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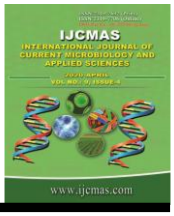

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Genetic Variation, Heritability and Diversity Analysis in Wheat Genotypes Based on Quantitative Traits

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ABSTRACT

The relationships between agronomic traits and grain yield were investigated in 30 genotypes of bread wheat. These genotypes raised in a randomised complete block design (RBD) with three replications during rabi season of 2016-17 at the Research Farm of Dept. of Genetics and Plant Breeding C.C.S. University Campus, Meerut (U.P.) India, using normal field management practices (i.e., 200 kg/ha fertilizer; N:P:K = 8:8:8). The data were recorded on 10 characters; days to heading (DTH), days to 50% flowering (DTA), days to maturity (DTM), plant height (PH), tiller number per plant (TNPP), number of spikelets per spike (NSPS), spike length (SL), grain number per spike (GNPS), 1000 grain weight (TGW) and grain yield per plant (GYPP). Statistical analyses were conducted for diversity; ANOVA, heritability (h^2), genetic advance (GA), coefficient of variation (CV), correlation, path analysis, genetic divergence etc. The result of ANOVA was significant almost all the traits between the treatments, similarly, the range of CV was from 0.34 (TGW) to 7.77 % (GYPP), the range of PCV and GCV were from 3.08 (DTM) to 45.02 (GYPP) and 2.98 (DTM) to 44.34 % (GYPP) respectively. The very high heritability was detected all the traits with the range from 93.75 (TNPP) to 99.95 % (TGW), the genetic advance (GA) was found with range from 2.62 (SL) to 18.19 (GYPP). Likewise, maximum positive correlation (0.92) was found between the DTH and DTA and the result of path analysis indicated, the tiller no showed maximum positive direct effect (0.56) on grain yield, while direct and negative effect of grain yield with DTA.

Introduction

Bread wheat (*Triticum aestivum* L.) is a major staple food for the world's population. Materialization of wheat yield fluctuates widely as a result of its interaction with environment because grain yield in wheat is a polygenic inherited trait and is the product of several contributing factors affecting yield directly or indirectly (Akram *et al.*, 2008; Kumar *et al.*, 2018). The need and importance of wheat is increasing day by day due to increase in human population. Different methods could be used to increase cereal production, such as increasing area of production, effective cultural practices, and using improved cultivars (Benbelkacem, 1996; Hannachi *et al.*, 2013). Use of varieties with better yield potential and wide range of adaptability is of prime importance for increasing wheat production. Thus development of high yielding wheat cultivars has always been a major objective of wheat breeding programs throughout the world

(Bhutta, 2006). Diversity studies facilitate the conservation and management aims of bread wheat. For the effective use of genetic diversity in plant breeding, knowledge of its extent and distribution plays a crucial role. Considering its significance, a large number of studies have been performed to estimate genetic diversity employing various methodologies in multiple crop species. The potential to select a superior line increases with genetic diversity, the discovery of which becomes an important tool in plant breeding. On depletion of genetic variability, plants are unable to cope with unfavourable environmental conditions (Khan *et al.*, 2015).

During the course of evolution, wheat gained sufficient genetic diversity along the road from einkorn to bread wheat. Today, however, its diversity is weakening due to repeated cultivation of landraces for specific characters, narrow adaptation, farmers' varietal selection and the requirement of uniform varieties in industrial seed grain processing (Bellon 1996; Heal *et al.*, 2004; Khan *et al.*, 2015). Heritability is a useful quantitative parameter, which considers the role of heredity and environment determining the expression of a trait (Allard, 1960). Effective selection can be achieved only when additive effects are substantial and environmental effects are small.

Study of correlation coefficient provides information on the relative importance of various quantitative characters in the expression of yield. Path coefficient (Standard partial regression) analysis, on the other hand provides an effective way of finding out direct and indirect sources of correlation. The use of this method requires a cause, and effect relationship among the characters. The path coefficient analysis was originally proposed by Wright (1921). Dewey and Lu (1959) were the first plant breeders, who used path coefficient analysis in plant breeding and found it to be a valuable tool in detection the real merit of characters contributing towards yield.

The study of path coefficient analysis reveals specific forces in the building of a given correlation. It permits the partitioning of correlation coefficient into components of direct and indirect effect and thus helps to elucidate the intrinsic nature of the observed association for complex characters such as given yield. Dewey and Lu (1959) applied the technique of path coefficient analysis for the first in the plant breeding using wheat grass (*Agropyron* spp.) as test genera. Subsequently, several studies on correlation coefficient and path coefficient analysis were conducted on wheat.

Materials and Methods

The study material was consisting of 30 diverse genotypes procured from – Indian Institute of Wheat and Barley Research (IIWBR) Haryana, India. These genotypes raised in a randomised complete block design (RBD) with three replications during rabi season of 2016-17 at the Research Farm of Dept. of Genetics and Plant Breeding C.C.S. University Campus, Meerut (U.P.) India, using normal field management practices (i.e., 200 kg/ha fertilizer; N:P:K = 8:8:8). Each genotype was raised in a plot of 3 rows of 1.5 m each, with a row to row distance of 0.25 m.

Phenotypic data were recorded for 10 different agronomic traits using ten competitive and healthy plants; (i) days to heading (DTH): The DTH was calculated as the number of days reacquired from sowing to heading in 75 % spikes, (ii) Days to anthesis (DTA): The DTA was calculated as the number of days required from sowing to anthesis in 75% spikes, (iii) plant height (PH): The PH was measured in cm from the soil surface to the tip of the tallest ear excluding the awns, (iv) days to maturity (DTM): The DTM was calculated as the number of days required for maturity (when 75 % spike tum yellow and dry) from sowing, (v) tiller number per plants (TNPP): at maturity, number of tiller per plant was counted for each genotype, (vi) spike length (SL): SL was measured in cm from the base of spike to the tip of the ear excluding the awns, (vii) Number of spikelets per spike (NSPP): at the time of spike maturation number of spikelet was calculated, (viii) grain number per spike (GNPS): the GNPS was measured as the average number of grain per spike, (ix) 1000 grain weight (TGW): a sample of 1000 grain of each genotype was counted and weight in gram (g) and (x) grain yield per plant (GYPP): total grain yield of a per plant was weight in g.

Statistical analyses; the analysis of variance was done on the basis of mean of the observations per replication and the following genetic parameters were worked out: (i) Variability; Means for all the characters were subjected for analysis of variance and of variance as given by Panse and Sukhatme (1967), (ii) Heritability (h^2); the h^2 in broad sense was calculated according to Burton (1952). Heritability and expected genetic gain were calculated according to the expected formulae given by Lush (1949) and later used by Burton and Davane (1953), (iii) Genetic advance; The expected genetic advance at 5% intensity of selection differential was calculated for each character following the formula suggested by Johnson *et al.*, (1955), (iv) Co-efficient of variability CV (%): The CV was calculated as given below : CV (%) = (SD x 100)/$\bar{X}$ (Where; SD = Standard deviation of the character , $\bar{X}$ = Mean of the character), (v) Correlation co-efficient; Simple correlation coefficients between pair of characters were calculated with two level (5 and 1 %) of significance, (vi) Path coefficient analysis: Path Coefficient was obtained according to Wright (1921) and as elaborated by Dewey and Lu (1959). Residual effect was also considered in the casual system representing all other factors, which might affect the final character and (vii) Genetic Divergence: The genetic divergence among all genotypes was worked out using non-hierarchical Euclidean cluster analysis following Beal (1969).

Results and Discussion

Analysis of variance (ANOVA): The detail result of analysis of variance is presented in Table 1. The mean squares due to genotypes were highly significant for all the characters, indicating thereby that there was sufficient amount of variability, which was presented in the material taken up for the present study, same results also found in the wheat (Ahmed *et al.*, 2018; Kumar *et al.*, 2018)

Variability: descriptive statistics of all the 30 genotypes of wheat (*Triticum aestivum* L.) exhibited highly significant differences for all the 10 characters indicating the presence of genetic variability among the genotypes studied. The estimates for range and coefficient of variation for the ten characters of thirty genotypes of wheat are given in Table 2. In the present investigation, wide range and coefficient of variability were noted for three characters including grain yield per plant(GYPP) (g) (7.77), tiller no. per plant(TNPP) (6.53), number of spikelet’s per spike (NSPS) (3.95).

This suggested that for these three characters high variability was available in thirty genotypes included in the present study. For the remaining six characters including plant height (PH) (cm), days to heading (DTH), days to 50 % flowering (DTA), days to maturity (DTM), grain number per spike (GNPS), spike length (SL) (cm), 1000 grain weight (TGW), the variability was low (Table 2).

The data of different characters along with the estimates of variability indicating genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV) in Table 2 and results are elaborated in the following text. The estimates of phenotypic coefficient of variation (PCV) ranged from (3.08) for DTM to (45.02) for GYPP. The other characters which had high phenotypic coefficients of variation (PCV), were NSPS (28.34), TNPP (26.14), GNPS (18.22), TGW (14.86), SL (14.22).Similarly the genotypic coefficients of variation (GCV) ranged from (2.98) for DTM to GYPP (44.34).

The other characters which showed high genotypic coefficients of variation (GCV) were GYPP (44.34), NSPS (28.06), TNPP (25.31), GNPS (18.22), TGW (14.86) and SL (14.21).It was also revealed from Table 2 that the estimates of phenotypic coefficients of variation (PCV) were higher than the genotypic coefficient of variation (GCV) for all the characters. Kabir *et al.,* (2015) and Rahman *et al.,* (2016) founded there was significant variation between the different varieties/lines for all the characters.

The variation midst the varieties/lines was judged at phenotypic and genotypic levels. The comparison of the estimates of the phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) suggested a parallel trend in the estimates of genotypic coefficient of variation and phenotypic coefficient of variation for different character, whereas the estimates of phenotypic coefficient of variation were, in general higher than the genotypic coefficient of variation for all the characters during the present investigation.

This may be result due to the involvement of high environment and genotypic x environment interaction effects in character expression. Arati yadawad *et al.,* (2015) reported a narrow range of PCV and GCV for NSPS, GYPP and TGW, whereas, Khan *et al.*, (2015) found moderate GCV and PCV for these traits.

Heritability (h^2): The h^2 was estimated for all 10 characters (Table 2). The estimate of heritability was highest for TGW (99.95%). while the lowest estimate of heritability was observed for TNPP (93.75%). The other characters which showed high to moderate estimates of heritability in order of their magnitude were SL (cm) (99.72), PH (98.69%), GNPS (98.63%), NSPS (98.06%), DTH (97.98%), DTA (97.93%), GYPP (97.02%) and DTM (93.77).

A genetic component of variation does not give the idea of total variation that is heritable. The relative amount of heritable portion of variation can be assessed through heritable estimates. Heritability indicates the effectiveness with the selection for the genotypes can be done on the basis of its phenotypic performance. The heritability (h^2) was estimated for all ten characters. The estimate of heritability was highest for 1000 grain weight, while the lowest estimates heritability was observed for TNPP.

Thus the material under study appears to be promising. High heritability value for quantitative characters are always preferred by the breeders as generally characters with high heritability estimates are comparatively less affected by the environment and these estimates, thus enable him to base his selection reliable on phenotypic expression of these character in individual plants.

Genetic advance: The highest estimate of genetic advances was recorded for GYPP (18.19), whereas, it was lowest for SL (2.62). The other characters which showed high estimated of genetic advance were PH (15.98), GNPS (17.70), 1000 grain weight

(12.15) and DTA (11.32; Table 2). High heritability estimates was associated with high predicted genetic advance for GYPP, PH, GNPS, TGW, which is encouraging since selection based for these characters being for additive in nature, is likely to be more efficient for their improvement. As such phenotypic selection for these traits is likely to be effective for their improvement. High heritability was recorded for plant height by Khan *et al.,* (2007) and Abinasa *et al.,* (2011). Chowdhry *et al.,* (1997) also reported moderate heritability with high genetic advance for number of tillers.

The high heritability with high genetic advance was reported for TGW. Saleem *et al.,* (2003) reported high heritability with high genetic advance for grain yield. Khan *et al.,* (2015) reported high heritability for traits like grain filling period, number of spikelets spike^{-1} and spike length and also reported low genetic gain for DTH, DTM, number of effective tillers m^{-1} and NSPS.

Correlation: All possible genotypic correlation coefficients are given in Table 3. The maximum and positive genotypic correlation coefficients (0.926) were observed between DTH and DTA. GYPP showed positive genotypic correlation coefficient with PH, DTM, TNPP, NSPS, GNPS, SL, TGW (Khan *et al.,* 1999; Usman *et al.,* 2006; Anwar *et al.,* 2009). 1000 grain weight showed positive genotypic correlation coefficient with DTM and TNPP. Spike length showed positive genotypic correlation coefficient with PH, DTH, DTM, TNPP, NSPS and GNPS. The details of all correlation between the different traits are presented in Table 3. These correlations suggested that more than two traits simultaneously improve in breeding programme. Singh & Sharma (1999) detected negative correlation of grains per spike and grain yield but numerous authors (Gautam and Sethi, 2002; Bergale *et al.,* 2001; Sufian 2005) had significant and positive correlation of grains per spike and grain yield. Similarly, TGW was positively correlated with GYPP same as previous reports (Singh and Tewari 1997; Navin *et al.,* 2014; Jat *et al.,* 2003; Zecevic *et al.,* 2004).

Path coefficient: The path coefficient analysis provides the effective means of entangling the direct and indirect causes of association and permits the critical examination and specific forces acting to produce a given correlation. It also measures the relative importance of cause factor. To ascertain the phenotypic direct and indirect effect of 9 characters, PH, DTH, DTA, DTM, TNPP, NSPS, GNPS, SL and TGW. The path analysis was done and results are presented in Table 4.

At the phenotypic level, it can be noticed that eight out of nine characters had positive direct effect on grain yield e.g. plant height, heading, maturity, tiller, number of spikekets, grain per spike, spike length, grain weight. Whereas, remaining one character viz. DTH had low and negative direct effect. It can be also noticed that the tiller number showed maximum positive direct effect (0.560) on grain yield. The path analysis was done and results are presented in Table 5. Direct effect was maximum at the genotypic level for the character of tiller number (0.526). Direct positive effect of yield with plant height, heading, maturity, tiller number, number of spikelets, grain number, SL and TGW.

While direct and negative effect of grain yield with DTA. It has been generally observed that if the correlation between yield and a character is due to direct effect of the character, it reveals true relationship between them and direct selection for these traits will be rewarding for yield improvement. On the other hand, if the correlation is mainly due to indirect effect through another component trait, indirect selection through such trait will be effective. In case, where the direct effect is positive and high but the correlation is negative, direct selection for such trait should be practiced to reduce the undesirable indirect effect. In genotypic path analysis our result revealed high direct positive effect of TNPP and GNPS. Spike yield also had positive and significant association with grain yield. Therefore, the direct selection for tiller and grain per spike shall prove useful for improvement of grain yield. Similarly in phenotypic path our result revealed high direct positive effect of tiller number and grain per spike.

Spike yield also had positive and significant association with grain yield. Therefore, the direct selection for tiller number and grain per spike shall prove useful for improvement of grain yield. Earlier research showed that path analysis delivers extra information on the interrelationships between yield components than correlation coefficients (Board *et al.*, 1997; Kozak and Kang, 2006; Sabaghnia *et al.*, 2010; Janmohammadi *et al.*, 2014). Path analysis helps to govern if yield component advantage is occurring and it occurs when two, or more, yield components affecting yield or any other yield component act inversely in their effects.

Genetic divergence: The knowledge of genetic divergence may be successfully utilized for selecting parents for hybridization. In the present study, the Non-Hierarchical Euclidean cluster analysis (Beale 1969; Spark 1973), a method numerical taxonomy, has been employed for estimating genetic divergence in bread wheat germplasm. The method has been found to be very useful tool for estimating diversity in a world collection of bread wheat (Jain *et al.*, 1975). Using this technique the 30 genotypes of bread wheat germplasm based on 10 characters were grouped into four (4) clusters indicating considerable amount of genetic diversity among the genotypes. The maximum number of genotypes (12) was group in cluster IV (Table 6).

The intra-cluster distances ranged from 1.198 (cluster III) to 1.828 (cluster IV) (Table 7). Thus the member of cluster III was least divergent and similarly the members of cluster IV were most divergent. However overall the genotypes included in the same cluster had little divergence from each other with respect to aggregate effect of the ten characters examined. Therefore hybridization among the genotypes of the same cluster may not provide a good scope for obtaining useful segregates. The putative parents for crossing programme should thus belong to different clusters separated by large inter-cluster distances.

Table.1 Analysis of variance mean sum square

Source of Variation	d.f.	PH (cm)	DTH	DTA	DTM	TNPP	NSPS	GNPS	SL	TGW	GYPP
Replication	1	2.02	0.60	0.07	4.27	0.82	1.07	1.35	0.01	0.28	3.41
Treatment	29	122.81**	41.99**	62.37**	27.61**	14.64*	27.85**	150.74**	3.24**	69.61**	163.19**
Error	29	0.81	0.43	0.65	0.89	0.47	0.27	1.04	0.00	0.02	2.47

df = degree of freedom*and ** significant at p=0.05 and 0.01 respectively, PH= Plant height, DTH = days to heading, DTA = days to anthesis, tiller number per plants (TNPP), NSPS= Number of spikelets per spike, GNPS = grain number per spike, SL= spike length 1000 grain weight, GYPP= grain yield per plant

Table.2 Estimation of mean, range, heritability, coefficient of variation, genetic advance (GA), genotypic coefficient variance (GCV), phenotypic coefficient variance (PCV) and contribution

Characters	Mean	Range		H^2 (%)	CV (%)	GA	GCV (%)	PCV (%)	Contribution (%)
		Min	Max						
PH (cm)	82.98	64.50	92.50	98.69	1.08	15.98	9.41	9.47	10.25
DTH	80.43	74.00	94.00	97.98	0.81	9.30	5.67	5.73	11.79
DTA	88.93	81.50	109.00	97.93	0.91	11.32	6.25	6.31	13.01
DTM	122.77	118.00	131.00	93.77	0.77	7.29	2.98	3.08	12.90
TNPP	10.52	6.00	15.50	93.75	6.53	5.31	25.31	26.14	12.93
NSPS	13.23	5.50	18.00	98.06	3.95	7.58	28.06	28.34	11.44
GNPS	47.48	30.00	61.50	98.63	2.15	17.70	18.22	18.35	10.76
SL (cm)	8.95	6.60	11.39	99.72	0.75	2.62	14.21	14.22	5.75
TGW	39.70	30.13	48.05	99.95	0.34	12.15	14.86	14.86	3.65
GYPP (g)	20.22	10.64	42.34	97.02	7.77	18.19	44.34	45.02	7.52

Table.3 Estimation of phenotypic correlation among different characters based on 30 genotypes of wheat (*T. aestivum* L.)

Traits	PH (cm)	DTH	DTA	DTM	TNPP	NSPS	GNPS	SL (cm)	TGW	GYPP (g)
PH (cm)	1.00	0.617**	0.585**	0.027	0.278*	0.783**	0.565**	0.484**	-0.437**	0.284*
DTH		1.00	0.909**	-0.093	0.081	0.761**	0.653**	0.309*	-0.545**	0.143
DTA			1.00	-0.177	0.011	0.653**	0.551**	0.226	-0.568**	0.036
DTM				1.00	0.650**	0.158	0.270*	0.393**	0.412**	0.737**
TNPP					1.00	0.486**	0.271*	0.394**	0.337**	0.890**
NSPS						1.00	0.681**	0.517**	-0.461**	0.453**
GNPS							1.00	0.589**	-0.281*	0.525**
SL (cm)								1.00	-0.158	0.485**
TGW									1.00	0.465**
GYPP (g)										1.000

Table.4 Estimation of phenotypic path correlation direct a (bold) and indirect effect of the measured variable attributed with number of grain number per spike

Traits	PH (cm)	DTH	DTA	DTM	TNPP	NSPS	GNPS	SL (cm)	TGW	R with GYPP (g)
PH (cm)	**0.032**	0.014	-0.013	0.002	0.155	0.024	0.229	0.009	-0.167	0.284*
DTH	0.020	**0.022**	-0.021	-0.008	0.045	0.024	0.264	0.005	-0.208	0.143
DTA	0.019	0.020	**-0.023**	-0.016	0.006	0.020	0.223	0.004	-0.217	0.036
DTM	0.001	-0.002	0.004	**0.091**	0.364	0.005	0.109	0.007	0.157	0.737**
TNPP	0.009	0.002	0.000	0.059	**0.560**	0.015	0.110	0.007	0.129	0.890**
NSPS	0.025	0.017	-0.015	0.014	0.272	**0.031**	0.276	0.009	-0.176	0.453**
GNPS	0.018	0.014	-0.013	0.025	0.152	0.021	**0.405**	0.010	-0.107	0.525**
SL (cm)	0.015	0.007	-0.005	0.036	0.221	0.016	0.238	**0.018**	-0.060	0.485**
TGW	-0.014	-0.012	0.013	0.038	0.189	-0.014	-0.114	-0.003	**0.382**	0.465**

Residual effect =0.01074

Table.5 Estimation of genotypic path correlation direct (Bold) and indirect effect of the measured variable attributes on number of seeds yield per plant (g) with variation of wheat genotypes

Traits	PH (cm)	DTH	DTA	DTM	TNPP	NSPS	GNPS	SL (cm)	TGW	R with GYPP(g)
PH (cm)	**0.033**	0.007	-0.010	0.003	0.152	0.042	0.229	0.009	-0.174	0.289*
DTH	0.020	**0.011**	-0.016	-0.009	0.045	0.041	0.264	0.006	-0.218	0.144
DTA	0.019	0.011	**-0.017**	-0.019	0.000	0.035	0.225	0.004	-0.228	0.029
DTM	0.001	-0.001	0.003	**0.103**	0.359	0.009	0.114	0.007	0.168	0.763**
TNPP	0.009	0.001	0.000	0.070	**0.526**	0.026	0.114	0.007	0.138	0.891**
NSPS	0.026	0.009	-0.011	0.017	0.257	**0.053**	0.277	0.009	-0.184	0.451**
GNPS	0.019	0.008	-0.010	0.029	0.149	0.036	**0.402**	0.011	-0.112	0.531**
SL (cm)	0.016	0.004	-0.004	0.042	0.215	0.028	0.238	**0.018**	-0.063	0.493**
TGW	-0.014	-0.006	0.010	0.044	0.183	-0.025	-0.114	-0.003	**0.396**	0.471**

Table.6 Grouping of thirty genotypes of wheat into four clusters

Clusters	No of genotypes	Genotype name
I	8	WH-711, HD-2009, PBW-343, PBW-373,Raj-3077, GM-173, WH-147, Lok-1
II	5	PBW-226, SFW-75, UP-2382, Raj-1482, HW-2004
III	5	HI-8498, Raj-3765, HD-2687, UP-262, PBW-154
IV	12	GW-322, GW366, HD-2189, HD-2733, HD-2851, HD-2894, HD-2967, HD-3043, HD-3086, HD-4672, H-1-1544, HD-2329.

Table.7 Inter and Intra Cluster distance (D^2) among five clusters in wheat

Clusters	I	II	III	IV
I	**1.578**			
II	2.354	**1.492**		
III	5.910	4.290	**1.198**	
IV	4.745	3.581	4.725	**1.828**

It can be concluded that the present study revealed that many traits have adequate genetic variability for the different agronomic traits genotypes studied and showed effectiveness for further breeding program. Inferior genetic advance restrictions the greater scope of improvement but higher GCV, PCV and higher heritability provides good chance for its further improvement. The results found from present research indicated that great amount of genetic variability were between wheat genotypes that could be used for development of new improved wheat varieties.

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