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GENETIC ANALYSIS FOR GRAIN YIELD AND YIELD RELATED TRAITS IN BREAD WHEAT (*TRITICUM AESTIVUM* L.)

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Abstract

Understanding the genetic basis and evolutionary history of drought-tolerant wheat genotypes was the principal aim of this investigation. Twenty-seven wheat genotypes were assessed under normal and drought conditions using a Randomized Complete Block Design (RCBD). Line × Tester analysis was employed to study combining ability, heritability and gene action in a plot size of 12.3 m². The experiment comprised four replications, two under normal irrigation and two under drought stress. Drought-tolerant genotypes Fareed-06, Ghazi-19, Sadiq-21, Bwp-79, Nishan-21 and Jauhar-16 were used as lines while three drought-susceptible genotypes (181601, NR-535 and NR-179) served as testers. Eighteen F_1 crosses were developed from these nine genotypes. Analysis of variance revealed statistically significant differences among crosses and genotypes for all parameters examined in both environments. Under normal conditions, significant differences were detected among lines for plant height, grains spike⁻¹ and biological yield plant⁻¹. Under water stress, significance was confined to grains spike⁻¹. Fareed-06 demonstrated maximum General Combining Ability (GCA) for tillers plant⁻¹, biological yield plant⁻¹ and grain yield plant⁻¹ in both environments. Cross combinations Jauhar-16 × 181601 and Bwp-79 × NR-535 proved superior in both conditions. Non-additive gene action was predominant for all traits except grains spike⁻¹ under both environments. Plant height, flag leaf area, tillers plant⁻¹, grains spike⁻¹ and biological yield plant⁻¹ exhibited high broad-sense heritability (h²). Genotypes Fareed-06 and 181601, together with crosses Jauhar-16 × 181601 and Bwp-79 × NR-535, are recommended for future drought-tolerance wheat breeding programs.

Keywords: *Bread wheat, Cmbining ability, Drought stress, Gene action, Heritability, Line × Tester analysis, Triticum aestivum*

INTRODUCTION

The cultivation of wheat dates historically to the delta of the Nile and the Fertile Crescent, from where it has spread across the globe (1). Wheat is an indispensable component of numerous breakfast cereals and bakery products. Its nutritional value, consumption, production potential and storability render it a cereal of unparalleled global importance (2). Wheat is particularly rich in dietary fibre, protein and carbohydrates, and contributes as the principal dietary calorie source for approximately 40% of mankind (3).

In Pakistan, wheat occupies a position of central dietary and economic significance. During 2022–23, 9,043,000 hectares were planted to wheat an increase of 0.7% from the preceding year's 8,977,000 hectares. Wheat contributes 1.9% to the national GDP and accounts for 8.2% of the value added in the agricultural sector. Total production reached 27.634 million tonnes in 2022–23 compared with 26.208 million tonnes in the previous year, representing an increase of approximately 5.4% (4).

Pakistan's population has surpassed 220 million and continues to grow, creating an ever-increasing demand for wheat. Concurrently, roughly 900,000 hectares of cultivated land are affected by recurrent drought. Drought, compounded by elevated temperatures during reproductive stages, induces premature maturity, grain shrivelling and leaf senescence, and causing sharp reductions in grain yield. Approximately

75% of total Pakistani wheat is cultivated in the Punjab province, of which 90% is grown under irrigated and 10% under rainfed conditions (5, 6).

Wheat breeders are thus challenged to develop cultivars that maximise productivity under both irrigated and water-deficit environments. Among mating designs employed to assess parental combining ability, the Line × Tester (L × T) design proposed by Kempthorne (1957) is particularly advantageous as it accommodates a relatively large number of parents in a complete set of crosses while minimising sampling error (7, 8). Combining ability analysis permits identification of superior parents based on progeny performance and quantifies the relative contributions of additive and non-additive gene action (9-11).

Heritability measures the proportion of phenotypic variance attributable to genotypic differences and serves as a predictor of the reliability of selection. High heritability facilitates the choice of parents and crosses for subsequent breeding cycles (12). The present study, therefore, deployed an L × T design with six drought-tolerant lines and three drought-susceptible testers to identify superior parents and F_1 crosses based on yield-related traits; to estimate combining ability effects (GCA and SCA), gene action, heritability and variance components; and to recommend breeding strategies for exploiting heterosis under drought-stress conditions.

MATERIALS AND METHODS

EXPERIMENTAL SITE AND GENETIC MATERIAL

The study was conducted at the experimental farm of the Department of Plant Breeding and Genetics, Faculty of Agriculture and Environment, The Islamia University of Bahawalpur, Pakistan, during 2022–24. The experimental material comprised nine wheat genotypes procured from the Regional Agricultural Research Institute (RARI), Bahawalpur. Six drought-tolerant genotypes (Fareed-06, Ghazi-19, Sadiq-21, Bwp-79, Nishan-21 and Jauhar-16) were designated as lines (females) and three drought-susceptible genotypes (181601, NR-535 and NR-179) were designated as testers (males), as detailed in Table I.

Table I. List of nine wheat genotypes used in Line × Tester mating design

Sr. No.	Code	Line/Tester	Genotype
1	G-1	L1 (Line)	Fareed-06
2	G-2	L2 (Line)	Ghazi-19
3	G-3	L3 (Line)	Sadiq-21
4	G-4	L4 (Line)	Bwp-79
5	G-5	L5 (Line)	Nishan-21
6	G-6	L6 (Line)	Jauhar-16
7	G-7	T1 (Tester)	181601
8	G-8	T2 (Tester)	NR-535
9	G-9	T3 (Tester)	NR-179

L = Line (female parent); T = Tester (male parent)

DEVELOPMENT OF F_1 CROSSES

Eighteen F_1 crosses were generated during 2022–23 through emasculation of the six female parents (lines) followed by controlled pollination with the three male parents (testers) in an L × T fashion. Emasculation was performed at the boot stage to prevent self-pollination. All 18 cross combinations plus the nine parental lines were evaluated as F_0 seed in the 2023–24 cropping season.

EXPERIMENTAL DESIGN AND CULTURAL PRACTICES

Both normal and water-deficit experiments were laid out in a Randomized Complete Block Design (RCBD) with four replications (two per environment) in a plot size of 12.3 m^2. Seeds were sown by the dibbling method with an intra-row spacing of 6 cm and row-to-row spacing of 30 cm. Under normal conditions, four irrigations were applied at critical crop growth stages, whereas the drought-stress block received only two irrigations. All other agronomic practices (fertilisation, weed management) were kept uniform and optimal across both environments.

TRAITS RECORDED

Data were recorded on eleven quantitative traits: plant height (cm), flag leaf area (cm^2), tillers $plant^{-1}$, spikelets $spike^{-1}$, spike length (cm), spike density, grains $spike^{-1}$, thousand-grain weight (g), biological yield $plant^{-1}$ (g), grain yield $plant^{-1}$ (g) and harvest index (%).

STATISTICAL ANALYSIS

Analysis of variance (ANOVA) was computed following Steel *et al.*, (1997) (13). Characters exhibiting significant variation were subjected to Line × Tester analysis as described by Kempthorne (1957) (7). General Combining Ability (GCA) effects for lines and testers and Specific Combining Ability (SCA) effects for all cross combinations were estimated using standard formulae. Genetic variance components (σ^2GCA and σ^2SCA) were calculated from the expected mean squares, and their ratio (σ^2GCA/σ^2SCA) was used to infer the prevailing mode of gene action: values > 1 indicate additive, values < 1 indicate dominance, and equality indicates epistasis. Broad-sense heritability (h^2) was also estimated for all traits in both environments.

RESULTS AND DISCUSSION

ANALYSIS OF VARIANCE

The mean squares from ANOVA were significant for nearly all traits in both environments, indicating adequate genetic diversity among the genotypes studied. Parental variation was significant for all traits except flag leaf area, thousand-grain weight and harvest index under normal conditions. Under water-deficit stress, significant parental variation was detected for all traits except flag leaf area, spikelets $spike^{-1}$, spike density and thousand-grain weight.

Variance due to parent vs. cross contrast was significant for all traits under normal conditions except flag leaf area and thousand-grain weight, indicating meaningful heterosis in most crosses. Line × Tester interaction was significant for all parameters under both environments, excluding flag leaf area, spike length, spike density and thousand-grain weight under normal conditions, and thousand-grain weight under drought. These results are consistent with earlier reports by Singh *et al.*, (2014) and Salman *et al.*, (2014), confirming that substantial genetic variation exists in these materials for exploitation in drought-tolerance breeding (14, 15).

Table II. Analysis of variance using L × T for various wheat characteristics in a normal environment

	PH	FLA	TP	SS	SL	SD	GS	TGW	BYP	GYP	HI
Genotypes	94.55**	28.21ns	229.86**	11.89**	7.51**	0.13**	249.55**	10.88ns	6.77**	0.59**	619.81**
Parents	103.43**	0.55ns	450.18**	24.68**	7.13**	0.21**	490.51**	15.72ns	6.39*	0.68*	35.72
P. vs C	49.34**	4.09ns	448.15**	15.56**	70.08**	0.46**	1776.3**	3.37ns	26.97**	2.98**	298.18**
Crosses	93.03**	42.65ns	113.35**	5.66ns	4.01**	0.08ns	46.35**	9.05ns	5.77**	0.41**	913.59**
Lines	132.36ns	47.12ns	21.78ns	3.92ns	5.98ns	0.05ns	38.64ns	2.66ns	3.98ns	0.45ns	699.41ns
Testers	12.44ns	24.26ns	108.53ns	6.75ns	4.08ns	0.09ns	33.36ns	13.37ns	1.82ns	0.06ns	523.27ns
L x T	89.48**	44.10ns	160.09**	6.32*	3.02ns	0.09ns	52.79*	11.38ns	7.45**	0.47**	1098.74*

MEAN PERFORMANCE OF PARENTS AND F_1 CROSSES

In the normal environment, mean plant height among parents ranged from 88 cm (NR-179) to 109 cm (Jauhar-16), while under drought the range was 86.5–108.5 cm. Among F_1 crosses, plant height varied from 91.5 cm (Fareed-06 × 181601) to 117.5 cm (Jauhar-16 × NR-535) under normal conditions. Wheat breeders typically prefer semi-dwarf cultivars in lodging-prone environments and taller types where water stress is prevalent (16).

Flag leaf area, an important determinant of post-anthesis photosynthesis and grain filling, ranged from 3.60 cm^2 (NR-535) to 4.97 cm^2 (Nishan-21) among parents under irrigation. Tillers $plant^{-1}$ is strongly associated with yield potential, with parental means ranging from 29 to 75 under normal conditions, and from 38 (181601) to 68 (Jauhar-16) under drought.

Grains spike^{-1} is a direct yield component. Parental values ranged from 20.5 to 72.5 under irrigation and from 35 to 59 under drought. Grain yield plant^{-1} ranged from 1.44 g (Bwp-79) to 3.35 g (Jauhar-16) among parents under irrigation, and from 1.55 g (Ghazi-19) to 3.30 g (Nishan-21) under drought stress. Overall, lines Ghazi-19 and Fareed-06 together with tester NR-535 performed consistently well in both environments, as did the crosses Jauhar-16 × NR-535, Sadiq-21 × NR-535 and Fareed-06 × NR-535.

GENERAL COMBINING ABILITY (GCA) EFFECTS

GCA effects quantify the average performance of a parent across all its hybrid combinations relative to the general mean, reflecting primarily additive gene action. Among lines, Fareed-06 exhibited the maximum GCA for the greatest number of traits—including tillers plant^{-1}, biological yield plant^{-1} and grain yield plant^{-1}—in both environments, establishing it as the most versatile general combiner in this study. Jauhar-16 demonstrated consistently positive and significant GCA for spikelets spike^{-1} and spike length under both conditions, while Ghazi-19 showed desirable GCA for plant height and spikelets spike^{-1}. These findings corroborate those of Majeed *et al.,* (2011) and Srivastava *et al.,* (2012) (17, 18).

Among testers, NR-179 showed significant GCA for grains spike^{-1} under both environments, and NR-535 performed as a good general combiner for grain yield plant^{-1} in both conditions. Parents exhibiting high GCA provide an additive genetic foundation and are candidates for recurrent selection schemes or use as parents in further hybridisation programs (19).

SPECIFIC COMBINING ABILITY (SCA) EFFECTS

SCA quantifies deviations of a specific cross from the performance predicted by the GCA of its parents, capturing non-additive (dominance and epistatic) gene effects. Among the 18 F_1 crosses evaluated, Jauhar-16 × 181601 recorded the highest positive SCA for thousand-grain weight (3.76) under normal conditions. For grain yield plant^{-1}, the two best crosses under normal conditions were Bwp-79 × NR-179 and Nishan-21 × 181601, whereas under drought the best crosses were Sadiq-21 × NR-535, Bwp-79 × NR-179 and Jauhar-16 × NR-535.

The cross Jauhar-16 × NR-535 emerged as the most consistent specific combiner, excelling across numerous traits in both environments; it is therefore recommended for immediate advancement in drought-tolerance breeding pipelines. These results are in agreement with Fellahi *et al.,* (2013) and Bibi *et al.,* (2013), who identified similar high-SCA cross combinations for yield traits in bread wheat under water-limited environments (20, 21).

Table III. General combining ability of parents in a normal environment

Parents	PH	FLA	TP	SS	SL	SD	GS	TGW	BYP	GYP	HI
Fareed-06	-5.13**	-1.99ns	-0.61ns	1.08*	1.25**	-0.08ns	1.61**	-0.99ns	-0.73**	-0.19**	-0.34ns
Ghazi-19	3.69**	-1.39ns	-0.94ns	0.25ns	0.08ns	0.01ns	3.44**	0.17ns	-0.12*	0.21**	21.62**
Sadiq-21	4.36**	-1.17ns	1.72ns	-0.75*	-1.41**	0.16*	-2.22**	0.03ns	-1.06**	-0.43**	-4.43*
Bwp-79	-4.13**	-1.06ns	0.55ns	-0.58ns	-0.08ns	-0.04ns	-3.22**	0.45ns	0.23*	0.01ns	-5.09*
Nishan-21	-3.47**	5.55**	-2.94*	-0.75*	-0.75*	0.03ns	-0.88*	0.85ns	0.57**	0.11*	-6.30**
Jauhar-16	4.69**	0.08ns	2.22*	0.75*	0.91*	-0.07ns	1.27*	-0.51ns	1.11**	0.29**	-5.44*
181601	-0.88*	-0.90ns	-1.77ns	0.75*	0.58**	-0.03*	-1.63**	0.99ns	-0.25**	0.01ns	-1.74ns
NR-535	1.11*	1.63*	3.47ns	-0.75*	0.00ns	-0.06*	-0.05ns	0.10ns	0.44**	0.06*	-5.55**
NR-179	-0.22ns	-0.73ns	-1.69ns	0.00ns	-0.58**	0.09*	1.69**	-1.10*	-0.19**	-0.07*	7.30**

**= Highly significant (P≤0.01), *=Significant (P≤0.05), ns=Non-significant, PH=Plant height (cm), FLA=Flag leaf area (cm^2), TP=Tillers plant^{-1}, SS=Spikelet's spike^{-1}, SL=Spike length (cm), SD=Spike density, GS=Grains spike^{-1}, TGW=Thousand grain weight (g), BYP=Biological yield plant^{-1} (g), GYP=Grain yield plant^{-1}(g), HI=harvest index (%)

Table IV. General combining ability of parents in water deficit stress environment

Parents	PH	FLA	TP	SS	SL	SD	GS	TGW	BYP	GYP	HI
Fareed-06	-4.72**	0.64**	6.38**	1.63*	-0.72*	0.27**	-6.02**	-1.68*	1.17**	0.00ns	-4.72**
Ghazi-19	4.111**	0.07ns	3.55*	0.63ns	-0.22ns	0.08*	4.47**	-0.70ns	0.90**	0.06ns	-3.25**
Sadiq-21	5.44**	0.16ns	0.72ns	-0.69ns	1.27**	-0.24**	8.13**	-0.80ns	0.001ns	0.38**	5.64**
Bwp-79	-1.72*	-0.82**	-6.11**	-0.19ns	-0.22ns	0.01ns	-1.02*	0.23ns	-0.49**	0.03ns	2.35*
Nishan-21	-4.88**	-0.56**	1.05ns	-3.86**	-1.22**	-0.17**	-5.02**	0.84ns	-0.66**	-0.03ns	2.03*
Jauhar-16	1.77*	0.49**	-5.61**	2.47**	1.11**	0.03ns	-0.52ns	2.12*	-0.92**	-0.45**	-2.05*
181601	0.52ns	-0.17*	-1.02ns	0.80*	-0.55*	0.16**	-0.36ns	-1.19*	0.43**	0.09**	-0.89ns
NR-535	1.69**	0.38**	0.72ns	0.05ns	0.61*	-0.08*	-0.52*	0.26ns	-0.31**	0.07**	3.16ns
NR-179	-2.22**	-0.21*	0.30ns	-0.86*	-0.05ns	-0.07*	0.88*	0.93*	-0.11ns	-0.16**	-2.27ns

**=Highly significant ($P \leq 0.01$), *=Significant ($P \leq 0.05$), ns=Non-significant, PH=Plant height (cm), FLA=Flag leaf area (cm^2), TP=Tillers plant$^{-1,}$ SS=Spikelet's spike^{-1}, SL=Spike length (cm), SD=Spike density, GS=Grains spike^{-1}, TGW=Thousand grain weight (g), BYP=Biological yield plant^{-1} (g), GYP=Grain yield plant^{-1}(g), HI=harvest index (%)

Table V. Specific combining ability of crosses in a normal environment

Crosses	PH	FLA	TP	SS	SL	SD	GS	TGW	BYP	GYP	HI
Fareed-06 × 181601	-5.94**	1.52ns	3.44ns	0.25ns	0.08ns	0.03ns	-1.02ns	-2.64*	0.31*	0.39**	8.21*
Fareed-06 × NR-535	-3.94**	-1.80ns	-11.3**	1.25*	-1.33*	0.27*	3.88**	1.51ns	1.37**	0.19*	-3.78ns
Fareed-06 × NR-179	9.88**	0.28ns	7.86**	-1.50*	1.25*	-0.3**	-2.86**	1.13ns	-1.69**	-0.58**	-4.43ns
Ghazi-19 × 181601	8.22**	0.74ns	-8.72**	1.58*	-0.25ns	0.16*	-3.36**	-1.06ns	1.49**	0.18*	-24.44**
Ghazi-19 × NR-535	-3.77**	-0.41ns	8.52*	-1.41*	0.83ns	-0.22*	0.05ns	-0.11ns	1.70**	-0.16*	-29.52**
Ghazi-19 × NR-179	-4.44**	-0.33ns	0.19ns	-0.16ns	-0.58ns	0.05ns	3.30**	1.18ns	-3.20**	-0.02ns	53.96**
Sadiq-21 × 181601	-0.44ns	1.03ns	11.61**	-1.41*	0.75ns	-0.23*	0.30ns	0.32ns	-0.31*	-0.11ns	4.69ns
Sadiq-21 × NR-535	-1.44ns	-2.53ns	-4.63*	-0.41ns	-1.16*	0.14ns	-8.27**	-1.46ns	-0.35*	-0.01ns	5.64*
Sadiq-21 × NR-179	1.88*	1.50ns	-6.97*	1.83*	0.41ns	0.08ns	7.97**	1.14ns	0.67**	0.12*	-10.33**
Bwp-79 × 181601	-0.94ns	0.28ns	5.27*	-1.08ns	-0.58ns	-0.00ns	3.80**	0.21ns	-1.72**	-0.71**	2.70ns
Bwp-79 ×NR-535	0.55ns	-2.20ns	2.52ns	2.41*	2**	-0.07ns	-0.77ns	-1.35ns	-0.4*	0.08ns	7.32*
Bwp-79 × NR-179	0.38ns	1.92ns	-7.80**	-1.33*	-1.41*	0.08ns	-3.02**	1.14ns	2.13**	0.62**	-10.03**
Nishan-21 × 181601	5.88**	-5.27*	-6.72*	-0.91ns	-0.41ns	-0.03ns	3.47**	-0.59ns	0.91**	0.53**	6.74*
Nishan-21 × NR-535	0.38ns	10.76**	-0.47ns	-0.91ns	0.66ns	-0.17*	0.88ns	3.04*	-0.89**	-0.01ns	9.64*
Nishan-21 × NR-179	-6.27**	-5.49*	7.19*	1.83*	-0.25ns	0.21*	-4.36**	-2.44*	-0.02ns	-0.52**	-16.38**
Jauhar-16 × 181601	-6.77**	1.68ns	-4.88*	1.58*	0.41ns	0.07ns	-3.19**	3.76*	-0.68**	-0.29**	2.07ns
Jauhar-16 × NR-535	8.22**	-3.79*	5.36*	-0.91ns	-1*	0.05ns	4.22**	-1.60ns	-1.42**	-0.09ns	10.69**
Jauhar-16 × NR-179	-1.44ns	2.11ns	-0.47ns	-0.66ns	0.58ns	-0.13ns	-1.02ns	-2.15ns	2.11**	0.38**	-12.76

**= Highly significant ($P \leq 0.01$), *=Significant ($P \leq 0.05$), ns=Non-significant, PH=Plant height (cm), FLA=Flag leaf area (cm^2), TP=Tillers plant^{-1}, SS=Spikelet's spike^{-1}, SL=Spike length (cm), SD=Spike density, GS=Grains spike^{-1}, TGW=Thousand grain weight (g), BYP=Biological yield plant^{-1} (g), GYP=Grain yield plant^{-1}(g), HI=harvest index (%)

GENE ACTION AND VARIANCE COMPONENTS

The ratio σ^2GCA/σ^2SCA was less than unity for all traits except grains spike^{-1} under both environments, demonstrating the predominance of non-additive (dominance) gene action in the expression of most yield-related traits. This is consistent with earlier findings by Srivastava *et al.*, (2012) and contrasts with the equal additive–dominance contribution reported by Riaz and Chowdhry (2007) for yield components under drought (18, 22). These results are further corroborated by Ingle et al. (2018), who used a 5-line × 8-tester L × T scheme in bread wheat and similarly documented a σ^2GCA/σ^2SCA ratio less than unity for grain yield and associated traits, concluding that non-additive gene effects were the predominant driving force across yield components. Comparable dominance effects were also reported by Fellahi *et al.*, (2013) under rainfed conditions in Algeria and by Bibi *et al.*, (2013) under moisture-stress in Pakistan, both employing the L × T design in bread wheat, providing strong multi-environment support for the conclusion that hybrid breeding rather than pure-line selection is the more effective exploitation strategy for yield improvement under drought.

The proportional contribution analysis revealed that female (line) parents were comparatively more influential than male (tester) parents for traits such as plant height, spike length, spike density, grains spike^{-1}, thousand-grain weight, grain yield plant^{-1}, biological yield plant^{-1} and harvest index in both environments, confirming a predominant maternal influence on these characters. Where non-additive gene effects predominate, exploitation through heterosis breeding rather than pure-line selection is more appropriate (23, 24).

Table VI. Specific combining ability of crosses in water deficit stress environment

	PH	FLA	TP	SS	SL	SD	GS	TGW	BYP	GYP	HI
Fareed-06 × 181601	0.63ns	0.10ns	-0.13ns	2.02*	-0.77ns	0.37**	0.52ns	-0.55ns	-0.12ns	0.32**	4.54**
Fareed-06 × NR-535	-0.52ns	0.50*	-2.38ns	0.77ns	0.05ns	0.005ns	1.19*	0.57ns	0.67**	-0.70**	-11.88**
Fareed-06 × NR-179	-0.11ns	-0.60**	2.52ns	-2.80*	0.72ns	-0.38**	-1.72*	-0.01ns	-0.55**	0.38**	7.33**
Ghazi-19 × 181601	-4.69**	1.06**	4.69*	0.02ns	0.22ns	-0.05ns	4.02**	0.01ns	0.01ns	-0.04ns	-0.02ns
Ghazi-19 × NR-535	1.63ns	-0.33*	-1.55ns	-1.22ns	0.05ns	-0.11ns	0.19ns	0.47ns	0.19ns	-0.12*	-3.41*
Ghazi-19 × NR-179	3.05*	-0.72**	-3.13ns	1.19ns	-0.27ns	0.16*	-4.22**	-0.48ns	-0.20ns	0.16*	3.43*
Sadiq-21 × 181601	1.97*	0.04ns	4.52*	-0.13ns	0.72ns	-0.12ns	-3.13**	1.66ns	1.10**	-0.15*	-7.15**
Sadiq-21 × NR-535	5.80**	0.50*	0.27ns	3.11**	0.55ns	0.17*	7.52**	0.49ns	-0.35*	0.75**	12.98**
Sadiq-21 × NR-179	-7.77**	-0.55*	-4.80*	-2.97**	-1.27*	-0.05ns	-4.38**	-2.16*	-0.75**	-0.60**	-5.82**
Bwp-79 × 181601	-2.86*	0.17ns	4.86*	2.36*	0.22ns	0.15*	8.52**	-0.58ns	0.50**	-0.08ns	-2.03ns
Bwp-79 ×NR-535	-5.52**	-0.56*	-7.88**	-3.38**	-2.44**	0.06ns	-4.80**	0.54ns	-0.50**	-0.69**	-9.06**
Bwp-79 × NR-179	8.38**	0.38*	3.02ns	1.02ns	2.22**	-0.21*	-3.72**	0.04ns	-0.001ns	0.70**	11.10**
Nishan-21 × 181601	5.30**	0.08ns	-7.30**	-0.47ns	0.22ns	-0.09ns	1.02ns	-0.97ns	-0.46*	0.05ns	3.47*
Nishan-21 × NR-535	-2.36*	-1.03**	4.44*	-0.22ns	0.55ns	-0.07ns	-11.8**	-0.61ns	0.37ns	0.37**	3.52*
Nishan-21 × NR-179	-2.94*	0.94**	2.86ns	0.69ns	-0.77ns	0.16*	10.77**	1.58ns	0.09ns	-0.43**	-6.99**
Jauhar-16 × 181601	-0.36ns	-1.47**	-6.63*	-3.80**	-0.61ns	-0.25*	-10.9**	0.43ns	-1.02**	-0.17*	1.19ns
Jauhar-16 × NR-535	0.97ns	0.92**	7.11**	0.94ns	1.22*	-0.06ns	7.69**	-1.47ns	-0.39*	0.39**	7.84**
Jauhar-16 × NR-179	-0.61ns	0.55*	-0.47ns	2.86*	-0.61ns	0.31**	3.27**	1.03ns	1.42**	-0.21*	-9.04**

**= Highly significant (P≤0.01), *=Significant (P≤0.05), ns=Non-significant, PH=Plant height (cm), FLA=Flag leaf area (cm^2), TP=Tillers plant^{-1}, SS=Spikelets spike^{-1}, SL=Spike length (cm), SD=Spike density, GS=Grains spike^{-1}, TGW=Thousand grain weight (g), BYP=Biological yield plant^{-1} (g), GYP=Grain yield plant^{-1}(g), HI=harvest index (%)

HERITABILITY ESTIMATES

Broad-sense heritability (h^2) provides a measure of the predictability of phenotypic selection. High heritability (>60%) was recorded for plant height, flag leaf area, tillers plant^{-1}, grains spike^{-1} and biological yield plant^{-1} under both environments, indicating that selection based on phenotype would be effective for these traits. Thousand-grain weight and harvest index exhibited moderate heritability under drought conditions, suggesting that selection for these traits should be practised in the target environment (25-28).

CONCLUSION

The Line × Tester mating design effectively partitioned genetic variance and identified superior combining parents and cross combinations for drought-tolerance breeding in bread wheat. Based on GCA values, Fareed-06 is recommended as the most versatile line parent, while 181601 and NR-535 are promising tester parents. Among the 18 F_1 crosses evaluated, Jauhar-16 × 181601, Bwp-79 × NR-535 and Jauhar-16 × NR-535 demonstrated consistently superior performance for key yield-related traits across both normal and drought-stress environments.

The prevalence of non-additive gene action for most traits suggests that heterosis breeding strategies, including the development of F_1 hybrids, would be most beneficial. Given the high heritability of plant height, tillers plant^{-1} and grains spike^{-1}, phenotypic selection for these traits is expected to be effective under both irrigated and rainfed conditions. These findings provide a sound genetic basis for the development of high-yielding, drought-tolerant wheat varieties to address food security challenges in water-scarce regions of Pakistan.

In practical terms, the identified superior parents and crosses can be integrated into ongoing wheat breeding programs through several complementary pathways. Fareed-06, which demonstrated maximum GCA for tillers plant^{-1}, biological yield plant^{-1} and grain yield plant^{-1} in both environments, is recommended as a recurrent parent in population improvement schemes, where repeated cycles of crossing and selection would progressively increase the frequency of drought-adaptive alleles. NR-535, confirmed as a superior tester for grain yield plant^{-1}, is recommended as a standard reference tester in future L × T evaluations to benchmark the combining ability of newly introduced lines against a fixed performance baseline. The top-performing crosses Jauhar-16 × NR-535 and Bwp-79 × NR-535, which showed consistently superior SCA and mean performance under both irrigated and water-deficit environments, are recommended for immediate advancement to multi-location replicated yield trials. Where hybrid seed production infrastructure exists, these F_1 combinations are strong candidates for commercial hybrid development targeting the irrigated agro-ecosystems of Southern Punjab. In environments where hybrid systems are not yet feasible, the same F_1 populations can serve as base material for pedigree or bulk selection to extract high-yielding, drought-tolerant pure lines in subsequent segregating generations.

Conflict of interest:

Authors declared no conflict of interest.

Authors' contribution:

HMSA Conceived the idea and supervised the research, study, and management; MS Collected the data and carried out the write-up and statistical analysis; AS Performed the interpretation of data and handled correspondence; FS carried out the grammar check and review; HI Performed the plagiarism check and correction; SATR Completed the results and discussion section; AF Handled the in-text citations and revision.

Declaration of generative AI-Assisted Tools:

No AI-assisted tools were used by the authors.

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