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# GENETICS OF SOME POLYGENIC TRAITS IN HEXAPLOID BREAD WHEAT IN HIGH TEMPERATURE STRESS

M. Irshad, I. Khaliq*, J. Iqbal**, N. Hussain, M. Aslam, K. Hussain and N. Din

Arid Zone Research Institute Bhakkar, Punjab, Pakistan.
*Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan. **Adaptive Research Station Gujranawala[3] Punjab, Pakistan.
Corresponding Author Email: niazfm@gmail.com

## ABSTRACT

A study was conducted to investigate the inheritance pathway of some physio-morphological traits of wheat in the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan from 2008-09 to 2010-11.Two hundred and twenty genotypes of spring wheat of diverse origin were preliminary screened in heat stress and stress free conditions during 2008-09 and out of these four high temperature stress tolerant and three thermolabile parental genotypes were selected. Forty two $F_1$progeniesof 7×7 diallel crosses alongwith parents were evaluated in stress free and heat stress environments during 2010-11.$F_1$ hybrids Bhakkar-02×SH-02 and its reciprocal had the highest grain yield per plant (28.00 and 27.33g) with a reduction of 29.42% and 26.78%, in heat stress respectively. The results revealed significant genotypic differences ($P< 0.01$) for all parameters. Adequacy tests indicated that data for spike length, grains per spike, 1000-grain weight and grain yield per plant were fit for additive dominance model, while those of dry biomass per plant at maturity were partially adequate. Additive component of variation (D) was significant ($P< 0.01$) and prominent over $H_1$ and $H_2$ components for days to anthesis, grains per spike, 1000-grain weight, grain yield per plant and dry biomass per plant at maturity while dominant genes were mainly controlling factors for spike length and was confidently sustained by the value of $H_1/D^{0.5}$. Values of $h^{\wedge 2}$ and$H_2/4H_1$ demonstrated asymmetrical and unequal distribution of dominant genes in parents for most of the characters. Spike length, dry biomass per plant at maturity, grains per spike, 1000-grain weight and grain yield per plant exhibited high narrow sense heritability due to the existence of additive gene action with partial dominance suggesting that these traits might be useful for the development of high temperature stress tolerant varieties by modified pedigree selection method.

**Keywords:** Spring wheat, terminal heat stress, physio-morphological traits, heritability, additive, asymmetrical, genetics, diallel.

## INTRODUCTION

Wheat is the most important crop and staple food of the peoples of Pakistan (Anonymous, 2008). In the subcontinent, the rising temperature of Spring during reproductive phase is a matter of great concern for wheat breeders targeting hot irrigated and late planting environments. The optimum temperature range for attaining maximum grain weight is 18-22ºC. In Pakistan temperatures above the optimum range are very common and this situation warrants the attention of researchers for apposite solution. The importance of short periods with very high temperatures have stimulated many studies (Calderini *et al.*, 1999) and wherein concluded that heat shocks decrease more individual grain weight than progressively increasing temperatures. If thermo tolerant varieties alongwith relevant production technologies are not deployed, significant yield loss may occur. Genetic potential for high yield does exist but terminal heat stress jeopardizes the yield stability. Therefore yield stability is key factor to ensure the food security. Farmers of hot irrigated climates demand varieties with high yield potential. Wheat grain weight is decreased from 4 to 8% per degree rise in mean temperature over the range of 12-26ºC during grain filling period (Wiegand and Cuellar 1981). Sharma *et al.* (2002) studied wheat heat tolerance through diallel approach and found both additive and dominance components of variance as significant for 000 grain weight and grain yield. Mohammadi *et al.* (2007) evaluated various screening techniques for heat tolerance in wheat and indicated that kernel weight was the most suited trait for heat stress screening. This study will be helpful to standardize and fine tune the selection criterion and understanding the mechanism of substantial yield losses in hot irrigated dry climate. Main objective of this study was to explore the genetic makeup of forty two $F_1$ progenies alongwith seven parents in stress free and heat stress environments. The results of this study are of vital importance for evolution of thermo tolerant wheat varieties.

## MATERIALS AND METHODS

Research work was conducted in the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad Pakistan (Latitude, 31.26°N; Longitude, 73.06°E; Altitude; 184.4m and soil pH 6.50) during the three spring wheat crop seasons from 2008-09 to 2010-11. Two hundred and twenty genotypes of diverse origin were preliminary screened in heat stress and stress free conditions during 2008-09 and four high temperature tolerant and three thermo-labile parental genotypes were selected. Experimental material was developed by crossing seven parental genotypes (Bhakkar-2002, SH-2002, V00183, Chakwal-86, 3C001, 93T347 and Punjab-96) in full diallel fashion during year 2009-10. Two separate experiments were conducted independently during wheat crop season 2010-11. First in stress free environment (Normal planting) was laid-out on 10th November 2010 and second in heat stress situation (late planting) was sown on December 20, 2010. Forty two $F_1$ progenies alongwith seven parents were laid out in each set according to randomized complete block design with three replications. Gross plot size was maintained 1.8m x 5m with plant to plant and row to row distance of 0.15 m and 0.30 m respectively. All standard agronomic practices were applied uniformly. These experiments were laid out adjacently in field in similar soil and weather conditions. The data were recorded on 10 randomly selected guarded plants of each genotype per replication per treatment of following different morphological traits.

**1. Days to anthesis (No.):** Days to 50% anthesis were recorded from date of sowing of each genotype by daily visiting the experiment in morning hours to ½ main culm spikes anthesis.

**2. Spike length (cm):** Spike length of mother shoot of selected plants at maturity was measured in centimeters from base to the tip of ear excluding awns and average value was computed.

**3. Number of grains per spike (No.):** Main spikes of all selected plants were threshed manually and grains from each main culm ear were counted, and finally average value of number of grains per main shoot spike was computed.

**4. 1000-grains weight (g):** Grain yield of ten selected plants in each replication of every genotype was bulked and 1000-grains were counted randomly from each bulk and weighed on electronic balance.

**5. Dry biomass per plant at maturity (g):** Biological yield was estimated by drying ten randomly selected plants at 65±5°C for 48 hours of every genotype in all replications in both stress and stress free conditions and then weighing separately by an electronic balance before threshing and finally average value was computed.

**6. Grain yield per plant (g):** Spikes of all individually selected plants were threshed manually and grains were weighed with electronic balance and finally average value for grain yield per plant was computed for each genotype in each replication. Data recorded for various parameters were statistically analyzed by adopting analysis of variance (ANOVA) procedure as described by Steel *et al*, (1997). Data were subjected to diallel analysis as given by Mather and Jinks (1982).

## RESULTS AND DISCUSSION

Genotypic differences were found highly significant for all the traits in both environments (Steel *et al.,* 1997). Analysis of variance of all characters under both normal and heat stress conditions are presented in (Table 1). The data collected were subjected to standard techniques of analysis of variance to establish level of genotypic differences for various attributes. The characters showing significant genotypic differences were further analyzed genetically following additive dominance model of genetic analysis developed by Mather and Jinks (1982).

### A. Plant response to high temperature

**1 Days to anthesis (No.):** Grand mean reduction of 17.50% was recorded for days to anthesis in heat stress condition. **(**Table 3**)**. Maximum reduction 20.99% was recorded in the parental genotype Punjab-96, followed by SH-02 with value 19.69%. However, minimum reduction of 15.24% for this trait was recorded in the genotype V00183.

**2 Spike length (cm):** All the genotypes showed grand mean reduction 16.30% in heat stress. Maximum reduction 39.23 % was recorded in parental genotype 3C001. V00183× SH-02 was best recombinant with value 16.7 cm and this hybrid showed reduction of 7.67 % in heat stress (Table 3). These results are in accordance with Hanchinal, *et al.* (1994) who reported 15.22 % reduction in spike length in heat stress.

**3. Grains per spike (N):** Grains per spike were maximum and at par (54.67) in two parental genotypes Bhakkar-02 and SH-02 in stress free climate while highest grain number (45.67) was recorded again in Bhakkar-02 closely followed by Chakwal-86 in heat stress among the parents. **(**Table-3**)**. Among crosses V00183 × SH-02 hybrid had the maximum (61.00) grains per spike in normal condition, while it was the highest (49.67) and at par in two crosses (Chakwal-86 x SH-02 and Bhakkar-02 x SH-02) in heat stress. However, grand mean reduction 24.56% was recorded for this trait in heat stress. These results are in accordance with, Hanchinal (1994), and Akbar *et al.* (2008).

**4 1000-grains weight (g):** Grand mean reduction 26.45% was recorded in heat stress. **(**Table-3**)**. Among crosses Bhakkar-02×SH-02 hybrid had the maximum (46.33 g)

1000 grains weight in stress free condition, while it was the highest (37.33 g) in hybrid (SH 02× Bhakkar-02) in heat stress. These results are in accordance with, Singh *et al*. (2005) and Mian*et al*. (2007)

**5. Dry biomass per plant at maturity (g):** Dry biomass per plant at maturity showed grand mean reduction 32.37% in heat stress (Table-3)**.** Similarly, in case of $F_1$ hybrids reduction in this trait ranged from 21.52 % (SH-02 × Bhakkar-02) to 42.34 % (Punjab-96 × V00183). Among crosses Bhakkar-02 × SH-02 showed maximum dry biomass per plant (97.00 g) at maturity in stress free climate and the highest value of 72.67 g was also recorded in the same cross in stress condition.

**6. Grain yield per plant (g):** Grain yield per plant was reduced 37.01% in heat stress (Table-3). The best parent was Bhakkar-02 in both stress free and heat stress regimes. Promising cross in stress free condition was Bhakkar-02 × SH-02 with grain yield 39.67 g per plant. $F_1$ hybrids Bhakkar-02 ×SH-02 and its reciprocal had the highest grain yield per plant (28.00 and 27.33g) with a reduction of 29.42% and 26.78% respectively in heat stress. Highest reduction in grain yield per plant (48.31%) was recorded in hybrid Punjab-96× V00183 which reduced grain yield from 24.67g in stress free clitmate to 12.75g in heat stress. These results get support from the findings of Wiegand and Cuellar (1981), Rajaram (1997), Singh *et al.* (2005) Rasal*et al.* (2006), Mian*et al.* (2007), Jagadish *et al*. (2007), Akbar *et al.* (2008) and Prasad *et al.* (2008).

**B Genetic analysis:** Primary analysis of variance displayed significant divergence among the genotypes for all the traits (Table 1). The mean squares showed high significance of 'F' test for all the attributes and indicated for further genetic manipulation.

**I Regression coefficient and analysis of array of variance:** Two scaling tests were employed for the validity of additive-dominance model following Mather and Jinks (1982). The joint regression coefficient test indicated that regression coefficient *b* differed significantly from zero but not from unity for days to anthesis, dry biomass per plant at anthesis, spike length, grains per spike, 1000 grain weight, dry biomass per plant at maturity and grain yield per plant in both stress conditions (Table-2).Thus the data fulfilled the assumptions of the model. Analysis of variance of arrays for dry biomass per plant at anthesis, 1000- grain weight, dry biomass per plant at maturity and grain yield per plant in heat stress showed absence of non-allelic interaction and data were considered fully adequate for further analysis. However in heat stress, second test for days to anthesis, spike length and grains per spike revealed significant differences for both Wr+Vr and Wr-Vr between arrays in heat stress. Therefore data were considered partially adequate to explain the genetic information in the presence of dominance and non-allelic interaction.

**II Estimates of genetic components of variation**

**1 Variation due to additive effects (D):** Genetic components of variation for days to anthesis, dry biomass per plant at anthesis, spike length, grains per spike, dry biomass per plant at maturity and grain yield per plant revealed that both additive (D) and dominance variations were significant in both conditions (Table-4). Genetic components of variations for 1000- grain weight revealed that only additive (D) gene action was significant in both conditions. However, additive component (D) was greater than H components for all the traits in both temperature regimes displaying predominance of additive effects.

**2 Variation due to dominance effect ($H_1$& $H_2$) and $H_2/4H_1$:** $H_1$ and $H_2$ values for days to anthesis in stress free climate were necessarily equal in magnitude displaying uniformity of distribution of positive and negative alleles among the parents. Unequal and significant values of $H_1$ and $H_2$ and ratios of $H_2/4H_1$ for dry biomass per plant at anthesis, spike length, grains per spike, dry biomass per plant at maturity and grain yield per plant in both environments indicated the unequal distribution of positive and negative alleles among the parents.

**3 Mean of 'Fr' over the arrays (F) and $4DH_1^{0.5}+F/4DH_1^{0.5}-F$:** Significant and positive F value and ratio of dominant to recessive genes (1.38) signified the important role of dominant genesfor dry biomass per plant at maturity in stress free environment. F value was non-significant and positive alongwith ratios of dominant to recessive genes being greater than 1 and signified the role of dominant genes for dry biomass per plant at anthesis, 1000-grain weight and grain yield per plant in both temperature regimes. F value was non-significant and positive for days to anthesis in non-stress environmentand ratio of dominant to recessive genes (1.24) indicated that the dominant genes were more frequent (Table-4).

**4 Dominance effect ($h^{\wedge 2}$):** Significant and positive value of $h^{\wedge 2}$ for dry biomass per plant at anthesis in stress free environment indicated the influential role of net dominant effect due to heterozygous loci for the expression of this trait. Non-significant and positive value of $h^{\wedge 2}$ for days to anthesis, spike length and grains per spike in stress free environment indicated un-important role of net dominant effect due to heterozygous loci in the expression of this trait.

**5 Environmental component of variation (E):** Significant value of E indicated the influence of environment on expression of traits viz., grains per spike and dry biomass per plant at maturity in both temperature regimes.Similarly, significant value of E indicated the influence of environment in expression of traits viz., dry biomass per plant at anthesis and grain yield per plant in heat stress

**6 Average degree of dominance** $(H_1/D)^{0.5}$: Average degree of dominance for days to anthesis, spike length, grains per spike, 1000-grain weight, dry biomass per plant at maturity and grain yield per plant in both temperature regimes suggested the presence of partial dominance(Table-4). Additive gene action with partial dominance for 1000 grain weight has earlier been reported by Hanchinal, (1994), Singh *et al.* (2002), Esmail (2002), Hamada *et al.* (2002), Yao-JinBao*et al.* (2004). Additive gene action with partial dominance for grain yield per plant has been reported also by Esmail, (2002), Hamada *et al.* (2002) and Chandrashekhar and Kerketta (2004).

**7 Heritability (N.S):** High narrow sense heritability estimates were recorded for days to heading, spike length, grains per spike, 1000-grains weight, dry biomass per plant at maturity and grain yield per plant (Table 4) indicating considerably large additive proportion in the total heritable genetic variation. High heritability estimates were also reported for spike length by Yao-JinBao*et al.* (2004), Koumber and Esmail (2005) and Khan *et al.* (2005). High narrow sense heritability estimates for 1000-grains weight were reported by Hamada, *et al.* (2002). High narrow sense heritability estimates for grain yield were reported by Hamada *et al.* (2002), Chandrashekhar and Kerketta (2004) and Khan *et al.* (2005).

**III Wr/Vr graph:**

**1Days to anthesis:** Placement of array points indicated (Figure 1a) that parental genotypes Punjab-96, 3C001,V00183 and Chakwal-86 occupied equal proportion of dominant and recessive genes . Genotypes, Bhakkar-02 and 93T347 had the least dominant, while SH-02 had maximum dominant genes. Figure 1b indicated that 3C001 had the maximum dominant genes, maximum recessive genes were found in Bhakkar-02 and V00183 while parental genotypes SH-02, Punjab-96 and Chakwal-86 had equal proportion of dominant and recessive genes in heat stress.

**2. Spike length (cm):** Figure 2a indicated that genotypes, Chakwal-86, Bhakkar-02, SH-02, V00183 and Punjab-96 had equal proportion of dominant and recessive genes. Genotype, 3C001 had the minimum dominant genes, while maximum dominant genes were found in 93T347 in stress free condition. Figure 2bexplained that genotypes SH-02, V00183, 93T347, Pb-96 and Ch-86 have equal proportion of dominant and recessive genes in heat stress. However maximum dominant genes were found in Bhakkar-02.

**3. Grains per spikes (N):** Figure 3a indicated that genotypes Chakwal-86, Bhakkar-02, SH-02 and V00183 had equal proportion of dominant and recessive genes. Genotypes Punjab-96 and 3C001 had minimum dominant genes, while maximum dominant genes were found in 93T347. Figure 3b indicated that minimum dominant genes were expressed in genotypes, Bhakkar-02, V00183 and Chakwal-86 alongwith equal proportion of dominant and recessive genes in two genotypes 3C001 and SH-02 in heat stress.

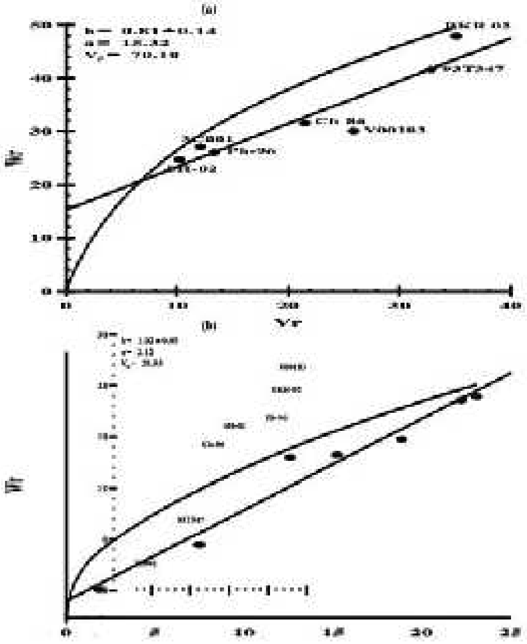

**Fig. 1: Wr/Vr graph for days to anthesis in (a) stress free and (b) heat stress environments**

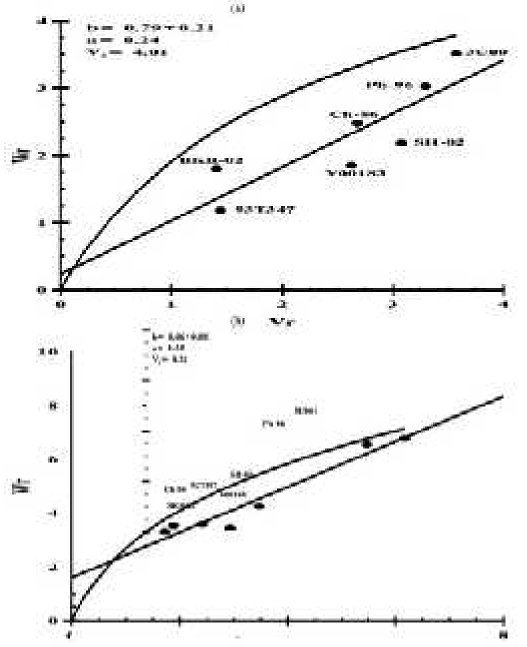

**Fig. 2: Wr/Vr graph for spike length in (a) stress free and (b) heat stress environments.**

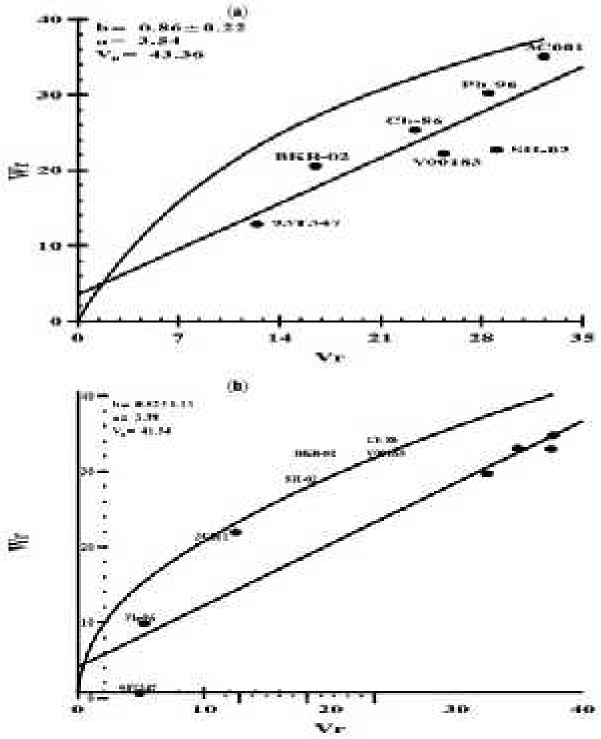

**Fig. 3 : Wr/Vr graph for grains per spike in (a) stress free and (b) heat stress environments.**

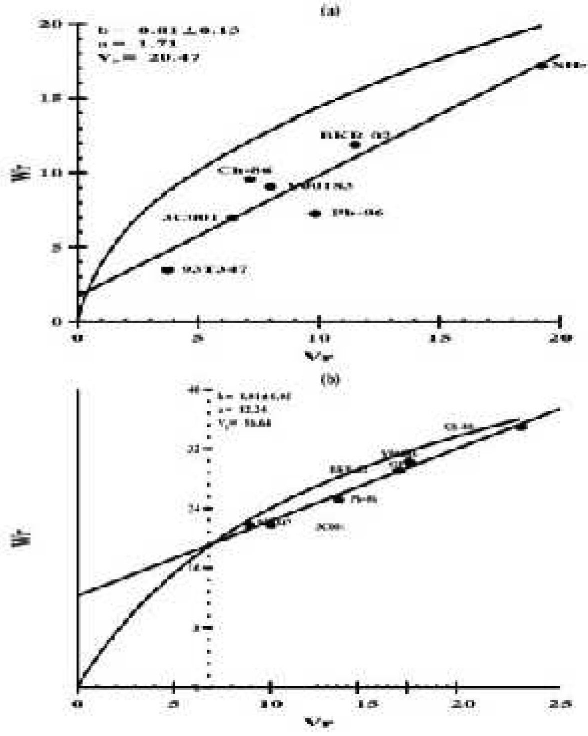

**Fig. 4: Wr/Vr graph for 1000-grain weight in (a) stress free and (b) heat stress environments.**

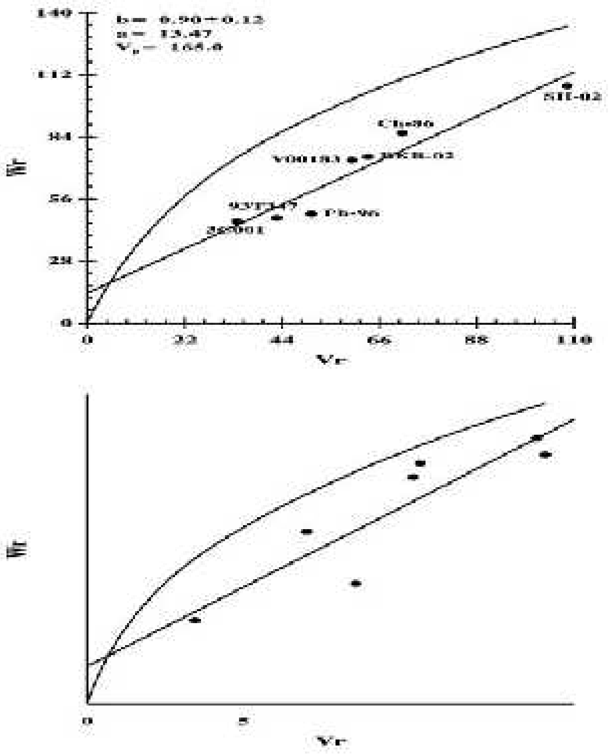

**Fig. 5 :Wr/Vr graph for dry biomass per plant at maturity in (a) stress free and (b) heat stress environment**

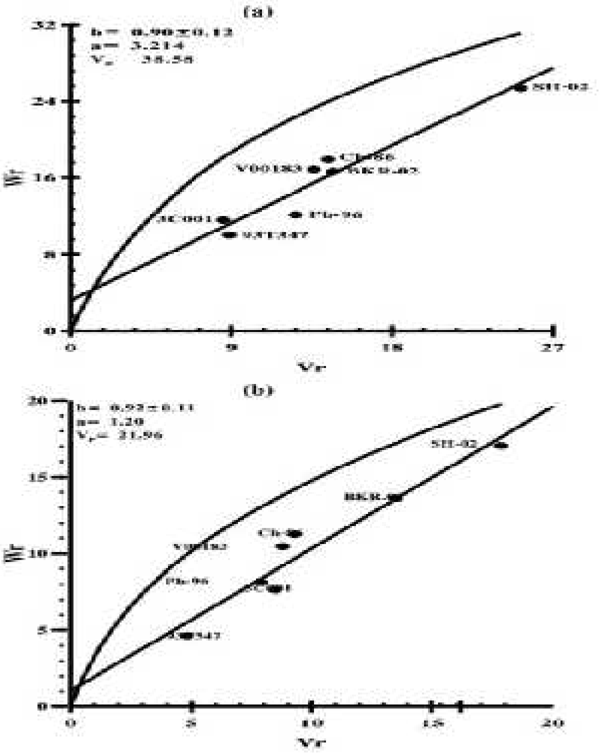

**Fig. 6 :Wr/Vr graph for grain yield per plant in (a) stress free and (b) heat stress environments.**

**4. 1000-grain weight (g):** Figure 4a explained that genotypes Chakwal-86, Bhakkar-02, 3C001, Punjab-96 and V00183 had equal proportion of dominant and recessive genes. Genotype SH-02 had minimum dominant genes, while maximum dominant genes were found in 93T347 in stress free condition. Figure 4b showed that minimum dominant genes were expressed in genotype Chakwal-86. However, 3C001, Punjab-96, Bhakkar-02, SH-02 and V00183 genotypes displayed equal proportion of dominant and recessive genes in heat stress, whilemaximum dominant genes were found in 93T347.

**5. Dry biomass per plant at maturity (g):** Figure 5a indicated that genotypes V00183, Punjab-96, Bhakkar-02, Chakwal-86 and 93T347 had equal proportion of dominant and recessive genes. Genotype SH-02 had the least dominant genes, while 3C001 had the maximum dominant genes.Figure 5bindicated that 93T347 had the maximum dominant genes, maximum recessive genes were found in Bhakkar-02 and V00183 whereas genotypes SH-02, 3C001, Punjab-96 and Chakwal-86 had equal proportion of dominant and recessive genes in heat stress.

**6. Grain yield per plant (g):** Placement of array point revealed that genotypes Chakwal-86, Bhakkar-02 and V00183 have equal proportion of dominant and recessive genes. Genotype SH-02 had minimum dominant genes, while 3C001, Punjab-96 and 93T347 had the maximum dominant genes **(**Figure6a**)**. Strain 93T347 had the maximum dominant genes, while maximum recessive genes were found in SH-02. Genotypes 3C001, V00183, Bhakkar-02, Punjabb-96 and Chakwal-86 had equal proportion of dominant and recessive genes in heat stress **(**Figure6b**)**.

**Table 1. Estimates for mean squares for quantitative traits in hexaploid bread wheat in stress free and heat stress environments.**

| S. No. | Traits | Mean squares df= 41 | | | |
|---|---|---|---|---|---|
| | | Stress free. | | Heat stress | |
| | | Genotypic | Error | Genotypic | Error |
| 1 | Days to anthesis | $97.689^{**}$ | 0.352 | $64.771^{**}$ | 0.301 |
| 2 | Spike length | $11.681^{**}$ | 0.232 | $16.076^{**}$ | 0.358 |
| 3 | Number of grains per spike | $110.927^{**}$ | 12.407 | $99.879^{**}$ | 20.049 |
| 4 | 1000 grain weights | $39.739^{**}$ | 3.468 | $76.638^{**}$ | 0.460 |
| 5 | Dry biomass per plant at maturity | $261.402^{**}$ | 22.586 | $438.519^{**}$ | 84.893 |
| 6 | Grain yield per plant | $59.421^{**}$ | 5.138 | $43.880^{*}$ | 3.902 |

**Table 2.Regression coefficient and analysis of array of variance for various traits in hexaploid bread wheat studied in stress free and heat stress environments.**

| S. No. | Characters | Stress free environment. | | | | Heat stress environment | | | |
|---|---|---|---|---|---|---|---|---|---|
| | | R Regression Analysis | | Analysis of array Variance | | Regression Analysis | | Analysis of array Variance | |
| | | b=0 | b=1 | Wr+Vr | Wr-Vr | b=0 | b=1 | Wr+Vr | Wr-Vr |
| 1 | Days to anthesis | $^{**}$ | NS | $^{**}$ | $^{**}$ | $^{**}$ | NS | $^{**}$ | $^{**}$ |
| 2 | Spike length | $^{*}$ | NS | $^{**}$ | NS | $^{**}$ | NS | $^{**}$ | $^{*}$ |
| 3 | Number of grains per spike | $^{*}$ | NS | $^{*}$ | NS | $^{**}$ | NS | $^{**}$ | NS |
| 4 | 1000-grain weight | $^{**}$ | NS | $^{**}$ | NS | $^{**}$ | NS | $^{**}$ | NS |
| 5 | Dry biomass per plant at maturity | $^{**}$ | NS | NS | NS | $^{**}$ | NS | NS | NS |
| 6 | Grain yield per plant | $^{**}$ | NS | $^{*}$ | NS | $^{**}$ | NS | $^{*}$ | NS |

$^{*}$=Significant $^{**}$ = Highly significant NS= Non-significant

**Table 3. Grand mean, coefficient of variability, LSD values and % deviation for quantitative traits in bread wheat in stress free and heat stress.**

| **Sr. No.** | **Trait** | **Condition** | **Grand mean** | **COV%** | **LSD (0. 05)** | **% deviation** | | |
|---|---|---|---|---|---|---|---|---|
| | | | | | | **Range** | | **Grand mean** |
| | | | | | | **Parents** | **$F_1$ hybrid** | |
| 1 | Days to anthesis (N) | Stress free | 107.71 | 0.55 | 0.959 | 15.24 - 19.69 | 8.59-21.70 | -17.50 |
| | | Heat stress | 88.85 | 0.62 | 0.887 | | | |
| 2 | Spike length (cm) | Stress free | 13.19 | 3.65. | 0.77 | 07.23-39.23 | 06.74-31.57 | -16.30 |
| | | Heat stress | 11.04 | 5.42 | 0.96 | | | |
| 3 | Grain per spike(N) | Stress free | 50.09 | 07.03 | 5.69 | 15.71-31.25 | 12.96-34.20 | -24.56 |
| | | Heat stress | 37.95 | 11.80 | 7.23 | | | |
| 4 | h^ 1000-grain weight (g) | Stress free | 38.26 | 04.87 | 3.01 | 15.02-37.67 | 12.39-43.74 | -26.45 |
| | | Heat stress | 28.14 | 02.41 | 1.10 | | | |
| 5 | Dry biomass per plant at maturity(g) | Stress free | 77.07 | 01.76 | 7.68 | 24.61-39.34 | 21.52-42.34 | -32.37 |
| | | Heat stress | 52.57 | 16.68 | 14.89 | | | |
| 6 | Grain yield per plant (g) | Stress free | 30.34 | 7.48 | 3.664 | 31.61-49.77 | 19.62-42.34 | -37.01 |
| | | Heat stress | 19.11 | 9.77 | 3.193 | | | |
| | | Heat stress | 19.11 | 9.77 | 3.193 | | | |

D = Variation due to additive effects.
H = variation due to dominance effect.
F = Mean of 'Fr' over the arrays
E = Environmental component of variation
$(H1/D)^{0.5}$ = Degree of dominance
$H_2/4H_1$ =Proportion of genes with positive and negative effects in the parents
$h^2_{(n.s)}$ = Heritability (N.S)
$4DH_1^{0.5}+F/4DH_1^{0.5}-F$ = Proportion of dominant and recessive genes in the parents
$h\wedge^2$ = Dominance effect (as the algebraic sum over all the loci in heterozygous phase in all loci)

**Table 4. Estimates of genetic components of variation for various traits of hexaploid bread wheat in normal temperature and heat stress.**

| **S. No** | **Character** | **Condition** | **D** | **$H_1$** | **$H_2$** | **F** | **$h\wedge^2$** | **E** | **$(H_1/D)^{0.5}$** | $H_2/4H_1$ | **$4DH_1^{0.5}+F/4DH_1^{0.5}-F$** | **$h^2_{(n.s)}$** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | Days to anthesis (N) | **Stress free** | 69.93$^*$ | 25.08$^*$ | 25.31$^*$ | 9.12 | 10.31 | 0.17 | 0.60 | 0.24 | 1.24 | 0.83 |
| | | **Heat stress** | 22.83$^*$ | 20.11$^*$ | 18.21$^*$ | -7.70$^*$ | 7.27$^*$ | 0.12 | 0.82 | 0.22 | 0.72 | 0.80 |
| 2 | Spike length(cm) | **Stress free** | 6.93$^*$ | 4.98$^*$ | 3.16$^*$ | -1.25 | 0.35 | 0.08 | 0.86 | 0.16 | 0.75 | 0.80 |
| | | **Heat stress** | 4.14$^*$ | 3.78$^*$ | 3.13$^*$ | -1.46 | 4.43$^*$ | 0.11 | 0.68 | 0.21 | 0.75 | 0.76 |
| 3 | Grain per spike(N) | **Stress free** | 39.23$^*$ | 31.10$^*$ | 19.06$^*$ | -15.85$^*$ | 3.58 | 4.12$^*$ | 0.89 | 0.15 | 0.63 | 0.79 |
| | | **Heat stress** | 34.94$^*$ | 27.39$^*$ | 24.63$^*$ | -16.85 | -0.33 | 6.60$^*$ | 0.88 | 0.22 | 0.57 | 0.68 |
| 4 | 1000-grain weight | **Stress free** | 19.28$^*$ | 17.51$^*$ | 16.80$^*$ | 1.89 | -0.19 | 1.18 | 0.95 | 0.24 | 1,11 | 0.62 |
| | | **Heat stress** | 56.46$^*$ | 6.75 | 5.53 | 2.73 | 0.06 | 0.18 | 0.34 | 0.20 | 1.15 | 0.95 |
| 5 | Dry biomass per plantat maturity(g) | **Stress free** | 157.20$^*$ | 113.18$^*$ | 97.77$^*$ | 42.65$^*$ | -2.82 | 7.82$^*$ | 0.85 | 0.22 | 1.38 | 0.67 |
| | | **Heat stress** | 236.97$^*$ | 66.28$^*$ | 75.29$^*$ | -10.06 | 17.95 | 29.38$^*$ | 0.52 | 0.28 | 0.92 | 0.71 |
| 6 | Grain yield per plant (g) | **Stress free** | 36.78$^*$ | 26.42$^*$ | 22.99$^*$ | 11.33 | -0.62 | 1.80 | 0.85 | 0.21 | 1.44 | 0.65 |
| | | Heat stress | 20.66$^*$ | 16.95$^*$ | 15.45$^*$ | 0.43 | -0.38 | 1.30$^*$ | 0.90 | 0.22 | 1.02 | 0.67 |

$^*$= Value is significant when it exceeds 1.96 after dividing with its standard error.

**Conclusions:** 1. Additive gene action with partial dominance was observed for all the traitsboth temperature stress conditions suggesting that these traits might be useful for the evolution of thermo-tolerant hexaploid spring wheat varieties for hot irrigated dry climate by modified pedigree selection empirical breeding technique. 2. $F_1$ progenies resulting from fore mentioned parents performed better in high temperature stress. Therefore outcome of this study indicated that future high yielding terminal heat stress tolerant varieties can be developed by involving genotypes Bhakkar-02, SH-02 and Chakwal-86 as parents and at the same time incorporating traits like 1000 grain weight and number of grains per spike to ensure the yield stability in present scenario of global warning and climate change.

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