

## Genetic Divergence Study in Improved Bread Wheat Varieties (*Triticum aestivum* L.) under Timely Sown Condition

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### Abstract

The genetic divergence study was conducted to estimate the nature and magnitude of diversity in improved varieties of bread wheat during Rabi season of 2015-16. The divergence analysis including Tocher's and Euclidian methods indicated the presence of appreciable amount of genetic diversity in the experimental materials. The sixty four wheat genotypes were grouped into 12 clusters by both Tocher's and Euclidian methods of divergence study. But the clusters of both methods were different on the basis of the genotypes and their numbers present in the cluster. The result obtained from different methods of divergence study was slightly different from each others. Promising genotypes for different traits were identified. The information obtained from this study can be used to plan crosses and maximized the use of genetic diversity and expression of heterosis.

**Key words:** Wheat, Genetic Divergence, Cluster Analysis.

### Introduction

Grain yield in wheat is a complex trait and is dependent on its main component, viz., number of spike number/plant and grain weight/spike. Morphological features of seed plant parts are the major components of identification of cultivar. However, it is rare for variety to be identified by the expression of the single morphology trait. Use of different morphological features in a sequential fashion is useful and convenient to distinguish the variety<sup>[7]</sup>. Thus for the improvement of grain yield, knowledge of genetic variability for traits of economic importance and cause and effect relationship of yield and yield components for the available genotypes are of almost importance, which help in planning of the future breeding programme. Besides these, the degree of divergence and relative contribution of different components to total divergence using Mahalanobis  $D^2$  technique helps in the identification of selection parameters to be used as criteria for the improvement of yield in wheat.

The present study was undertaken with the aim of examining the magnitude of genetic diversity and traits contributing to genetic diversity among bread wheat genotypes for utilization in wheat breeding programme.

### Materials and Methods

The experiment was carried out under Wheat Improvement Project at Seed Breeding Farm, Department of Genetics and Plant Breeding, College of Agriculture, JNKVV, Jabalpur (M.P.). The experimental materials consist of 64 diverse promising bread wheat genotypes grown in Randomized Block Design with three replications. The observations were recorded for traits viz., Days to 50% flowering, Days to maturity, Plant height, Number of effective tillers plant<sup>-1</sup>, Ear length, Ear weight, Peduncle length, Number of spikes/plant, Number of spikelets/spike, Number of grains spike<sup>-1</sup>, 1000 grain weight, Biological yield plant<sup>-1</sup> and Harvest index from mean of five randomly selected plants from each variety per

replication. Days to 50% heading, days to maturity and grain yield were recorded on plot basis. The effective number of tillers was measured in per square meter of the plot. The  $D^2$  values were also calculated.

**Results and Discussion**

The maximum number of genotypes (16) were found in the cluster II, followed by cluster V (11), cluster I (9), cluster IV (9), cluster VI (7) and cluster XI (6). While remaining cluster III, cluster VII, cluster VIII,

cluster IX, cluster X and cluster XII were monogenotypic (Table - 1). From the composition of genotypes of most of the clusters, it was found that the genotypes included in clusters are heterogeneous in terms of their origins. These results revealed that geographic diversity might not be an important factor in determining genetic divergence. These findings are in agreement with the results obtained by many others [1, 2, 3, 4, 5, 6, 8].

**Table 1 Distribution of genotypes into different clusters based on genetic divergence**

Cluster	Number of genotype	Name of genotypes
I	9	PYT.SB.14.83, PYT.SB.14.13, PYT.SB.14.50, PYT.SB.14.67, PYT.SB.14.47, PYT.SB.14.45, PYT.SB.14.84, PYT.SB.14.33 & PYT.SB.14.27
II	16	PYT.SB.14.10, PYT.SB.14.16, PYT.SB.14.07, PYT.SB.14.25, PYT.SB.14.98, PYT.SB.14.100, PYT.SB.14.15, PYT.SB.14.71, PYT.SB.14.68, PYT.SB.14.87, PYT.SB.14.43, PYT.SB.14.24, PYT.SB.14.12, PYT.SB.14.56, PYT.SB.14.31 & PYT.SB.14.55
III	1	PYT.SB.14.89
IV	9	PYT.SB.14.04, PYT.SB.14.03, PYT.SB.14.09, PYT.SB.14.05, PYT.SB.14.41, PYT.SB.14.89, PYT.SB.14.38, PYT.SB.14.34 & PYT.SB.14.39
V	11	PYT.SB.14.06, PYT.SB.14.88, PYT.SB.14.72, PYT.SB.14.62, PYT.SB.14.70, PYT.SB.14.69, PYT.SB.14.81, GW 322, GW 366, HI 1544 & JW 1201
VI	7	PYT.SB.14.11, PYT.SB.14.91, PYT.SB.14.86, PYT.SB.14.58, PYT.SB.14.99, PYT.SB.14.24 & PYT.SB.14.32
VII	1	PYT.SB.14.40
VIII	1	PYT.SB.14.49
IX	1	PYT.SB.14.93
X	1	PYT.SB.14.64
XI	6	PYT.SB.14.44, PYT.SB.14.66, PYT.SB.14.78, PYT.SB.14.85, PYT.SB.14.85 & PYT.SB.14.52
XII	1	PYT.SB.14.36

The inter cluster distances were found higher than the intra cluster distance revealing a considerable amount of genetic diversity among the genotypes studied. The highest inter cluster distance was observed between cluster V and cluster XII (PYT.SB.14.06, PYT.SB.14.88, PYT.SB.14.72, PYT.SB.14.62, PYT.SB.14.70, PYT.SB.14.69, PYT.SB.14.81, GW 322, GW 366, HI 1544, JW

1201 and PYT.SB.14.36), followed by cluster III and XII, cluster X and XII, cluster VII and XII, cluster VI and XII, cluster I and V and cluster II and XII (Table - 2). The genotypes grouped in these clusters can be used in breeding programme in order to get a wide spectrum of variability and transgressive segregates [1,2,3,8].

**Table 2 Average intra (diagonal) and inter- cluster  $D^2$  values**

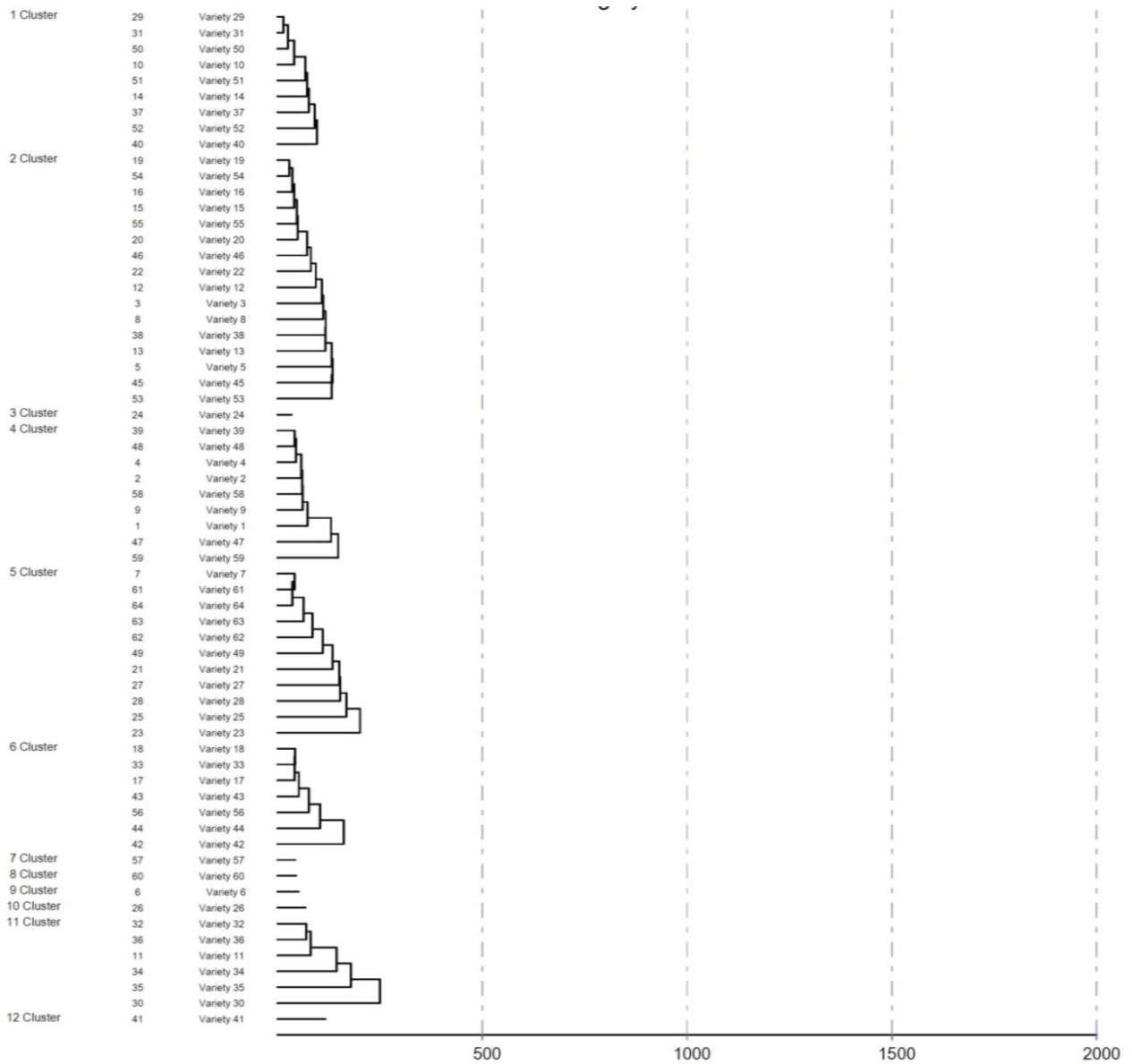
Cluster No.	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	233.51	884.72	1408.54	487.88	1676.84	1552.59	1265.76	649.30	449.09	1106.86	505.10	633.39
II		312.29	473.45	655.30	734.31	638.30	510.11	448.66	440.95	770.46	896.30	1624.46
III			0.0	1355.28	466.84	745.50	178.29	845.31	549.44	347.90	1154.90	2660.48
IV				293.49	1509.61	920.55	1388.23	569.51	603.84	1524.24	713.17	671.45
V					432.15	855.43	638.52	1345.26	753.78	699.47	1272.85	3186.61
VI						319.16	1181.87	1211.54	888.42	1513.78	1275.95	2235.56
VII							0.0	724.66	561.73	202.01	1181.21	2413.99
VIII								0.0	696.70	1016.09	971.30	1078.75
IX									0.0	457.95	437.16	1372.28
X										0.0	993.78	2555.65
XI											583.18	1276.03
XII												0.0

The inter cluster distance was minimum between clusters III and VII (178.29), cluster VII and X (202.01) and cluster III and X (347.90). Cluster V and cluster III were farthest from clusters VII (638.50) to cluster XII (3186.61) and clusters VII (178.28) to cluster XII (2660.48), respectively, and cluster I and VI (1552.59), cluster IV and X (1524.24), cluster VI and X (1513.78), and cluster IV and V (1509.61) were observed to be the nearest.

Maximum intra cluster distance was revealed in cluster XI (583.18), followed by cluster V (432.15), cluster VI (319.16), cluster II (312.29) and cluster IV (293.49). The minimum (233.51) intra cluster distance was expressed by cluster I. The remaining clusters

viz. cluster III, cluster VII, cluster VIII, cluster IX, cluster X and cluster XII were monogenotypic hence having zero intra cluster distance.

Highest mean value for a large number of traits was exhibited in cluster VIII for biological yield/plant, harvest index and grain yield/plant, followed by cluster X for ear weight, number of spikelets/spike and number of grains/spike, cluster VI for number of effective tillers/plant and number of spikes/plant, cluster XII for days to maturity and plant height, cluster III for days to 50% heading, cluster V for peduncle length, cluster VII for 1000 grain weight and cluster XI for ear length [Fig. 1]. These findings are in close harmony with the earlier findings<sup>[1, 3, 4, 8]</sup>.



**Fig. 1. Clustering by Tocher’s method**

Crossing among the genotypes in cluster V (PYT.SB.14.06, PYT.SB.14.88, PYT.SB.14.72, PYT.SB.14.62, PYT.SB.14.70, PYT.SB.14.69, PYT.SB.14.81, GW 322, GW 366, HI 1544 and JW 1201) and cluster XII (PYT.SB.14.36) were identified as genetically most diverse parents, which can be utilized for future wheat improvement programme may

lead to maximum diversity in the segregating population and develop high yielding varieties in wheat. Number of grains/spike, 1000 grain weight, harvest index, biological yield per plant, number of spikelets/spike peduncle length and effective tillers/ plant contributed substantially towards genetic divergence need more attention of wheat breeders<sup>[4]</sup>.

**Table 3 Cluster means for yield and yield attributing traits**

<b>Traits</b>	<b>Days to 50% heading</b>	<b>Days to maturity</b>	<b>Plant height</b>	<b>Number of effective tillers /plant</b>	<b>Ear length</b>	<b>Ear weight</b>	<b>Peduncle length</b>	<b>Number of spikes/ plant</b>	<b>Number of spikelets/ spike</b>	<b>Number of grains/ spike</b>	<b>1000 grain weight</b>	<b>Biological yield/ plant</b>	<b>Harvest index</b>	<b>Grain yield/ plant</b>
<b>Cluster I</b>	67.93	117.33	98.71	10.93	9.52	2.62	14.38	10.71	16.79	34.86	40.91	55.04	28.38	15.45
<b>Cluster II</b>	68.40	116.85	101.93	15.10	9.99	2.89	15.65	14.91	17.39	45.07	40.60	70.17	36.32	25.53
<b>Cluster III</b>	74.33	121.33	106.14	12.60	10.05	3.17	10.71	12.49	21.66	54.78	39.59	71.18	37.82	26.92
<b>Cluster IV</b>	69.56	118.44	96.22	15.42	10.05	2.45	16.06	15.02	15.53	33.49	39.15	63.79	31.56	20.02
<b>Cluster V</b>	68.00	115.79	86.83	13.42	10.49	2.83	20.01	13.12	17.79	51.66	37.35	60.28	33.90	20.46
<b>Cluster VI</b>	68.19	114.76	98.53	17.08	10.73	2.44	15.14	16.86	15.67	42.61	34.16	75.08	30.91	23.30
<b>Cluster VII</b>	69.67	116.33	104.40	11.87	10.79	3.37	14.11	11.48	20.27	55.22	43.69	79.79	33.30	26.57
<b>Cluster VIII</b>	64.67	122.00	101.06	13.68	9.71	2.77	15.27	13.46	19.77	42.37	43.12	82.28	39.37	32.39
<b>Cluster IX</b>	68.67	114.33	97.15	10.68	9.77	2.65	11.00	10.49	15.57	42.64	39.51	48.52	34.22	16.60
<b>Cluster X</b>	61.67	110.67	91.23	9.25	9.80	3.41	12.48	9.08	21.74	55.40	42.70	64.89	30.69	19.91
<b>Cluster XI</b>	69.44	117.94	100.08	10.10	11.43	2.55	15.25	9.84	17.05	37.39	37.44	50.64	27.78	13.65
<b>Cluster XII</b>	71.67	127.00	110.80	14.45	9.80	2.23	10.55	13.71	15.36	26.01	42.63	71.73	24.41	17.50

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