**Assessment of Genetic Variability and Character Association in Wheat (*Triticum aestivum* L.) Under Timely Sown Irrigated Condition**

**Abstract**

Wheat (*Triticum aestivum* L. em Thell.), a key staple crop globally, contributes significantly to food security and nutrition, providing 20% of the world’s resources. This study aimed to evaluate the genetic variability, heritability, and path analysis of 105 wheat genotypes, including four checks, under timely sown irrigated conditions in Uttar Pradesh, India during the rabi season 2022-23. The experiment was conducted using an Augmented Block Design across seven blocks, assessing traits such as days to flowering, days to maturity, plant height, tillers per plant, spike length, spikelets per spike, peduncle length, grains per spike, 1000-grain weight, biological yield, harvest index, and grain yield per plant. Results revealed significant variation among genotypes for all traits. High heritability was observed for traits such as number of grains per spike (99.82%) and grain yield per plant (99.35%). Genetic advance was notably high for grain yield per plant (65.49%) and biological yield (61.52%). The phenotypic coefficient of variation (PCV) generally exceeded the genotypic coefficient of variation (GCV), indicating environmental influence on trait expression. Grain yield per plant showed strong positive correlations with biological yield, grains per spike, and other yield-related traits. Path coefficient analysis indicated that biological yield had the highest direct effect on grain yield. This study provides valuable insights into the genetic diversity and variability of wheat genotypes, essential for breeding programs aiming to improve yield and adaptability.

**Key words:** Genetic variability, Heritability, Path analysis, Genetic advance, Path coefficient analysis

**1. Introduction**

Wheat is a self-pollinated crop belonging to the Gramineae family. *Triticum aestivum* is hexaploidy wheat (2n=6x=42). Wheat is a widely grown cereal crop across the world. It offers 20% of the world’s resources. The nutritional content of 100 g of bread wheat revealed that it contains 71 g of carbohydrate, 14 g of protein, 2.5 g of fat, 2 g of minerals and significant amounts of vitamins (thiamine and vitamin B) and minerals (zinc and iron) (**Kumar and Nagarajan, 1998; Iquebal and Mishra, 2021**). Wheat is the predominant staple food crop crucial for nourishing 2.5 billion individuals worldwide. The cultivation of wheat accounts for roughly 19% of the overall major cereal production globally as reported by (**FAOSTAT 2020-21**). This cereal holds significant agronomic and nutritional importance in ensuring food security, reducing poverty, and enhancing livelihoods. In the more recent 2020-21 period, the worldwide wheat cultivation area expanded to 224.49 million hectares, yielding 792.40 million tons of wheat with an average productivity of 31.45 quintals per hectare, as reported (**anonymously, 2021**). In India, the mean approximations for wheat cultivation during the timeframe of 2015-16 to 2020-21 suggest an area of 30.31 million hectares, a production of 100.42 million tonnes, and a yield of 3314 kg per hectare (**Agriculture Statistics at a Glance report, 2021**). Analysis of variability among the traits and the association of a particular character with other traits contributing to yield of a crop would be of a great importance in planning a successful breeding programme (**Mary and Gopalan, 2006**). It is essential for a breeder to measure the variability with the help of parameters like phenotypic coefficient of variation, genotypic coefficient of variation, heritability and genetic advance. Hence, these above said parameters give the information regarding the availability of genetic variability for different characters in germplasm (**Yagi, 2009**). Genetic variability is crucial in plant breeding because hybrids between lines of different origins have more heterosis than hybrids between closely related parents and can provide a wide range of genetic variability in segregating populations (**Arunachala, 1981**). Therefore, the present investigation was undertaken to study the genetic variability and character association analysis in wheat (*T. aestivum* L.) during Rabi season 2022-2023.

**2. Materials and Methods**

The field experiment was conducted at Main Experimental Station of Department of Genetics & Plant Breeding, A.N.D.U.A.&T. Kumarganj, Ayodhya (U.P.) during rabi season 2022-23 under timely sown irrigated condition. A total 105 wheat genotypes including four checks (**DBW-222, DBW-187, HD-2967 and NW-5054**), in Augmented block design. The experimental field were divided into 7 blocks and 19 plots (15 genotypes along with 4 checks) accommodated in each Block. Each plot consists two rows of 3 m length with spacing of 5 cm plant to plant with in the row and 20 cm between the rows. The observation was recorded on 5 randomly selected plants from each plot except days to 50% flowering and days to maturity, where their data will be recorded on plot basis. Observations were recorded on grain yield and its related traits, viz. days to 50% flowering, days to maturity, plant height (cm.), productive tillers per plant, spike length (cm.), spikelets per spike, peduncle length (cm.), grains per spike, 1000-grain weight (g), biological yield (g), harvest index (%), grain yield per plant (g). The data was analysed by INDOSTAT software (version 8.0). The phenotypic and genotypic coefficients of variation (PCV, GCV) were calculated as per method suggested by (**Burton, 1954**). The correlation coefficients at genotypic and phenotypic level were computed as per method suggested by (**Johnson *et al*., 1955**). Path coefficient analysis was done by using correlation coefficients as suggested by (**Dewey and Lu**, **1959**).

**3. Results and Discussion**

**3.1 Analysis of Variance**

**Table-1** shows the result of an analysis of variance for augmented block design obtained for 105 genotypes along with four checks for all 12 characters to determine the significant differences across various treatments, checks, and blocks. The treatment showed highly significant for all the traits. Computing means and ranges was used to examine the existing variability in the indigenous collections. Simple correlations (**Robinson *et al.* 1951)** and path -coefficient analysis was used to investigate the nature of link between distinct features (**Wright, 1921; Dewey and Lu, 1959**). The genetic variability of 94 genotypes was studied by Euclidean2 cluster analysis (**Rao, 1952**). The experiment’s findings have been analysed in light of relevant wheat literature.

**3.2 Heritability, genetic advance, and coefficient of variability analysis**

Heritability and genetic advance in percent of mean were estimated for all 12 characters and are presented in **Table 2**. High estimates of broad sense heritability were recorded for all the traits like No. of grains/spike (99.82%), followed by grain yield per plant (g) (99.35%), plant height (cm) (98.53), biological yield (g) (98.03%) and no. of spikelet’s/spike (92.49%). The high estimates of genetic advance were showed in grain yield per plant (g) (65.49%) followed by biological yield (g) (61.52%) followed by no. of grain/ spike (28.60%), and No. of spikelets/spike (22.84%). The magnitude of the PCV is always higher than the GCV for all the characters due to environmental influence on the expression of the traits. The following PCV and GCV for all 12 traits are given in **Table 2**. The character which exhibited higher estimates of GCV and PCV by grain yield per plant (g) GVC (31.89%) and PCV (32.00%) followed by biological yield (g) GCV (30.16%) and PCV (30.46%), and No. of grains/spike (29.14%) GCV and PCV (29.17%). The characters that exhibited moderate estimates of GCV and PCV were in no. of tillers/plant (12.75%), GCV and PCV (14.09%), and No. of spikelets/spike (11.53%) GCV where PCV (11.98%). The remaining characters showed low estimates of GCV and PCV like heading date, days to maturity, plant height (cm), spike length (cm), peduncle length (cm), 1000 grain weight (g), and H.I. (%).

**3.3 Correlation coefficients**

The estimates of simple correlation coefficients between twelve characters have been presented in **Table 3**. The grain yield per plant showed a highly significant and positive correlation with spike length (cm.) (0.231) followed by no. of spikelets per spike (0.303), no. of tillers per plant (0.354), grains per spike (0.867), 1000 grain wt. (g.) (0.301), biological yield (0.954), and harvest index (%) (0.271). Heading date (0.076) and plant height (cm.) (0.067) showed a non-significant and positive correlation. Days to maturity (-0.222) showed a negative and significant correlation and peduncle length (cm) (-0.222) showed a non-significant and negative correlation. The strong positive association of grain yield with one or more of the above traits has also been observed by previous workers**, (Dishevel *et al.*, 2016), (Wane *et al.*, 2018), (Bhang *et al.*, 2018), (Gate *et al.*, 2018), (Rather *et al.*, 2019).**

**3.4 Path coefficient analysis**

Path coefficient analysis is a tool to partition the observed correlation coefficients into direct and indirect effects of independent variables on the dependent variable. The path coefficient analysis was carried out by using simple correlation coefficients to assess the direct and indirect effects of twelve independent characters on dependent character grain yield per plant have been presented in **Table-4**. High order positive direct effect on biological yield (0.9387) followed by harvest index (%) (0.2688), no. of tillers per plant (0.0256), grains per spike (0.0214) and days to maturity (0.0008). High order indirect effect on grain yield via biological yield (0.954), grain yield via grain per spike (0.867), grain yield per plant via no. of tillers per plant (0.354), grain yield via spikelets per spike (0.303), grain yield via 1000-grain weight (g) (0.301) and grain yield per plant via harvest index (0.271).

The results of path coefficient analysis carried out using simple correlation coefficients among 12 characters are given in **Table 4**. Similar result of direct and indirect effect in path coefficient analysis were also recorded by **Desheva *et al.*; (2016), Ayer *et al.*; (2017), Rathod *et al.*; (2019), Chauhan *et al.*; (2022).**

**4. Conclusion**

All genotypes differed significantly among themselves for all 12 characters studied. the genotypes **IBWSN-1107 (20.22 g)** has the highest yield followed by **IBWSN-1119 (20.01 g), IBWSN-1122 (19.71 g), IBWSN-1114,** which showed the highest grain yield among 105 genotypes and four checks which may be used in the further breeding program. Genetic variability evaluated in this study of wheat can be useful for the improvement of quantitative traits through traditional and advanced breeding programs. The developmental program is further augmented and aided by the identification of desirable parents possessing significant genetic variability for the yield and yield-attributing traits.

**References**

**Agriculture Statistics at a Glance (2021).** Government of India, Ministry of Agriculture and Farmers Welfare, Department of Agriculture and Farmer Welfare, Director of Economics and Statistics 2021.: *www.agricoop.nic.in*

**Anonymous:** Crop Prospectus and Food Situation (2021). Food and Agriculture

**Ayer, D. K., Sharma, A., Ojha, B. R., Paudel, A. and Dhakal, K. (2017).** Correlation and path coefficient analysis in advanced wheat genotypes. *SAARC J. Agri.,* 15(1): 1-12.

**Bhanu, A. N., Arun, B., and Mishra, V. K. (2018)**. Genetic variability, heritability and correlation study of physiological and yield traits in relation to heat tolerance in wheat (*Triticum aestivum* L.). *Biomedical Journal of Scientific & Technical Research*, 2(1), 2112-2116.

**Burton, G.W. (1952).** Quantitative inheritance in grasses. Pro VI Int Grass l Cong.1952: 277-283.

**Chauhan, S., Tyagi, S. D., Gupta, A., and Singh, S. (2022).** Genetic variability, correlation, path coefficient and cluster analysis in bread wheat (*Triticum aestivum* L.) under rained conditions.

**Desheva, G. (2016)**. Correlation and path-coefficient analysis of quantitative characters in winter bread wheat varieties.

**Dewey, D. R., and Lu, K. H., (1959).** A correlation and path co-efficient analysis of component of crested wheat grass seed production. *Argon. J.,* 51: 515- 518.

**Food and Agriculture Organization Corporate Statistical Database** (FAOSAT 2020-21).

**Gite, V. D., Bankar, D. N., Baviskar, V. S., Honrao, B. K., Chavan, A. M., Surve, V. D. and Khade, V. M. (2018)**. Genetic variability parameters and correlation study in elite genotypes of bread wheat (*Triticum aestivum* L.). *Journal of Pharmacognosy and Phytochemistry*, 7(1S), 3118-3123.

**Iquebal, M.A., Mishra, P., Maurya, R., Jaiswal, S., Rai, A. and Kumar, D. (2021)**. Centenary of soil and air borne wheat Karnal bunt disease research: *A review. Biology*.10(11):1152.

**Johanson, H. W., Robinson, H. F. and Comstock, R. E. (1955).** Estimation of genetic and environmental variability in soybeans. *Agron. J.,* 47: 314 - 318.

**Kumar, J. and Nagarajan, S. (1998)**. Role of flag leaf and spike emergence stage on the incidence of Karnal bunt in wheat. *Plant Disease*. 82(12): 1368-1370.

**Mary, S.S. and Gopalan, A. (2006)**. Dissection of genetic attributes yield traits of fodder cowpea in F3 and F4. *J. Appl. Sci. Res*. 2(6): 805-808.

**Mittal, V. P., and Brar, K. S. (2008)**. Divergence analysis for some yield contributing characters in wheat (*Triticum aestivum* L.). *Crop Improvement*, 35(1), 1.

**Rao, C.R. (1952)**. Advanced Statistical Methods in Biometric Research. By C. Radhakrishna Rao. John Wiley and Sons, Inc., New York, N.Y. 390 pp.

**Rathod, S., Parmar, V. L., and Patel, A. I. (2019)**. Correlation and path coefficient analysis in for quantitative traits in f₂ population in okra [*Abelmoschus esculentus* (L.) Moench]. *International Journal of Chemical Studies*, 7(5), 1030-1033.

**Robinson, H. F., Constock, R. E. and Harvey, P. H. (1951).** Genotypic and phenotypic correlation in corn and their implications in selection. *Agron. J.,* 43: 262-67.

**Sapi, S., Marker, S., and Bhattacharjee, I. (2017)**. Evaluation of genetic divergence in bread wheat (*Triticum aestivum* L.) genotypes for yield parameters and heat tolerance traits. *Journal of Pharmacognosy and Phytochemistry*, 6(4), 253-257.

**Wani, Shabir H., Sheikh, F. A., Najeeb, S., Sofi, Mehraj-u-din., Iqbal, Asif M., Kordrostami, Mojtaba., Parray, G. A. and Jeberson, M. Samuel (2018).** Genetic variability study in bread wheat (*Triticum aestivum* L.) under temperate conditions. *Curr. Agri. Res*., 6(3): 268-277.

**Yagdi, K. (2009)**. Path coefficient analysis of some yield components in durum wheat (*Triticum durum*.). *Pak. J. Bot*. 41(2):745-751.

**Table 1: Analysis of variance of augmented block design for 12 characters in wheat genotypes under the timely sown irrigated condition**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **S.V.** | **d.f.** | **Heading**  **date** | **Days to maturity** | **Plant height (cm)** | **Spike length**  **(cm)** | **No. of spikelet/**  **Spike** | **Peduncle length (cm)** | **No. of tillers /plant** | **No. of grains/ spike** | **1000 grain weight (g)** | **Biological yield (g)** | **H.I. (%)** | **Grain yield/plant** |
| **Block** | 6 | 1.121 | 1.163 | 0.388 | 0.075 | 0.269 | 0.117 | 0.117 | 0.257 | 0.037 | 1.270 | 0.604 | 0.140 |
| **Treatment** | 108 | 10.781 \*\* | 11.979 \*\* | 64.478\*\* | 2.162 \*\* | 6.419 \*\* | 5.935 \*\* | 1.113 \*\* | 230.798 \*\* | 6.311 \*\* | 88.402 \*\* | 16.465 \*\* | 18.540 \*\* |
| **Checks** | 3 | 67.857 \*\* | 79.083 \*\* | 757.074 \*\* | 36.234 \*\* | 8.716 \*\* | 11.120 \*\*\* | 4.549 \*\*\* | 22.999 \*\*\* | 57.704 \*\*\* | 173.558 \*\*\* | 54.518 \*\*\* | 8.907 \*\*\* |
| **Varieties** | 104 | 4.824 \*\* | 8.249\*\* | 30.560 \*\* | 1.197 \*\* | 5.791 \*\* | 4.570 \*\*\* | 1.015 \*\*\* | 234.440 \*\*\* | 4.738 \*\* | 84.961 \*\*\* | 10.210 \*\*\* | 18.967 \*\*\* |
| **Checks vs. Variety** | 1 | 459.072 \*\*\* | 198.632 \*\*\* | 1514.186 \*\*\* | 0.322 | 64.872 \*\*\* | 132.280 \*\*\* | 0.981 \* | 475.413 \*\*\* | 15.655\*\*\* | 190.810 \*\*\* | 552.855 \*\*\* | 3.011 \*\*\* |
| **Error** | 18 | 0.801 | 0.914 | 0.371 | 0.112 | 0.364 | 0.362 | 0.156 | 0.356 | 0.311 | 1.385 | 0.686 | 0.101 |

**\*, \*\* significant at 5% and 1% probability levels respectively**

**Table 2: Estimation of mean, range, coefficient of variation%, and heritability (broad sense) %, genetic advance, and genetic advance % of the mean for 12 characters in wheat genotype under timely sown irrigated condition**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Characters** | **Mean** | **Range** | **GCV (%)** | **PCV (%)** | **Heritability (broadsense) %** | **Genetic**  **Advance** | **Genetic advance**  **5% of mean** |
| **Heading date** | 79.20 | 71-86 | 2.34 | 2.61 | 80.56 | 3.36 | 4.33 |
| **Days to maturity** | 128.86 | 122-138 | 1.89 | 2.02 | 86.88 | 4.72 | 3.63 |
| **Plant height (cm)** | 88.85 | 72.10-101.60 | 5.82 | 5.87 | 98.53 | 10.20 | 11.91 |
| **Spike length (cm)** | 11.15 | 8- 13.78 | 8.65 | 9.18 | 88.90 | 1.83 | 16.81 |
| **No. of spikelets/spike** | 19.55 | 12.56-24.89 | 11.53 | 11.98 | 92.49 | 4.19 | 22.84 |
| **Peduncle length (cm)** | 30.90 | 26.4-36.7 | 6.06 | 6.37 | 90.55 | 3.65 | 11.89 |
| **No. of tillers /plant** | 6.77 | 4.5- 8.6 | 12.75 | 14.09 | 81.95 | 1.57 | 23.79 |
| **No. of grains/spike** | 65.86 | 18.54-70.26 | 29.14 | 29.17 | 99.82 | 28.60 | 59.98 |
| **1000 grain weight (g)** | 40.98 | 35.12-45.89 | 4.77 | 4.97 | 92.17 | 3.78 | 9.43 |
| **Biological yield (g)** | 38.78 | 11.37-45.51 | 30.16 | 30.46 | 98.03 | 16.94 | 61.52 |
| **H.I. (%)** | 40.25 | 37.1-54.4 | 6.26 | 6.53 | 91.98 | 5.53 | 12.38 |
| **Grain yield per plant (g)** | 17.47 | 5.09-20.22 | 31.89 | 32.00 | 99.35 | 8.10 | 65.49 |

**\*GCV-** genotypic coefficient of variation, **\*PVC**- phenotypic coefficient of variation

**Table 3: Estimates of simple correlation coefficients between 12 characters in wheat genotypes under timely sown irrigated conditions.**

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Traits** | **Days to maturity** | **Plant height (cm.)** | **Spike length(cm.)** | **Spikelets per spike** | **Peduncle length (cm.)** | **No. of tillers per plant** | **Grains per spike** | **1000 grain wt.(g.)** | **Biological yield** | **Harvest Index (%)** | **grain yield per plant (g)** |
| **Heading date** | -0.395\*\* | 0.522\*\* | -0.005 | 0.258\*\* | 0.291\*\* | 0.041 | 0.052 | -0.195\* | 0.163 | -0.250\*\* | 0.076 |
| **Days to maturity** | **1.000** | -0.018 | -0.264\*\* | -0.283\*\* | -0.042 | 0.072 | -0.201\* | 0.083 | -0.342\*\* | 0.336\*\* | -0.222\* |
| **Plant height (cm.)** |  | **1.000** | -0.126 | 0.191\* | 0.424\*\* | 0.080 | 0.058 | -0.023 | 0.063 | -0.010 | 0.067 |
| **Spike length (cm.)** |  |  | **1.000** | 0.687\*\* | 0.149 | 0.194\* | 0.193\* | -0.141 | 0.290\*\* | -0.129 | 0.231\*\* |
| **Spikelets per spike** |  |  |  | **1.000** | 0.329\*\* | 0.108 | 0.255\*\* | -0.030 | 0.342\*\* | -0.069 | 0.303\*\* |
| **Peduncle length (cm.)** |  |  |  |  | **1.000** | 0.107 | -0.031 | -0.175\* | -0.024 | -0.063 | -0.046 |
| **No. of tillers per plant** |  |  |  |  |  | **1.000** | 0.058 | 0.030 | 0.294\*\* | 0.202\* | 0.354\*\* |
| **Grains per spike** |  |  |  |  |  |  | **1.000** | 0.212\* | 0.804\*\* | 0.336\*\* | 0.867\*\* |
| **1000 grain wt. (g.)** |  |  |  |  |  |  |  | **1.000** | 0.245\*\* | 0.218\* | 0.301\*\* |
| **Biological yield** |  |  |  |  |  |  |  |  | **1.000** | -0.019 | 0.954\*\* |
| **Harvest Index (%)** |  |  |  |  |  |  |  |  |  | **1.000** | 0.271\*\* |

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

**Table 4: Direct and indirect effects of 12 characters on grain yield per plant in wheat genotype under timely sown irrigated condition**

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Traits** | **Heading date** | **Days to maturity** | **Plant height (cm.)** | **Spike length (cm.)** | **Spikelets per spike** | **Peduncle length (cm.)** | **No. of tillers per plant** | **Grains per spike** | **1000 grain wt.(g.)** | **Biological yield** | **Harvest Index (%)** | **Grain yield per plant (g)** |
| **Heading date** | **-0.0213** | -0.0003 | 0.0096 | 0.0001 | 0.0030 | -0.0033 | 0.0011 | 0.0011 | 0.0002 | 0.1530 | -0.0672 | 0.076 |
| **Days to maturity** | 0.0084 | **0.0008** | -0.0003 | 0.0052 | -0.0033 | 0.0005 | 0.0018 | -0.0043 | -0.0001 | -0.3210 | 0.0903 | -0.222\* |
| **plant height (cm.)** | -0.0111 | 0.0000 | **0.0184** | 0.0025 | 0.0022 | -0.0048 | 0.0021 | 0.0012 | 0.0000 | 0.0591 | -0.0027 | 0.067 |
| **Spike length (cm.)** | 0.0001 | -0.0002 | -0.0023 | **-0.0198** | 0.0081 | -0.0017 | 0.0050 | 0.0041 | 0.0002 | 0.2722 | -0.0347 | 0.231\*\* |
| **Spikelets per spike** | -0.0055 | -0.0002 | 0.0035 | -0.0136 | **0.0118** | -0.0037 | 0.0028 | 0.0055 | 0.0000 | 0.3210 | -0.0186 | 0.303\*\* |
| **Peduncle length (cm.)** | -0.0062 | 0.0000 | 0.0078 | -0.0029 | 0.0039 | **-0.0113** | 0.0027 | -0.0007 | 0.0002 | -0.0225 | -0.0169 | -0.046 |
| **No. of tillers per plant** | -0.0009 | 0.0001 | 0.0015 | -0.0038 | 0.0013 | -0.0012 | **0.0256** | 0.0012 | 0.0000 | 0.2760 | 0.0543 | 0.354\*\* |
| **Grains per spike** | -0.0011 | -0.0002 | 0.0011 | -0.0038 | 0.0030 | 0.0004 | 0.0015 | **0.0214** | -0.0002 | 0.7547 | 0.0903 | 0.867\*\* |
| **1000 grain wt.(g.)** | 0.0042 | 0.0001 | -0.0004 | 0.0028 | -0.0004 | 0.0020 | 0.0008 | 0.0045 | **-0.0011** | 0.2300 | 0.0586 | 0.301\*\* |
| **Biological yield** | -0.0035 | -0.0003 | 0.0012 | -0.0057 | 0.0040 | 0.0003 | 0.0075 | 0.0172 | -0.0003 | **0.9387** | -0.0051 | 0.954\*\* |
| **Harvest Index (%)** | 0.0053 | 0.0003 | -0.0002 | 0.0026 | -0.0008 | 0.0007 | 0.0052 | 0.0072 | -0.0002 | -0.0178 | **0.2688** | 0.271\*\* |

RESIDUAL EFFECT = 0.07354649

***Bold values show direct and normal values show indirect***