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Phenotypic Screening for Drought Tolerance in Algerian Bread Wheat (*Triticum aestivum* L.) Genotypes under Semi-Arid Conditions

Cribado fenotípico para la tolerancia a la sequía en genotipos argelinos de trigo harinero (*Triticum aestivum* L.) bajo condiciones semiáridas

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ABSTRACT

Bread wheat production in semi-arid regions is strongly constrained by environmental variability, particularly drought stress, which limits yield stability. This study evaluated the agro-morphological performance, yield components, and stress tolerance of 55 bread wheat genotypes in six different rainfed environments defined by three locations in northeastern Algeria over two cropping seasons (2021–2022 and 2022–2023), using an augmented block design. The combined analysis of variance showed highly significant effects of environment and genotype for all traits, while genotype × environment interactions were trait-dependent, being significant for spike length, thousand-kernel weight, and aboveground biomass. Environmental effects accounted for the largest share of total variation (38.76 to 81.80%). Substantial phenotypic variability was observed, with moderate to high broad-sense heritability (36.59 to 79.24%), indicating reasonable selection prospects despite pronounced environmental influence. Correlation analyses revealed that yield formation was predominantly driven by kernel number, spike density, and biomass under both conditions, while flag leaf area contributed more specifically under stress. Based on the Stress Tolerance Index, breeding line T22 followed by T2, and T23 combined high yield potential with strong stability, exhibiting the highest STI values (0.786, 0.485, and 0.463, respectively). Future breeding efforts should prioritize crossing these superior lines with locally adapted cultivars and expanding multi-environment trials across wider semi-arid agroecosystems to accelerate the development of climate-resilient wheat varieties.

Palabras clave:
Variabilidad genética
Heredabilidad
Eficiencia de selección
Respuesta al estrés
Rendimiento

RESUMEN

La producción de trigo harinero en regiones semiáridas está fuertemente limitada por la variabilidad ambiental, en particular el estrés hídrico, que restringe la estabilidad del rendimiento. Este estudio evaluó el desempeño agromorfológico, los componentes del rendimiento y la tolerancia al estrés de 55 genotipos en seis ambientes de secano en el noreste de Argelia durante dos temporadas de cultivo (2021–2022 y 2022–2023), utilizando un diseño aumentado de bloques. El análisis combinado de varianza mostró efectos altamente significativos del ambiente y del genotipo para todos los caracteres, mientras que las interacciones genotipo × ambiente fueron significativas únicamente para la longitud de espiga, el peso de mil granos y la biomasa aérea. Los efectos ambientales explicaron la mayor proporción de la variación total (38,76 a 81,80%). Se observó variabilidad fenotípica considerable, con heredabilidad en sentido amplio de moderada a alta (36,59 a 79,24%), indicando perspectivas razonables de selección pese a la marcada influencia ambiental. Los análisis de correlación revelaron que el rendimiento estuvo determinado principalmente por el número de granos, la densidad de espigas y la biomasa, mientras que el área de la hoja bandera contribuyó más específicamente bajo estrés. Con base en el Índice de Tolerancia al Estrés, las líneas T22, T2 y T23 combinaron alto potencial de rendimiento con amplia estabilidad (0,786, 0,485 y 0,463, respectivamente). Los programas futuros deben priorizar el cruzamiento de estas líneas con cultivares localmente adaptados y ampliar los ensayos multiambientales para desarrollar variedades resilientes al clima en agroecosistemas semiáridos.

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Bread wheat (*Triticum aestivum* L.) is a cornerstone of global food security and human nutrition (Govindan et al. 2022). Worldwide, its cultivation covers over 220 million hectares, producing approximately 799 million tonnes annually (FAOSTAT 2025). In Algeria, wheat is a vital staple crop; however, national production satisfies less than 10% of domestic demand, leading to a heavy reliance on imports (Selt 2025). This massive production gap is primarily driven by severe environmental constraints in semi-arid regions, where water scarcity and climate variability strictly limit potential productivity (Djenadi et al. 2025).

The semi-arid Mediterranean climate of Algeria is marked by irregular rainfall and recurrent droughts, often exposing wheat to terminal water stress during grain filling (Djenadi et al. 2025). Under these conditions, agro-morphological traits related to growth and phenology contribute significantly to adaptation and yield stability (Bekaddour et al. 2024; Ladoui et al. 2025). Within this challenging context, water deficit emerges as the dominant constraint shaping wheat performance and yield stability, with impacts depending on stress intensity, duration, and timing (Haghpanah et al. 2024). Consequently, mitigating these effects through targeted breeding programs has become a primary objective to improve wheat productivity under water-limited conditions.

To address this challenge, breeding strategies increasingly focus on developing genotypes combining high grain yield with enhanced drought tolerance (Fellahi et al. 2020; Bentouati et al. 2026), which requires the identification of high-potential, genetically diverse germplasm and traits associated with adaptation and yield performance under stress conditions (Bekaddour et al. 2024; Ladoui et al. 2025).

In this framework, multi-environment trials (METs) are widely used to assess genotype × environment interactions and to identify stable and high-performing genotypes across contrasting conditions (Crossa et al. 2017). Such approaches are particularly relevant in semi-arid regions, where strong environmental heterogeneity leads to variable genotype responses and unstable yield performance (Rabti et al. 2020).

Despite these advances, important gaps remain. In particular, the combined analysis of phenotypic variability and genotype × environment interaction under the specific terminal drought conditions of the Algerian high plains is still insufficiently explored for modern advanced breeding lines (Kirouani et al. 2023). Furthermore, the integration of biplot analysis and stability indices to support efficient selection strategies remains limited in this region. Addressing these gaps is essential to bridge the yield gap and identify genotypes combining high yield and stability. The findings of this study are expected to provide breeders with validated selection criteria and superior donor lines to accelerate the development of climate-resilient wheat genotypes for the North African cereal belt.

In this context, the main aim of the present study was to evaluate the phenotypic variability of 55 bread wheat (*Triticum aestivum* L.) genotypes across three semi-arid environments in Algeria over two crop seasons. Specifically, this study aimed to (i) assess genotype × environment interactions, (ii) identify stable and high-yielding genotypes using stress tolerance index, and (iii) analyze the relationships between grain yield and key agro-morphological traits to support indirect selection.

MATERIALS AND METHODS

Plant Materials

The plant material consisted of 55 bread wheat (*Triticum aestivum* L.) genotypes (Table 1), including 50 advanced breeding lines developed through Algerian selection programs using genetic material from diverse origins including the International Maize and Wheat Improvement Center (CIMMYT) and The International Center for Agricultural Research in the Dry Areas (ICARDA), alongside landraces and old and modern cultivars. Five local check cultivars named Hidhab, Arz, Ain Abid, Akhamokh and Boumerzoug were also included. These checks are widely cultivated in Algeria and have been extensively characterized for their responses to diverse abiotic and biotic stresses under semi-arid conditions, serving as references for performance comparison.

Table 1. List of bread wheat (*Triticum aestivum* L.) genotypes evaluated in the study.

Code	Name / Pedigree	Type
T1	NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR/5/KACHU/6/KACHU (CMSS06B00734T-099TOPY-099ZTM-099Y-099M-13WGY-0B)	MV
T2	KACHU#1//WBLL1*2/KUKUNA (CMSS07Y00129S-0B-099Y-099M-099NJ-099NJ-14WGY-0B)	MV
T3	ITP40/AKURI (CMSS07Y00441S-0B-099Y-099M-099NJ-099NJ-14WGY-0B)	MV
T4	KAUZ*2/MNV//KAUZ/3/MILAN/4/BAV92/5/CHYAK (CMSS07B00100S-099M-099Y-099M-3WGY-0B)	MV
T5	7 CERROS	OV
T6	LALOUB-2	OV
T7	BECARD/QUAIU #1	BL
T8	YAMAMA/SD8036	BL
T9	KIRITATI/WBLL1//MESIA/3/KIRITATI/WBLL1	BL
T10	TUKURU//BAV92/RAYON/3/FRNCLN	BL
T11	QUAIU/5/FRET2*2/4/SNI/TRAP#1/3/KAUS*2/TRAP//...	BL
T12	YACINE (OASIS/SKAUZ//4*BCN*2/3/PASTOR)	MV
T13	CAL/NH//H567.71/3/SERI/4/CAL/NH//H567.71/5/2*KAUZ/6/...	BL
T14	GK.ARON/AG.SECO7846//2180/4/2*MILAN/KAUZ//...	BL
T15	SOKOLL*^{2}/TROST	BL
T16	EL ZINA (ACSAD$_{1135}$/RMADA)	MV
T17	MOROCCO	L
T18	SOKOLL/3/PASTOR//HXL7573/2*BAU/4/SOKOLL/WBLL1/5/PIHA//WORRAKATTA/2*PASTOR/3/PRL/2*PASTOR (PTSS14Y00057S-0B-099Y-099B-26Y-020Y-0B)	BL
T19	SOKOLL/WBLL1/4/PIHA//WORRAKATTA/2*PASTOR/3/PRL/2*PASTOR (PTSS14Y00079S-0B-099Y-099B-1Y-020Y-0B)	BL
T20	SOKOLL (CMSS97M00316S-0P20M-0P20Y-43M-010Y)	OV
T21	WBLL4//OAX93.24.35/WBLL1/5/CROC1/AE.SQUARROSA(205)//BORL95/3/PRL/SARA//TSI/VEE#5/4/FRET2/6/D67.2/PARANA66.270//AE.SQUARROSA(320)/3/CUNNINGHAM/4/VORB (PTSS15Y00024S-099B-099Y-099M-2Y-020Y)	BL
T22	WBLL4//OAX93.24.35/WBLL1/5/CROC1/AE.SQUARROSA(205)//BORL95/3/PRL/SARA//TSI/VEE#5/4/FRET2/6/D67.2/PARANA66.270//AE.SQUARROSA(320)/3/CUNNINGHAM/4/VORB (PTSS15Y00024S-099B-099Y-099M-2Y-020Y)	BL
T23	WBLL4//OAX93.24.35/WBLL1/5/CROC1/AE.SQUARROSA(205)//BORL95/3/PRL/SARA//TSI/VEE#5/4/FRET2/6/D67.2/PARANA66.270//AE.SQUARROSA(320)/3/CUNNINGHAM/4/VORB (PTSS15Y00024S-099B-099Y-099M-2Y-020Y)	BL
T24	STOT//ALTAR84/ALD/3/PATKA.7/YAZI.1/4/SOMAT.3/PHAX.1//TIL0.1/LOTUS.4/5/SOOTY9/RASCON37//WODUCK/CHAM3/12/1A.1D5+1.06/3*MOJO//RCOL/4/ARMENT//SRN.3/NIGRIS.4/3/CANELO.9.1/11/PLATA.10/6/MQUE/4/USDA573/QFN/AA.7/3/ALBA.D/5/AVO/HUI/7/PLATA.13/8/RAFI97/9 (CDSS13Y00283S-099Y-021M-33Y-1M-0Y)	BL
T25	FRTL//ATTILA/3*BCN/5/D67.2/PARANA 66.270//AE.SQUARROSA(320)/3/CUNNINGHAM/4/VORB (PTSS15Y00010S-099B-099Y-099M-2Y-020Y)	BL

Table 1

Code	Name / Pedigree	Type
T26	SOKOLL/3/PASTOR//HXL7573/2*BAU/5/CROC_1/AE.SQUARROSA(205)//BORL95/3/PRL/SARA//TSI/VEE#5/4/FRET2/6/D67.2/PARANA66.270//AE.SQUARROSA (320)/3/CUNNINGHAM/4/VORB (PTSS15Y00023S-099B-099Y-099M-23Y-020Y)	BL
T27	CROC_1/AE.SQUARROSA(205)//BORL95/3/PRL/SARA//TSI/VEE#5/4/FRET2/5/P IHA//WORRAKATTA/2*PASTOR/3/PRL/2*PASTOR (PTSS15Y00046S-099B-099Y-099M-7Y-020Y)	BL
T28	SOKOLL/3/PASTOR//HXL7573/2*BAU/4/PARUS/PASTOR/5/PIHA//WORRAKATTA/2*PASTOR/3/PRL/2*PASTOR (PTSS14Y00062S-0B-099Y-099B-39Y-020Y)	BL
T29	SOKOLL/WBLL1/4/PIHA//WORRAKATTA/2*PASTOR/3/PRL/2*PASTOR (PTSS14Y00079S-0B-099Y-099B-1Y-020Y-0B)	BL
T30	ATTILA*^{2}/PBW65*^{2}//KACHU (CMSS06Y00582T-099TOPM-099Y-099ZTM-13WGY-0B)	BL
T31	MUTUS*^{2}/ATUKI..	BL
T32	FLORENCE AURORE (FLORENCE X AURORE$_{588}$)	OV
T33	AIN EL BEY (MAHON DEMIAS/BOUMERZOUG)	MV
T34	KACHU/KIRITATI	BL
T35	PFAU/SERI.1B//AMAD/3/WAXWING/4/WBLL1*^{2}/BRAMBLING	BL
T36	MAHON DEMIAS	L
T37	MUNAL#1/FRANCOLIN#1	BL
T38	KBIRD//WBLL1*^{2}/KUKURU	BL
T39	CNO79//PF70354/MUS/3/PASTOR/4/BAV92/5/FRET/KUKUNA//...	BL
T40	ACHTAR*3//KAUZ/KS85-8.5/4/MILAN/LAUZ//PRINIA/3/BAV92/5/...	BL
T41	FRET2/KUKUNA//FRET2/3/PASTOR//HXL7573/2*BAU/5/FRET2*2/...	BL
T42	CROC-1/AE.SQUARROSA(224)//OPATA/3/PASTOR	BL
T43	MILAN/S87230//HUITES	BL
T44	MEXIPAK	OV
T45	*Triticum dicoccum*	L
T46	ZIAD (ALONDRA'S/ERA//SON64/ALONDRA'S)	OV
T47	TIDDIS (IRENA CM91575-28Y-OM-0Y-2M-0Y)	MV
T48	PRL/PASTOR	MV
T49	MASSINE (PASTOR CM85295-0101TOPY-2M-0Y-0M-3Y-0M-0SY)	MV
T50	ANZA (LR/N10B x ANE3)	OV
C1	HIDHAB (HD1220/3*KAL/NAL CM40454)	OV
C2	ARZ (MAYO$_{54}$E/LR$_{6}$4//H$_{490}$/3/LR$_{64}$//TPP/YAKTANA$_{54}$)	OV
C3	AIN ABID (AS8189'A')	MV
C4	AKHAMOKH (IRENA/BADAX//PASTOR CMSS96 M05638T -040Y -010S-010M-010S-4M-0Y)	MV
C5	BOUMERZOUG (CMSS93B00255S-48Y-010M-010Y-010M-7Y-0M-4KBY-0KBY-0M)	MV

L: Landrace, OV: Old variety, MV: Modern variety; BL: Advanced breeding line.

Sites description

Field experiments were conducted over two successive cropping seasons (2021-2022 and 2022-2023) at three contrasting locations in northeastern Algeria under rainfed conditions. The first site was located at El Khroub, at the experimental field of the National Agronomic Research Institute of Algeria (INRAA), south of Constantine [36°16' N, 6°37′ E; 640 meters above sea level (masl)]. The second site was situated at the Debbah pilot farm in Didouche Mourad, north of Constantine [36°29' N, 6°37' E; 500 (masl)]. The third site was established at the INRAA experimental station in Sétif [36°09' N, 5°22′ E; 981 (masl)]. The six test environments were defined as combinations of site and cropping season: Environment 1 (E1) corresponded to El Khroub during 2021-2022, Environment 2 (E2) to Didouche Mourad during 2021-2022, and Environment 3 (E3) to Sétif during 2021-2022. Similarly, Environment 4 (E4), Environment 5 (E5), and Environment 6 (E6) corresponded respectively to El Khroub, Didouche Mourad, and Sétif during 2022-2023.

Soil characteristics and climatic conditions

Soil samples were collected from the 0–40 cm layer at each site prior to sowing. Soils at El Khroub were clay-loam with alkaline pH (8.32) and high available phosphorus; those at Didouche Mourad were clay-silt with neutral to slightly alkaline pH typical of Mediterranean calcareous soils; and Sétif soils were heavy clay with alkaline pH (7.91), high carbonate content, and low available phosphorus and potassium. Monthly rainfall and mean, maximum, and minimum temperatures recorded during both cropping seasons at the three sites are presented in Figure 1.

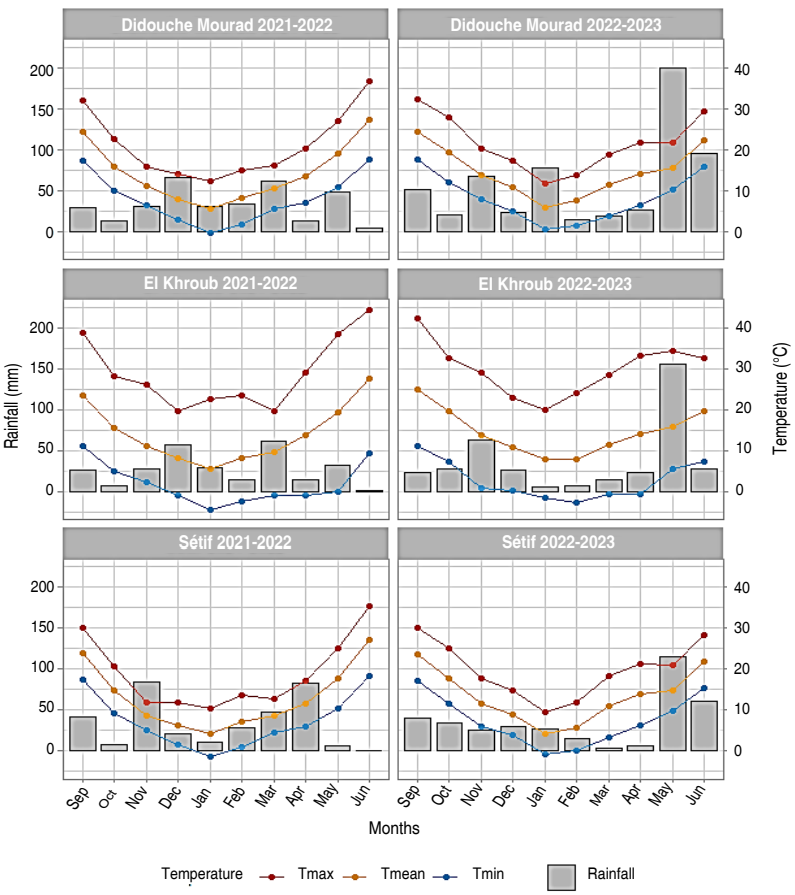


Figure 1. Monthly rainfall and mean, maximum, and minimum temperatures recorded during the 2021-2022 and 2022-2023 cropping seasons at the three experimental sites (El Khroub, Didouche Mourad, and Sétif).

Experimental design

The field experiments were established using an augmented block design (Burgueño et al. 2018), a specifically suited for evaluating large numbers of unreplicated test genotypes alongside replicated checks. This design was selected to optimize screening efficiency for the genotypes and minimize the experimental area, thereby controlling intra-block soil heterogeneity. The design comprised four incomplete blocks, each containing the five local check cultivars replicated across all blocks. The 50 test genotypes were distributed across blocks without replication: blocks 1 and 2 each contained 18 test genotypes, while blocks 3 and 4 each contained 17. Each genotype was grown in two rows, 2 m long, with 0.2 m row spacing, resulting in a total plot size of 0.8 m². Blank rows were maintained between adjacent plots to minimize border effects, and blocks were separated by 1 m alleys. Sowing was carried out in early December of each season at all three sites, at a seeding rate of 300 viable seeds m^{-2}. Nitrogen fertilization was applied at a rate of 100 kg N ha^{-1}, split between basal application at sowing and top-dressing at tillering. Weed control was performed using selective herbicides at the tillering stage, and no irrigation was applied, as all trials were conducted under strictly rainfed conditions. These agronomic practices were applied uniformly across all sites and seasons in accordance with local recommendations.

Measurements of agro-morphological traits

Eight agro-morphological traits were measured at the plot level, with values calculated as the mean of three representative plants per plot selected at random at physiological maturity, unless otherwise specified. Plant height (PH, cm) was measured at physiological maturity from the soil surface to the tip of the spike, excluding awns. Spike length (SL, cm) was measured from the base of the lowest spikelet to the tip of the uppermost spikelet, excluding awns, on the main stem spike at physiological maturity. Flag leaf area (FLA, cm²) was assessed at heading stage on the flag leaf of the main stem, calculated as the product of flag leaf length and maximum width multiplied by a correction factor of 0.75, following Yang et al. (2016). Spike density (NS, spikes m^{-2}) was determined by counting all productive spikes within a known area of 0.5 m^2 per plot at maturity and converting to spikes per square meter. Number of kernels per square meter (NK, kernels m^{-2}) was estimated by multiplying spike density by the average number of kernels per spike, the latter determined by threshing and counting kernels from 10 representative spikes per plot. Thousand-kernel weight (TKW, g) was determined by counting and weighing three samples of 1,000 seeds per plot using a precision balance. Grain yield (GY, g m^{-2}) was obtained by harvesting, threshing, and weighing all grains from each plot. Aboveground biomass (BIO, g m^{-2}) was determined by cutting and weighing all aboveground plant material at soil level within the harvested plot area at maturity.

Statistical analysis

A combined two-way analysis of variance (ANOVA) was performed to assess the effects of genotype (G), environment (E), and their interaction (G×E). Since test genotypes were unreplicated within each environment, adjusted means were estimated to correct for block effects, using the replicated check cultivars, which appeared in all blocks, as a reference for block-effect estimation. Observed plot values were then corrected accordingly, following the standard augmented design procedure (Burgueño et al. 2018). These adjusted means replaced raw values in all subsequent analyses, ensuring unbiased genotype comparisons. Where ANOVA revealed significant differences, mean comparisons were performed using Tukey's Honestly Significant Difference (HSD) test at the 5% probability level. Phenotypic (σ^2_p), genotypic (σ^2_g), and environmental (σ^2_e) variances were estimated from ANOVA mean squares. The phenotypic (CV_p), genotypic (CV_g) and environmental (CV_e) coefficients of variation were computed as follows: $CV_p\ (\%) = (\sigma^2_p / \mu) \times 100$; $CV_g\ (\%) = (\sigma^2_g / \mu) \times 100$; $CV_e\ (\%) = (\sigma^2_e / \mu) \times 100$, where μ is the trait mean (Abdurezake et al. 2024). The CV_g/CV_e ratio was used to assess the relative importance of genetic versus environmental variation. Broad-sense heritability (h^2_{bs}) was estimated as: $h^2_{bs}\ (\%) = (\sigma^2_g / \sigma^2_p) \times 100$ (Acquaah 2020). All analyses were performed using GENES software (Cruz 2013).

Phenotypic correlations among traits were computed separately for the most favorable (E3) and the most stressful (E4) environments to examine changes in trait interrelationships across contrasting conditions. Environment classification was based on mean grain yield across all genotypes: E3 recorded the highest mean GY (203.54 g m^{-2}) and was designated as the favorable environment, while E4 recorded the lowest mean GY (23.11 g m^{-2}) and was designated as the stressful environment.

Correlation matrices were visualized using the '*corrplot*' package in R (Wei et al. 2017).

Stress tolerance was assessed using the Stress tolerance Index (STI), calculated as: $STI = (Y_p \times Y_s) / \overline{X}_p^2$, where Y_p and Y_s are the grain yield of a given genotype under the most favorable and most stressful environments respectively, and $\overline{X}_p$ is the mean grain yield of all genotypes under the favorable environment (Fernandez 1992). STI was computed using the iPASTIC toolkit (Pour-Aboughadareh et al. 2019).

RESULTS AND DISCUSSION

Variance analysis and mean comparison

The combined analysis of variance (ANOVA) for the 55 bread wheat genotypes evaluated across six environments revealed highly significant effects (P<0.01) of environment (Env.) and genotype (Gen.) for all eight traits (Table 2), indicating substantial environmental heterogeneity and exploitable genetic diversity within the studied material. The genotype × environment (G × E) interaction was trait-dependent: significant for SL (P<0.05), highly significant (P<0.01) for TKW, and BIO, and remained non-significant for PH, FLA, NS, NK, and GY. The absence of significant G × E interaction for these later traits suggests relatively stable genotypic performance across environments, while significant interactions for SL, TKW, and BIO indicate differential genotypic responses to environmental variation, a key consideration for selection strategies (Rabti et al. 2020; Menzir et al. 2025).

Environmental effects were the predominant source of variation for all traits, accounting for 38.76% (SL) to 81.80% (PH) of total variation, reflecting the strong influence of contrasting climatic and edaphic conditions across sites and seasons, a common feature in multi-environment trials conducted under rainfed systems (Rabti et al. 2020; Kirouani et al. 2023). G × E interaction constituted the second largest source, contributing 9.89% (PH) to 38.78% (BIO), while genotypic effects, though smaller in magnitude (4.94% for PH to 27.26% for SL), remained highly significant for all traits, confirming the presence of diversity suitable for selection. Coefficients of variation (CV) ranged from 3.39% (TKW) to 11.66% (GY), indicating acceptable experimental precision under field conditions.

Table 2. Combined analysis of variance of the agro-morphological traits of bread wheat genotypes under six environments.

SV	df	PH	SL	FLA	NS	NK	TKW	GY	BIO
Env. (E)	5	1605.38**	0.31**	1.78**	2.66**	7.87**	0.22**	8.27**	2.19**
Gen. (G)	49	98.99**	0.02**	0.02**	0.03**	0.12**	0.01**	0.13**	0.07**
G × E	245	39.61^{ns}	0.00*	0.01^{ns}	0.02^{ns}	0.05^{ns}	0.00**	0.06^{ns}	0.04**
Error	72	45.87	0.00	0.01	0.02	0.05	0.00	0.05	0.01
CV (%)	/	11.50	6.06	9.39	5.24	6.42	3.39	11.66	4.32

SV: Source of variation, Env.: Environment, Gen.: Genotype, CV: Coefficient of variation (%), df: Degrees of freedom, PH: Plant height (cm), SL: Spike length (cm), FLA: Flag leaf area (cm²), NS: Number of spikes per square meter, NK: Number of kernels per square meter (No), TKW: Thousand-kernel weight (g), GY: Grain yield (g m^{-2}), BIO: Aboveground biomass (g m^{-2}). ^{ns}, * and **: non-significant and significant effects at 5 and 1% probability levels.

Marked phenotypic variability was observed for all traits across the six environments. PH averaged 58.92 cm, ranging from 50.86 cm (T41) to 73.58 cm (T36). SL averaged 8.45 cm, varying from 3.95 cm (T45) to 9.96 cm (T23). FLA averaged 14.37 cm², with genotypic values ranging from 9.90 cm² (T48) to 19.39 cm² (T22). NS averaged 304.88 spikes m^{-2}, ranging from 182.28 spikes m^{-2} (T27) to 448.14 spikes m^{-2} (T36), and NK averaged 2992.58 kernels m^{-2}, ranging from 1134.58 kernels m^{-2} (T27) to 5323.13 kernels m^{-2} (T22). TKW showed a mean value of 27.89 g, varying from 21.88 g (T45) to 34.07 g (T1). GY averaged 83.42 g m^{-2}, ranging from 31.97 g m^{-2} (T27) to 154.08 g m^{-2} (T22), while BIO averaged 592.89 g m^{-2}, varying between 313.57 g m^{-2} (T27) and 889.88 g m^{-2} (T20). These results confirm the integrative contribution of yield components and biomass production to final grain yield under semi-arid conditions (Rabti et al. 2020; Ladoui et al. 2025). Comparison between test genotypes and local checks revealed no significant differences for most traits, though test

genotypes exhibited significantly higher TKW (27.99 g vs. 26.93 g, $P<0.05$), suggesting positive genetic progress for grain filling capacity under water-limited conditions (Fellahi et al. 2024; Ladoui et al. 2025).

Pronounced differences were recorded among the six environments for all traits (Figure 2). Environment E3 emerged as the most favorable, ranking first for seven of eight traits including PH (89.35 cm), SL (11.39 cm), FLA (28.66 cm^2), NS (505.08 spikes m^{-2}), NK (8701.44), GY (203.54 g m^{-2}), and BIO (1181.42 g m^{-2}), reflecting adequate water availability and moderate temperatures during critical growth stages (Jing et al. 2024; Wang et al. 2024). Despite this overall superiority, E3 ranked last for TKW (23.06 g), illustrating the classic compensation between grain number and weight under high sink density (Bekaddour et al. 2024). In contrast, E4 was the least productive, recording the lowest NS (135.70 spikes m^{-2}), NK (961.43 kernels m^{-2}), GY (23.11 g m^{-2}), and BIO (499.12 g m^{-2}), consistent with severe drought stress limiting spike fertility and kernel set (Rabti et al. 2020; Ladoui et al. 2025).

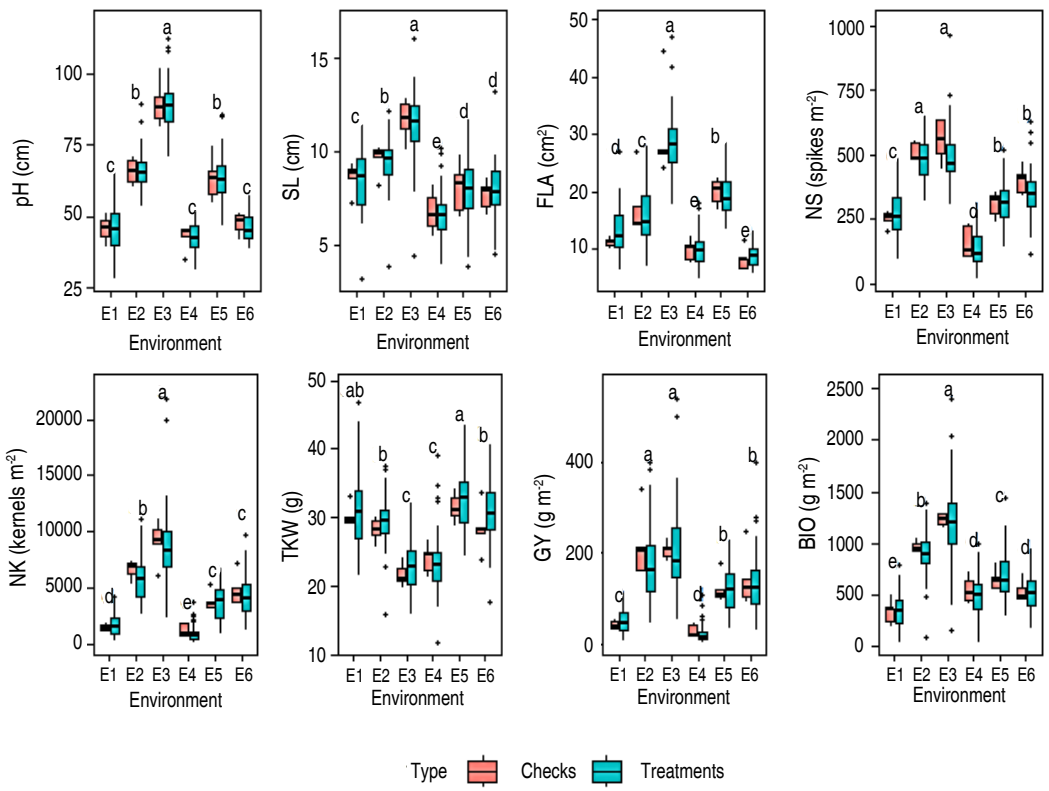


Figure 2. Comparison of environment means for agro-morphological and yield-related traits of bread wheat genotypes across six environments.

Environment E5 recorded the highest TKW (32.70 g), suggesting reduced sink competition and enhanced assimilate remobilization during the post-anthesis period (Fellahi et al. 2024). Environment E2 ranked second for most traits, showing balanced growing conditions that supported both sink formation and biomass accumulation.

Genetic and non-genetic parameters analysis

CV_g/CV_e ratios ranged from 0.34 (NS) to 0.96 (SL), and broad-sense heritability (h^2_{bs}) estimates varied from 36.59% (NS) to 79.24% (SL) (Table 3). All CV_g/CV_e ratios fell below unity, indicating predominance of environmental over genetic effects and reduced predictability of phenotypic performance across contrasting conditions

Table 3. Estimates of genetic and non-genetic parameters of eight agro-morphological bread wheat traits.

Traits	PH	SL	FLA	NS	NK	TKW	GY	BIO
CV_g/CV_e	0.46	0.96	0.39	0.34	0.46	0.63	0.48	0.58
h^2_{bs} (%)	59.99	79.24	50.91	36.59	55.18	59.06	53.19	41.74

h^2_{bs}: Broad-sense heritability, CV_g: Genotypic coefficient of variation, CV_e: Environmental coefficient of variation, PH: Plant height (cm), SL: Spike length (cm), FLA: Flag leaf area (cm^2), NS: Number of spikes per square meter, NK: Number of kernels per square meter, TKW: Thousand-kernel weight (g), GY: Grain yield (g m^{-2}), BIO: Aboveground biomass (g m^{-2}).

(Fellahi et al. 2020). SL exhibited the highest heritability (79.24%), suggesting strong genetic control and favorable prospects for selection.

PH (59.99%), FLA (50.91%), NK (55.18%), TKW (59.06%), GY (53.19%), and BIO (41.74%) showed moderate heritability, while NS (36.59%) was moderate-to-low, reflecting greater sensitivity to environmental fluctuations. These results confirm that most traits are governed by both genetic and environmental components, and that effective selection will require evaluation across diverse environments over multiple breeding cycles. Variability in heritability estimates across studies (Fellahi et al. 2020; Hossain et al. 2021; Wafa and Heakel 2023) reflect differences in environmental conditions, genetic background, experimental design, and G × E magnitude, and should therefore be interpreted within the specific context of each study rather than as fixed properties of the traits.

Phenotypic correlations under contrasting environments

Phenotypic correlations were computed separately for the most favorable (E3) and the most stressful (E4) environments to examine environment-specific trait interrelationships (Figure 3).

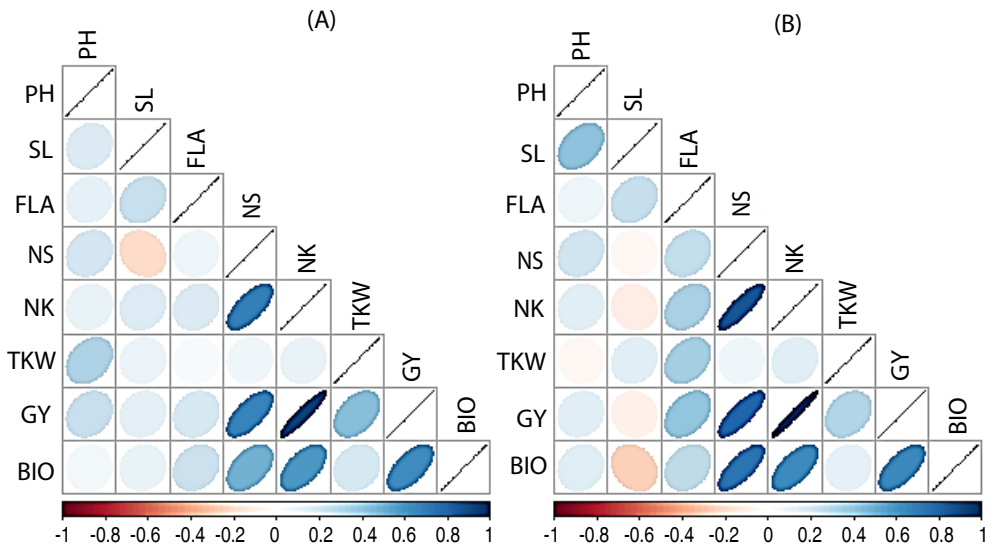


Figure 3. Phenotypic correlation matrices among agro-morphological and yield-related traits in wheat under favorable (**A**) and stressful (**B**) environments.

Under both conditions, GY was most strongly associated with NK (r = 0.921** in E3; r = 0.969** in E4), confirming kernel number as the central yield determinant regardless of growing conditions. Strong positive correlations of GY with NS and BIO were observed in both environments, reflecting the coordinated contribution of tillering capacity and biomass accumulation to yield formation (Fellahi et al. 2020; Kirouani et al. 2023).

The main difference between environments concerns the role of FLA and TKW. Under favorable conditions (E3), neither FLA nor architectural traits (PH, SL) showed

significant associations with GY, indicating that yield relied primarily on sink size and assimilate supply through a balanced source–sink framework (Zhang et al. 2025). Under stress (E4), FLA emerged as a significant contributor to GY (r = 0.395*), TKW (r = 0.331*), and NK (r = 0.329*), suggesting a compensatory role of photosynthetic surface in sustaining assimilate supply when source limitations prevail. TKW also showed a modest but significant association with GY under stress (r = 0.298*), indicating that grain filling, though constrained, still contributed modestly to yield variation. The tightening of correlations among NK, NS, and BIO under E4 further reflects coordinated drought responses of tillering, biomass, and kernel set (Fellahi et al. 2020). These findings highlight that indirect selection for NK, NS, and BIO would be effective across environments, while FLA becomes an additional relevant criterion specifically under stress conditions.

Screening wheat genotypes based on Stress Tolerance Index (STI)

STI values ranged from 0.009 to 0.786, indicating wide genetic variability in stress response (Figure 4). Twenty-seven genotypes exceeded the median STI (0.078), reflecting a substantial proportion with moderate to high tolerance. Breeding line T22 recorded the highest STI (0.786), indicating superior and stable productivity under both favorable and stressful conditions, making it the most promising candidate for stress-tolerant breeding. Lines T2 (0.485) and T23 (0.463) also showed high STI values, followed by varieties T46 (0.320) and T33 (0.292), suggesting good adaptability across contrasting environments. Treatments including breeding lines T42 (0.243) and T10 (0.238), landrace T37 (0.238), and checks C3 (0.238) and C1 (0.212) showed moderate tolerance, while T20, T14, T3, T5, T24, and T1 displayed

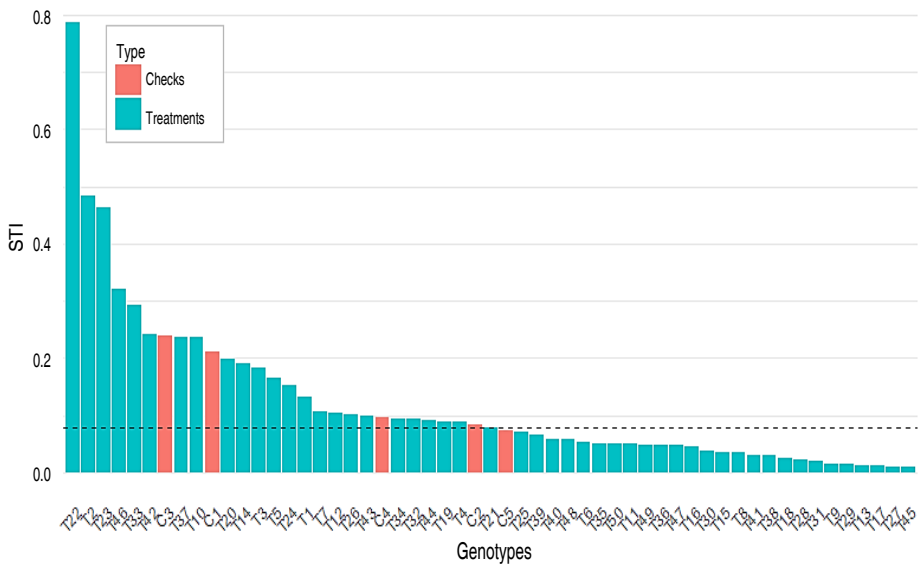


Figure 4. Stress tolerance index (STI) of bread wheat genotypes based on grain yield under favorable (E3) and stressful (E4) environments. The dash line indicates the median STI value.

lower but non-negligible values, representing potential genetic resources for future breeding efforts rather than immediate candidates for cultivar release.

Based on the Fernandez (1992) classification, genotypes were assigned to four groups (Figure 5). Group A, combining high yield under both favorable and stressful conditions, contained only T22 (STI = 0.786), confirming its exceptional combining ability for productivity and stability and making it the most promising candidate for stress-tolerant breeding. Group B, comprising genotypes with high yield under favorable but reduced performance under stress, included T46, T10, T3, and T12, representing stress-sensitive yet agronomically valuable materials under optimal management (Chirag et al. 2025).

No genotype was assigned to Group C, indicating that stress tolerance within the studied panel was largely associated with overall yield potential rather than stress-

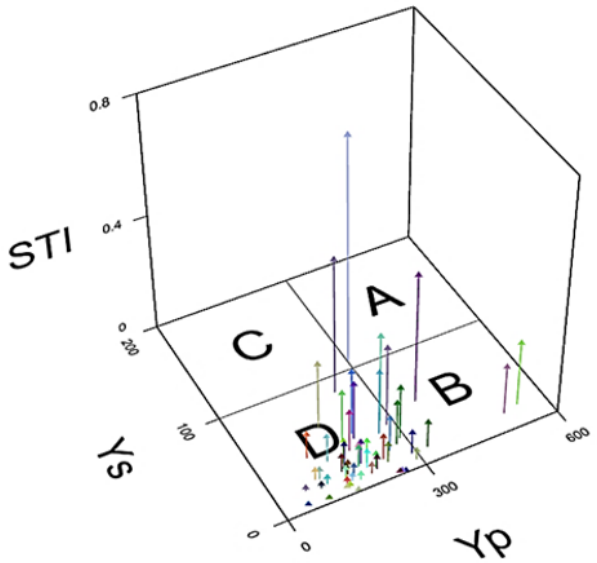


Figure 5. Three-dimensional biplot for grouping stress-tolerant and stress-susceptible bread wheat genotypes based on Y_p, Y_s and STI.

specific adaptation. The predominance of Group D genotypes, characterized by low STI values and poor performance under both conditions, suggests a generally limited adaptive capacity of the evaluated germplasm to contrasting moisture regimes, a trend commonly observed when diverse collections are screened under harsh environments (Sallam et al. 2019; Duma et al. 2022). These materials may nonetheless harbor specific traits of interest for targeted breeding purposes.

CONCLUSION

This study revealed substantial genetic variability and moderate to high heritability for most agro-morphological traits in bread wheat under semi-arid conditions, confirming meaningful prospects for genetic improvement. Kernel number, spike density, and biomass were consistently the primary yield determinants, while flag leaf area emerged as an additional relevant criterion under drought stress. STI-based screening identified T22 as the most promising genotype, combining exceptional yield potential with broad stability, followed by T2, T23, T46, and T33 as candidates for advanced breeding cycles. The predominance of low-STI genotypes underscores the need to broaden the genetic base of Algerian breeding programs through incorporation of diverse drought-tolerant germplasm. Integrating multi-environment trials with STI-based selection provides a practical framework for identifying broadly adapted genotypes, and future efforts should prioritize crossing superior lines with locally adapted cultivars to accelerate the development of climate-resilient wheat varieties for semi-arid agroecosystems.

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CONFLICT OF INTERESTS

The authors declare that there is no conflict of interest of any kind in the preparation and publication of the manuscript.

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