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# Genetic variability of wheat (*Triticum aestivum* L.) genotypes for agro-morphological traits and their correlation and path analysis

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## Abstract

In the present study, 98 wheat genotypes were evaluated for estimation of heritability, variability, correlation and path analysis. The wheat genotypes were sown in randomized block design in two replications in the field of Wheat and Barley Section, Department of Genetics and Plant Breeding, CCS HAU, Hisar (India) during *Rabi*, 2018-2019. Phenotypic data was recorded for nine characters *viz*. plant height, number of effective tillers per meter, spike length, number of grains per spike, number of Spikelets per spike, 1000-grain weight, grain yield per plot, and biological yield per plot. The highest value for GCV and PCV was observed for biological yield per plot (18.09 & 19.18 % respectively). Heritability for broad sense ($h^2$) and genetic advance as 5% of mean were highest for harvest index (96.50 %) and biological yield (35.17%), respectively. Grain yield per plot was highly and significantly correlated with all the traits except plant height and grain yield per plot. Path analysis revealed that biological yield per plot had the maximum direct positive effect on grain yield per plot and harvest index, whereas, all other traits except plant height contributed indirectly towards grain yield per plot via biological yield per plot. Thus, these component traits may be used in wheat breeding program for further improvement in grain yield.

**Keywords:** Wheat, variability, correlation, path analysis

## Introduction

Wheat (*Triticum aestivum* L.) is the 'King of Cereals' as it is one of the most commonly grown & consumed food grain and occupies a major acreage under its cultivation, worldwide. Wheat cultivars are the result of extensive selection by breeders to meet both the quality and the agronomic requirements for the wide range of end products. Thus wheat quality becomes a major target in wheat breeding program for the world wheat trade (Gross *et al*., 2007) [6].

Grain yield is a multigenic trait and evaluations of the inter association between grain yield & other yield traits and among themselves simplifies effective selection outlines to expand the yield. Chances of succeeding improvement in any crop plant depend greatly on the scale of genetic variability. The magnitude of genotypic variability on yield and its constituent characters affects selection approaches to be accepted by the plant breeders as it is the heritable constitute of the variability. In bread wheat varieties, many agro-morphological characters (plant height, flag leaf length, flag leaf hairs on auricle, flag leaf waxiness of blade, flag leaf attitude, spike length, spikelet number, peduncle waxiness, spike density, peduncle length and awns presence) reveal main variability (Rehman *et al*., 2009).

Heritability is a quantity having analytical role to determine phenotypic variability in the traits which can be ascribed to genetic differences in plant breeding experiments. The phenotypic data can be recorded directly whereas the genetic values are deliberated by the appropriate analyses. The amount of phenotypic value which will be inherited to the succeeding generation is estimated by genotypic values (Rehman & Alam 1994) [14]. Heritability shows a direct association with the response of selection known as genetic advance (GA) or progress. Higher the value of heritability, the simpler is selection event (Khan *et al*., 2007) [9]. The evaluation of heritability depends on the environment along with the nature of the test population (Gemechu, 1996) [5]. The combination of high heritability and high genetic advance provide the effectual selection conditions (Larik *et al*., 2000) [10].

Analysis of variance reveals significant difference among genotypes for traits like days to maturity, plant height, 1000-seed weight, spike height, seed yield, protein yield and percentage, grain filling rate and number of spikes. Path analysis along with correlation studies provides a detailed understanding of association of various traits with grain yield. It not only provides means to quantify the interrelationship of different yield components but also indicates whether the influence is directly reflected in the yield or takes some other path for

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ultimate effects (Kashif & Khaliq, 2004) [8]. The information of correlation that occurs between significant characters may simplify proper clarification of results and offers a basis for development of more efficient breeding programs. Phenotypic correlation is the association between recorded two value or traits, while genotypic correlation is the natural association between characters. The information of interrelationship of many yield constituents is of supreme significance for a plant breeder for making the results regarding range conditions.

It is required to increase the productivity of wheat to fulfill the increasing demand of food. The knowledge of genetic variability, heritability, correlation coefficient and other related parameters can help in further increasing the grain yield. Their understanding can direct the selection of yield related traits and their relationship with the yield. The estimation of variability, heritability and correlation coefficient done in this study could be utilized for further increase in grain yield of the wheat genotypes.

## Materials and Methods

### Experimental Material and Design

All the wheat genotypes listed in Table 1, were sown during *Rabi* season 2018-19 in the field of Wheat & Barley Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar, India. Each genotype was planted in 1.5-meter plot with two tiers of it. As much as 30 seeds per line were sown in rows arranged in Randomized Block Design. Two replications were grown for each line. All the plant protection methods & recommended package of practices needed for cultivation of a healthy crop were followed.

**Table 1:** List of genotypes used in the present study

| Sr. No. | Genotype | Sr. No. | Genotype | Sr. No. | Genotype | Sr. No. | Genotype |
|---|---|---|---|---|---|---|---|
| 1. | DBW-14 | 26. | KALYANSON-9 | 51. | RMR-1 | 76. | WH-1105 |
| 2. | DBW-17 | 27. | C-306 | 52. | RAJ-3765 | 77. | WH-1123 |
| 3. | DBW-88 | 28. | LOK-54 | 53. | SYM-2 | 78. | WH-1124 |
| 4. | DBW-90 | 29. | MR-1 | 54. | SYM- 4 | 79. | WH-1126 |
| 5. | DBW-95 | 30. | MACS-6222 | 55. | SYM-22 | 80. | WH-1127 |
| 6. | HD-2009 | 31. | NI-5439 | 56. | SYM-24 | 81. | WH-1129 |
| 7. | HD-2285 | 32. | NGSN-2 | 57. | UP-2338 | 82. | WH-1132 |
| 8. | HD-2329 | 33. | NW-2059 | 58. | UP-2425 | 83. | WH-1134 |
| 9. | HD-2687 | 34. | NW-2306 | 59. | UP-2463 | 84. | WH-1135 |
| 10. | HD-2733 | 35. | NW-6064 | 60. | UP-2565 | 85. | WH-1136 |
| 11. | HD-2851 | 36. | NW-6098 | 61. | UP-2660 | 86. | WH-1137 |
| 12. | HD-2880 | 37. | P-9141 | 62. | UP-2902 | 87. | WH-1138 |
| 13. | HD-2888 | 38. | P-11638 | 63. | UP-2906 | 88. | WH-1142 |
| 14. | HD-2967 | 39. | PBW-116 | 64. | WH-147 | 89. | WH-1152 |
| 15. | HD-3059 | 40. | PBW-343 | 65. | WH-157 | 90. | WH-1153 |
| 16. | HD-3086 | 41. | PBW-502 | 66. | WH-283 | 91. | WH-1154 |
| 17. | HD-3126 | 42. | PBW-550 | 67. | WH-542 | 92. | WH-1155 |
| 18. | HUW-234 | 43. | DBW-621-50 | 68. | WH-711 | 93. | WH-1157 |
| 19. | HUW-704 | 44. | PBW-693 | 69. | WL-711 | 94. | WH-1158 |
| 20. | HW-3190 | 45. | PBW-698 | 70. | WH-730 | 95. | WH-1159 |
| 21. | HPBW-2 | 46. | PBW-715 | 71. | WH-1021 | 96. | WH-1184 |
| 22. | K-307 | 47. | PBW-723 | 72. | WH-1025 | 97. | WH-1186 |
| 23. | KRL-19 | 48. | PBW-725 | 73. | WH-1063 | 98. | WH-1188 |
| 24. | KRL-210 | 49. | PBW-726 | 74. | WH-1080 | | |
| 25. | KH-65 | 50. | PBW-729 | 75. | WH-1097 | | |

### Morphological data collection

Data for different agro-morphological traits was collected on plant and plot basis. Plant height (cm), spike length (cm), number of grains per spike, and number of spikelets per spike were taken on plant basis; whereas thousand grain weight (g), grain yield (g), biological yield (g), harvest index (%) and number of effective tillers per meter were evaluated on plot basis.

### Statistical analysis

The analysis of variance for complete randomized complete block design was done for individual character to test the importance of difference among the genotypes, using the method given by Fisher (1925) and named by Panse and Sukhatme (1967). Genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV) were estimated by the formula suggested by Burton (1953). Heritability in broad sense was calculated according to the formula suggested by Hanson *et al.* (1956). Estimates of appropriate variance components were substituted for the parameters as recommended by Lush (1949) and Johnson *et al.* (1955), to predict expected genetic gain which was calculated at 5 per cent selection intensity. Coefficients of correlation were determined by using the variance and covariance components as suggested by Al-Jibouri *et al.* (1958). The estimation of direct and indirect effect of 8 independent characters on grain yield as dependent character was performed. The genotypic correlations coefficients were used to carry out path coefficient analysis as suggested by Wright (1934) and illustrated by Dewey and Lu (1959) [3].

## Results

The mean sum of squares values is shown in Table 2. The perusal of this data revealed that variance due to genotype was significant for all the characters which indicated that genetic variance was present among the 98 genotypes for all the traits studied.

**Table 2:** Analysis of Variance (ANOVA) for different traits of wheat genotypes

| Source of variation (SV) | Degree of freedom (df) | Mean sum of squares (MSS) | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | Plant height (cm) | Number of effective tillers/m | Spike length (cm) | Number of grains/spike | Number of spikelets/spike | 1000 Grain Weight(g) | Biological yield/plot (g) | Grain yield/plot (g) | Harvest index (%) |
| Replication | 1 | 2.94 | 3.45 | 0.04 | 24.79 | 0.33 | 7.14 | 215.63 | 57.22 | 215.63 |
| Treatment | 97 | 244.10* | 30.20* | 0.80* | 154.17* | 5.20* | 60.49* | 16.15* | 9702.15* | 136.15* |
| Error | 97 | 16.64 | 2.40 | 0.07 | 3.25 | 0.31 | 3.88 | 8.79 | 173.55 | 8.79 |

* Significant at 5 % level of significance

Heritability and genetic advance

## Genetic variability

The lower value of GCV as compared to PCV for all the traits indicated that the effect of environment was negligible on the development of plants (Table 3). Biological yield per plot depicted the highest value of GCV (18.09%) and PCV (19.18%) followed by harvest index (GCV- 15.76%, PCV- 16.04%), number of grains per spike (GCV- 14.29%, PCV- 14.60%) and 1000 grain weight (GCV- 13.11%, PCV- 13.97%). The GCV and PCV values observed for rest of the traits were comparatively lower (<10) such as plant height, number of spikelets per spike, spike length, grain yield per plot and number of tillers per meter. Broad sense ($h^2$) heritability was in range from 97% to 78%. The highest $h^2$ value was recorded for harvest index (96.50) followed by number of grains per spike (95.90%), biological yield per plot (89%), number of spikelets per spike (88.60%), 1000 grain weight (88%), plant height (87.20%), number of tillers per meter (85.30%), spike length (83.10%) and grain yield per plot (78.50%).

**Table 3:** Estimation of phenotypic and genotypic coefficient of variance, heritability and genetic advance for grain yield and component traits in wheat

| Sr. No | Traits | Phenotypic Parameters | | | Genetic Parameters | | | |
|---|---|---|---|---|---|---|---|---|
| | | Overall Mean | Min. | Max. | GCV (%) | PCV (%) | Heritability (%) | Genetic advance as 5% of mean |
| 1 | Plant height (cm) | 116.45 | 85.80 | 125.20 | 9.158 | 9.805 | 87.20 | 17.620 |
| 2 | Number of effective tillers/ m | 106.28 | 94.00 | 115.00 | 3.508 | 3.799 | 85.30 | 6.674 |
| 3 | Spike length (cm) | 12.53 | 11.28 | 14.50 | 4.822 | 5.289 | 83.10 | 9.054 |
| 4 | Number of grains/spike | 60.00 | 40.00 | 77.00 | 14.297 | 14.601 | 95.90 | 28.838 |
| 5 | Number of spikelets/spike | 17.00 | 13.00 | 21.00 | 8.840 | 9.389 | 88.60 | 17.146 |
| 6 | 1000 Grain weight (g) | 40.58 | 27.95 | 44.00 | 13.110 | 13.979 | 88.00 | 25.328 |
| 7 | Biological yield/ plot (g) | 1019.77 | 655.00 | 1520.00 | 18.098 | 19.184 | 89.00 | 35.170 |
| 8 | Grain yield/ plot (g) | 437.87 | 300.00 | 638.30 | 4.582 | 8.432 | 78.50 | 5.129 |
| 9 | Harvest index (%) | 41.87 | 33.30 | 45.40 | 15.764 | 16.048 | 96.50 | 31.897 |

Genetic advance as 5% of mean indicated a good scope for improvement for biological yield (35.17%), harvest index (31.89%), number of grains per spike (28.83%) and 1000 grain weight (25.32%) while, traits *viz*. plant height (17.62%), number of spikelets per spike (17.14%), spike length (9.05%), number of tillers per meter (6.67%) and grain yield per plot (5.12%) showed lower value of genetic advance. The traits *viz.* biological yield per plot, harvest index and number of grains per spike showed high GCV, PCV, heritability and genetic advance as 5% of mean.

## Correlation coefficients

The phenotypic and genotypic correlation coefficients were appraised to find out the associations among different quantitative characters at phenotypic level (Table 4). Grain yield per plot was positively and highly significantly correlated with number of effective tillers per metre (0.448), spike length (0.551), number of grains per spike (0.611), number of spikelets per spike (0.588), 1000 grain weight (0.585), biological yield per plot (0.805) and harvest index (0.113). Harvest index showed negative correlation with biological yield per plot (-0.044). Biological yield per plot showed positive significant association with number of effective tillers per meter (0.457), spike length (0.550), number of grains per spike (0.626), number of spikelets per spike (0.540) and 1000 grain weight (0.610). It was observed that 1000 grain weight had positive significant correlation with all traits *viz.* number of effective tillers per meter (0.530), spike length (0.629) and number of spikelets per spike (0.560) except plant height (-0.072) and number of grains per spike (-0.661).

## Path coefficient

It was revealed that biological yield per plot had the maximum direct positive effect on grain yield per plot (0.600) followed by harvest index (0.573). Rest of traits such as number of spikelets per spike (0.172), 1000 grain weight (0.064), spike length (0.035), number of effective tillers per meter (0.033) and number of grains per spike (0.012) showed moderate direct positive effect on grain yield. Plant height had direct negative effect on grain yield per plot (-0.079) (Table 5). For indirect effects, it was observed that all the characters contributed towards grain yield per plot via biological yield per plot except plant height (-0202). It was also observed that all the characters contributed towards grain yield per plot through harvest index.

**Table 4:** Phenotypic and Genotypic correlation coefficient for various traits in wheat genotypes

| Traits | | Plant height (cm) | No. of effective tillers/meter | Spike length (cm) | Number of grains/spike | Number of spikelets/spike | 1000 Grain Weight (g) | Biological yield/plot (g) | Grain yield/plot (g) | Harvest Index % |
|---|---|---|---|---|---|---|---|---|---|---|
| Number of effective tillers/ meter | $r_p$ | -0.018 | | | | | | | | |
| | $r_g$ | -0.021 | | | | | | | | |
| Spike length (cm) | $r_p$ | -0.231$^{**}$ | 0.493$^{**}$ | | | | | | | |
| | $r_g$ | -0.256$^{**}$ | 0.595$^{**}$ | | | | | | | |
| Number of grains/ spike | $r_p$ | -0.188$^{**}$ | 0.475$^{**}$ | 0.672$^{**}$ | | | | | | |
| | $r_g$ | -0.205$^{**}$ | 0.522$^{**}$ | 0.743$^{**}$ | | | | | | |
| Number of spikelets/ spike | $r_p$ | -0.138 | 0.434$^{**}$ | 0.568$^{**}$ | 0.674$^{**}$ | | | | | |
| | $r_g$ | -0.144$^{*}$ | 0.507$^{**}$ | 0.638$^{**}$ | 0.722$^{**}$ | | | | | |
| 1000 Grain Weight (g) | $r_p$ | -0.072 | 0.530$^{**}$ | 0.629$^{**}$ | 0.661$^{**}$ | 0.560$^{**}$ | | | | |
| | $r_g$ | -0.098 | 0.576$^{**}$ | 0.689$^{**}$ | 0.706$^{**}$ | 0.627$^{**}$ | | | | |
| Biological yield/ plot (g) | $r_p$ | -0.338$^{**}$ | 0.457$^{**}$ | 0.550$^{**}$ | 0.626$^{**}$ | 0.540$^{**}$ | 0.610$^{**}$ | | | |
| | $r_g$ | -0.393$^{**}$ | 0.502$^{**}$ | 0.633$^{**}$ | 0.671$^{**}$ | 0.594$^{**}$ | 0.677$^{**}$ | | | |
| Grain yield/ plot(g) | $r_p$ | -0.321$^{**}$ | 0.448$^{**}$ | 0.551$^{**}$ | 0.611$^{**}$ | 0.588$^{**}$ | 0.585$^{**}$ | 0.805$^{**}$ | | |
| | $r_g$ | -0.337$^{**}$ | 0.478$^{**}$ | 0.608$^{**}$ | 0.634$^{**}$ | 0.631$^{**}$ | 0.627$^{**}$ | 0.854$^{**}$ | | |
| Harvest Index (%) | $r_p$ | 0.006 | 0.093 | 0.049 | 0.129 | 0.023 | 0.056 | 0.044 | 0.113 | |
| | $r_g$ | 0.003 | 0.224$^{**}$ | 0.176$^{*}$ | 0.247$^{**}$ | 0.005 | 0.121 | 0.110 | 0.178$^{*}$ | |

rp- Phenotypic coefficient of correlation
rg- Genotypic coefficient of correlation

**Table 5:** Direct (diagonal value) and indirect effects of grain yield and its component traits in wheat genotypes

| Traits | Plant height (cm) | No. of tillers /meter | Spike length (cm) | Number of grains /spike | Number of spikelets/ spike | 1000 Grain weight (g) | Biological yield/ plot (g) | Harvest index (%) |
|---|---|---|---|---|---|---|---|---|
| Plant height (cm) | -0.0790 | 0.0015 | 0.0183 | 0.0149 | 0.0109 | 0.0057 | 0.0267 | -0.0005 |
| Number of effective tillers/ meter | -0.0006 | 0.0335 | 0.0165 | 0.0159 | 0.0146 | 0.0178 | 0.0153 | 0.0031 |
| Spike length (cm) | -0.0082 | 0.0174 | 0.0354 | 0.0238 | 0.0201 | 0.0222 | 0.0195 | 0.0017 |
| Number of grains/ spike | -0.0023 | 0.0059 | 0.0083 | 0.0124 | 0.0084 | 0.0082 | 0.0078 | 0.0016 |
| Number of spikelets/ spike | -0.0238 | 0.0747 | 0.0979 | 0.1159 | 0.1722 | 0.0964 | 0.0930 | 0.0040 |
| 1000 Grain weight (g) | -0.0046 | 0.0340 | 0.0403 | 0.0424 | 0.0359 | 0.0641 | 0.0391 | 0.0036 |
| Biological yield/ plot (g) | -0.2027 | 0.2742 | 0.3303 | 0.3760 | 0.3244 | 0.3661 | 0.6003 | 0.0266 |
| Harvest index (%) | 0.0004 | 0.0068 | 0.0036 | 0.0094 | 0.0017 | 0.0041 | 0.0032 | 0.5730 |
| Correlation with grain yield | 0.213$^{**}$ | 0.143$^{*}$ | 0.495$^{**}$ | 0.362$^{**}$ | 0.410$^{**}$ | -0.071 | 0.656$^{**}$ | 0.396$^{**}$ |

** Significant at 1 % level of significance

## Discussion

### Genetic Variability

The analysis of variance showed the existence of adequate genetic variation among the various wheat genotypes for all the traits studied. Jee *et al.* (2019) [7] also found that the analysis of variance was highly significant between the genotypes under their study. It shows that the material selected for this study carries significant diversity which is required by any breeding program. It was observed that value of PCV was slightly higher than the value of GCV. Similar results were observed by Singh *et al.* (2018) [17] indicating less effect of environment on the expression of characters studied. The highest GCV and PCV were recorded for biological yield per plot and harvest index. Morteza *et al.* (2018) [11] also observed highest GCV and PCV for biological yield followed by harvest index. Two important selection parameters were heritability and genetic advance. These were useful in selection for genetic improvement of various traits to improve grain yield of wheat (Johnson *et al.*, 1995). Harvest index, number of grains per spike and biological yield per plot showed high heritability and genetic advance as 5% mean. Singh *et al.* (2018) [17] also found high GCV and PCV along with high heritability and high genetic advance which indicated substantial involvement of additive gene action in the expression. They also observed that number of grains per ear and 1000-grain weight had high heritability and genetic advance which could be improved. They also recorded that biological yield per plant and number of grains per ear had high GCV, heritability and genetic advance.

The study of correlation provided information about degree and direct association of grain yield contributing characters. In the present study, phenotypic and genotypic correlation were estimated. Phenotypic includes both genotypes and environmental influence. It was revealed that number of effective tillers per meter, spike length; number of grains per spike, number of spikelets per spike, 1000 grain weight, biological yield per plot and harvest index had positive and significant correlation with grain yield per plot. Nazem and Arzani (2013) [12] also found significant association of grain yield with the other traits *viz,* 1000 grain weight and number of grains per spike. Analogous results were observed by Bhushan *et al.* (2013) [2] that positive significant correlation of test weight, biological weight and number of spikelets per spike with grain yield per plant. These results signified that selection of these traits would lead to grain yield improvement of crop. It was observed that harvest index showed negative and highly significant correlation with biological yield per plot. Rajput (2019) [16] also revealed in his study that harvest index was negatively and highly significantly correlated with biological yield. This result indicated that direct selection for these characters might not be helpful.

Path coefficient analysis provided the information of the direct effect of various characters on yield as well as their indirect effects via other component characters. It also calculates residual effect, which describes the role of other independent variables which are not included in this study. It was recorded that highest positive direct effect towards grain yield per plot was of biological yield per plot followed by harvest index. A similar result was observed by Jee *et al.* (2019) [7] that the maximum positive direct effects towards grain yield were via biological yield and harvest index. It was demonstrated that plant height had negative direct effect on grain yield per plot. Rajput (2018) [16] also observed similar result regarding direct negative effect of plant height on grain yield. Biological yield per plot had positive indirect effect on grain yield per plot via number of tillers per meter, spike length, number of grains per spike, number of spikelets per spike and 1000 grain weight. Analogous results were found by Rajput (2018) [16] that biological yield had positive indirect effect on grain yield via weight of grains per spike, spike length and number of tillers per plant. It was noted that many traits had either direct positive effect on the grain yield per plot or indirect effect on grain yield via other traits. Similar findings were gained by Nukasani *et al*. (2013) [13] for spike length, grain weight and 1000-grain weight.

## Conclusion

The present study demonstrated the presence of wide range of variations for all of the traits among wheat genotypes and which provide the opportunities of the genetic gain through selection or hybridization. Phenotypic and genotypic correlation analysis showed the positive correlation of grain yield with studied agro-morphological characters. Hence, improving one or more of the traits could result in high grain yield for wheat variety. Biological yield, harvest index and number of tillers per meter had positive phenotypic and genotypic direct effect and correlation with grain yield suggesting the possibility of improving grain yield through direct selection of these traits.

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