**Genetic studies on variability for quantitative traits in bread wheat (*Triticum aestivum* L. em. Thell)**

**ABSTRACT**

Ten bread wheat genotype and their all possible cross combinations excluding their reciprocals (10 parents+45 F1s) were evaluated in a randomized block design with three replications during *Rabi* 2022-2023 at Student’s Instructional Farm, C. S. Azad University of Agriculture and Technology-208002, Kanpur, U.P to get the extent of variability and related parameters to select effectively for grain yield and quality character. It is the big challenge for researchers to get high grain yield with high protein. The data was recorded on fourteen characters *viz*., days to heading (50%), days to maturity, plant height (cm), chlorophyll content, number of productive tillers per plant, spike length (cm), number of spikelets per spike, number of grains per spike, weight of grain per spike (g), 1000 grain weight (g), biological yield (g), harvest index (%), protein content (%) and grain yield per plant (g). The variability among parents was highest for days to maturity it ranged from 117.33 to 137.67 with the mean value 126.60. The variation in F1 progenies was highest for plant height ranged from 85.97 to 120.53 with the mean value of 96.71. The result showed higher estimated values for phenotypic coefficient of variability (PCV) of all the fourteen characters as compared to their corresponding genotypic coefficient of variability (GCV). Highest value of PCV and GCV were noted for grain yield per plant in F1s generation except GCV were observed for none of the character F1s. high heritability estimates were recorded for all characters in F1s generation. High genetic gain was observed for grain yield per plant followed by biological yield per plant in F1s generation.

**Keywords**: Variability, heritability, genetic advance, range, quantitative traits

**INTRODUCTION**

Wheat (*Triticum aestivum* L*.*) is one of the most important cereal crop grown in different environments due to its versatile nature over the world. It is used as food for consumption. At global level, it’s cultivated over 220.40 million ha and production of 798.97 million tons with an average productivity of 36.25 quintals per hectare. In India, it is grown in area of 31.40 million hectares with a production of 110.55 million tons and productivity of 35.20 quintals per hectare **(FAO, 2023**) [1]. Wheat is grown under diverse agro-climatic conditions leading to wide fluctuation in productivity from region to region. Wheat is used for both human and animal nutrition and plays an important role in the nutrition of rapidly growing populations both in our country and the world. A number of biometrical techniques are extensively used for genetic evaluation of plants. Out of them, diallel, partial diallel and line X tester analyses have been frequently used by breeders for genetic study because they provide more genetic information about the material studied. Wheat has been playing an important role in the economy of several countries. The present study was based on fourteen quantitative characters measured on ten genotypes with one check. Information on the variability was measured by estimating the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance for individual quantitative character and through equilibrium distance over the characters. In addition, the present study will also helpful in identification of high yielding genotypes with better quality. In crop improvement only the genetic components of variation are important because this is the only component which transmits to the next generation. Heritability is an important parameter in the selection process as it determines the response to selection. Estimates of heritability (narrow sense) and genetic advance for 14 characters in F1s generations. Heritability is used by plant breeders to enhance the precision of single field trial and /or of series of trials [2]. Estimates of genetic advance in per cent over mean various range in F1s generations. The research on the genetic studies on variability provide significant information specifically in breeding programs. Variability is the core foundation for aiming improvement of traits for biotic and abiotic stresses, as well as for traits that has economically important. Study of the estimates of heritability with genetic advance is more meaningful and reliable than considering the parameters individually [3,4].

**MATERIAL AND METHODS**

Ten genetically divers genotypes were crossed in all possible combinations excluding reciprocal during *Rabi* 2022-23 at Student’s Instructional Farm, C. S. Azad University of Agriculture & Technology, Kanpur-208002 U.P. Basic material consisting of ten morphological diverse genotype *viz*., HD 2733, DBW 222, HD 3086, HUW 666, DBW 187, K 1317, KRL 19, HI 1563, DBW 14 and K 9423. The salient features of these parental genotypes are given in **Table-1**.

**Table 1**: Salient features of parental genotypes

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Sr. No.** | **Name of Parents** | **Pedigree** | **Salient feature** | **Origin place** |
| **1.** | HD 2733 | ATTILA/3/TUI/CARC//CHEN/CHTO/4/ATTILA | Resistance to brown rust and tolerant to leaf blight. | IARI, N. Delhi |
| **2.** | DBW 187 | NAC/TH.AC//3\*PVN/3/MIRLO/BUC/4/2\*PASTOR/5/KACHU/6/KACHU | Good biscuit spread factor (8.6cm), High Fe content (43.1 ppm), resistance to yellow and brown rust | IIWBR, Karnal |
| **3.** | DBW 222 | KACHU/SAUAL/8/ATTILA\*2/PBW65/6/PVN//CAR422/ANA/5/BOW/CROW//BUC/PVN/3/YR/4/TRAP#1/7/ATTILA/2\*PASTOR | Resistant for stripe and leaf rust; Highly resistant to Karnal bunt (9.1%) and loose smut (4.9%). Chapatti quality score (7.5/10). | IIWBR, Karnal |
| **4.** | HD 3086 | DBW 14/ HD 2733/HUW 468 | Resistance to yellow and brown rust | IARI, N. Delhi |
| **5.** | HUW 666 | - | Drought tolerance | BHU, Varanasi |
| **6.** | K1317 | K 0307/K9162 | Resistant to brown rust and leaf blight. Good Chapatti quality | CSAUA&T, Kanpur |
| **7.** | KRL 19 | PBW 255/KRL 1-4 | Salt affected Wheat Varieties Also suitable for water logging area and tolerant to yellow and brown rust | CSSRI, Karnal |
| **8.** | HI 1563 | MACS 9496\*2/MC10 | Resistance to all the pathotypes of the three rusts at seedling stage | IARI, RS, Indore |
| **9.** | DBW 14 | RAJ 3765/PBW 343 | Tolerant to leaf blight | IIWBR, Karnal |
| **10.** | K 9423 | HP1633/KAL/UP262 | Tolerance to heat at grain development stage | CSAUA&T, Kanpur |

The genotype parents were sown in a randomized complete block design (RCBD) with three replications where each replication, there were 100 rows in three tiers. Parents were sown of single row while F1s were sown in two row plots. The length of each line was 3 meters with row to row spacing of 22.5 cm and plant to plant spacing of 10 cm. All the recommended agronomical practices were adopted to raise the crop. For fourteen characters *viz.,* days to heading (50%), days to maturity, plant height (cm), number of productive tillers per plant, chlorophyll content, spike length (cm), number of spikelets per spike, number of grains per spike, weight of grain per spike(g), 1000 grain weight (g), biological yield (g), harvest index (%),protein content (%) and grain yield per plant (g) observation were recorded from the five randomly selected plants from each genotype HD 3086 bread wheat variety of this region were used as ‘check varieties’ in this experiment.

**Estimation of coefficient of variability:** The computation of genotypic coefficient of variability (GCV) and phenotypic coefficient of variability (PCV) was done by the formula given by **Burton and de Vane (1953)** [5].

GCV = $\frac{\sqrt{V\_{g}}}{\overline{X}}$ X 100

Where,

Vg = Genotypic variance, and

$\overline{X}$= Germplasmmean

PCV = $\frac{\sqrt{V\_{p}}}{\overline{X}}$ X 100

Where,

Vp = phenotypic variance, and

$\overline{X}$ = Germplasm mean

**Heritability (in narrow sense):** In $F\_{1}$ generation was calculated by the formula proposed by **Crumpacker and Allard (1962),** [6] which is as follows:

$\begin{matrix}\^\\h^{2}\end{matrix}$ = $\frac{(\frac{1}{4})\begin{matrix}\^\\D\end{matrix}}{(\frac{1}{4}) \begin{matrix}\^\\D\end{matrix}+(\frac{1}{4})\begin{matrix}\^\\H\_{1}\end{matrix}- (\frac{1}{4})\begin{matrix}\^\\F\end{matrix}+\begin{matrix}\^\\E\end{matrix}}$

Heritability (in per cent) = Heritability coefficient ( $\begin{matrix}\^\\h^{2}\end{matrix}$ ) × 100

Where,

$\begin{matrix}\^\\h^{2}\end{matrix}$ = estimate of heritability coefficient and$\begin{matrix}\^\\D\end{matrix}, \begin{matrix}\^\\H\_{1}\end{matrix}$, $\begin{matrix}\^\\F\end{matrix}$ and $\begin{matrix}\^\\E\end{matrix}$ are the

**Genetic advance:** The calculation of the estimates of genetic advance was done according to the formula given by **Robinson *et al.* (1949)** [7]**.**

 GA = (k) ($\begin{matrix}\^\\h^{2}\end{matrix}$) ($δ\_{ph}$)

and genetic advance over mean of the character

 GA (%) = $\frac{GA}{\overline{X}}$ × 100

Where,

 GA = estimate of genetic advance

 k = selection differential at 5% selection intensity, i.e., 2.06

 $σ\_{ph}$ = phenotypic standard deviation

 $\hat{h}^{2}$ = estimate of heritability coefficient (broad sense)

 $\overline{x}$ = mean of the character concerned

**RESULT AND DISCUSSION**

**A. Analysis of variance (ANOVA)**

The analyses of variance (ANOVA) for parents + F1s for all the fourteen characters are presented in **Table-2**.

In case of **Table-2**, highly significant differences were observed among the parents for all the 14 characters. Similarly, highly significant differences were found among F1s for all the 14 traits. It was indicated significant variability in the base material as well as the material generated subsequently, involved all possible combinations except reciprocal cross. Highly significant differences were noted among parents *vs.* F1s for all characters except for days to 50% heading, chlorophyll content and weight of grain per spike which reflected significant amount of heterotic response in these attributes [8] [9].

The magnitude of variability in F1s was higher for days to heading (50%), days to maturity, plant height, number of productive tillers per plant, spike length, weight of grains per spike, biological yield per plant [10] [11].

**B. Mean and Range**

The mean values and range of parents, their F1 progenies for all the fourteen traits are presented in **Table-3**.

The variability among parents was highest for days to maturity it ranged from 117.33 to 137.67 with the mean value 126.60. Mean value for plant height reported 90.94 with the ranged from 80.60 to 100.83. The average days to heading (50%) was 81.77 with the minimum 74.33 and maximum values 93.67.Biological yield per plant ranged from 35.53 to 51.27 with the mean value of 41.57.Harvest index ranged from 30.61 to 45.64 with the mean value 38.21 and the average grain yield per plant 15.99 ranged from 12.33 to 23.40 while number of grains/spike ranged from 30.47 to 38.1 with the mean value of 34.28.1000 grain weight ranged from 38.98 to 44.31 with the average value of 41.72.Chlorophyll content range from 38.47 to 43.39 with the mean value of 40.56 and the average spike length 11.12 ranged from 9.27 to 13.47 while number of productive tillers/plant ranged from 6.33 to 10.00 with the mean value of 7.50. Mean number of spikelets/spike found 17.05 with the ranged of 15.47 to 18.87 while the average protein content found 10.34 with the minimum and maximum values 9.22 and 11.54 respectively. Weight of grains/spike ranged from 1.53 to 1.87 with the mean value of 1.67.[12] [13] [14].

The variation in F1 progenies was highest for plant height ranged from 85.97 to 120.53 with the mean value of 96.71 followed by biological yield per plant ranged from 20.67 to 52.07 with the mean value of 38.77. Days to maturity ranged from 118.00 to 138.67 with the mean value of 125.88 and the average days to heading (50%) 81.20 ranged from 72.00 to 89.67 while grain yield per plant ranged from 8.53 to 22.87 with the mean value of 15.59. chlorophyll content ranged from 34.23 to 48.07 with the mean value of 40.27. number of grains per spike ranged value 28.53 to 41.60 with the mean value of 36.95 and the average harvest index 40.24 ranged from 36.78 to 44.98 while 1000 grain weight ranged from 39.12 to 46.12 with the mean value of 42.88. Mean number of spikelets per spike found 18.43 with the ranged of 14.80 to 21.20 while the average number of productive tillers 8.63 with the minimum and maximum values 6.00 and 11.67 respectively. Spike length ranged from 8.30 to 13.47 with the mean value of 10.63 and the average protein content 10.14 ranged from 8.81 to 11.26 while and weight of grain per spike ranged from 1.30 to 2.13 with the mean value of 1.66[15] [16].

**C. Coefficients of variation**

In **Table-4** the estimates variability parameters i.e., genotypic coefficient of variation and phenotypic coefficient of variation were computed for all the traits having significant difference between the genotypes. GCV and PCV are categories *viz*., high (above 20%), moderate (above 10 and below 20%) and low (below 10 %).

In F1 generation, at level of phenotypic coefficient of variation high values of phenotypic coefficient of variation (PCV) were observed for grain yield per plant and exhibited moderate for number of productive tillers per plant, biological yield per plant, spike length and weight of grain per spike. whereas recorded low for number of spikelets per spike, number of grains per spike, chlorophyll content, plant height, harvest index, protein content, days to heading (50 %), days to maturity and 1000 grain weight. At level of genotypic coefficient of variation, high values of genotypic coefficient of variation (GCV) were observed for none of the characters and exhibited moderate for grain yield per plant, biological yield per plant, number of productive tiller per plant, spike length and weight of grain per spike whereas recorded low for number of spikelets per spike, number of grains per spike, plant height, chlorophyll content, harvest index, protein content, days to heading (50 %), days to maturity and 1000 grain weight. [17] [18] [19]

**D. heritability and genetic advance**

Estimates of heritability (narrow sense) and genetic advance for 14 characters in F1 generations, are presented in **Table-4.** There are three categories for the expression of heritability *viz*., high (above 30%), moderate (above 10 and below 30%) and low (below 10%) and genetic advance *viz*., high (above 20%), moderate (above 10 and below 20%) and low (below 10%).

**(a) Heritability**

In F1 generation, high heritability estimates were recorded for all characters namely days to heading (50%), days to maturity, plant height (cm), number of productive tillers per plant, chlorophyll content (%), spike length (cm), number of spikelets per spike, number of grains per spike, weight of grain per spike(g), 1000 grain weight (g), biological yield (g), harvest index (%),protein content (%) and grain yield per plant (g) [20] [21].

**(b) Genetic advance:-**

Estimates of genetic advance in per cent over mean ranged from 7.74 (1000 grain weight) to 37.88 (grain yield per plant) in F1 generation. High genetic gain was observed for grain yield per plant followed by biological yield per plant, number of productive tillers per plant, spike length and weight of grain per spike. Moderate genetic advance was recorded for number of spikelets per spike followed by number of grains per spike, plant height, chlorophyll content, harvest index and protein content and low for days to heading followed by days to maturity and 1000 grain weight [22] [23].

**CONCLUTIONS**

The present study generally indicated there was plenty of genetic variability among the genotypes. Thus, there is vast opportunity in the improvement of protein content and grain yield in bread wheat genotype. Therefore, the result and information generated from current study need to be used by interested plant breeders. These results showed the major involvement of additive genetic component and marginal role of non-additive component in controlling the inheritance of these characters. Similarly reported for plant height, number of productive tillers per plants, number of grain per spike by **Dhonde *et al.* (2000)**; [24] days to maturity, plant height, number of productive tillers per plant, number of grain per spike, biological yield per plant, 1000 grain weight, harvest index, protein content and grain yield per plant. Studies revealed that the days to maturity with high heritability and low genetics advance over mean followed by biological yield per plant and grain yield per plant high heritability and low genetics advance over mean in F1s generation. plant height, chlorophyll content, number of spikelets per spike, number of grains per spike, harvest index and protein content were the major yield attributing characters coupled with moderate genetic advance over mean in F1s generation, so emphasis should be given for these characters at the time of sample selection. [25, 26 &27].

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Details of the AI usage are given below:

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2.

3.

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**Table-2 Analysis of variance for fourteen characters of 10 Parents and their 45 F1s in bread wheat**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Source of variation** | **d. f.** | **No. of grains/spike)** | **Weight of grain/ spike(g)** | **1000 grain weight (g)** | **Biological yield/plant (g)** | **Harvest index (%)** | **Protein content (%)** | **Grain yield /plant (g)** |
| **Replication** | 2 | 1.98 | 0.008 | 0.19 | 2.30 | 0.72 | 0.028 | 0.17 |
| **Treatment** | 54 | 31.79\*\* | 0.109\*\* | 10.05\*\* | 145.23\*\* | 21.96\*\* | 1.178\*\* | 27.88\*\* |
| **Parents** | 9 | 26.94\*\* | 0.051\*\* | 11.94\*\* | 84.27\*\* | 58.18\*\* | 1.700\*\* | 36.62\*\* |
| **F1** | 44 | 29.54\*\* | 0.124\*\* | 9.14\*\* | 156.61\*\* | 12.77\*\* | 1.076\*\* | 26.64\*\* |
| **Parents vs F1** | 1 | 174.44\*\* | 0.002 | 33.08\*\* | 193.55\*\* | 100.59\*\* | 0.979\*\* | 4.02\* |
| **Error** | 108 | 1.23 | 0.009 | 0.68 | 3.31 | 2.05 | 0.069 | 0.80 |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Source of variation** | d. f. | **Days to heading (50%)** | **Days to maturity** | **Plant height (cm)** | **Chlorophyll content** | **No. of productive tillers/plant** | **Spike length (cm)** | **No. of spikelets/spike** |
| **Replication** | 2 | 3.28 | 7.17 | 5.05 | 2.41 | 0.03 | 0.34 | 0.52 |
| **Treatment** | 54 | 61.51\*\* | 109.64\*\* | 149.93\*\* | 25.90\*\* | 6.99\*\* | 5.27\*\* | 9.27\*\* |
| **Parents** | 9 | 111.93\*\* | 143.91\*\* | 96.82\*\* | 8.16\*\* | 4.46\*\* | 6.69\*\* | 5.81\*\* |
| **F1** | 44 | 52.42\*\* | 104.84\*\* | 145.68\*\* | 30.06\*\* | 6.95\*\* | 4.96\*\* | 9.14\*\* |
| **Parents vs F1** | 1 | 7.89 | 12.68\*\* | 815.79\*\* | 2.07 | 31.53\*\* | 5.93\*\* | 46.24\*\* |
| **Error** | 108 | 4.64 | 2.38 | 3.54 | 1.37 | 0.58 | 0.12 | 0.27 |

**Table-2 continued**

**\*, \*\* significant at 5% and 1% level, respectively**

**Table-3 Mean and range of parents and their F1s for fourteen characters based on ten parents diallel in bread wheat.**

|  |  |  |  |
| --- | --- | --- | --- |
| **S. No.** | **Characters** | **Parent** | **F1** |
| **Mean** | **Range** | **Mean** | **Range** |
| **Min.** | **Max.** | **Min.** | **Max.** |
| **1** | **Days to heading (50%)** | **81.77** | 74.33 | 93.67 | **81.20** | 72.00 | 89.67 |
| **2** | **Days to maturity** | **126.60** | 117.33 | 137.67 | **125.88** | 118.00 | 138.67 |
| **3** | **Plant height (cm)** | **90.94** | 80.60 | 100.83 | **96.71** | 85.97 | 120.53 |
| **4** | **Chlorophyll content**  | **40.56** | 38.47 | 43.39 | **40.27** | 34.23 | 48.07 |
| **5** | **No. of productive tillers/plant** | **7.50** | 6.33 | 10.00 | **8.63** | 6.00 | 11.67 |
| **6** | **Spike length (cm)** | **11.12** | 9.27 | 13.47 | **10.63** | 8.30 | 13.47 |
| **7** | **No. of spikelets/spike** | **17.05** | 15.47 | 18.87 | **18.43** | 14.80 | 21.20 |
| **8** | **No. of grains/spike** | **34.28** | 30.47 | 38.10 | **36.95** | 28.53 | 41.60 |
| **9** | **Weight of grain/ spike(g)** | **1.67** | 1.53 | 1.87 | **1.66** | 1.30 | 2.13 |
| **10** | **1000 grain weight (g)** | **41.72** | 38.98 | 44.31 | **42.88** | 39.12 | 46.12 |
| **11** | **Biological yield/plant (g)** | **41.57** | 35.53 | 51.27 | **38.77** | 20.67 | 52.07 |
| **12** | **Harvest index (%)** | **38.21** | 30.61 | 45.64 | **40.24** | 36.78 | 44.98 |
| **13** | **Protein content (%)** | **10.34** | 9.22 | 11.54 | **10.14** | 8.81 | 11.26 |
| **14** | **Grain yield /plant (g)** | **15.99** | 12.33 | 23.40 | **15.59** | 8.53 | 22.87 |

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **S. No.** | **Characters** | **Mean** | **Heritability (%)** | **GA** | **GA% mean** | **GCV (%)** | **PCV (%)** |
| **1** | **Days to heading (50%)** | 81.30 | 80.35 | 8.04 | 9.89 | 5.36 | 5.97 |
| **2** | **Days to Maturity** | 126.01 | 93.76 | 11.93 | 9.47 | 4.75 | 4.90 |
| **3** | **Plant height (cm)** | 95.66 | 93.22 | 13.89 | 14.52 | 7.30 | 7.56 |
| **4** | **Chlorophyll content** | 40.32 | 85.62 | 5.45 | 13.52 | 7.09 | 7.66 |
| **5** | **Number of productive tillers plant** | 8.43 | 78.72 | 2.67 | 31.71 | 17.35 | 19.56 |
| **6** | **Spike length** | 10.71 | 93.22 | 2.60 | 24.30 | 12.22 | 12.65 |
| **7** | **Number of spikelets per spike** | 18.18 | 91.81 | 3.42 | 18.81 | 9.53 | 9.95 |
| **8** | **No. of grains per spike** | 36.46 | 89.19 | 6.21 | 17.03 | 8.75 | 9.27 |
| **9** | **Weight of grain/ spike(g)** | 1.66 | 79.68 | 0.34 | 20.29 | 11.03 | 12.36 |
| **10** | **1000 seeds grain weight (g)** | 42.67 | 82.16 | 3.30 | 7.74 | 4.14 | 4.57 |
| **11** | **Biological yield per plant (g)** | 39.28 | 93.45 | 13.70 | 34.87 | 17.51 | 18.11 |
| **12** | **Harvest index (%)** | 39.87 | 76.37 | 4.64 | 11.63 | 6.46 | 7.39 |
| **13** | **Protein content (%)** | 10.18 | 84.32 | 1.15 | 11.30 | 5.97 | 6.50 |
| **14** | **Grain yield per plant (g)** | 15.66 | 91.84 | 5.93 | 37.88 | 19.19 | 20.02 |

**Table-4 Estimates of components of genetic variability for yield and its components in bread wheat.**