

# Genetic Variability Studies for Yield and Yield Attributing Traits of Wheat (*Triticum aestivum* L.)

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## ABSTRACT

Diversity analysis was carried out in 93 wheat genotypes including three checks with help of cluster analysis, path analysis, heritability in broad sense, genetic advance as per cent of mean, coefficient of variation and correlation coefficient.  $D^2$  statistics showed existence of 10 clusters which clearly indicated presence of considerable genetic divergence in the experimental material. In Path analysis, traits *viz.*, tillers per plant, spike length and grains per spike displayed positive and direct effect on yield per plot; indicating that selection of those traits can be practiced to improve yield. Grain yield per plot showed positive correlation with days to maturity, plant height, tillers per meter, tillers per plant, spike length and grain per spike. All traits show high heritability in broad sense. Genetic advance in percent of mean estimates were high in all traits except days to maturity and days to fifty percent heading; which recorded low and moderate estimates of genetic advance, respectively. The difference between PCV and GCV was less indicating less impact of environment in the expression of various yield contributing traits.

**Key words:** Wheat, Cluster analysis, Path coefficient, Coefficient of variation, Heritability and genetic advance as percent of mean

## Introduction

Wheat is one of the important cereal crop in world, and second most important crops in India. Wheat is cultivated in spring and winter in western countries depending on severity of winter; however in India it is raised in *Rabi* season. Wheat is staple food and fulfills the daily requirement of 20% of the total calories and protein of an individual around the world (Braun *et al.*, 2010). Wheat is consumed in form of: bread, chapatti, biscuits, pasta, and fermented food products. With increasing population, demand of wheat will be increasing in future, and thus this necessitates increase wheat production. As suggested by Grafius (1956) in his "Geometrical Concept" that yield can be increased by selection of yield attribut-

ing traits which are easily inherited than yield per se. The Geometrical concept can be applied in wheat to increase yield.

Existence of genetic variability in an experimental material is essential to any breeding program, as a diverse population assures high heterosis in hybridization program, and the chance of obtaining transgressive segregants increase. Studies on genetic diversity provide a medium to screen given population for presence of variation for different traits of the experimental material. In crop improvement program, varieties with desirable traits are selected from a population but selection process can become more effective when a population possess high genetic variability. If trait is non-heritable in such case selection of phenotypically superior plants will not

lead to any improvement. So, along with genetic variability high heritability of traits become prime factor, which impact the success of selection process. Genetic advance estimates the superiority of new population in respect to the base population from which it was derived. Genetic advance along with heritability estimates can be used to assess the genetic gain possible from a selection process. Path coefficient and correlation coefficient studies are applied to illustrate the genetic and phenotypic relationship between yield and yield attributing traits.

Understanding the importance of genetic variability in plant breeding an experiment was conducted by utilizing 93 wheat genotypes to explore genetic diversity with the help of  $D^2$  statistics; and estimate the direct and indirect effect of yield attributing traits on yield per plot, heritability, coefficient of variation, correlation coefficient, correlation, and genetic advance for nine yield traits of wheat.

## Materials and Methods

### Experimental material and Design

The experiment was conducted at Agricultural Research Farm, Institute of Agricultural Sciences, BHU, Varanasi, Uttar Pradesh. The experimental material constituted of 90 wheat genotypes and three checks (Table 1) were planted in three blocks, with checks replicated in each block in an Augmented Block Design in *Rabi* 2017-18.

### Data collection

Five plants were randomly selected from each of the 90 lines and three checks (from each blocks) and tagged to collect data in field as well as in laboratory. Data was collected on following traits: days to 50% heading, days to maturity, plant height, tillers per plant, spike length, number of tillers per plant, num-

**Table 1.** List of Genotypes used in the experiment with serial number

S. No	Name of Genotype	S. No	Name of Genotype	S. No	Name of Genotype
1.	DBW 17	31	MACS 4028(d)	61	FLW 22
2.	DBW 71	32	MP 3336	62	HI 8708 (d)
3.	DBW 88	33	MP 3382	63	KBRL 79-2
4.	DBW 93	34	MPO 1255(d)	64	KBRL 82-2
5.	DBW 107	35	NIAW 1994	65	PHSL 5
6.	DBW 110	36	NW 5054	66	PHSL 10
7.	DBW 168	37	PBW 681	67	PHSL 11
8.	DBW 173	38	PBW 723	68	AKAW 4899
9.	DBW 39	39	UAS 446(d)	69	DWAP 1530
10.	GW 451	40	WB 2	70	DWAP 1531
11.	GW 463	41	WH 147	71	DWAP 1541
12.	HD 2009	42	DDK 1048 (dic)	72	GW 2013-491
13.	HD 3043	43	DDK 1049 (dic)	73	GW 2014-544
14.	HD 3086	44	DDW 31(d)	74	GW 2014-547
15.	HD 3171	45	HS 597	75	HI 1609
16.	HD 4728(d)	46	HS 599	76	HI 1610
17.	HD 4730(d)	47	HUW 695	77	LBPY 2015-07
18.	HD 4758(d)	48	K 1314	78	NIAW 2844
19.	HI 1612	49	K 1315	79	DBW 129
20.	HI 8737(d)	50	MACS 3972(d)	80	DBW 172
21.	HI 8777(d)	51	MACS 4020(d)	81	DBW 187
22.	HPW 360	52	MACS 5041(dic)	82	GRU-2017-18/7
23.	HPW 368	53	PBW 719	83	KRL 350
24.	HPW 373	54	TL 3003 (T)	84	KRL 370
25.	K 0402	55	TL 3004 (T)	85	KRL 386
26.	K 0607	56	UAS 455 (d)	86	NIAW 3553
27.	K 1006	57	WB 5	87	NIAW 3584
28.	K 1317	58	DBW 150	88	DBW 166
29.	Lok 1	59	FLW 10	89	UASD DT-6
30.	MACS 3949(d)	60	FLW 16	90	Raj 4480
Check	HI 8713(d)	Check	HD 2967	Check	Sonalika

ber of grains per spike, thousand grain weights and grain yield per plot. Package of practice was followed precisely to ensure a healthy crop stand.

### Statistical analysis

Analysis of variance of Augmented Block Design was done according to Federer, (1956). The analysis of variance and covariance was estimated by Panse and Sukhatme (1967). Correlation coefficient analysis was done by using formulae developed by Johnson *et al.* (1955). The path coefficient analysis was done according to Dewey and Lu (1959). Heritability in broad sense ( $h^2_b$ ) was calculated and classified into low (below 30%), medium (30- 60%) and high (above 60%); and genetic advance as percent over mean (at 5%) were computed and categorized into low (0-10%), moderate (10-20%) and high ( $e''$  20%) as given by Johnson *et al.* (1955). Estimates of PCV and GCV was calculated following Burton and De Vane (1953) and categorized into low (<10%), moderate (10-20%) and high (>20%) according to Sivasubramanian and Madhavamenon (1973). Collected data was subjected to statistical analysis for genetic diversity analysis using Mahalanobis's  $D^2$  statistics (Mahalanobis, 1936). The genotypes were grouped into clusters as per Ward's method (1963).

### Results and Discussion

Analysis of variance showed significant differences for all traits in blocks and checks except for test weight among checks (Table 2).

Cluster analysis was carried out following  $D^2$  statistics which divide a population into certain num-

**Table 2.** Analysis of variance of Augmented Block Design with 3 blocks and 3 checks for nine characters in 93 wheat (*Triticum aestivum* L.) during Rabi 2017-18.

Source of variation	Blocks	Checks	Error
df	2	2	4
DH	375.22**	194.77**	4.28
DM	119.75**	124.00**	2.33
PH	502.44**	49.27*	5.69
TPM	474.67**	447.44**	2.44
TPP	9.60**	0.96**	0.009
SPL	15.14**	3.17**	0.034
GPS	176.67**	65.77**	0.44
TW	199.47**	3.74	0.76
YP	2878.07**	4421.33**	1.15

ber of groups; these groups represent cluster. Distance between two clusters is directly proportional to genetic diversity present between the groups. Genotypes which fall in same group are genetically more related to each other. Ten clusters were identified from  $D^2$  analysis (Table 3), among which cluster IX included maximum number of genotypes while Cluster III included only single genotype. Contribution of test weight (65.31%) towards genetic divergence was maximum, followed by tillers per meter (24.92%) and plant height (3.51%). Contribution of tillers per plant and spike length to genetic divergence was negligible while very less genetic divergence was observed for days to maturity and yield per plot (Table 4). The maximum intra-cluster distance was recorded for cluster V while minimum intra-cluster distance was observed for cluster III (Table 5). Cluster III and VIII showed the highest inter-cluster distance while lowest inter-cluster distance was recorded between clusters VII and cluster IX. From the cluster mean results, contrasting genotypes for various yield contributing traits may be used for generating divergent crosses. These findings are in congruence with work of Sandhya *et al.* (2019).

The coefficient of phenotypic, genotypic and environmental variations can be used to assess the genetic variability present in a population (Singh and Singh, 1975). In the present findings coefficient of PCV was higher than GCV (Table 6). Similar results were found in literature of Choudhary *et al.* (2015)

**Table 3.** Distribution of clusters by following Ward's method

Clusters	Genotypes included	Number of genotypes in each Clusters
I.	1,3,65,66,72,67,86,2,5,35,12,3 (Check),4,29,90	15
II.	33,37,32	3
III.	30	1
IV.	6,48,28,81,74,75,70,73,82	9
V.	53,84,54,55,61,63,79,89,87,83,85,76,78,77	14
VI.	7,9,8,38,13,41,49,69,1 (Check),68,71,45	12
VII.	10,14,26,19,52,23,57,25,46	9
VIII.	42,43,11	3
IX.	15,47,16,40,59,58,20,21,62,17,18,24,27,60,22,80,39,2 (Check),36,64,88,56	22
X.	31,34,51,44,50	5

**Table 4.** Mean value of different clusters with respect to nine yield traits of 93 wheat genotypes

CLUSTERS	DH	DM	PH	TPM	TPP	SPL	GPS	TW	YP
I.	71.05	105.84	82.43	60.59	4.87	8.89	41.45	41.88	106.48
II.	64.88	101	70.81	82.77	5.75	6.62	31.44	37.11	145
III.	88.88	101.33	64.31	27.77	3.02	6.68	29.77	25.87	26.33
IV.	73.33	113.29	96.75	50	4.23	9.65	45.55	49.21	90.4
V.	72.22	113.16	89.49	72.65	4.32	8.51	38.65	42.57	160.16
VI.	85.23	117.22	95.52	70.15	5.88	9.54	47.82	40.54	145.88
VII.	81	113.22	86.32	79.22	6.37	7.93	32.55	39.67	121
VIII.	88.55	119.77	85.92	140.11	9.24	8.08	33.77	39.82	107.77
IX.	85.51	118	80.65	48.95	4.27	7.95	38.09	40.23	108.87
X.	85.28	117	94.35	32.57	3.95	5.66	34.77	43.4	58.4
Contribution % of each trait towards genetic divergence	2.73	0.28	3.51	24.92	0	0	2.83	65.31	0.42

**Table 5.** Average intra and inter cluster distance values among ten clusters of 93 wheat (*Triticum aestivum* L.) Genotypes using Ward's method during Rabi-2017-18

Clusters	I.	II.	III.	IV.	V.	VI.	VII.	VIII.	IX.	X.
I.	8.76	17.13	33.81	15.82	13.64	18.12	14.39	40.06	16.22	25.3
II.		9.56	33.79	38.47	22.15	35.57	18.59	41.27	28.1	38.79
III.			0	55.22	47.45	53.94	36.88	72.66	29.5	33.58
IV.				11.01	17.37	17.2	22.2	48.32	19.6	23.77
V.					11.09	15.07	14.02	37.02	15.82	25.62
VI.						6.85	13.91	27.55	15.21	26.97
VII.							7.38	19.55	13	21.14
VIII.								9.8	35.73	48.47
IX.									8.03	15.15
X.										10.21

and Rajput *et al.* (2018). Genotypic coefficient of variation does not give a clear idea about the amount of genetic gain to be expected from selection traits based on phenotypes unless the heritability is known Burton (1952). The method selected for population improvement is largely influenced by the heritability of the trait.

Heritability explains about magnitude of impact of genetic variance to the phenotypic expression of a trait. So, when we need to measure genetic improvement in a plant population; estimate of genetic advance becomes a necessity. The estimates of heritability and genetic advance together are more useful in assessing the genetic gain possible due to selection (Johnson *et al.*, 1955a). High heritability indicates lesser influence of environment on the expression of traits. Genetic advance is genetic improvement found in new population in comparison to the population from which it has been derived. So, in view of aforementioned information in the present study heritability and genetic advance both were

estimated to work out the extent of genetic improvement possible in the present experimental material. All traits in the present study showed high value for heritability (Table 6). Among the different traits studied in the experiment, highest genetic advance as percentage of mean was observed in all traits except days to maturity and days to heading, which showed low and moderate genetic advance in percent of mean, respectively. Such findings are in congruent with work of Panwar and Singh (2000), Gahalain (2009), and Fellahi *et al.* (2013). High heritability along with high genetic advance indicates role of additive gene action in inheritance of traits.

Path analysis can be used to understand whether the independent traits have direct effect on dependent trait or they are affecting dependent through other traits indirectly. In the present study, Path analysis was carried out by taking yield per plot as dependent factor and remaining traits as independent factors (Table 7). Results indicated that highest positive direct effect was exhibited by tillers per

**Table 6.** Summary table of the range of variation, grand mean, genotypic, phenotypic, error variance, heritability, genetic advance, phenotypic, genotypic and environmental coefficient of variation in 93 wheat (*Triticum aestivum* L.) genotypes

		DH	DM	PH	TPM	TPP	SPL	GPS	TW	YP
Range	Min	61.22	100	64.31	24.44	2.82	4.78	22.44	25.87	26
	Max	91.88	122	113.01	159.77	9.75	12.98	58.44	53.37	235.66
Grand mean		78.98	113.57	86.71	63.09	4.96	8.38	39.54	41.61	117.9
Genotypic variance		58.64	32.27	82.5	555.75	1.72	1.91	54.81	26.96	1584.62
Phenotypic variance		62.92	34.61	88.19	558.19	1.73	1.94	55.26	27.73	1585.78
Error Variance		4.28	2.33	5.69	2.44	0.0094	0.03	0.44	0.76	1.15
h <sup>2</sup> (Broad sense) %		93.2	93.26	93.55	99.56	99.46	98.23	99.2	97.23	99.93
Genetic advancement as % of mean		19.32	9.96	20.86	76.91	54.53	33.67	38.51	25.29	69.31
PCV (%)		10.06	5.18	10.82	37.5	26.61	16.64	18.84	12.63	33.67
GCV (%)		9.71	5	10.47	37.42	26.54	16.49	18.77	12.45	33.66
ECV (%)		2.62	1.34	2.74	2.48	1.96	2.21	1.69	2.1	0.91

**Table 7.** Genotypic path matrix of nine traits on grain yield per plot in 93 wheat (*Triticum aestivum* L.) genotypes during Rabi 2017-18

Traits	DH	DM	PH	TPM	TPP	SPL	GPS	TW
DH	-0.42	-0.32	0.01	0.01	-0.07	0.05	0.02	0.14
DM	0.32	0.41	0.1	0	0.05	-0.02	0.02	-0.03
PH	0	-0.05	-0.19	-0.01	0	-0.07	-0.04	-0.08
TPM	-0.01	0	0.03	0.37	0.25	0.01	-0.06	-0.07
TPP	-0.01	0	0	-0.02	-0.03	0	0	0
SPL	-0.03	-0.01	0.1	0.01	0.01	0.27	0.12	0.06
GPS	-0.01	0.01	0.03	-0.02	-0.02	0.06	0.13	0.03
TW	0.02	0	-0.02	0.01	0	-0.01	-0.01	-0.05
YP	-0.14	0.03	0.05	0.34	0.18	0.28	0.19	-0.01

**Table 8.** Genotypic correlation coefficient of nine traits of 93 wheat (*Triticum aestivum* L.) genotypes studied during Rabi 2017-18

Character	DH	DM	PH	TPM	TPP	SPL	GPS	TW
DH	1							
DM	0.77**	1						
PH	-0.01	0.26	1					
TPM	-0.03	0	0.07	1				
TPP	0.17	0.11	0.01	0.67	1			
SPL	-0.12	-0.05	0.37*	0.02	0.04	1		
GPS	-0.06	0.05	0.23*	-0.16	-0.15	0.46	1	
TW	-0.33*	-0.07	0.45*	-0.2	-0.09	0.24	0.21	1
YP	-0.14	0.03	0.05	0.34**	0.18	0.28*	0.19	-0.01

meter (0.343) followed by spike length (0.283) and grains per spike (0.170) while negative direct effect on yield was observed maximum for days to 50% heading (-0.141). Such findings complement with the results reported by Saleh *et al.* (2018) where they found positive and higher direct effect of effective tillers per plant and grain weight per spike on grain yield. Maximum positive indirect effect on yield per plot was exhibited by days to 50% heading via days

to maturity. Negative indirect effect was recorded by tillers per meter (-0.012), tillers per plant (-0.006), spike length (-0.032), grains per spike (-0.007) on grain yield per plot via days to 50% heading.

Simple correlation studies for different traits in a experimental population gives information on co-variation or co-inheritance between traits. Character association studies indicated a positive significant genotypic correlation between yield per plot with ef-

fective tillers per meter and spike length (Table 8). Positive significant correlation of yield per plot was recorded in traits viz., days to maturity, effective tillers per plant, grain filling duration, length of spike, grains per spike, and 1000 grain weight by Mallik *et al.* (2018). Mecha *et al.* (2017) observed that grain yield per plant was positively correlated with grain filling period, effective tillers per plant, spike length, number of spikelets per spike, grains per spike, test weight, yield per plot and harvest index at both phenotypic and genotypic levels. Sandhya *et al.* (2019) observed significant positive correlation of yield per plant with day to maturity, days to flowering, and plant height in barley crop. Yield per plant showed negative correlation with days to 50% heading and test weight.

## Conclusion

The present study showed that the experimental material possess ample amount of genetic diversity which can be utilized in future crop improvement program for the improvement of traits which can contribute positively in increment of yield. Ten clusters possessed different magnitude for intra-cluster group mean for all nine traits suggesting if genotypes of high cluster mean for specific traits are utilized in future hybridization program can yield high heterosis. Additive genetic variance played a predominant role in inheritance of traits as high heritability followed by high genetic advance as per cent of mean was recorded for most of the traits studied in the present experiment.

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