The Pharma Innovation

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Genetic divergence and character association studies in bread wheat (*Triticum aestivum* L.) genotypes

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Abstract
The experimental material consists of 35 genotypes. Observations recorded on 12 characters and the data obtained was subjected to estimation of genetic Variablity, path and correlation analysis. The estimation of analysis of variance revealed mean sum of square due to genotypes were significant for all the characters indicating sufficient genetic variability among the genotypes. The present study revealed that the phenotypic coefficient of variation was higher than the corresponding genotypic coefficient of variation for all the traits. High PCV and high GCV was observed for plant height. Heritability for broad sense was estimated for all the characters under study and observed range from 61.54 to 99.94%. Genetic advance as percentage of mean ranged from 6.34 to 99.94%. Out of 12 characters, 7 characters showed positive and direct effect with grain yield per plant. A method based on Mahalanobis D^2 suggested by Tocher (Rao, 1952) was used to group the genotypes into different clusters based on the D^2 values. 35 genotypes were grouped into 10 clusters. As cluster 1 is having maximum number of genotypes (11). Highest percent contribution towards divergence was due to plant height.

Keywords: Bread wheat, genotypes, genetic divergence, correlation and path analysis, d^2 analysis

Introduction
For majority of the world's population, wheat (*Triticum aestivum* L.) is the most important cereal crop. It is nearly two billion people's most significant staple food (36 percent of the world population). Wheat is recognised as the "King of Cereals" due to its extensive cultivation, high production, and significant position in the international food grain market. Wheat-growing areas in India are divided into six zones: The principal wheat tract is formed by the Indo-Genetic plains, which include the N-E Plains Zone and the N-W Plains Zone, followed by the Peninsular Zone, Central Zone, Southern Hill Zone, and Northern Hill Zone. Wheat is adaptable due to its high yield potential and ease of cultivation in a variety of agro-ecological situations. Almost all the popular wheat varieties are low of protein content as well as of essential amino acids such as lysine and tryptophan. Breeders can boost the nutritional value through genetic modification, we can improve the yield of this vital crop. Grain yield is a complex polygenic trait with a lot of genetic, physic-morphological, and environmental influences. It is necessary to investigate the nature of genetic variability for quality components and yield related characteristics in wheat in order to genetically modify grain production and quality.

This is an area that requires extensive study, as the majority of wheat quality components have an unfavorable association with production. When heritability, which measures the genetic connection of a characteristic in the population, is high, it should be relatively straight forward to increase that trait. In an experiment, genetic advance provides an estimate of the improvement in the mean performance of the selected clusters over the base populations. Correlation coefficient analysis appears to be quiet powerful tool to study the connection of various yield characteristics. This parameter also provides estimates of the interrelationships between grain yield and other qualities, as well as between the attributes themselves. Path coefficient analysis deals with the amount of direct and indirect influence of the independent variables on a dependent variable by separating the correlation coefficient of grain yield and the relevant characteristic.

Keeping these views in the mind, the present study entitled "Genetic Divergence and Character Association Studies in Bread wheat (*Triticum aestivum* L.) genotypes." has been planned to work out information on genetic variation, character association and genetic divergence for yield and yield contributing characters in wheat.

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Materials and Methods

Table 1: The present experimental material consists of 35 genotypes

S. No	Genotypes	S. No	Genotypes
1	IC 73570	19	IC 75331
2	IC 532087	20	IC 532456
3	IC 58012	21	IC 78972
4	IC 534755	22	IC 82421
5	IC 104611	23	IC 82435
6	IC 107910	24	IC 532502
7	IC 534801	25	IC 532247
8	IC 78972	26	IC 82555
9	IC 104636	27	IC 534816
10	IC 82184	28	IC 82187
11	IC 532057	29	IC 138874
12	IC 104586	30	IC 104570
13	IC 79023	31	IC 82264
14	IC 104555A	32	IC 57578
15	IC 57579	33	IC 532283
16	IC 212173	34	IC 104586
17	IC 104570	35	IC 79023
18	IC 82264		

The experiment was carried out under Agriculture Research Farm, Department of Plant Breeding and Genetics, Lovely Professional University, Phagwara (Punjab). The experimental area occupied was quite uniform in respect of topography and fertility. 35 different genotypes of Wheat grown in Randomized Complete Block Design with three replications during *rabi* 2018-19. The sowing was done by dibbling seeds in rows with row to row distance 22.5 cm, plant to plant distance 3 cm, row length is 2m. All genotypes were sown in 5 lines each. The recommended packages of practices were adopted for optimum crop growth. Observations on yield and yield attributing characters were recorded *viz.* Days to 50% heading, days to maturity, plant height, Number of productive tillers per plant, Ear length, ear weight, number of grains per spike, 1000-grain weight, grain yield, biological yield per plant, harvest index, chlorophyll content. Leaving border plants in each replication. In each plot, five randomly selected competitive plants were tagged to record observations except for days to 50% heading and days to maturity which were recorded on plot basis. The data obtained in respect of all the characters has been subjected to the following statistical analyses: Analysis of Variance (Panse and Sukhatme, 1962) [17], Heritability (Hanson et.al., 1956) [11], Genetic advance (Johnson *et al.*, 1955) [13], Correlation coefficient analysis (Miller *et al.*, 1958) [16], path coefficient analysis (Dewey an Lu 1959), Genetic diversity using D^2 analysis (Mahalanobis 1936) [15].

Results and Discussion

The presence of genetic variability in available gene pool provides an opportunity for selecting superior genotypes. Association between yield and yield components as determined by correlation coefficient is useful for selecting desirable plant types. The efficiency of selection depends on the direction and magnitude of association between yield and its components. The genetic diversity which is the basis of plant breeding produced due to inherent genetic differences in the plant species and is of major interest to the plant breeder. The identification of superior genotypes for further breeding programme to develop varieties to yield and yield related characters. Hence keeping in view, this topic was undertaken to identify the diverse parents for crossing programme and their results have been discussed in the light of available literature and explanation wherever possible is provided under the following subheads:

Analysis of variance

Analysis of variance indicated that the mean sum of square (MSS) due to genotypes were highly significant for all the characters at 1% and 5% level of significance and it indicated the presence of consisted amount of genetic variability for all the traits. Similar kind of results were also found by haydar *et al.,* (2020), Dabi *et al.,* (2019), Anas *et al.,* (2021), Bhuwal *et al.,* (2019) [10, 4, 1, 3].

Table 2: Analysis of Variance for Grain Yield and its Component in Wheat

Source of Variation	D.f.	Days to 50% Maturity	Days to Maturity	Plant Height	Number of Productive Tiller per Plant	Ear Length	Ear Weight	Number of Grain per Plant
Replication	2	2.466	1.40	1.43	1.26	0.06	0.01	0.55
Genotypes	34	48.25**	51.25**	1207.53**	8.48**	5.11**	0.36**	75.83**
Error	68	1.35	0.58	0.69	0.52	0.15	0.01	2.62
CV	-	1.3471	0.5774	0.8246	5.2375	3.5145	3.0565	2.8286

Source of Variation	d.f	1000 Seed Weight	Grain Yield	Biological Yield	Harvest Index	Chlorophyll Content
Replication	2	2.88	0.38	14.01	0.17	12.63
Genotypes	34	91.65**	7.47**	2404.11**	10.60**	21.12**
Error	68	0.64	0.59	21.97	0.39	8.08
CV	-	1.8683	4.4927	2.7908	5.9499	6.2242

Heritability and Genetic Advance: High or moderate heritability coupled with high or moderate genetic advance indicates presence of additive gene effects in the inheritance of concerned traits and selection may be effective in this case, while high or moderate heritability coupled with low genetic advance or high or moderate genetic advance coupled with low heritability indicates presence of non-additive gene effects and selection may be ineffective.
Heritability estimates have been broadly classified into low (below 30%), medium (30% and 60%) and high (above 60%) and genetic advance estimates classified into low (below 10%); medium (10-20%) and high (above 20%) in order to draw conclusions about these parameters.

High heritability estimates were observed for days to maturity, days to 50% heading, plant height, ear length, Number of grains per ear. The moderate heritability was observed for traits like ear weight, 1000 grain weight, biological yield per plant, harvest index, chlorophyll content

and grain yield per plant. The low heritability was observed for Number of productive tillers per plant.

High genetic advance as percentage of mean estimates were observed for plant height, biological yield per plant, harvest index and grain yield per plant. It indicates that maximum genetic gain can be received by using these characters and these characters are transferred from parent to their offspring. Moderate genetic advance as percentage of mean was recorded for days to 50% maturity, ear length, ear weight, Number of grains per ear and 1000-grain weight. It indicates partially genetic gain by selection. Low genetic advance as

percentage of mean was recorded for days to maturity, Number of productive tillers per plant and chlorophyll content. Coupled high heritability with high genetic advance observed in traits *viz*., for plant height. High heritability coupled with moderate genetic advance observed in traits *viz*., ear length and Number of grains per ear while, moderate heritability with moderate genetic advance observed in traits *viz*., number of grains per ear and low heritability with low genetic advance observed in number of productive tillers per plant. Present findings are presented in Table 3.

Table 3: Genetic parameters of variation for grain yield and its components in wheat

Characters	Maximum	Minimum	Range	Mean	GCV	PCV	Heritability	Genetic Advance	Genetic Advance % of Mean
1)Days to 50% Heading	96.66	82.66	14	86.53	4.56	4.63	97.18	8.02	9.27
2)Days to Maturity	139.00	125.00	14	132.60	3.09	3.11	98.86	8.41	6.34
3)Plant Height	129.97	76.54	53.43	101.23	19.81	19.81	99.94	41.30	40.80
4)Number of Tillers per Plant	16.20	11.06	5.14	13.83	11.77	12.15	93.81	3.25	23.49
5)Ear Length	14.10	8.80	5.3	11.27	11.40	11.57	96.93	2.60	23.12
6)Ear Weight	4.32	2.98	1.34	3.57	9.65	9.81	96.76	0.69	19.55
7)Numberof Grains per Ear	69.26	49.80	19.46	57.26	8.62	8.78	96.54	9.99	17.46
8)1000Seed Weight	53.46	30.66	22.8	42.88	12.84	12.88	99.30	11.30	26.36
9)Grain Yield	20.52	10.60	9.92	17.21	8.79	9.17	92.00	2.99	17.38
10) Biological Yield	227.70	120.73	106.97	167.97	16.77	16.85	99.09	57.78	34.39
11) Harvest Index	14.82	8.24	6.58	10.50	17.56	17.89	96.32	3.73	35.51
12)Chlorophyll Content	52.08	41.06	11.02	45.67	4.56	5.80	61.54	3.37	7.38

Phenotypic and Genotypic Coefficient of Variance

Presence of higher magnitude of variability in genotypes provides the opportunity for crop improvement. Phenotypic and genotypic coefficient of variation was computed for the 35 genotypes of 12 traits. Therefore, these parameters were made unit free by estimating phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV). As GCV represents the heritable genetic component of the total variation, it would be high appropriate to use this parameter for comparing variability of different traits.

In the present study, the phenotypic coefficient of variation was greater than genotypic coefficient of variation for all the traits. It means the observed variation is not only due to the genotypes, but also due to suitable influence of environment. Highest estimates of PCV and GCV indicates that these characters have quantitative inheritance and considerably more or less influenced by environmental factors. While, low estimates of PCV and GCV indicates that less influenced by environmental factors. PCV and GCV estimates classified into low (below 10%); medium (10-20%) and high (above 20%) in order to draw conclusions about these parameters.

In the present study, there is only high PCV for harvest index and grain yield while, there is no high GCV for any other character. The magnitude of PCV and GCV were moderate for plant height, ear weight, Number of grains per ear, biological yield per plant. The magnitude of moderate PCV and low GCV were observed for Number of productive tiller per plant, 1000-grain weight and Number of ear per plant. Low PCV and low GCV were observed for traits *viz*., days to maturity, days to 50% maturity, ear length, chlorophyll content. The PCV and GCV of present study results were presented in table 4. Similar kind of result were found by Dabi *et al*., (2019) [4] and Santosh *et al*., (2019) [22].

Correlation Coefficient Analysis

The grain yield or economic yield, almost in all of the crops, is referred to as super character which results from the interactions of several component characters that are termed as yield and yield contributing components. Thus, genetic construction of grain yield, in wheat as well as in other crops, is based on the balance or overall net effect construct by various yield components directly or indirectly by interacting with each other. Therefore, correlation studies are of considerable importance in understanding the relationship of any two given characters or any number of characters with each other. A positive correlation between desirable character is helpful to the plant breeder because it helps in simultaneous improvement of both the characters. Negative correlation on the other hand, will hinder the parallel expression of both the characters. In the present study, correlation coefficients were worked out for all possible pairs of characters particularly the grain yield per plant and its components at genotypic and phenotypic levels.

In the present findings, the magnitudes of genotypic correlation coefficient were greater than corresponding phenotypic correlation coefficient (in general also) similar findings by Verma *et al*., (2019) [25]. The significant phenotypic and genotypic correlation of grain yield per plant was found for the characters namely, number of productive tillers per plant, biological yield per plant and harvest index and in genotypic correlation ear length, ear weight and biological yield per plant also shows positive significant. Thus, these characters revealed as most important association of grain yield per plant in wheat. It showed that the above mentioned characters must be included in selection criteria during improvement of grain yield in wheat.

The characters like days to 50% maturity shows negative

association at both genotypic and phenotypic level for grain yield per plant, but days to maturity shows positive association at genotypic and phenotypic level. Similarly, others characters have shown apparent magnitude of variations on other yield contributing characters and are presented in Table 4 and table 5.

Table 4: Genotypic correlation between grain yield and its contributing characters in wheat

Characters	X1	X2	X3	X4	X5	X6	X7	X8	X10	X11	X12
X1	1.0000	0.1073	-0.0088	-0.0024	-0.1907	*-0.2067	-0.1744	0.0275	*0.1960	*-0.2853	-0.0620
X2		1.0000	-0.0405	*-0.1996	0.0617	0.1121	*0.2245	**-0.3038	0.1168	-0.0789	*-0.2496
X3			1.0000	-0.0147	0.4267	**0.4361	**0.3678	-0.0041	*0.1963	-0.0447	-0.1498
X4				1.0000	*-0.1948	-0.1988	*-0.2127	0.0133	**-0.3411	**0.2506	**0.3304
X5					1.0000	**1.0124	**0.8805	-0.1766	0.0084	**0.3203	**-0.5635
X6						1.0000	**0.9365	-0.1722	0.0494	**0.3421	**-0.6365
X7							1.0000	*-0.2472	0.0918	**0.2534	**-0.6087
X8								1.0000	0.0244	0.0982	**-0.2617
X10									1.0000	**-0.8301	**-0.4263
X11										1.0000	0.0100
X12											1.0000
X9	-0.1764	0.1348	**0.3476	-0.0706	**0.5975	**0.7043	**0.6480	*0.2399	0.1894	**0.3630	**-0.7421

Table 5: Phenotypic correlation between grain yield and yield contributing characters in wheat

Characters	X1	X2	X3	X4	X5	X6	X7	X8	X10	X11	X12
X1	1.0000	0.102	-0.0079	-0.0036	-0.1828	-0.1988*	-0.1650	0.0268	0.1915	-0.2740**	-0.0646
X2		1.000	-0.0401	-0.1906	0.0648	0.1081	0.2146*	-0.3010**	0.1149	-0.0777	-0.2078*
X3			1.0000	-0.0134	0.4200**	0.4293**	0.3613**	-0.0040	0.1957*	-0.0444	-0.1146
X4				1.0000	-0.1826	-0.1950*	-0.1949*	0.0108	-0.3298**	0.2491*	0.2535**
X5					1.0000	0.9773**	0.8554**	-0.1724	0.0061	0.3111**	-0.4465**
X6						1.0000	0.9086**	-0.1700	0.0493	0.3236**	-0.4641**
X7							1.0000	-0.2386**	0.0901	0.2456*	-0.4509**
X8								1.0000	0.0265	0.0934	-0.2018*
X10									1.0000	-0.8220**	-0.3205**
X11										1.0000	-0.0093
X12											1.000
X9	-0.1631	0.1269	0.3330**	-0.0482	0.5636**	0.6549**	0.6142**	0.2289*	0.1811	0.3831**	-0.5695**

X1: Days to 50% heading; X2: Days to maturity; X3: Plant height (cm); X4: Number of productive tillers per plant; X5: Ear length (cm); X6: Ear weight (g); X7: Number of grains per spike; X8: 1000-grains weight (g); X9: grain yield; X10: Biological yield per plant; X11: Harvest index (%); X12: Chlorophyll content

Path coefficient analysis
Path coefficient analysis can be defined as the ratio of the standard deviation of the effect due to a given cause to the total standard deviation of the effect, also called standard partial regression coefficients which splits the correlation coefficient into the measures of direct and indirect effects, i.e. it measures the direct and indirect contribution of various independent characters on a dependent character. They are free from units, directional and may be more or less than unity and therefore, enable easy interpretation. The basic assumption of path analysis is that the path diagram utilizes a complete representation of the casual factor involved in determining the end product i.e., grain yield per plant.

The path coefficient analysis of different characters revealed that positive direct effect on grain yield per plant was observed by days to maturity, plant height, No. of tillers/plant, No of grains/plant, 1000 seed weight, biological yield and harvest index. Negative direct effect on grain yield per plant was observed by days to 50% heading, ear length, ear weight and chlorophyll content.

Thus, these characters need special attention during the time of selection strategy due to their contrasting direct and indirect effects. The present study results were presented in table 6. Similar kind of result were found by Kumar *et al*., (2019), Verma *et al*., (2019) and Baye *et al.,* (2020) [25, 2].
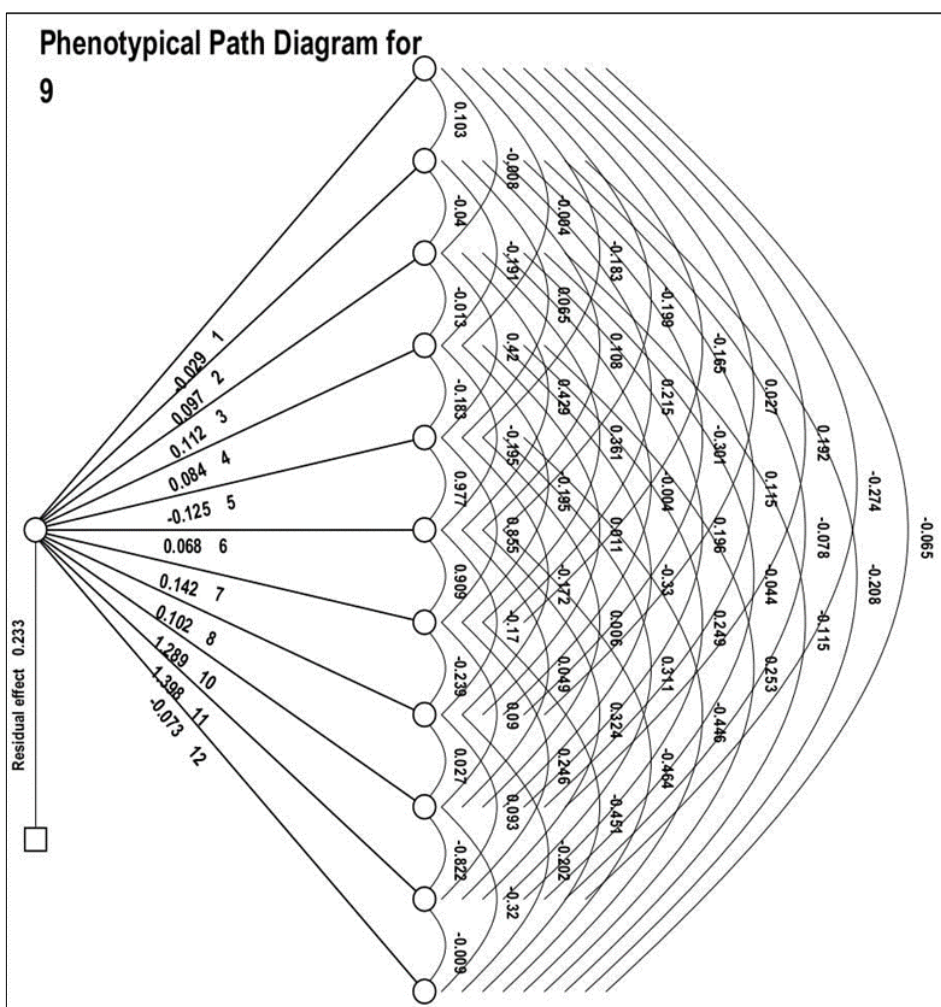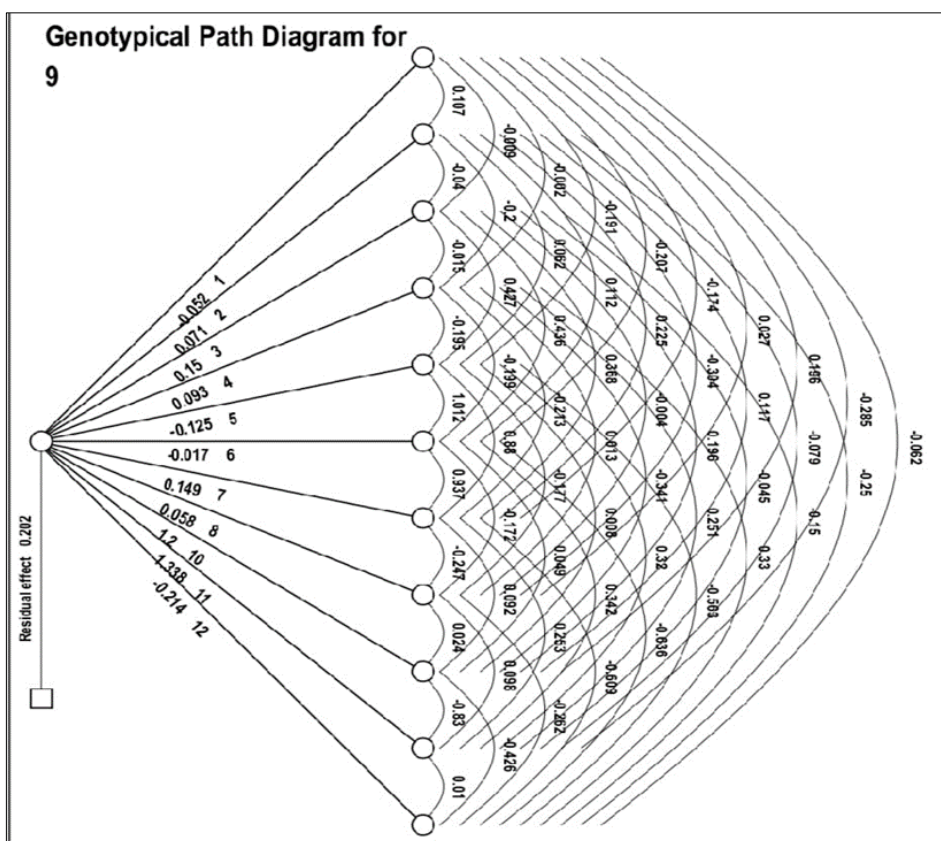
Fig 1, 2: Representing genotypic and phenotypic path diagrams

Table 6: Genotypic path coefficient showing direct and indirect effects of different contributing characters on grain yield per plant in wheat

Characters	X1	X2	X3	X4	X5	X6	X7	X8	X10	X11	X12
X1	-0.0523	0.0056	0.0005	0.0001	0.0100	0.0108	0.0091	-0.0014	-0.0103	0.0149	0.0032
X2	0.0076	0.0708	-0.0029	-0.0141	0.0044	0.0079	0.0159	-0.0215	0.0083	-0.0056	-0.0177
X3	-0.0013	-0.0061	0.1499	-0.0022	0.0640	0.0654	0.0551	-0.0006	0.0294	-0.0067	-0.0225
X4	-0.0002	-0.0187	-0.0014	0.0935	-0.0182	-0.0186	-0.0199	0.0012	-0.0319	0.0234	0.0309
X5	0.0239	-0.0077	0.0535	0.0244	-0.1254	-0.1270	-0.1104	0.0221	0.0011	0.0402	0.0707
X6	0.0035	-0.0019	-0.0075	0.0034	0.0173	-0.0171	-0.0160	0.0029	-0.0008	-0.0058	0.0109
X7	-0.0260	0.0335	0.0549	-0.0318	0.1314	0.1398	0.1493	-0.0369	0.0137	0.0378	-0.0909
X8	0.0016	-0.0175	-0.0002	0.0008	-0.0102	-0.0099	-0.0142	0.0575	0.0014	0.0056	-0.0150
X9	-0.1764	0.1348	0.3476	-0.0706	0.5975	0.7043	0.6480	0.2399	0.1894	0.3630	-0.7421
X10	0.2352	0.1402	0.2356	-0.4094	0.0101	0.0593	0.1102	0.0292	1.2000	-0.9961	-0.5116
X11	-0.3816	-0.1056	-0.0598	0.3353	0.4285	0.4577	0.3390	0.1314	-1.1104	1.3377	0.0134
X12	0.0132	0.0533	0.0320	-0.0706	0.1203	0.1359	0.1300	0.0559	0.0910	-0.0021	-0.2135

Genetic divergence

The amount of diversity available in the crop decides the success of any crop improvement programme with manifold objectives.

In the present study, 35 genotypes of wheat were considered for the assessment of nature of genetic diversity by multivariate analysis. The genetic diversity present in the genotypes was assessed by adopting Mahalanobis (1936) [15] concept of generalized distance (D^2).

Group Constellations

Genetic divergence analysis based on Mahalanobis D^2 suggested by Tocher (Rao, 1952) statistics resulted in grouping of 35 genotypes into 10 clusters. Among 10 clusters, cluster I was the biggest with 11 genotypes followed by cluster VI (9 genotypes), cluster IV (6 genotypes), V (3 genotypes), VII (1 genotype), cluster II (1 genotype), cluster III (1 genotype), cluster VIII (1 genotype), cluster IX (1 genotype) and cluster X (1 genotype).The discrimination of genotypes in to discrete clusters suggested presence of high degree of genetic diversity in the material evaluated. Presence of substantial genetic diversity among the parental material screened in the present study indicated that this material may serve as good source for selecting the diverse parents for hybridization programme. In conformity to the present investigation, similar findings were found by Santosh *et al.,* (2019), Yadav *et al*., (2019), and Devesh *et al*., (2019) [22, 5] The clustering pattern and the distribution of genotypes into different clusters were presented in table 7.

Inter and intra cluster divergence

Maximum differences among the genotypes within the same cluster (intra-cluster) were shown by Cluster VI followed by cluster V, Clusters IV and cluster I while, cluster II, III, VII, VIII, IX and X showed zero intra-cluster distance. Diversity among the clusters varied from 15.94 to 97.60 where as cluster VII and IX showed maximum inter cluster distance followed by that between cluster IV and VII, cluster VII and X, cluster VII and VIII, cluster II and VII, cluster V and VII, cluster I and VII, cluster III and VII, minimum inter cluster was found between cluster II and I. The intra and inter cluster D^2 values of wheat genotypes are presented in table 8.

Table 7: Distribution of 35 genotypes in to different clusters

| Group	No. of genotypes	Name of genotypes
Cluster I	11	IC-78972, IC-57578, IC-82555, IC-104555A, IC-57579, IC-107910, IC-534755, IC-78978, IC-532087, IC-58012, IC-82435
Cluster II	1	IC-534801
Cluster III	1	IC-118721
Cluster IV	6	IC-138868, IC-532247, IC-212173, IC-79023, IC-82184, IC-82421
Cluster V	3	IC-104636, IC-78962, IC-532502
Cluster VI	9	IC-104570, IC-104586, IC-532283, IC-75331, IC- 532057, IC-534816, IC-82264, IC-73570, IC-82187
Cluster VII	1	IC-82296
Cluster VIII	1	IC-532456
Cluster IX	1	IC-138874
Cluster X	1	IC-104611

Clustering by Tocher Method
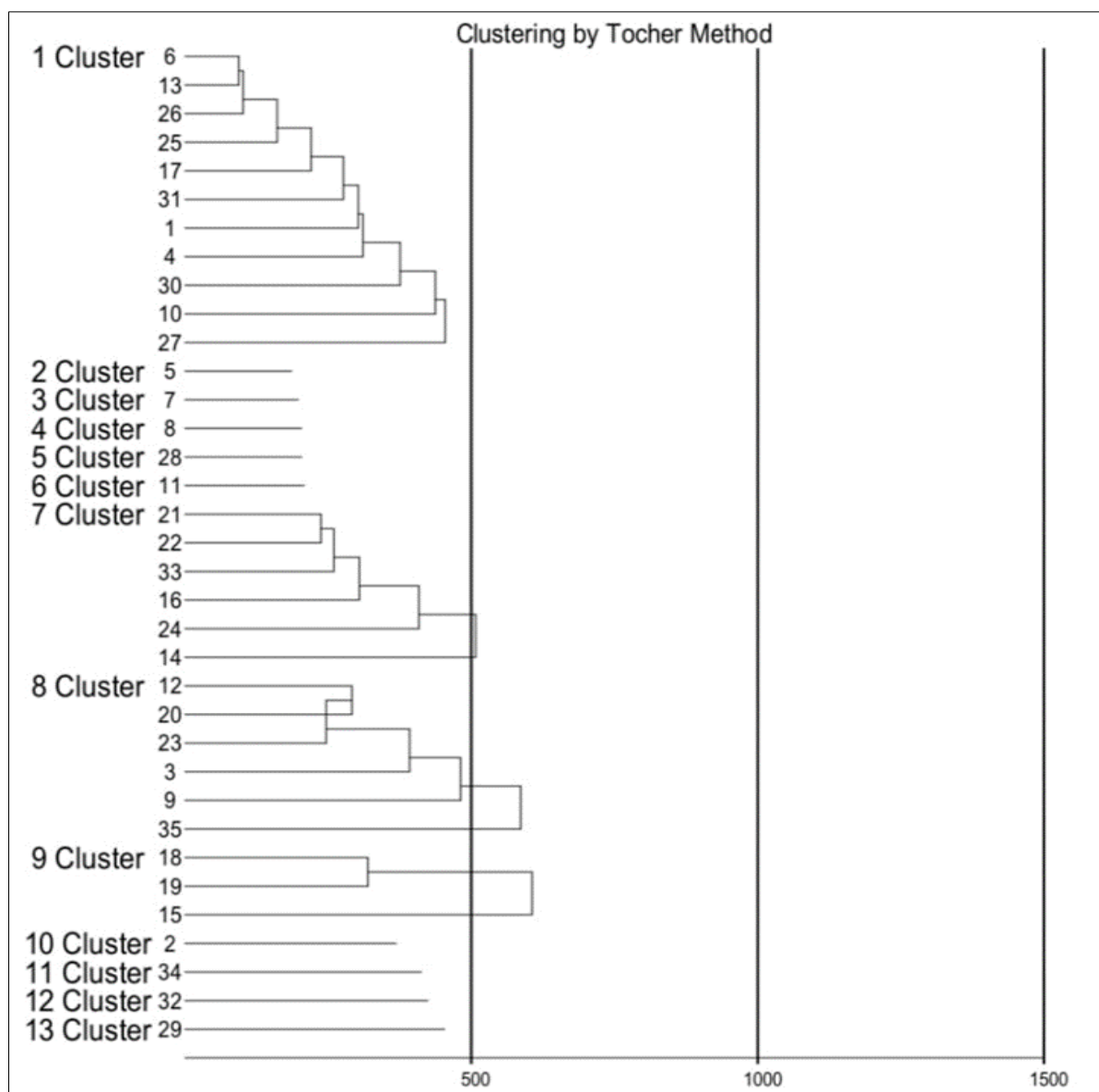
Table 8: Average intra and inter cluster D^2 values of wheat genotypes

Group	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X
Cluster I	19.29	24.64	23.87	32.01	27.13	46.39	72.38	27.85	36.18	30.55
Cluster II		0.00	15.94	24.31	19.75	55.93	83.95	26.10	36.76	24.80
Cluster III			0.00	33.53	17.52	45.34	71.24	29.54	42.07	33.93
Cluster IV				20.22	32.63	68.61	96.16	35.00	33.79	28.58
Cluster V					22.37	49.28	74.90	36.69	47.01	29.53
Cluster VI						25.74	36.43	57.73	70.21	59.04
Cluster VII							0.00	85.04	97.60	86.52
Cluster VIII								0.00	20.90	41.10
Cluster IX									0.00	46.36
Cluster X										0.00

Percent contribution of characters towards divergence
It was observed that plant height was highest contributor towards divergence followed by 1000 grain weight, biological yield per plant, harvest index, days to maturity, days to 50% heading and grain yield showed same percent of contribution where as ear length and number of grains per spike showed

same percent of contribution towards divergence while, number of tillers per plant, chlorophyll content and ear weight did not contribute significantly towards divergence. Percentage contribution of characters towards divergence of 35 wheat genotypes is presented in below table 9.

Table 9: Percentage contribution of characters towards divergence of 35 wheat genotypes

SI Number	Characters	Percent contribution	Rank
1	Days to 50% heading	0.67	VI
2	Days to maturity	3.87	V
3	Plant height (cm)	67.56	I
4	Number of productive tillers per plant	0.00	
5	Ear length (cm)	0.34	VII
6	Ear weight (g)	0.00	
7	Number of grains per ear	0.34	VII
8	1000-grain weight (g)	13.45	II
9	Biological yield plant (g)	0.67	VI
10	Harvest index (%)	7.56	III
11	Chlorophyll content	5.55	IV
12	Grain yield per plant (g)	0.00	

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