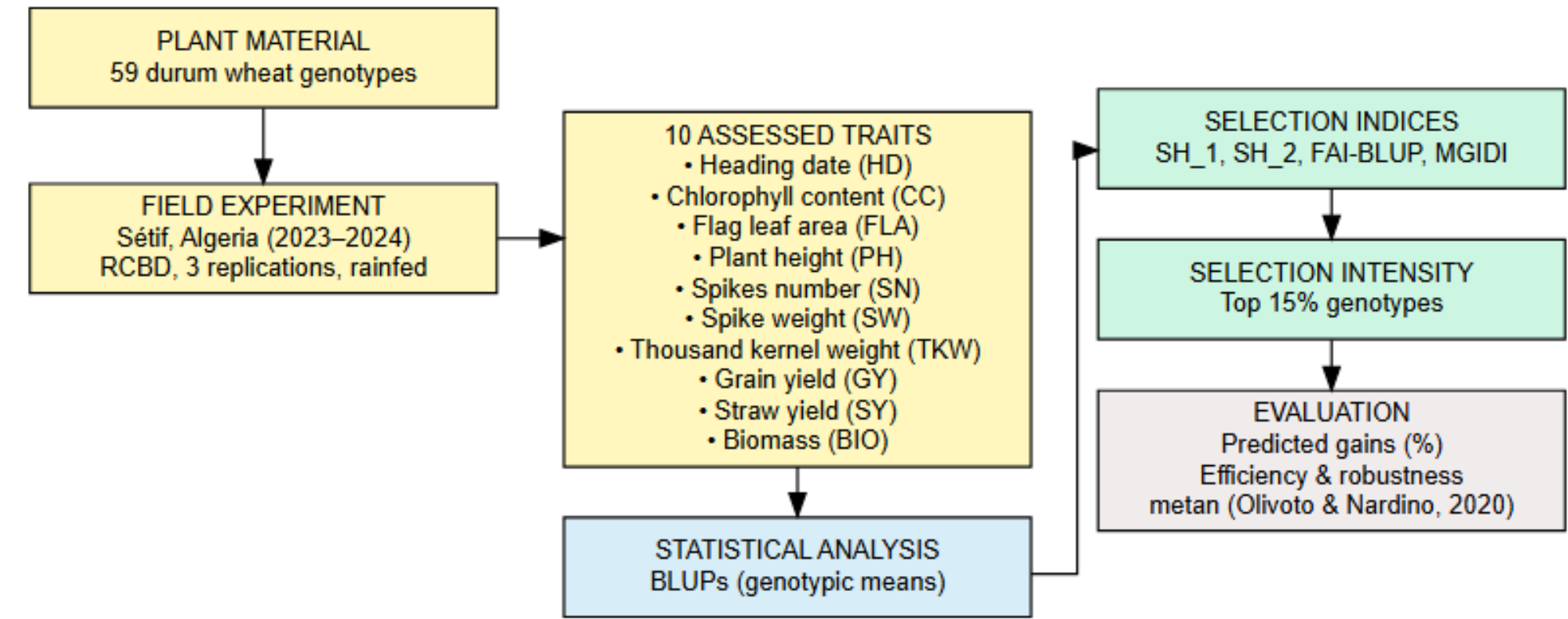
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INTRODUCTION & AIM

Durum wheat (*Triticum durum* Desf.) is a staple cereal in the Mediterranean basin and North Africa, providing essential calories and proteins to millions. However, its productivity is constrained by erratic rainfall, high temperatures, and soil degradation—major challenges in semi-arid regions such as Algeria [1]. Traditional single-trait selection often fails to capture complex relationships among yield components, physiological traits, and adaptability. Moreover, classical multi-trait indices like Smith–Hazel (SH) are sensitive to multicollinearity, leading to unstable genetic gains [2,3]. Recent advances have introduced ideotype- and factor analysis–based indices, including the Multi-Trait Genotype-Ideotype Distance Index (MGIDI) and the Factor Analysis and Ideotype-Design Based BLUP (FAI-BLUP), which integrate correlated traits and target genotypes close to an “ideotype,” enhancing selection accuracy and efficiency [4,5]. This study aims to evaluate the efficiency of MGIDI, FAI-BLUP, and SH indices in identifying superior durum wheat genotypes under semi-arid conditions.

METHOD



RESULTS & DISCUSSION

Table 1: Deviance analysis and genetic parameters for durum wheat traits assessed.

Parameters	HD	CC	FLA	PH	SN	SW	TKW	GY	SY	BIO
Genotype effect	**	**	**	**	*	*	**	**	**	*
H ²	0.91	0.44	0.33	0.59	0.19	0.16	0.29	0.22	0.39	0.20
Accuracy	0.98	0.84	0.77	0.90	0.64	0.60	0.74	0.68	0.81	0.66
CV _g	3.04	12.76	13.74	12.20	14.90	13.55	7.09	16.13	24.76	14.81
CV _e	0.95	14.53	19.57	10.23	31.06	31.15	11.13	30.15	30.87	29.53
CV _g /CV _e	3.20	0.88	0.70	1.19	0.48	0.44	0.64	0.53	0.80	0.50

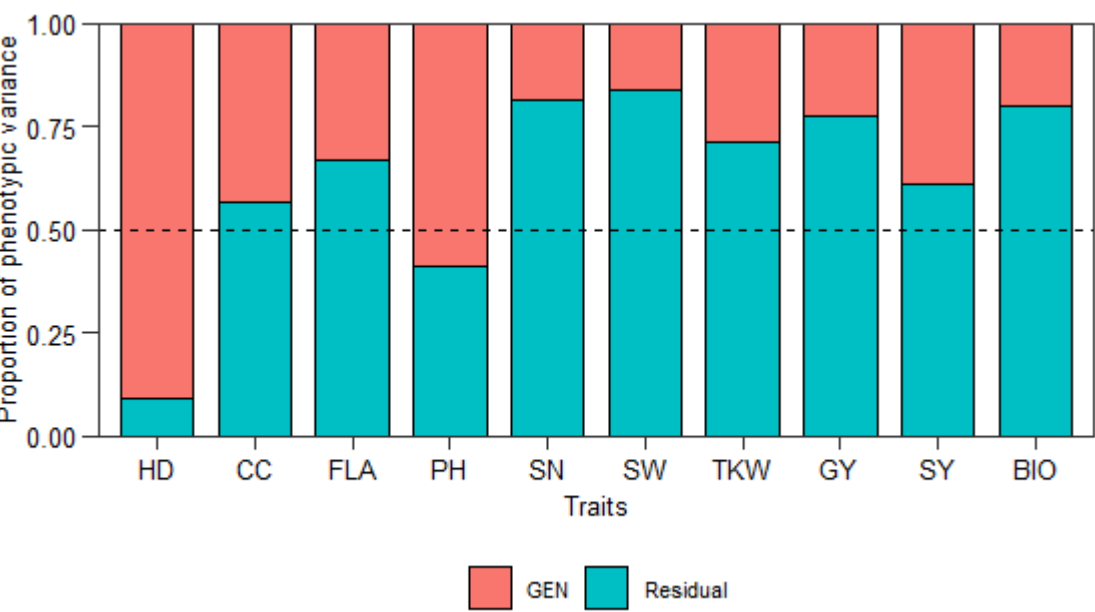


Figure 1: Variance components for the assessed traits in durum wheat.

Table 2: Eigenvalues, explained variance, factorial loadings after varimax rotation, and communalities obtained in the factor analysis.

Trait	FA1	FA2	FA3	Communality
SN	-0.90	0.02	-0.24	0.86
SW	-0.96	-0.13	-0.03	0.93
GY	-0.89	-0.34	0.02	0.91
BIO	-0.90	0.38	-0.09	0.97
HD	-0.17	-0.88	0.12	0.82
CC	-0.11	-0.57	-0.41	0.50
FLA	-0.10	0.76	0.04	0.59
PH	0.01	0.85	-0.10	0.73
SY	-0.63	0.68	-0.12	0.87
TKW	0.14	-0.11	0.92	0.88
Eigenvalues	3.97	3.08	1.02	
Variance (%)	39.8	30.8	10.2	
Cum. variance (%)	39.8	70.5	80.8	

Bold values indicate the variables grouped within each factor.

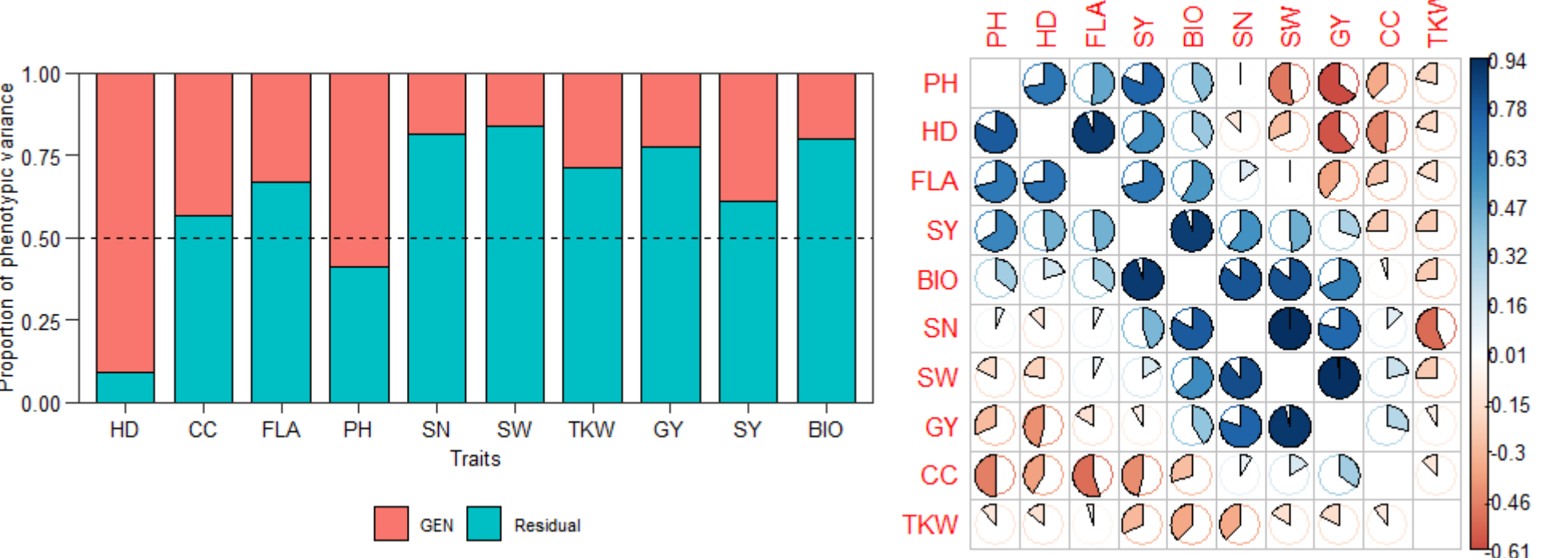


Figure 2: Phenotypic (lower diagonal) and genotypic (upper diagonal) correlation between assessed traits in durum wheat.

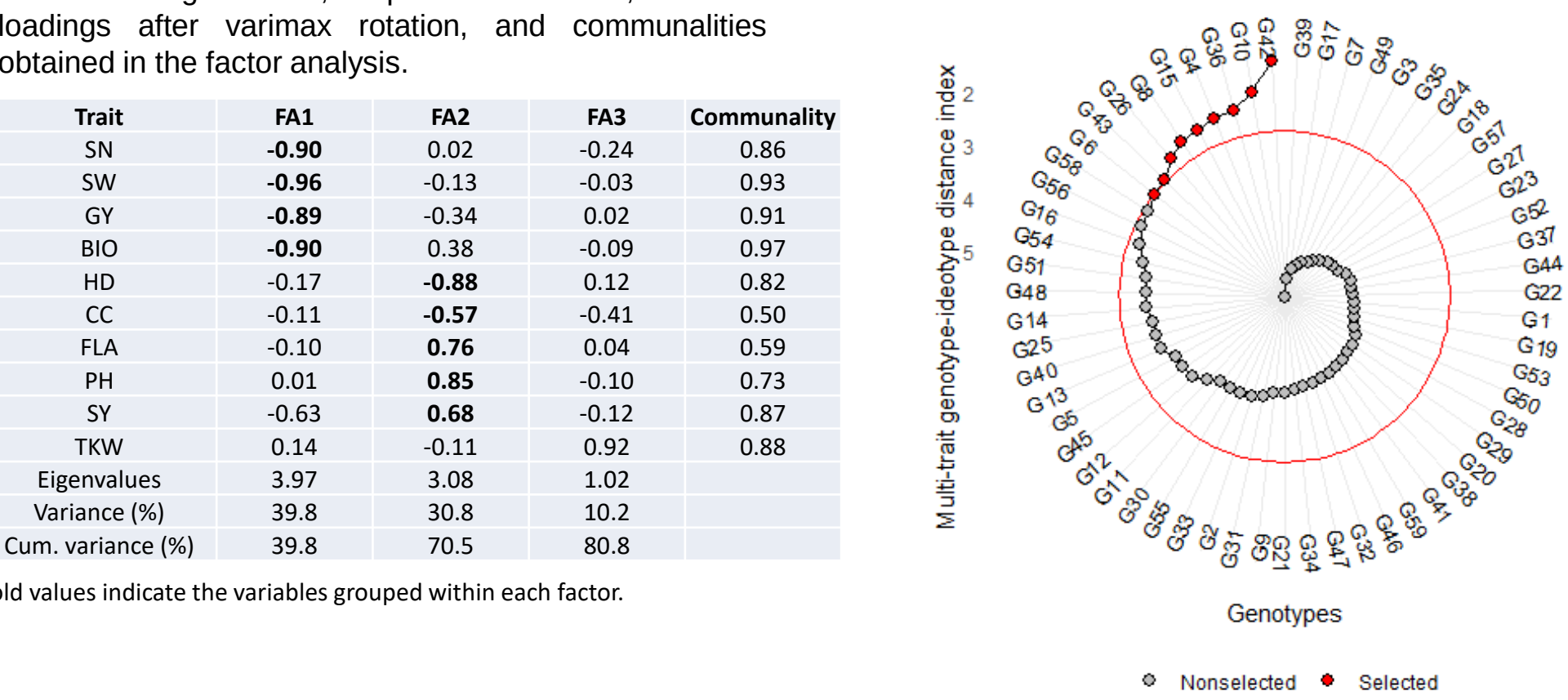


Figure 3: Genotypes ranking based on the MGIDI index.

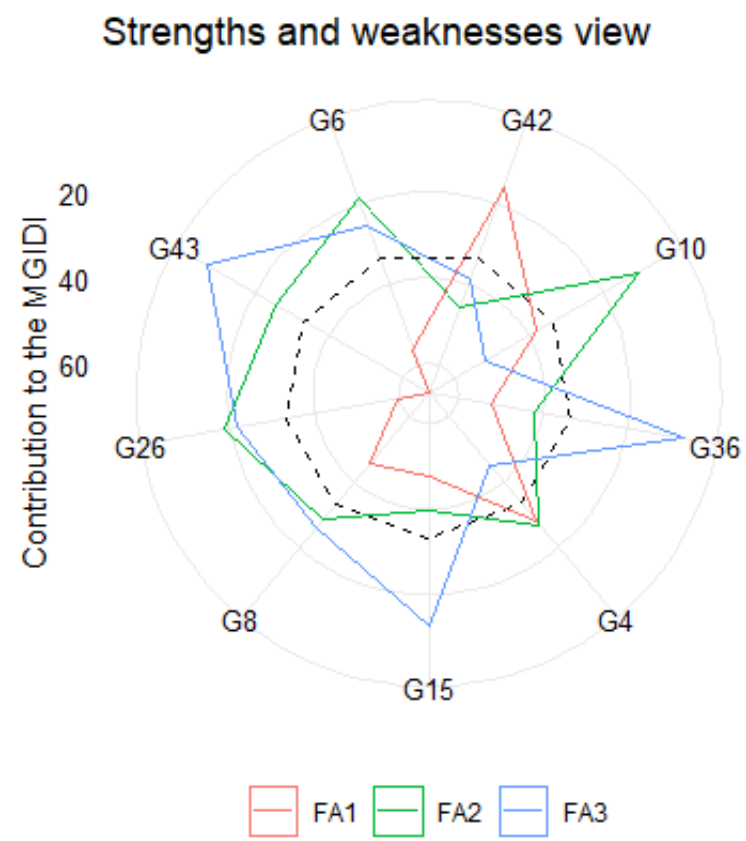


Figure 4: Strengths and weaknesses view of the selected genotypes identified by MGIDI index.

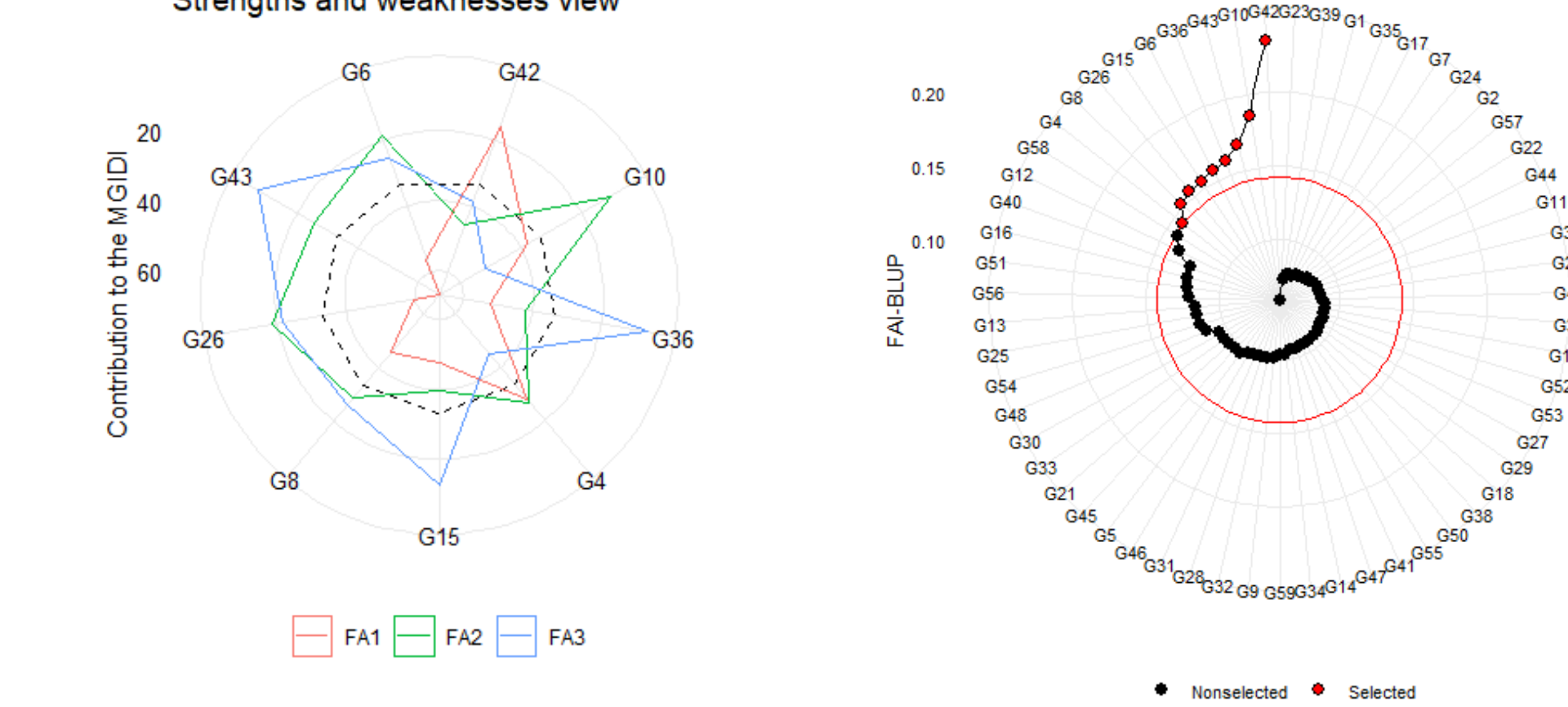


Figure 5: Genotypes ranking based on the FAI-BLUP index.

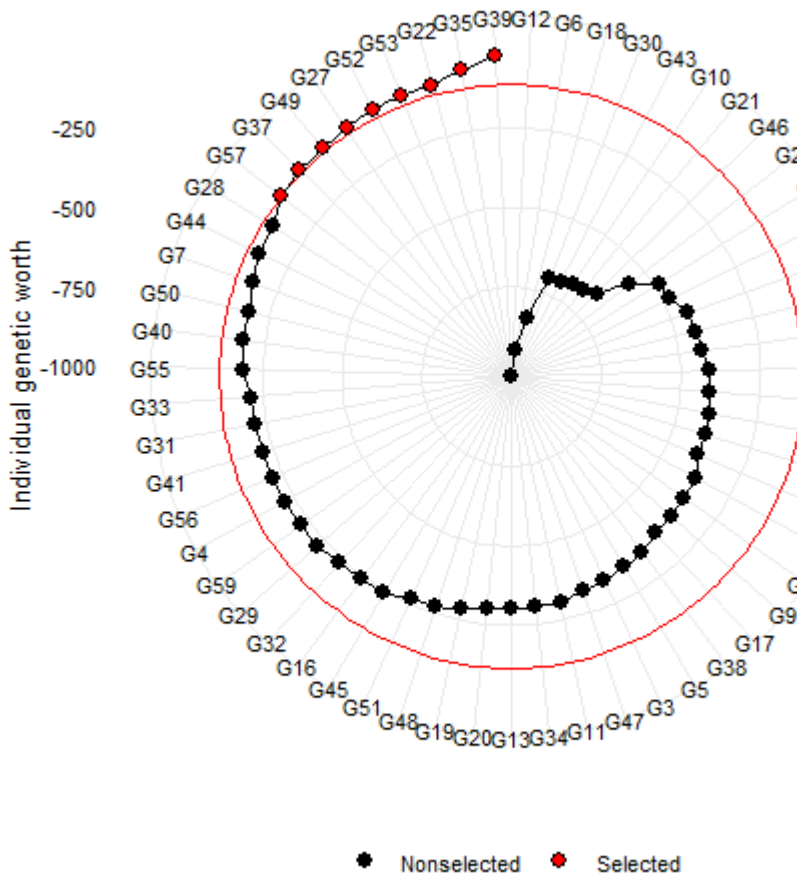


Figure 6: Genotypes ranking based on the SH_1 index.

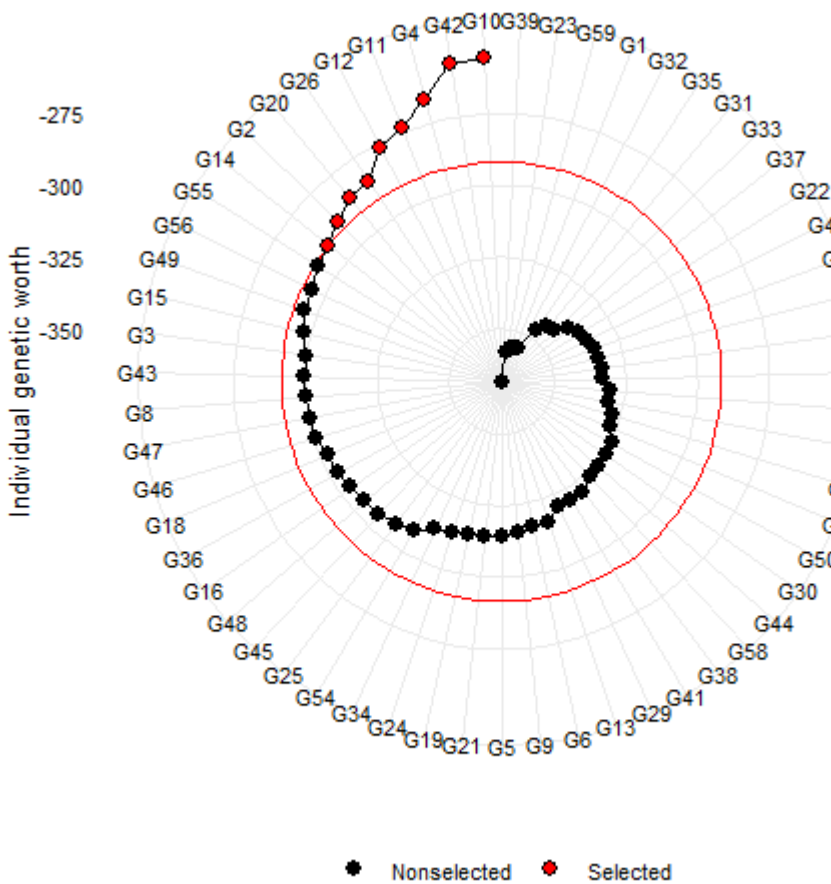


Figure 7: Genotypes ranking based on the SH_2 index.

Table 3: Coincidence index and shared genotypes for each pair of indexes evaluated.

Index 1	Index 2	Coincidence	Shared genotypes
MGIDI	FAI-BLUP	100	G42,G10,G36,G4,G15,G8,G26,G43,G6
MGIDI	SH_1	-17.65	None
MGIDI	SH_2	34.67	G42,G10,G4,G26
FAI-BLUP	SH_1	-17.65	None
FAI-BLUP	SH_2	5.88	G42,G10,G26,G4
SH_1	SH_2	76.47	None

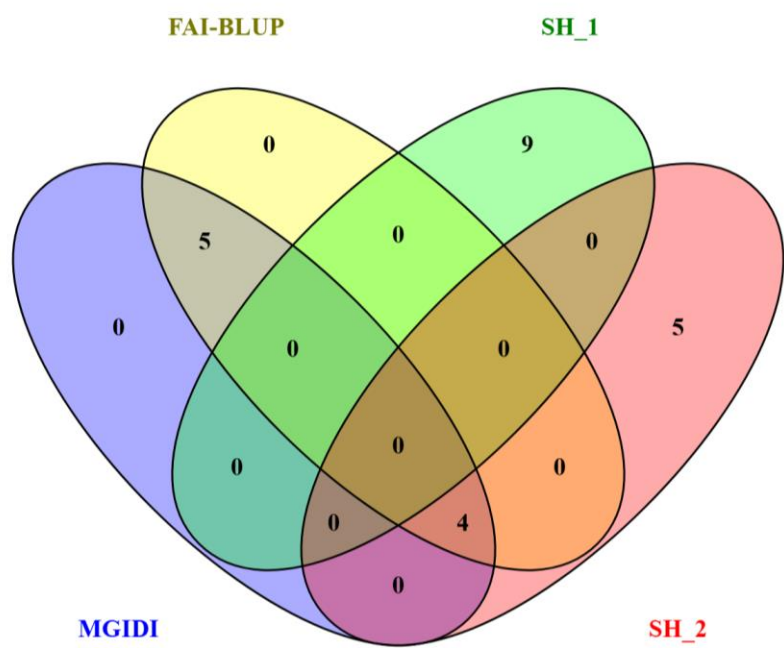


Figure 8: Number of common genotypes between the selection indexes based on coincidence index.

Table 4: Predicted genetic gains for the indexes MGIDI, FAI-BLUP, SH_1 and SH_2.

Factor	Trait	Goal	Genetic value	MGIDI	FAI-BLUP	SH_1	SH_2
FA1	SN	Increase	350.9±4.35	3.97	3.97	-3.18	5.54
FA1	SW	Increase	60.35±0.64	3.48	3.48	-2.02	3.60
FA1	GY	Increase	34.92±0.5	5.49	5.49	-2.87	5.72
FA1	BIO*	Increase	118.53±1.5	5.64	5.64	-4.90	NA
FA2	HD	Decrease	127.49±0.5	-0.01	-0.01	-0.63	-1.15
FA2	CC	Increase	35.78±0.5	-5.12	-5.12	1.62	1.03
FA2	FLA	Increase	20.15±0.28	3.73	3.73	-1.94	1.94
FA2	PH	Increase	89.96±1.29	3.19	3.19	-4.92	2.03
FA2	SY	Increase	57.95±1.52	15.10	15.10	-16.60	13.70
FA3	TKW	Increase	33.68±0.23	0.81	0.81	-0.53	-1.65
Total (Increase)				36.29	36.29	-35.34	31.91
Total (Decrease)				-0.01	-0.01	-0.63	-1.15

*: Traits removed from SH_2 due to multicollinearity issues.

CONCLUSION

Modern indices MGIDI and FAI-BLUP promoted substantial gains in key productivity-related traits, and substantially outperformed SH_2 and especially SH_1, which was negatively affected by multicollinearity. Genotypes G42, G10, G26, and G4 were consistently selected across MGIDI, FAI-BLUP, and SH_2, confirming their superior multi-trait performance and breeding potential. Crosses involving these genotypes are expected to increase the frequency of favorable alleles in the resulting progenies while maximizing genetic variability and heterosis.

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