



Study of variability, correlation, path and diversity analysis in wheat (*Triticum aestivum* L.)

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Abstract

The wide range of different characters and comparison of mean of germplasm lines using least significant differences indicated existence of very high degree of variability for all the characters in the germplasm collection evaluated. The genetic variability present for the trait in the plant height, tillers/plant, biological yield, grain filling duration, spikelets per ear, grain yield per plant, grain weight/ear and harvest index showing high estimates of PCV. The highest heritability was for plant height, grain weight per ear, spikelets per spike, days to flowering, grain filling duration, biological yield, tillers/plant, grain yield per plant. Grain yield per plant showed very strong positive association with biological yield per plant and harvest index. Existence of significant positive associations among yield and important yield components suggested that selection would be highly effective and efficient in improving these traits due to possibility of correlated response. Path analysis identified biological yield per plant followed by, harvest index, grain filling duration and days to flowering, as major direct contributor towards expression of grain yield per plant. The character identified above as important direct and indirect yield components merit due to consideration in formulating effective selection strategy for developing high yielding varieties in wheat. The highest intra cluster distance was observed within cluster-III (HD-2967 and PBW-730) indicate that genotype in this cluster was genetically more divergent.

Keywords: Wheat, Variability, Correlation, Path analysis, Diversity

Introduction

One-fifth calories from hexaploid wheat is provided to the globe [Sehgal, *et al.*, 2015] ^[17]. The global number of persons can almost be more than nine billion till 2050. [United Nations, 2015] ^[26], causing the need of food by 60% in the coming years. This crop is extremely essential than the rest of the crops for the survival of humans, because 20% dietary calories as well as proteins are obtained by males, females and children in the form of golden crop [FAO, 2018] ^[5].

Grain yield is a complex quantitative parameter which is more affected by the environment and less by the genotype and is also contributed by lots of factors affecting directly and indirectly. Interaction between genotype and environment creates fluctuation in the sustainable production of hexaploid wheat which has been a considerable demand of rising food and herbivores. To complete this gap between production and the speed of utilization, plant breeding needs the breeders who can seed the germplasm for the choice, improvement and development of stable and high yield cultivars [Zameer, *et al.*, 2015] ^[27].

Correlation is a statistical technique that can show where and how strong pairs of variables are related to one another. Among useful breeding characteristics, character association is applied to determine the extent of correlation of certain yield contributing traits with yield (Ali *et al.*, 2008) ^[1]. The relationship between morphological characteristics is of very much importance in selecting appropriate selection criteria. The association between yield traits could be better understood with the assistance of correlation study.

Heritability is known as one of the most genetic analysis, because it notifies about the structure of a population. Its most vital function is that it tells that how much percentage of the attributes transfer from parents to the children or offspring in the form of genes which also assist a plant breeder in foreseeing about the gene interaction in upcoming generations. The highest transmissibility of any trait is estimated from its highest heritability to the progeny [Subhani, *et al.*, 2013] ^[6]. Heritability is found in three ranges like low, moderate and high with the ranges of 1-30%, 31-60% and 61-100%. These amounts of heritability estimates are caused by the interaction between genes and environment. When the contribution of an environment for the expression of a character is always greater than that of genes, low heritability expresses itself. High heritability come into existence when genes performs better than environmental conditions, whereas if both genotypes and environment equally contribute to a trait, moderate heritability is produced. The value of heritability must always be high or moderate which are regarded more effective in selection process. Genetic distance is very vital for genetic analysis in the field of breeding as it functions as auxiliary equipment and a strong connection between conservation and the utilization of present genetic resources [Mohammadi, 2003] ^[16]. Therefore, this investigation was undertaken to find out the genotypes having good estimates of variability, correlation, path analysis and genetic diversity for yield and yield attributes so that a better selection can be made for the development of new cultivars with desirable attributes.

Material and Methods

Fifty eight wheat genotypes were grown during rabi season 2022-2023 at the research Farm of Department of Genetics and Plant Breeding, R.M. P. (PG) College, Gurukul Narsan, Haridwar, Uttarakhand, India. The 58 genotypes of wheat were sown in a randomized block design (RBD) with three replications at the research farm. Each genotype was grown in two rows per replication of 3 meter length and row to row and plant to plant spacing was kept 30 and 10cm, respectively. The variability, correlation, path coefficient and genetic diversity

were calculated as per the standard statistical procedures.

Result and Discussion

Analysis of variance

The results of analysis of variance for various characters are presented in Table 1. The mean squares due to treatment for all the traits were highly significant, thereby suggesting the presence of considerable amount of variability among the 58 wheat genotypes with respect to the traits studied under present investigation.

Table 1: Analysis of variance for eleven characters in wheat (*Triticum aestivum* L.)

Characters												
Source of variation	d.f	1	2	3	4	5	6	7	8	9	10	11
Replication	2	1.21	0.78	0.24	1.93	0.55	0.36	8.25	4.01	0.00	0.18	0.00
Treatment	57	7.73**	264.92**	2.30**	14.44**	10.47**	4.34**	20.51**	6.35**	0.44**	2.42	0.11**
Error	114	0.66	1.21	0.09	0.58	0.85	0.37	1.85	1.11	0.00	0.32	0.00

Mean, Range, PCV

The estimates of mean, range, phenotypic coefficient of variation, heritability and expected genetic advance for 11 traits of 58 wheat genotypes are presented in Table 2. The estimates of means showed wide range of values for the 58 genotypes of wheat for all the characters. The growth response of all the traits of wheat cultivars to varying dates of sowing was distinct at various growth stages. The mean values suggested that normal sowing resulted into performance of the traits, such as in days to flowering (87.97), plant height (82.08), tillers/plant (9.20), days to maturity (137.62), grain filling duration (49.65), spikelets per spike (17.74), biological yield (28.17), grain yield per plant (14.70), 100 grain weight (3.37), grain weight per ear (1.92) and harvest index (52.22).

Variability

Genetic variability is the tendency of individuals in a population to vary from one another. Variability is different from genetic variation, which is the actual amount of phenotypic variation seen in a particular population. The variability of a trait describes how much that trait tends to vary in response to changes in the genetics of a population. Genetic variability in a population is very important, because without variability, it becomes difficult for a population to adapt to environmental changes, creating a static population. Variability is an important factor in [evolution](#) since it provides the potential for genetic variation, the raw material for [natural selection](#).

The estimates of phenotypic coefficient of variation were high for many traits such as days to flowering (3.24), plant height (12.29), tillers /plant (12.84), days to maturity (1.82), grain filling duration (8.30), spikelets per ear (10.17), biological yield (12.35), grain yield per plant (15.44), 100 grain weight (9.73), grain weight per ear (17.55) and harvest index (10.80). In the present study, a wide range of variation was displayed by different traits. The success of selection depends on the extent of genetic variability present for the trait in the plant height, tillers/plant, biological yield, grain filling duration,

spikelets per ear, grain yield per plant, grain weight/ear and harvest index showing high estimates of PCV. Suggested that adequate variability is present for these traits and hence there is a scope for employing suitable breeding programs for brining about improvement in these traits.

A large number of studies have been conducted, which gives information about the degree of variability present in wheat for various traits. Chaudhary *et al.* (1977) ^[4] observed the high PCV for harvest index in wheat. Bhatt (1976) ^[2] also observed large variability along with high heritability and genetic advance for harvest index in several wheat crosses.

Heritability and expected genetic advance

High PCV or GCV did not provide a clear picture of the extent of genetic gain to be achieved from selection for the phenotypic traits unless the heritable fraction of the trait was known (Burton 1952) ^[3]. If the value of heritability in broad sense is high, it indicates that the character is least influenced by the environmental effects, and there exists sufficient genetic variability for that trait leading to the proposition that selection would be effective for improvement of such character. Broad sense heritability is based on total genetic variance which includes both fixable (additive) and non-fixable (dominance and epistatic) variances. If broad sense heritability is low, it reveals that the character is highly influenced by environmental effects and genetic improvement through selection will be difficult due to masking effects of the environment on the genotypic effects.

Data in Table 2 Revealed that heritability were highest for plant height (97.0), grain weight per ear (94.0), spikelets per spike (87.0), days to flowering (86.0), grain filling duration (86.0) biological yield (83.0), tillers/plant (82.0), grain yield per plant (72.00) and lowest value for heritability were found for the trait days to maturity (69.0), harvest index (66.0), 100 grain weight (57.0) and improvement in the mean genotypic value of selected plant progeny over the parental (base) population is known as genetic advance. It is the measure of genetic gain under selection. The genetic advance from the mixtures of pure

lines or clones should be calculated using broad sense heritability estimates and from segregating population using narrow sense heritability.

Khan (1990) ^[9] reported high heritability along with high genetic advance for yield and its components, indicating the importance of additive genetic variation. High heritability estimates indicate that large portion of the total variance was attributed to the genotypic variance and that individual of the population differ for this trait. Wheat breeders considered heritability (h^2) estimates along with the genetic advance values because h^2 alone is not good indicator of the amount of usable genetic variability (Masood *et al.*, 1986) ^[14].

Data in table 2 indicate that estimates of expected genetic advance (EGA) for different traits such as days to flowering (5.06), plant height (20.35), tillers/plant (2.00), days to maturity (3.60), grain filling duration (7.10), spikelets per spike (3.26), biological yield (6.02), grain yield per plant (3.41), 100 grain weight (0.39), grain weight per ear (0.66) and harvest index (7.25).

In the present study the value of EGA was high for five traits days to flowering, plant height, grain filling duration, biological yield and harvest index. High value of genetic advance for these traits, such as days to flowering, plant height, grain filling duration, biological yield and harvest index shows that these characters are governed by additive gene action and selection will be rewarding for improvement of such traits. If the value of genetic advance is low, it indicates that the character is likely to be governed by non-additive gene action and the heterosis breeding may be useful for such traits.

From Table 2 it can be seen that the high estimates of heritability and EGA were observed for the traits: plant height, days to flowering, grain filling duration and biological yield which suggested that selection may be effective for these traits. In contrast high estimates of heritability coupled with low expected genetic advance were observed for the traits: effective tillers, spikelets per spike and grain weight per ear indicating non-additive gene action.

Table 2: Estimates of mean, range, phenotypic coefficient of variation, heritability and genetic advance for 11 traits in bread wheat (*Triticum aestivum* L.)

S. No.	Traits	Parameters				
		Mean	Range	PCV	H ²	EGA
1	Days to flowering	87.97	81.87 -93.33	3.24	86.0	5.06
2	Plant height	82.08	0.67 – 103.07	12.29	97.0	20.35
3	Tillers per plant	9.20	5.20 – 9.63	12.84	82.0	2.00
4	Days to maturity	137.62	134.03 – 143.17	1.82	69.0	3.60
5	Grain filling duration	49.65	41.60 – 59.97	8.30	86.0	7.10
6	Spikelets per spike	17.74	13.07 – 21.07	10.17	87.0	3.26
7	Biological yield	28.17	22.77 – 36.19	12.35	83.0	6.02
8	Grain yield per plant	14.70	10.42 – 17.62	15.44	72.0	3.41
9	100 grain weight	3.37	2.89 – 4.01	9.73	57.0	0.39
10	Grain weight per ear	1.92	1.31 – 2.99	17.55	94.0	0.66
11	Harvest index	52.22	40.85 – 58.96	10.80	66.0	7.25

Character association

Correlation between different traits is generally due to the presence of linked genes and epistatic effect of different genes. Environment plays an important role in correlation. In some cases, environment affects both the traits simultaneously in same direction or some time in different directions. Genetic and environmental causes of correlation combine together and give phenotypic correlation. The dual nature of phenotypic correlation makes it clear that the magnitude of genetic correlation cannot be determined from phenotypic correlation. The correlation coefficients among 11 traits are presented in Table 3. The traits which showed significant positive correlations were: days to flowering with plant height (0.47**), tillers per plant (0.33*); plant height with tillers per plant (0.59**), days to maturity (0.58**); days to maturity with grain filling duration (0.67**); biological yield with grain yield per plant (0.68**); grains yield per plant with harvest index (0.61**).

The significant negative correlations of traits were: plant height with 100 grain weight (g) (-0.39*); tillers/plant with 100 grain

weight (-0.37**), days to maturity with 100 grain weight (g) (-0.30*) and grain filling duration with 100 grain weight (-0.33*).

Similar pattern of correlation was also observed by Singh *et al.* (1998) ^[24], Sharma (1998) ^[19], Singh and Singh (1999) ^[21], Khumkar *et al.* (2001) ^[10], Sultan *et al.* (2002) ^[25] and Sharma *et al.* (2000) ^[20]. The traits exhibiting significant positive association with grain yield suggest that such traits may be important for improving the grain yield, and indirect selection for these traits would be effective for increasing grain yield of the wheat genotypes under study.

These results suggested that selection for one trait would result into negative/adverse correlated response in other trait, which had negative correlation.

Sharma (2000) ^[20] reported that under normal environment, grain yield was positively correlated with plant height, biological yield and grain number whereas under terminal heat stress conditions grain yield was correlated with biological yield, harvest index, grain number and 100-grain weight.

Table 3: Estimates of phenotypic correlation coefficients for eleven traits in wheat (*Triticum aestivum* L.)

S. No.	Characters	1	2	3	4	5	6	7	8	9	10	11
1	Days to flowering	1.00	0.47**	0.33*	0.52**	-0.26	-0.18	0.02	-0.04	-0.01	-0.25	-0.11
2	Plant height (cm)			0.59**	0.58**	0.24	-0.05	0.23	0.27	-0.39**	0.00	0.10
3	Tillers/plant				0.14	-0.13	0.02	0.25	0.27	-0.37**	0.08	0.08
4	Days to maturity					0.67**	-0.16	-0.02	0.00	-0.30*	-0.07	0.02
5	Grain filling duration						-0.02	-0.05	0.05	-0.33*	0.13	0.13
6	Spikelets / spike							-0.23	-0.21	0.08	0.24	0.03
7	Biological yield (g)								0.68**	-0.21	-0.08	-0.15
8	Grain yield / plant (g)									-0.06	0.12	0.61**
9	100 grain weight (g)										0.09	0.15
10	Grain weight / ear(g)											0.25
11	Harvest index%											1.00

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. The result of path analysis is presented in Table 4. The phenotypic path analysis is described in view of them to making visual or direct selection. However, the direct and indirect effects were not consistent in all environments. For description, magnitude of different values was taken into consideration while describing results.

The estimates of direct and indirect effects of different character on grain yield per plant are presented in table 4. The

path coefficient analysis revealed that yield contributing traits like Days to anthesis (0.11) produced positive and non-significant. direct effect on grain yield and negative indirect effect was noted through grain filling duration (-0.18). Grain filling duration showed direct effect on grain yield and negative indirect effect via rate of grain filling (-0.26). Biological yield (0.46) showed maximum positive direct effect on grain yield, maximum positive indirect effect was produced through rate of grain filling (0.34).The grain filling duration (0.46) produced positive direct effect on grain yield and positive indirect effect was noted through biological yield (0.34) and harvest index (0.40) and also exhibited positive direct effect on grain yield, while positive indirect effect on grain yield was noted through rate of grain filling (0.22). Similar result also reported by Shalini *et al.* (2000) ^[18], Singh and Singh (2010) ^[23], Mahla *et al.* (2003) ^[13], and Kumar *et al.* (2016) ^[11].

Table 4: Estimate phenotypic direct and indirect effect on grain yield for eleven characters in wheat (*Triticum aestivum* L.)

Characters	1	2	3	4	5	6	7	8	9	10	Correlation with grain yield
Days to flowering	0.11	-0.00	0.00	0.00	-0.18	-0.00	0.08	0.00	0.00	-0.01	0.12
Plant height(cm)	0.00	-0.00	0.00	0.00	-0.04	-0.00	0.18	-0.00	0.00	-0.11	0.11
Tillers per plant	0.00	-0.00	-0.00	0.00	-0.04	-0.00	0.09	-0.00	0.00	-0.04	0.08
Days to maturity	-0.00	0.00	0.000	-0.00	0.16	0.00	-0.11	0.00	-0.00	-0.03	-0.13
Grain filling duration	-0.00	0.00	0.00	-0.00	0.22	0.00	-0.13	0.00	-0.00	0.02	-0.16
Spikelets per spike	0.00	-0.00	-0.00	0.00	-0.03	-0.01	-0.02	-0.00	0.00	-0.09	-0.19
Biological yield (g)	0.00	-0.00	0.00	0.00	-0.06	0.00	0.46	0.00	-0.00	-0.01	0.74**
100 Grain weight (g)	0.00	-0.00	0.00	0.00	-0.00	-0.00	-0.05	-0.01	0.00	-0.00	-0.10
grain weight per ear (g)	0.00	0.00	-0.00	0.00	-0.05	-0.00	-0.04	-0.00	0.01	-0.01	-0.09
Harvest index	0.00	0.00	0.00	0.00	0.01	0.00	-0.01	0.00	0.00	0.40	0.63**

Genetic divergence

D2 analysis was carried out as per Mahalanobis as described (Rao, 1952) ^[15] for fifty eight genotypes for respect to sixteen characters presented in table 5. to 7. On the basis of D2 values all 58 genotypes were grouped in 4 clusters in normal sowing condition. Twenty eight genotypes were grouped in cluster I, Twenty two in cluster II, two in cluster III and six in cluster IV Table 5. Intra cluster distance ranged from 2.768 to 3.158. The

cluster II had maximum intra cluster distance (3.158) followed by cluster IV (3.158), I (2.883) and III (2.768). The inter cluster distance ranged from 3.001 to 4.955. The maximum inter cluster distance was observed between cluster II and III (4.955) and II and IV (4.955), followed by the distance between cluster I and IV (4.832), III and IV (4.105), I and II (3.059). The lowest inter cluster distance was found between cluster I and III (3.001) Table 6.

Table 5: Distribution of Fifty eight genotypes of wheat in different cluster

Clusters No.	No of Genotypes	Name of Genotypes
I	28	PBW-726, WP-705/17, K-31, WP-708/17, DBW-6602, DBW-945, WP-711/17, K-27, K-54, WP-702/17, HD-3123, HD-3086, BW-5572, PBW-725, SP-goal, WP-703/17, DW-17, PBW-703, HD-3091, HACS-3949, RAJ-4539, PBW-543, Cahu Canada, WP-710/17, WP-712/17, K-35, HI-1544, HI-1605,
II	22	HD-3128, Tall-3, VL-907, Jalwa, Mahycogal, PBW-154, DBW-730, CPAN-3061, PBW-343, WP-707/17, K-23, WP-709/17, K-34, PBW-166, PBW-703, HD-2733, ARAW-4498, K-26, K-33, PBW-292, Tall-2, HD-3194,
III	2	HD-2967, PBW-730
IV	6	WP-702/17, Sarwottam, WH-1105, HD-8189, DBW-147, K-55,

Table 6: Intra – cluster (diagonal) and inter cluster genotypic divergence values in wheat

Cluster No	I	II	III	IV
I	2.883			
II	3.259	3.158		
III	3.001	4.955	2.768	
IV	4.832	4.955	4.105	3.131

The cluster mean values for eleven different characters in

wheat is presented in table 7. The lowest and highest cluster means respectively for different traits were observed i.e. for days to flowering (II and III), plant height (II and III), tillers per plant (II and IV), days to maturity (III and I), grain filling duration (III and II), spikelets per spike (II and III), spikelets per spike (II and III), biological yield (II and IV), grain yield (III and IV), 100 grain weight (II and I), grain weight per ear (II and III) and harvest index (III and IV).

Table 7: Mean values of eleven characters in four cluster constructed from fifty eight genotypes of wheat

Cluster no	Days to flowering	Plant height	Tillers per plant	Days to maturity	Grain filling duration	Spikelets/spike	Biological yield	Grain yield	100 grain weight	Grain weight/ear	Harvest index
I	87.15	82.43	8.73	139.98	52.83	18.28	27.39	13.77	3.58	1.97	50.34
II	85.67	76.33	8.61	139.70	54.03	16.65	26.59	14.69	3.19	1.83	55.20
III	88.94	96.92	9.16	137.08	48.14	18.75	29.37	13.45	3.52	2.23	46.07
IV	88.78	84.39	9.41	137.14	48.35	17.84	30.01	16.04	3.42	2.04	53.55

The perusal of reveals that cluster III contained genotypes depicting significantly higher mean performance for four traits as compared to general means over all the 58 genotypes. In that context, cluster III (HD-2967 & PBW-730) showed higher mean performance for days to flowering, plant height, spikelets per spike and grain weight per ear. Cluster I showed higher means for days to maturity and 100 grain weight. Similarly, cluster II depicting higher means for grain filling duration and cluster IV showed higher means for tillers/plant, biological yield and harvest index.

Mahalanobis (1936) [12] have suggested D2 analysis taken place in plant breeding. D2 analysis is a powerful tool for determining genetic divergence within a population. In past numerous studies on genetic divergence had been carried out by several workers in wheat as estimated by Joshi and Singh (1979) [8], and Gashaw *et al.*, (2007) [7]. Fifty eight genotypes of wheat in the present study were grouped in 4 clusters.

A perusal of table revealed that the genotype of the same cluster has little divergence of each cluster with respect aggregate effects of the character studied. The hybridization between the genotypes of the same cluster, thus may not provide good segregants, the crosses may attempted clusters reported by the large inter cluster distance. This can give desirable transgressive segregants. The highest inter cluster distance was noted between cluster II and cluster III. The greater genetic distance between the clusters, showed higher genetic divergence among genotypes and this help in crop improvement.

Different methods for selection of parents for a hybridization programme have been suggested in the part of several crops. Usually, it is suggested that parents be selected on the basis of D2 analysis of Mahalanobis (1936) [12]. This is a useful tool in quantifying the degree of divergence between populations and also aids in the choice of genetically diverse parents to obtain better recombinants in the segregating generations. In the present study, genetic divergence among 58 genotypes was worked out,

The presence of significant genetic variability among genotypes suggests an opportunity for improvement of grain yield through hybridization of genotypes from clusters III and subsequent selection from the segregating generations.

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