

Study of Character Association and D² For Yield Attributing Traits of Wheat [*Triticum aestivum* L.]

V.N. Pathak*, Shivansh Kumar Pandey*, S.P. Verma*, and K.K. Pandey#

*Department of Genetics & Plant Breeding, S.M.M. Town Post Graduate College, Ballia

Department of Agronomy, S.M.M. Town Post Graduate College, Ballia

Corresponding author: V.N. Pathak Email of corresponding author - vijyanad.pathak76@gmail.com

Abstract

The present study was aimed at estimating the extent of genetic variability for grain yield & its components, character association, path coefficient analysis and genetic diversity in twenty-five diverse genotypes of hexaploid wheat (*Triticum aestivum* L.). Analysis of variance (ANOVA) revealed significant differences among the genotypes for all the traits under study. The genotypes showed that PCV was slightly higher than GCV for all traits. The highest genotypic and phenotypic coefficient of variation was recorded for Harvest Index, Grain yield, Tillers/plant, Biological yield and No of grains/ear. High heritability (h^2) coupled with high genetic advance were recorded for Harvest index, Biological yield, No of grains/ear and Plant height that these characters are governed by additive gene effects and directional selection for these traits would be more effective. Grain yield per plant showed a highly significant and positive correlation with Harvest index (0.789), Test weight (0.545), Plant height (0.486), Flag leaf area (0.469), Spike length (0.328) and Tillers/plant (0.279). It revealed that by increasing the value of these traits, grain yield can be drastically increased. Path coefficient analysis revealed that the maximum positive direct contribution toward yield by Harvest index (1.217), Biological yield (0.815), 50% flowering (0.058) and Days to maturity (0.035). The results revealed that these traits may serve as effective selection attributes during selection in a breeding program for yield improvement in wheat. All the genotypes were grouped into six distinct and non-overlapping clusters. Cluster (II) emerged with the highest number of 7 genotypes.

Key words: Wheat, genetic variability, D₂, correlation, path analysis.

I. Introduction

Wheat (*Triticum aestivum* L. 2n=42), a self-pollinated crop of the Gramineae family and genus *Triticum*, is the world's largest famous energy-rich cereal crop. The dependency of the global human population on wheat makes it a vital cereal crop for food and nutritional security (Zewdu et al., 2024). It covers more than 200 million of area under wheat cultivation, thus making an important trade commodity for global trade.

The pre-requisite of any wheat breeding program is to screen the available wheat germplasm for different yield-related attributes, determine genetic diversity, sort out best yield-performing lines, and assess their genetic advance and heritability. Such best-performing lines and desired traits with high heritability are the base of a successful wheat breeding program aimed at developing best yield-producing cultivars. Genetic diversity plays an important role in generating new, effective plant species under different environments (Mary and Gopalan, 2006).

Wheat may be compared with other cereals in nutritive value. It has a good nutrition profile with 12.1% protein, 1.8% lipids, 1.8 % ash, 2.0% reducing sugar, 6.7% pentose sugar, 59.2% starch, 70% total carbohydrates and provides 314 Kcal/100 g of food. It is also a good source of minerals and vitamins viz, calcium (37 mg. /100 g), Iron (4.1 mg. /100 g), Thiamine (0.45 mg. /100 g), riboflavin (0.1 – 3 mg. / 100 g), and nicotinic acid (5.4 mg. / 100 g). The uniqueness of wheat in contrast to other cereals is that wheat contains gluten protein, which enables leavened dough to rise by forming carbon dioxide gas cells and this property enables bakers to produce light breads.

Yield is a complex attribute comprised of multiple components. Some of these have an immediate impact on yield, while others have an indirect effect. Thus, understanding the relationship between yield and its components is required. Correlation coefficient analysis assesses the mutual influence between numerous plant traits and identifies the component characters on which to base selection for genetic yield improvement. If there is a high association between a set of desirable features, we will select one character, and the other will be taken care of automatically.

II. Materials and Methods

The experiment comprising 25 germplasm accessions was laid out in a Randomized block design with three replications during *Rabi 2018-19*. These lines were grown in a row plot of 3 meters in length. The spacing between row to rows and plant to plants was 30cm and 30cm, respectively. It was maintained by repaired to raise a good crop. Five competitive plants were randomly tagged for recording observations for each entry in each replication for observing all the quantitative characters except for days to 50 percent flowering, days to maturity, plant height, Tillers per plant, spike length, flag leaf area, No. of seed per spike, biological yield per plant, 1000-grain weight, harvest index and grain yield per plant.

Statistical analysis

The analysis of variances and covariances for different characters was computed according to Panse and Shukhatme (1961).

The coefficient of variation was calculated with the help of formulae suggested by Burton (1952). The correlation coefficient analysis was done as per the method described by Singh and Chaudhary (1971). The original concept of path analysis was discussed by Wright (1921). Path co-efficient analysis was calculated by the following formula suggested by Dewey and Lu (1959).

III. Result and Discussion

The most prime objective of a plant breeding programme is to make an improvement in yield, but yield is a complex character and is a combination of a number of traits, each of which is often polygenic in nature and also affected by environmental factors.

A vast range of variation was expressed for 11 characters in 23 genotypes, along with 2 checks HLBSN-17 produced the highest grain yield per plant followed by IBWSN1006, HD-3086 and WR544. Apart from grain yield many other characters important in breeding programme and which can be used as a donor parent for transfer of character were observed as WR-544 for days to 50% flowering, IBWSN-1082 for flag leaf area, plant height HLBSN-22, GW-366 for tillers per plant, STEMRRSN-6110 for spike length, number of seed per spike STEMRRSN -6060, WR-544 for days to maturity, STEMRRSN6110 for biological yield per plant, IBWSN-1082 for harvest index, GW-366 for number of grains per ear and HLBSN-17 for test weight.

A high amount of inherent variability was found for characters. The genotype coefficient of variation was found to be less than the phenotypic coefficient of variation, indicating the effect of the environment in the development of character. This laid the basis for a large scope of selection due to genotypic coefficient of variation as these characters were genetically potent for selection in crop like wheat. The high heritability of the number of seed per spike, biological yield per plant, harvest index, 1000 grain weight per plant, and grain yield per plant is equal and high genetic gain. The presence of the additive nature of genetic variability was indicated. It can be concluded that since these characters are highly responsible for selection. Superior genotype can be evolved through selection on the expression of these characters. Shah and Deora (2002), Singh et al., (2013) and Jee et al (2019) also highlighted the importance of variability in tillers per plant, plant height.

Grain yield per plant was positively and significantly correlated with flag leaf area, plant height, tillers per plant, spike length, harvest index, and 1000-grain weight per plant. It implies that by increasing the value of these component traits, grain yield can be drastically increased. Non-significant association of grain yield per plant was found with days to 50% flowering, number of seeds per spike, days to maturity and biological yield per plant. Harvest index showed a non-significant association with most of the characters, including grain yield, it should not be taken into consideration in breeding programmes. Selection for test weight showed an increase in harvest index because they were positively significant. Similar results have been reported by Saini et. al. (1990), Kumar and Chaudhari (1986), Verma *et al.* 2019, Kumar *et al.* 2019 and Saini et al.(2024).

Plant height had a positive and highly significant association with grain yield, probably due to the positive direct effect of this character and the positive direct effects of spike length, number of seeds per spike and harvest index. A positive and significant correlation was shown between tillers per plant with grain yield per plant despite the direct effect of negative character and indirect effect of plant height, spike length, no of seed per spike days to maturity and biological yield.

Spike length per plant was positively and highly significantly correlated with grain yield per plant, probably due to the direct effect was positive and the indirect effect of days to 50% flowering, plant height, biological yield and harvest index. Harvest index showed correlated with positively and highly significant of grains grain yield per plant expressed due to direct effect was positive and spike length, number of seed per spike, and days to maturity. 1000Grain yield correlated with highly and positive significant with grain yield per plant and direct effect was negative and positive indirect effect of plant height, spike length per plant, biological yield per plant, and harvest index.

The non-significant association of the number of grains per ear with grain yield per plant, despite a direct positive effect, indicated a residual effect that needed to be studied. The non-significant association of harvest

index with grain yield per plant despite a positive direct effect and most of the indirect effects being positive, indicates residual effects. The association between test weight and grain yield per plant was positive and highly significant due to the positive direct effect of this character and indirect positive effects of days to 50% flowering, tillers per plant, flag leaf area, plant height, ear length, biological yield per plant and ear weight. This is supported by the findings of Kumar et al (2019), Singh et al (2021), Mishra et al. (2024), Sharma et al. (2023) and Joshi et al. (2024).

The Non-hierarchical Euclidean cluster analysis grouped 22 genotypes and 3 check varieties into 6 distinct and non-overlapping clusters. The discrimination of varieties/lines into so many discrete clusters suggested the presence of a high degree of genetic diversity in the material evaluated. Earlier workers have also reported substantial genetic divergence in the wheat materials (Singh and Dwivedi 2002, Verma et al. 2006, Saini et al. 2017). The highest inter-cluster distance was expressed between cluster (III) and cluster (IV) followed by cluster (II) and cluster (VI). Thus, crossing between the genotypes belonging to cluster pairs separated by very high inter-cluster distances mentioned above, may through desirable transgressive segregants, which indicates that the genotypes belonging to these cluster pair separated by very high inter-cluster distances, mentioned above, may produce desirable transgressive segregants.

The maximum intra-cluster distance was shown for cluster (IV) followed by cluster (I) and cluster (II). The minimum intra-cluster distance was recorded for clusters (V) and (VI) are equal and followed by cluster (III). Cluster (I) having 6 genotypes and expressing the lowest mean performance for flag leaf area, plant height, 1000-grain weight per plant and grain yield per plant and possessed moderate means for the remaining characters. Cluster (II), having 7 genotypes, expressed the highest cluster mean for days to 50% flowering and showed a moderate mean for remaining characters. Cluster (III) having 04 genotypes expressed the highest cluster mean for two characters no of seeds per spike and biological yield per plant and showed moderate means for the remaining characters.

Cluster (IV), having 06 genotypes, showed the highest cluster mean for harvest index and grain yield per plant and a moderate mean for remaining characters. Clusters (V) and (VI) have equal genotypes. Cluster (V) having 1 genotype and expressing the highest cluster mean for four character flag leaf area, tillers per plant, spike length per plant, and 1000-grain weight per plant, and lowest mean for number of seeds per spike and showing average mean for other remaining characters. Cluster (VI) having 1 genotype showed the highest cluster mean for plant height, days to maturity and showed the lowest mean for tillers per plant and biological yield per plant and moderate for remaining characters. These findings are similar to those of, Saini et al. 2017, and Verma et al 2019.

The above discussion clearly shows wide variation from one cluster to another in respect of cluster mean for 11 characters, indicating that genotypes having distinctly different mean performance for various characters were separated into different clusters. The crossing between the entries belonging to cluster pairs having large inter-cluster distances and possessing high cluster means for one or other characters to be improved, may be recommended for isolating desirable recombinants in the segregating generations in wheat.

References

- [1]. Dewey, S. R. and Lu, K. H. (1959). Correlation and path coefficient analysis of crested wheat gross seed production. *Agron. J.*, 51: 515-518.
- [2]. Jee, C, Pathak, V.N., Verma, S.P., Verma, O.P., Singh, O.P. (2019). Association studies for grain yield and its contributing components in diverse genotypes of wheat (*Triticum aestivum* L. em Thell). *Journal of Pharmacognosy and Phytochemistry*, 8(3):1177-1180.
- [3]. Joshi, S., Jaiswal, J. P., & Kumar, A. (2024). Estimation of genetic diversity among bread wheat (*Triticum aestivum* L.) genotypes. *Journal of Scientific Research and Reports*, 30(7), 953-962
- [4]. Kumar, A. and Chaudhary, R.K. (1986). Studies on biological yield and harvest index in durum wheat information services 61/62: 72-79
- [5]. Kumar S, Singh Brijesh, Verma SP, Pathak VN, Jee Chaman and Singh, J.P. (2019). Studies on Genetic Variability, Heritability, Genetic Advance, Correlation and Path Analysis for Grain Yield and Its Contributing Traits in Indigenous Wheat (*Triticum aestivum* L.). *Int. J. Curr. Micro. biol. App. Sci.* 8(08): 1408-1416.
- [6]. Mary SS, & Gopalan A. 2006. Dissection of genetic attributes among yield traits of fodder cowpea F3 and F4. *J. Applied Sci. Res.* 2, 805-808.
- [7]. Mishra, S.K., Surin, S. S., Verma, N., Bhargaw, P.K., Kumari, M., & Mishra, D.K. (2024). Studies on genetic variability, correlation and path coefficient analysis for yield and yield contributing traits in bread wheat (*Triticum aestivum* L.). *Journal of Experimental Agriculture International*, 46(6), 389-397.
- [8]. Panse, V. G., & Sukhatme, P. V. (Ed.). (1995). *Statistical methods for agricultural workers* (381 pp.). ICAR.
- [9]. Saini, D. P. and Gautam, P. L. (1990) Early generation selection in durum wheat. *Indian J. Genet.* (Golden Jubilee) Vol. 50 (2): 147-152
- [10]. Saini, P. K., Singh, S. V., Yadav, R. K., Singh, L., Singh, S., Tripathi, H., Dwivedi, S., & Tiwari, U. (2024). Correlation and path coefficient analyses for grain yield and its contributing traits in bread wheat (*Triticum aestivum* L.). *Journal of Advances in Biology and Biotechnology*, 27(3), 208-218.
- [11]. Saini Manisha; Shweta; Paswan, S. K. (2017). Genetic divergence analysis in bread wheat (*Triticum aestivum* L.). *International Journal of Plant Sciences (Muzaffarnagar)*.12(2):249-252.
- [12]. Shah, M. A. and Deora, V. S. 2002. Genetic variability and association studies in Wheat for grain yield and temperature tolerance parameters. *Indian J. Agril. Res.*, 36(3):123-125.

Study of Character Association and D² For Yield Attributing Traits of Wheat [Triticum aestivum L.]

- [13]. Sharma, S., Tripathi, M. K., Tiwari, S., Solanki, R. S., Chauhan, S., Tripathi, N., Dwivedi, N., & Kandalkar, V. S. (2023). The exploitation of genetic variability and trait association analysis for diverse quantitative traits in bread wheat (*Triticum aestivum* L.). *Current Journal of Applied Science and Technology*, 42, 19-33
- [14]. Singh, J.B., Verma, A., Satya Prakash, Patidar, I., Prakash, T.L., Prasad, S.V. S. Singh, A.K. and Mishra, A.N. 2013. Variability and interrelationship analysis in bread wheat under moisture stress conditions. *J. Wheat Res.*, 5(2): 27-34.
- [15]. Singh, S. P. and Dwivedi, V. K. (2002). Genetic divergence in wheat (*Triticum aestivum* L.). *New Agriculturist*. 13(1/2):5-7.
- [16]. Singh OP, Verma SP, Singh Brijesh, Pathak VN and Rajbhar SK (2021) Assessment of genetic variability, heritability, genetic advance and relationship of yield and its contributing traits in wheat genotypes (*Triticum aestivum* L.). *J. of Progressive Science*, Vol.12 No. 1&2: 24-33.
- [17]. Verma SP, VN Pathak, OP Verma. (2019). Interrelationship between Yield and its Contributing Traits in Wheat (*Triticum aestivum* L.). *Int. J Curr. Microbiol. App. Sci.*; 8(2): 3209-3215.
- [18]. Verma, A. K.; Singh, P. K.; Vishwakarma, S. R.; Tripathi, R.M. (2006). Genetic divergence in wheat (*Triticum aestivum* L.). *Farm Science Journal*. 15(1):32-34.
- [19]. Verma SP, Pathak VN and Verma OP. (2020). D2 analysis for yield and yield components in indigenous wheat germplasm (*Triticum aestivum* L.). *Wesleyan j. of Research*. 12(4): 73-78
- [20]. Zewdu D, Mekonnen F, Geleta N, & Abebe K. 2024 Genetic Variability, Heritability and Genetic Advance for Yield and Yield Related Traits of Bread Wheat (*Triticum aestivum* L.) Genotypes. *International Journal of Economic Plants*; 11(Feb, 1): 038-047

Table 1. Anova for 11 Characters in Wheat (*Triticum aestivum* L.)

| S.No. | Source of Variation | d.f. | Days to 50% Flowering | Tillers/ Plant | Flag Leaf Area (cm) ² | Plants Height (cm) | Ear of Length/Plant (cm) | Days to Maturity | Biological Yield/Plant (g) | No of Grains/Ear | Harvest Index (%) | Test Weight (g) | Grain Yield/Plant (g) |
|-------|---------------------|------|-----------------------|----------------|----------------------------------|--------------------|--------------------------|------------------|----------------------------|------------------|-------------------|-----------------|-----------------------|
| 1 | Replication | 2 | 4.01 | 0.42** | 2.17 | 0.47* | 0.16 | 6.84* | 0.14* | 0.03 | 0.06 | 0.03 | 0.02 |
| 2 | Treatments | 24 | 69.36** | 15.06** | 40.73** | 109.09** | 2.37** | 4.97** | 199.66** | 181.35** | 489.34** | 74.72** | 52.45** |
| 3 | Error | 48 | 2.83 | 0.08 | 1.02 | 0.10 | 0.06 | 2.20 | 0.04 | 0.21 | 0.06 | 0.09 | 0.02 |

Graph:- Mean of all Characters in Wheat.

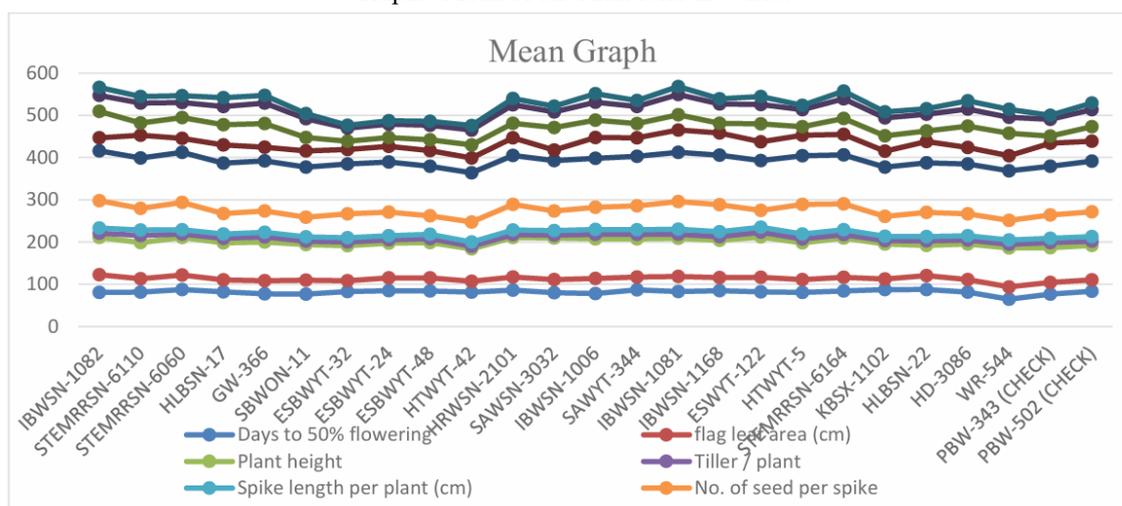


Table 2 - Grand Mean, PCV, GCV, ECV, Standard Error and CD of 11 Characters in Wheat (*Triticum aestivum* L.)

| S. No. | Characters | Grand Mean | PCV | GCV | ECV | Standard Error | CD 5% | Heritability(h ²) broad sense | Genetic advancement (5%) | Genetic advance as % of mean |
|--------|----------------------------|------------|-------|-------|------|----------------|-------|---|--------------------------|------------------------------|
| 1 | Days to 50% Flowering | 81.87 | 6.11 | 5.75 | 2.06 | 0.97 | 2.76 | 0.89 | 9.14 | 14.30 |
| 2 | Flag leaf area(cm) | 31.05 | 12.16 | 11.72 | 3.25 | 0.58 | 1.66 | 0.93 | 7.22 | 29.81 |
| 3 | Plant Height (cm) | 86.98 | 6.94 | 6.93 | 0.36 | 0.18 | 0.52 | 1.00 | 12.40 | 18.27 |
| 4 | Tiller/plant | 9.67 | 23.29 | 23.10 | 2.93 | 0.16 | 0.46 | 0.98 | 4.57 | 60.51 |
| 5 | Ear of Length/Plant (cm) | 10.71 | 8.51 | 8.21 | 2.26 | 0.14 | 0.40 | 0.93 | 1.75 | 20.88 |
| 6 | No of Grains/Ear | 54.64 | 14.25 | 14.22 | 0.83 | 0.26 | 0.74 | 1.00 | 15.98 | 37.48 |
| 7 | Days to maturity | 117.52 | 1.50 | 0.82 | 1.26 | 0.86 | 2.44 | 0.30 | 1.08 | 1.18 |
| 8 | Biological Yield/Plant (g) | 41.77 | 19.54 | 19.53 | 0.51 | 0.12 | 0.35 | 1.00 | 16.80 | 51.54 |
| 9 | Harvest Index (%) | 36.51 | 34.98 | 34.98 | 0.69 | 0.14 | 0.41 | 1.00 | 26.30 | 92.32 |
| 10 | Test Weight (g) | 40.87 | 12.23 | 12.20 | 0.72 | 0.17 | 0.48 | 1.00 | 10.26 | 32.16 |
| 11 | Grain Yield/Plant (g) | 14.70 | 28.47 | 28.45 | 0.96 | 0.08 | 0.23 | 1.00 | 8.61 | 75.06 |

Table 3- Genotypic and Phenotypic Correlation Coefficient for 11 Characters in Wheat (*Triticum aestivum* L.)

| No | Character | Days to 50% Flowering | Flag Leaf Area (cm) ² | Plants Height (cm) | Tiller/plant | Spike Length/Plant (cm) | No of seed/spike | Days to Maturity | Biological yield/plant | Harvest Index (%) | 1000 grain weight/plant(g) | Grain yield/plant (g) |
|----|----------------------------------|-----------------------|----------------------------------|--------------------|------------------|-------------------------|--------------------|--------------------|------------------------|----------------------|----------------------------|-----------------------|
| 1 | Days to 50% Flowering | r(g) r(p) | 0.007 -0.003 | -0.250* -0.233* | -0.164 -0.160 | 0.123 0.102 | 0.347** 0.327** | 0.059 0.029 | 0.145 0.136 | -0.313** -0.293** | -0.029 -0.028 | -0.226 -0.212 |
| 2 | Flag Leaf Area (cm) ² | | r(g) r(p) | 0.381** 0.364** | 0.153 0.145 | 0.660** 0.613** | 0.271* 0.265* | 0.048 0.048 | 0.001 0.001 | 0.443** 0.427** | 0.273* 0.266* | 0.486** 0.469** |
| 3 | Plants Height (cm) | | | r(g) r(p) | 0.003 0.002 | 0.417** 0.402** | -0.017 -0.016 | -0.016 -0.015 | -0.161 -0.161 | 0.514** 0.513** | 0.357** 0.355** | 0.487** 0.486** |
| 4 | Tiller/plant | | | | r(g) r(p) | 0.401** 0.383** | -0.115 -0.117 | 0.193 0.087 | 0.481** 0.479** | -0.001 -0.002 | 0.429** 0.426** | 0.281* 0.279* |
| 5 | Spike Length/Plant (cm) | | | | | r(g) r(p) | 0.400** 0.388** | -0.260* -0.132 | 0.376** 0.362** | 0.107 0.103 | 0.523** 0.502** | 0.342** 0.328** |
| 6 | No of seed/spike | | | | | | r(g) r(p) | -0.301** -0.168 | 0.311** 0.310** | -0.180 -0.180 | 0.015 0.015 | -0.067 -0.067 |
| 7 | Days to Maturity | | | | | | | r(g) r(p) | -0.475** -0.263* | 0.482** 0.264* | -0.035 -0.019 | 0.281* 0.154 |
| 8 | Biological yield/plant | | | | | | | | r(g) r(p) | -0.544** -0.544** | 0.512** 0.511** | 0.046 0.047 |
| 9 | Harvest Index (%) | | | | | | | | | r(g) r(p) | 0.166 0.165 | 0.789** 0.789** |
| 10 | 1000 Grain weight/plant | | | | | | | | | | r(g) r(p) | 0.546** 0.545** |

Table 4- Direct and Indirect Effect at Genotypic Level of different Quantitative Characters on yield in Wheat (*Triticum aestivum* L.)

| No | Character | Days to 50% Flowering | Flag Leaf Area (cm) ² | Plants Height (cm) | Tillers/Plant | Ear of Length/Plant (cm) | No of Grains/Ear | Days to maturity | Biological Yield/Plant (g) | Harvest Index (%) | Test Weight (g) | Grain Yield/ Plant (g) |
|----|-----------------------------------|-----------------------|----------------------------------|--------------------|---------------|--------------------------|------------------|------------------|----------------------------|-------------------|-----------------|------------------------|
| 1 | Days to 50% Flowering | 0.058 | 0.000 | -0.003 | 0.017 | 0.002 | -0.042 | 0.001 | 0.111 | -0.356 | 0.001 | -0.212 |
| 2 | Flag Leaf Area (cm) ² | -0.000 | -0.009 | 0.005 | -0.016 | 0.009 | -0.034 | 0.002 | 0.001 | 0.520 | -0.009 | 0.469** |
| 3 | Plants Height (cm) | -0.014 | -0.003 | 0.014 | -0.000 | 0.006 | 0.002 | -0.000 | -0.131 | 0.624 | -0.012 | 0.486** |
| 4 | Tillers/Plant | -0.009 | -0.001 | 0.000 | -0.108 | 0.006 | 0.015 | 0.003 | 0.390 | -0.002 | -0.014 | 0.279* |
| 5 | Ear of Length/Plant (cm) | 0.006 | -0.006 | 0.006 | -0.041 | 0.014 | -0.050 | -0.005 | 0.295 | 0.125 | -0.016 | 0.328** |
| 6 | No of Grains/Ear | 0.019 | -0.002 | -0.000 | 0.013 | 0.006 | -0.129 | -0.006 | 0.253 | -0.219 | -0.000 | -0.067 |
| 7 | Days to maturity | 0.002 | -0.000 | -0.000 | -0.009 | -0.002 | 0.022 | 0.035 | -0.214 | 0.322 | 0.001 | 0.154 |
| 8 | Biological Yield/Plant (g) | 0.008 | 0.000 | -0.002 | -0.052 | 0.005 | -0.040 | -0.009 | 0.815 | -0.662 | -0.016 | 0.047 |
| 9 | Harvest Index (%) | -0.017 | -0.004 | 0.007 | 0.000 | 0.002 | 0.023 | 0.009 | -0.443 | 1.217 | -0.005 | 0.789** |
| 10 | Test 1000 Grain Weight/Plants (g) | -0.002 | -0.002 | 0.005 | -0.046 | 0.007 | -0.002 | -0.001 | 0.416 | 0.201 | -0.032 | 0.545** |

R SQUARE = 0.9594 RESIDUAL EFFECT=0.2016

Table 5- Clustering pattern of 25 wheat genotypes on the basis of Non-hierarchical Euclidean Cluster analysis for 6 characters.

| No of cluster | No of genotype | Genotype |
|---------------|----------------|---|
| 1 | 6 | ESBWYT-32, ESBWYT-24, ESBWYT-48, HTWYT-42, SBWON-11, IBWSN-1168 |
| 2 | 7 | HRWSN-2101, SAWYT-344, HTEMRRSN-6164, IBWSN-10006, PBW302, IBWSN-181, HTEMRRSN-6110 |
| 3 | 4 | IBWSN-1168, HTWYT-5, PBW-343, HLBSN-22 |
| 4 | 6 | HLBSN-17, HD-3086, HTEMRRSN-6060, WR-544, GW-366, IBWSN-1082 |
| 5 | 1 | ESWYT-122 |
| 6 | 1 | SAWSN-3032 |

Table 6- Estimates of average intra- and inter-cluster distances for 6 clusters in wheat

| No of Cluster | Cluster 1 | Cluster 2 | Cluster 3 | Cluster 4 | Cluster 5 | Cluster 6 |
|---------------|--------------|--------------|---------------|---------------|---------------|---------------|
| Cluster 1 | 58.75 | | 127.21 | 140.35 | 109.44 | 170.49 |
| Cluster 2 | | 57.87 | 103.11 | 146.11 | 90.41 | 198.10 |
| Cluster 3 | | | 56.59 | 216.43 | 166.96 | 265.60 |
| Cluster 4 | | | | 73.65 | 106.43 | 93.67 |
| Cluster 5 | | | | | 0.00 | 139.55 |
| Cluster 6 | | | | | | 0.00 |

Table 7- Clusters means for 11 characters in wheat

| No of character | Days to 50% flowering | Flag leaf area | Plant height | Tillers per plant | Spike length per plant | No of seed per spike | Days to maturity | Biological yield per plant | Harvest index | 1000grain weight per plan | Grain yield per plant |
|-----------------|-----------------------|----------------|--------------|-------------------|------------------------|----------------------|------------------|----------------------------|---------------|---------------------------|-----------------------|
| Cluster 1 | 82.83 | 28.56 | 81.97 | 8.06 | 10.04 | 49.68 | 117.56 | 36.55 | 27.61 | 36.64 | 10.10 |
| Cluster 2 | 83.24 | 32.11 | 89.54 | 10.53 | 11.43 | 58.09 | 117.29 | 48.09 | 35.14 | 44.16 | 16.85 |
| Cluster 3 | 82.67 | 30.09 | 82.55 | 10.18 | 10.70 | 61.77 | 116.25 | 51.39 | 21.43 | 41.46 | 10.98 |
| Cluster 4 | 79.00 | 32.42 | 88.67 | 10.08 | 10.41 | 54.57 | 118.33 | 35.49 | 53.39 | 40.52 | 18.78 |
| Cluster 5 | 82.33 | 34.38 | 95.15 | 11.47 | 11.50 | 40.10 | 118.00 | 44.28 | 42.20 | 46.30 | 18.69 |
| Cluster 6 | 80.00 | 30.81 | 98.56 | 7.13 | 10.52 | 46.79 | 118.67 | 25.40 | 52.91 | 37.50 | 13.51 |