Assessment of genetic variability, heritability and genetic advance in wheat (*Triticum aestivum* L.) genotypes under normal and heat stress environment

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**ABSTRACT**

One ninety diverse wheat genotypes were evaluated for genetic variability, heritability and genetic advance under normal and heat stress environment at the Research Farm of Department of Genetics and Plant Breeding, Chaudhary Charan Singh University, Meerut U. P. (India). The genotypes were grown in simple augmented block design and data were collected on fifteen morpho-agronomic characters. Analysis of observed data showed that the mean squares due to treatments for all the traits in both the environment were highly significant. GCV and PCV were highest for canopy temperature depression, grain weight/spike, biological yield/plant, grain yield/plant and lowest for days to anthesis. Heritability (bs) estimates were high for canopy temperature depression (CTD), followed by biological yield/plant, grain weight/spike, grain number/spike, 1000- grain weight, grain yield/plant, tiller number/plant and lowest for days to heading and days to anthesis in case of both environments. The estimates of genetic advance (GA) were highest for canopy temperature depression followed by grain weight/spike, biological yield/plant, grain yield/spike, tiller number/plant, grain number/spike and lowest for days to heading and days to anthesis under both (normal and heat stress) environment. This study suggests that the presence of adequate genetic variability, heritability and genetic advance for these traits under normal and heat stress environment is suitable for breeding programs and crop improvement.

**Key words:** Analysis of variance, Genetic advance, GCV, Heat stress, Hertitibility, PCV.

**INTRODUCTION**

Wheat (*T. aestivum* L. em. Thell; 2n=42) is the second most important staple food crop of the world after rice. It is a self-pollinated crop, member of Poaceae family and is one of the leading cereals of many countries of the world including India. It is the most important food crop of India and accounts for 20% of human consumption of calories and is an important source of protein, vitamins and minerals. Wheat has relatively high content of niacin and thiamine which are principally concerned in providing the special protein called ‘Gluten’. The majority of the cultivated wheat varieties belong to three main species of the genus *Triticum*. These are the hexaploid (2n=6x=42) *T. aestivum* (bread wheat), the tetraploid (2n=4x=28) *T. durum* and the diploid (2n=2x=14) *T. dicoccum*. Wheat genome is reported 17 gigabase (1.7 x10^9 bp), which is about 100 times larger than the *Arabidopsis* genome, 40 times that of rice and 6 time that of maize. Globally, *aestivum* wheat is most important species which covers 90 per cent of the area. Next popular wheat being durum wheat which covers about 9 per cent of the total area while *T. dicoccum* and *T. monococcum* cover less than the 1 per cent of the total area.

The area under wheat cultivation and productivity varies in different wheat growing states of India. For example, Uttar Pradesh accounts for 9.67 mha area which is 33.97% of the total area under wheat cultivation in India. The wheat productivity in Uttar Pradesh stands at 3,113 kg/ha. In Punjab, wheat grown on 3.52 mha area, which accounts for 12.38% of total area under wheat cultivation in India with a highest productivity of 4,693kg/ha.

The major wheat producing states are Uttar Pradesh, Punjab, Haryana, Madhya Pradesh, Rajasthan, Bihar, Maharashtra, Gujrat, Karnataka, West Bengal, Uttarakhand, Himachal Pradesh and Jammu and Kashmir. These states contribute about 99.5 per cent of total wheat production in the country, while remaining states, namely, Jharkhand, Assam, Chhattisgarh, Delhi and other North East states contribute only about 0.5 per cent of the total wheat production in the country.

Heat stress is an important production constraint of wheat during grain-filling period in India and in other parts of the world where the temperature becomes high during anthesis to maturity (grain-filling) stage of plant growth (Dhanda and Munjal, 2009). Extremely high temperatures are the factors causing the greatest problems for agriculture and crop production (Ball et al. 2009). Heat tolerance, a quantitative trait for direct selection. A thorough
understanding of physiological responses of plants to high temperature, mechanisms of heat tolerance and identification of screening indices for development of heat-tolerant genotypes are imperative (Modarresi et al. 2011).

The development of an effective plant breeding program is dependent upon the existence of genetic variability. The efficiency of selection largely depends upon the magnitude of genetic variability present in the plant population. Thus, the success of genetic improvement in any character depends on the nature of variability present in the gene pool for that character. Hence, an insight into the magnitude of variability present in the gene pool of a crop species is of paramount importance to a plant breeder for starting a judicious plant breeding program (Farshadfar et al. 2013). Heritability and genetic advance are important selection parameters. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimate alone. Heritability, is a measure of the phenotypic variance attributable to genetic causes, has predictive function in breeding crops (Songsri et al. 2008). It provides an estimate of the genetic advance a breeder can expect from selection applied to a population under certain environment. The higher the heritability estimates, the simpler are the selection procedures (Khan et al. 2008). High heritability (bs) associated with high genetic advance reveals strong contribution of additive genetic variance for expression of the traits and the selection based on these traits could play a vital role in improving grain yield (Iqbal and Khan, 2003). The estimation of heritability helps the plant breeder in selection of elite genotypes from diverse genetic populations. The principle objective of this study was to estimate the genetic variability, heritability and genetic advance under normal and heat stress environments which can be further used in breeding and crop improvement programmes.

**MATERIALS AND METHODS**

The experimental material consisted of 190 diverse genotypes of bread wheat along with four check genotypes were evaluated in simple augmented block design experiment under normal and heat stress environments during *rabi* season of 2014-15 at Research Farm, Department of Genetics and Plant Breeding, C.C.S. University, Meerut. Number of blocks in each environment / experiment was 19 and number of genotypes in each block was 10 with four check genotypes repeated in each block. Standard agronomic practices were adopted in each experiment to raise a good crop. Observations were recorded on five plants which are randomly selected from each genotype for various quantitative characters viz, days to heading, days to anthesis, days to maturity, grain filling duration (GFD), canopy temperature depression (CTD), chlorophyll content, plant height (cm), grain weight per spike (gm), grain number per spike, 1000- grain weight (gm), grain yield per plant (gm), tiller number per plant, biological yield per plant (gm), grain protein content and grain carotenoids content.

**Statistical analysis:** Following statistical analysis were carried out using the mean values of individual genotypes under normal and heat stress environment at 0.05% of probability level.

Recorded data of both environment (normal and heat stress) were subjected to statistical analysis and analysis of variance calculated by using the statistical software WINDOSTAT version 9.2 programme. Heritability (h^2) and genetic advance (GA) were estimated suggested by Allard et al. (1960) and variability was estimated by the Burton and De Vane (1953).

**RESULTS AND DISCUSSIONS**

**Analysis of variance:** The results of analysis of variance for various characters under stress and non stress (normal) environments are presented in Table 1 and Table 2. The mean squares due to treatments for all the traits in both the environment were highly significant, thereby suggesting the presence of considerable amount of variability among the one hundred ninety (190) wheat genotypes with respect to traits studied under present study.

**Variability:** Knowledge of genetic diversity among existing varieties is highly useful. It is the basic requirement for successful breeding program. Secondly, the future breeding program also depends upon the availability of genetic variability to increase the grains in productivity, so to achieve self-sufficiency and sustainability. There is a need to develop cultivars with a diverse genetic base. Heat stress is known to adversely affect many traits resulting into decline in grain yield.

The estimates of mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) for fifteen traits of wheat varieties in timely sowing (normal) and late sowing (heat stress) environments are presented in Table 3 and Table 4. The estimates of means showed wide range of values for all the characters. The magnitude of phenotypic coefficient of variation (PCV) values for all the traits were higher than the corresponding genotypic coefficient of variation (GCV) values indicating that these characters are influenced by environmental effects. The traits which have higher PCV and GCV values under normal environment are: CTD (29.59) and (29.52), grain weight/spike (18.61) and (18.55), tiller number/ plant (17.48) and (17.37), biological yield/plant (16.11) and (16.07), and the traits which have higher PCV and GCV values under heat stress environment are: CTD (28.55) and (28.48), grain weight/spike (25.52) and (25.48), grain yield/plant (22.84) and (22.74), biological yield/plant (22.65) and (22.60). The higher estimates of PCV, suggested that
### Table 1: Analysis of variance for physiological traits of 190 bread wheat genotypes evaluated in augmented block design under normal (non-stress) environment.

<table>
<thead>
<tr>
<th>Source of variation/trait</th>
<th>df</th>
<th>DTH</th>
<th>DTA</th>
<th>DTM</th>
<th>GFD</th>
<th>CTD</th>
<th>CC</th>
<th>T/PP</th>
<th>PH</th>
<th>BY/P</th>
<th>GW/S</th>
<th>GN/S</th>
<th>Y/PLA</th>
<th>TGW</th>
<th>GPC</th>
<th>BCE</th>
</tr>
</thead>
<tbody>
<tr>
<td>Block (adj.)</td>
<td>18</td>
<td>5.92</td>
<td>6.52</td>
<td>18.70</td>
<td>23.06</td>
<td>7.83</td>
<td>51.15</td>
<td>4.40</td>
<td>47.26</td>
<td>963.56</td>
<td>0.35</td>
<td>87.95</td>
<td>3.37</td>
<td>51.09</td>
<td>1.45</td>
<td>0.78</td>
</tr>
<tr>
<td>Treatment (adj)</td>
<td>193</td>
<td>3.28</td>
<td>3.50</td>
<td>24.39</td>
<td>21.51</td>
<td>1.19</td>
<td>30.44</td>
<td>1.97</td>
<td>22.58</td>
<td>678.56</td>
<td>0.17</td>
<td>75.76</td>
<td>2.93</td>
<td>25.62</td>
<td>0.42</td>
<td>0.64</td>
</tr>
<tr>
<td>Checks</td>
<td>3</td>
<td>4.37</td>
<td>5.35</td>
<td>26.21</td>
<td>15.21</td>
<td>0.93</td>
<td>60.83</td>
<td>6.59</td>
<td>249.43</td>
<td>1313.50</td>
<td>0.85</td>
<td>235.38</td>
<td>9.83</td>
<td>197.17</td>
<td>0.88</td>
<td>0.60</td>
</tr>
<tr>
<td>Varieties</td>
<td>189</td>
<td>3.65</td>
<td>3.79</td>
<td>22.38</td>
<td>20.78</td>
<td>1.94</td>
<td>34.66</td>
<td>2.31</td>
<td>22.32</td>
<td>849.03</td>
<td>0.19</td>
<td>70.01</td>
<td>2.90</td>
<td>27.71</td>
<td>0.51</td>
<td>0.72</td>
</tr>
<tr>
<td>Checks vs. Varieties</td>
<td>1.00</td>
<td>0.87</td>
<td>1.47</td>
<td>661.01</td>
<td>590.23</td>
<td>0.00</td>
<td>54.91</td>
<td>4.02</td>
<td>194.02</td>
<td>1830.98</td>
<td>1.92</td>
<td>251.06</td>
<td>47.66</td>
<td>29.38</td>
<td>7.78</td>
<td>0.18</td>
</tr>
<tr>
<td>Error</td>
<td>54.00</td>
<td>2.68</td>
<td>2.18</td>
<td>5.74</td>
<td>0.39</td>
<td>0.01</td>
<td>0.24</td>
<td>0.02</td>
<td>2.08</td>
<td>3.60</td>
<td>0.00</td>
<td>0.82</td>
<td>0.07</td>
<td>0.44</td>
<td>0.09</td>
<td>0.02</td>
</tr>
</tbody>
</table>

*Significant at 0.05%; and **Significant at 0.01%; respectively. Where, df=degrees of freedom, DTH=days to heading, DTA=days to anthesis, DTM=days to maturity, GFD=grain filling duration, CTD=canopy temperature depression, CC=chlorophyll content, TGW=1000-grain weight, GN/S=grain number per spike, GW/S=grain weight per spike, PH=plant height, Y/PLA=yield per plant, GPC=grain protein content, T/PP=tiller number per plant, BY/P=Biological yield per plant, BCE=Beta carotene.

### Table 2: Analysis of variance for physiological traits of 190 bread wheat genotypes evaluated in augmented block design under heat-stress condition.

<table>
<thead>
<tr>
<th>Source of variation/trait</th>
<th>df</th>
<th>DTH</th>
<th>DTA</th>
<th>DTM</th>
<th>GFD</th>
<th>CTD</th>
<th>CC</th>
<th>T/PP</th>
<th>PH</th>
<th>BY/P</th>
<th>GW/S</th>
<th>GN/S</th>
<th>Y/PLA</th>
<th>TGW</th>
<th>GPC</th>
<th>BCE</th>
</tr>
</thead>
<tbody>
<tr>
<td>Block (adj.)</td>
<td>18</td>
<td>7.25</td>
<td>6.58</td>
<td>13.93</td>
<td>15.16</td>
<td>15.18</td>
<td>45.06</td>
<td>1.31</td>
<td>68.27</td>
<td>1037.34</td>
<td>0.13</td>
<td>90.31</td>
<td>3.56</td>
<td>45.24</td>
<td>0.83</td>
<td>0.57</td>
</tr>
<tr>
<td>Treatment (adj)</td>
<td>193</td>
<td>5.15</td>
<td>2.98</td>
<td>11.14</td>
<td>8.68</td>
<td>1.43</td>
<td>24.66</td>
<td>0.76</td>
<td>25.43</td>
<td>259.23</td>
<td>0.09</td>
<td>69.50</td>
<td>1.62</td>
<td>32.79</td>
<td>0.32</td>
<td>0.36</td>
</tr>
<tr>
<td>Checks</td>
<td>3</td>
<td>24.61</td>
<td>14.75</td>
<td>14.14</td>
<td>2.01</td>
<td>1.37</td>
<td>16.33</td>
<td>5.45</td>
<td>197.98</td>
<td>128.78</td>
<td>0.37</td>
<td>68.04</td>
<td>1.37</td>
<td>255.26</td>
<td>0.61</td>
<td>0.25</td>
</tr>
<tr>
<td>Varieties</td>
<td>189</td>
<td>4.43</td>
<td>2.96</td>
<td>9.00</td>
<td>8.71</td>
<td>2.87</td>
<td>29.16</td>
<td>0.84</td>
<td>28.61</td>
<td>360.03</td>
<td>0.10</td>
<td>76.81</td>
<td>1.93</td>
<td>33.52</td>
<td>0.39</td>
<td>0.42</td>
</tr>
<tr>
<td>Checks vs. Varieties</td>
<td>1.00</td>
<td>189.51</td>
<td>58.06</td>
<td>610.18</td>
<td>291.79</td>
<td>1.71</td>
<td>0.71</td>
<td>1.17</td>
<td>105.32</td>
<td>254.81</td>
<td>0.40</td>
<td>308.24</td>
<td>8.77</td>
<td>38.16</td>
<td>1.15</td>
<td>0.22</td>
</tr>
<tr>
<td>Error</td>
<td>54.00</td>
<td>1.67</td>
<td>1.38</td>
<td>3.60</td>
<td>0.24</td>
<td>0.01</td>
<td>0.30</td>
<td>0.01</td>
<td>1.33</td>
<td>0.80</td>
<td>0.00</td>
<td>0.47</td>
<td>0.01</td>
<td>0.20</td>
<td>0.10</td>
<td>0.02</td>
</tr>
</tbody>
</table>

*Significant at 0.05%; and **Significant at 0.01%; respectively. Where, df=degrees of freedom, DTH=days to heading, DTA=days to anthesis, DTM=days to maturity, GFD=grain filling duration, CTD=canopy temperature depression, CC=chlorophyll content, TGW=1000-grain weight, GN/S=grain number per spike, GW/S=grain weight per spike, PH=plant height, Y/PLA=yield per plant, GPC=grain protein content, T/PP=tiller number per plant, BY/P=Biological yield per plant, BCE=Beta carotene.
adequate variability is present for these traits and hence there is a scope for employing suitable breeding programs for bringing about improvement in these traits under heat stress environment. In normal environment experiment, the estimates of GCV and PCV showed wide range, the GCV and PCV respectively, varied from 1.02 to 2.19 for days to heading, and from 29.52 to 29.59 for CTD and under heat stress, the GCV and PCV values varied from 1.53 to 2.23 for days to anthesis and from 28.48 to 28.55 for CTD. The wide range of GCV and PCV indicates the presence of considerable amount of variability among all the characters.

By following the studies conducted by Geeta et al. (2014), Kyosev and Desheva (2015) and Kumar et al. (2014), for ten metric traits in RAJ-4037 wheat genotypes, for eight quantitative traits in thirty eight emmer wheat genotypes, for eleven quantitative traits in fifty wheat genotypes, respectively, we can conclude that the degree of variability present in wheat for various traits and their results follows the same variability pattern i.e. higher PCV and GCV values for CTD followed by grain weight/spike and biological yield/plant, as concluded in our study and similar results were agreement with the work of Jitendra et al. (2014), whose finding are maximum values of GCV and PCV for GY/P and similarly Kumar et al. (2017), confirmed high GCV, PCV values for CTD and GY/P in *Triticum aestivum* but different genotypes.

**Heritability and expected genetic advance:** The estimation of heritability and expected genetic advance for fifteen traits of wheat varieties in timely sowing (normal) and late sowing (heat stress) environments are presented in Table 3 and Table 4. It was found that heritability estimates for all the traits were high in case of both environments. Heritability estimates in normal environment were highest for canopy temperature depression CTD (99.55), followed by biological yield/plant, as concluded in our study and similar results were presented in Table 3 and Table 4.
(99.44), grain weight/ spike (99.31), chlorophyll content (99.09), tiller number /plant (98.74), grain number/spike (98.48) and lowest for days to heading (21.65). In heat stress environment, heritability estimates were highest for grain weight/spike (99.83), followed by biological yield/plant (99.70), canopy temperature depression (99.48), 1000 grain weight (99.22), grain number/spike (99.19), grain yield/plant (99.19) and lowest for days to anthesis (46.73).

High heritability indicated that the characters such as CTD, BY/P, GW/S, CC, GN/S, FY/P. 1000- Grain weight and TPP are less influenced by environment and low heritability of characters, DTH and DTA suggest that these characters would not be effective for selection due to predominant effects of non additive genes. The above finding of heritability were in agreement with the work of Ramanuj et al. (2018), Kumar et al. (2018), Hakimi et al. (2017) and Kumar et al. (2017). High value of heritability for GW/S and 1000- Grain weight in wheat have also been reported by Naveen et al. (2014), Rajput (2018), Kyosev and Desheva (2017) in different genotype of wheat.

Data given in Tables 3 and 4 indicate that estimates of genetic advance (GA) in normal environment were high for traits such as canopy temperature depression (60.68), grain weight/spike (38.08), tiller number/plant (35.55), biological yield/plant (33.01), grain number/spike (27.90) and lowest for the days to heading (0.97) and genetic advance (GA) in heat stress environment was highest for canopy temperature depression (58.52), grain weight/spike (52.39), grain yield/spike (46.65), biological yield/plant (46.49) and lowest for days to anthesis (2.15) and the similar findings have been earlier reported by Rathwa et al. (2018), Kumar et al. (2017) and Kyosev et. al (2015).

CONCLUSION
Following major conclusion has been drawn from the present study in which 190 wheat genotypes were evaluated in augmented block design in two environment (normal and heat stress) to access the genetic diversity based on qualitative characters and yield components.

- Analysis of variance showed significant differences among the wheat genotypes for all the fifteen quantitative traits.
- In the analysis of variability, GCV and PCV in normal environment were high for CTD, GW/S, T/PP and BY/P and in heat stress environment. GCV and PCV were high for CTD, GW/S, Y/PLA and BY/P.
- In normal environment, traits including CTD, BY/P, GW/S, T/PP, CC, GN/S, 1000-GW, FY/P, GFD and BCE showed high heritability and CTD, BY/P, GW/S and T/PP were coupled with high genetic advance. In case of heat stress environment, traits including CTD, BY/P, GW/S, FY/P, GN/S, 1000-GW, CC and T/PP showed high heritability and CTD, BY/P, GW/S and FY/P were coupled with high genetic advance.

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REFERENCES


