

Genetic Variability, Correlation And Path Analysis In Wheat (*Triticum aestivum* L.)

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Abstract

A study was conducted at Agricultural Research Farm, R.B.S. College, Bichpuri, Agra (U.P.) during rabi season. Range, CV, genotypic, phenotypic and environment variance, genotypic and phenotypic coefficient of variation, heritability, genetic advance, correlation coefficient and path analysis were performed for yield and its contributing characters in 27 wheat genotypes. Analysis of variance for significant differences was among the all characters except, number of effective tillers per plant and spike length. A broad range of variation was observed for grain yield per ha⁻¹, plant height at maturity and number of grain per spike. Phenotypic variance value for most characters was closer than the corresponding genotypic variance value showing little environment effect on the expression of these characters. The estimated value of broad sense heritability was found between 50.10% (Spike length) and 97.20% (grain yield ha⁻¹). Heritability values were determined as 85.60%, 74.80%, 90.10%, 96.40%, 69.40%, 88.10%, 96.10%, and 87.90%, for number of effective tillers per plant, initiation of spike, days to maturity, plant height at maturity, number of spikelet's per spike, 1000 grain weight, number of grain per spike and grain yield per plant respectively. High heritability coupled with high genetic advance as percent over mean was observed for grain yield ha⁻¹, plant height at maturity, number of grain per spike and days to maturity suggesting selection for these traits would give good responses. Grain yield ha⁻¹ showed significant positive genotypic and phenotypic correlation with grain yield per plant ($r_g=0.454$, $r_p=0.442$) and spike length ($r_g=0.536$). Grain yield ha⁻¹ (0.938, 0.502) had highest positive direct effect on grain yield per plant followed by 1000 grain weight (0.490, 0.336). It is suggested that these characters can be considered as selection criteria in improving the grain yield.

Key words: Genetic variability, heritability, genetic advance, correlation, path analysis and *Triticum aestivum* L.

Wheat (*Triticum aestivum* L.) is belongs to Gramineae family. It is the prime and staple food in the world. It is originated in south west Asia in the area is known as the fertile crescent. In India evidence from Mohan-Jo-daro excavations indicate that wheat was cultivated more than 5000 year ago.

Wheat is grown in peninsular India, East Pakistan, Burma, Thailand and other countries of South and southern Asia since the hot humid climate in these area is unfavorable for good wheat production. In India, it is cultivated on 28.89 mh area and 88.31 mt production in 2011-12. The average productivity of wheat is estimated to be 30.57 q ha⁻¹ in 2011-12, which is lower than the china, USA and russia. The development of high yielding varieties with desirable quality breeding programme. Analysis of

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variability among the traits and the association of a particular character with other traits contributing to yield of a crop would be great importance in planning a successful breeding programme (Mary and Gopalan, 2006). Genetic variability among wheat genotypes can be estimated based on quantitative traits. The choice of parents is of paramount importance in breeding programme. For effective selection, information on nature and magnitude of variation in population, association of character with yield and among themselves and the extent of environmental influence on the expression of these characters are necessary (Yagdi and Sozen, 2009).

Heritability, degree to which the variability of a character is transmitted to the progeny, serves as a guide to the reliable phenotypic variability in the selection programme and hence determines its success (Hamdi, 1992). However, Johnson *et al.* (1955) stated that heritability estimates together with genetic advance are more important than heritability alone to predict the resulting effect of selecting the best individuals. Genetic advance is also of considerable importance, because it indicates the magnitude of the expected genetic gain from one cycle of selection (Hamdi *et al.* 2003). High genetic advance coupled with high heritability estimates, offer the most effective condition for selection (Larik *et al.* 2000). Correlation and path coefficient analysis could be used as an important tool to bring information about appropriate cause and effects relationship between yield and some yield components (Khan *et al.*, 2003).

Path coefficient analysis provides means to quantify the inter-relationship of different yield components and indicate whether the influence is directly reflected in the yield or take some other path ways to produce an effect. Path analysis was used for different crops to determine the direct and indirect effect of yield components (Khaliq *et al.* 2004; Chaudhary and Joshi, 2005; Yagdi, 2009; Yasin and Singh, 2010). The present investigation was conducted with the objectives to determine the variability of traits, provide information on inter-relationship of yield with some important yield

components and to partition the observed genotypic correlations into their direct and indirect effects.

Material and methods

The field experimental materials for the present investigation comprised twenty seven wheat (*Triticum aestivum* L.) genotypes. The genotypes were received from Department of Plant Breeding and Genetics, R.B.S. College, Bichpuri, Agra-283105 (U.P.). These were UP-2338 (UP 368/VL 421/UP26), Raj-6560 (TOPDY-6), PBW-435 (HD 2160/CAL/DAD), Raj-1555 (COCRIT 'S' /RAJ 911), Lok-1 (S308/S331), HD 2687 (CAPAN 2009/HD/2329), WH-542 (JUP/BJY/VRES), WH-896 (SIN 'S' /WH 852), Raj-3765 (HD2402/VL 639), HD-2329 (HD1962//E4870/K65/3/HD 1553/UP262), HD-4672 (BRED/PBW 34// I ALTER/84), UP-2425 (HD 2320/UP 2263), A-9-30-1 (8206/GA2A), HD-2285 (249/HD2160 // HD 2186), HW-2004 (C306/7/TR 380-14* 7/3 AG 14), PBW-373 (ND/VG 1944 // KA 2// BB/3 /VACO 'S' /4/VEE # 5'S'), Raj-3777 (RAJ 3160/HD 2499), Durgapura-65 (Selection from RS 31-1), CNN-RV-1 (J 24/AVS 15854), Raj-4037 (DL 788-2 /RAJ 3717), Raj-3077 (HD 2267/RAJ 1482 // RAJ 1802), Kharachiya-65 (Selection from kharachia local), Raj -1482 (NAPOTOB 'S' / C8156/CAL-Bb), PBW-343 (ND/VG 1944 // KA 2//BB/3/VACO 'S' /4/ VEE# 5 'S'), Bijara (Local selection), Kalyansona (PUNJAB Mo'S GABO 55) and Kundan (DL 788-2) (K 7537/HD 2160/HD 278/LR 24 K-4-14). The genotypes were sown in randomized block design with three replications at Agricultural Research Farm, R.B.S. College, Bichpuri, Agra in rabi season 2007-08. In each replication there was a three row of each genotype with a row length of 3.5 meter. The following quantitative data were recorded on five randomly selected plants from each genotype in each replication for ten characters *viz.* number of effective tillers per plant, initiation of spike (days), days to maturity (days), plant height at maturity (cm), spike length (cm), number of spikelet per spike, 1000-grain weight (gm), number of grain per spike, grain yield per plant (gm) and grain yield ha⁻¹ (quintal) except initiation of spike (days), days to maturity (days) and grain yield ha⁻¹ (quintal) recorded on the plot basis.

All the recommended agronomic cultural practices and plant protection measures were followed. Replication wise mean data for each character were subjected for analysis of variance (Panse and Sukhatme, 1985), coefficient of variance (CV) (Burton, 1953), heritability in board sense (Johnson, Robinson and Cornstock, 1955), genetic advance (Johnson et al., 1955), correlation (Searle et al., 1961 and Snedecar et al. 1967) and Path analysis (Sewall Wright, 1921 and Deway et al. 1952) were calculated as per statistical method.

Result and discussion

Genetic Variability, Heritability and Genetic advance

Highly significant differences ($P < 0.01$) were observed among genotypes for initiation of spike, days to maturity, plant height at maturity, 1000 grain weight, number of grain per spike, grain yield per plant and grain yield ha^{-1} and significant differences ($P < 0.05$) was observed for number of spikelets per spike demonstrating the presence of genetic variability among genotypes. However, number of effective tillers per plant, and spike length were not significantly different for these genotypes (Table 1). The variability parameters showing phenotypic variation (σ^2_p), genotypic variation (σ^2_g), environment variation (σ^2_e), phenotypic coefficient of variance (PCV), genotypic coefficient of variance (GCV), heritability in broad sense (h^2), genetic advance (GA) and genetic advance as percentage (GA%) over the mean among with mean, range, coefficient of variance (CV) are presented in Table – 2.

Maximum phenotypic coefficient of variance (PCV) was observed on grain yield ha^{-1} (27.02%), grain yield per plant (23.37%), number of effective tillers per plant (21.10%) and number of grain per spike (21.05%) and minimum for initiation of spike (3.08%) and days to maturity (4.11%). The genotypic coefficient of variance (GCV) was also maximum for grain yield ha^{-1} (26.64%) followed by grain yield per

plant (21.91%), number of grain per spike (20.66%) and number of effective tillers per plant (19.52%) and minimum for initiation of spike (2.67%) and days to maturity (3.91%).

The higher PCV and GCV values for most of the characters could be evidence for the existence of a wide range of variation for such characters. In general, the PCV values for most characters were closer than the corresponding GCV values showing little environment effect on the expression of these characters. Similar results were also observed by Bhoite et al. (2008). Selection on a phenotypic basis may be effective for the genetic improvement of such traits. Initiation of spike and days to maturity were showed low PCV and GCV values implying the difficulty of improving these traits through simple selection. However, contradicting results were obtained from the works of Tazeen et al. (2009).

High heritability values were exhibited for grain yield ha^{-1} (97.20%), plant height at maturity (96.40%), number of grain per spike (96.30%), grain yield per plant (87.90), days to maturity (90.10%), 1000 grain weight (88.10%) and number of effective tillers per plant (85.60%) showed that these characters were governed by additive genes. High heritability related to grain yield ha^{-1} , Plant height at maturity and number of grain per spike were obtained in the studied conducted previously (Singh et al., 2006 and Bhoite et al, 2008). The high heritability magnitude indicates the reliability with which the high chance of the genotype to be recognized by its phenotypic expression (Chandrababu and Sharma, 1999). Moderate heritability value were observed for spike length (50.10%), number of spikelets per spike (69.40%) and initiation of spike (74.80%) suggesting selection for these characters would not be effective due to predominant effects of non additive genes in this population.

Maximum expected genetic advance as percentage of mean was observed on grain yield ha^{-1} (54.09%) followed by grain yield per plant (42.33%), number of grain per spike (91.26%) and number of tillers per

plant (37.17%) indicating the presence of additive gene effects; while the same was minimum for initiation of spike (4.75%), days to maturity (7.64%) and spike length (13.83%). Similar results were found in other findings (Thakhur, et al., 1998; Gupta et al., 1979 and Bhoite et al., 2008).

High heritability coupled with high genetic advance percentage over mean was recorded on grain yield ha^{-1} , number grain per spike, grain yield per plant and number of effective tillers per plant indicating selection for these characters would be more effective.

Phenotypic and genotypic correlation coefficient of grain yield ha^{-1} with other characters is presented in Table 3. Grain yield ha^{-1} had positive significant phenotypic correlation with grain yield per plant (0.442%) and positive phenotypic correlation with spike length (0.337) and 1000 grain weight (0.227%) and negative significant phenotypic association with days to maturity (-0.437) and negative association with initiation of spike (-0.234%), number of effective tillers per plant (-0.224), number of grains per spike (-0.121), plant height at maturity (-0.091) and number of spikelets per spike (-0.044). Similar results were observed by (Budak, 2000, Yogdi and Sozen 2009). The negative association of grain yield ha^{-1} with days to maturity and initiation of spike suggested that early initiation of spike and maturity genotypes would give high grain yield. At genotypic level, grain yield ha^{-1} had positive significant correlation with spike length (0.536) and grain yield per plant (0.454) and positive correlation with 1000 grain weight (0.245) and negatively significant association with days to maturity (-0.433) and negative association with initiation spike (-0.272), number of tillers per plant (-0.234), number of grain per spike (-6.124), Plant height at maturity (-0.092) and number of spikelet's per spike (-0.046). Similar results were observed by (Dawari and Luthra 1991 and Moghaddam et al., 1997).

The genotypic correlation coefficient value for most of the characters were higher in magnitude than the

corresponding phenotypic values showing the existence of inherent association among the traits.

The path coefficient analysis was done with ten characters using estimates of direct and indirect effects of nine characters on grain yield based on phenotypic and genotypic correlation coefficient (Table -4). High and positive phenotypic direct effects on grain yield per plant were exhibited by grain yield ha^{-1} (0.502) followed by 1000 grain weight (0.336) and number of effective tillers per plant (0.281) which supports the findings by Moghaddam et al. (1997). Hence, these traits should be considered in further selection procedures for higher grain yield. Grain yield ha^{-1} showed indirect effect on grain yield per plant through spike length and number of effective tillers per plant. Spike length, days to maturity and number of grain per spike had negative phenotypic direct effect on grain yield per plant. Genotypic path coefficient analysis showed that positive direct effects grain yield per plant were extracted by grain yield ha^{-1} (0.938), 1000 grain weight (0.490), number of spikelets per spike (0.486), plant height at maturity (0.405) and number of effective tillers per plant (0.364) while negative direct effect by spike length (-1.030) and days to maturity (-0.317). Similar result were found (Jain et al. 1975 and Maghaddam et al. 1997).

Residual effect was $P = 0.4889$, $G=0.122$ showing the variability in the grain yield in wheat was contributed by the characters studied in path analysis.

Conclusion

The present study illustrated the existence of wide ranges of variations for most of the trait among the wheat genotypes and opportunities of the genetic gain through selection or hybridization. Phenotypic and genotypic correlation analysis showed the positive correlation of grain yield with important agromorphology characters. Hence, improving one or more of these traits could result in high grain yield for wheat. Grain yield ha^{-1} 1000 grain weight,

number of spikelet per spike and number of tillers per plant had positive phenotypic and genotypic direct effect and correlation with grain yield suggesting the possibility of improving grain yield through direct selection of these traits.

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