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Evaluation of Different Traits to Find Out Genetic Divergence of Some Rice (*Oryza sativa* L.) Genotypes

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

The goal of the study was to quantify the genetic divergence among the different genotypes of rice. The experiment was conducted under the agro-climatic zone of Western ghat region. The experimental trial was carried out for thirteen characters of 40 rice genotypes during *kharif* 2021 at Agricultural Research Station, Vadgaon Maval, Pune. Total 11 clusters were formed out of which Cluster I contained 12 genotypes and cluster II, III, IV, X contained 6,9,3 and 4 genotypes respectively. While cluster V, VI, VII, VIII, IX and XI were monogenotypic. The maximum inter-

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cluster distance observed within cluster VII and XI (24.29) followed by cluster III and XI (24.03), cluster X and XI (23.69), cluster IV and VII (23.39), cluster I and IX (22.21). Hybridization between genetically distant cluster ensure the greater genetic variability in the progeny thereby increases the chance of obtaining superior hybrid. Greater the genetic diversity is directly linked to the extend of heterosis and also reduce the chance of inbreeding depression. The variance of cluster mean showed that, the trait test weight followed by flag leaf length, days to 50% flowering, flag leaf breadth, panicle length, fertile spikelets per panicle, days to maturity were the main characters for contributing divergence in current study. In present analysis productive tillers per plant, spikelet fertility %, infertile spikelets per panicle, grain yield per plant, plant height and total spikelets per panicle had comparatively much low contribution in divergence. Based on the divergence classes the genotypes *viz*., Karjat 5, VDN 1930, Karjat 5-4, VDN 1902, Phule Samruddhi, RTN 4, Ratnagiri 24, TKR 34, VDN 1832 and KJT TCR 39 may be used as potential donor for future hybridisation program to develop high yielders. Although the intercluster distance between cluster V (test weight- highest value) and cluster IX (flag leaf length- highest value) is 13.61 was not the maximum, it still represents sufficient genetic diversity to warrant hybridization. The high contribution percentages of test weight (25.13%) and flag leaf length (23.59%) highlight the importance of these traits in crop improvement. Hybridization between these clusters could lead to varieties with superior traits, including higher yield, better grain quality and improved stress adaptability. These traits are complementary and together ensure the efficiency of resource utilization (photosynthesis and grain filling), making them priorities in a breeding program.

Keywords: Divergence; grain yield; inter-cluster; intra-cluster; variance.

1. INTRODUCTION

Rice is generally considering a semi aquatic annual crop, although it could survive as a perennial in the tropics or subtropics areas. Cultivars of the two cultivated species are *Oryza sativa* L. and *O. glaberrima* L. Rice i.e., *Oryza sativa* L. is monocot plant having genus *Oryza* in wild Oryzeae in grasses like member of family Poaceae or Gramineae. For the majority of the world's population, particularly in Asia, it is the most extensively consumed staple food as a cereal grain. There is need to enhance rice production in order for satisfy the demands of the growing population and sustain self-sufficiency.

India is the second-largest producer of rice in the world, after china. According to Foreign Agriculture Service-U. S. Department of agriculture, in 2023-24, area under rice crop is 47.60 million hactare; production is 1370.00 lakh tonnes. Rice is cultivated in 32 districts of Maharashtra and none of the region comes under the high productivity area. Pune district (experimental trial area) is also come under low productivity district with a 1-1.5 tonnes/ha.

A breeding program's long-term success depends on knowing the genetic diversity among existing cultivars of any crop, which maximizes the exploitation of genetic resources (Belaj et al., 2002). One of the main tools for improving a crop that requires genetic diversity analysis for parent selection (Singh, 1983) is hybridization; furthermore, genetic diversity evaluation is crucial for the source genes of specific traits across the existing germplasm (Roy and Panwar, 1993).

In order to properly select parents for a better search for heterosis, it is crucial to quantify genetic diversity both within and between groups or clusters (Murty and Arunachalam, 1966). Multivariate analysis using the D2 technique evaluates the relative contributions of several components to the overall divergence and quantifies the level of genetic variety in a given population with regard to multiple features (Zahan et al., 2008). In light of the aforementioned situation, the purpose of this study was to ascertain rice's genetic diversity in order to maximize the use of genetic resources and choose donor parents appropriately. The goal of the current study is to better understand the genetic diversity among promising rice genotypes in order to increase output.

2. MATERIALS AND METHODS

The present investigation was carried out during *kharif* 2021 at Agricultural Research Station, Vadgaon Maval, Pune. In the present study fourty genotypes with thirteen character were

assessed to study the genetic diversity for yield and its components. Each genotype was sown in three rows of 4 m length following a spacing of 20 between the rows and 15 cm between the plants in randomized block design (RBD) with three replications. Standard agronomic practices were performed uniformly for all the experimental units. Phenological data for days to 50% flowering was recorded on plots basis for each genotype in each replication. At maturity five plants from each accession were selected randomly for recording data on grain yield per plant and; yield component traits, namely, plant height, productive tillers per plant, panicle length, grains per panicle and test weight.

2.1 Statistical Methods

The statistical analysis was done by standard statistical method suggested by Panse and Sukhatme (1995). The generalized distance (D^2) between two population is defined by Mahalanobis (1936). The D^2 value obtained for a pair of population is taken as the calculated value of x^2 and is tested against the tabulated values x^2 for "p" degrees of freedoms where p is number of characters considered (Singh and Chaudhary, 1977). Tocher´s method as described by Rao (1952) was followed for cluster formation. Genetic diversity as an index of selecting desirable parents for hybridization. The possible limits of parental divergence within which there were reasonably high chances for occurrence of heterosis were calculated following Arunachalam and Bandopadhyay (1984).

3. RESULTS AND DISCUSSION

The analysis of variance showed genotypes differed significantly for all the characters studied indicated presence of variability in the genotypes studied. Heritable improvement is based on genetic divergence, which is influenced by genetic factors. Therefore, comprehensive knowledge of genetic divergence is essential for a successful breeding effort. High heterotic effects from genetically different parents are known to result in desirable progenies in breeding method. A technique/method known as the multivariate analysis (D^2 statistic) quantifies the genetic diversity among genotype population given by Mahalanobis (1936). Therefore, the genetic diversity of the 40 genotypes under study was evaluated using 13 characteristics. There are 11 clusters formed of these 40 genotypes. The cluster I contained 12 genotypes, cluster II contained 6 genotypes, cluster III contained 9 genotypes, cluster X contained 4 genotypes, cluster IV contained 3 genotypes and remaining 6 cluster V, VI, VII, VIII, IX, XI are monogenotypic (Mohammad *et al*. (2017) observed genotypes divided into 11 clusters in that only one monogenotypic cluster was observed. Devi *et. al.* (2020) reported 11 clusters were cluster I and II was consisted with 33 and 29 genotypes respectively and remaining others was monogenotypic showing high diversity among genotypes. Current experiment was agreement with these by showing six (6) monogenotypic clusters among 11 clusters. Genetic divergences in 40 genotypes of rice were analysed by following Mahalanobis's D^2 statistic. The D^2 values for the pair of comparisons between these genotypes were in the ranged from 8.42 to 24.29 (Table 1). This high range for D^2 values indicated high amount of genetic diversity present in the genotypes. While the highest value was between clusters VII and XI, the lowest value is between the clusters V and VIII.

Determining intra- and inter-cluster distance is the fundamental idea behind cluster formation. This acts as an index to select parents of diverse origins. The D^2 values of the cluster elements are the basis for the intra and inter cluster values. Crossing between genotypes in various clusters with high inter-cluster D^2 values shall prove to be the better approach for achieving the desired results. D^2 values through divergence analysis were used to estimate the D^2 and D values of intra and inter cluster. The minimum intra cluster distance was observed in cluster II (8.95) followed by cluster I (9.17), cluster IV (10.78), cluster III (11.46) and cluster X (14.31). Other clusters are monogenotypic in nature hence indicated no intra cluster distance. The maximum inter cluster distance was observed between cluster VII and XI (24.29). The cluster VII had single genotype Karjat 5 which was short in height, medium in days to maturity and days to 50% flowering, more flag leaf length, more spikelet fertility %, high test weight and medium grain yield. Cluster XI had one genotype (VDN-1930), which was short in height, higher flag leaf length, highest flag leaf breadth, more fertile spikelets per panicle, higher spikelet fertility % and more test weight. The second maximum inter cluster distance D^2 was 24.03 (cluster III and XI) followed by 23.69 (cluster X and XI), 23.39 (cluster IV and VII), 22.21 (cluster I and IX). The minimum inter cluster distance was observed between cluster V and VIII (8.42) signifying their proximity to one another. Both of the cluster's constituents are monogenotypic. Cluster I was even further distant from the cluster IX (22.21), followed by cluster XI (22.18), cluster

X (19.14), cluster IV (18.30), cluster VIII (17.98), cluster V (15.96), cluster II (14.01), cluster III (12.68), cluster VI (11.26). While cluster II indicated the highest distance from the cluster X (22.17) followed by cluster XI (19.34), cluster VII (18.79), cluster IX (18.12), cluster III (17.28), cluster VI (14.61), cluster IV (14.41), cluster VIII (13.01), cluster V (12.32). Cluster III showed the maximum distance from cluster XI (24.03) followed by cluster IX (21.31), cluster VIII (19.54), cluster V (19.42), cluster IV (17.01), cluster X (15.20), cluster VI (14.67). The maximum distance by Cluster IV showed from cluster VII (23.39) followed by cluster XI (20.65), cluster X (19.21), cluster VI (18.25), cluster V (18.01), cluster IX (17.40), cluster VIII (15.43). Cluster V observed the maximum distance from cluster X (20.79) followed by cluster VII (16.23), cluster IX (13.61), cluster XI (12.82), cluster VI (10.40), cluster VIII (8.42). Cluster VI observed the highest distance from cluster IX and X (17.47), followed by cluster VII (16.27), cluster XI (16.06), cluster VIII (12.62). Cluster VII observed maximum distance from cluster XI (24.29) followed by cluster IX (20.85), cluster VIII (19.23), cluster X (17.81). Cluster VIII observed maximum distance from cluster X (20.04) followed by cluster XI (11.01), cluster IX (8.71). Cluster IX observed maximum distance from cluster X (19.02) and cluster XI (11.37). Cluster X observed maximum distance from cluster XI (23.69).

The highest inter cluster distance showed between cluster- VII & XI (24.29) demonstrating that the genetic composition- of the genotypes represented in cluster VII and cluster XI may be completely different. The cluster V, VIII, VII, IX, VI and XI with genotypes i.e., RTN 1410-1, RTN 1513-2, Karjat 5, RTN 2012-5, TKR 34, VDN 1930 respectively showed great diversity from other genotypes -present in clusters I, II, III, IV and X.

Cluster X showed the higher mean for traits like days to 50% flowering, days to maturity and productive tillers per plant. Cluster XI showed the high value for flag leaf breadth, spikelet fertility and grain yield per plant. Cluster XI observed lowest mean value for traits days to 50 % flowering, days to maturity and spikelet fertility. Cluster IV showed highest value for fertile spikelets and total spikelets per panicle, cluster V for test weight, cluster IX for flag leaf length and cluster VI for panicle length. From the results, it was indicated that no single cluster contained all desirable characters, which indicated no possibility of direct selecting one genotype for immediate use. Therefore, hybridization programme between the desirable genotypes from different clusters is essential to combine all the targeted traits to improve phenotypic performance.

The study of genetic divergence has limitations, including a limited representation of the genetic pool, as it often relies on a small sample of varieties that may not fully capture the genetic diversity of a species. Environmental factors and phenotypic plasticity can obscure genetic differences, making it difficult to attribute observed traits to genetic variation alone. Additionally, the choice of traits and markers may introduce bias and complex traits influenced by multiple genes are challenging to quantify accurately. Inbreeding or genetic bottlenecks in breeding lines can reduce the available genetic diversity.

The percent contribution of thirteen characters studied for total divergence is represented in Table 3. It was showed that test weight (1000 grain weight) contributed highest (25.13%) for divergence followed by flag leaf length (23.59%), days to 50% flowering (19.87%), flag leaf breadth (12.95%), panicle length (6.54%), fertile spikelets per panicle (4.10%), days to maturity (3.46%), productive tillers per plant (1.79%), spikelet fertility % (1.03%), infertile spikelets per panicle (0.77%), grain yield per plant (0.64%) and plant height (0.13%).The character panicle length is also responsible for divergence with 6.54 % (Sathyaraj et al. 2024). In genetic divergence studies of rice, plant height, flag leaf breadth, and infertile spikelets per panicle show lower contributions because they exhibit low variability, have been stabilized through breeding, traits play a supportive role, not direct (less) impact on yield or productivity compared to other traits. These traits are less effective in differentiating genotypes and therefore contribute minimally to overall divergence. The traits like test weight, flag leaf length and panicle length shows the maximum divergence because they are more directly correlated with productivity and often show higher variability.

The variance of cluster means was high for test weight followed by flag leaf length, days to 50 % flowering, flag leaf breadth, panicle length, days to maturity and fertile spikelets per panicle. This result were in similar with reports of Reddy *et al.* (2006), Hossain et al. (2021) for test weight. Saha *et al.* (2007) for flag leaf length, test weight and number of filled grains (fertile spikelets) per

Table 1. Average intra and inter cluster D^2 and D values of 11 clusters formed from 40 genotypes

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	9.17 (3.02)	14.01 (3.74)	12.68 (3.56)	18.30 (4.27)	15.96 (3.99)	11.26 (3.35)	16.06 (4.00)	17.98 (4.24)	22.21 (4.71)	19.14 (4.37)	22.18 (4.70)
II		8.95 (2.99)	17.28 (4.15)	14.41 (3.79)	12.32 (3.50)	14.61 (3.82)	18.79 (4.33)	13.01 (3.60)	18.12 (4.25)	22.17 (4.70)	19.34 (4.39)
III			11.46 (3.38)	17.01 (4.12)	19.42 (4.40)	14.67 (3.83)	16.53 (4.06)	19.54 (4.42)	21.31 (4.61)	15.20 (3.89)	24.03 (4.90)
IV				10.78 (3.28)	18.01 (4.24)	18.25 (4.27)	23.39 (4.83)	15.43 (3.92)	17.40 (4.17)	19.21 (4.38)	20.65 (4.54)
V					0.00 (0.00)	10.40 (3.22)	16.23 (4.02)	8.42 (2.90)	13.61 (3.68)	20.79 (4.55)	12.82 (3.58)
VI						0.00 (0.00)	16.27 (4.03)	12.62 (3.55)	17.47 (4.17)	17.47 (4.17)	16.06 (4.00)
VII							0.00 (0.00)	19.23 (4.38)	20.85 (4.56)	17.81 (4.22)	24.29 (4.92)
VIII								0.00 (0.00)	8.71 (2.95)	20.04 (4.47)	11.01 (3.31)
IX									0.00 (0.00)	19.02 (4.36)	11.37 (3.37)
X										14.31 (3.78)	23.69 (4.86)
XI											0.00 (0.00)

Table 2. Distribution of 40 rice genotypes into different cluster

Clusterno.	No. of genotypes included	Genotypes
I	12	RTN 1401-4, IGP 14-2, Indrayani, Phule Samruddhi, VDN 1822, IGP 13-11, RTN 4, VDN 1848, RTN 15 M6-22, IGP 12-1, KJT 2, KJT R-3.
II	6	Karjat 3, KJT 7, VDN 1902, RTN 1409-1, KJT-184, KJT 11012-8.
III	9	SKL 09-30, VDN 1942, RDN 20-10, PKV Ganesh, KJT 5-4, Kundalika, IGP Local, Palghar 1, RP 4-14
IV	3	Phule Radha, Ratnagiri 5, Ratnagiri-24
V	1	RTN 1410-1
VI	1	RTN 1513-2
VII	1	Karjat 5
VIII	1	RTN 2012-5
IX	1	TKR 34
X	4	VDN 1832, RDN 20-03, Super Basmati 1, KJT TCR 39
XI	1	VDN 1930

Table 3. Percent Distribution of 40 rice genotypes into different cluster

Sr. No.	Characters	Times ranked 1st	Contribution %
1.	Days to 50 % flowering	155	19.87
2.	Days to maturity	27	3.46
3.	Plant height	1	0.13
4.	Productive tillers/plant	14	1.79
5.	Panicle length	51	6.54
6.	Flag leaf length	184	23.59
7.	Flag leaf breadth	101	12.95
8.	Fertile spikelets per panicle	32	4.10
9.	Infertile spikelets per panicle	6	0.77
10.	Spikelet fertility	8	1.03
11.	Test weight (1000 grain weight)	196	25.13
12.	Grain yield/plant	5	0.64
	Total		**100**

Table 4. Mean performance of different clusters in rice

Cluster	Days to 50% Flower-ing (no.)	Days to maturiy (no.)	Plant Height (cm)	Productive Tillers per plant (no.)	Panicle length (cm)	Flag leaf length (cm)	Flag leaf breadth (cm)	Fertile spikelets per panicle (no)	Infertile spikelets per panicle (no)	Total spikelets per panicle (no)	Spikelet fertility %	Test weight (g)	Grain yield per plant (g)
I	102.63	134.46	78.50	6.48	22.37	29.73	1.80	159.17	21.17	180.33	88.25	23.48	23.18
II	88.42	116.67	68.46	5.75	21.81	30.49	1.68	163.25	22.67	185.92	87.25	23.40	21.27
III	104.83	135.50	79.86	6.36	21.62	32.59	1.64	184.83	25.00	209.83	88.04	16.88	18.70
IV	90.17	115.83	75.17	6.25	21.17	31.90	1.70	229.67	27.17	256.83	89.40	13.82	18.95
V	93.00	119.50	79.50	5.90	26.75	41.95	2.15	164.00	16.00	180.00	91.10	29.85	26.90
VI	104.50	134.50	92.00	5.65	27.05	38.60	2.35	166.50	21.00	187.50	88.80	26.25	23.65
VII	104.50	134.50	81.25	5.85	22.50	41.00	1.35	142.00	18.50	160.50	88.45	28.25	22.55
VIII	89.50	115.50	96.75	5.10	24.70	42.05	2.20	158.50	25.00	183.50	86.40	24.15	19.20
IX	87.50	113.50	85.50	5.60	23.80	50.80	2.25	171.50	27.00	198.50	86.40	20.05	19.00
X	106.38	136.50	93.56	6.50	25.14	43.40	1.71	212.50	27.88	240.38	88.39	16.00	20.36
XI	88.00	118.00	84.75	6.05	22.55	48.95	2.85	187.00	18.00	205.00	91.20	25.85	27.25

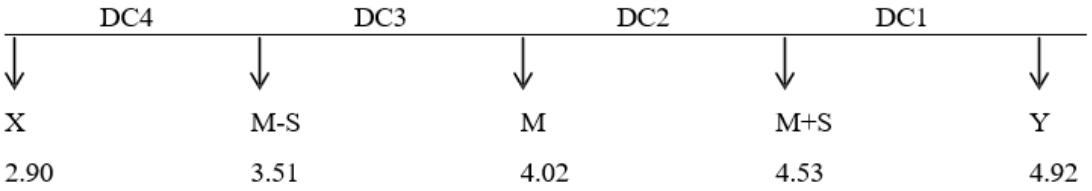

Fig. 1. Genetic divergence and selection of potent parents

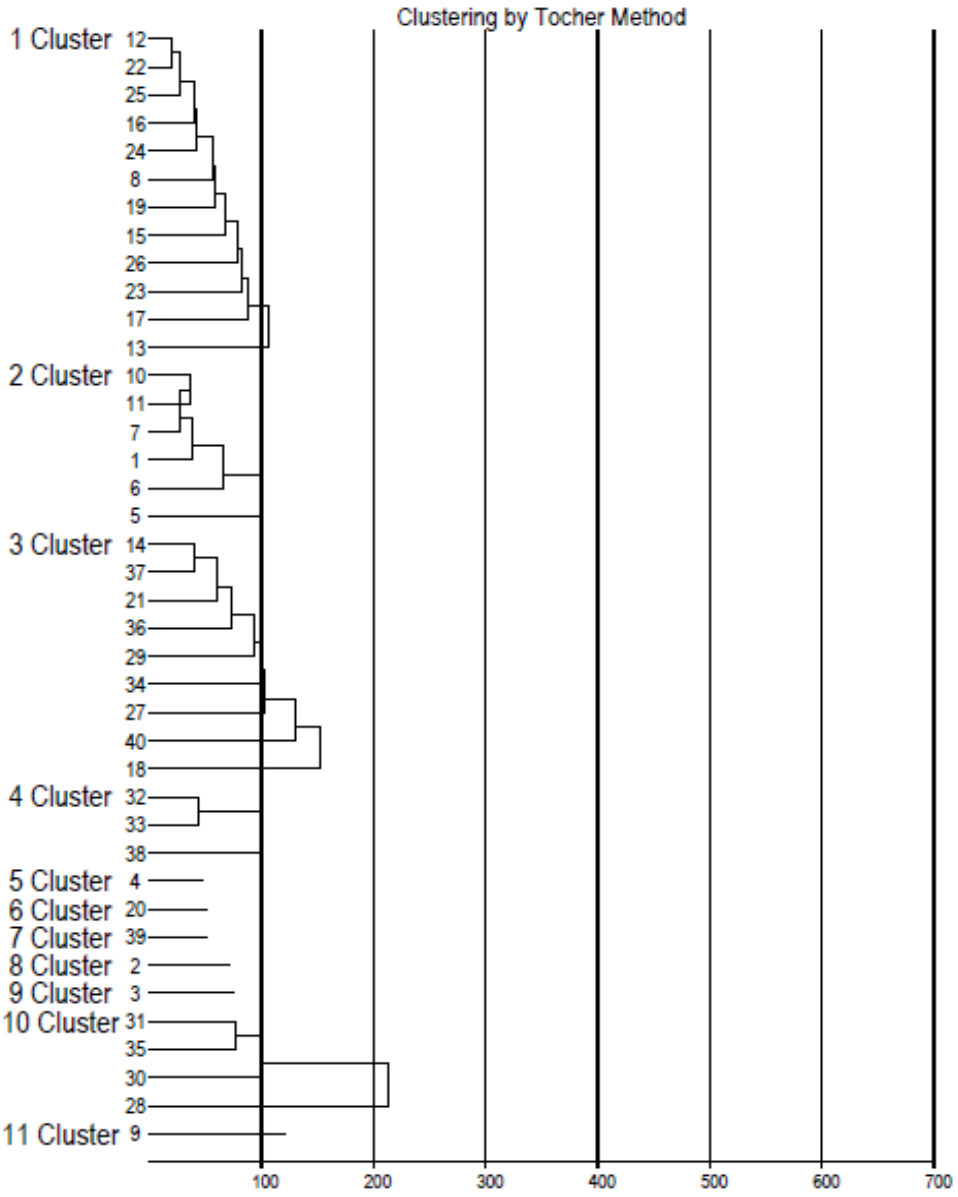

Fig. 2. Dendrogram: Cluster formation of genotypes

List of genotypes- *1) RTN 1409-1 2) RTN 2012-5 3) TKR 34 4) RTN 1410-1 5) KJT-184 6) KJT 11012-8 7) VDN 1902 8) IGP 13-11 9) VDN 1930 10) Karjat 3 11) KJT 7 12) RTN 1401-4 13) KJT R-3 14) SKL 09-30 15) VDN 1848 16) Phule Samruddhi 17) KJT 2 18) RP 4-14 19) RTN4 20) RTN 1513-2 21) RDN 2010 22) IGP 14-2 23) IGP 12-1 24) VDN 1822 25) Indrayani 26) RTN 15 M6-22 27) IGP Local 28) Super Basmati 29) KJT 5-4 30) VDN 1832 31) RDN 20-03 32) Ratnagiri 5 33) Phule Radha 34) Kundalika 35) KJT TCR 39 36) PKV Ganesh 37) VDN 1942 38) Ratnagiri-24 39) Karjat 5 40) Palghar1*

panicle. Agreement with Kavurikalpa *et al.* (2018) and Mishra *et al.* (2018) was observed high contribution of test weight. Sujitha *et al.* (2020) for days to 50 % flowering. Devi *et a*l. (2020) for test weight, days to 50% flowering and panicle length. Rai *et al.* (2014) to flag leaf length. Kumari *et al*. (2018) for days to 50 % flowering. In the present study plant height, productive tillers per plant, infertile spikelets per panicle, total spikelets per panicle, spikelet fertility and grain yield per plant had relatively low contribution towards divergence. Such type of result were reported by Shanmugam et al. (2023) and Devi *et al.* (2019) to number of productive tillers per plant. Kumari *et al*. (2018) for grains per panicle.

Genetic divergence and selection of potent parents: The success of a crop improvement programme is depend on the selection of the best parents with high potential for economically important characteristics. Among the various approaches of selecting parents, diversity-based selection is significant since diversity is a basic requirement for crop improvement. Studies of diversity among the different genotypes provided valuable information in the present study, which could be helpful in recommending potent parents in crossing.

The possible limits of the parental divergence at which there were relatively high chances of heterosis occurrence were calculated by following method of Arunachalam and Bandopadhyay (1984). They suggested classifying parental divergence into four (4) divergence classes. The mean (m) and standard deviation (s) of the divergence values were determined to account for the varying magnitude of variation in the parental divergence. The divergence classes are defined as follows:

They postulated that when two parents with genetic divergence between (m+s) and (m-s), that is in the classes DC2 and DC3, when crossed they have a higher chance of producing high frequency along with high magnitude of heterosis than a cross with parental divergence outside the limits [(m+s), (m-s)].

Table 5. Distribution of different cluster combinations in to four divergence classes based on D values between them

DC1	DC2	DC3	DC4
(I, IX) (I, XI) (II, X) (III, IX) (IV, VII) (V, X) (VII, IX) (VII, XI) (X, XI)	(I, VIII) (I, X) (II, III) (II, VII) (II, IX) (II, XI) (III, IV) (III, V) (III, VIII) (IV, V) (IV, VI) (IV, IX) (IV, X) (IV, XI) (VI, IX) (VI, X) (VII, VIII) (VII, X) (VIII, X) (IX, X)	(I, IV) (I, II) (I, III) (I, V) (II, IV) (II, VI) (II, VIII) (III, VI) (III, VII) (X, X) (III, X) (IV, VIII) (V, VII) (V, IX) (V, XI) (VI, VII) (VI, VIII) (VI, XI)	(I, I) (I, VI) (I, VII) (II, II) (II, V) (III, III) (IV, IV) (V, VI) (V, VIII) (VIII, IX) (VIII, XI) (IX, XI)

Table 6. Better performance of genotypes selected for breeding programme based on inter-cluster distances

Sr. No	Genotype	Better performance for traits
1	Karjat 5	Grain yield, more test weight, flag leaf length, spikelet fertility % and medium maturity.
2	VDN 1930	Grain yield, early flowering and maturity, flag leaf length and breadth, total spikelets per panicle, spikelet fertility% and more test weight.
3	Karjat 5-4	Grain yield, productive tiller per plant, plant height, total spikelets per panicle, spikelet fertility%, medium maturity and less test weight.
4	VDN 1902	Grain yield, early flowering and maturity, plant height, productive tillers per plant, panicle length, spikelet fertility% and more test weight.
5	Phule Samruddhi	Grain yield, productive tillers per plant, panicle length, flag leaf length and breadth, spikelet fertility % and medium test weight.
6	RTN 4	Grain yield, medium maturity, productive tillers per plant, more test weight and spikelet fertility%.

Sr. No	Genotype	Better performance for traits
7	Ratnagiri -24	Grain yield, early flowering and maturity, productive tillers per plant, panicle length, flag leaf length and breadth, total spikelets per panicle spikelet fertility % and medium test weight.
8	TKR 34	Early flowering and maturity, flag leaf length and breadth, plant height and medium test weight.
9	VDN-1832	Grain yield, medium maturity, productive tillers per plant, flag leaf length, total spikelets per panicle, spikelet fertility % and less test weight.
10	KJT TCR 39	Grain yield, medium maturity, productive tillers per plant, flag leaf length and breadth, total spikelets per panicle, spikelet fertility % and less test weight.

The cluster combinations were classified into four divergence classes, following the method suggested by Arunachalam and Bandopadhyay (1984). On the basis of the results, the parents should be chosen from the cluster combinations in the divergence classes DC1, DC2, and DC3. However, when selecting among the genotypes from a cluster, the per se performance for the genotypes of different characteristics (Table 4) such as grain yield per plant, test weight, flag leaf length and breadth, days to 50% flowering, plant height, fertile spikelets per panicle, productive tillers per plant etc. should be considered so that desirable segregates can be obtained after the hybridization.

4. CONCLUSIONS

On the basis of divergence classes, the genotypes *viz*., Karjat 5, VDN 1930, Karjat 5-4, VDN 1902, Phule Samruddhi, RTN 4, Ratnagiri 24, TKR 34, VDN 1832 and KJT TCR 39 were found superior to the most of the traits and will be used for the future breeding programme. Based on the studies these genotypes it is observed that best genotypes having all the desired outcomes of grain yield along with yield contributing components and higher inter-cluster distances could be used in the future breeding improvement for yield.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of this manuscript.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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