

# Multi-trait selection of bread wheat (*Triticum aestivum* L.) genotypes under semi-arid conditions in Algeria

Selección de múltiples características de genotipos de trigo harinero (*Triticum aestivum* L.) bajo condiciones semiáridas en Argelia

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## ABSTRACT

### Keywords:

Agronomic traits  
ANOVA  
Correlation  
LSI  
MGIDI  
Wheat



The selection of high-yielding bread wheat (*Triticum aestivum* L.) genotypes with superior agronomic traits is critical for improving productivity in semi-arid regions like Algeria. To address national reliance on wheat imports and enhance local production, a preliminary yield trial was conducted in Constantine (36°16' N, 6°40' E) during the 2018–2019 cropping season. A total of 112 bread wheat genotypes, including local and international entries and five local checks, were evaluated using an augmented design with four blocks. Significant variability was detected among genotypes and checks for most traits, confirming the presence of exploitable genetic diversity. Phenotypic correlations showed that grain yield was positively associated with spike density ( $r=0.463$ ) and thousand-kernel weight ( $r=0.557$ ), while it was negatively correlated with days to heading ( $r=-0.293$ ), indicating the advantage of early heading under drought conditions. Using the Least Significant Increase (LSI) method, genotypes G29, G38, and G9 were found to be significantly earlier than several local checks, while G65 outperformed at least one check across all traits. In parallel, the Multi-Trait Genotype-Ideotype Distance Index (MGIDI) enabled the identification of 17 high-performing genotypes such as G60, G41, G65, and G111 alongside two superior local checks (C3 and C4). These genotypes combine favorable traits and are promising candidates for inclusion in breeding programs targeting yield stability and stress resilience. Overall, the study provides valuable insights into trait associations and highlights elite genetic materials suitable for advancing wheat improvement efforts in challenging semi-arid environments.


## RESUMEN


### Palabras clave:

Características agronómicas  
ANOVA  
Correlación  
LSI  
MGIDI  
Trigo

La selección de genotipos de trigo harinero (*Triticum aestivum* L.) de alto rendimiento con rasgos agronómicos superiores es fundamental para mejorar la productividad en regiones semiáridas como Argelia. Para reducir la dependencia nacional de las importaciones de trigo y aumentar la producción local, se llevó a cabo un ensayo preliminar de rendimiento en Constantina (36°16' N, 6°40' E) durante la temporada agrícola 2018–2019. Se evaluaron un total de 112 genotipos de trigo harinero, incluidos materiales locales e internacionales y cinco testigos locales, utilizando un diseño aumentado con cuatro bloques. Se detectó una variabilidad significativa entre genotipos y testigos para la mayoría de los rasgos, lo que confirma la presencia de diversidad genética aprovechable. Las correlaciones fenotípicas mostraron que el rendimiento en grano se asoció positivamente con la densidad de espigas ( $r=0.463$ ) y el peso de mil granos ( $r=0.557$ ), mientras que se correlacionó negativamente con los días hasta el espigado ( $r=-0.293$ ), lo que indica la ventaja de un espigado temprano en condiciones de sequía. Utilizando el método de Least Significant Increase (LSI), se encontró que los genotipos G29, G38 y G9 fueron significativamente más precoces que varios testigos locales, mientras que G65 superó al menos a un testigo en todos los rasgos. Paralelamente, Multi-trait genotype-ideotype distance index (MGIDI) permitió la identificación de 17 genotipos de alto rendimiento tales como G60, G41, G65 y G111, junto con dos testigos locales superiores (C3 y C4). Estos genotipos combinan características favorables y son candidatos prometedores para ser incluidos en programas de mejora enfocados a la estabilidad del rendimiento y la resiliencia al estrés. En general, el estudio proporciona información valiosa sobre las asociaciones entre rasgos y destaca materiales genéticos elite adecuados para avanzar en los esfuerzos de mejora del trigo en entornos semiáridos desafiantes.

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Bread wheat (*Triticum aestivum* L.) stands as one of the most important staple crops worldwide, owing to its exceptional adaptability across a wide range of temperate agro-climatic zones and its diverse applications as a source of food, animal feed, seed, and raw material for various industrial uses (Venske et al. 2019; Sivakumar and Kumar 2023). Its dominance in global agriculture is further underscored by its central role in food security, providing approximately 20% of the calories and proteins consumed by the global population. In Algeria, despite favorable agro-ecological conditions in certain regions, the country remains highly dependent on cereal imports, particularly bread wheat to meet its growing consumption needs. This dependency is largely driven by the persistent mismatch between domestic wheat production and increasing national demand, which continues to exert pressure on food security and public finances (Bekkis et al. 2023). Illustratively, national cereal output fell from 4.39 million tons in the 2019–2020 growing season to 2.76 million tons in 2020–2021, while wheat import expenditures reached 6 billion dollars in 2022 (ONS 2023a, 2023b). Addressing this imbalance necessitates a profound transformation, with a particular focus on increasing local wheat productivity and resilience through strategic breeding and germplasm enhancement.

In this context, the identification and evaluation of high-potential genotypes and genetically enriched germplasm constitute a critical foundation for achieving durable improvements in yield and resilience to environmental stressors. The enhancement of genetic resources through the incorporation of diverse materials such as landraces and wild relatives enables the introduction of novel alleles into elite pools, thereby expanding genetic diversity and mitigating the limitations resulting from historical selection pressures and genetic erosion. This strategy is particularly relevant for selection programs in marginal and semi-arid environments, where crop performance is frequently constrained by abiotic challenges including drought, heat, and erratic precipitation. The implementation of these strategies is grounded in the detailed characterization and assessment of available germplasm, which provides a rich pool of adaptive traits. Detailed agro-morphological, physiological, and molecular analyses allow for the identification of accessions with beneficial features such as early vigor, robust root systems, efficient nutrient

uptake, or resistance to foliar diseases that may otherwise remain unexploited. This critical step transforms raw genetic variability into materials suitable for integration into selection pipelines. Incorporating such diversity facilitates the alleviation of genetic bottlenecks, enhances resilience to stress, and supports the development of improved genotypes tailored to the demands of semi-arid agro-ecosystems.

Current wheat selection strategies increasingly emphasize the integration of traits associated with adaptation, such as early flowering, drought avoidance, heat tolerance, and optimized root architecture, while simultaneously maintaining or enhancing yield-related attributes. Due to the complex genetic architecture of grain yield and its strong interaction with environmental factors, indirect selection based on correlated traits like plant height, spike density, and thousand-kernel weight is often preferred. These traits, typically characterized by higher heritability, serve as effective proxies for identifying superior genotypes under variable and stress-prone field conditions (Ullah et al. 2021; Khodarahmi et al. 2023).

The challenge lies in efficiently integrating multiple traits with varying levels of heritability and agronomic relevance into a single selection index. Traditional linear selection indices often fall short due to their reliance on arbitrarily assigned weights and assumptions of trait independence. To address this limitation, multivariate selection tools such as the Multi-Trait Genotype–Ideotype Distance Index (MGIDI) have been developed. MGIDI offers a holistic approach by quantifying the distance between a genotype's standardized multi-trait profile and that of an "ideotype". This approach enables the simultaneous consideration of multiple agronomic criteria without the need for predetermined economic weights, making it highly adaptable across breeding contexts (Olivoto and Nardino 2021; Olivoto et al. 2022).

The efficacy of MGIDI has been validated in numerous studies across diverse crops and agro-climatic environments. In wheat, it has been successfully applied to identify genotypes with balanced performance across yield components, stress tolerance traits, and phenological attributes (Pour-Aboughadareh and Poczaï 2021; Mamun et al. 2022; Romena et al. 2022). When integrated into early-stage field trials, MGIDI enhances the efficiency

of genotype ranking and supports data-driven decision-making in breeding pipelines.

The aim of the present study are threefold: (i) to assess the agro-morphological variability within a diverse panel of bread wheat genotypes cultivated under semi-arid conditions in Algeria, (ii) to investigate the phenotypic relationships between grain yield and key agronomic traits, and (iii) to identify superior genotypes outperforming local checks. Genotype selection was based on two complementary approaches: The Least Significant Increase (LSI) method and the Multi-Trait Genotype–Ideotype Distance Index (MGIDI). Together, these tools enable the efficient identification of high-performing lines, thereby supporting the development of bread wheat cultivars with improved yield potential, enhanced adaptability, and greater resilience to stress in the context of challenging agro-climatic environments.

## MATERIALS AND METHODS

### Genetic materials, location, and experimental design

The germplasm evaluated in this study comprised 107 bread

wheat (*Triticum aestivum* L.) genotypes sourced from diverse origins, including the International Center for Agricultural Research in the Dry Areas (ICARDA), the International Maize and Wheat Improvement Center (CIMMYT), as well as locally adapted varieties. Additionally, five local check cultivars were included for comparative assessment (Table 1). The field trial was conducted during the 2018–2019 cropping season at the El Baraouia experimental farm, located in the Constantine region (36°16'N, 6°40'E), a site characterized by cold, wet winters and hot, dry summers (Table 2).

The experimental soil was classified as a clayey–loamy soil with moderately alkaline pH (8.32), high phosphorus content (338.33 ppm), elevated lime content (28.63%), moderate organic matter (1.96%), and low nitrogen levels (0.098%). The soil texture was predominantly clay (69.25%), with a smaller fraction of loam (19.5%). Overall, the soil was classified as moderately alkaline, clayey–loam with a relatively low organic matter content.

**Table 1.** Code, pedigrees, and origin of local checks.

Code	Name	Pedigrees	Origin
C1	Anza	Lr/N10B//3*Ane II8739-4R-1M-1R	USA
C2	Arz	Mayo 54 ILR64/ "TAC S".	Cimmyt-Mexico
C3	Tidis	BUCKBUCK/FLICKER/MYNA/VULTURE	Cimmyt-Mexico
C4	Hidhab	HD1220/3*Kal/Nac	Cimmyt-Mexico
C5	Massine	PFAU/SERI-82/(SIB)BOBWHITE	Cimmyt-Mexico

**Table 2.** Climatic data of Constantine region during the 2018–2019 cropping season.

Month	Temperature (°C)	Precipitation (mm)
September	22.50	7.61
October	15.80	143.01
November	11.40	5.59
December	8.30	20.08
January	5.60	101.1
February	6.90	48.01
March	9.80	48.76
April	12.90	40.13
May	15.00	60.19
June	25.30	0.25
July	27.60	0.25
Mean	14.60	43.20

(Tutiempo 2024).

An augmented block design, following the methodology outlined by Federer (1956), was implemented to evaluate the agro-morphological performance of the bread wheat (*Triticum aestivum* L.) germplasm. The experimental layout consisted of four blocks, each containing five local check varieties sown in two replications to facilitate intra-block adjustment, while the test genotypes were evaluated without replication. The first three blocks included 27 genotypes each, whereas the fourth block comprised 26 genotypes, resulting in a total of 107 unique entries. Each entry sown in two rows of 1 m in length, spaced 25 cm apart, and planted at a soil depth of 2 to 3 cm. A total of 147 experimental plots were established following a standardized technical itinerary suitable for wheat cultivation under semi-arid conditions. The trial was conducted under rainfed conditions.

The agro-morphological traits assessed in the bread wheat germplasm under rainfed conditions were selected for their agronomic relevance to yield potential and adaptability in semi-arid environments. These traits included days to heading (DTH, days), recorded as the number of days from sowing to the emergence of the spike in 50% of the plants, and plant height (HGT, cm), measured from the base of the stem to the base of the spike, excluding the awns. The number of kernels per spike (NKS) was calculated as the average grain count from three representative spikes. In addition, the number of spikes per square meter (NS m<sup>2</sup>), the thousand-kernel weight (TKW, g), and grain yield (YLD, t ha<sup>-1</sup>) were also estimated. Together, these traits provided a comprehensive framework for evaluating genotypic performance under water-limited conditions.

### Statistical analysis

An analysis of variance was conducted on the quantitative data following the method described by Federer (1961). The analysis was carried out using the “*augmentedRCBD*” package (Aravind et al. 2023) within the R statistical software environment (R Core Team 2024). Adjusted means were estimated for the unreplicated treatments.

The error mean square obtained from this analysis was used to calculate different standard errors of differences for various comparisons, including: the means of two check varieties ( $SE_c$ ), the adjusted means of two new selections within the same block ( $SE_d$ ), the adjusted means of two new selections in different blocks ( $SE_v$ ), and the adjusted

mean of a new selection and a check variety ( $SE_{vc}$ ), as described by Federer (1961) (Equations 1–4).

$$SE_c = \sqrt{2MSE / r} \quad (1)$$

$$SE_d = \sqrt{2MSE} \quad (2)$$

$$SE_v = \sqrt{2(C + 1) MSE / c} \quad (3)$$

$$SE_{vc} = \sqrt{2(r + 1)(c + 1)MSE / rc} \quad (4)$$

Since the aim was to identify new selections that outperformed the checks, the Least Significant Increase (LSI) was computed using the formula (Equation 5):

$$LSI = SE_{vc} \times t_{\alpha} \quad (\text{at error df}) \quad (5)$$

In this case, a one-sided *t*-test was performed at a 5% level of significance, using the degrees of freedom associated with the error term. Where *t* is the one-tailed *t*-test at  $\alpha$  probability level at error degree of freedom (df) (Equation 6) and  $S_{vc}$  from Equation 4.

$$df \ t(\alpha = 0.05) = 1.694 \quad (6)$$

To describe the variability among genotypes, several basic univariate statistics were calculated, including the minimum, maximum, range, mean, and standard deviation.

Correlation analysis between the studied traits was carried out using the “*metan*” package in R (Olivoto and Lúcio 2020). Pearson correlation coefficients were calculated to examine the relationships between variables. A heatmap was used to visualize the results, making it easier to identify strong positive or negative correlations among the traits, as well as their statistical significance.

The Multi-trait Genotype–Ideotype Distance Index (MGIDI) was applied to identify the most promising genotypes based on their overall performance across multiple traits. This index estimates the weighted Euclidean distance of each genotype from an ideotype that represents the ideal combination of trait values, using scores derived from factor analysis to account for multicollinearity among traits.

The MGIDI value for each genotype was calculated using the following equation (Equation 7):

$$MGIDI = \left[ \sum_{i=1}^f (i\gamma_{ij} - \gamma_j)^2 \right]^{0.5} \quad (7)$$

Where  $i$ , is for the genotype,  $\gamma_{ij}$  is the  $j^{\text{th}}$  score of the  $i^{\text{th}}$  genotype, and  $\gamma_i$  is the  $j^{\text{th}}$  score of ideotype ( $i = 1, 2, \dots, t$ ;  $j = 1, 2, \dots, f$ ).  $t$  and  $f$  the number of genotypes and traits.

Genotypes with lower MGIDI values were considered closer to the ideotype and thus more desirable. A selection intensity of 15% was applied, enabling differential selection for each trait and the identification of superior genotypes combining multiple desirable characteristics.

The calculation of the strengths and weaknesses of genotypes is based on the proportion of the MGIDI value of the  $i^{\text{th}}$  genotype that is explained by the  $j^{\text{th}}$  factor, denoted as  $\omega_{ij}$  (Equation 8):

$$\omega_{ij} = \frac{\sqrt{D_{ij}^2}}{\sum_{j=1}^f \sqrt{D_{ij}^2}} \quad (8)$$

Where  $D_{ij}$  represents the distance between the  $i^{\text{th}}$  genotype and the ideal genotype for the  $j^{\text{th}}$  trait.

A low contribution of a given factor suggests that the traits associated with it are close to the ideotype, indicating the strength of the genotype.

## RESULTS AND DISCUSSION

### Genotypic performance across traits

The analysis of variance (ANOVA) presented in Table 3 showed significant differences among genotypes and local checks for all traits studied. The comparison between genotypes and checks was also significant ( $P \leq 0.001$ ) for most traits, except for NKS and TKW, for which no significant difference was observed. Table 3 also includes a summary of basic statistics for each trait.

**Table 3.** Analysis of variance for the studied agronomic traits.

Source of variation	DF	MS					
		DTH	HGT	NKS	NS m <sup>2</sup>	TKW	YLD
Blocks (Eliminating treatments)	3	58.29**	4.09**	18.99	9706**	39.13	214.00
Treatments (Eliminating blocks)	111	31.22***	162.93**	104.54***	3465.00**	55.88*	280.20**
Genotypes	106	27.21***	165.70**	98.76***	3447.00*	57.46*	282.00**
Checks	4	83.84***	292.84**	285.01***	6869.00**	120.25**	402.00*
Genotypes vs Checks	1	154.32***	14.85***	101.33	28323.00***	75.27	5177.00***
Error	32	9.65	21.14	30.76	1603.00	29.52	131.20
CV%		2.55	5.09	9.66	17.18	15.66	31.15

DTH: Date to heading; HGT: Plant height; NKS: Number of kernels per spike; NS m<sup>2</sup>: Number of spikes per square meter; TKW: Thousand kernel weight; YLD: Grain yield; SD: Standard deviation; LSI: Least significant increase, CV%: Coefficient of variation; \*: Represents significance at ( $P < 0.05$ ) level; \*\*: Represents significance at ( $P < 0.01$ ) level; \*\*\*: Represents significance at ( $P < 0.001$ ) level.

The descriptive statistics (Table 4) of the evaluated agromorphological traits reveal considerable phenotypic variability within the studied germplasm, emphasizing its potential for genetic enhancement under semi-arid conditions. The observed standard deviations across traits further illustrate the extent of this variability, indicating a wide range of expressions that can be exploited in breeding programs aimed at improving yield performance and adaptability in water-limited environments. DTH ranged from 103.9 to 136.7 days, with a mean of 122.3 days, reflecting a broad spectrum of earliness among genotypes, an essential adaptation

trait under terminal drought stress. Earliness to heading is a key criterion for improving cereal production in rainfed environments, as it enables genotypes to complete their cycle before the drought period. HGT exhibited variation, from 65.92 to 137.62 cm (mean = 90.31 cm), highlighting the coexistence of dwarf and tall genotypes. Genotypes with medium straw are more desirable in semi-arid regions, as they ensure structural robustness while maintaining harvestable yield. The NKS varied from 21.64 to 84.94, with an average of 58.2, suggesting significant differences in spike fertility, a major determinant of final grain number. NS m<sup>2</sup>



ranged from 57.15 to 319.15 spikes  $m^{-2}$  (mean = 226.6), indicating broad variability in tillering ability and grain filling capacity. TKW showed a wide distribution, from 8.62 to 51.12 g (mean = 35.3 g), pointing to genotypic differences in grain size and filling efficiency. YLD

exhibited variability, ranging from 0.63 to 7.33  $t\ ha^{-1}$ , with a mean of 3.35  $t\ ha^{-1}$ , reflecting differences in yield potential among genotypes. This variability emphasizes the opportunity to identify and promote high-performing lines specifically adapted to water-limited conditions.

**Table 4.** Univariate statistics of the studied agronomic traits.

Statistics	DTH	HGT	NKS	NS $m^{-2}$	TKW	YLD
Min	103.90	65.92	21.64	57.15	8.62	0.63
Max	136.70	137.62	84.94	319.15	51.12	7.32
Range	32.70	71.70	63.30	262.00	42.50	6.71
Mean	122.30	90.31	58.23	226.62	35.34	3.35
SD	2.57	4.59	5.54	40.03	5.43	11.45
LSI	6.45	9.54	11.51	83.09	11.28	23.77

DTH: Days to heading; HGT: Plant height; NKS: Number of kernels per spike; NS  $m^{-2}$ : Number of spikes per square meter; TKW: Thousand kernel weight; YLD: Grain yield; SD: Standard deviation; LSI: Least significant increase.

The univariate statistics including minimum, maximum, mean, range, and standard deviation as well as the analysis of variance, revealed significant differences among treatments for all assessed traits. These findings are essential for the efficient identification and selection of superior genotypes adapted to the agro-ecological conditions of Constantine. The results are in line with previous studies conducted under similar semi-arid conditions in Algeria, which have demonstrated comparable relationships between grain yield and associated agronomic traits (Fellahi et al. 2013; Frih et al. 2022; Lamara et al. 2022; Hannachi and Fellahi 2023; Djoudi et al. 2024). Overall, the observed phenotypic variability constitutes a

valuable resource for targeted selection and the design of crossing strategies in wheat breeding programs aimed at improving productivity, resilience to environmental stress, and resource use efficiency in semi-arid agro-ecosystems.

According to the Least Significant Increase (LSI) criterion, genotypes exhibiting earlier heading than the mean performance of the local check – LSI value are considered desirable for the DTH. In this regard, genotypes G29, G38, and G9 were significantly earlier than four local checks (C1, C2, C4, and C5), while genotypes G111, G28, G40, G60, G61, G62, G65, G71, G8, G83, and G99 exhibited earliness superior to that of checks C4 and C5 (Table 5).

**Table 5.** Local checks average, least significant increase outperforming genotypes number.

Checks	DTH-LSI	Out GN	NS $m^{-2}$ +LSI	Out GN	NKS+LSI	Out GN	TKW+LSI	Out GN	YLD+LSI	Out GN
C1	113.05	3	324.84	0	75.34	2	44.01	10	70.10	1
C2	113.68	3	330.59	0	58.55	57	42.98	10	52.98	14
C3	108.55	0	345.09	0	68.09	13	51.46	0	70.37	1
C4	115.43	6	385.59	0	68.26	14	41.44	20	69.10	1
C5	117.18	14	308.09	5	67.68	14	44.09	10	60.85	4

Out GN: Outperforming genotypes number.

For traits where higher values are desirable, namely NKS, NS  $m^{-2}$ , TKW, and YLD genotypes that exceed the mean performance of the local checks plus LSI threshold are considered superior. Based on this criterion, 22 out of the 107 tested genotypes exhibited YLD values significantly

higher than the benchmark set by the local checks, thereby demonstrating promising agronomic potential. Among these, genotypes such as G111, G11, G54, G30, G57, G60, G61, G62, G67, and G8 notably outperformed the local check C2 in terms of grain yield. Genotype G87 was

particularly outstanding, registering the highest yield at  $7.33 \text{ t ha}^{-1}$ , thus surpassing all five local checks. Furthermore, G87 also exceeded the population mean for NKS (63 grains),  $\text{NS m}^{-2}$  (235 spikes  $\text{m}^{-2}$ ), and TKW (36.65 g), indicating a robust and well-balanced performance across key yield-contributing traits.

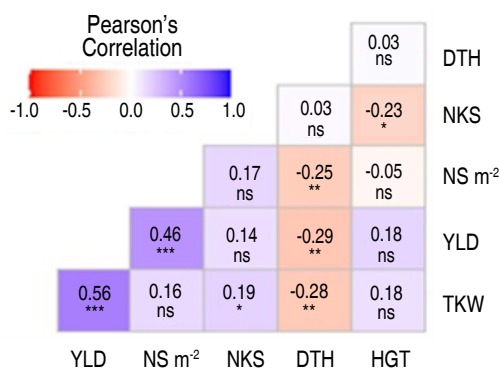
For the number of kernels per spike, the mean value recorded among the local checks was 58.27 grains. Genotypes G26 and G49 exceeded this threshold and outperformed all checks based on the LSI criteria, indicating superior spike fertility. Notably, the local check C4 registered TKW across the entire collection, confirming its strong performance for grain size. Among the tested entries, genotype G65 stood out by surpassing at least one local check for every trait evaluated, reflecting its broad and consistent agronomic superiority.

Selection based on LSI thus enables the identification of genotypes with statistically significant improvements. Specifically, genotypes with trait values greater than (check mean + LSI) for NKS,  $\text{NS m}^{-2}$ , TKW, and YLD or less than (check mean – LSI) for DTH can be classified

as statistically superior. The utility of LSI in identifying promising donors of yield-related traits has been previously validated in bread wheat (Kumar et al. 2018) as well as in rice (Hasan et al. 2020; Mustikarini et al. 2023). If in a new germplasm, YG, exceeds  $\text{YC} + \text{LSI}$ , the resulting increase in yield is considered statistically significant at the 100% level. However, the results reported in the present study do not fully align with those of Kumar et al. (2018).

### Trait relationships and their contribution to grain yield

Strong correlations were observed among the six agro-morphological traits assessed in the bread wheat genotypes (Figure 1). Correlation analysis revealed that early heading, high spike density, and increased thousand-kernel weight positively contributed to higher grain yield, particularly in genotype G87. Early-heading genotypes are of particular interest to breeders, as earliness is often associated with improved yield performance under rainfed and drought-prone conditions. Therefore, such genotypes represent valuable candidates for selection programs aiming to combine early maturity with yield-enhancing traits.



ns  $P \geq 0.05$ ; \*  $P < 0.05$ ; \*\*  $P < 0.01$ ; and \*\*\*  $P < 0.001$

**Figure 1.** Correlation heat maps of grain yield and its related traits of studied bread wheat genotypes. DTH: Days to heading; HGT: Plant height; NKS: Number of kernels per spike;  $\text{NS m}^{-2}$ : Number of spikes per square meter; TKW: Thousand kernel weight; YLD: Grain yield; ns: no significant at ( $P \geq 0.05$ ); \*: Represents significance at ( $P < 0.05$ ) level; \*\*: Represents significance at ( $P < 0.01$ ) level; \*\*\*: represents significance at ( $P < 0.001$ ) level.

These findings agree with earlier reports demonstrating significant positive associations between yield and traits such as TKW and  $\text{NS m}^{-2}$  (Kumar et al. 2020; Ullah et al. 2021). In contrast, Kumar et al. (2018) reported a significant negative correlation between DTH and YLD,

which aligns with the present findings. A negative but statistically non-significant relationship was observed between the NKS and HGT, consistent with the results of Arain et al. (2018). Furthermore, Fellahi et al. (2013) identified a significant inverse relationship between NKS

and TKW, suggesting a possible trade-off between spike fertility and grain weight. However, this contrasts with other studies (Djuric et al. 2018), which reported positive associations between these traits. Such discrepancies highlight the complexity of trait interactions and emphasize the importance of context-specific validation in different genetic backgrounds and environmental conditions.

### MGIDI-Based Multi-Trait Selection

In selection based on MGIDI (Table 6), six traits were employed to assess variation among 107 genotypes. The genotype selection aimed at selecting genotypes with lower values (negative gains) for DTH, and higher values (positive gains) for NKS, NS m<sup>2</sup>, TKW, and YLD. For HGT, based on the average height of the germplasm

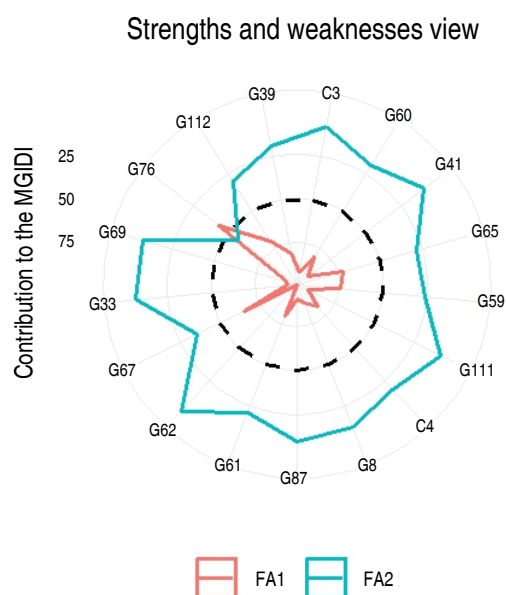
(90.31 cm), medium straw genotypes are more desirable than short straw genotypes. A selection with a positive gain is more desirable for this study.

The Multi-Trait Genotype-Ideotype Index classifies the studied genotypes by trait interest and exhibits significant genetic gains across all examined traits, resulting in a total genetic gain of 31.19%. The YLD shows the highest selection gain at 20%, while NKS is the only trait exhibiting an undesired gain (Table 6). Among the five local checks, C3 and C4 were chosen. The genotypes G39 and G112 were observed to be near to the cut point, indicated by the red line in Figure 2. These genotypes may serve as promising candidates exhibiting noteworthy traits for future breeding programs.

**Table 6.** Factorial loadings after varimax rotation and predicted genetic gains (PSG) based on the MGIDI.

Traits	Factors	FA1	FA2	SG	SG (%)	Sense	Goal
DTH	FA1	0.60	-0.02	-1.85	-1.52	decrease	100
NS-m <sup>2</sup>	FA1	0.64	0.22	10.10	4.30	increase	100
TKW	FA1	0.69	-0.06	1.65	4.75	increase	100
YLD	FA1	0.85	-0.04	7.40	19.97	increase	100
HGT	FA2	0.17	-0.79	3.83	4.24	increase	100
NKS	FA2	0.19	0.75	-0.34	-0.59	increase	0

SG: Selection gain; SG %: Selection gain percent.

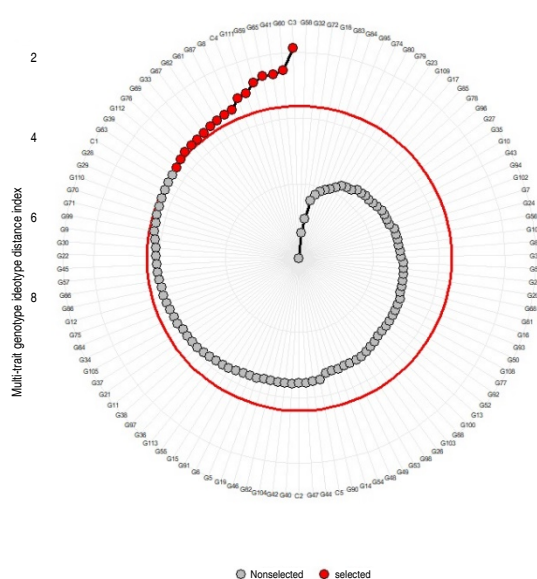


**Figure 2.** View of strengths and weaknesses of selected bread wheat genotypes.



According to Olivoto et al. (2022), the genotype with the lowest MGIDI value is considered the closest to the ideal genotype, exhibiting favorable performance across all traits under evaluation. Understanding the strengths and weaknesses of genotypes provides critical insights for parental selection in future breeding efforts. Out of the 107 evaluated genotypes, 17 were selected, including the

two local checks (C3 and C4). These selected genotypes demonstrated outstanding agronomic performance, particularly in YLD, but also across other desirable traits. Similar Multi-Trait selection (Figure 3) approaches have been successfully applied in wheat (Pour-Aboughadareh and Poczaï 2021; Romena et al. 2022), barley (Pour-Aboughadareh et al. 2021), and rice (Mamun et al. 2022).



**Figure 3.** Selected bread wheat genotypes using Multi-Trait Genotype Ideotype Index.

## CONCLUSION

The present study revealed significant agro-morphological variability among the evaluated bread wheat genotypes, underscoring the genetic diversity available for selection under semi-arid conditions. The application of both the Least Significant Increase (LSI) method and the Multi-Trait Genotype–Ideotype Distance Index (MGIDI) facilitated the identification of superior genotypes combining desirable agronomic traits. Notably, genotype G65 outperformed at least one local check across all studied traits, while MGIDI highlighted 15 promising genotypes alongside two local checks (C3 and C4) as candidates for future breeding efforts. These findings emphasize the importance of early heading (DTH), high kernel number per spike (NKS), and high thousand-kernel weight (TKW) as key traits positively associated with grain yield performance. These results suggest that integrating genotypes expressing such traits into crossing programs could substantially contribute to the development of high-yielding and well-adapted cultivars

suited to the constraints of semi-arid environments like those found in Algeria. From a broader perspective, the success of breeding programs relies not only on trait-based selection but also on a comprehensive understanding of the interrelationships among traits. Such knowledge is essential for making strategic decisions that maximize genetic gain while minimizing negative correlations. Future research should therefore focus on combining phenotypic data with molecular and genomic approaches to improve selection accuracy. Moreover, the incorporation of diverse germplasm, including landraces and improved lines, into pre-breeding pipelines remains crucial for broadening the genetic base and reinforcing the adaptive potential of new cultivars. The integration of robust statistical tools such as MGIDI with well-designed field evaluations represents a promising strategy for accelerating wheat genetic improvement. These approaches will play a vital role in ensuring food security and climate resilience in regions facing increasing agricultural challenges.

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## CONFLICT OF INTERESTS

No competing interests declared.

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