Evaluation of wheat genotypes (*Triticum aestivum* L.) for assessment of character association, path coefficient and cluster analysis

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**ABSTRACT**

Thirty wheat genotypes (*Triticum aestivum* L.) were evaluated for 11 morphological and yield trait for analysis of character association (phenotypic and genotypic correlation coefficient), path analysis and cluster analysis. The experiment was conducted during *rabi* seasons of 2014-2015 in a randomized block design with three replication. Days to 50% heading showed positive and significant correlation with flag leaf area and number of spikelet per ear; flag leaf area showed positive and significant correlation with 1000 grain weight; Plant height showed positive and significant correlation with spike length; spike length showed positive and significant correlation with 1000 grain weight. Phenotypic path analysis showed biological yield and number of grain per spike had highly positive and direct effect on grain yield. Direct and highly positive effect on grain yield was shown by number of productive tillers, plant height, spike length, number of spikelet per spike genotypic path coefficient. Biological yield and grains per plant show highly positive and direct effect on yield with number of productive tillers, plant height, number of spikelet per spike and spike length. In cluster analysis the intra cluster distance ranged from 1.61 (cluster II) to 2.37 (cluster III and VI). Thus the member of cluster II were least divergent and similarly the member of cluster III and IV were most divergent. The maximum inter cluster distance was between cluster II and III followed by cluster IV and V, cluster VI and III and cluster VI and V that order therefore the accessions grouped in the five pair of cluster may be considered as most divergent.

**Key words:** Character association, Cluster analysis, Genotypic path coefficient, Phenotypic path coefficient, Wheat.

**INTRODUCTION**

Wheat (*Triticum aestivum* L.) is an important cereal crop grown in temperate environments worldwide. Due to gradual increase in the world’s population demands a substantial increase in its productivity. Wheat has always been subjected to both broad and endless research so as to maximize grain production and also to improve grain yield per unit area (Islam *et al.*, 2012). So world largest cropped area is devoted for the cultivation of wheat to minimise the foods demand of the population in the world and it is the world’s most important crops in the other all cereal crops in the area and its production, thereby providing about 20.0 per cent of total food calories for the people of the world. Wheat is consumed in various ways such as chapatti, Bread, suji, flour, porridge, macaroni, biscuits, cookies, cakes, pasta, noodles etc. In cereal crop grain yield is the complex quantitative character, which is incentive by a numerous yield contributing characters. These characters influence grain production both directly and indirectly and the breeder is naturally interested in investigating the extent and type of association of such traits (Zafarnaderi *et al.*, 2013). Yield is the result of the value of the yield component such as number of spike/ m², thousand kernels mass.; height of plant, number of productive tillers, number of spikelet/ spike, number of kernel/ spike, kernel mass/ spike, and others beside yield component environment factor such levels of water, fertilizer, pesticide application play important roles in wheat yield increasing (Valencia *et al.*, 2009). It is also widely recognized that genetic architecture of yield can be resolved better by studying its component characters. This enables the plant breeder to breed for high yielding genotypes with desired combinations of traits. Yield of wheat is the important quantitative character which obtained by the action and interaction of various traits (Singh and Diwivedi, 2002). Correlation and path coefficient analysis are used as an important tool to bring information about appropriate cause and effects relationship between yield and some yield components (Khan *et al.*, 2003). Correlation coefficient is an important statistical procedure to evaluate breeding programs for high yield, as well as to examine direct and indirect contribution of the yield variables. Path analysis has been used in many studies on wheat (Mohamed, 1999).

The study of the correlation coefficient provide the knowledge of a association between character and yield. This study among various traits is very useful for breeder in selecting genotypes possessing group of desired traits (Ali, 2008)

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MATERIALS AND METHODS

The experimental material comprised of thirty wheat genotypes presented in Table 1 for the evaluation of character association, path coefficient and cluster analysis. The experiment was conducted at the research farm of Department of Genetics and Plant Breeding Chaudhary Charan Singh University, Meerut in randomized block design with three replications during the winter season of 2014-2015. In this experiment, row-to-row and plant-to-plant distances were kept at 25 cm and 10 cm, respectively and standard agronomic practices were adopted in each experiment to raise the good crops. The data was recorded on five randomly selected plants for each line for 11 quantitative traits viz. plant height, days to 50% heading, days to maturity, number of productive tillers per plant, number of spikelets per spike, flag leaf area, chlorophyll contents, biological yield, harvest index (%), 1000-grain weight and grain yield per plant. The character association was estimated from variance and covariance components (Al-Jibouri et al., 1958). (Dewey and Lu, 1959) was adopted for estimation of direct and indirect contribution of various characters to grain yield calculated through Path coefficient analysis and cluster analysis was performed using the squared Euclidean method.

Table 1: Name of genotypes with pedigree and their releasing year.

| Genotypes  | Pedigree                                      | Year |
|------------|-----------------------------------------------|------|
| 101HP-1633 | RL 6010 / 5* SKA                              | 1992 |
| 102HP-1731 | LIRA//PARULA//TONICHI                         | 1994 |
| 103HP-1744 | CIANO//PARULA//CHILERO//GARUDA                 | 1996 |
| HP-1761    | RL6010/6*INIA//3*KAUZ                          | 1996 |
| 105HPW-42  | VEE’S/4/PVN’/S’/CBB/CNO’S’/3/JAR/ORZ’S’ OR VRR/3/PVN . SIB/CNO SIB//JAR/ORZ SIB | 1992 |
| HPW-89     | INTERMED/0 RODI/HD 2248                       | 1997 |
| HPW-147    | CPAN 1869/HIM 10 BA (WS)                      | 1999 |
| HPW-155    | BT 2549/EX                                 | 2005 |
| HPW-184    | ND/VG9144/KAL/BB/YACO/4/VEE#5                | 2003 |
| HPW-251    | WW 24/LEHMI/P2-III49 OR WW 24/LEHMI           | 2007 |
| GW-322     | PBW 173/GW 196                               | 2002 |
| 49GW-273   | CPAN2084/VW 205                              | 1997 |
| 48GW-190   | VEE/3/BB’ S’/SKA//ARJUN                      | 1994 |
| 47GW-173   | TW275/7/6/1/ KOK-1                           | 1994 |
| 46GW-120   | INIA66/CNO/INIA66/BB/3/Y50E/3*KAL            | 1985 |
| 45GW-89    | KAL ‘S’/LR64A//SKA                           | 1994 |
| 44GW-18    | S331/NP890                                   | 1978 |
| 43GW-10    | S308/WS217                                   | 1973 |
| 2AJANTA    | PW5/Y53                                      | 1981 |
| AKW-381    | S-308/N5439                                  | 1991 |
| AKW-1071   | VEE’S/ 3 FLN ACC/ ANA                        | 1995 |
| 8C-306     | RGN/CSK3/2*C591/3/C217/N14//C281             | 1969 |
| 9BW-11     | KVZ/TI-71/TITTO                              | 1985 |
| VL-404     | KT/BAGE//FN/GU/3/ST464(DR)/P174106(DR)       | 1978 |
| HD-2967    | ALD/COC/URES/HD2160M/HD2278                 | 1989 |
| 91HI-1077  | GALL-AUST-HI-61-151/CNO-NO66-K913           | 1999 |
| 92HI-1418  | H1076/CC505/H1 1136                         | 2002 |
| 93HI-1464  | HW 2002*2/STREMPALLI/PNC 5                  | 2005 |
| 94HI-1500  | HI 1182/CPAN 1990                           |      |

RESULTS AND DISCUSSION

Correlation coefficient: In the estimates of genotypic correlation coefficients and phenotypic correlation coefficients the magnitude of the genotypic correlation coefficients is higher than phenotypic correlation coefficients presented in Table 2. In the genotypic correlation coefficients Days to 50% heading showed positive and significant correlation with flag leaf area, plant height and number of spikelet per ear; flag leaf area showed positive and significant correlation with spike length and 1000 grain weight which agree with the statement of Rohani et al., 2016. Plant height showed positive and significant correlation with biological yield; Spike length showed positive and significant correlation with 1000 grain weight, grain yield and biological yield. Similar results had been reported by Hama et al., 2016 that spike length has positive significant correlation with 1000 grain weight and biological yield.

Number of grain per spike showed positive and significant correlation with chlorophyll content, grain yield and biological yield; chlorophyll content showed positive and significant correlation with grain yield and biological yield; 1000 grain weight showed positive and significant correlation with grain yield and biological yield; grain yield
**Table 2:** Estimates of genotypic correlation (upper diagonal) and phenotypic correlation (lower diagonal) among eleven traits in wheat.

| Genotypes | Days of 50% heading (t) | Number of Productive Tillers (t) | Flag leaf area (cm²) | Plant height (cm) | Spike length (cm) | No spiklet per ear (t) | Number of grains / spike (t) | Chlorophyll content (mg) | 1000 grain wt. (g/plant) | Grain yield (g/plant) | Biological yield (g/plant) |
|-----------|--------------------------|----------------------------------|----------------------|------------------|------------------|------------------------|-----------------------------|--------------------------|------------------------|----------------------|----------------------------|
| Days of 50% heading | - | 0.092 | 0.272** 0.312** | -0.150 0.372** | -0.079 | -0.026 | 0.108 | -0.076 | 0.053 |
| Number of Productive Tillers | 0.101 | - | -0.067 -0.362** -0.197 0.111 | -0.135 | -0.091 | -0.453** -0.130 | -0.239* |
| Flag leaf area (cm²) | 0.254* | -0.069 | - | -0.267* 0.229* 0.149 | -0.086 | -0.072 | 0.260* -0.031 | -0.025 |
| Plant height (cm) | 0.176 | -0.298** -0.218* | - | 0.164 | -0.160 | -0.102 | -0.015 | 0.032 | 0.106 | 0.208* |
| Spike length (cm) | -0.138 | -0.140 | 0.177 0.234* | - | -0.149 | 0.196 | 0.112 | 0.257* | 0.444** | 0.300** |
| No spiklet per ear | 0.249* | 0.125 | 0.118 -0.056 | -0.067 | - | 0.151 | 0.182 | -0.080 | 0.124 | -0.094 |
| Number of grains per spike | -0.079 | -0.119 | -0.082 -0.047 | 0.181 | 0.151 | - | | | |
| Chlorophyll content (mg) | -0.037 | -0.067 | -0.053 0.027 | 0.090 | 0.111 | 0.512** | - | | |
| 1000 grain wt. (g) | 0.074 | -0.381** | 0.216* 0.035 | 0.210* -0.152 | 0.074 | 0.016 | - | 0.338** | 0.468** |
| Grain yield (g/plant) | -0.059 | -0.124 | -0.023 0.109 | 0.380** 0.090 | 0.606** | 0.500** | 0.242* | - | 0.748** |
| Biological yield (g/plant) | 0.023 | -0.233* | -0.023 0.184 | 0.242* -0.067 | 0.403** | 0.400** | 0.386** | 0.700** | - |

*,** = Significant at P=0.05 and P=0.01 levels, respectively.

showed positive and significant correlation biological yield. While number of productive tillers showed negative and significant correlation with plant height, 1000 grain weight and biological yield earlier similar result observed by Kalimullah et al. (2012); flag leaf area showed negative and significant correlation with plant height; flag leaf area showed negative and significant correlation with plant height.

In the estimation of phenotypic correlation coefficients among 11 different traits in 30 genotypes days to heading showed positive and significant correlation with flag leaf area and number of spiklet per ear; flag leaf area showed positive and significant correlation with 1000 grain weight; similar result was reported by Rohani et al., 2016.

Spike length showed positive and significant correlation with 1000 grain weight, grain yield and biological yield; number of grain per spike showed positive and significant correlation with chlorophyll content, grain yield and biological yield; chlorophyll content showed positive and significant correlation with grain yield and biological yield; 1000 grain weight showed positive and significant correlation with grain yield and biological yield; grain yield showed positive and significant correlation biological yield. While number of productive tillers showed negative and significant correlation with plant height, 1000 grain weight and biological yield; flag leaf area showed negative and significant correlation with plant height. In the present study, character association among 11 important plant characters recorded on thirty genotypes revealed that spike length, number of grain per spike, chlorophyll content, 1000 grain weight and biological yield were the most important characters that determine grain yield potential.

**Path coefficient analysis:** The path coefficient analysis was carried out with the objective of assessing the direct and indirect contribution of different traits under study towards the grain yield. Since the mutual relationship of component characters may vary both in magnitude and direction and tend to vitiate the association of grain yield with other attributes, so it is necessary to partition the correlation into direct and indirect effects of each character.

Estimation of genotypic and phenotypic path coefficients the magnitude of genotypic path coefficients are higher than phenotypic path coefficients among 11 different quantitative traits in 30 wheat (Triticum aestivum L.) genotypes presented in Table 3. In genotypic path coefficients estimation the biological yield and also of grains per spike had a highly positive and direct effect on grain yield. Number of productive tillers, flag leaf area, plant height, number of spiklet per spike, chlorophyll content, and 1000 grain weight had moderate to low positive direct effect. The only one trait Days of 50% heading had negative direct effect on grain yield.
Table 3: Estimates of genotypic and phenotypic path correlation coefficient of 11 different qualitative traits in wheat (*Triticum aestivum* L.) genotypes.

| Genotypes                        | Days of 50% heading | Number of Productive Tillers | Flag leaf area (cm²) | Plant height (cm) | Spike length (cm) | No spiklet per ear | Number of grains/spike | Chlorophyll content (mg) | 1000 grain wt. (g) | Biological yield (g/plant) | correlation with Grain yield (g/plant) |
|----------------------------------|---------------------|------------------------------|----------------------|-------------------|-------------------|---------------------|--------------------------|--------------------------|--------------------------|-------------------------------|---------------------------------------|
| Days of 50% heading              | Genotypic path      | -0.260                       | 0.023                | 0.011             | 0.074             | -0.026              | 0.087                    | -0.028                   | -0.003                   | 0.023                        | 0.023                   | -0.076          |
| heading                          | Phenotypic path     | -0.045                       | 0.007                | -0.004            | 0.002             | -0.027              | 0.022                    | -0.024                   | -0.005                   | 0.002                        | 0.011                   | -0.059          |
| Number of Productive Tillers    | Genotypic path      | -0.024                       | 0.248                | -0.003            | -0.086            | -0.034              | 0.026                    | -0.047                   | -0.011                   | -0.094                       | -0.105                  | -0.130          |
|                                | Phenotypic path     | -0.005                       | 0.071                | 0.001             | -0.004            | -0.028              | 0.011                    | -0.035                   | -0.008                   | -0.013                       | -0.114                  | -0.124          |
| Flag leaf area (cm²)            | Genotypic path      | -0.071                       | -0.017               | 0.041             | -0.063            | 0.040               | 0.035                    | -0.030                   | -0.009                   | 0.054                        | -0.011                  | -0.031          |
|                                | Phenotypic path     | -0.012                       | -0.005               | -0.014            | -0.003            | 0.035               | 0.010                    | -0.024                   | -0.007                   | 0.007                        | -0.011                  | -0.023          |
| Plant height (cm)               | Genotypic path      | -0.081                       | -0.090               | -0.011            | 0.236             | 0.028               | -0.037                   | -0.036                   | -0.002                   | 0.007                        | 0.091                   | 0.106           |
|                                | Phenotypic path     | -0.008                       | -0.021               | 0.003             | 0.013             | 0.046               | -0.005                   | -0.014                   | 0.003                    | 0.001                        | 0.090                   | 0.109           |
| Spike length (cm)               | Genotypic path      | 0.039                        | -0.049               | 0.009             | 0.039             | 0.173               | -0.035                   | 0.069                    | 0.014                    | 0.054                        | 0.132                   | 0.444**       |
|                                | Phenotypic path     | 0.006                        | -0.010               | -0.003            | 0.003             | 0.198               | -0.006                   | 0.054                    | 0.011                    | 0.007                        | 0.119                   | 0.380**       |
| No spiklet per ear             | Genotypic path      | -0.097                       | 0.028                | 0.006             | -0.038            | -0.026              | 0.234                    | 0.053                    | 0.022                    | -0.017                       | -0.041                  | 0.124           |
|                                | Phenotypic path     | -0.011                       | 0.009                | -0.002            | -0.001            | -0.013              | 0.088                    | 0.045                    | 0.014                    | -0.005                       | -0.033                  | 0.090           |
| Number of grains per spike      | Genotypic path      | 0.020                        | -0.034               | -0.004            | -0.024            | 0.034               | 0.035                    | 0.350                    | 0.070                    | 0.011                        | 0.187                   | 0.646**       |
|                                | Phenotypic path     | 0.004                        | -0.008               | 0.001             | -0.001            | 0.036               | 0.013                    | 0.296                    | 0.064                    | 0.002                        | 0.198                   | 0.606**       |
| Chlorophyll content (mg)        | Genotypic path      | 0.007                        | -0.022               | -0.003            | -0.004            | 0.019               | 0.043                    | 0.200                    | 0.122                    | 0.005                        | 0.205                   | 0.572**       |
|                                | Phenotypic path     | 0.002                        | -0.005               | 0.001             | 0.000             | 0.018               | 0.010                    | 0.152                    | 0.126                    | 0.001                        | 0.196                   | 0.500**       |
| 1000 grain wt. (g)              | Genotypic path      | -0.028                       | -0.112               | 0.011             | 0.008             | 0.045               | -0.019                   | 0.018                    | 0.003                    | 0.208                        | 0.206                   | 0.338**       |
|                                | Phenotypic path     | -0.003                       | -0.027               | -0.003            | 0.000             | 0.042               | -0.013                   | 0.022                    | 0.002                    | 0.034                        | 0.190                   | 0.242*        |
| Biological yield (g/plant)      | Genotypic path      | -0.014                       | -0.059               | -0.001            | 0.049             | 0.052               | -0.022                   | 0.149                    | 0.057                    | 0.098                        | 0.439                   | 0.748**       |
|                                | Phenotypic path     | -0.001                       | -0.017               | 0.000             | 0.002             | 0.048               | -0.006                   | 0.119                    | 0.050                    | 0.013                        | 0.491                   | 0.700**       |

Residual effect: 0.0380, *, ** = Significant at P=0.05 and P=0.01 levels, respectively.
While phenotypic path coefficients showed that biological yield and number of grain per spike had highly positive and direct effect on grain yield. Number of productive tillers, plant height, spike length, number of spikelet per spike, chlorophyll contents and 1000 grain weight had moderate to low positive direct effect. The only two traits two traits including days to 50% heading and flag leaf area had negative direct effect on grain yield.

**Cluster analysis:** In the present study the non-hierarchical eduecliden cluster analysis. Using this technique the 30 genotypes of wheat based on 11 character were grouped into six cluster indicating considerable amount of genetic diversity among the genotypes presented in Table 4. The maximum number of genotypes was grouped into cluster V while the minimum of genotypes in cluster (2) in cluster II. The intra cluster distance ranged from 1.61 (cluster II) to 2.37 (cluster III and VI) presenting in the Table 5. Thus the member of cluster II were least divergent and similarly the member of cluster III and IV were most divergents. The maximum inter cluster distance was between cluster II and III followed by cluster IV and V, cluster VI and cluster III and VI and cluster V that order therefor the accessions grouped in the five pair of cluster may be considered as most divergent.

An examination as mean values of genotypes clustered in each of the six different cluster presented in the Table 5. The lowest and highest cluster means respectively for different traits were observed i.e. for days to 50% heading (I and II), number of productive tillers (II and IV), flag leaf area (II and VI), plant height (I and II), spike length (II and VI), number of spikelet per spike (III and VI), number of grains per spike (III and II), chlorophyll contents (III and II), 1000 grains weight (I and VI), biological yield (III and V) and grain yield (III and V). Estimation of mean values of the six different cluster suggested that mean values for different traits of the genotypes grouped into four most divergent cluster II, III, IV, and V was desirable.

Therefore desirable and diverse accessions from these four cluster may be selected for involving hybridization programme. the genotypes HPW-155 and 43GW-10 belonging to cluster III, HPW-184 belonging to cluster IV, and 91HI-1077 belonging to cluster V had high mean values for different yield contributing character presented in Table 5. Therefore these genotypes may be involved in hybridization programme for recovering desirable segregates. Genetic divergence among wheat genotypes through cluster analysis was also reported by Khodadadi *et al.* (2011), Mollasadeghi *et al.* (2012), Talebi and Fayyaz (2012).

### Table 4: Distribution of 30 genotypes of wheat genotype into different clusters.

| Clusters | No of genotypes | Genotype name |
|-----------|-----------------|---------------|
| I         | 8               | 103HP-1744, HP-1761, GW-322, 47GW-173, 46GW-120, AKW-381, 9BW-11, VL-404 |
| II        | 2               | HPW-184, 8C-306 |
| III       | 4               | HPW-155, 44GW-18, 43GW-10, 2AJANTA |
| IV        | 3               | 105HPW-42, HPW-251, 48GW-190 |
| V         | 9               | 101HP-1633, 102HP-1731, AKW-1071, HD-2967, 91HI-1077, 92HI-1418, 93HI-1464, 94HI-1500 |
| VI        | 4               | HPW-89, HPW-147, 49GW-273, 45GW-89 |

### Table 5: Inter and intra Clusters distance of different cluster of 30 wheat genotypes.

| Clusters | I   | II  | III | IV  | V   | VI  |
|----------|-----|-----|-----|-----|-----|-----|
| I        | 2.33|     |     |     |     |     |
| II       | 3.93| 1.61|     |     |     |     |
| III      | 3.47| 5.41| 2.37|     |     |     |
| IV       | 3.01| 5.06| 4.12| 2.25|     |     |
| V        | 2.69| 2.53| 4.29| 4.26| 2.36|     |
| VI       | 3.89| 3.95| 4.40| 4.58| 3.33| 2.37|

### Table 6: Estimates of cluster mean of different qualitative traits in 30 wheat (*Triticum aestivum* L.) genotypes.

| Clusters | Days of 50% flowering | Number of productive Tillers | Flag leaf area (cm²) | Plant height (cm) | Spike length (cm) | No spikelet per ear | Number of grains/spike | Chlorophyll content 1000 grain wt. (g/plant) | Grain yield (g/plant) | Biological yield (g/plant) |
|----------|------------------------|------------------------------|----------------------|------------------|------------------|---------------------|-----------------------|---------------------------------|------------------------|--------------------------|
| I        | Mean 84.63             | 8.18                         | 41.64                | 78.47            | 11.36            | 20.03               | 42.42                 | 46.54                           | 38.22                  | 8.39                     | 16.01                     |
| II       | Mean 86.67             | 6.23                         | 35.97                | 94.60            | 11.45            | 19.57               | 52.00                 | 51.02                           | 41.44                  | 11.45                    | 20.92                     |
| III      | Mean 86.08             | 7.61                         | 40.83                | 86.72            | 11.40            | 18.92               | 32.00                 | 35.51                           | 41.44                  | 6.42                     | 14.09                     |
| IV       | Mean 89.89             | 9.60                         | 42.31                | 79.58            | 9.85             | 20.51               | 42.89                 | 43.48                           | 38.29                  | 7.74                     | 16.83                     |
| V        | Mean 85.30             | 7.24                         | 42.34                | 83.12            | 11.75            | 19.07               | 47.52                 | 45.38                           | 41.72                  | 11.82                    | 21.70                     |
| VI       | Mean 89.25             | 6.51                         | 58.33                | 86.93            | 12.24            | 20.62               | 41.67                 | 45.53                           | 44.86                  | 9.54                     | 18.76                     |
Tahmasebi et al. (2013) used cluster analysis based on squared Euclidean distance and ward’s method, categorized the 16 wheat lines into three groups. Aharizad et al. (2012) used cluster analysis based on all the traits using Ward’s algorithm and squared Euclidean distances assigned the lines into three groups.

Kumar et al. (2013) used cluster analysis based on Euclidian dissimilarity distance, the separated the 30 wheat genotypes into eight different clusters. Ahlawat et al. (2008) carried out genotypic divergence analysis, carried out according to Mahalanobis $D^2$ statistics, categorized 36 genotypes into 9 clusters.

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