



Heterosis and combining ability in Algerian durum wheat (*Triticum durum* Desf.) for adaptation and production related traits. Heterose e capacidade de combinação em trigo duro argelino (*Triticum durum* Desf.) para características relacionadas à adaptação e produção.

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Abstract

Wheat landraces constitute valuable genetic resources for breeding resilient genotypes in response to environmental stress and climate variability. A Line $\times$ Tester analysis was conducted on three oasis wheat landraces that were used as testers, and two varieties of durum wheat to obtain 6 combinations (F_2) that were evaluated along with their relative parents for adaptation-related. The analysis revealed that non-additive genetic effects played a dominant role in determining the inheritance patterns of all studied traits except FLA, PH, AL, HT, ST, and HD. Correlation analysis revealed that GCA values of parental lines and testers HYB can be more effectively predicted based on GCA of parental lines in almost all traits.

Keywords: Durum wheat. Heterosis. Combining ability. Correlation analysis.

Resumo

As raças locais de trigo constituem recursos genéticos valiosos para a criação de genótipos resilientes em resposta ao estresse ambiental e à variabilidade climática. Uma análise de Linha $\times$ Testador foi conduzida em três raças locais de trigo oásis que foram usadas como testadores e duas variedades de trigo duro para obter 6 combinações (F_2) que foram avaliadas junto com seus pais relativos para adaptação relacionada. A análise revelou que os efeitos genéticos não aditivos desempenharam um papel dominante na determinação dos padrões de herança de todas as características estudadas, exceto FLA, PH, AL, HT, ST e HD. A análise de correlação revelou que os valores de GCA das linhagens parentais e testadores HYB podem ser previstos de forma mais eficaz com base na GCA das linhagens parentais em quase todas as características.

Palavras-chave: Trigo duro. Heterose. Capacidade de combinação. Análise de correlação.



Introduction

Wheat farming covers vast expanses of agricultural land in Algeria spanning approximately 1.9 million hectares, mostly in its Mediterranean region and high plateaus, coastal plains, and sublittoral plains (DSASI, 2021). However, wheat production in the region is subject to various challenges of irregular annual rainfall distribution, intermittent droughts, and urbanization (MEBERKANI, 2012). This highlights the importance of leveraging and utilizing the phylogenetic resources found in the oases of the Sahara which possess much potential in boosting wheat cultivation and production in Algeria.

The initial phase of a systematic breeding program with clearly defined objectives involves the comprehensive evaluation and selection of germplasm resources that possess variation in the traits aligned with the targeted breeding goals. The genetic variation can be sourced from landraces, cultivars, advanced lines and wild relatives (MOURAD et al., 2019). Notably, the utilization of local wheat landraces in breeding programs holds significance for developing varieties adapted to the specific agro-climatic conditions. Old-time cultivars and landraces are considered repositories of extensive genetic diversity, harboring many valuable traits. This wide range of genetic variation within these landraces is instrumental in breeding new varieties with desirable characteristics.

Systematic crossing using appropriate mating design facilitates the estimation of quantitative genetic parameters like combining ability and heterosis. For instance, the line $\times$ tester mating design involves crossing a set of inbred lines (lines) with a few widely adapted and genetically divergent testers. It is one of the genetic-statistical methodologies devised to aid in the selection of parental candidates, considering their combining capacity and ability to generate advantageous segregating populations (OKELLO et al., 2006).

Combining ability analysis is a crucial genetic tool to evaluate the performance of parental lines and their hybrid offspring. The estimates general combining ability measure a parent's capacity to transmit desirable traits to its progeny, while specific combining ability quantifies the extent to which the performance of particular hybrid combinations deviates from the expected performance. In breeding programs, this analysis directs the selection of superior parents and cross combinations (DAR et al., 2017; ALIU et al., 2008). By analyzing GCA and SCA, breeders can identify lines with good combining ability and select promising hybrid combinations that exhibit heterosis for traits of interest. Additionally, it is complementary to study the correlation coefficients among GCA, SCA and heterosis as they provide valuable insights into how the selection affects other attributes (KHALED et al., 2013).

The primary objective of this investigation is to assess the heterosis and combining ability of some the adaptation-related traits and production-related traits of wheat hybrids and their parents that were developed via crossing Algerian wheat varieties.

Material and methods

This investigation used six hybrids of durum wheat (*Triticum durum* Desf.) and their parents that were developed via a Line $\times$ Tester mating design (Table 1). The experiment was carried out during the 2022/2023 growing season at the Chaabat Erassas experimental station in the University of Constantine 1, Algeria. The experimental design employed a complete randomized block arrangement with four replications. The soil at the site exhibited a clay-loam texture, comprising 67.4% clay, 19.7% silt, 6.97% fine sand, and 5.81% coarse sand. Additionally, the soil had a pH of

8.16, an electrical conductivity of 813.66 $\mu\text{S}\cdot\text{cm}^{-1}$, and a total limestone content of 22.1%. Standard agronomic practices, including fertilization, weed control, and pest and disease management, were meticulously observed throughout the study, from planting to harvest.

Table 1 - Name, source and code of used landraces (Testers), and local varieties (Lines) and their corresponding hybrids.

	Code	Parent name	Source	Hybrid	Code
Testers ♂	T1	Bassa	Touggourt	Djenah khetaifa × Bassa	HD1
	T2	fritass	Touggourt	Djenah khetaifa × fritass	HD2
	T3	Bourione	Touggourt	Djenah khetaifa × Magarin	HD3
	T4	Magarin	Touggourt	Guemgoum Rkham × Bassa	HD4
Lines ♀	L1	Djenah khetaifa	Tunisia	Guemgoum Rkham × fritass	HD5
	L2	Guemgoum Rkham (GGR)	Tiaret (Algeria)	Guemgoum Rkham × Magarin	HD6

Five plants from each replication were randomly chosen and data recorded for plant height (pH, cm), peduncle length (PL, cm), spike length without awns (SL, cm), awns length (AL, cm), ear density (ED, mm), number of spikelets (NS), flag leaf area (FLA, cm^2), number of herbaceous tillers (Nb HT), number of spike tillers (Nb ST), number of grains per spike (Nb G/S), spikes number per m^2 (Nb S/m^2), thousand grains weight (TGW, g), and grain yield (GY, $\text{q}\cdot\text{h}^{-1}$). Chlorophyll content was estimated using the SPAD-502 meter (Chl, SPAD), number of days to heading (DH, days).

Statistical analysis

Collected data were analyzed using RStudio 2023.09.1-494 (Posit PBC, Boston, Massachusetts, United States). The package “Agricolae” was used to conduct a $L \times T$ analysis including: ANOVA for $L \times T$ analysis with replications, treatments, parents, parents versus crosses, crosses, lines, testers, $L \times T$, GCA effects of lines and testers and SCA effects of hybrids. genetic components: General combining ability variance (σ^2_{GCA}), specific combining ability variance (σ^2_{SCA}), additive variance (σ^2_{A}), dominance variance (σ^2_{D}). Heterotic effects were assessed in relation to average performance of the two parents (mid-parent heterosis) and superior performing parent (better-parent heterosis) using the TNAU-STAT-Statistical package (MANIVANNAN, 2014).

Results and discussion

Line Tester ANOVA

ANOVA for $L \times T$ (Table 2) indicates significant differences ($p < 0.01$) among the genotypes (crosses and parents) for all the traits under investigation HT and ST, this suggests that the genetic variability introduced by these genotypes does not significantly influence the variation observed in HT and ST. In addition, these traits are likely influenced by environmental factors or other sources of variation rather than genetic differences among the genotypes.

The parental effects were found to be extremely significant for all traits excluding GY, HT and ST, indicating substantial genetic variability among the parents (lines and testers together) in

these trait. This indicates that they constitute promising breeding material, particularly for traits associated with adaptation, where notable divergence among them was observed. However, the partitioning of the parental effects revealed a significant effect of testers only for FLA, PH and AL. While the mean squares of lines were not significant for all the studied traits. This results could be explained by the fact that the variation contributed by lines and testers is not large enough to be detected as significant when considered separately. Despite this, their combined effect (as parents) is significant. In addition, it might be possible that the testers used are relatively similar or homogeneous for the traits evaluated. Furthermore, the interaction effect between lines and testers ($L \times T$) was observed to be significant only for PL, Nb S, ED, HD, TGW, Nb G.S⁻¹ and GY. This points toward the genetic interactions between lines and testers being a driving force in shaping the phenotypic characteristics of these traits. On the other hand, for traits that showed no significant effect of $L \times T$ interaction, the genetic backgrounds represented by the lines and testers do not interact to produce significant differences in the expression of these traits.

The mean squares of parents versus crosses was very significant ($p < 0.01$) for SL, AL, Nb S, ED, HD and Nb S.m⁻² indicating that the mean performance of parents is significantly different from the mean performance of the crosses for these traits. Thus, there is potential for exploiting heterosis or hybrid vigor for these traits in a breeding program. Finally, the effect of crosses was highly significant for all studied characters except for Chl, HT and ST. From this findings, we can conclude that selection among crosses may not be as effective for improving Chl, HT and ST. Although, the significance effect for other traits suggests that the performance of the crosses differs substantially from one another in term of these traits, and there is a potential to identify superior cross combinations for that trait, and therefore, selection among these crosses can be effective for improving or manipulating these traits in a breeding program.

Mean performance of parents and hybrids

The results of mean performance of parents and crosses for different measured traits are displayed in Figure 1. The best performance for of PH, Chl, FLA, ED, HD, HT, Nb S.m⁻², Nb G.S⁻¹ and GY was obtained by testers. On the other hand, lines registered the highest records for PL, SL, AL Nb S and TGW. Although, the performance of both parental lines and testers exhibited remarkably similar performance for SL and ST. This close resemblance in performance complicates the determination of unequivocal superiority between the parental lines and testers.

The evaluation of hybrid performance revealed substantial variation across the traits under study. The hybrid H_D1 recorded the highest values for PL and ST, while it obtained the lowest values of Chl, Nb S and Nb G.S⁻¹. Hybrid H_D2 exhibited the highest Nb S among the evaluated hybrids. However, its yield performance was compromised, as it recorded the lowest values for TGW and GY, all this was accompanied with the most prolonged heading period. H_D3 displayed the longest spike, highest HT, Nb G.S⁻¹ and achieved the earliest heading compared to other crosses. On the other side, it registered the shortest height and PL, it had low ED and lesser Nb S.m⁻². H_D4 displayed the highest Chl and had long stem holding the densest spikes with long awns. It also achieved the highest number of spikes per area. Yet, it registered the lowest values of FLA and had the shortest spikes. Furthermore, H_D5 displayed the largest FLA and the lowest number of ST and Nb S.m⁻². H_D6 was the highest yielding cross and performed best for TGW, it had the shortest awns and the least HT.

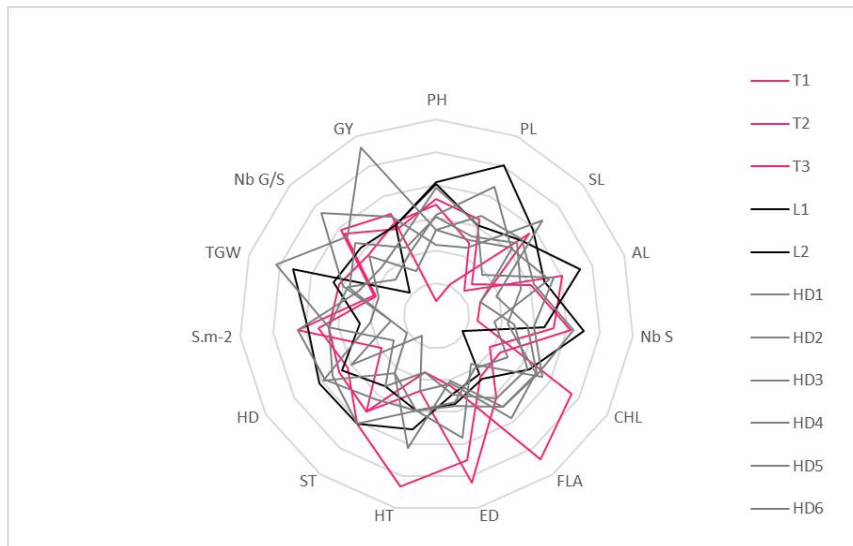


Figure 1 - comparison of performance of parents and hybrids for adaptation related and production related traits.

Heterosis

The phenomenon of heterosis describes the manifestation of superior phenotypic characteristics in hybrid individuals compared to their inbred parental lines, encompassing traits such as enhanced growth vigor, reproductive fitness, and yield potential (LIPPMAN; ZAMIR, 2007). Positive heterosis values are desirable for traits where higher values correspond to enhanced performance, such as GY, its contributing components, and Chl. Conversely, negative heterosis values are preferable for traits in which lower values indicate superior performance, including PH, HD.

The estimates of mid-parents and better-parents heterosis of durum wheat F_1 hybrids are displayed in Table 2. Significant heterosis was registered in 9 traits out of 15 studied traits. The proportion of hybrid combinations exhibiting significant heterosis varied considerably across different traits. For H_{MP} , the range spanned from 0% in Nb S, AL, ED, HT and Nb $S.m^{-2}$ to 66% in PH. When considering H_{BP} , the percentages ranged from lowest at 0% in for PL, AL, Nb S, ED, HT, ST, Nb $S.m^{-2}$ and Nb $G.S^{-1}$ to highest at 83% in PH. Consequently, PH exhibited the highest incidence of hybrids displaying significant positive heterosis amongst all the studied traits. Moreover, crosses didn't show any improvement in performance of AL, Nb S, ED, HT and Nb $S.m^{-2}$ as compared to their parents.

Crosses H_{D2} and H_{D5} showed a significant increase of Chl compared to respective mid-parent's values, however, when compared to the better-parent, only the cross H_{D2} displayed a significant enhancement in Chl. H_{MP} of FLA was significant in three crosses and amounted up to 50.31% in H_{D5} , over better parent, only H_{D4} and H_{D5} manifested significant enhancement with the observed values being very similar to their respective H_{MP} estimates. The heterosis observed for PH exhibited a greater magnitude and frequency when compared to better-parent than when compared to the mid-parent. For H_{BP} , all hybrids expressed significant heterosis except H_{D4} , the values ranged from -14.88% in H_{D5} to 28.52% H_{D3} . Heterosis of PL was only significant when compared to the mid-parent values, with the maximum increase being 10.89% 10.89 in H_{D6} . Regarding spike morphology, H_{D2} and H_{D5} showed significant increase in SL of 9.49% and 10.56% over H_{MP} , while only the H_{D6} cross exhibited significant increase of 6.96% over H_{BP} .

Table 2 - Estimates of mid-parent and better-parent heterosis in F1 hybrids of durum wheat.

		HD1	HD2	HD3	HD4	HD5	HD6
Chl	HMP %	-0.26	9.67**	3.23	7.99*	-1.87	1.37
	HBP %	-2.91	7.49*	1.18	5.11	4.59	-5.79
FLA	HMP %	-20.69*	-24.19**	35.37**	52.31**	-9.15	15.11**
	HBP %	-27.98**	-32.55**	34.02**	50.38**	-31.33**	-36.81**
PH	HMP %	-10.57*	3.01	-18.63**	-11.81*	-1.83	7.79
	HBP %	-15.07**	-1.79	-21.78**	-14.88**	-28.52**	-21.30**
PL	HMP %	9.49*	6.20	-11.88**	-5.15*	-13.65**	10.89*
	HBP%	-9.30**	0.42	-22.43**	-9.58*	-36.42**	8.99
SL	HMP%	6.10	-5.26	9.49**	10.56**	5.08	-5.31
	HBP%	-9.13*	-17.03**	-4.56	-1.40	4.18	6.96*
AL	HMP %	-1.54	-6.00	-1.76	-12.79**	-6.90	-20.13**
	HBP %	-4.59	-8.84*	-4.28	-19.49**	-18.34**	-33.51**
Nb S	HMP %	-15.05*	-3.14	-0.66	-10.27**	-0.72	0.76
	HBP %	-17.53**	-4.14	-1.95	-12.67**	-11.04**	-6.34
ED	HMP %	-21.31**	-0.04	-14.06**	-24.97**	-10.37*	2.96
	H BP %	-34.75**	-19.28**	-25.63**	-36.86**	-15.38**	0.42
HT	HMP %	9.09	0.00	-25.00	-41.18	60.00	-27.27
	HBP %	0.00	14.29	-40.00	50.00	33.33	-42.86
ST	HMP %	28.57	-17.65	-33.33	77.78**	-28.57	-29.41
	HBP %	12.15	-22.22	-44.44	-77.78*	-37.50	-33.33
HD	HMP %	1.70*	0.95*	4.83**	-3.91**	-10.64**	-9.86**
	HBP %	1.34**	-1.11*	4.31**	-6.73	-14.59**	-15.80**
Nb S/m2	HMP %	4.11	5.13	-8.11*	-18.99**	-15.79**	-6.17*
	HBP %	0.00	2.50	-12.82**	-20.00**	-21.95**	-7.32*
TGW	HMP %	-4.93**	-17.50**	-11.53**	-6.68**	4.87**	24.61**
	HBP%	-6.08**	-24.47**	-19.74**	-20.97**	4.33**	6.07**
Nb G/S	HMP %	-16.20**	4.42	-8.49	12.60*	14.52**	15.44**
	HBP %	-17.88**	-7.18	-11.97*	-4.87	9.02	-3.14
GY	HMP %	-17.03**	-8.40	25.08**	11.76	1.60	39.48**
	HBP %	-17.76*	-9.13	-25.75**	-12.63	-1.54	35.29**

The hybrid H_D6 exhibited earlier heading compared to both its respective mid-parent and better parent values. Additionally, it displayed higher TGW and a greater Nb G.S⁻¹ relative to its mid-parent values. Furthermore, this hybrid exhibited enhanced GY over both its mid-parent and better parent values, with the yield enhancement reaching 39.48% and 35.29% for H_{MP} and H_{BP}, respectively. Actually, 33% of hybrids exhibited noteworthy and desirable H_{MP} effects for GY while only 16% exhibited significant H_{BP}. 50% of hybrids showed desirable significant H_{BP} and H_{MP} for HD. The hybrid H_D3 exhibited earliness in heading time when compared to both its respective mid-parent and better parent values. Concurrently, it showcased superior performance for TGW and a greater Nb G.S⁻¹ relative to its mid-parent estimates. Furthermore, H_D5 showed significant H_{MP} for ST, HD and Nb G.S⁻¹. H_D4 also manifested substantial GY heterosis outperforming its mid-parents

value. As demonstrated by earlier research, hybrid bread and durum wheat exhibit a H_{MP} for grain yield of about 10% (GOWDA et al., 2010) and amounted up to 20% in other studied Akel et al. (2019). Hnnachi (2013) documented higher values for grain yield heterosis that reached 72% in some durum wheat crosses.

General combining ability

All traits showed significant desirable effect of GCA for at least one parent in all the studied traits except in Chl, PH, Nb S, HT and ST. Results showed that L1 exhibited significant effect of GCA for PL and SL (Table 3). L2 exhibited favorable GCA for yield-related traits $S.m^{-2}$, TGW and GY, indicating its potential as a valuable parent for improving these characteristics. For tester, T1 was good combiner for PL, AL and $S.m^{-2}$. Additionally, T2 register significant effect for FLA only, suggesting its potential as a promising parental genotype for improving FLA. T3 was the only good combiner for HD, in addition it showed positive significant values of GCA for TGW, Gr, GY.

Table 3 - GCA effects of parents in durum wheat.

	L1	L2	T1	T2	T3
Chl	-0.26	0.26	-0.42	0.38	0.04
FLA	0.14	-0.14	-9.33**	6.35**	2.98
PH	-5.46	5.46	11.36*	-1.43	9.94*
PL	1.58*	-1.58*	3.76**	-0.19	-3.57**
SL	0.39**	-0.39**	-0.66**	0.19	0.48**
AL	0.21	-0.21	1.51**	0.25	-1.76**
Nb S	0.33	-0.33	-0.56	0.78	-0.22
ED	-0.10	0.10	0.44**	-0.14	-0.30**
HT	0.14	-0.14	0.03	-0.06	0.03
ST	0.11	-0.11	0.39	-0.36	-0.03
HD	0.36	-0.36	8.19**	5.75**	-14.14**
$S.m^{-2}$	-7.20*	7.20*	22.63**	-17.49**	-5.14
TGW	-3.34**	3.34**	-2.59**	-5.24**	7.83**
Gr	-0.08	0.08	-5.42**	-0.09	5.51**
GY	-4.83**	4.83**	-4.60**	-8.02**	12.62**

The identification of parental lines and testers exhibiting good general combining ability can help recognize potential donors for favorable alleles or genes that contribute to the expression of desirable traits. By leveraging these superior combiners in breeding programs, breeders can enhance the probability of obtaining progeny with the desired trait.

Specific combining ability

SCA is associated with the non-additive genetic effects (including dominance and epistatic interactions) in a specific hybrid (AKTER et al., 2010; ELMYHUN et al., 2020). It represents the deviation of a hybrid's performance from what would be expected based on GCA of its parents. The results of SCA are shown in Table 4. Significant and desirable effect of SCA were registered in all

traits except Chl, PH, Nb S, ED, HT, ST. This suggests that non-additive gene interactions, such as dominance and epistasis, do not play a substantial role in the expression of these traits in the hybrid combinations evaluated. These traits might be primarily governed by additive gene action, where the performance of the hybrid can be predicted based on the average performance of the parents. Significant and positive SCA effects for PL were registered in two crosses H_D1 and H_D4. H_D4 and H_D2 expressed significant SCA for SPK and ED. For HD, three crosses registered significant negative SCA namely: H_D1, H_D4 and H_D3. These crosses provide valuable genetic resources and opportunities for breeding programs aimed at developing cultivars with optimized heading time. Yield components showed significant desirable effect in H_D3 for S.m⁻², H_D1 and H_D5 for TGW, H_D5 for GY.

Table 4 - SCA effects of hybrids in durum wheat.

	HD1	HD2	HD3	HD4	HD5	HD6	SE
Chl	-0.89	0.89	0.32	-0.32	0.57	-0.57	0.82
FLA	0.65	-0.65	-2.03	2.02	1.38	-1.38	2.76
PH	-2.64	2.64	1.44	-1.44	1.20	-1.20	5.55
PL	2.01*	-2.01*	0.31	-0.31	-2.33*	2.33*	0.87
SL	0.14	0.14	-0.31	0.31	0.17	-0.17	0.19
AL	-0.33	0.33	0.12	-0.12	0.21	-0.214	0.36
SPK	-1.33*	1.33*	1.33*	-1.33*	-0.00	0.00	0.54
ED	-0.30*	0.30*	0.36**	-0.36**	-0.0	0.06	0.11
HT	-0.14	0.14	-0.06	0.06	0.19	-0.19	0.25
ST	0.06	-0.06	0.14	-0.14	-0.19	0.19	0.31
HD	-1.60**	1.60**	4.06**	-4.06**	-2.46**	2.46**	0.46
S.m-2	-2.06	2.06	13.37*	-13.37*	-11.32	11.32	5.40
TGW	4.79**	-4.76**	-0.13	0.13	-4.66**	4.66**	0.76
Gr	-1.29	1.29	-1.43	1.43	2.72*	2.72	0.86
GY	2.75	-2.75	1.69	-1.69	-4.44**	4.44**	1.51

Genetic components of the total variance

σ^2_{SCA} was higher than σ^2_{GCA} in all studied traits except in FLA, PH, AL, HT, ST and HD (Table 5), This suggests that a substantial portion of the total genetic variation for the trait is attributable to non-additive gene interactions, similar findings in durum wheat were verified by Gorjanovic et al. (2007). These results are substantiated by the ratio $\sigma^2_{GCA}/\sigma^2_{SCA}$ that were lower than unit in these traits, in addition to the value of σ^2_D that was higher than σ^2_A for the same traits for PH.

Correlation analysis

To optimize hybrid breeding programs, it is essential to understand the correlation between the performance of individual lines and their hybrids, as well as the relationship between GCA effects and the performance of individual lines (LONGIN et al., 2013). Studies of association

between different genetic parameters like heterosis, combining ability, the sum of combining abilities, and hybrid performance and *per se* of parents have been studied in crop plants like wheat, barely and rice hybrids by many researchers (GOWDA et al., 2010; FELLAHI, 2013; HANNACHI, 2013; LONGIN et al., 2013; ZHANG et al., 2015; GRAMAJE et al., 2020; BIRADAR et al., 2020).

Table 5 - Estimates of genetic components of the total variance for the studied traits in durum wheat.

	σ^2_{GCA}	σ^2_{SCA}	σ^2_A	σ^2_D	$\sigma^2_{GCA}/\sigma^2_{SCA}$	σ^2_A/σ^2_D
Chl	-0.12	0.54	-0.50	2.19	-0.22	-0.23
FLA	12.05	1.19	48.23	-4.76	10.13	-10.13
PH	28.90	-20.45	115.62	-81.83	-1.41	-1.41
PL	1.90	8.81	7.61	35.25	0.22	0.22
SL	0.09	0.10	0.36	0.41	0.90	0.88
AL	0.50	0.03	2.03	0.14	16.67	14.50
SPK	-0.38	3.25	-1.53	13.02	-0.12	-0.12
ED	-0.0008	0.21	-0.003	0.84	0.00	0.00
HT	-0.002	-0.005	-0.01	-0.02	0.40	0.50
ST	0.02	-0.03	0.08	-0.15	-0.67	-0.53
HD	25.35	24.89	101.40	99.59	1.02	1.02
S.m-2	50.81	281.94	203.27	1127.77	0.18	0.18
TGW	5.89	44.13	23.58	176.52	0.13	0.13
Gr	4.09	10.37	16.39	41.51	0.39	0.39
GY	25.64	27.90	102.56	111.61	0.92	0.92

Simple linear correlation coefficients were utilized to elucidate the relationships among HYB, H_{MP} , H_{BP} , SCA, GCA, GSCA, *per se* (Table 6). HYB performance showed significant positive correlation with H_{MP} in some traits: FLA, HT, HD, Nb S.m⁻² and TGW. Positive correlations were also observed with H_{BP} for PH, AL, Nb S, ST, HD, Nb S.m⁻², Nb G.S⁻¹ and GY. The positive correlation between HYB and heterosis levels suggests that selecting for hybrids with superior trait expression (higher values) is likely to result in a greater manifestation of hybrid vigor or heterotic advantage over the parental lines for the corresponding trait. these findings have important implications for hybrid breeding programs by allowing for more efficient selection of promising cross combinations based on hybrid performance data.

HYB was positively and significantly correlated with SCA in two traits: Chl and Nb S, these results differ from those of Hannachi (2013) who registered higher correlations coefficients with HYB for yield and yield related traits in durum wheat crosses. the absence of correlation between HYB and SCA suggests that while SCA provides valuable insights into specific genetic interactions between parent lines, it does not fully explain or predict hybrid performance in the studied durum wheat crosses. Understanding this can guide more nuanced breeding strategies that take into account the complex genetic architecture underlying desirable traits in hybrids. On the other hand, HYB correlation with GSCA was marked in FLA, PL, SL, AL, ST, HD, Nb S.m⁻², TGW, Nb G.S⁻¹ and GY. This means that hybrids produced from parents with higher GCA values are more likely to exhibit superior performance compared to hybrids produced from parents with lower GCA values. It also indicates that a significant portion of the hybrid's trait expression is influenced by the additive gene effects contributed by the parents. Similar findings were obtained by Yu et al. (2020).

the association estimates were stronger than those of HYB/H_{MP} and HYB/H_{BP}. Consequently, the GCA of parental lines appeared to be a more reliable predictor of hybrid performance across the evaluated traits and genetic backgrounds.

Table 6 - Association between HYB, *per se*, heterosis, and combining ability in durum wheat.

	HYB VS HMP	HYB VS HBP	HYB VS SCA	HYB VS GSCA	SCA VS HMP	SCA VS HBP	SGCA VS HMP	SGCA VS HBP	<i>Per se</i> VS GCA
Chl	0.542	0.717	0.835	0.550	0.341	0.778	0.470	0.123	-0.181
FLA	0.836	0.640	0.212	0.977	0.011	0.139	0.853	0.625	0.063
PH	0.133	0.999	0.178	0.489	0.141	0.177	0.907	0.507	-0.545
PL	0.390	0.134	0.468	0.884	0.578	0.522	0.137	-0.122	0.489
SL	0.582	0.753	-0.059	0.944	0.151	-0.210	0.464	0.744	0.555
AL	0.762	0.890	0.174	0.985	0.289	0.252	0.723	0.859	0.722
Nb S	0.655	0.841	0.861	0.516	0.755	0.923	0.018	0.101	0.477
ED	0.443	0.030	0.601	0.771	0.671	0.489	0.032	-0.339	0.632
HT	0.876	0.408	0.680	0.717	0.511	0.748	0.718	-0.144	-0.486
ST	-0.348	0.989	0.405	0.917	-0.376	0.333	-0.214	0.938	-0.514
HD	0.971	0.957	0.276	0.961	0.357	0.285	0.908	0.914	0.700
Nb S.m-2	0.924	0.964	0.487	0.873	0.463	0.472	0.800	0.841	0.022
TGW	0.927	0.733	0.508	0.862	0.483	0.337	0.791	0.651	0.076
Nb G.S-1	0.811	0.939	0.765	0.918	0.958	0.859	0.716	0.766	0.340
GY	0.538	0.998	0.296	0.955	0.455	0.316	0.422	0.947	0.826

Values in bold indicate significant at level $\alpha=0.05$

SCA exhibited a limited number of significant correlations with measures of heterosis for the evaluated traits, it was positively correlated with H_{MP} in Nb G.S⁻¹, and with H_{BP} Nb S and Nb G.S⁻¹, indicating they operate somewhat independently in the genetic expression of hybrid vigor. On the other hand, GSCA was correlated with H_{MP} in FLA, PH and HD, and with H_{BP} in AL, ST, Nb S.m⁻², this suggests that GCA values can serve as indicators of hybrid performance potential.

Finally, the *per se* was unexpectedly not correlated with the GCA of parents, which confirms that the phenotypic performance of parents for the studied traits does not necessarily reflect their GCA values as parents with high or low phenotypic performance may not necessarily have correspondingly high or low GCA values. These results are contradictory to those of Zhang et al. (2015).

Conclusion

The study revealed significant heterotic effects for the majority of traits evaluated, with particularly pronounced manifestations in PH, TGW, and GY. Notably, PH exhibited the highest frequency of hybrids displaying significant positive heterosis among all traits studied. This finding suggests that these hybrid combinations offer considerable potential for the improvement of durum wheat architecture and stature in durum wheat breeding programs. Moreover, the investigation elucidated the predominance of non-additive genetic effects in the inheritance of the majority of

traits under study. However, FLA, PH, AL, HT, ST, and HD exhibited a preponderance of additive genetic control. These findings provide critical insights into the genetic architecture underlying key agronomic traits, thereby informing future breeding strategies for their improvement. Correlation analysis indicted that superior hybrid values are indicative of greater heterotic effects, thereby providing a potential predictive tool for estimating hybrid vigor. The correlation analysis further revealed that HYB can be more effectively predicted based on GCA of both parental lines, rather than SCA of the hybrids themselves. This finding underscores the paramount importance of parental GCA in determining offspring performance and suggests that careful selection of parental lines with high GCA values may be a more efficient strategy for developing high-performing hybrids than focusing solely on SCA effects.

Conflicts of interest

There was no conflict of interest of the authors.

Authors' contribution

Boulacel Mouad – original idea, direction, evaluation; Hadji Toka – study performing, data collection, editing, data analysis, corrections and text review; Ghennai Awatef – data collection, text editing and text review; Souilah Nabila – review.

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