

Genetic Variability and Trait Association Analysis in Yield and Yield Components in Bread Wheat (*Triticum aestivum* L.) Genotypes under Rainfed Condition

Arpit Gaur¹, Vikaram Singh², Sonia Sheoran³, Deepak Kaushik⁴ and Yogesh Jindal^{5*}

^{1,2,4,5}Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar-125004, Haryana

³Crop Improvement, ICAR-Indian Institute of Wheat and Barley Research, Karnal-32001, India

*Corresponding Author E-mail: yjindalhau@gmail.com

Received: 1.07.2020 | Revised: 4.08.2020 | Accepted: 11.08.2020

ABSTRACT

One hundred bread wheat (*Triticum aestivum* L.) were evaluated for genetic variability and yield performance under rainfed condition in two replication using alpha-lattice design. Substantial variations were reported among genotypes with ANOVA for all the fourteen studied traits. Low to moderate range of GCV (1.7-17.1%) and low to high PCV (2.3-23.4%), GAM (3.5-32.6%) and heritability (42.9-79.2%) were reported. At genotypic level GY showed positive and highly significant correlation with DTH, DTA, DTM, NOT, SL, BM, HI, TKW and TNG at genotypic level and with DTM, BM, HI, TKW and TNG at phenotypic level. TKW and TNG showed highest positive and direct effect on GY in path analysis. Genotypes HI1531, HI1581 and C306 were showed highest yield.

Keywords: Wheat, Rainfed, Genetic variability, Correlation, Path analysis.

INTRODUCTION

Global food security for the coming generations is a prime issue across the continents due to rapidly diminishing natural resources and climate change (Behnassi et al., 2018). Wheat (*Triticum aestivum* L.) is one of the most important pillars of global food security. It provides 41% of total calories and 50% of total proteins consumed from cereals globally (Shiferaw et al., 2013). Across the globe, it cultivated on nearly 220 million hectares area with an average 670 million tons of annual production (Ramadas et al., 2019). In near future, wheat demand is expected to be

raise by 60%. At present climatic anomalies are the major threat for crop productions. Climate change has significantly affected the global food security by means of affecting the crop production across the world through many ways among them water stress in one (Shan et al., 2020). Therefore, development of climate resilient crop varieties has become a major objective for plant breeders. Wheat crop is highly sensitive to water availability (Choudhury & Kumar, 1980). Water stress at any point of wheat plant lifecycle significantly reduces grain yield and quality.

Cite this article: Gaur, A., Singh, V., Sheoran, S., Kaushik, D., & Jindal, Y. (2020). Genetic Variability and Trait Association Analysis in Yield and Yield Components in Bread Wheat (*Triticum Aestivum* L.) Genotypes under Rainfed Condition, *Ind. J. Pure App. Biosci.* 8(5), 240-247. doi: <http://dx.doi.org/10.18782/2582-2845.8278>

In past few years due to climate change incidences of water stress have substantially increased throughout the world with a great impact on wheat production. Therefore, development of drought tolerant wheat varieties is a major goal for both national and international wheat breeding programs.

Pre-breeding which includes evaluation and development of genetic resources, development of selection indices, and estimation of genetic variability is the base of a successful sustainable breeding program. With this reason, here in this study we have studied a set of one hundred bread wheat (*Triticum aestivum* L.) genotypes for their yield performance, genetic variability and trait association under rainfed conditions.

MATERIALS AND METHODS

Filed experiment: The field experiment was conducted during Rabi 2018-19 at experimental farms of Section of Wheat and Barely Breeding, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University. A total of 100 bread wheat (*Triticum aestivum* L.) genotypes were field planted in alpha lattice experimental design with two replications in first week of November-2018. Each genotype was sown using dibbling method with following planting specification: seed depth: 10 cm, plant to plant spacing: 10 cm, row to row spacing: 20 cm, plot to plot spacing: 100 cm, block to block spacing: 150 cm. No irrigation was given throughout the life cycle rest agronomic practices were carried out as per recommended package of practices.

Data collection: The following agronomic data were collected on per plant basis: 1) days to heading (DTH) were measured as the number of days until 75% of the plants had fully emerged spikes, 2) days to flowering (DTA) were measured as the number of days until 75% of the plants had fully emerged anthers, 3) days to maturity (DTM) were measured as the number of days until 75% of the plants had reached senescence, 4) grain filling duration (GFD) period between DTA and DTM, 5) productive tiller number (NOT) was measured as the number of tillers that had managed to set seed, 6) plant height (PH) was measured as the height from base of the plant to the point where the spike emerged, 7) peduncle length (PL) was measured from first internode to base of the spike. 8) spike length (SL) was measured from the base of the spike to the tip of the spike, 9) spikelets per spike (SPS) were measured by counting the number of spikelets per spike, 10) biomass (BM) was measured as mass of all above-ground plant parts, 11) grain yield (GY) was measured after harvesting using an electronic balance, 12) harvest index (HI) percentage ration between GY and BM, 13) thousand kernel weight (TKW) was measured by randomly sampling 1000 kernels and weighing them, and 14) Total number of grains per plant (TNG) were measured by counting total number of grains harvested.

Data analysis:

Analysis of variance for each trait was calculated using restricted maximum likelihood (ReML) method in R environment with following model.

$$Y_{ijk} = \mu + Rep_i + Block_j \times Rep_i + Gen_k + \epsilon_{ijk}$$

Broad sense heritability (H^2) was calculated as

$$H^2 = \frac{\sigma_g^2}{\sigma_g^2 + \frac{\sigma_e^2}{r}} \times 100$$

where ' σ_g^2 ', ' σ_e^2 ' and ' r ' are genetic variance, residual variance and number of replications, respectively.

genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was calculated as a percentage ratio between under

root of corresponding variance ($\sigma_{g\text{ or }p}^2$) and grand mean (\bar{X}).

Genetic advance and genetic advance over grand mean were calculated for each

environment, management and across the environment as per (Johnson et al., 1955).

a. Genetic advance (GA)

$$GA = k \cdot h^2 \cdot \sigma^2$$

b. Genetic advance over mean (GAM)

$$GAM = \frac{GA}{\bar{X}}$$

Where: k is standardized selection differential at 5% selection intensity (2.06), h^2 is broad sense heritability for the trait, \bar{X} is population mean for the trait.

Furthermore, categorization of GCV and PCV was done as suggested by Sivasubramanin and Menon (1973) and for heritability and GAM% categorization suggested by Johnson et al. (1955).

| Category | GCV and PCV | Heritability | GAM |
|----------|-------------|--------------|--------|
| Low | <10% | <30% | <10% |
| Moderate | 11-20% | 31-60% | 11-20% |
| High | >20% | 60> | >20% |

Phenotypic and genotypic correlation coefficients of all the characters were worked-out as per Al-Jibouri et al. (1958) and path coefficient analysis was carried-out as per the method suggested by Dewey and Lu (1959).

RESULTS AND DISCUSSION

In present investigation, ANOVA advocated the existence of substantial genetic variability at significance level $p > 0.01$ in the study material for all the fourteen studied traits (Table 1). For some traits such as GY, BM and TNG we reported difference among replications. This expected difference among replications was due to uncontrollable errors which generated due to uneven distribution of water stress in the open fields however, effects of these errors on present study were negligible or in acceptable range. The coefficient of variation (CV%) ranged between 1.4% and 18.7% (Table 2). High values (>10%) of CV for the traits NOT, PH, BM, GY, HI and TNG show that these traits are under the influence of environment thus selection based on these traits can be misleading. With this reason traits with low

CV could be used with more reliability. Similar results were reported by (Shamuyarira et al., 2019). We reported a wide range for all the studied traits (Table 2). Among the evaluated genotypes, HI1531, HI1581 and C306 were the highest yielder. These genotypes are identified drought tolerant varieties thus the present investigation also supported previous claims and recommendations to use these genotypes for limited water conditions.

Estimation of genetic variance (Table 2) revealed that for all the traits PCV was greater from the corresponding GCV. For DTH, DTA and DTM both GCV, PCV and GAM were low. PH, SPS and TKW were recorded with low GCV and moderate PCV and GAM. Both GCV and PCV were reported moderate for GFD, PL, SL, GY and TNG whereas, for NOT, BM and HI GCV and PCV were moderate and high, respectively. Furthermore, moderate GAM was reported for GFD, PH, SPS, and TKW and high GAM was reported for NOT, PL, SL, BM, GY, HI and TNG. We reported high broad sense heritability (H^2) for all the traits excluding PH, BM and TNG

which had moderate level of H^2 . Results from GCV and PCV illustrate that variability in the present study material is largely influenced with environmental factors rather than genetic factors. Furthermore, traits with high heritability and high GAM indicates the high responsiveness to selection and presence of additive effects whereas, for traits with high heritability to moderate heritability and moderate to low GAM indicates the presence of non-additive effects thus multiple selection cycle will be needed for these traits. Our results are in agreement with many previous studies however some contradiction arises due to difference in plant material and climatic conditions during studies (Shamuyarira et al., 2019; Mathew et al., 2018; Mwadzingeni et al., 2016; Jatoi et al., 2012).

Relatedness between studied traits in the present study material was estimated at both genotypic and phenotypic levels. At genotypic level GY showed positive and highly significant correlation with DTH, DTA, DTM, NOT, SL, BM, HI, TKW and TNG at $p > 0.01$ and with PH and SPS at $p > 0.05$. In contrast to this at phenotypic GY showed significantly positive association with DTM, BM, HI, TKW and TNG. Detailed results on correlation studies are presented in Table 3. Correlation studies are affirmative with Qaseem et al. (2019), Malav et al. (2017) and Mia et al. (2017). Furthermore, to partition and estimate the effect of individual trait on GY path coefficient analysis was carried out (Table 4). Results from the path analysis revealed that in the scenario of present investigation, DTH, DTM, TKW and TNG had a higher magnitude of direct effect on GY in positive direction whereas DTA and GFD had it in negative direction. Rest of the traits showed a very low magnitude of direct effect

on GY among which PL, SL and BM had positive effect and NOT, PH, SPS and HI had negative effect. Since, TKW and TNG had largest direct on GY we pursued the indirect effect of other traits on GY *via* these traits. DTH, DTA, SPS and SL showed negative indirect effect of low magnitudes on GY *via* TKW whereas rest of the traits imposed positive indirect effects. TKW increases GY by means of weight. Indirect effect of various traits on GY *via* TKW can be understood by physiological basis of growth and development of wheat kernel. GFD increases with early DTH/DTA and delayed maturity. A longer GFD allows increased accumulation of assimilates in developing grain which lead to increase in the kernel weight. Higher number of NOT and PL are associated with increased green area of plant which allow more assimilation of photosynthates. Additionally, PL stores water soluble carbohydrates which works as reservoirs under water stressed conditions. High HI further indicates the transformation of BM into GY. Unlike TKW, TNG contributes in GY by means of numbers. In present investigation all the traits excluding GFD and PL showed positive indirect effect on GY *via* TNG. These traits increase TNG by maintain pollen fertility under water stress conditions. Early DTH and DTA are associated with escape mechanism. Increased NOT improves the canopy cover and green area which improve assimilation and carbon mobilization necessary to maintain the pollen fertility. Longer SL assures a greater number of spikelets thus a greater number of grains. These results are in agreement with previous studies of Malav et al. (2017), Gelalcha & Hanchinal (2013), Khan et al. (2005) and many others.

Table 1: Mean squares analysis of variance involving fourteen phenotypic traits of hundred wheat genotypes evaluated in two replications under rainfed conditions

| Source | Mean Sum of Squares | | | | | | | | | | | | | |
|----------|---------------------|-------|-------|--------|--------|---------|-------|------|------|-------|--------|---------|-------|-----------|
| | DTH | DTA | DTM | GFD | NOT | PH | PL | SL | SPS | BM | GY | HI | TKW | TNG |
| Rep | 67.28 | 74.30 | 26.65 | 199.80 | 337.73 | 2349.99 | 5.55 | 3.20 | 2.00 | 0.38 | 488.50 | 5932.96 | 0.60 | 318140.47 |
| Block | 30.43 | 32.62 | 18.84 | 16.96 | 3.35 | 321.76 | 33.23 | 1.10 | 5.38 | 39.14 | 4.62 | 73.20 | 20.22 | 2974.45 |
| Genotype | 23.74 | 25.20 | 10.54 | 21.01 | 4.46 | 246.46 | 27.90 | 3.26 | 7.35 | 62.99 | 5.71 | 76.10 | 27.33 | 3047.03 |
| Error | 8.31 | 10.90 | 3.10 | 8.68 | 1.81 | 160.77 | 7.35 | 0.94 | 2.34 | 25.93 | 1.82 | 19.82 | 6.93 | 1509.06 |

Table 2: Genetic parameters for yield and associated traits in hundred wheat genotypes under rainfed condition

| Statistic | DTH | DTA | DTM | GFD | NOT | PH | PL | SL | SPS | BM | GY | HI | TKW | TNG |
|--------------|-------|-------|--------|-------|-------|--------|-------|-------|-------|-------|-------|-------|-------|---------|
| □ | 81.79 | 89.76 | 117.91 | 28.11 | 7.85 | 94.52 | 30.19 | 10.86 | 19.75 | 29.06 | 10.17 | 35.96 | 39.43 | 259.06 |
| Minimum | 70.50 | 78.00 | 112.00 | 22.00 | 4.95 | 73.95 | 22.03 | 7.95 | 15.00 | 18.94 | 5.88 | 19.92 | 31.26 | 169.84 |
| Maximum | 90.50 | 98.00 | 123.50 | 37.50 | 14.13 | 127.35 | 44.06 | 17.85 | 24.00 | 48.33 | 14.93 | 61.76 | 48.72 | 360.78 |
| σ^2 | 11.06 | 10.25 | 4.45 | 8.18 | 1.81 | 57.99 | 13.11 | 1.27 | 2.93 | 16.60 | 2.28 | 34.08 | 12.31 | 956.78 |
| σ_p^2 | 18.73 | 20.27 | 7.41 | 16.06 | 3.36 | 211.82 | 19.98 | 2.13 | 5.28 | 46.23 | 4.17 | 53.59 | 19.08 | 2492.67 |
| σ_e^2 | 7.67 | 10.02 | 2.95 | 7.87 | 1.55 | 153.83 | 6.87 | 0.86 | 2.35 | 29.64 | 1.89 | 19.51 | 6.76 | 1535.89 |
| H^2 (%) | 74.26 | 67.15 | 75.09 | 67.52 | 70.03 | 42.99 | 79.25 | 74.63 | 71.35 | 52.83 | 70.65 | 77.75 | 78.46 | 55.47 |
| GCV (%) | 4.07 | 3.57 | 1.79 | 10.18 | 17.15 | 8.06 | 11.99 | 10.36 | 8.66 | 14.02 | 14.84 | 16.23 | 8.90 | 11.94 |
| PCV (%) | 5.29 | 5.02 | 2.31 | 14.26 | 23.37 | 15.40 | 14.80 | 13.43 | 11.63 | 23.40 | 20.08 | 20.36 | 11.08 | 19.27 |
| GA | 6.62 | 6.23 | 4.21 | 5.57 | 2.65 | 12.89 | 7.30 | 2.24 | 3.38 | 7.40 | 2.97 | 11.73 | 7.06 | 57.05 |
| GAM (5%) | 8.09 | 6.94 | 3.57 | 19.83 | 33.71 | 13.64 | 24.17 | 20.64 | 17.10 | 25.47 | 29.23 | 32.60 | 17.90 | 22.02 |
| LSD (5%) | 4.83 | 5.27 | 3.18 | 4.60 | 2.08 | 16.45 | 4.85 | 1.60 | 2.59 | 7.90 | 2.31 | 8.02 | 4.59 | 58.20 |
| CV (%) | 3.39 | 3.53 | 1.46 | 9.98 | 15.87 | 13.12 | 8.68 | 8.54 | 7.76 | 18.74 | 13.53 | 12.28 | 6.60 | 15.13 |

Table 3: Genotypic (below diagonal) and phenotypic (above diagonal) correlation coefficients among fourteen characters in hundred genotypes of bread wheat under rainfed condition

| | DTH | DTA | DTM | GFD | NOT | PH | PL | SL | SPS | BM | GY | HI | TKW | TNG |
|-----|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|
| DTH | 1 | 0.974** | 0.449** | - | -0.143* | 0.111 | -0.023 | -0.041 | -0.042 | 0.052 | 0.054 | 0.004 | -0.103 | 0.119 |
| DTA | 0.997** | 1 | 0.476** | - | -0.147* | 0.115 | 0.007 | -0.045 | -0.048 | 0.057 | 0.018 | -0.037 | -0.138 | 0.105 |
| DTM | 0.521** | 0.554** | 1 | - | -0.044 | 0.327** | 0.325** | -0.01 | 0.078 | 0.276** | 0.196** | -0.139* | 0.082 | 0.150* |
| GFD | - | - | 0.112 | 1 | 0.144* | 0.103 | 0.241** | 0.033 | 0.111 | 0.129 | 0.121 | -0.051 | 0.225** | -0.015 |
| NOT | - | - | - | 0.319** | 1 | -0.037 | -0.001 | 0.005 | -0.058 | -0.042 | 0.103 | 0.157* | 0.087 | 0.058 |
| PH | 0.298** | 0.400** | 0.840** | 0.194** | 0.089 | 1 | 0.474** | -0.025 | 0.054 | 0.305** | 0.065 | - | 0.105 | -0.002 |
| PL | -0.013 | 0.013 | 0.507** | 0.354** | 0.003 | 1.130** | 1 | -0.057 | 0.032 | 0.276** | 0.071 | - | 0.114 | 0.001 |
| SL | -0.012 | -0.007 | 0.051 | 0.05 | 0.103 | 0.012 | -0.155* | 1 | 0.293** | 0.022 | 0.12 | 0.073 | -0.025 | 0.140* |
| SPS | 0.215** | 0.215** | 0.240** | -0.02 | -0.127 | 0.03 | 0.01 | 0.419** | 1 | 0.073 | 0.059 | -0.07 | -0.079 | 0.11 |
| BM | 0.240** | 0.313** | 0.703** | 0.202** | 0.033 | 0.967** | 0.583** | 0.127 | 0.260** | 1 | 0.548** | - | 0.1 | 0.513** |
| GY | 0.212** | 0.202** | 0.450** | 0.134 | 0.251** | 0.171* | 0.098 | 0.223** | 0.174* | 0.340** | 1 | - | 0.350** | 0.837** |
| HI | -0.076 | -0.142* | - | 0.009 | 0.218** | - | - | 0.076 | -0.109 | - | 0.651** | 1 | 0.231** | 0.224** |
| TKW | -0.073 | -0.106 | 0.238** | 0.290** | 0.194** | 0.172* | 0.178* | -0.033 | - | 0.214** | 0.609** | 0.403** | 1 | - |
| TNG | 0.308** | 0.317** | 0.391** | -0.031 | 0.163* | 0.047 | -0.026 | 0.302** | 0.409** | 0.269** | 0.807** | 0.519** | 0.019 | 1 |

*, ** Significant at 5% and 1% levels, respectively

Table 4: Genotypic path coefficient analysis showing direct (diagonal and bold) and indirect effects of different characters on grain yield in 50 genotypes of bread wheat

| | DTH | DTA | DTM | GFD | NOT | PH | PL | SL | SPS | BM | HI | TKW | TNG | GY# |
|-----|--------------|---------------|--------------|---------------|---------------|---------------|--------------|--------------|---------------|--------------|---------------|--------------|--------------|---------|
| DTH | 0.260 | -0.559 | 0.092 | 0.218 | 0.005 | -0.023 | -0.001 | 0.000 | -0.017 | 0.010 | 0.005 | -0.044 | 0.267 | 0.212** |
| DTA | 0.259 | -0.561 | 0.098 | 0.213 | 0.006 | -0.031 | 0.001 | 0.000 | -0.017 | 0.013 | 0.009 | -0.063 | 0.275 | 0.202** |
| DTM | 0.136 | -0.311 | 0.177 | -0.031 | 0.003 | -0.066 | 0.039 | 0.002 | -0.019 | 0.028 | 0.011 | 0.142 | 0.339 | 0.450** |
| GFD | -0.205 | 0.432 | 0.020 | -0.277 | -0.005 | -0.015 | 0.027 | 0.002 | 0.002 | 0.008 | -0.001 | 0.173 | -0.027 | 0.134 |
| NOT | -0.090 | 0.225 | -0.033 | -0.088 | -0.015 | -0.007 | 0.000 | 0.003 | 0.010 | 0.001 | -0.013 | 0.115 | 0.142 | 0.251** |
| PH | 0.078 | -0.224 | 0.149 | -0.054 | -0.001 | -0.078 | 0.087 | 0.000 | -0.002 | 0.039 | 0.035 | 0.102 | 0.041 | 0.171* |
| PL | -0.004 | -0.007 | 0.090 | -0.098 | 0.000 | -0.089 | 0.077 | -0.005 | -0.001 | 0.023 | 0.028 | 0.106 | -0.023 | 0.098 |
| SL | -0.003 | 0.004 | 0.009 | -0.014 | -0.002 | -0.001 | -0.012 | 0.031 | -0.033 | 0.005 | -0.005 | -0.019 | 0.262 | 0.223** |
| SPS | 0.056 | -0.120 | 0.043 | 0.006 | 0.002 | -0.002 | 0.001 | 0.013 | -0.078 | 0.010 | 0.007 | -0.116 | 0.354 | 0.174* |
| BM | 0.063 | -0.175 | 0.124 | -0.056 | -0.001 | -0.076 | 0.045 | 0.004 | -0.020 | 0.040 | 0.031 | 0.127 | 0.234 | 0.340** |
| HI | -0.020 | 0.080 | -0.033 | -0.003 | -0.003 | 0.045 | -0.035 | 0.002 | 0.009 | -0.020 | -0.062 | 0.240 | 0.450 | 0.341** |
| TKW | -0.019 | 0.060 | 0.042 | -0.080 | -0.003 | -0.013 | 0.014 | -0.001 | 0.015 | 0.009 | -0.025 | 0.595 | 0.017 | 0.350** |
| TNG | 0.080 | -0.178 | 0.069 | 0.009 | -0.002 | -0.004 | -0.002 | 0.010 | -0.032 | 0.011 | -0.032 | 0.011 | 0.867 | 0.837** |

Residual are -0.00424, *, ** Significant at 5% and 1% levels, respectively, # Genetic correlation

| Genotype | DTH | DTA | DTM | GFD | NOT | PH | PL | SL | SPS | BM | GY | HI | TKW | TNG |
|----------|-------|-------|--------|-------|-------|--------|-------|-------|-------|-------|------|-------|-------|--------|
| DBW39 | 87.50 | 96.00 | 118.00 | 22.00 | 7.05 | 82.95 | 24.03 | 10.05 | 20.00 | 23.88 | 8.46 | 36.91 | 32.71 | 262.55 |
| HI1579 | 89.00 | 94.50 | 119.00 | 24.50 | 8.65 | 94.05 | 26.03 | 10.17 | 21.00 | 22.29 | 8.46 | 37.88 | 40.56 | 208.23 |
| GW496 | 76.00 | 84.00 | 118.50 | 34.50 | 7.10 | 81.90 | 31.24 | 10.43 | 18.00 | 26.99 | 8.37 | 30.93 | 38.83 | 214.98 |
| BWL9022 | 85.50 | 93.50 | 117.50 | 24.00 | 6.15 | 93.15 | 35.24 | 11.10 | 23.00 | 30.46 | 8.34 | 26.93 | 38.29 | 218.44 |
| GW451 | 78.00 | 85.00 | 113.00 | 28.00 | 8.85 | 77.55 | 26.83 | 9.68 | 17.00 | 20.77 | 8.34 | 40.37 | 37.54 | 227.16 |
| WL711 | 84.50 | 92.50 | 116.50 | 24.00 | 6.65 | 85.05 | 28.04 | 9.68 | 19.00 | 30.11 | 8.28 | 28.01 | 40.79 | 203.40 |
| HD1981 | 77.50 | 86.00 | 117.00 | 31.00 | 10.50 | 84.30 | 28.44 | 11.18 | 18.00 | 28.70 | 7.95 | 29.15 | 39.24 | 202.21 |
| DBW31 | 77.00 | 84.50 | 119.50 | 35.00 | 7.95 | 90.00 | 30.84 | 12.30 | 23.00 | 28.55 | 7.86 | 27.47 | 45.30 | 175.23 |
| GW273 | 81.50 | 88.50 | 118.00 | 29.50 | 9.15 | 92.70 | 33.64 | 11.85 | 22.00 | 32.02 | 7.68 | 24.05 | 38.03 | 203.04 |
| DBW110 | 81.00 | 89.00 | 113.50 | 24.50 | 9.00 | 88.20 | 29.24 | 11.03 | 17.00 | 19.71 | 7.59 | 38.24 | 39.08 | 195.13 |
| WH1097 | 85.50 | 93.00 | 118.50 | 25.50 | 6.15 | 99.45 | 30.44 | 10.73 | 18.00 | 33.66 | 7.59 | 23.83 | 33.16 | 230.53 |
| AKW1071 | 85.00 | 93.00 | 118.00 | 25.00 | 7.55 | 96.60 | 28.84 | 10.20 | 19.00 | 18.94 | 7.56 | 40.24 | 35.78 | 211.03 |
| WBM1591 | 82.00 | 89.50 | 121.00 | 31.50 | 6.20 | 116.37 | 36.29 | 8.55 | 19.00 | 26.89 | 7.56 | 28.53 | 32.90 | 229.50 |
| GW391 | 83.50 | 92.50 | 119.00 | 26.50 | 5.60 | 89.55 | 27.23 | 9.87 | 21.00 | 29.37 | 7.32 | 24.74 | 42.41 | 175.34 |
| FLW5 | 83.50 | 92.25 | 119.00 | 26.00 | 6.15 | 82.35 | 29.64 | 10.07 | 19.00 | 27.08 | 7.10 | 26.28 | 31.88 | 223.93 |
| WH595 | 76.50 | 83.50 | 114.00 | 30.50 | 7.55 | 79.80 | 26.83 | 10.58 | 18.00 | 22.20 | 7.02 | 31.10 | 32.65 | 210.15 |
| GL27 | 77.00 | 85.50 | 118.00 | 32.50 | 5.85 | 127.35 | 37.65 | 9.75 | 20.00 | 32.74 | 6.33 | 19.92 | 37.60 | 169.84 |
| WH147 | 78.00 | 86.50 | 114.00 | 27.50 | 6.85 | 94.50 | 28.04 | 9.90 | 21.00 | 21.47 | 5.88 | 27.37 | 32.60 | 181.24 |

REFERENCES

- Al-Jibouri, H., Miller, P. A., & Robinson, H. F. (1958). Genotypic and environmental variances and covariances in an upland Cotton cross of interspecific origin 1. *Agronomy journal*, 50(10), 633-636.
- Dewey, D. R., & Lu, K. (1959). A Correlation and Path-Coefficient Analysis of Components of Crested Wheatgrass Seed Production 1. *Agronomy journal*, 51(9), 515-518.
- Behnassi, M., Pollmann, O., & Gupta, H. (Eds.). (2018). *Climate Change, Food Security and Natural Resource Management: Regional Case Studies from Three Continents*. Springer.
- Choudhury, P. N., & Kumar, V. (1980). The sensitivity of growth and yield of dwarf wheat to water stress at three growth stages. *Irrigation Science*, 1(4), 223–231.
- Gelalcha, S., & Hanchinal, R. R. (2013). Correlation and path analysis in yield and yield components in spring bread wheat (*Triticum aestivum* L.) genotypes under irrigated condition in Southern India. *African Journal of Agricultural Research*, 8(24), 3186–3192.
- Jatoi, W. A., Baloch, M. J., Kumbhar, M. B., & Keerio, M. I. (2012). Heritability and correlation studies of morpho-physiological traits for drought tolerance in spring wheat. *Pakistan Journal of Agriculture, Agricultural Engineering Veterinary Sciences (Pakistan)*, 28(2), 100–114.
- Johnson, H. W., Robinson, H. F., & Comstock, R. E. (1955). Estimates of Genetic and Environmental Variability in Soybeans I. *Agronomy Journal*, 47(7), 314.
- Khan, A. J., Azam, F., Ali, A., Tariq, M., & Amin, M. (2005). Inter-relationship and Path Coefficient Analysis for Biometric Traits in Drought Tolerant Wheat (*Triticum aestivum* L.). *Asian Journal of Plant Sciences*, 4(5), 540–543.
- Malav, A. K., Monpara, B. A., Gaur, A., & Bhati, S. S. (2017). Character association analysis in yield and yield components in bread wheat (*Triticum aestivum* L.) genotypes. *Journal of Plant Development Sciences*. 9(2), 77-83.
- Mathew, I., Shimelis, H., Mwadzingeni, L., Zengeni, R., Mutema, M., & Chaplot, V. (2018). Variance components and heritability of traits related to root: shoot biomass allocation and drought tolerance in wheat. *Euphytica*, 214(12), 1–12.
- Mia, M. S., Liu, H., Wang, X., Lu, Z., & Yan, G. (2017). Response of wheat to post-anthesis water stress, and the nature of gene action as revealed by combining ability analysis. *Crop and Pasture Science*, 68(6), 534–543.
- Mwadzingeni, L., Shimelis, H., Tesfay, S., & Tsilo, T. J. (2016). Screening of bread wheat genotypes for drought tolerance using phenotypic and proline analyses. *Frontiers in Plant Science*, 7, 1276.

- Gaur et al.** *Ind. J. Pure App. Biosci.* (2020) 8(5), 240-247 ISSN: 2582 – 2845
- Qaseem, M. F., Qureshi, R., & Shaheen, H. (2019). Effects of Pre-Anthesis Drought, Heat and Their Combination on the Growth, Yield and Physiology of diverse Wheat (*Triticum aestivum* L.) Genotypes Varying in Sensitivity to Heat and drought stress. *Scientific Reports*, 9(1), 1–12.
- Ramadas, S., Kumar, K., Singh, G. P., Kiran Kumar, T. M., & Pratap Singh, G. (2019). Wheat Production in India: Trends and Prospects. *Intech*, i, 13. <https://doi.org/http://dx.doi.org/10.5772/57353>
- Shamuyarira, K. W., Shimelis, H., Tapera, T., & Tsilo, T. J. (2019). Genetic Advancement of Newly Developed Wheat Populations Under Drought-Stressed and Non-Stressed Conditions. *Journal of Crop Science and Biotechnology*, 22(2), 169–176.
- Shan, V., Singh, S. K., & Haritash, A. K. (2020). Water Crisis in the Asian Countries: Status and Future Trends. In *Resilience, Response, and Risk in Water Systems* (pp. 173–194). Springer, Singapore.
- Sivasubramanian, S., & Menon, M. (1973). Heterosis and inbreeding depression in rice. *Madras Agricultural journal*, 60(7), 1139-1140.