

Original Research Article

Genetic Divergence Study in Advance Indica Rice (*Oryza sativa* L.) Lines for Yield and Quality Attributes

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ABSTRACT

An experiment was conducted during Kharif 2014 and 2015 with two different conditions (Control and Reproductive stress) at research farm of Bihar Agricultural University, Sabour (Bhagalpur) to study the existing genetic diversity in thirty six advance rice lines through Mahalanobis D^2 statistics for grain yield and quality traits. Based on the D^2 analysis, the genotypes were grouped into six clusters revealed the presence of considerable amount of genetic diversity in the material with each other for different yield and quality traits. The inter-cluster distances were higher than intra-cluster distances indicating wider genetic diversity among the genotypes of different clusters. The intra-cluster distances were lower in all the cases reflecting homogeneity of the genotypes within the clusters. The cluster II contained the highest number of genotypes (17) followed by cluster I (12), cluster III (4) and the clusters IV, V and VI are mono-genotypic. The highest intra-cluster distance was noticed for the cluster I followed by cluster II, cluster III and nil distance for clusters IV, V and VI. The highest inter-cluster distance was observed between cluster I and III, followed by cluster III and V, cluster III and IV and the lowest between cluster IV and V. The above results indicate that these genotypes have maximum genetic diversity and useful for developing a large number of segregants through crossing program by using maximum diverse genotypes. Cluster VI showed highest mean value for grain yield per plant, grain yield kilogram per hectare, 1000-grain weight, harvest index, number of spikelet's per panicle, number of productive tillers/m², amylose content and days to maturity. Cluster V showed highest mean value for number of tillers/plant, milling%, kernel length before cooking, L/B ratio and volume expansion ratio. The crosses between the genotypes/parents of cluster VI and cluster V would exhibit high heterosis as well as higher level of yield potential. Therefore, more emphasis should be given for selection of the genotypes from clusters VI and V for future breeding program. Among the twenty one traits studied, maximum contribution was made by Kernel elongation ratio (71.90%) followed by biological yield per plant (4.76%), amylase content (4.60%) and 1000-grain eight (4.13%). Therefore, these characters may be given importance during hybridization program.

Keywords

Rice, genetic diversity, D^2 statistics, grain yield, grain quality

Introduction

Rice is the principal food crop and a primary food source for more than one third of the world's population. The population growth

in most of the Asian countries, except China, continues to be around 2% per year. Hence it is very pertinent to critically

consider whether the rice production can be further increased to keep pace with population growth. In order to meet the food requirement of growing population, development of high yielding varieties is essential. The success of any breeding program depends on the selection of parents for hybridization. The parents involved in the development of varieties should be divergent. The germplasm provides immense scope for wider variability. Diversity analysis is a useful tool in quantifying the degree of divergence between biological population at genotypic level and to assess relative contribution of different components to the total divergence both at intra and inter cluster levels (Murty and Arunachalam, 1966; Ram and Panwar, 1970). Information on nature and degree of genetic divergence would help the plant breeder in choosing the right parents for the breeding program (Vivekanandan and Subramaniam, 1993). It also permits to select the genetically diverged parents which can produce new recombinants with desirable traits when they are crossed together. Keeping this in view, the present study was undertaken to assess the genetic diversity of promising rice genotypes using Mahalanobis D^2 statistics.

Materials and Methods

Thirty six advance lines of rice consisting genotypes of IRRI were raised at field experimentation centre, Bihar Agricultural University, Sabour (Bhagalpur), Bihar during Kharif, 2014 and 2015 with control and reproductive stress condition to identify diverse genotypes. The experiment was laid out in randomized complete block design with three replications. The genotypes were raised in plot size $4 \times 2 = 8\text{m}^2$. Row to row and plant to plant spacing was maintained at 20×20 cm. The recommended agronomic practices were followed. They were

evaluated for twenty one yield and quality attributing characters viz., days to 50% flowering, plant height (cm), days to maturity, number of tillers per plant, number of productive tillers / meter², panicle length (cm), number of spikelet's per panicle, grain yield per plant (g), biological yield per plant (g), harvest index (%), 1000-grain weight (g), hulling (%), milling (%), head rice recovery (%), kernel length before cooking (mm), kernel breadth before cooking(mm), L/B ratio, amylose content, volume expansion ratio, kernel elongation ratio, grain yield per plot (kg/ha). Five random plants per replication per genotype were tagged for recording observations for above mentioned characters except days to 50% flowering, days to maturity and grain yield kilogram per hectare which were recorded on plot basis. The genetic distance between the genotypes was worked out using Mahalanobis D^2 analysis (1936) and grouping of varieties into clusters was done following the Tocher's method as detailed by Rao, (1952).

Results and Discussion

Analysis of variance showed significant differences for all the twenty one characters studied among the genotypes. Based on D^2 values, 36 genotypes were grouped into 6 clusters (Table – 1 and Figure - 1) in such a way that the genotypes within a cluster had a small or low D^2 values than those of in between the characters. Among the different clusters cluster II had maximum number of genotypes (17 genotypes) followed by cluster I (12 genotypes), cluster III (4 genotypes) while, cluster IV, V and VI are mono-genotypic. The pattern of group constellation proved the existence of significant amount of variability. The overall composition of the clustering pattern showed that genotypes collected from the same geographic origin were distributed in

different clusters. Similar findings of non-correspondence of geographic origin with genetic diversity were also reported by Shanmugasundaram, *et al.*, 2000 and Nayak, *et al.*, 2004. The inter-cluster distance is higher than intra-cluster, indicating wide genetic diversity among the genotypes. The highest inter - cluster distance varied from 3.335 to 36.777. The highest inter-cluster distance was observed between cluster I and III (36.777) (Table - 2 and Fig - 2) followed by cluster III and V (26.638), cluster III and IV (24.814) and cluster I and VI (21.356). On the other hand minimum distance was observed between cluster IV and V (3.335), indicating close relationship between these clusters would not provide any good result. The greater the distance between clusters wider the genetic diversity between the genotypes. Highly divergent genotype would produce a broad spectrum of variability in the subsequent generations enabling further selection and improvement. The hybrids developed from the selected genotypes within the limit of compatibility of these clusters may produce desirable transgressive segregants or higher magnitude of heterosis. This would be useful in rice breeding program to evolve miracle varieties with high yield potential along with better quality traits. Highly divergent genotypes deem to produce wide variability that may help further selection for genetic improvement (Rahaman *et al.*, 1997). Hybrid developed from the genotypes within the limit of compatibility of those clusters may manifest high heterosis or desirable transgressive segregants, which would be beneficial for genetic improvement. Dey *et al.*, (2011) also suggested the use of divergent genotypes for development of lines with high yielding potential and better adaptability. Hybridization between genetically divergent parents to generate high heterotic segregants reported promising (Roy and Panwar, 1993;

Vivekanandan and Subramaniam 1993; Sharma *et al.*, 1997) and a similar finding was of Sarawgi and Rastogi (2000), Nayak *et al.*, (2004) and Parikh *et al.*, (2011). The maximum intra cluster distance was observed for cluster I (3.512) followed by cluster II (3.386) and cluster III (2.603) (Table - 2 and Figure - 2). Maximum intra-cluster distance was observed among the genotypes, viz., IR 92527-6-2-1-2, IR 92527-6-2-1-4, IR 92517-1-3-1-1, IR 92523-37-1-1-2, IR 92523-35-1-1-1, IR 93339:40-B-18-13-B-B-1, IR 92545-53-4-1-3, IR 88287-383-1-B-B-1-1-B, IR 94313:18-4-1-4-1-B, IR 92522-61-3-1-4, MTU 1010, IR 94314-20-2-1-B in cluster I, indicating existence of wide genetic divergence among the constituent genotypes in it. High degree of divergence among the genotypes within a cluster would produce more segregating breeding materials and selection within such cluster might be executed based on maximum mean value for the desirable characters. It was reported that genotypes within the cluster with high degree of divergence would produce more desirable breeding material for achieving maximum genetic advance (Bose and Pradhan, 2005). The minimum intra-cluster distance was observed in cluster IV, V and VI (0.000) indicating homogeneous nature of the genotypes with no deviation between the genotypes, therefore selection will be ineffective. Similar findings were also reported by Rajesh *et al.*, 2010 and Nayak *et al.*, (2004). A perusal of results on cluster means (Table - 3) revealed that the cluster VI showed highest mean value for grain yield/plant, grain yield/plot (Kg/ha), 1000-grain weight, harvest index, number of spikelet's per panicle, number of productive tillers/m², amylose content and days to maturity. Cluster V showed highest mean value for number of tillers/plant, milling%, kernel length before cooking, L/B ratio and volume expansion ratio.

Table.1 Distribution of 36 advance rice lines in various clusters

Clusters ↓	Number of Genotypes	Name of Genotypes
Cluster I	12	IR 92527-6-2-1-2, IR 92527-6-2-1-4, IR 92517-1-3-1-1, IR 92523-37-1-1-2, IR 92523-35-1-1-1, IR 93339:40-B-18-13-B-B-1, IR 92545-53-4-1-3, IR 88287-383-1-B-B-1-1-B, IR 94313:18-4-1-4-1-B, IR 92522-61-3-1-4, MTU 1010, IR 94314-20-2-1-B
Cluster II	17	IR 92546-7-1-1-3, IR 92546-33-3-1-1, IR 92546-17-6-4-4, RP-1-27-7-6-1-2-1, IR 64,IR 94391-587-1-2-B, IR 92516-8-3-3-4, IR 92545-51-1-1-4, IR 92545-24-3-1-1, IR 92545-23-2-1-1, IR 92545-54-6-1-4, LALAT, IR 92546-17-6-4-3, IR 92522-47-2-1-1, CRR 724-1-B (IR 88889-44), CRR 719-1-B (IR 88903-34), IR 92546-33-4-2-3
Cluster III	4	IR 92521-23-6-1-3, IR 92521-24-5-1-3, IR 92521-5-3-1-2, IR 92521-7-5-1-1
Cluster IV	1	IR 92545-40-2-2-3
Cluster V	1	IR 92522-47-2-1-4
Cluster VI	1	IR 92522-45-3-1-4

Table.2 Average intra and inter cluster distance among six clusters for thirty six advanced lines of rice

Clusters → ↓	Cluster - I	Cluster - II	Cluster - III	Cluster - IV	Cluster - V	Cluster - VI
Cluster - I	3.512	10.020	36.777	4.619	4.754	21.356
Cluster - II		3.386	13.753	5.649	5.953	7.449
Cluster - III			2.603	24.814	26.638	10.146
Cluster - IV				0.000	3.335	11.736
Cluster - V					0.000	12.613
Cluster - VI						0.000

Table.3 Mean values of clusters for different characters towards genetic divergence in thirty six advance rice lines

Characters	Cluster (I)	Cluster (II)	Cluster (III)	Cluster (IV)	Cluster (V)	Cluster (VI)
Days to 50% flowering	83.458	83.304	82.542	84.500	82.167	83.717
Plant height (cm)	97.462	99.752	107.086	104.396	96.633	96.750
Days to maturity	115.806	115.824	115.500	115.300	115.917	116.583
No. of tillers per plant	11.285	10.775	9.604	10.083	11.500	10.750
No. of productive tillers/m²	234.896	230.608	205.708	230.167	205.000	237.917
Panicle length (cm)	26.293	25.901	25.872	27.405	25.522	25.738
No. of spikelets per panicle	146.153	148.034	194.396	159.417	130.750	150.083
Grain yield per plant (g)	27.951	27.574	27.333	24.667	26.500	29.500
Biological yield per plant	67.632	66.770	69.125	72.833	70.167	62.417
Harvest index (%)	41.689	41.696	39.823	34.197	37.758	47.467
1000-grain weight (g)	24.103	24.125	23.410	27.800	24.242	27.958
Hulling (%)	73.960	74.755	74.415	77.345	75.102	73.741
Milling (%)	63.113	62.460	62.713	62.883	65.258	56.983
Head rice recovery (%)	44.331	50.195	56.177	43.133	40.008	42.158
Kernel Length before cooking	7.292	6.982	6.450	7.175	7.708	6.792
Kernel Breadth before cooking	2.065	2.097	2.165	2.183	1.925	2.117
L/B ratio	3.557	3.348	2.992	3.301	4.018	3.222
Amylose content	21.774	22.464	21.305	21.342	23.332	23.716
Volume expansion ratio	3.384	3.372	3.414	3.322	3.417	3.352
Kernel elongation ratio	0.754	0.645	0.533	0.701	0.697	0.586
Grain yield/plot (Kg/ha)	4474.299	4318.172	4135.729	3913.583	3965.084	4563.333

Table.4 Contribution of different yield and quality traits towards genetic divergence of 36 advance rice lines

S. No.	Source	Contribution %	Times Ranked 1st
1	Days to 50% flowering	0.01	0
2	Plant height (cm)	0.01	0
3	Days to maturity	0.16	1
4	No. of tillers per plant	0.01	0
5	No. of productive tillers/m ²	0.48	3
6	Panicle length (cm)	0.16	1
7	No. of spikelets per panicle	1.90	12
8	Grain yield per plant (g)	0.01	0
9	Biological yield per plant	4.76	30
10	Harvest index (%)	0.01	0
11	1000-grain weight (g)	4.13	26
12	Hulling (%)	0.63	4
13	Milling (%)	0.01	0
14	Head rice recovery (%)	7.78	49
15	Kernel Length before cooking	1.11	7
16	Kernel Breadth before cooking	0.16	1
17	L/B ratio	0.01	0
18	Amylose content	4.60	29
19	Volume expansion rate	0.01	0
20	Kernel elongation ratio	71.90	453
21	Grain yield/plot (Kg/ha)	2.22	14

Fig.1 Distribution of 36 advance rice lines in various clusters

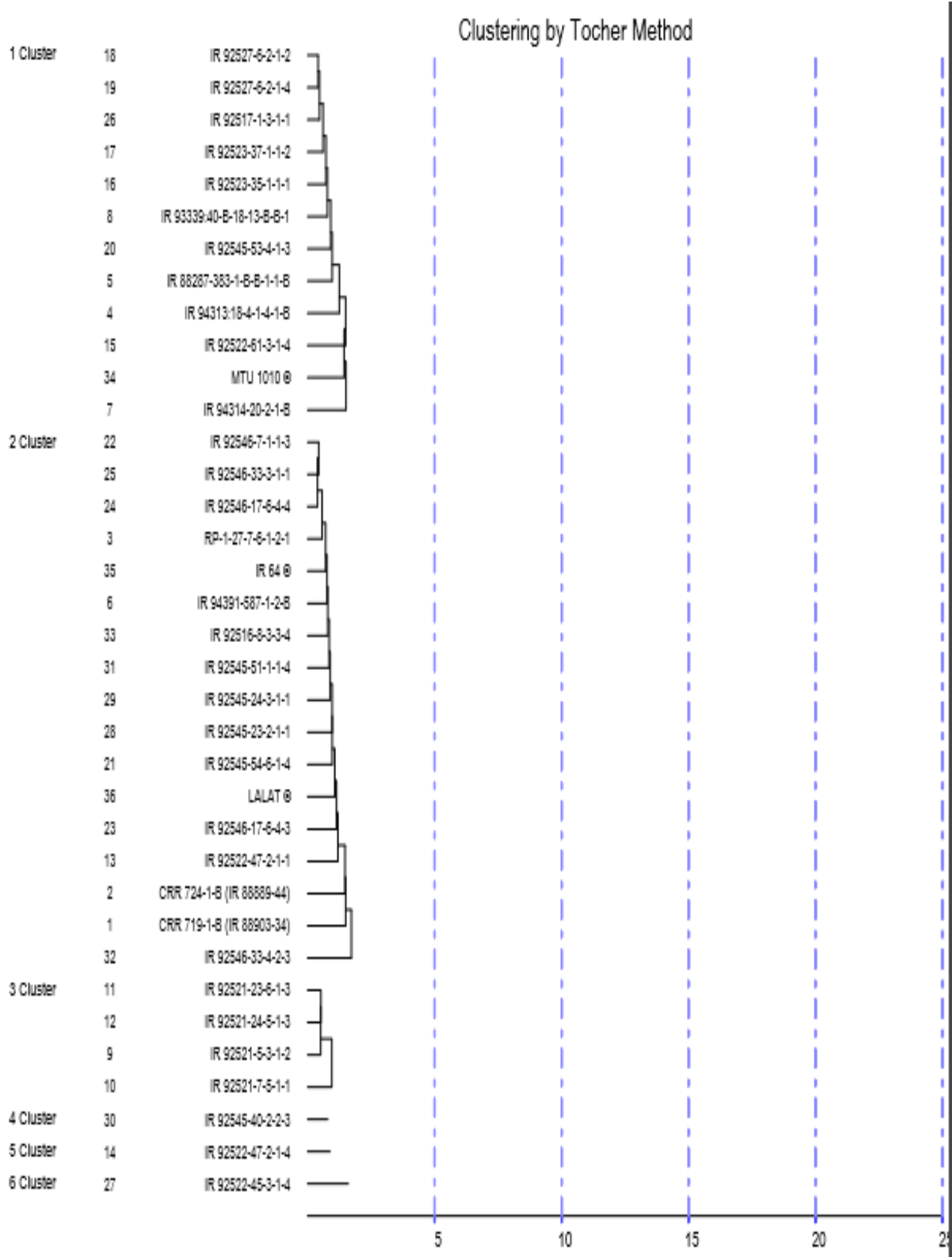


Fig.2 Average intra and inter cluster distance among six clusters for thirty six advanced lines of rice

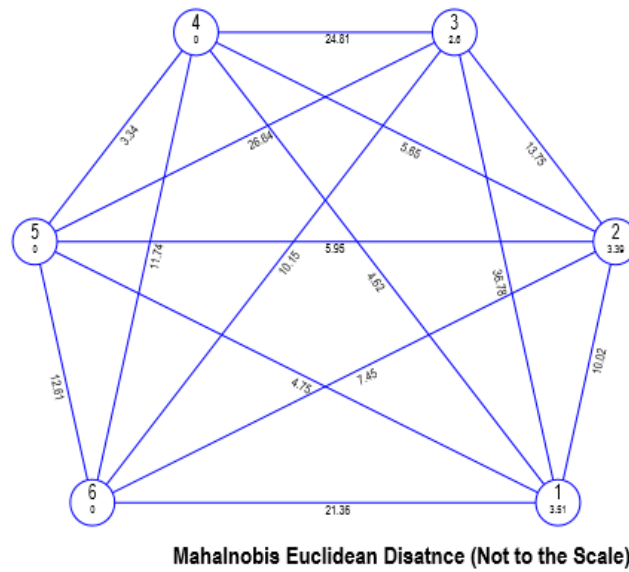
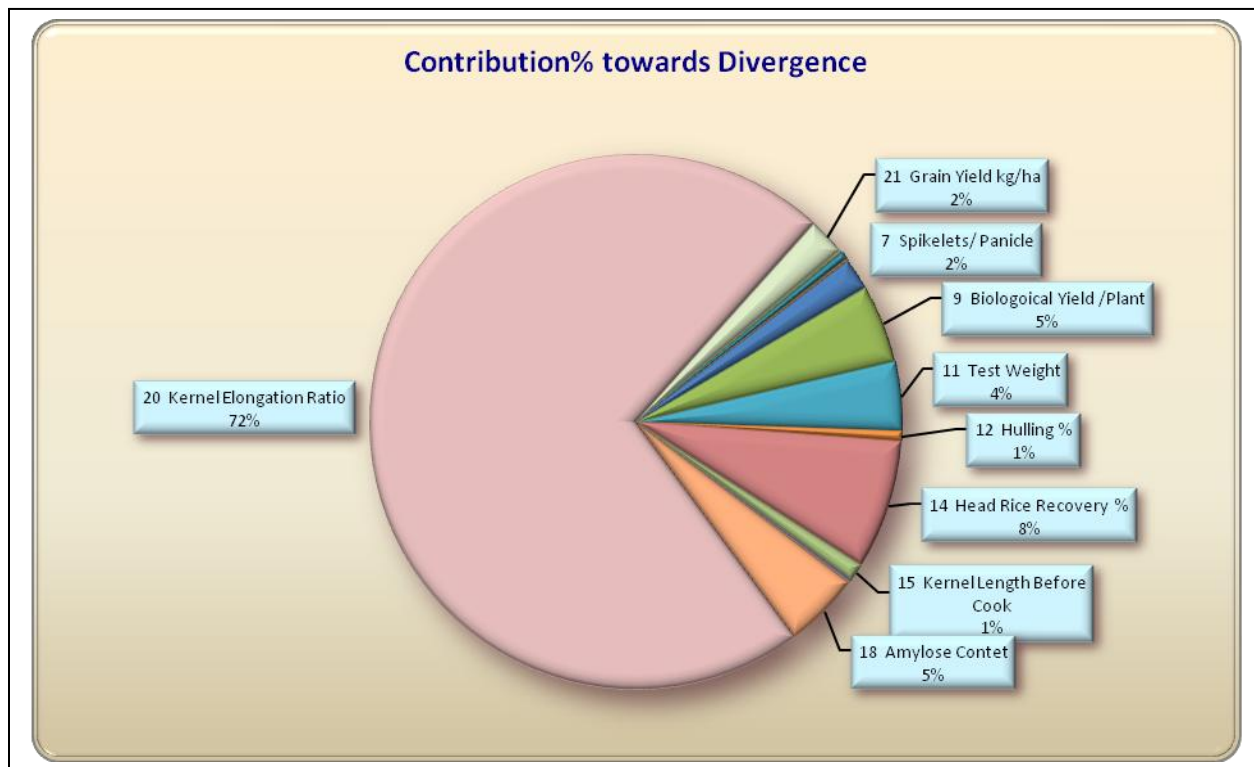


Fig.3 Contribution of different yield and quality traits towards genetic divergence of 36 advance rice lines



Cluster IV showed highest mean value for days to 50% flowering with better panicle length, biological yield per plant, hulling% and kernel breadth before cooking. Cluster III showed highest mean value for plant height with head rice recovery%. While cluster I showed highest mean value for kernel elongation ratio. The results suggest that intercrossing of genotypes from different cluster showing good mean performance may help in obtaining high yield. Inclusion of more diverse parents in hybridization is believed to increase the chances of obtaining better heterosis and give broad spectrum of variability in segregating generation. The better genotypes can be selected for most of characters on the basis of mean performance in the cluster. The promising genotypes for grain yield per plant, grain yield per plot (Kg/ha), 1000-grain weight, harvest index, number of spikelet's per panicle, number of productive tillers/m², amylase content and number of tillers per plant, milling (%), kernel length before cooking, L/B ratio and volume expansion rate were identified from cluster VI and V on the basis of mean values which could be utilized for hybridization program for the development of high yielding genotypes.

The utility of D² analysis, which is a potent tool to quantify the extent of divergence in biological populations at genetic level, is further enhanced by its applicability to estimate the relative contribution of the various plant characters to genetic divergence. The present study revealed that out of twenty one traits studied, maximum contribution was made by Kernel elongation ratio (71.90%) (Table – 4 and Figure 3) followed by biological yield per plant (4.76%), amylose content (4.60%) and 1000-grain weight (4.13%). Therefore, these characters may be given importance during hybridization program.

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