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Genetic variability, correlation and path analysis in bread wheat (*Triticum aestivum*) genotypes for yield and its contributing traits

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Abstract

Fifty-seven bread wheat genotypes were evaluated for genetic variability, correlation and path analysis to identify the traits associated with grain yield. The experimental material was sown in Randomized Block Design in three replications at Research area of Wheat & Barley Section, Department of Genetics & Plant Breeding, CCS HAU, Hisar situated during *Rabi*, 2015-16. The analysis of variance revealed the presence of significant genetic variability for all the characters under study. High heritability along with high genetic advance as percent of the mean was recorded for grains/spike, grain yield/plot (g), number of effective tillers per meter, spike length (cm), biological yield per plot (g/plot) and harvest index (%). Correlation analysis explained that grain yield per plot had a significant and positive correlation with the number of effective tillers/meter, spike length (cm), number of spikelets/spike, number of grains/spikes, 1000-grain weight (g), biological yield/plot (g) and harvest index (%). Harvest index, spike length, days to heading and 1000-grain weight (g) were found directly correlated with grain yield (g/plot). Path analysis showed that harvest index and biological yield had positive effect on grain yield followed direct effect of spike length, days to 50% heading and 1000-grain weight thereby indicated that these were main contributors to the grain yield. So breeders should concentrate on these traits for improving grain yield per plant in wheat breeding program.

Keywords: Bread wheat, genetic variability, correlation, path analysis

Introduction

Wheat (*Triticum aestivum* L., $2n=6x=42$) is a monocot plant, belongs to the tribe *triticeae*, under the grass family *poaceae*. Wheat grain has a high nutritional value with 70-75% starch, 14% water, 8-20% proteins, 2-3% non-starch polysaccharides, 2% lipids, 1.6% minerals, antioxidants *etc.* and is main staple food crop for a huge world population (Goesaert *et al.*, 2005) [12]. The growing pace of population is declining the cultivated land which is a great concern for the world's food security and alarming us to raise the grain yield production by crop improvement. The genetic variability observed in the plant population of a species is result of the both heredity effects of concerned genes and the environment. Therefore, Grain yield is a complex trait and is strongly influenced by many genetic and environmental factors. Thus, direct selection for yield can be misleads and deaccelerate the pace of breeding program. Successful selection of high yielding genotypes depends on information available for genetic variability and the association of morpho-agronomic traits with grain yield. The degree of association between two or more variables is estimated by the correlation coefficient (*r*). The correlation analysis measures the degree of association but does not indicate the relative importance of each factor. Therefore, it is necessary to perform a more detailed examination using an analysis of the path coefficient, a statistical technique to decompose the correlation coefficient into direct and indirect effects, which facilitates the estimation of the contribution of each component (independent cause) to the grain yield (dependent variable) (Suleiman *et al.*, 2014) [21]. Keeping in mind the above facts, the present study was planned to estimate the correlation and path coefficients analysis between grain yield and its contributing traits in wheat genotypes and to identify the yield contributing traits that could be used as selection criteria to improve grain yield.

Material and Methods

The experiment was carried out in the research area of Wheat & Barley Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar. Geographically, Hisar is located at latitude $29^{\circ}10'N$, longitude of $75^{\circ}46'E$ and altitude of 215.2 m above sea level in the semi-tropical region of Western Haryana.

A total of 57 genotypes, including released varieties and advance breeding lines were used in the present study. The crop was sown in four rows of 3-meter length with three replicates in a Randomized Block Design (RBD) during *Rabi* 2015-16. Five plants from middle rows of plot were selected randomly and tagged to record the data of different morpho-agronomical traits *viz.*, days to 50% flowering, plant height (cm), number of effective tillers/plant, spike length (cm), number of spikelets/spike, number of grains/spike, grain yield/plot (g), 1000-grain weight (g), biological yield/plot(g), harvest index(%). Harvest index was calculated as per formula given by Donald and Humblin (1976) [8]. The mean performance of individual genotypes was used for statistical analysis. Statistical analysis of recorded phenotypic data was performed using a computer based statistical package INDOSTAT program. Analysis of variance of the observations recorded on all characteristics was carried out as per the standard procedure suggested by Fisher (1925) [11]. Genotypic and phenotypic coefficients of variation were estimated according to Burton *et al.* (1953) [4]. Heritability in broad sense was calculated as the ratio of genotypic to phenotypic variance and expressed in percentage (Falconer, 1981) [10]. Genetic advance as percent of mean of each character was worked out adopting the formula given by Johnson *et al.* (1955) [14]. Similarly, correlation coefficient and path analysis were carried out using the method suggested by

Al-Jibouri *et al.* (1958) [1] and Dewey and Lu (1959) [7], respectively.

Results and Discussion

The glimpses of the ANOVA (Table 1) for different traits revealed that the mean sum of squares due to genotypes was significant for all the characters under study indicating substantial variability in the material taken under study. This variability indicates that there is ample scope for improvement of traits under study. Many workers, including Drikvand *et al.*, (2013) [9], Bhutto *et al.* (2016) [3], and Khan *et al.* (2017) [15] and Phougat *et al.*, (2016) [17] reported high variability for different traits in wheat.

Variability and heritability parameters

The extent of variability present in the genotypes was measured in terms of range, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad sense heritability and expected genetic advance (GA) (Table 2). It is clearly marked that a significant amount of variation was present among genotypes for the character under study. The magnitude of phenotypic coefficient of variation (PCV) was higher than the corresponding genotypic coefficient of variation (GCV) for all the characters under the study (Table 2) indicating influence of environmental factors on their expression.

Table 1: Analysis of variance (ANOVA) for various traits in different genotypes of wheat

| Source of Variations | DF | Mean sum of squares | | | | | | | | | | |
|----------------------|-----|---------------------|-------|---------|---------|-------|-------|---------|--------|-----------|------------|-------|
| | | DH | DM | PH | ET | SL | S/S | G/S | GW | GY | BY | HI |
| Replication | 2 | 17.38 | 4.32 | 318.30 | 153.29 | 1.40 | 29.44 | 925.45 | 20.73 | 8716.33 | 46782.13 | 0.97 |
| Genotypes | 56 | 19.01* | 6.29* | 100.83* | 400.33* | 2.27* | 6.21* | 132.38* | 24.93* | 89176.41* | 373329.62* | 33.11 |
| Error | 112 | 1.31 | 0.58 | 10.09 | 156.72 | 0.76 | 1.40 | 49.53 | 13.66 | 10831.26 | 50864.41 | 2.97 |

*Significant at p=0.01% level of significance

DH: Days to 50% heading; DM: Days to maturity; PH: Plant height (cm); ET: Number of effective tillers/meter; SL: Spike length (cm); S/S: Number of spikelets/spike; G/S: Number of grain/spike; GW: 1000-grain weight (g); GY: Grain yield/plot (g/plot); BY: Biological yield/plot (g/plot); HI: Harvest index (%).

Table 2: Range, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance (GA) in different genotypes of wheat

| Characters | Range | Coefficient of variation (%) | | h ² (bs) | GA as % of mean |
|------------|-----------------|------------------------------|-------|---------------------|-----------------|
| | | GCV | PCV | | |
| DH | 90.67-104.33 | 2.56 | 2.83 | 81.85 | 4.77 |
| DM | 132.33-139.33 | 1.02 | 1.16 | 76.72 | 1.84 |
| PH | 89.33-121.40 | 5.10 | 5.89 | 74.99 | 9.10 |
| ET | 76.33-130.00 | 10.24 | 13.75 | 55.44 | 15.71 |
| SL | 8.90-13.90 | 7.34 | 9.20 | 63.59 | 12.05 |
| S/S | 20.50-25.75 | 5.48 | 7.52 | 53.24 | 8.24 |
| G/S | 39.00-77.00 | 12.87 | 15.51 | 68.85 | 21.99 |
| GW | 34.22-45.88 | 5.45 | 7.09 | 59.09 | 8.63 |
| BY | 2080.00-3920.00 | 10.22 | 12.41 | 67.90 | 17.35 |
| HI | 21.25-45.52 | 7.91 | 9.00 | 77.17 | 14.31 |
| GY | 753.33-1633.67 | 12.60 | 14.98 | 70.60 | 21.81 |

Heritability and Genetic Advance

The genotypic coefficient of variation does not offer full scope to estimate the variation that is heritable or environmental and therefore, estimation of heritability becomes necessary. The magnitude of heritability ranged from 53.24% (number of spikelet/spike) to 81.85% (Days to 50% heading). Heritability(h²) estimates were moderate to high (>60%) for days to 50% heading (81.85), days to maturity (76.72%), plant height (74.99%), spike length (63.59%), number of grain per spike (68.85%), biological yield per plot (67.90%), harvest index (77.17%) and grain yield per plot (70.60%) (Table 2).

The high heritability estimates would be helpful for selection and breeding of superior genotypes on the basis of phenotypic performance of quantitative characters. However, Johnson *et al.* (1955) [14] reported that heritability (h²) estimates along with genetic advance were more useful than the heritability alone while selecting the best genotypes. So, heritability along with high genetic advance was considered an important selection parameter. High heritability estimates along with genetic advance as per cent of mean were recorded for characters number of grains/spike, grain yield/ plot (g), number of effective tillers per meter, spike length (cm), biological yield per plot (g/plot) and harvest index (%). This

demonstrates the presence of additive gene effects indicating the effectiveness of selection for these traits in crop improvement programme. Similar results were also reported by Kumar *et al.* (2014)^[2] for tiller number per row.

Correlation coefficient analysis

Grain yield is a complex trait and is influenced by several component characters. It is also very difficult to improve yield by directly selecting for grain yield per plant. So, it was felt that it would be of great help in selecting the desirable genotypes for yield if there is a certain association of grain yield with certain easily measurable plant characters.

Correlation between traits could be due to linkage or pleiotropy. Correlation due to linkages can be modified through recombination, but correlation due to pleiotropy or developmental causes may not be easy to overcome. In later cases, the genetic improvement in yield is not possible without bringing an improvement in yield component traits. The inclusion of various component characters in a selection scheme is obviously not practicable and under these

situations, and knowledge with respect to the association of various traits with grain yield would be of immense help in formulating an effective and efficient selection and screening programme.

Correlation among wheat genotypes showed that grain yield per plot had significant and positive correlation with biological yield per plot (g) (0.779**), harvest index (%) (0.552**), 1000-grain weight (g) (0.370**), spike length (cm) (0.261**), number of spikelets/spike (0.252**), number of grains/spike (0.250**) and number of effective tillers/metre (0.243**) while negative correlation with days to heading (0.152*) and days to maturity (0.236**) (Table 3). Days to heading was positively correlated with days to maturity (0.694**). Spike length exhibited highly significant and positive association with number of spikelets per spike (0.245**), grain per spike (0.270**), and harvest index (0.285**). Similarly, the association of grain yield with either one or more than one trait has also been reported by Desheva (2016)^[6], Phougat *et al.* (2017)^[18] and Arya *et al.* (2017)^[2].

Table 3: Phenotypic correlation coefficients among various morphological traits of wheat genotypes

| Characters | DH | DM | PH | ET | SL | S/S | G/S | GW | BY | HI |
|------------|----------|----------|---------|---------|---------|---------|---------|---------|---------|---------|
| DH | | | | | | | | | | |
| DM | 0.694** | | | | | | | | | |
| PH | -0.296** | -0.168* | | | | | | | | |
| ET | 0.033 | 0.028 | 0.039 | | | | | | | |
| SL | -0.076 | -0.213** | 0.077 | 0.068 | | | | | | |
| S/S | 0.075 | 0.049 | 0.168* | -0.039 | 0.245** | | | | | |
| G/S | -0.036 | -0.065 | 0.098 | -0.043 | 0.270** | 0.331** | | | | |
| GW | -0.135 | -0.152* | 0.065 | 0.166* | 0.212** | 0.019 | 0.063 | | | |
| BY | -0.251** | -0.088 | 0.291** | 0.204** | 0.083 | 0.123 | 0.160* | 0.197** | | |
| HI | 0.097 | -0.239** | -0.141 | 0.103 | 0.285** | 0.236** | 0.204** | 0.317** | -0.099 | |
| GY | -0.152* | -0.236** | 0.148 | 0.243** | 0.261** | 0.252** | 0.250** | 0.370** | 0.773** | 0.552** |

*significant at p= 0.05, ** Significant at p= 0.01

Path coefficient analysis

Partitioning of total correlation into direct and indirect effects provide a direct and indirect contribution of characters and thus form the basis for selection to improve the yield. Considering grain yield as effect and other characters as causes, genotypic correlation coefficients were partitioned by using the method of path analysis to find out the direct and indirect effects. Shrivastava and Sharma (1976)^[19] suggested that only direct yield components should be used for selection purpose. In the present study, the magnitude of direct effects revealed that biological yield per plot (0.8369) was the most important trait followed by harvest index (0.6261), spike

length (0.0129), days to 50% heading and 1000-grain weight for improvement of grain yield. Similar findings were observed by, Hussain *et al.* (2012)^[13], Wahidy *et al.* (2016)^[22], Desheva (2016)^[6], Phougat *et al.* (2017)^[18] and Arya *et al.* (2017)^[2]. Indirect effects of independent traits indicated that biological yield (0.773) was the most important followed by harvest index (0.552). This revealed that in addition to the grain yield components biological yield and harvest index are important for grain yield determining characters. Very low residual effects (0.00276) indicated that contribution of characters included in this study explained almost all of the variation for grain yield as shown in Table 4.

Table 4: Direct (diagonal) & Indirect (off-diagonal) effects of component traits on Grain Yield per plot of wheat

| Characters | DH | DM | PH | ET | SL | S/S | G/S | GW | BY | HI |
|------------------------------|---------|----------|---------|---------|---------|---------|---------|---------|---------|---------|
| DH | 0.0067 | 0.0046 | -0.0019 | 0.0002 | -0.0005 | 0.0005 | -0.0003 | -0.0009 | -0.0017 | 0.0007 |
| DM | -0.0117 | -0.0169 | 0.0029 | -0.0005 | 0.0036 | -0.0008 | 0.0011 | 0.0026 | 0.0015 | 0.0040 |
| PH | 0.0025 | 0.0014 | -0.0083 | -0.0003 | -0.0006 | -0.0014 | -0.0008 | -0.0005 | -0.0020 | 0.0012 |
| ET | 0.0002 | 0.0002 | 0.0003 | 0.0064 | 0.0004 | -0.0003 | -0.0003 | 0.0011 | 0.0013 | 0.0007 |
| SL | -0.0009 | -0.0028 | 0.0001 | 0.0008 | 0.0129 | 0.0032 | 0.0035 | 0.0027 | 0.0011 | 0.0037 |
| S/S | 0.0004 | 0.0003 | 0.0009 | -0.0002 | 0.0014 | 0.0056 | 0.00184 | 0.0001 | 0.0007 | 0.0013 |
| G/S | 0.0006 | 0.0011 | -0.0016 | 0.0007 | -0.0044 | -0.0054 | -0.0164 | -0.0010 | -0.0020 | -0.0033 |
| GW | -0.0002 | -0.0003 | 0.0001 | 0.0003 | 0.0004 | 0.0001 | 0.0001 | 0.0018 | 0.0004 | 0.0006 |
| BY | -0.2096 | -0.0735 | 0.2436 | 0.1711 | 0.0691 | 0.1026 | 0.1337 | 0.1653 | 0.8369 | -0.0827 |
| HI | 0.0605 | -0.1497 | -0.0885 | 0.0648 | 0.1782 | 0.1476 | 0.1279 | 0.1986 | -0.0619 | 0.6261 |
| Correlation with grain yield | -0.152* | -0.236** | 0.148 | 0.243** | 0.261** | 0.252** | 0.250** | 0.370** | 0.773** | 0.552** |

Residual effect 0.002

Conclusion

The result obtained from the present study will be useful in understanding the current status of genetic variation present in

the studied wheat genotypes for studied morpho-agronomical traits that could be useful in further breeding program. Considering the nature and magnitude of character

associations and their direct and indirect effects, it can be inferred that biological yield and harvest index, number of productive tillers per plant, 1000-grain weight and number of spikelets per spike could serve as important traits in any selection programme for developing high yielding wheat varieties.

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