

## Genetic Diversity and Path Coefficient in *Triticum* System under Temperate Conditions

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### Abstract

Genetic diversity, clustering pattern and path analysis were studied in 45 lines of wheat for yield and yield contributing traits. The magnitude of PCV and GCV for all the traits under study were low to moderate, which indicated that the traits were less influenced by environment and are genetically controlled. Plant height, number of grains/spike and grain yield/plot showed high heritability and genetic advance. Grain yield was found to be positively correlated with plant height, peduncle length, number of spikelets/spike, number of grains/spike, grain yield/spike and grain yield/plot. Path coefficient analysis revealed that grain yield/spike had maximum positive direct effect on grain yield followed by awn length, number of grains/spike and peduncle length, indicating true and perfect relationship. The high positive correlation between grain yield and peduncle length, number of grains/spike, grain yield/spike was obtained mainly through indirect effect via grain yield/spike, awn length. Clustering pattern divides the germplasm into three different clusters. On mean basis, cluster II is characterized by for having prominent traits like high grain yield/plot, number of spikelets/spike, number of grains/spike, grain yield/spike. Such clustering helps in selecting desirable lines and traits for crossing program. PCV revealed that informative components accounted for 79.40% variance. Most of the important traits with higher weight age were grain yield/spike, 1,000-grain weight, awn length, plant height, peduncle length and spike length were in PCI.

**Key words :** Wheat, *Triticum*, Variability, Heritability, Path coefficient.

For any crop improvement program the selection of parents for hybridization is largely based on diversity, adaptation and high yield. The base material which includes germplasm, landraces, varieties, lines, genotypes and wild relatives always play great role by providing variability for different traits under consideration for improvement and the studies related to genetic variability, heritability and association between grain yield and its component characters may be helpful to exercise an efficient selection program. Enhancing the genetic potential and productivity of wheat continue to be an important objective in varietal improvement program. Mahantashivayogayya et al. (1) observed the highest GCV and PCV for spikelets/spike, grains/spike, productive tillers/plant, 1,000-seed weight and yield/plant. Ahmad et al. (2) reported differences among the genotypes in terms of number of plant height, number of spikelets per spike grain yield and 100-kernel weight were significant. Sahu et al. (3) reported that genotypic correlation coefficients

were higher than the phenotypic correlation coefficients and number of spikes per plant and 1,000-grain weight was positively and significantly correlated with grain yield. Therefore, the present study was planned to analyze the nature and extent of genetic variability and diversity present in the wheat material for grain yield and other morphological traits when tested under temperate conditions.

### Methods

Forty five diverse lines received from national nurseries which consists of yield component screening nursery (YCSN), short duration nursery (SDN), NBPGR material and winter wheat were evaluated in randomized block design with three replications at Plant Breeding and Genetics Farm of Regional Research Station, SKUAST-K, Wadura, Sopore, Kashmir (34°17' N and 74°33' E at an altitude of 1,524 m amsl) under rainfed conditions. Each line was accom-

**Table 1.** Estimates of different genetic parameters for different traits in wheat. PH = Plant height, PDL = Peduncle length (cm), SPKL = Spike length (cm), SKT/Pnc = Number of spikelets/ spike, GRN/Pnc = Number of grains/spike, GY/Spk = Grain yield/ spike (g), SD = 1000 seed weight (g), AL = Awn length (cm), GY = Grain yield (g)/plot.

Traits/ Parameters	PH	PDL	SPKL	SKT/Pnc	GRN/Pnc	GY/Spk	SD	AL	GY
Mean	86.06	14.55	6.81	15.0	29.42	1.29	4.43	6.47	219.64
Range	70.3-112.0	5.3-25.8	4.2-12.5	11-18.6	17.3-48	0.38-2.0	3.3-6.3	4.9-11.3	98.3-473.3
PCV (%)	11.40	28.74	23.10	14.29	27.94	30.39	14.10	22.24	43.42
GCV (%)	9.66	26.07	20.03	10.08	23.46	26.14	13.79	16.61	38.13
CV (%)	6.06	12.08	11.49	10.12	15.18	15.51	2.90	14.79	20.76
h <sup>2</sup> (%)	71.7	82.3	75.2	49.8	70.5	74.0	95.8	55.8	77.1
GA	14.50	7.09	2.44	2.19	11.93	0.60	1.23	1.65	151.54
GA as % of mean	16.85	48.74	35.80	14.65	40.57	46.31	27.81	25.56	68.99

modated in three rows of 3.0 m length with line-line spacing of 30 cm. Recommended package of practices were followed to raise a good crop.

Five randomly selected competitive plants in each plot were selected for data on the following traits viz., plant height (PH), peduncle length (PDL) (cm), spike length (SPKL) (cm), number of spikelets/spike (SKT/Pnc), number of grains/spike (GRN/Pnc), grain yield/spike (GY/Spk) (g), 1,000-grain weight (SD) (g), awn length (AL) (cm), grain yield (g)/plot (GY).

Average values were statistically analyzed for variance, genotypic and phenotypic coefficients of variation, heritability, genetic advance and correlation coefficients following standard procedure described by Panse and Sukhatme (4) and Burton and De Vane (5). Path analysis was done as described by Dewey and Lu (6) to assess the associations, direct and indirect influence of various components on grain yield. Mahalanobis D<sup>2</sup> statistics was used to assess genetic diversity. Genotypes were grouped

on the basis of minimum generalized distance using Tocher's method as described by Rao (7).

## Results and Discussion

Estimates of variability, heritability and genetic advance are presented in Table 1. A close resemblance between the corresponding estimates of PCV and GCV suggested little role of environment in the expression of different traits. Grain yield/plot (43.42 and 38.13 g) showed highest PCV and GCV followed by grain yield/spike (30.39 and 26.14 g), peduncle length (28.74 and 26.07 cm), number of grains/spike (27.94 and 23.46) and spike length (23.10 and 20.03 cm). Plant height, number of spikelets/spike and 1000 grain weight shows low PCV and GCV values. Heritability estimates varied from 49.80% for number of spikelets/spike to 95.80% for 1,000-grain weight. High to moderately high variability for GCV and PCV coupled with high estimates of heritability were observed for the

**Table 2.** Genotypic correlation matrix for grain yield and related traits. PH = Plant height, PDL = Peduncle length (cm), SPKL = Spike length (cm), SKT/Pnc = Number of spikelets/spike, GRN/Pnc = Number of grains/spike, GY/Spk = Grain yield/spike (g), SD = 1000 seed weight (g), AL = Awn length (cm), GY = Grain yield (g)/plot.

Characters	PH	PDL	SPKL	SKT/Pnc	GRN/Pnc	GY/Spk	SD	AL	GY
PH	<b>1.00</b>								
PDL	0.571	<b>1.00</b>							
SPKL	0.156	0.264	<b>1.00</b>						
SKT/Pnc	0.123	0.129	0.172	<b>1.00</b>					
GRN/Pnc	0.081	0.192	0.197	0.836	<b>1.00</b>				
GY/Spk	0.394	0.415	0.382	0.630	0.796	<b>1.00</b>			
SD	0.384	0.370	0.591	-0.086	0.093	0.456	<b>1.00</b>		
AL	0.224	0.130	0.807	0.335	0.335	0.488	0.562	<b>1.00</b>	
GY	0.088	0.152	-0.061	0.061	0.204	0.272	-0.001	0.025	<b>1.00</b>

**Table 3.** Estimates of direct and indirect effects on grain yield and related traits. PH = Plant height, PDL = Peduncle length (cm), SPKL = Spike length (cm), SKT/Pnc = Number of spikelets/spike, GRN/Pnc = Number of grains/spike, GY/Spk = Grain yield/spike (g), SD = 1000 seed weight (g), AL = Awn length (cm), GY = Grain yield (g)/plot. R square = 0.191, Residual effect = 0.899.

Characters	PH	PDL	SPKL	SKT/Pnc	GRN/Pnc	GY/Spk	SD	AL
PH	<b>-0.053</b>	-0.030	-0.008	-0.006	-0.004	-0.021	-0.020	-0.012
PDL	0.086	<b>0.151</b>	0.040	0.019	0.029	0.062	0.056	0.019
SPKL	-0.041	-0.070	<b>-0.264</b>	-0.045	-0.052	-0.101	-0.156	-0.214
SKT/Pnc	-0.062	-0.064	-0.086	<b>-0.501</b>	-0.419	-0.315	0.043	-0.168
GRN/Pnc	0.012	0.029	0.030	0.130	<b>0.155</b>	0.124	0.014	0.052
GY/Spk	0.215	0.227	0.209	0.344	0.435	<b>0.546</b>	0.249	0.266
SD	-0.130	-0.126	-0.201	0.029	-0.031	-0.155	<b>-0.339</b>	-0.191
AL	0.061	0.035	0.219	0.091	0.091	0.132	0.153	<b>0.272</b>
GY	0.088	0.152	-0.061	0.061	0.204	0.272	-0.001	0.025

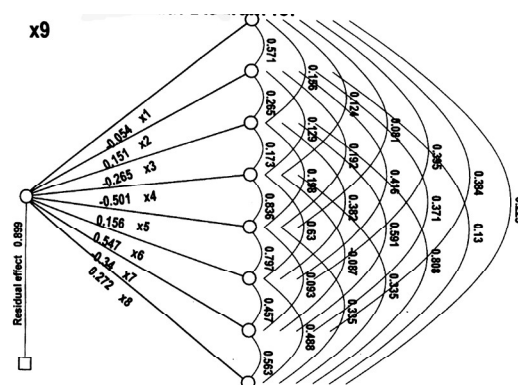
characters viz., peduncle length, spike length, grain yield/spike, number of grains/spike and grain yield/plot which indicate an advantage through selection. All the traits except, plant height and number of spikelets/panicle exhibited comparatively higher estimates of GCV, heritability and genetic advance as percent of mean which is indicative of predominance of additive gene action in expression of these traits therefore for these characters selection appears to be effective. The GA as percent mean was found to be highest for grain yield/plot (68.90) followed by peduncle length (48.74), grain yield/spike (46.31), number of grains/spike (40.57) and spike length (35.80). The results are in accordance with earlier findings of Kumar et al. (8). High heritability estimates coupled with high GA percent of mean were observed for peduncle length, spike length, number of grains/spike, grain yield/spike, 1,000 grain weight, awn length and grain yield/plot. High heritability of these characters may be due to additive gene effects ; hence these characters are likely to respond to direct selection.

The grain yield/plot showed maximum magnitude of positive correlation (Table 2) with grain yield/spike

(0.272) followed by number of grains/spike (0.204), peduncle length (0.152), plant height (0.088) and number of spikelets/spike (0.061). Such types of associations are expected to improve grain yield. Most of the traits studied showed positive correlation with each other except number of spikelets/spike with 1,000 grain weight (-0.086). Negative correlation of grain yield/plot was observed for the character, spike length (-0.061) and 1,000-grain weight (-0.001). The highest positive correlation was observed between number of spikelets/spike and number of grains /spike (0.836) followed by spike length and awn length (0.807), number of grains/spike and grain yield/spike (0.796) and number of spikelets/spike and grain yield/spike

**Table 4.** Inter and Intra cluster (underlined) distances. PH = Plant height, PDL = Peduncle length (cm), SPKL = Spike length (cm), SKT/Pnc = Number of spikelets/spike, GRN/Pnc = Number of grains/spike, GY/Spk = Grain yield/spike (g), SD = 1000 seed weight (g), AL = Awn length (cm), GY = Grain yield (g)/plot.

	Cluster I	Cluster II	Cluster III
Cluster I	<b>79.13</b>	186.35	408.64
Cluster II		<b>0.00</b>	859.77
Cluster III			<b>0.00</b>



**Figure 1.** Genotypic path diagram for grain yield (X9) and related traits. X9 = Grain yield (g)/plot, X1 = Plant height, X2 = Peduncle length (cm), X3 = Spike length (cm), X4 = Number of spikelets/spike, X5 = Number of grains/spike, X6 = Grain yield/spike (g), X7 = 1000 grain weight (g), X8 = Awn length (cm).

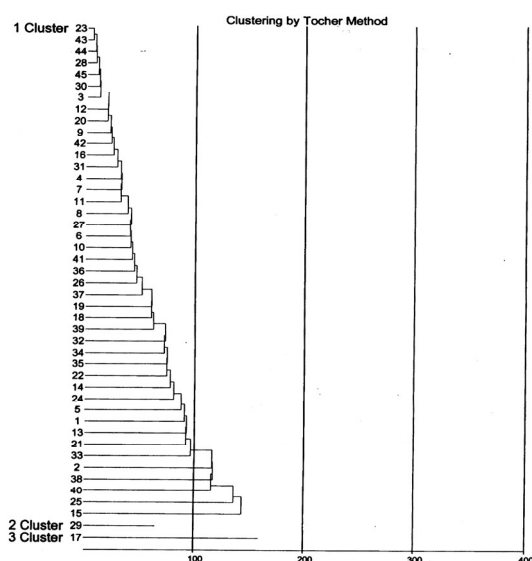


Figure 2. Clustering pattern of lines used in the study.

(0.630). Similar results were presented by Singh et al. (9).

Positive correlation of a particular character with yield does not necessarily mean a direct, positive effect of that trait on yield. Path coefficient analysis measures the direct and indirect influence of a variable on the dependent trait and is an effective device for selecting meritorious characters to be used in selection programme to get maximum yield. Therefore, path coefficient analysis which analyzes cause and effect relationships and partitions the correlation into direct and indirect effects were carried out. Path analysis (Table 3) showed that maximum amount of positive direct effect on grain yield was exerted by grain yield/spike (0.272) followed by number of grains/spike (0.204), peduncle length (0.152), plant height (0.088), number of spikelets/spike (0.061) and awn length

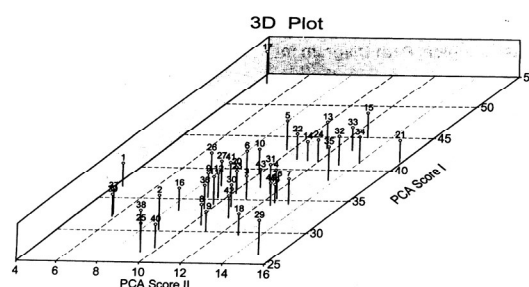


Figure 3. 3D Principal component scatter plot.

(0.025) indicating the importance of these traits in determining the grain yield. Therefore, these traits should be given preference while practicing selection which aimed at the improvement of yield. Number of grains/spike had an influence on grain yield through positive indirect effect of grain yield/spike (0.435), whereas number of spikelets/spike through number of grains/spike (0.130) and grain yield/spike (0.344), grain yield/spike via number of grains/spike (0.124) and awn length (0.132), plant height and peduncle length through grain yield/spike (0.215 and 0.227) respectively (Fig. 1). On the other hand, direct effects of number of spikelets/spike, 1000 grain weight, spike length, and plant height were negative. Greater role of grain yield/spike, number of grains/spike, peduncle length and awn length was observed in determining the grain yield, as the magnitude of their direct effects were very high. The results are in agreement with earlier findings of Singh et al. (10), Lad et al. (11). Kumar et al. (12) reported that grain yield had positive and significant correlations with days taken to maturity, test weight and number of spikes/meter row length in PBW 343, WH 711, Raj 3765 and Sonak. This is due to the direct and indirect effects of the yield components on each other. Nayem and Baig

Table 5. Means of different yield affecting traits in different clusters. PH = Plant height, PDL = Peduncle length (cm), SPKL = Spike length (cm), SKT/Pnc = Number of spikelets/spike, GRN/Pnc = Number of grains/spike, GY/Spk = Grain yield/spike (g), SD = 1000 seed weight (g), AL = Awn length (cm), GY = Grain yield (g)/plot.

Traits	PH	PDL	SPKL	SKT/Pnc	GRN/Pnc	GY/Spk	SD	AL	GY
Cluster I	86.18	14.61	6.69	14.94	29.29	1.30	4.41	6.36	215.85
Cluster II	84.13	13.00	6.70	17.60	41.67	1.38	3.38	6.70	473.33
Cluster III	82.73	14.00	12.50	15.00	23.00	1.26	6.40	11.37	129.00
Contribution to diversity (%)	4.34	12.93	5.15	0.51	5.66	4.14	56.16	2.32	8.70

**Table 6.** Canonical root, cumulative variance of the first three principal components (PCs) and factor loading between PCs and traits studied.

	PC1	PC2	PC3
Root	1257	275	194
Percent of variance	57.79	12.64	8.95
Cumulative variance	57.79	70.44	79.40
Traits	Factor loading		
PH	0.135	0.385	0.141
PDL	0.180	0.615	0.313
SPKL	0.201	-0.086	-0.371
SKT/Pnc	-0.063	0.090	-0.358
GRN/Pnc	-0.045	0.228	-0.591
GY/Spk	0.185	0.272	0.127
SD	0.920	-0.171	-0.029
AL	0.135	0.058	-0.441
GY	-0.055	0.545	-0.231

(13) emphasized the importance of number of grains/ear, test weight and number of tillers/m during selection to increase the yield in *T. durum*.

Different clearly defined clusters were obtained from clustering method which was based on morphological traits. The lines were grouped into three clusters based on distance ranges for the tree shown in Fig. 2. Cluster I includes 43 lines and cluster II and III had 1 line each. The maximum inter cluster distance observed was 859.77 (Table 4) between cluster II and III followed by cluster I and III (408.64), suggesting diversity between lines of these clusters. So crossing between lines belonging to these clusters may result into high heterosis. High inter cluster values also suggests that a good amount of genetic diversity in the material. The cluster I with intra cluster values of 79.13 suggests that this cluster is different from other two clusters (Table 4). Cluster means for different traits are presented in Table 5. The cluster II is characterized by prominent traits like higher number of spikelets/spike, high number of grains/spike, high grain yield/spike and high grain yield/plot. The prominent traits in cluster I were more plant height and peduncle length and in cluster III were more spike length, high 1,000-grain weight and more awn length. Such clustering helps in selecting desirable traits for crossing programme. Peduncle length, 1,000-grain weight and grain yield/plot have contributed more towards divergence, so the direct selection for these traits would be helpful.

Principal components analysis revealed that the first three most informative components accounted

for 79.40% variance (Table 6). Traits were determined on the basis of estimated factor loadings. Traits with higher weightings were grain yield/spike, 1,000-grain weight, awn length, plant height, peduncle length and spike length in PC1; plant height, peduncle length, number of grains/spike, grain yield/spike and grain yield/plot in PC2 and plant height, peduncle length and grain yield/spike in PC3. The scatter plot of PC scores of first two PC axes is presented in Fig. 3.0. The principal component analysis (PCV) in general confirmed the groupings obtained through cluster analysis. Two distinct line could be marked which falls in two different clusters (cluster II and III). Whereas, in cluster I, 43 lines were present, a pair of different lines could be prepared clearly. This shows that cluster appears to be homogeneous but heterogeneous within the cluster. The study helps in finding out the diversity available in the lines and selection of desirable types of traits which will be utilized during crossing program.

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