Utilization of multi-trait genotype-ideotype distance index (MGIDI) increases expected genetic gains for simultaneous improvement of wheat traits

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INTRODUCTION

Multi-trait-based selection has a great potential to increase genetic gain in wheat (*Triticum aestivum* L.) breeding programs (Fellahi *et al.*, 2020). In this study, the Smith-Hazel classic indexes (SH1 and SH2), the modern ideotype-design index (FAI-BLUP) and the recently proposed multi-trait genotype-ideotype distance index (MGIDI) were compared and used to select superior wheat genotypes for thirteen important agronomic traits with negative and positive desired gains.

MATERIALS AND METHODS

- **Plant Materials :** 34 local and introduced bread wheat genotypes.
- **Experimental design :** all genotypes were tested in a randomized complete block design with three replications at the Agricultural Experimental Station of the ITGC institute, Setif (Algeria).
- **Traits scoring :** heading date (DVP), canopy temperature (CT), membrane thermostability (MT), chlorophyll content (CC), relative water content (RWC), flag leaf area (FLA), plant height (PH), thousand grain weight (TGW), number of spikes/m² (NS), number of grains/m² (NG), grain yield (GY), biomass (BIO) and harvest index (HI).
- **Statistical analysis :** data collected were analyzed using 'metan' package in R software (Olivoto and Nardino, 2020).

RESULTS AND DISCUSSION

Variance components, genetic parameters and correlations :

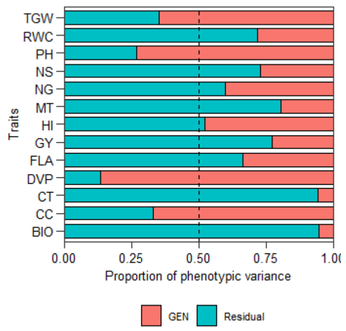

Figure 1: Estimated variance components for the traits evaluated.

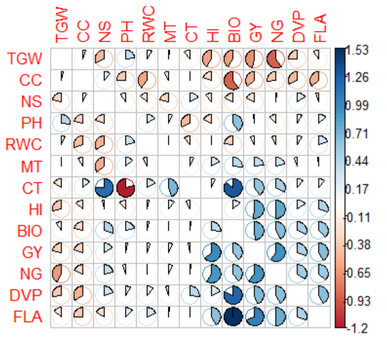

Figure 2: Phenotypic (lower diagonal) and genotypic (upper diagonal) correlation between the traits evaluated.

Traits	h²	CV_g	CV_g/CV_e	p-value	Traits	h²	CV_g	CV_g/CV_e	p-value
DVP	0.95	3.17	2.54	2.1e-23	TGW	0.85	8.46	1.36	1.2e-10
CT	0.16	1.68	0.25	5.6e-01	NS	0.53	10.75	0.61	9.7e-03
MT	0.42	16.85	0.49	6.3e-02	NG	0.67	18.69	0.82	1.4e-04
CC	0.86	14.05	1.43	1.5e-11	GY	0.47	12.78	0.54	3.1e-02
RWC	0.54	3.03	0.63	7.3e-03	BIO	0.15	4.6	0.24	5.9e-01
FLA	0.61	13.37	0.71	1.4e-03	HI	0.73	10.86	0.95	5.5e-06
PH	0.89	9.9	1.65	4.6e-14					

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

Selected genotypes, coincidence index and predicted selection gains :

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

Traits	FA1	FA2	FA3	FA4	FA5	h†
TGW	**-0.64**	-0.45	0.03	-0.04	-0.24	0.66
NG	**0.89**	0.10	0.12	0.41	0.00	0.98
GY	**0.81**	-0.10	0.16	0.49	-0.10	0.95
HI	**0.93**	-0.06	0.07	-0.09	-0.12	0.90
CT	0.13	**-0.90**	-0.01	-0.15	0.15	0.88
PH	-0.27	**-0.68**	0.32	0.39	-0.19	0.83
DVP	-0.30	-0.26	**-0.53**	-0.47	-0.14	0.68
CC	-0.12	-0.01	**-0.82**	-0.19	0.12	0.73
RWC	-0.02	-0.20	**0.77**	-0.18	0.09	0.68
FLA	0.49	-0.09	**0.51**	0.33	-0.14	0.64
NS	0.07	0.30	-0.27	**0.64**	0.49	0.81
BIO	0.31	-0.10	0.17	**0.88**	-0.04	0.91
MT	-0.09	-0.07	0.02	0.02	**0.92**	0.87
Eigenvalues	4.46	2.30	1.51	1.21	1.04	
Variance	34.3	17.7	11.6	9.27	8.02	
Accumulated	34.3	52	63.6	72.8	80.9	

†: Communality, bold values indicate the variables grouped within each factor.

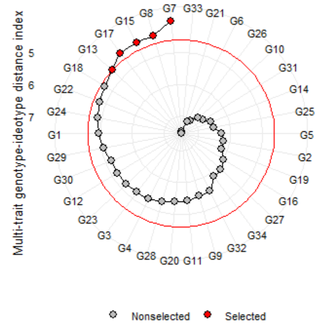

Figure 3: Genotypes ranking based on the MGIDI index.

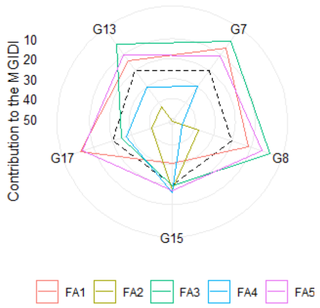

Figure 4: Strengths and weaknesses view of the selected genotypes identified by MGIDI index.

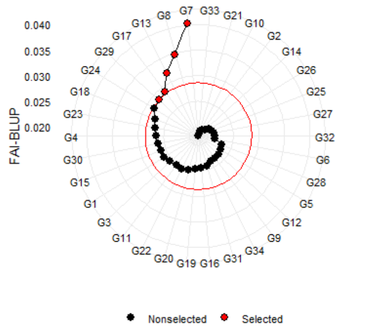

Figure 5: Genotypes ranking based on the FAI-BLUP index.

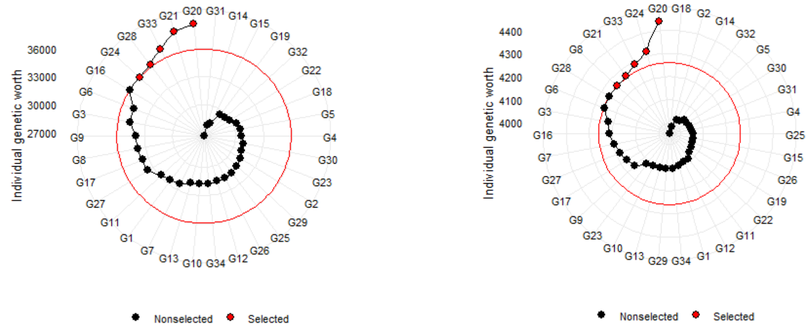

Figure 6: Genotypes ranking based on the SH-1 (left) and SH-2 (right) indexes.

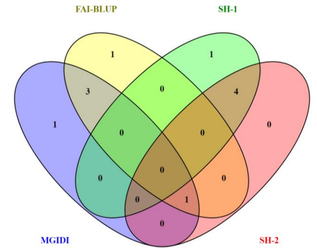

Figure 7: Number of common genotypes between the indexes MGIDI, FAI-BLUP, SH-1 and SH-2 based on coincidence index.

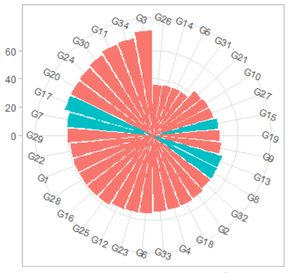

Figure 8: Grain yield for the evaluated genotypes. The selected genotypes by the MGIDI index are highlighted in blue color.

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

Index 1	Index 2	Coincidence	Shared genotypes
MGIDI	FAI-BLUP	76.47	G7,G8,G17,G13
MGIDI	SH-1	-17.65	None
MGIDI	SH-2	5.88	G8
FAI-BLUP	SH-1	-17.65	None
FAI-BLUP	SH-2	5.88	G8
SH-1	SH-2	76.47	G20,G21,G33,G24

Table 4: Predicted genetic gains for the indexes MGIDI, FAI-BLUP, SH-1 and SH-2.

Factor	Trait	Goal	Genetic value	Genetic gain (%)			
				MGIDI	FAI-BLUP	SH-1	SH-2
FA1	TGW	Increase	39.95±0.53	0.81	-2.33	-7.12	-2.85
FA1	NG†	Increase	13727.29±359.74	0.02	3.92	6.89	NA
FA1	GY†	Increase	54.14±0.81	0.27	1.41	1.25	NA
FA1	HI	Increase	35.39±0.56	1.3	2.62	7.09	-3.43
FA2	CT	Decrease	18.89±0.02	-0.13	-0.09	0.03	0.02
FA2	PH	Increase	86.05±1.38	6.59	0.14	-2.07	5.12
FA3	DVP	Decrease	118.48±0.63	-2.2	-1.23	2.43	2.94
FA3	CC	Increase	33.66±0.75	4.16	4.77	-4.58	-8.46
FA3	RWC	Increase	88.65±0.34	-0.41	-0.62	-0.19	-0.03
FA3	FLA	Increase	16.34±0.29	0.4	-0.67	-0.78	1.15
FA4	NS	Increase	954.71±12.82	1.2	3.05	-0.53	5.7
FA4	BIO	Increase	152.43±0.46	-0.02	0.04	-0.15	0.39
FA5	MT	Decrease	32.91±0.62	-2.39	-4.12	2.17	-0.87
Total (positive)				**14.32**	**12.31**	**-0.19**	**-2.41**
Total (negative)				**-4.71**	**-5.44**	**4.63**	**2.09**

†: Traits removed from SH-2 due to multicollinearity issues.

CONCLUSION

The most efficient selection was obtained by MGIDI index, which outperformed the Smith-Hazel and FAI-BLUP indices with higher desired gains considering all traits simultaneously.

The MGIDI provided negative gains (-2.20% ≤ gains ≤ -0.07%, a total of -4.71%) for all the three traits that wanted to decrease and positive gains (-0.41% ≤ gains ≤ +6.59%, a total of +14.32%) for eight of the ten traits that wanted to increase.

MGIDI can greatly increase the efficiency of selection for multiple traits in wheat breeding programs.

REFERENCES

Fellahi, Z., Hannachi, A., & Bouzerzour, H. (2020). Expected genetic gains from mono trait and index-based selection in advanced bread wheat (*Triticum aestivum* L.) populations. *Revista Facultad Nacional de Agronomía*, 73(2), 9131-9141.

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