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GENETIC VARIABILITY AND CORRELATION STUDIES FOR DIFFERENT MORPHOLOGICAL TRAITS OF WHEAT (*TRITICUM AESTIVUM* L. EM. THELL.)

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Abstract

A field experiment was conducted on 135 bread wheat genotype under timely sown, in order to determine the genetic variability, heritability, degree and direction of the association between grain yield and its attributing characters. The experimental findings indicated highly significant differences in genotypes for all 12 morphological traits taken under study. PCV was more than GCV for all the 12characters. Correlation coefficients showed highly significant and positive association with number of grains per spike, tillers per plant, biological yield per plant, and 1000 seed-weight and harvest index. Direct impact on grain yield was shown by biological yield per plant, harvest index, peduncle length, and flag leaf area. However, other traits have a significant indirect effect on grain yield. Accordingto this, choosing genotypes with higher yield would be more effective if selection were based on these traits.

Keywords: Genetic variability, heritability, GCV, PCV, Correlation coefficients and Grain yield.

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Introduction

Wheat (Triticum aestivum L. em. Thell.) is an important cereal crop of the family Graminae (Poaceae), the largest family within the monocots. It is an all ohexaploid with chromosome number 42 (2n = 6x = 42) comprising three genetically related genomes A, B, and D (Sears, 1969). Wheat originated in the Ethiopian highlands and the Levant region of the Near East, although it is now grown all over the world. A substantial percentage of many people's daily dietary energy comes from wheat, a staple crop. Forty per cent of the global population is fed on wheat. By 2050, it is predicted that there will be 8.9 to 10.6 billion people on the planet, meaning that more wheat will need to be produced in order to guarantee food security. In order to meet the demands of a growing global population by 2050, wheat grain must be upgraded nutritionally by 850 Million tones, both in terms of GPC and health-promoting mineral elements like iron (Fe) and zinc (Zn), which can be achieved through the use of bio-fortification. The production of wheat worldwide in 2021-2022 was 779 million metric tons. According to /, https://wheat.org/wheat-in-the-world it is consumed by around 2.5 billion people in 89 countries and makes up 20% of all the calories in a person's diet. With a production of 103.86 million metric tons in 2021–2022, India is the world's second-largest producer of wheat, surpassing the average production of 103.88 million tonnes over the previous five years by 2.96 million tonnes (IIWBR, Annual report, 22-23). Wheat offers the greatest genetic diversity, which allows desired genes to hybridize and recombine to create new potential genotypes with broader adaption. Increased grain yield of wheat crop is main concern of wheat breeders; they have been utilizing the available genetic resources to change the existing varieties and evolving new crop varieties to meet the ever-changing requirements of the societies. Therefore, the present investigation was undertaken to study the "Genetic variability and correlation studies for different morphological traits of wheat (Triticum aestivum L. em. Thell.) under normal sown condition, using the genetic material available in the department of Genetics and Plant Breeding, ANDUAT, Kumarganj, Ayodhya.

Materials and Methods

The study was conducted at Acharya Narendra Deva University of Agriculture and Technology, Ayodhya, U.P during the *Rabi* season of 2021-22 under timely sown condition. A total of 135 genotypes were grown in an Augmented Block Design with four checks in a single row plot with a plot size of 22.5 x 10 cm and recommended agronomic practices were followed to raise the healthy crop. Observations were recorded

on grain yield and its related traits, *viz.*, days to flowering, days to maturity, plant height, spike length, flag leaf area, peduncle length, number of tillers per plant, number of seeds per spike, 1000-seed weight, biological yield per plant, harvest index and grain yield per plant. The data was analysed using OPSTAT (software available at <u>http:</u>//www.hau.ernet.in.), INDOSTAT (version 8.0), SPSS (version 24.0), and STAR (Statistical Tool for Agricultural Research) software.

Results and Discussion

Analysis of variance

The analysis of variance (ANOVA) for the Augmented Block Design obtained for 135 genotypes along with four checks for all the 12 characters and presented (**Table 1**). The variance analyses indicated the presence of adequate variability. The perusal of table revealed high significant differences among all the genotypes for all the 12 characters. The variations due to checks were highly significant for all the traits.

Coefficient of Variability, Heritability (Broad sense) and Genetic advance The mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in broad sense (h^2b) and genetic advance (GA) of one hundred and thirty five genotypes of different characters have been shown (Table 2).

The number of seeds per spike (35.98-70.12) recorded the highest range of variation followed by plant height (68.20 - 101.67 cm), days to maturity (107-134 days), biological yield per plant (21.92 - 45.51 g), peduncle length (14.56 - 32.88 cm), flag leaf area $(14.93-31.04 \text{ cm}^2)$, days to heading (70-85 days), harvest index (36.25 - 51.26 %), 1000-seed weight (32.52 - 45.89 g), grain yield per plant (9.50-20.22 g) and it was minimum in spike length (4.20-13.80 cm) and no. of tillers per plant (4.38-9.00). The phenotypic and genotypic coefficient of variability (PCV and GCV) of all the twelve characters is given (**Table 2**). Usually phenotypic coefficient of variability (PCV) was more than genotypic coefficient of variability (GCV) for all the twelve characters. The high estimate (> 20 %) of PCV and GCV was not found for any traits, whereas, moderate estimate (10-20 %) of PCV and GCV was recorded for peduncle length (11.03% and 14.35%) respectively. The lowest estimates (< 10 %) of PCV and GCV were recorded for rest of the traits. These all were in concurrence with the earlier reports of **Nuksani** *et al.* (2013), Arya *et al.* (2017), Dabi *et al.* (2020) and Prasad *et al.* (2021). The estimates of the heritability gives the idea about transmission of characters from parents to their offspring. The heritability estimates in

broad sense were calculated for all 12 characters and have been illustrated (Table 2). The heritability ranged from 16.69 % (Flag leaf area) to 92.92 % (Biological yield per plant). The High estimates of heritability in broad sense (>75 %) were recorded for biological yield per plant (92.92 %) followed by days to heading (75.64 %). Whereas, moderate heritability (50-75%) were observed in days to maturity (56%), peduncle length (59.03%), number of seeds per spike (54.14 %). Comparatively, low estimates of heritability (< 50%) were observed for harvest index (44.42 %), plant height (31.00 %), 1000-seed weight (28.86 %), tillers per plant (24.37 %), spike length (17.18 %) and flag leaf area (16.69 %). The genetic advance (GA) gives a thought of expected advancement through selection in the next generation. The high estimates of GA coupled with high heritability without a doubt indicates the possibility of improvement through selection. The Genetic advance (GA) in % of mean shows significant variations for different traits. The GA in percent of mean ranged from 0.40 % (tillers per plant) to 6.09 % (days to heading). None of the character showed high estimates (> 20%) of genetic advance in % of mean meanwhile, moderate estimates (10-20 %) were noted in grain yield per plant (10.15 %), biological yield per plant (2.97 %) and peduncle length (17.45 %). rest of the traits showed low estimates of genetic advance. The above findings are in accordance with those of **Kumar** et al. (2013), Khattab et al. (2010), Abinas et al. (2011), Huang et al. (2012), Hussain et al. (2013), Kumar et al. (2014) and Abbas et al. (2020).

Correlation coefficient

The values of simple correlation coefficient were calculated for all the 12 quantitative characters and have been illustrated (**Table 3**). The character days to heading exhibited positive and significant correlation with peduncle length (0.17). The trait days to maturity exhibited highly significant and positive correlation with spike length (0.24) and negative significant correlation with tillers per plant (-0.24) followed by harvest index (-0.25) and grain yield per plant (-0.34). Plant height exhibited positive and significant correlation with number of seeds per spike (0.27), Spike length exhibited negative and significant correlation with grain yield per plant (-0.16) and positive significant correlation with grain yield per plant (0.21) while, positive and highly significant correlation with peduncle length (0.23). Peduncle length showed positive and significant correlation with 1000-seed weight (0.20) and harvest index (0.21) and 1000-seed weight (0.20). Number of seeds per spike of seeds per spike and highly significant positive association with number of seeds per spike (0.21) and 1000-seed weight (0.20). Number of seeds per spike possessed significant and high

positive association with tillers per plant (0.20), biological yield per plant (0.25), harvest index (0.34) and grain yield per plant (0.47). Tillers per plant showed positive and highly significant difference with 1000-seed weight (0.34), biological yield per plant (0.49) and grain yield per plant (0.52). The 1000-seed weight showed positive and highly significant correlation with grain yield per plant (0.27) and biological yield per plant (0.21). Biological yield per plant possessed significant positive association with grain yield per plant (0.69) and negative and highly significant correlation with harvest index (-0.25). Whereas, harvest index possessed significant and high positive association with grain yield per plant (0.51). Akram *et al.* (2008), Tsagaye *et al.* (2012), Bhushan *et al.* (2013), Baye *et al.* (2020), Kadam *et al.* (2020) and Bradauskiene *et al.* (2023) reported the similar results for seed yield and most of its components.

Path coefficient

The correlation coefficient of grain yield per plant with other characters under investigation was further divided into direct and indirect effect using path coefficient analysis and is presented (Table 4). Path coefficient analysis under normal situation showed that that biological yield had highest positive direct effect (0.887) on grain yield per plant followed by harvest index (0.732). Days to heading (0.0028), peduncle length (0.0097) and flag leaf area (0.0059). While, days to maturity (-0.024), plant height (-0.0012), spike length (-0.002), tillers per plant (-0.0105) and 1000-seed weight (-0.0033) showed negative direct effect on grain yield per plant while Biological yield per plant via days to maturity (0.0037), spike length (0.0004) and seeds per spike (0.0004) showed positive indirect effect on grain yield per plant while, it exerted negative indirect effects on grain yield via plant height (-0.0001), peduncle length (-0.0008), flag leaf area (-0.0001), tillers per plant (-0.0053), 1000-seed weight (-0.0033). Harvest index via daysto maturity (0.0062), spike length (0.0002), peduncle length (0.0017), flag leaf area (0.0009)and grain yield per plant (0.0006) exerted positive indirect effects on grain yield. Remaining traits had negative effects. The estimates of residual effects were (0.0344). These results are in close agreement with the finding of Khan et al. (2013), Mecha et al. (2017), Gholizadeh et al. (2017), Singh et al. (2022) and Hinson et al. (2022).

Conclusion

Adequate variability was found in the Augmented Block Design analysis of variance for 135 germplasm, which included four checks for each of the 12 characters. For each of the 12 traits under study, there were notable differences between each genotype. The variances

due to checks were highly significant for all the traits. Phenotypic coefficient of variability was more than genotypic coefficient of variability for all the twelve characters. The moderate estimates of PCV and GCV was recorded for peduncle length (11.03 % and 14.35 %) respectively. Lowest estimates of PCV and GCV were recorded for all the remaining traits. The high estimates of heritability in broad sense were recorded in biological yield per plant and days to heading. Moderate estimates of heritability were observed in days to maturity, peduncle length, and number of seeds per spike. Rest of the trait had low estimates of heritability. Moderate estimates of genetic advance in percent of mean were noted for grain yield per plant, biological yield per plant and peduncle length. Rest of the traits had low estimates of genetic advance. Days to maturity exhibited negative significant correlation with grain yield per plant. Whereas, spike length, number of seeds per spike, tillers per plant, biological yield per plant, 1000-seed weight and harvest index possessed positive and high positive association with grain yield per plant. Biological yield per plant, harvest index, days to heading, peduncle length and flag leaf area showed positive direct effect on grain yield per plant. While, days to maturity, plant height, spike length, tillers per plant and 1000-seed weight showed negative direct effect on grain yield per plant. Biological yield per plant via days to maturity showed positive indirect effect on grain yield per plant and it exerted negative indirect effects on grain yield via days to maturity. Remaining traits had negligible direct/indirect effects.

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| Source of variation | DF | Days to heading | Days to maturity | Plant height (cm) | No. of tillers per plant | Flag leaf area (cm ²) | Spike length (cm) | Peduncle length (cm) | No. of seeds per spike | 1000- seed weight (g) | Biological yield per plant (g) | Harvest index (%) | Grain yield per plant (g) |
|------------------------|-----|--------------------|---------------------|-------------------------|-----------------------------------|--|-------------------------|----------------------------|---------------------------------|--------------------------------|--------------------------------------|-------------------------|---------------------------------------|
| Block | 8 | 68.79** | 594.62** | 165.73** | 6.24** | 23.49** | 5.26** | 175.18** | 167.87** | 27.00** | 41.73** | 69.94** | 18.65** |
| Checks | 3 | 26.32** | 18.99** | 545.52** | 2.45** | 7.81** | 12.66** | 5.50** | 39.45** | 21.50** | 51.85** | 39.81** | 3.87** |
| Error | 24 | 3.72 | 2.99 | 21.82 | 0.47 | 5.74 | 1.24 | 4.33 | 9.98 | 2.52 | 0.33 | 4.34 | 0.40 |
| Total | 170 | 44.28 | 43.34 | 60.42 | 1.26 | 10.32 | 3.07 | 32.64 | 55.67 | 7.00 | 16.48 | 18.68 | 3.59 |

Table 1: ANOVA of Augmented Block Design for 12 characters of wheat

*, ** significant at 5% and 1% level of probability

| Genotypes | Mean | Min. | Max. | Var. (g) | Var. (p) | Heritability (%) | Genetic advance (GA) | GA% mean | GCV (%) | PCV (%) |
|-----------------------------------|--------|--------|--------|-------------|-------------|---------------------|-------------------------|-------------|------------|------------|
| Days to heading | 78.26 | 70.00 | 85.00 | 11.55 | 15.27 | 75.64 | 6.09 | 7.78 | 4.34 | 4.99 |
| Days to maturity | 123.90 | 107.00 | 134.00 | 3.85 | 6.84 | 56.29 | 3.03 | 2.45 | 1.58 | 2.11 |
| Plant height (cm) | 83.62 | 68.20 | 101.67 | 9.80 | 31.62 | 31.00 | 3.59 | 4.29 | 3.74 | 6.72 |
| No. of tillers per plant | 6.24 | 4.38 | 9.00 | 0.15 | 0.62 | 24.37 | 0.40 | 6.35 | 6.24 | 12.65 |
| Flag leaf area (cm ²) | 23.53 | 14.93 | 31.04 | 1.15 | 6.90 | 16.69 | 0.90 | 3.84 | 4.56 | 11.16 |
| Spike length (cm) | 11.02 | 4.20 | 13.80 | 0.36 | 2.10 | 17.18 | 0.51 | 4.65 | 5.45 | 13.14 |
| Peduncle length (cm) | 22.66 | 14.56 | 32.88 | 6.24 | 10.57 | 59.03 | 3.95 | 17.45 | 11.03 | 14.35 |
| No. of seeds per spike | 52.80 | 35.98 | 70.12 | 11.78 | 21.76 | 54.14 | 5.20 | 9.85 | 6.50 | 8.84 |
| 1000-seed weight (g) | 39.45 | 32.52 | 45.89 | 1.02 | 3.55 | 28.86 | 1.12 | 2.84 | 2.56 | 4.77 |
| Biological yield per plant (g) | 32.02 | 21.92 | 45.51 | 4.37 | 4.71 | 92.92 | 4.15 | 12.97 | 6.53 | 6.78 |
| Harvest index (%) | 42.99 | 36.25 | 51.26 | 3.47 | 7.80 | 44.42 | 2.56 | 5.95 | 4.33 | 6.50 |
| Grain yield per plant (g) | 13.78 | 9.50 | 20.22 | 0.72 | 1.12 | 64.30 | 1.40 | 10.15 | 6.15 | 7.66 |

| Tuble 21 fillung funger genoty ple und phenoty ple coefficient of variability (/ 0) and genote advance in percent of ma | able 2: Mean, rang | ge, genotypic and phenotypic | c coefficient of variability, | heritability (%) and | genetic advance in p | percent of mean |
|--|--------------------|------------------------------|-------------------------------|----------------------|-----------------------------|-----------------|
|--|--------------------|------------------------------|-------------------------------|----------------------|-----------------------------|-----------------|

| Characters | Days to heading | Plant height (cm) | Days to maturity | Spike length (cm) | Peduncle length (cm) | Flag leaf area (cm ²) | No. of seeds per spike | No. of tillers per plant | 1000- seed weight (g) | Biological yield per plant (g) | Harvest index (%) | Grain yield per plant (g) |
|-----------------------------------|--------------------|-------------------------|---------------------|-------------------------|----------------------------|--|---------------------------------|--------------------------------|--------------------------------|--------------------------------------|-------------------------|---------------------------------|
| Days to heading | 1.000 | -0.029 | -0.024 | 0.086 | 0.179* | 0.019 | -0.016 | -0.111 | 0.035 | -0.003 | -0.059 | -0.040 |
| Plant height (cm) | | 1.000 | 0.165 | 0.119 | -0.143 | 0.013 | 0.274** | 0.101 | 0.066 | 0.074 | 0.104 | 0.133 |
| Days to maturity | | | 1.000 | 0.245** | -0.155 | -0.147 | -0.012 | -0.242** | 0.030 | -0.149 | -0.251** | -0.341** |
| Spike length(cm) | | | | 1.000 | 0.232** | 0.015 | -0.011 | -0.191* | 0.036 | -0.169* | -0.084 | 0.216* |
| Peduncle length(cm) | | | | | 1.000 | 0.134 | 0.012 | -0.017 | 0.208* | -0.083 | 0.176* | 0.067 |
| Flag leaf area (cm ²) | | | | | | 1.000 | 0.214* | 0.116 | 0.208* | -0.024 | 0.156 | 0.100 |
| No. of seeds per spike | | | | | | | 1.000 | 0.205* | 0.065 | 0.252** | 0.349** | 0.479** |
| No. of tillers per plant | | | | | | | | 1.000 | 0.341** | 0.499** | 0.129 | 0.528** |
| 1000-seed weight(g) | | | | | | | | | 1.000 | 0.217* | 0.134 | 0.274** |
| Biological yield per plant (g) | | | | | | | | | | 1.000 | -0.257** | 0.694** |
| Harvest index (%) | | | | | | | | | | | 1.000 | 0.510** |
| Grain yield per plant (g) | | | | | | | | | | | | 1.000 |

Table 3: Simple correlation coefficient between 12 characters of wheat

*, ** significant at 5% and 1% level of probability respectively

| Characters | Days to heading | Plant height (cm) | Days to maturity | Spike length (cm) | Peduncle length (cm) | Flag leaf area (cm ²) | No. of seeds per spike | No. of tillers per plant | 1000- seed weight (g) | Biological yield per plant (g) | Harvest index (%) | Correlation coefficient with Grain yield per plant (g) |
|---------------------------------------|--------------------|-------------------------|---------------------|-------------------------|----------------------------|--|---------------------------------|-----------------------------------|--------------------------------|--------------------------------------|-------------------------|--|
| Days to heading | 0.0028 | 0.0000 | 0.0006 | -0.0002 | 0.0017 | 0.0001 | 0.0000 | 0.0012 | -0.0005 | -0.0027 | -0.0431 | -0.040 |
| Plant height (cm) | -0.0001 | -0.0012 | -0.0040 | -0.0003 | -0.0014 | 0.0001 | 0.0004 | -0.0011 | -0.0010 | 0.0654 | 0.0761 | 0.133 |
| Days to maturity | -0.0001 | -0.0002 | -0.0245 | -0.0005 | -0.0015 | -0.0009 | 0.0000 | 0.0026 | -0.0005 | -0.1322 | -0.1836 | -0.341** |
| Spike length (cm) | 0.0002 | -0.0002 | -0.0060 | -0.0021 | 0.0022 | 0.0001 | 0.0000 | 0.0020 | -0.0006 | -0.1500 | -0.0618 | -0.216* |
| Peduncle length (cm) | 0.0005 | 0.0002 | 0.0038 | -0.0005 | 0.0097 | 0.0008 | 0.0000 | 0.0002 | -0.0032 | -0.0740 | 0.1291 | 0.067 |
| Flag leaf area(cm ²) | 0.0001 | 0.0000 | 0.0036 | 0.0000 | 0.0013 | 0.0059 | 0.0003 | -0.0012 | -0.0032 | -0.0216 | 0.1146 | 0.100 |
| No. of seeds per spike | -0.0001 | -0.0003 | 0.0003 | 0.0000 | 0.0001 | 0.0013 | 0.0016 | -0.0022 | -0.0010 | 0.2235 | 0.2559 | 0.479** |
| No. of tillers per plant | -0.0003 | -0.0001 | 0.0060 | 0.0004 | -0.0002 | 0.0007 | 0.0003 | -0.0105 | -0.0052 | 0.4430 | 0.0943 | 0.528** |
| 1000-seed weight (g) | 0.0001 | -0.0001 | -0.0007 | -0.0001 | 0.0020 | 0.0012 | 0.0001 | -0.0036 | -0.0152 | 0.1924 | 0.0978 | 0.274** |
| Biological yield per plant (g) | 0.0000 | -0.0001 | 0.0037 | 0.0004 | -0.0008 | -0.0001 | 0.0004 | -0.0053 | -0.0033 | 0.8873 | -0.1883 | 0.694** |
| Harvest index (%) | -0.0002 | -0.0001 | 0.0062 | 0.0002 | 0.0017 | 0.0009 | 0.0006 | -0.0014 | -0.0020 | -0.2280 | 0.7326 | 0.510** |

| Table 4: Direct and indirect effects of 12 characters on | grain | yield | per plan | t (g) |
|--|-------|-------|----------|-------|
|--|-------|-------|----------|-------|

Residual = 0.0344

*, ** Significant at 5% and 1% level of probability.