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**Research Article****Genetic insights into spike trait inheritance in wheat for drought resilience****Nadeem Ahmad¹, Ahsan Javed¹, Suleman Gohar², Muhammad Makky Javaid³, Muhammad Sarwar¹, Muhammad Owais¹, Muhammad Kashif Aziz⁴, Muhammad Zulkiffal¹, Muhammad Hammad Tanveer¹, Javed Ahmad¹, Muhammad Abdullah¹**¹ Wheat Research Institute, AARI, Faisalabad, Punjab, Pakistan.² Cotton Research Station, 55000, Sahiwal, Punjab, Pakistan.³ Agricultural Biotechnology Research Institute, AARI, Faisalabad, Punjab, Pakistan.⁴ Maize research station, AARI, Faisalabad, Punjab, Pakistan.**ABSTRACT**

This study genetic insights of spike-related inheritance traits in wheat (*Triticum aestivum* L.) under water stress. Seven wheat genotypes, comprising five drought-tolerant and two drought-sensitive lines, were crossed in all possible combinations in complete diallel fashion. The F1 hybrids and parental lines were tested under both irrigated and drought conditions in a randomized complete block design. Traits such as spikes plant-1, spike length, spikelets spike-1, spike weight, grains spike-1, spike harvest index, and grain yield plant-1 were recorded and analyzed.

Significant genotypic variation was observed across all traits, with additive gene and partial dominance identified as the primary genetic mechanisms. Heritability estimates were moderate to high (40%–78%), highlighting the potential for genetic improvement. Traits like spikes per plant and spike length displayed high heritability under drought conditions, making them suitable targets for early-generation selection. The findings suggest that breeding programs focusing on additive gene action can enhance drought tolerance and yield potential in wheat. This research provides a framework for developing high-yielding, resilient wheat varieties suited for water-limited environments, through Identification of drought resilient crosses on the basis studied traits contributing to sustainable food production also.

Keywords *Triticum aestivum*; screening; genetic analysis; spike traits; moisture stress.

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INTRODUCTION

Wheat serves as the primary source of calories for the population of Pakistan, providing sustenance for both humans and livestock. It occupies 37% of the total cultivated land and contributes 76% of the country's total grain production (Ullah et al., 2020). In 2023, Pakistan achieved a record wheat production of 27.634 million tonnes from 9.043 million hectares, with an average yield of 3.056 tonnes per hectare (Anonymous, 2023). Although Pakistan ranks 10th globally in terms of agricultural land area, its productivity stands at 59th. Wheat yields vary significantly across regions and farms due to factors such as weather conditions and irrigation availability (Javed et al., 2025). The average yield per acre is approximately 20–25 maunds, and achieving higher yields demands additional resources and favorable climatic conditions (Javaid et al., 2022). The boosting requirement of foodstuff is suggesting that enhancement of wheat production is essential. This can be achieved through either increasing the cultivated area or improving productivity per unit area by adopting advanced farming practices (Kashif et al., 2023). While productivity has increased from 2.833 tonnes per hectare in 2010-11 to 3.056 tonnes per hectare in

2022-23 (Anonymous, 2023), it has not kept pace with the country's population growth, now at approximately 237.28 million (Anonymous, 2023). With a per capita wheat consumption of 115 kilograms, the domestic requirement stands at 27.29 million tonnes annually (Ahmad et al., 2023).

There is need to develop such wheat varieties that have ability to deliver higher yield under normal and water-stressed environment. In Pakistan wheat production in rainfed area is riskier due to erratic and scarce rainfall. Rainfed areas contribute only 12% to national wheat output. There is high need to develop new climate resilient, drought tolerant and high yielding wheat genotypes (Iqbal et al., 2022).

Water scarcity is a significant challenge to wheat production. Limited irrigation water availability has made it crucial to breed drought-resistant varieties to ensure higher yield under water stress conditions (Noorka et al., 2013). Stress due to deficit water not only impacts yield-related traits but also presents a major challenge for plant breeders (HongBo et al., 2006). This stress is further compounded by shifting climate patterns, which significantly affect wheat yields (Ahmad et al., 2022).

In Punjab, irrigation relies heavily on groundwater, much of which is saline and requires mixing with canal water to sustain productivity (Zakir-Hassan et al., 2021). High electricity costs also discourage tube well use. Addressing these challenges is critical, as incentives for farmers previously resulted in record wheat yields despite resource constraints. Farmers are now facing additional difficulties due to inflation and rising input costs, underlining the need for policy interventions and research-driven solutions.

Pakistan's farming sector must overcome challenges like water scarcity, to meet the food needs of its population (Kashif et al., 2023). During the 2022-23 cropping season, water availability was 29.8% below requirements (Anonymous, 2023). Variability in wheat genotypes for yield and drought tolerance highlights opportunities for breeding programs focused on resilient traits (Javed et al., 2022). Developing drought-resistant wheat varieties is crucial for achieving sustainable self-sufficiency, enabling surplus production to support the national economy. This study will help to identify climate smart drought resilient wheat genotypes.

MATERIALS AND METHODS

The study was conducted at the Wheat Research Institute, Faisalabad. During the 2020–2021 cropping season, a total of seventy-five wheat genotypes from local and international sources were collected and evaluated for drought tolerance using seedling traits. The experiment was performed in glasshouse in petri dishes. 20% PEG-6000 solution was used to induced drought. Seedlings were harvested after 15 days. Based on their performance, five drought-tolerant and two drought-sensitive genotypes were selected for further research (Table 1).

Table 1. Parents selected for crossing.

Codes	Variety/Line	Source	Status
G1	MRNG/BUC'S//BLO'S/PSN'S'	CIMMYT	Tolerant
G2	PVN/PBW65/3/KAUZ*2/TRAP//KAUZ	CIMMYT	Tolerant
G3	SERI/NKT//2*KAUZ	CIMMYT	Tolerant
G4	SITE/MO/3/VORONA/BAU//BAU	CIMMYT	Tolerant
G5	VS73.600/MRL'S/3/BOW'S//YR/TRF'S'	CIMMYT	Tolerant
G6	BOW'S//VRE'S//VEE'S'	CIMMYT	Sensitive
G7	HD2329/SABUF	PAKISTAN	Sensitive

In the 2021–2022 season, the selected seven genotypes were crossed in all possible combinations in complete diallel fashion. During the first week of November 2021, the resulting F1 hybrids (42 genotypes) and the original parent lines (seven genotypes) were planted in a randomized complete block design. The replications were kept three planted in two separate experimental sets. One set was irrigated regularly, while the other was subjected to drought stress by limiting irrigation. Under normal condition, the crop received four irrigations at various times, including pre-sowing, tillering, booting and at grain filling stage. On the other hand, just two irrigations were applied during pre-sowing and at tillering in drought stress. Each genotype was grown in two rows of 3 meters' length, maintaining a plant-to-plant spacing of 15 cm and a row-to-row spacing of 30 cm. Two seeds were sown per hole, and after germination, thinning was done to retain one healthy seedling per hole. To minimize edge effects, non-experimental rows were planted at the beginning and end of each replication.

At maturity, data was recorded for spike traits (spikes plant⁻¹, spike length, spikelets spike⁻¹, spike weight, grains spike⁻¹, spike harvest index) and grain yield plant⁻¹ under both water regimes from ten randomly selected plants per replication. Analysis of variance (ANOVA), as described by Steel et al. (1997), was used to identify significant differences among genotypes. The genetic analysis was conducted using diallel cross methodology as detailed by Mather and Jinks (1982). Genetic basis of spike related traits were estimated following the methods described by Hayman (1954a, b) and Mather and Jinks (1982).

RESULTS AND DISCUSSION

Genotypic Variation Assessment

Significant differences ($P \leq 0.01$) among all genotypes for the evaluated traits under both environments (normal and drought) were noted (Table 2). These differences confirmed the presence of substantial genetic variability, enabling further analysis using the methodologies of Hayman (1954a, b) and Mather and Jinks (1982). The Mean squares of various spike traits in a 7x7 diallel cross under normal and drought also suggested useful variation (Table 3).

Additivity and Dominance Model Validation

Regression analysis, involving variance (V_r) and covariance (W_r), along with ANOVA for ($W_r + V_r$) and ($W_r - V_r$), was utilized to evaluate spike-related traits under normal and drought conditions. The regression coefficient 'b' showed significant deviation from zero, confirming the suitability of the Mather and Jinks genetic model for the analyzed traits (Table 4).

Under normal water conditions, traits such as spike weight, spikelets per spike, and spike length demonstrated dominance effects, evidenced by significant differences in ($W_r + V_r$) values between arrays. For drought conditions, similar dominance patterns were observed in traits including grain yield, spikes per plant, and spike length. However, non-significant ($W_r - V_r$) differences within arrays for these traits under both conditions indicated the absence of epistasis, supporting the model's adequacy.

Partial adequacy was observed for certain traits where non-significant variations between arrays ($W_r + V_r$) were detected. This highlights the presence of partial dominance or complex interactions in the genetic control of these traits. Overall, the findings validate the model's applicability to dissect genetic inheritance patterns in both normal and water-stressed environments.

Spikes Plant⁻¹ (SP)

Table 5 demonstrates that both additive (D) and dominance (H) genetic effects significantly influenced SP under both environmental conditions. Under normal water conditions, dominance effects (H_1) were greater than additive effects (D), indicating the presence of over-dominance. In contrast, under drought stress, additive effects (D) exceeded dominance effects (H_1), suggesting partial dominance. Gene distribution was unequal under normal conditions, as indicated by H_1 values surpassing H_2 and an $H_2/4H_1$ ratio of 0.22, which is below the theoretical value of 0.25. However, gene distribution under drought conditions was nearly equal, with H_1 and H_2 values being similar, further supported by an $H_2/4H_1$ ratio close to 0.25. The dominance of positive genes was evident under both conditions, as shown by the positive (F) value. This was confirmed by the ratio $\sqrt{(4DH_1 + F)}/\sqrt{(4DH_1 - F)}$, which exceeded one (1.36 under normal and 2.95 under drought). Heritability estimates were moderate, with values of 40% under normal and 58% under drought. Over-dominance under normal conditions was evident from a degree of dominance greater than one and a regression line intercepting below the origin (Figure 1a). Conversely, under drought stress, partial dominance was indicated by a degree of dominance less than one (0.51) and a regression line intercepting above the origin (Figure 1b). Dominant genes were more prevalent in genotypes G7 and G3, which were located near the origin under both water regimes. In contrast, G1 and G4, positioned farther from the origin, exhibiting the highest number of recessive genes under normal and drought conditions, respectively. These findings align with previous research by Khalilzadeh (2018), which identified additive genetic effects for SP in wheat.

Spike Length (SL)

Table 5 indicates that both additive (D) and dominance (H) genetic effects significantly influenced spike length (SL) under both environmental conditions. Additive effects (D) were more pronounced, especially under drought stress, as their values surpassed those of dominance effects (H_1).

Gene distribution was observed to be unequal across both water regimes, with H_1 values exceeding H_2 . This was further confirmed by the $H_2/4H_1$ ratios, which were below the expected 0.25 (0.17 under normal and 0.15 under drought conditions). Dominant gene action was evident, supported by positive (F) values under both regimes. The ratio $\sqrt{(4DH_1 + F)}/\sqrt{(4DH_1 - F)}$

F)/ $\sqrt{(4DH_1 - F)}$ exceeded one in both conditions (1.99 for normal and 2.12 for drought), reinforcing the role of dominant genes. The degree of dominance values was less than one under both water conditions, indicating partial dominance (0.77 under normal and 0.93 under drought). This partial dominance was further validated by regression lines intercepting above the origin in Figures 2a and 2b. Heritability estimates were relatively high, with values of 74% under normal conditions and 67% under drought stress, indicating a strong potential for genetic improvement through selection. Dominant genes were more prevalent in genotype G5, which was situated near the origin under both conditions. In contrast, genotype G1 was positioned farther from the origin, exhibiting the highest number of recessive genes under both water regimes. Kumar et al. (2018) confirmed additive gene action with partial dominance for SL in wheat.

Table 2. Analysis of variance of various spike traits under both the regimes in a 7x7 diallel cross of *Triticum aestivum*.

Source of variation (Normal)	Degree of freedom	Spikes plant ⁻¹	Spike length	Spikelets spike ⁻¹	Spike weight	Grains spike ⁻¹	Spike harvest index	Grain Yield plant ⁻¹
Replications	2	0.291	0.042	8.4782	0.011	5.55	16.05	0.18
Male	6	2.48**	7.61**	23.3636**	0.514**	115.4**	37.41*	40.70**
Female	6	4.83**	1.73**	23.1216**	0.48**	27.25*	58.01**	45.00**
Male x Female	36	1.22**	0.65**	3.5358**	0.16 ^{NS}	16.54*	14.48 ^{NS}	7.19 ^{NS}
Error	96	0.448	0.048	0.7338	0.11	10.06	12.05	5.40
Total	146							
Reciprocals	21	1.77**	0.99**	4.6605**	0.24**	31.23**	19.12 ^{NS}	7.26 ^{NS}
Drought								
Replications	2	0.5213	0.027	3.5927	0.179	6.83	7.52	6.065
Male	6	2.36**	9.24**	6.4077**	1.419**	123.09**	60.51**	40.79**
Female	6	2.056**	2.40**	13.0318**	0.89**	57.72**	65.07**	36.09**
Male x Female	36	0.72**	0.85**	2.1028**	0.092 ^{NS}	10.55 ^{NS}	5.80 ^{NS}	5.91*
Error	96	0.20	0.15	0.5847	0.083	8.94	7.30	3.27
Total	146							
Reciprocals	21	1.16**	0.95**	1.4790**	0.165*	32.98**	12.62 ^{NS}	6.83 ^{NS}

**=Significant at P ≤ 0.01; *=Significant at P ≤ 0.05; NS=Non-significant.

Table 3. Mean squares of various spike traits in a 7x7 diallel cross under normal and drought.

Traits (Normal)	Replications (df=2)	Genotypes (df=49)	Error (df=96)
Spikes per plant	0.287	1.833**	0.448
Spike length	0.0418	1.6550**	0.0480
Spikelets per spike	8.474	8.462**	0.734
Spike weight	0.02	0.31**	0.02
Grains per spike	5.57	30.24**	10.06
Spike harvest index	56.57	44.76**	25.31
Grain yield	0.213	16.11**	5.40
Traits (Drought)			
Spikes per plant	0.523	1.096**	0.203
Spike length	0.0281	2.0919**	0.1449
Spikelets per spike	3.572	4.006**	0.585
Spike weight	0.06	0.41**	0.030
Grains per spike	7.010	30.518**	8.939
Spike harvest index	6.12	17.59**	10.49
Grain yield	6.07	14.04**	3.27

**=Significant at P ≤ 0.01.

Table 4. Scaling tests for adequacy of additive-dominance model for various traits under normal and drought.

Traits (Normal)	Regression slope		Mean squares		Remarks	Joint regression(b)
	b ₀	b ₁	W _r + V _r	W _r - V _r		

Spikes per plant	4.21*	0.59 ^{NS}	0.34 ^{NS}	3.95 ^{NS}	partially adequate	0.8772 ± 0.2085
Spike length	11.01*	-1.23 ^{NS}	0.63**	0.009 ^{NS}	fully adequate	1.1254±0.1022
Spikelets per spike	6.01*	0.083 ^{NS}	3.49*	0.48 ^{NS}	fully adequate	0.9863 ± 0.1640
Spike weight	3.75*	0.95 ^{NS}	0.009**	0.002 ^{NS}	fully adequate	0.7978 ± 0.2129
Grains per spike	6.10*	0.85 ^{NS}	34.94 ^{NS}	7.75 ^{NS}	partially adequate	0.8771±0.1438
Spike harvest index	8.06*	0.015 ^{NS}	248.5 ^{NS}	108.2 ^{NS}	partially adequate	0.9982±0.1238
Grain Yield	3.08*	0.63 ^{NS}	42.90 ^{NS}	2.31 ^{NS}	partially adequate	0.8296± 0.2689
Traits (Drought)						
Spikes per plant	9.06*	-1.60 ^{NS}	0.23*	5.70 ^{NS}	fully adequate	1.2156 ± 0.1342
Spike length	6.21*	0.58 ^{NS}	2.08**	0.075 ^{NS}	fully adequate	0.9144±0.1473
Spikelets per spike	3.50*	0.75 ^{NS}	2.20 ^{NS}	0.19 ^{NS}	partially adequate	0.8237 ± 0.2353
Spike weight	6.69*	0.54 ^{NS}	0.005 ^{NS}	0.0006 ^{NS}	partially adequate	0.9253± 0.1383
Grains per spike	10.49*	1.30 ^{NS}	27.29 ^{NS}	4.27 ^{NS}	partially adequate	0.8901±0.0848
Spike harvest index	6.57*	0.31 ^{NS}	14.42 ^{NS}	13.61 ^{NS}	partially adequate	0.9547±0.1453
Grain Yield	5.04*	1.14 ^{NS}	39.44*	1.82 ^{NS}	fully adequate	0.8152± 0.1618

*=Significant at P ≤ 0.05; NS=Non-significant. Where, b₀: coefficient of regression deviating from zero, b₁: coefficient of regression deviating from unity, b: regression coefficient, Mean squares are from analysis of variance of values (Wr + Vr between arrays) and (Wr - Vr with in arrays).

Table 5. Components of genetic variation under both regimes.

Components (Normal)	Spikes plant ⁻¹	Spike length	Spikelets spike ⁻¹	Spike weight	Grains spike ⁻¹	Spike harvest index	Grain Yield plant ⁻¹
D	0.46 ± 0.06*	1.03 ± 0.04*	3.77 ± 0.14*	0.04 ± 0.008*	7.46 ± 0.34*	16.42±0.23*	6.68 ± 0.69*
H ₁	0.52 ± 0.15*	0.62 ± 0.10*	1.07 ± 0.34*	0.02 ± 0.02	4.51 ± 0.82*	-14.3±1.54*	1.08 ± 1.67
H ₂	0.46 ± 0.13*	0.42 ± 0.09*	1.00 ± 0.30*	0.01 ± 0.02	2.51 ± 0.72*	-9.9±1.36*	1.03 ± 1.47
F	0.15 ± 0.15	0.53 ± 0.10*	-0.15 ± 0.34	-0.03 ± 0.02	-3.87 ± 0.81*	-3.36±1.53*	-0.18 ± 1.66
(h ²)	0.05 ± 0.09	0.02 ± 0.06	-0.15 ± 0.20	-0.005 ± 0.01	-1.73 ± 0.48*	-3.49±0.91*	-0.89 ± 0.99
E	0.16 ± 0.02*	0.02 ± 0.01	0.32 ± 0.05*	0.04 ± 0.003*	3.54 ± 0.12*	9.21±0.23*	1.88 ± 0.25*
√H ₁ /D	1.06	0.77	0.53	0.65	0.78	0.93	0.40
(H ₂ / 4H ₁)	0.22	0.17	0.23	0.19	0.14	0.17	0.24
(√4DH ₁ + F) / √4DH ₁ - F)	1.36	1.99	0.93	0.28	0.50	0.80	0.93
h ² (n.s)	40 %	74 %	78 %	49 %	62 %	53%	62 %
Drought							
D	0.55 ± 0.03*	1.28 ± 0.11*	1.10 ± 0.18*	0.14 ± 0.006*	5.95 ± 0.20*	1.71±0.16*	7.07 ± 0.67*
H ₁	0.14 ± 0.08*	1.12 ± 0.27*	1.18 ± 0.43*	0.03 ± 0.01*	4.85 ± 0.48*	-8.74±0.39*	2.39 ± 1.62
H ₂	0.13 ± 0.07*	0.66 ± 0.23*	1.17 ± 0.38*	0.02 ± 0.01*	3.42 ± 0.42*	-6.35±0.35*	2.29 ± 1.43
F	0.28 ± 0.07*	0.86 ± 0.27*	0.57 ± 0.43	-0.06 ± 0.01*	-5.38 ± 0.48*	-5.03±0.39*	1.41 ± 1.61
(h ²)	-0.01 ± 0.04	0.20 ± 0.16	0.16 ± 0.25	-0.01 ± 0.01	-1.52 ± 0.28*	-1.55±0.23*	-0.46 ± 0.96
E	0.07 ± 0.01*	0.05 ± 0.04	0.23 ± 0.06*	0.03 ± 0.002*	3.16 ± 0.07*	3.69±0.06*	18 ± 0.24*

$\sqrt{H_1/D}$	0.51	0.93	0.99	0.47	0.90	0.92	0.58
$(H_2 / 4H_1)$	0.24	0.15	0.25	0.17	0.18	0.18	0.24
$(\sqrt{4DH_1 + F} / \sqrt{4DH_1 - F})$	2.95	2.12	1.12	0.35	0.33	0.21	1.41
$h^2(n.s)$	58 %	67 %	62 %	79 %	68 %	51%	62 %

D: additive variance, H_1 : Dominance variance, H_2 : Proportion of positive and negative genes in the parent, F: Relative frequency of dominant and recessive alleles in the parents, h^2 : Dominance effect (over all loci in heterozygous phase), E: Environmental Variance, $\sqrt{H_1/D}$: Mean degree of dominance, $(\sqrt{4DH_1 + F} / \sqrt{4DH_1 - F})$: Proportion of dominant and recessive genes in the parents, $(H_2 / 4H_1)$: Proportion of genes with positive and negative effects in the parents, $h^2(n.s)$: Heritability narrow sense. (Note: The value of variance is significant (*) when the value exceeds 1.9996 after dividing with its standard error.

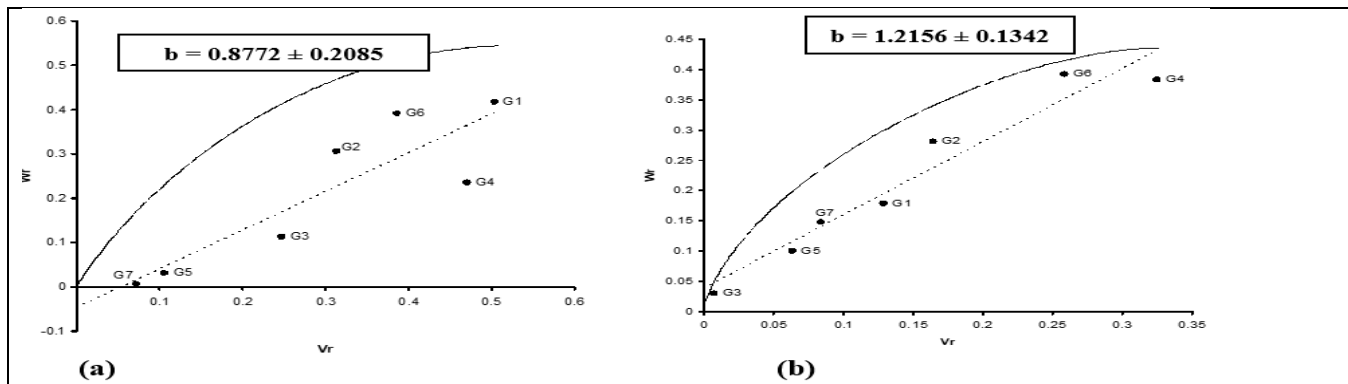


Figure 1. W_r/V_r graph for spikes per plant under normal (a) & drought (b) conditions.

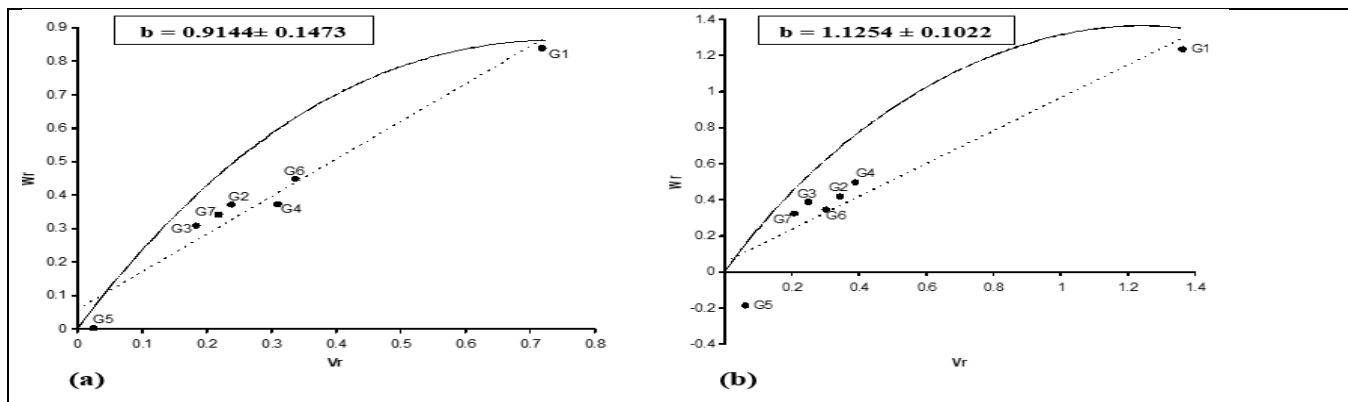


Figure 2. W_r/V_r graph for spike length under Normal (a) & drought (b) conditions.

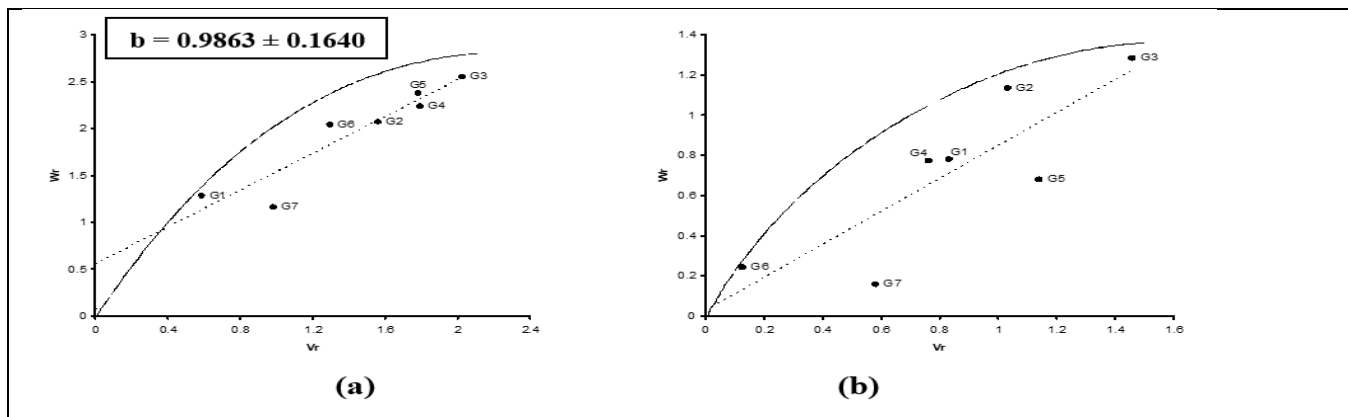


Figure 3. W_r/V_r graph for spikelets per spike under Normal (a) & drought (b) conditions.

Spikelets Spike⁻¹ (SLS)

Table (5) reveals that both additive (D) and dominance (H) genetic effects played significant roles in determining spikelets per spike (SLS) under both normal and drought conditions. Under normal conditions, the additive effects (D) were more prominent, as their values exceeded those of dominance effects (H₁). Conversely, under drought conditions, dominance effects (H₁) were greater, highlighting the role of dominance under stress.

Gene distribution was unequal under normal conditions, as indicated by H₁ values being higher than H₂ and an H₂/4H₁ ratio of 0.23, which is less than 0.25. However, under drought stress, gene distribution became balanced, with H₁ and H₂ values being approximately equal, as confirmed by an H₂/4H₁ ratio of 0.25.

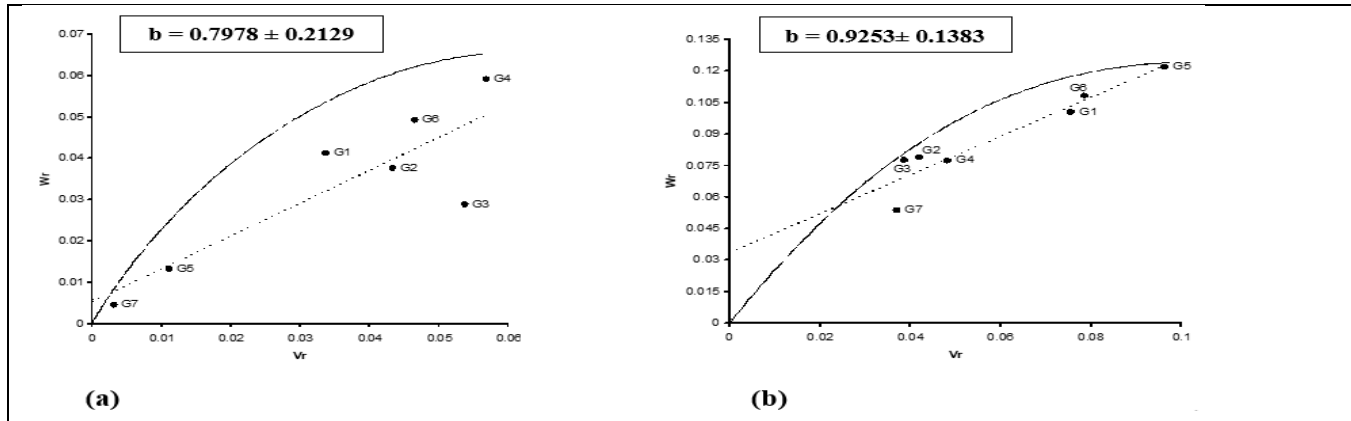


Figure 4. W_r/V_r graph for spike weight under Normal (a) & drought (b) conditions.

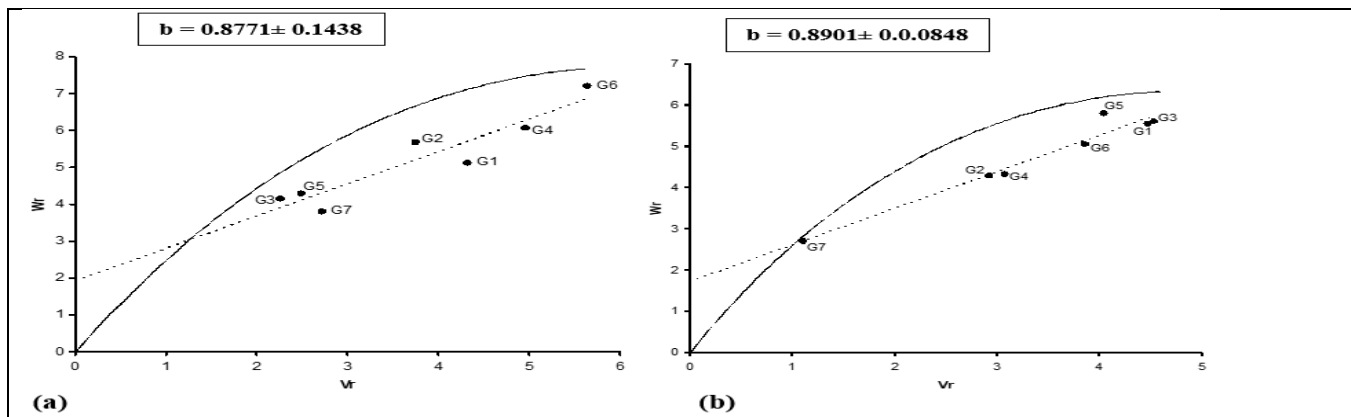


Figure 5. W_r/V_r graph for grains per spike under Normal (a) & drought (b) conditions.

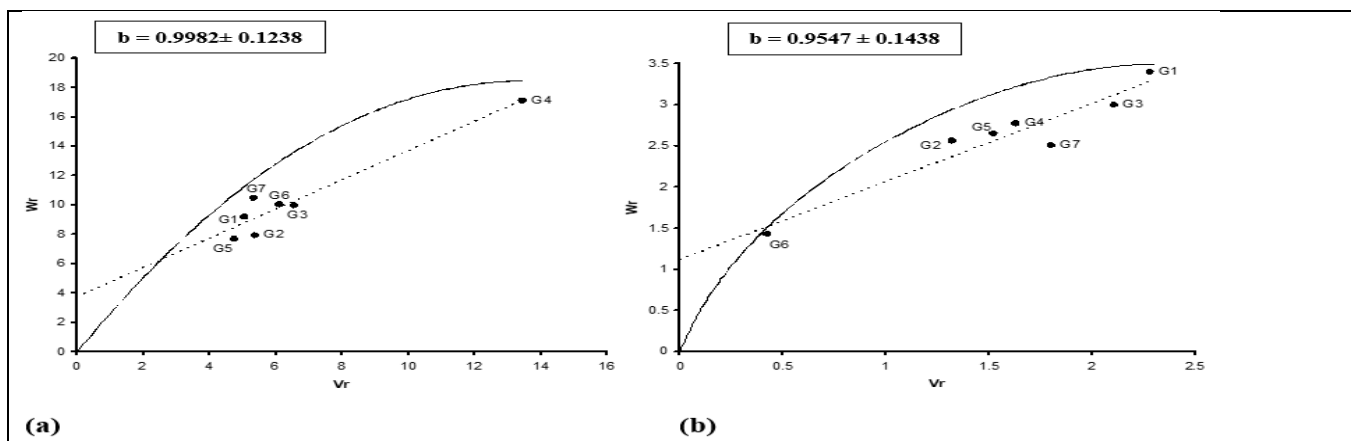


Figure 6. W_r/V_r graph for spike harvest index under Normal (a) & drought (b) conditions.

Recessive gene action was evident under normal conditions, supported by the negative and non-significant (F) value. This was further validated by the ratio $\sqrt{(4DH_1 + F)/\sqrt{(4DH_1 - F)}}$, which was less than one (0.93). Under drought conditions, dominant gene action became prominent, as indicated by a positive (F) value and a ratio $\sqrt{(4DH_1 +$

$F)/\sqrt{(4DH_1 - F)}$ greater than one (1.12). Partial dominance was evident under normal conditions, with a degree of dominance value less than one (0.53), as shown by the regression line intercepting above the origin in Figure 3a. Under drought conditions, complete dominance was observed, with a degree of dominance value equal to one, supported by the regression line intercepting at the origin in Figure 3b. Heritability estimates were high, with values of 78% under normal conditions and 62% under drought stress, indicating good potential for selection.

Dominant genes were more prevalent in genotypes G5 and G6, which were located closer to the origin under normal and drought conditions, respectively. In contrast, genotype G3, positioned farther from the origin, exhibited the highest number of recessive genes in both conditions. These findings align with Rana et al. (2023), who observed both additive

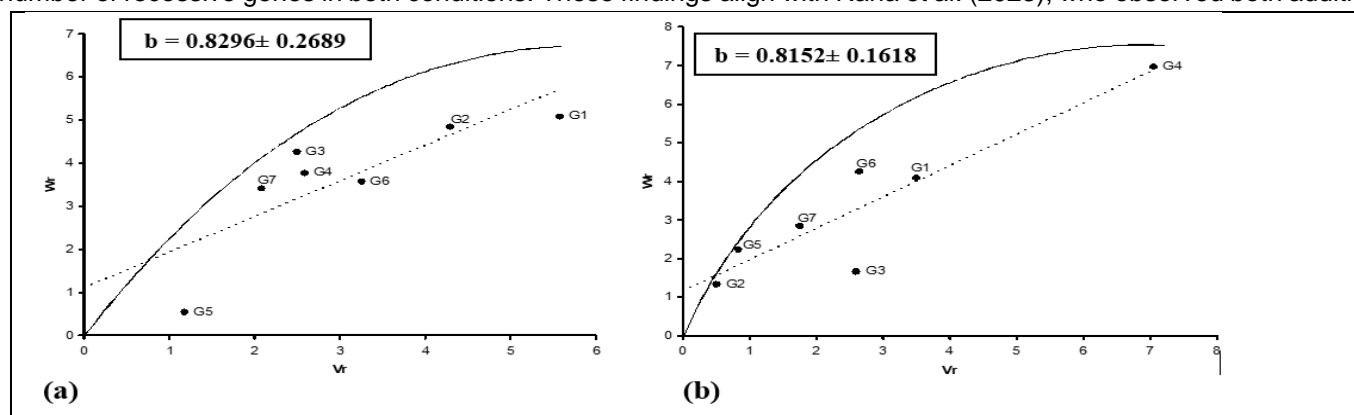


Figure 7. W_r/V_r graph for grain yield per plant under Normal (a) & drought (b) conditions

and dominance gene action in wheat, while Khalilzadeh (2018) and Ishaq et al. (2018) reported over-dominance effects for this trait.

Spike Weight (SW)

Table (5) shows that additive genetic effects significantly influenced spike weight (SW) under both normal and drought conditions. Non-additive genetic effects were negligible under normal conditions but became significant under drought stress. The higher values of additive components in both conditions highlight the stability of additive inheritance for this trait. Gene distribution was unequal across both water regimes, as indicated by H_1 values exceeding H_2 . This was confirmed by $H_2/4H_1$ ratios of 0.19 under drought and 0.17 under normal conditions, both below the theoretical value of 0.25. Recessive gene action was predominant in both conditions, reflected by the negative and non-significant (F) values. The ratio $\sqrt{(4DH_1 + F)}/\sqrt{(4DH_1 - F)}$ was less than one, with values of 0.28 for normal and 0.35 for drought, further supporting the role of recessive genes.

Partial dominance was observed under both water regimes, with degree of dominance values below one (0.65 for normal and 0.47 for drought). This partial dominance was validated by regression lines intercepting above the origin in Figures 4a and 4b. Heritability estimates were moderate under normal conditions (49%) and high under drought stress (79%), indicating greater potential for selection under water-limited environments.

Genotype G7 exhibited a higher number of dominant genes, as it was located closer to the origin under both water regimes. Conversely, genotypes G4 and G5, positioned farther from the origin, contained the highest number of recessive genes under normal and drought conditions, respectively.

Grains Spike-1 (GPS)

Table 5 indicates that grains per spike (GPS) were significantly influenced by both additive (D) and dominance (H) genetic effects under normal and drought conditions. Under both regimes, additive effects (D) were more pronounced, as their values exceeded those of dominance effects (H_1), emphasizing the stability of additive inheritance for this trait. Gene distribution was unequal across both conditions, with H_1 values surpassing H_2 . This was supported by $H_2/4H_1$ ratios of 0.14 for normal and 0.18 for drought, both below the expected 0.25. Recessive gene action was more apparent, as indicated by the negative (F) values under both conditions. This was further confirmed by the ratio $\sqrt{(4DH_1 + F)}/\sqrt{(4DH_1 - F)}$, which was less than one, specifically 0.50 under normal and 0.33 under drought stress. Partial dominance was evident in both environments, with the degree of dominance values below one (0.78 under normal and 0.90 under drought). This partial dominance was further validated by regression lines intercepting above the origin in Figures (5a) and (5b). Heritability estimates were moderate, with values of 62% under normal conditions and 68% under drought stress, suggesting good potential for genetic improvement through selection.

Genotypes G3 and G7 contained a greater number of dominant genes, as they were located closer to the origin under normal and drought conditions, respectively. In contrast, genotypes G6 and G3, positioned farther from the origin under both environmental conditions, respectively, exhibited the highest number of recessive genes. These findings align with Al-Bakry et al. (2017), who reported additive control with partial dominance for GPS, although Esmail (2007) highlighted non-additive genetic effects in similar studies.

Spike Harvest Index (SHI)

Table 5 highlights that spike harvest index (SHI) was controlled by additive genetic effects (D) under both normal and drought conditions, as evidenced by significant differences among the genotypes. Non-additive genetic effects (H) were found to be negatively significant under both water regimes, indicating their limited contribution to this trait's inheritance. Gene distribution was unequal in both conditions, with H_1 values exceeding H_2 . This was further confirmed by $H_2/4H_1$ ratios of 0.17 for normal and 0.21 for drought, both below the theoretical value of 0.25. Recessive gene action was more pronounced, supported by negative (F) values under both conditions. The ratio $\sqrt{(4DH_1 + F)}/\sqrt{(4DH_1 - F)}$ was less than one, with values of 0.80 under normal and 0.18 under drought, further emphasizing the dominance of recessive genes. Partial dominance was observed in both water regimes, as indicated by the degree of dominance values being less than one (0.93 under normal and 0.75 under drought). This was validated by regression lines intercepting above the origin in Figures 6a and 6b. Heritability estimates were moderately high, recorded at 53% under normal conditions and 51% under drought stress, suggesting good potential for selection.

Genotype G7 exhibited a higher number of dominant genes, as it was positioned closer to the origin under both conditions. In contrast, genotypes G4 and G6, located farther from the origin under both environmental conditions, respectively, exhibited the highest number of recessive genes.

Grain Yield Plant-1 (GYP)

Table (5) demonstrates that grain yield per plant (GYP) was significantly influenced by additive genetic effects (D) under both normal and drought conditions. While non-additive genetic effects (H) were positively non-significant under normal conditions, they became significant under drought stress, suggesting their importance in stressed environments. Gene distribution was balanced under both water regimes, as H_1 values closely matched H_2 . This was confirmed by $H_2/4H_1$ ratios of 0.24 for both conditions, aligning with the theoretical value of 0.25. Recessive genes played a dominant role under normal conditions, as directed by the negative (F) value. The ratio $\sqrt{(4DH_1 + F)}/\sqrt{(4DH_1 - F)}$ was less than one (0.93), reinforcing this finding. Under drought conditions, dominant gene action became evident with a positive (F) value and a ratio $\sqrt{(4DH_1 + F)}/\sqrt{(4DH_1 - F)}$ exceeding one (1.41).

Partial dominance was evident in both environments, with the degree of dominance values less than one (0.40 under normal and 0.58 under drought). This was supported by regression lines intercepting above the origin in Figures 7a and 7b. Heritability estimates were moderate, recorded at 62% for both conditions, suggesting strong potential for genetic improvement through selection.

Genotypes G5 and G2 exhibited a higher number of dominant genes, as they were located closer to the origin under both environmental conditions, respectively. In contrast, genotypes G1 and G4, positioned farther from the origin under normal and drought conditions, respectively, contained the highest number of recessive genes. These findings are consistent with Ahmad et al. (2017) who reported additive genetic control for grain yield under both irrigated and stressed conditions, while Rana et al. (2023) confirmed non-additive genetic control for this trait.

CONCLUSION

This study gives information about genetic mechanisms governing spike-related traits in wheat (*Triticum aestivum* L.) under drought conditions. Significant genotypic variability was observed for all traits, with additive gene action and partial dominance as key mechanisms influencing traits such as spike length, spikelets spike-1, and grain yield plant-1. Heritability ranged from moderate to high (40%–78%), indicating a strong potential for genetic improvement through selection. Under drought stress, traits like spikes per plant and spike length exhibited heritability values as high as 67%, suggesting their resilience and suitability for early-generation selection. The predominance of additive genetic effects (D) over dominance effects (H) for most traits underscores the stability of inheritance under water-limited conditions. Grain yield per plant, with a heritability of 62% under both water regimes, demonstrated consistent genetic patterns, supporting the efficacy of pedigree-based selection methods for breeding drought-tolerant wheat varieties. In conclusion, prioritizing traits governed by additive genetic effects in wheat breeding programs can significantly enhance resilience and yield potential in drought-prone areas.

AUTHOR'S CONTRIBUTION

Nadeem Ahmad and Ahsan Javed executed the research and performed write-up. Suleman Gohar and Muhammad Makky Javaid analysed the data. Muhammad Sarwar and Muhammad Owais collected helped in data compilation. Muhammad Kashif Aziz, Muhammad Zulkiffal and Muhammad Hammad Tanveer helped in collection of the data of normal & drought set. Javed Ahmad supervised the research work. Muhammad Abdullah assisted in write-up.

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AVAILABILITY OF DATA AND MATERIAL

The datasets are available from the corresponding author on reasonable request.

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Not applicable.

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CONFLICT OF INTERESTS

No conflict of interest is confirmed by all authors for publication of this article

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REFERENCES

- Ahmad, N., Javed, A., Gohar, S., Ahmed., Sher, J. A., Abdullah, M., Asghar, S., Javed, K., Iqbal, J., S. Kumar & Qayyum, A. 2022. Estimation of Drought Effects on Different Bread Wheat Genotypes Using Morpho-Physiological Traits. *Biochemical Systematics and Ecology*: (104): 104483. <https://doi.org/10.1016/j.bse.2022.104483>
- Ahmad, N., Rehman, A., Gulnaz, S., Javed, A., Sultana, R., Ajmal, S., Ahsan, A., Shamim, S., Nadeem, M., Shair, H., Abdullah, M., Ahmad and J., Sarwar, M. 2023. Appraisal of bread wheat germplasm for quality attributes and their relationship with grain yield. *SABRAO Journal of Breeding and Genetics*. 55(2): 388-398. <http://doi.org/10.54910/sabrao2023.55.2.11>.
- Anonymous, 2023. *Agricultural Statistics of Pakistan*. Ministry of Food, Agriculture and Cooperative, Food and Agriculture Div., Economic Wing, Islamabad.
- Ahmad, N., Khan, A.S., Khaliq, I and Ayub, M. 2017. Genetic analysis of dry matter partitioning in wheat (*Triticum aestivum* L.) Under drought conditions. *Journal of Agricultural Research* (03681157), 55(3).
- Al-Bakry, M. R., Al-Naggar, A.M.M., Ghareeb, Z.E and Mohamed, S.G. 2017. Gene effects and interrelationships of spike traits in bread wheat. *Egyptian Journal of Plant Breeding*, 21(1), pp.85-98.
- Anonymous, 2023. *Economic Survey of Pakistan*. Economic Adviser's Wing, Finance Division Government of Pakistan, Islamabad.
- Esmail, R. M. 2007. Detection of genetic components through triple test cross and line tester analysis in bread wheat. *WJAS*, (2): 184-190.
- Hayman, B. I. 1954a. The theory of analysis of diallel crosses. *Genetics*. 39: 739-809.
- Hayman, B. I. 1954b. The analysis of variance of diallel crosses. *Biometrics*. 10: 235-245.
- HongBo, S., ZongSuo, L and MingAu, S. 2006. Osmotic regulation of 10 wheat (*Triticum aestivum* L.) genotypes at soil water deficits. *Colloids Surf B Biointerfaces*. 47(2), 132-139.
- Iqbal, J., Ahmad, N., Tabassum, M. I., Rabbani, G., Hassan, F., Rafique, M., Iqbal, M., Mustafa, R., Ashraf, S., Javed, A. and Abdullah, S., 2022. MA-21: a disease tolerant and long-rooted wheat variety depicting long-stay in the rainfed regime. *Journal of Agricultural Research (JAR)*., 60(2), pp.107-113.
- Ishaq, M., Ahmad, G., Afridi, K., Ali, M., Khan, T.U., Shah, I.A., Ahmad, B., Ahmad, N., Ahmad, I., Saleem, A and Miraj, M. 2018. Combining ability and inheritance studies for morphological and yield contributing attributes through line tester mating design in wheat (*Triticum aestivum* L.). *Pure and Applied Biology (PAB)*, 7(1), pp.160-168.
- Javed, A., Ahmad, N., Ahmed, J., Gohar, S., Abdullah, M., Iqbal, J., Qayyum, A., Ashraf, S., Alarfaj, A.A., Alharbi, S.A. and Ansari, M.J. 2025. Computation of Drought Effects on Yield and Quality of Wheat (*Triticum aestivum* L.) Via Reckoning of Morpho-Physiological Responses. Pp 407-416. <http://doi.org/10.59665/rar4236>

- Javed, A., Ahmad, N., Ahmed, J., Hameed, A., Ashraf, M. A., Zafar, S. A., Maqbool, A., amrah, H. Al- H., Alatawi, A., Alharbi M.S and Ali, E. F. 2022. Grain yield, chlorophyll and protein contents of elite wheat genotypes under drought stress. *Journal of King Saud University-Science*. (34): 102279
- Javaid, M.M., Ahmad, N., Javed, A., Makhdoom, M., Saleem, M., Owais, M., Nadeem, M. Rahman, S., Mehboob, S., Naz, S., Rehman, A., Ahmed, J and Tanveer, M.H. 2022. Monitoring and detection of wheat blast disease caused by *Magnaporthe oryzae* Triticum pathotype in Punjab, Pakistan. *SABRAO Journal of Breeding and Genetics*. 54(5): 1004- 1015. <http://doi.org/10.54910/sabrao2022.54.5.4>.
- Kashif, M., Usman, M., Ahmad, N., Owais, M., Javed, A., Ahmad, J and Ahmad, A. 2023. Selection of stable wheat genotypes under different agro-ecological zones of Punjab, Pakistan. *SABRAO Journal of Breeding and Genetics*. 55(4): 1038-1050. <http://doi.org/10.54910/sabrao2023.55.4.3>.
- Khalilzadeh, G. R. 2018. Genetic investigation of grain yield and its components in bread wheat genotypes using diallel method. *Iranian Dryland Agronomy Journal*, 6(2), pp.165-186.
- Kumar, S., Kumar, P., Arya, V.K., Kumar, R and Kerkhi, S.A. 2018. Estimates of genetic components and regression analysis for grain yield and various morphological traits in bread wheat (*Triticum aestivum* L.). *Journal of Applied and Natural Science*, 10(1), pp.6-11.
- Mather, K., Jinks, J. L., Mather, K and Jinks, J. L. 1982. Diallels. *Biometrical Genetics: The study of continuous variation*, pp.255-291.
- Noorka I. R., Batool, A., Rauf, S., Jaime, A., Silva, T and Ashraf, E. 2013. Estimation of heterosis in wheat under contrasting water regimes. *International Journal of Plant Breeding and Genetics*. 7(1), 55-60.
- Rana, U.S., Azmat, M. A. and Khan, A. S. 2023. Genetic analysis of yield related traits in 5× 5 diallel crosses of spring wheat (*Triticum aestivum* L.). *Journal of Agriculture and Biology*, 1(2), pp.71-77.
- Steel, R. G. D., Torrie, J. H and Dickey, D. A. 1997. *Principles and procedures of statistics: A biometrical approach*, 3rd ed. McGraw Hill Book Co., New York.
- Ullah, I., Khan, M., Khan, M., Khan, H and Azra. 2020. Factors affecting different wheat varieties yield in district Peshawar, Khyber Pakhtunkhwa, Pakistan: A comparative analysis. *Sarhad Journal of Agriculture*, 36(4): 1063-1066. <http://dx.doi.org/10.17582/journal.sja/2020/36.4.1063.1066>
- Zakir-Hassan, G., Hassan, F. R., Punthakey, J.F. and Shabir, G. 2021. "Challenges for Groundwater-Irrigated Agriculture and Management Opportunities in Punjab Province of Pakistan." *International Journal of Research in Agronomy*, 4(2), 142–153.