

Assessment of Genetic Diversity in Rice (*Oryza sativa* L.) under Irrigated and Drought Stress Condition

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Authors' contributions

This work was carried out in collaboration among all authors. Author SP designed the study, conducted the experiment and wrote the first draft. Author MC performed the statistical analysis. Author AK managed the analyses and edited the first draft of the study. Author BDP managed the literature searches. All authors read and approved the final manuscript.

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ABSTRACT

A set of 48 rice genotypes were evaluated to assess the magnitude of genetic diversity under irrigated (control) and reproductive stage drought stress conditions during *Kharif*, 2018 at Rice Research Farm, Bihar Agricultural University, Sabour (Bhagalpur), India. On the basis of D² statistics, all the genotypes were grouped into nineteen clusters in irrigated condition with cluster I consisting of maximum number of genotypes (24) followed by cluster III (7) and rest of the clusters were represented by single genotype in irrigated condition. Under drought stress condition, forty eight genotypes were grouped into eleven clusters, cluster I consisted of maximum number of genotypes (24) followed by cluster II and III (8 genotypes in each cluster) and rest of the clusters were mono-genotypic. The highest inter-cluster distance was recorded between cluster XVIII and

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XIX (28.53), followed by cluster X and VIII (24.20), cluster XIII and XVIII (23.98) and cluster VII and XVIII (23.79) in irrigated condition while in drought stress condition the highest inter-cluster distance was observed between cluster IX and X (31.72), followed by cluster V and IX (28.77), cluster VI and VII (25.98) and cluster IV and IX (25.98) indicating wider genetic diversity among the genotypes between these clusters. The hybridisation programme involving genotype of cluster XVIII and cluster XIX under irrigated condition and the genotypes of cluster IX and X under drought stress condition could be undertaken to isolate high yielding segregants, since these genotypes have high yielding potential, number of effective tillers per hill, relative water content, leaf area, root biomass, panicle length, biological yield, harvest index, plant height, number of fertile grains per panicle, total number of spikelets per panicle, leaf area and proline content with more genetic distances. The parents for hybridisation could be selected on the basis of their large inter-cluster distance for isolating useful recombinants in the segregating generations. Hence, these genotypes might be used in a multiple crossing programme to recover transgressive segregants. Therefore, it is suggested that if the diverse genotypes from these groups along with the other desirable attributes are used in breeding programmes, it is expected to produce better segregants for high grain yield and yield contributing traits due to non-allelic interaction.

Keywords: Rice; genetic diversity; irrigated; drought stress; clusters.

1. INTRODUCTION

Rice (*Oryza sativa* L.) is the most important food crop and a primary food source for more than one third of the world's population. It is a self-pollinated crop belonging to family *Poaceae* with a genome size of 430 mb. Globally rice is grown over an area of about 164 million hectares with an annual production of 723 million tons. The area, production and productivity of rice in India is 43.19 million hectares, 110.15 million tonnes and 2550 kg/hectare, respectively [1]. In Bihar the area under rice cultivation was 3.31 million hectares with productivity 2447 kg/ha (Directorate of Economics & Statistics, 2017-18). The report by International Food Policy Research Institute (IFPRI) stated that by 2025 rice prices will increase between 32-37% as a result of climate change and yield losses in rice could be between 10-15% [2]. Rainfed rice accounts for around 45% of the world's rice area and around 40 million hectares of rain-fed area is concentrated in South and South East Asia alone [3]. Rainfed rice growing areas are highly prone to abiotic stresses such as drought, high temperature and submergence depending upon the distribution of rainfall and topography. In India, out of the total 43.19 million hectares approximately 16.2 million hectares is present in eastern-India, of which 6.3 million hectares of upland and 7.3 million hectares of lowland area are highly susceptible to drought [4]. Rice crop is highly sensitive to temperature and soil moisture deficit stresses at reproductive stage.

Germplasm is the basic material for genetic improvement of the crop. The pace and magnitude of genetic improvement generally

depend on the amount of genetic variability present in a population. It is essential to assess the genetic divergence in available germplasm. The importance of genetic diversity for successful selection of parents to be used in hybridization has been emphasized earlier. Precise information on the nature and degree of genetic divergence of the parents is the prerequisite of an effective breeding program. The D^2 technique developed by Mahalanobis [5] had been found to be a potent tool in quantifying the degree of divergence in germplasm. This analysis provides a measurement of relative contribution of different components on diversity both at inter-cluster and intra-cluster level and genotypes drawn from widely divergent clusters are likely to produce heterotic combinations and wide variability in segregating generation [6]. In the present study genetic divergence among 48 rice genotypes has been studied to help the breeders in selecting promising and genetically diverse parents for desired improvement in rice under rainfed condition of eastern India as well as under irrigated conditions. Along with study of the magnitude of genetic divergence, the characters contributing towards the genetic divergence in rice under irrigated and reproductive stage drought stress conditions were also identified to help the breeders in selecting promising and genetically diverse parents for improvement of rice under rainfed condition of eastern India.

2. MATERIALS AND METHODS

A set of forty eight rice genotypes (Table 1) including two checks viz., Sahbhagidhan and Sabour Deep were evaluated in two

environments, irrigated condition and reproductive drought stress conditions during *kharif* 2018 in a randomized block design with three replications at rice research farm, Bihar Agricultural University, Sabour, Bhagalpur, Bihar. In the control set of experiment, standing water was maintained from transplanting to 20 days before maturity by supplying water through rain or through supplementary irrigation as and when required. The reproductive stage drought stress experiment was irrigated like the control experiment by allowing standing water up to 28 days after transplanting. Thereafter, the field was drained to enable them to dry for the development of stress. Supplemental irrigation was prohibited in the drought stress experiment. During the reproductive stage stress period soil moisture content was monitored through tensiometer reading. All the recommended package of practices for rice was followed to raise a healthy crop. Data were recorded on five randomly and competitive plants of each genotype from each replications for nineteen quantitative characters viz., number of effective tillers per hill, plant height (cm), panicle length (cm), number of fertile grains per panicle, spikelet sterility (%), panicle density index, total number of spikelets per panicle, 1000 grain weight (g), grain yield per plant (g), biological yield (g), harvest index (%), proline content, chlorophyll index, canopy temperature, leaf area, relative water content and root biomass. Data on days to 50 % flowering and days to maturity were recorded on plot basis. Genetic divergence was determined by using D^2 statistics of Mahalanobis [5] and clustering of genotypes was done according to Tocher's method. The percentage contribution of studied characters towards genetic divergence was computed according to Singh and Chaudhary [7].

3. RESULTS AND DISCUSSION

The analysis of variance (Table 2) revealed that there was highly significant variation among the genotypes for all the traits studied under both the environments. This in turn indicated that there was sufficient variability in the material studied under both drought stress and irrigated conditions, which could be utilized in breeding programme. Based on relative magnitude of D^2 values, forty eight genotypes were grouped into nineteen clusters in irrigated condition and eleven clusters in drought stress conditions (Table 3 and Table 4). The cluster diagram by Tocher method for irrigated and drought stress

condition is given in Figs. 1 and 2, respectively. Among the nineteen clusters, cluster I consisted of a maximum number of genotypes (24) followed by cluster III (7) and rest of the clusters were represented by single genotype in irrigated condition (Table 3). Under drought stress condition, forty eight genotypes were grouped into eleven clusters, cluster I consisted of a maximum number of genotypes (24) followed by cluster II and III (8 genotypes in each cluster) and rest of the clusters were mono-genotypic (Table 4). The pattern of distribution of genotypes from diverse geographical region into different clusters was random. It revealed that genotypes collected from same geographic region got distributed in different clusters. It might be due to selection differential or genetic drift under diverse environmental conditions within the same geographical region. Similarly genotypes collected from different places coexisted in the same clusters. Thus the distribution of genotypes into different clusters was not associated with their geographical region. The results are in agreement with earlier findings of Roy et al. [8]. This tendency of genotypes occurring in the same cluster cutting across the geographical boundaries demonstrated that geographical diversity might not always be useful index in assessing genotypic diversity in rice.

The inter cluster distances were greater than intra cluster indicating wide genetic diversity among genotypes (Table 5 and Table 6). The similar results were reported by Banumathy et al. (2010) and Hosan et al. [9]. The intra-cluster D^2 value ranged from 0.00 to 9.76 (Table 5) and 0.00 to 12.01 (Table 6) under irrigated and drought stress conditions, respectively. The maximum intra cluster distance was exhibited by cluster III (9.76) followed by cluster I (8.92) in irrigated condition (Table 5), whereas, in drought stress condition the highest intra-cluster distance was recorded for cluster III (12.01) followed by cluster II (10.7) and cluster I (9.7) (Table 6) indicating wide genetic variability within the genotypes of these clusters. The highest intra-cluster distance was recorded for genotypes from these clusters could be utilized as parental lines for hybrid breeding programmes owing to their higher mean performance within group. The least intra cluster distance indicated homogenous nature of the genotypes with less deviation between the genotypes. Hence, selection will be ineffective. Similar findings were reported by Rajesh et al. [10].

Table 1. List of genotypes

S. no.	Genotypes	Sources	S. no.	Genotypes	Sources
1	IR 95785-31-2-1-2	IRRI	25	IRRI 123	IRRI
2	IR 14L155	IRRI	26	IR 107891-B-B-111-2-1	IRRI
3	IR 107891-B-B-845-1-1	IRRI	27	IR 107891-B-B-1019-1-1	IRRI
4	IR 90257-B-577-1-1-B	IRRI	28	IR 107891-B-B-548-1-1	IRRI
5	IR 14L157	IRRI	29	IR 107891-B-B-664-3-1	IRRI
6	IR 107891-B-B-846-2-1	IRRI	30	DRR dhan 44	IIRR, Hyderabad
7	IR 107891-B-B-1110-3-1	IRRI	31	IR 107891-B-B-1394-1-1	IRRI
8	IR 14L362	IRRI	32	Sahbhagidhan	Hazaribag, Jharkhand
9	IR 90257-B-577-1-1-B-1	IRRI	33	IR 108198-23-1-1-B	IRRI
10	IR 95817-5-1-1-2	IRRI	34	SWARNA	Maruteru (ANGRAU)
11	Sabour Deep (C)	Sabour, Bhagalpur	35	IR 14L613	IRRI
12	MTU 1010	APPRI, Maruteru	36	IR 107891-B-B-359-3-1	IRRI
13	IR 106312-50-1-1-1	IRRI	37	IR 107891-B-B-1284-2-1	IRRI
14	IR 107891-B-B-785-2-1	IRRI	38	IR 107891-B-B-1023-1-1	IRRI
15	IR 107891-B-B-1253-1-1	IRRI	39	IR 90257-B-577-2-1-3-B	IRRI
16	Sambha Mahsuri		40	IR 108198-23-24-1-B	IRRI
17	IR 107891-B-B-90-3-1	IRRI	41	IR 64	IRRI
18	IR 107891-B-B-379-2-1	IRRI	42	TRP-20-7-1-B-2-B	IRRI
19	IR 106516-1-2-2-2	IRRI	43	IR 107891-B-B-1304-1-1	IRRI
20	IR 107891-B-B-447-2-2	IRRI	44	IR 127363-76-1	IRRI
21	IR 103587-22-5-5-B	IRRI	45	IR 13L378	IRRI
22	IR 108199-24-32-1-1-B	IRRI	46	IR 107891-B-B-1216-1-1	IRRI
23	IR 107891-B-B-1432-2-1	IRRI	47	IR 107891-B-B-447-3-1	IRRI
24	IR 93827-29-1-1-4	IRRI	48	IR 93827-29-2-1-3	IRRI

The inter-cluster D^2 value ranged from 7.45 to 28.53 and 9.64 to 31.71 under irrigated and drought stress conditions, respectively (Table 5 and Table 6). The highest inter-cluster distance was recorded between cluster XVIII and XIX (28.53), followed by cluster X and VIII (24.20), cluster XIII and XVIII (23.98) and cluster VII and XVIII (23.79) in irrigated condition (Table 5) while in drought stress condition the highest inter-cluster distance was observed between cluster IX and X (31.72), followed by cluster V and IX (28.77), cluster VI and VII (25.98) and cluster IV and IX (25.98) (Table 6) indicating wider genetic diversity among the genotypes between these clusters. These findings are in accordance with the results of Bose et al. [11], Abarshahr et al. [12], Chakravorty and Ghosh [13], Chandramohan et al. [14] and Devi et al. [15]. The greater distance between clusters revealed wider genetic diversity between genotypes. Selection of genotypes belonging to distant clusters is expected to produce highly variable population in the segregating generation. Hence,

genotypes belonging to these clusters may be utilized in hybridization programme for rice improvement.

In the present study, a considerable variation in cluster mean values was revealed for all the characters (Table 7 and Table 8). Cluster XVIII had the highest mean value for grain yield per plant, leaf area, root biomass and days to flowering and days to maturity in irrigated condition indicating directly towards better yield potential while, Cluster XIX had the noticed highest mean value for effective tillers per hill and relative water content (Table 7). Cluster X had highest mean value for 1000 grain weight, number of fertile grains per panicle, total number of grains per panicle and panicle density index in irrigated condition (Table 7) indicating directly towards better yield potential in irrigated condition while, cluster VII had noticed the highest mean value for harvest index, relative water content and proline and cluster XIII noticed the highest mean value for panicle length (Table 7).

Table 2. Analysis of variance for nineteen different characters in forty eight rice genotypes under control and stress conditions

S. no.	Characters	Mean sum of squares					
		Replication (d.f. =02)		Treatment (d.f. =47)		Error (d.f. =94)	
		c	s	c	s	c	S
1	Days to 50% flowering	10.54	12.79	18.191**	18.454**	7.32	7.15
2	Days to maturity	5.15	2.31	23.786**	23.106**	13.61	5.55
3	Effective tillers per hill	1.79	0.17	3.359**	1.624**	0.35	0.42
4	Plant height (cm)	88.73	112.75	157.206**	208.411**	32.68	62.89
5	Panicle length (cm)	0.49	0.98	7.527**	9.056**	2.01	2.17
6	No. of fertile grains panicle ⁻¹	53.24	495.58	1128.890**	581.411**	91.29	47.55
7	No. of sterile grains panicle ⁻¹	1.01	7.79	92.410**	133.375**	3.30	4.69
8	Sterility %	1.96	29.36	40.423**	61.311**	2.28	3.16
9	Total no. of spikelets panicle ⁻¹	41.47	386.54	1318.710**	868.453**	92.34	51.45
10	Panicle density index	0.18	0.89	1.972**	1.353**	0.23	0.19
11	1000 grain weight	1.15	3.00	13.919**	11.699**	1.38	1.83
12	Biological yield (g)	14.88	17.06	45.945**	32.791**	12.07	12.77
13	H.I. (%)	9.73	16.74	19.097**	56.939**	11.05	23.83
14	Grain yield plant ⁻¹	2.89	4.65	20.919**	13.202**	3.58	1.47
15	Leaf area	13.15	0.72	110.514**	120.04	2.99	1.72
16	RWC	1.59	0.37	46.047**	39.526**	2.98	0.65
17	Proline	1.46	2.71	7.246**	7.464**	0.31	0.48
18	Root biomass	1.36	1.45	66.496**	29.590**	3.50	1.94
19	Chlorophyll Index	9.77	0.20	26.627**	13.903**	12.69	2.67

Cluster XII had exhibited high biological yield while, cluster XV had the lowest mean value for flowering and maturity (Table 7).

Under drought stress condition, cluster X had the highest mean value for panicle fertile grains per panicle, total number of grains per panicle, tall plant stature, leaf area, relative water content and proline while, cluster IX had high mean value for panicle length, biological yield, harvest index and grain yield per plant (Table 8). Cluster XI had noticed the highest mean value for chlorophyll index and panicle density index while, cluster VIII had high mean value for effective tillers per hill (Table 8). Cluster VII had the highest mean value for leaf area, early flowering and early maturity while, cluster V had exhibited high mean value for 1000-grain weight and root biomass (Table 8). These results are in agreement with the result of Tirkey et al. [16]. The findings of present study suggested that inter-crossing of genotypes from different clusters exhibiting good mean performance may be helpful for obtaining higher yield (Table 11 and Table 12) and thus, selection of more diverse parents for hybridization is

believed to provide the chances of getting better heterosis and give broad spectrum of variability in segregating generation.

The selection and desirability of parents mainly depend upon contribution of characters towards divergence. In the present investigation the highest contribution in manifestation of genetic divergence was exhibited by leaf area followed by fertile grains per panicle, proline, root biomass, relative water content, total grains per panicle, effective tillers per hill, grain yield per plant, 1000-grain weight and panicle length in irrigated condition (Table 9). Under drought stress condition, relative water content contributed maximum towards genetic divergence followed by leaf area, number of fertile grains per panicle and root biomass, proline, grain yield per plant, 1000-grain weight and harvest index (%) (Table 10). Therefore, these characters may be given importance during hybridization programme. The present findings were in accordance with the results of Banumathy et al. (2010), Mina et al. [17], Mahalingam et al. [18] and Basavaraja et al. [19].

Table 3. Distribution of 48 genotypes under irrigated (control) condition

Cluster	No. of genotypes	Name of genotypes
I	24	IR 103587-22-5-5-B, IR 107891-B-B-1304-1-1, IR 14L157, IR 127363-76-1, TRP-20-7-1-B-2-B, IR 107891-B-B-846-2-1, IR 107891-B-B-1432-2-1, IR 108199-24-32-1-1-B, IRR1 123, IR 90257-B-577-2-1-3-B, IR 14L613, IR 107891-B-B-379-2-1, IR 107891-B-B-1394-1-1, IR 107891-B-B-447-2-2, MTU 1010, IR 107891-B-B-359-3-1, IR 107891-B-B-785-2-1, IR 107891-B-B-90-3-1, IR 108198-23-1-1-B, IR 108198-23-24-1-B, IR 127363-76-1, IR 106312-50-1-1-1, IR 107891-B-B-1019-1-1, IR 107891-B-B-1216-1-1
II	1	IR 64
III	7	IR 107891-B-B-111-2-1, IR 107891-B-B-548-1-1, IR 107891-B-B-1023-1-1, IR 107891-B-B-1284-2-1, IR 93827-29-1-1-4, Sahbhagidhan, DRR dhan 44
IV	1	IR 90257-B-577-1-1-B
V	1	IR 107891-B-B-1253-1-1
VI	1	IR 107891-B-B-1110-3-1
VII	1	IR 107891-B-B-845-1-1
VIII	1	IR 14L362
IX	1	IR 95785-31-2-1-2
X	1	IR 106516-1-2-2-2
XI	1	Sambha Mahsuri
XII	1	IR 14L155
XIII	1	IR 107891-B-B-664-3-1
XIV	1	SWARNA
XV	1	IR 90257-B-577-1-1-B-1
XVI	1	IR 95817-5-1-1-2
XVII	1	Sabour Deep
XVIII	1	IR 107891-B-B-447-3-1
XIX	1	IR 13L378

Table 4. Distribution of 48 rice genotypes under drought stress condition

Cluster	No. of genotypes	Name of genotypes
I	24	MTU 1010, IR 107891-B-B-1019-1-1, IR 107891-B-B-785-2-1, IR 14L155, IRR1 123, IR 107891-B-B-379-2-1, IR 64, IR 107891-B-B-1304-1-1, IR 106516-1-2-2-2, IR 127363-76-1, IR 107891-B-B-359-3-1, IR 107891-B-B-1394-1-1, SWARNA, IR 108198-23-24-1-B, IR 107891-B-B-447-2-2, TRP-20-7-1-B-2-B, IR 107891-B-B-90-3-1, IR 93827-29-2-1-3, IR 107891-B-B-845-1-1, IR 14L613, IR 108198-23-1-1-B, IR 107891-B-B-1110-3-1, Sambha Mahsuri and IR 107891-B-B-664-3-1
II	8	IR 103587-22-5-5-B, IR 107891-B-B-1432-2-1, IR 108199-24-32-1-1-B, IR 90257-B-577-1-1-B, IR 107891-B-B-846-2-1, IR 95785-31-2-1-2, IR 14L362, IR 90257-B-577-1-1-B-1
III	8	IR 107891-B-B-1284-2-1, IR 107891-B-B-1216-1-1, Sahbhagidhan, IR 93827-29-1-1-4, IR 107891-B-B-548-1-1, IR 107891-B-B-1023-1-1, IR 90257-B-577-2-1-3-B, DRR dhan 44
IV	1	IR 107891-B-B-1253-1-1
V	1	IR 107891-B-B-111-2-1
VI	1	IR 106312-50-1-1-1
VII	1	IR 107891-B-B-447-3-1
VIII	1	IR 13L378
IX	1	IR 14L157
X	1	IR 95817-5-1-1-2
XI	1	Sabour Deep

Table 5. Average intra and inter cluster distance values among nineteen clusters for forty eight genotypes of rice under irrigated condition

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI	XVII	XVIII	XIX
I	8.92	11.11	12.83	11.51	10.65	11.11	11.07	10.7	10.91	12.15	11.01	11.17	12.94	11.42	13.17	15.26	12.78	19.55	16.85
II		0	14.43	11.91	9.62	7.45	13.97	12.18	13.04	16.4	10.98	12.1	15.36	15.01	14.68	15.69	15.01	21	17.67
III			9.76	13.55	14.18	12.24	14.96	13.68	13.69	16.73	12.13	15.03	17.48	14.42	17.17	14.45	13.74	14.09	23.28
IV				0	13.97	11.45	14.68	12.18	10.7	13.39	15.75	12.26	9.11	10.36	8.9	9.37	13.1	19.02	15.78
V					0	8.42	11.71	13.59	11.72	17.58	8.54	12.92	17.23	14.55	16.76	18.4	16.2	21.29	21.37
VI						0	14.44	11.12	9.47	16.57	10.33	13.67	16.76	12.69	16.75	16.03	16.51	18.15	21.75
VII							0	9.59	11.78	12.47	12.12	9.63	13.58	13.82	15.65	18.11	12.21	23.79	18.5
VIII								0	8.95	9.34	14.59	11.64	13.02	10.73	15.09	16.18	13.85	21.72	18.34
IX									0	12.44	13.33	12.64	14.18	8.93	15.93	17.26	15.07	20.95	20.26
X										0	18.11	13.21	11.28	10.87	12.88	17.31	13.66	24.2	15.53
XI											0	13.23	18.38	15.48	17.87	18.12	14.82	18.03	22.22
XII												0	12.8	15.9	13.47	15.15	13.85	21.58	16.63
XIII													0	11.65	8.86	12.83	14.38	23.98	10.21
XIV														0	14.07	15.87	14.51	20.84	17.79
XV															0	10.3	14.17	22.38	12.52
XVI																0	16.04	15.42	18
XVII																	0	21.09	17.9
XVIII																		0	28.53
XIX																			0

Table 6. Average intra and inter cluster distance values among nineteen clusters for forty eight genotypes of rice under drought stress condition

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	9.7	13.85	14.27	15.03	19.31	13.15	22.18	13.41	16.51	21.07	15.87
II		10.7	17.59	14.25	18.24	14.1	21.25	16.32	24.15	15.49	21.57
III			12.01	21.42	15.14	15.63	15.92	18.7	19.01	19.51	16.61
IV				0	21.66	12.82	25.75	20.18	25.98	22.35	25.94
V					0	14.33	9.64	24.56	28.77	15.21	24.28
VI						0	19.6	18.88	22.64	19.45	22.81
VII							0	27.32	29.12	16.48	24.78
VIII								0	16.63	22.93	12.66
IX									0	31.72	13.97
X										0	25.6
XI											0

Table 7. Mean values of clusters of different characters towards genetic divergence in 48 rice genotypes under irrigated condition

	DFF	DM	EBT	PHT	PL	NFG PP	NSG PP	SS%	TNS PP	PDI	1000 GR WT	BY	HI %	LA	RWC	PROLINE	RB	CI	GYPP
Cluster I	89.42	117.93	8.5	103.58	27.11	115.49	13.94	10.84	129.43	4.8	25.87	45.81	48.82	23.82	86.66	32.61	20.65	44.23	24.84
Cluster II	88	116.33	8.27	86	25.78	110.74	16.94	13.24	127.68	4.96	21.31	39.84	48.5	20.68	90.4	35.14	19.73	47.4	18.28
Cluster III	88.71	118.67	8.31	99.68	26.46	126.83	11.71	8.52	138.55	5.27	26.43	44.19	49	36.04	91.14	32.87	22.46	44.94	24.04
Cluster IV	87.33	115.33	9.47	107.33	28	123.77	22.25	15.23	146.03	5.23	25.42	47.94	48.6	30.01	92.1	34.53	12.48	43.38	25.4
Cluster V	88.33	116.67	8.12	105.33	28	88	6.35	6.8	94.36	3.39	23.72	43.02	48.07	19.28	90.56	34.24	19.66	42.83	23.6
Cluster VI	90.67	120	9.35	89	26.89	124.56	9.97	7.44	134.53	5.01	23.79	45.53	47.83	23.23	93.43	30.86	18.24	44.03	25.38
Cluster VII	91	119.67	7.22	117.22	23.67	120.23	7.65	5.98	127.88	5.42	21.72	41.03	51.63	22.64	87.64	36.02	14.44	45.33	20.75
Cluster VIII	92	122	7.83	110.22	27.67	164.66	11.71	6.65	176.37	6.37	22.78	41.25	49.92	23.78	91.79	33.4	14.91	43.23	22.19
Cluster IX	88	115	10.78	103.34	26.34	136.74	6.98	4.88	143.71	5.46	25.92	47.08	48.2	24.87	90.41	34.23	13.23	47.2	27.79
Cluster X	87	115.67	8.3	106.78	26.11	182.36	17.94	9.04	200.3	7.73	28.67	48.06	47.54	22.29	87.11	31.35	16.68	49.73	24.96
Cluster XI	90.67	119.67	8.81	86.33	22.44	90.58	7.02	7.19	97.61	4.38	25.03	45.16	48.8	24.25	85.52	32.61	24.79	45.27	24.01
Cluster XII	90.67	118.33	7.11	105.67	25.56	118.02	13.28	10.13	131.3	5.15	22.31	56.61	36.89	24.8	81.21	33.71	12.37	48.63	20.3
Cluster XIII	87	116	8.7	104.44	28.78	122.7	25.59	17.34	148.29	5.15	23.01	47.05	50.1	26.02	87.77	31.11	10.46	42.23	25.59
Cluster XIV	85	116.67	8.7	99.89	25.89	140.81	16.41	10.44	157.22	6.1	26.16	47.73	48.76	24.39	79.39	31.49	21.19	44.67	30.28
Cluster XV	81.33	110.67	7.44	113.11	27.34	139.5	26.91	16.16	166.41	6.09	27.04	42.3	49.65	26.16	84.62	33.29	14.56	42.1	23.08
Cluster XVI	90.67	121	7.88	114.22	28.33	143.82	26.24	15.42	170.06	6	22.89	42.77	49.72	37.85	87.19	34.24	17.68	44.13	23.32
Cluster XVII	91.33	122	6.94	108.78	21.35	98.07	20.67	17.5	118.74	5.58	27.91	33.3	49.54	32.17	91.08	30.5	18.6	55.4	18.93
Cluster XVIII	97.67	126.33	9.02	91.11	25.33	124.69	14.62	10.49	139.31	5.5	26.92	47.84	48.11	45.47	85.28	34.52	31.27	42.53	31.36
Cluster XIX	88.67	118.67	10.85	101.22	27.89	98.99	32.11	24.45	131.1	4.71	21.55	37.9	45.67	20.63	94.42	30.26	17.1	44.2	19.45

DFF= days to 50% flowering; DM=days to maturity; EBT= number of effective tillers per hill; PHT= plant height; PL= panicle length; NFGPP= number of fertile grains per panicle; NSGPP= number of sterile grains per panicle; SS%= spikelet sterility %; TNSPP= total number of spikelets per panicle; PDI= panicle density index; GR WT= grain weight; BY= biological yield; HI= harvest index; LA= leaf area; RWC= relative water content; RB= root biomass; CI= chlorophyll index; GYPP= grain yield per plant

Table 8. Mean values of clusters of different characters towards genetic divergence in 48 rice genotypes under drought stress condition

	DFF	DM	EBT	PHT	PL	NFGPP	NSGPP	SS%	TNSPP	PDI	1000 GR WT	BY	HI%	LA	RWC	PRO LINE	RB	CI	GYP P
Cluster I	84.61	113.87	7.75	98.45	25.86	92.49	19.63	17.32	112.12	4.37	20.73	40.57	38.79	17.39	72.28	44.24	13.69	42.06	15.61
Cluster II	84.42	113.38	8.2	96.88	26.66	119.49	21.85	15.28	141.34	5.32	22.91	41.29	41.41	18.91	77.02	45.04	12.38	40.83	16.96
Cluster III	85.04	115.75	8.14	97	26.09	96.78	19.22	16.66	115.99	4.47	20.25	40.07	40.91	28.25	71.15	44.14	15.02	41.49	16.25
Cluster IV	93.67	123.67	7.38	99.89	27.7	84.18	8.74	9.39	92.92	3.38	24.24	39.52	42.42	12.39	77.79	45.39	12.57	39.33	16.7
Cluster V	83.67	113.00	8.04	85	25.42	86.51	17.18	16.64	103.69	4.12	24.88	42.08	41.41	34.3	78.84	43.52	21.27	41.28	17.44
Cluster VI	85.33	115.33	8.6	99.67	25.77	87.08	11.23	11.5	98.31	3.48	23.54	43.57	40.27	18.68	75.85	42.55	21.13	42.33	17.8
Cluster VII	83.33	113.00	7.31	86.11	24.34	99.31	17.59	15.12	116.89	4.8	21.66	43.46	42.94	40.5	75.7	43.72	15.62	38.47	18.62
Cluster VIII	84.67	116.33	8.63	96.22	26.96	89.18	37.16	29.44	126.35	4.69	22.09	33.52	33.29	14.67	72.55	41.7	12.05	43.4	11.04
Cluster IX	87.33	114.67	8.17	97.34	28.24	90.75	24.84	21.48	115.6	4.5	19.27	44.18	47.69	16.33	63.03	41.21	9.72	38.63	21.07
Cluster X	86.33	116.00	7.76	110.22	27.49	124.02	31.47	20.29	155.49	5.68	19.98	39.27	45.56	32.07	79.29	46.71	14.09	43.87	17.8
Cluster XI	87.00	118.00	6.6	104.78	20.58	82.24	35.5	30.24	117.73	5.72	18.71	29.8	36.02	24.82	67.92	43.01	10.36	41.4	10.45

DFF= days to 50% flowering; DM=days to maturity; EBT= number of effective tillers per hill; PHT= plant height; PL= panicle length; NFGPP= number of fertile grains per panicle; NSGPP= number of sterile grains per panicle; SS%= spikelet sterility %; TNSPP= total number of spikelets per panicle; PDI= panicle density index; GR WT= grain weight; BY= biological yield; HI= harvest index; LA= leaf area; RWC= relative water content; RB= root biomass; CI= chlorophyll index; GYPP= grain yield per plant

Table 9. Contribution of different characters towards genetic divergence of forty eight rice genotypes under irrigated condition

Source	Times Ranked 1st	Contribution %
Days to 50% flowering	0	0.00%
Days to maturity	0	0.00%
Number of effective tillers per hill	45	3.99%
Plant height (cm)	3	0.27%
Panicle length (cm)	16	1.42%
Number of fertile grains per panicle	206	18.26%
Spikelet sterility (%)	4	0.35%
Total number of spikelets per panicle	65	5.76%
Panicle density index	1	0.09%
1000 grain weight (g)	28	2.48%
Biological yield	6	0.53%
Harvest index (%)	2	0.18%
Leaf area	268	23.76%
Relative water content (RWC)	89	7.89%
Proline content	198	17.55%
Root biomass	159	14.10%
Chlorophyll index	4	0.35%
Grain yield per plant (g)	34	3.01%

Table 10. Contribution of different characters towards genetic divergence of forty eight rice genotypes under drought stress condition

Source	Times Ranked	Contribution %
Days to 50% flowering	0	0.00%
Days to maturity	0	0.00%
Number of effective tillers per hill	1	0.09%
Plant height (cm)	3	0.27%
Panicle length (cm)	3	0.27%
Number of fertile grains per panicle	170	15.07%
Spikelet sterility (%)	14	1.24%
Total number of spikelets per panicle	0	0.00%
Panicle density index	0	0.00%
1000 grain weight (g)	13	1.15%
Biological yield	1	0.09%
Harvest index (%)	12	1.06%
Leaf area	325	28.81%
Relative water content (RWC)	407	36.08%
Proline content	61	5.41%
Root biomass	68	6.03%
Chlorophyll index	25	2.22%
Grain yield per plant (g)	25	2.22%

Table 11. Selection of parents based on D² values, clusters mean and mean performance of genotypes under irrigated condition

Clusters	Genotypes	Specific characters
XV	IR 90257-B-577-1-1-B-1	Early flowering, early maturity
XIX	IR 13L378	Effective tillers per hill, RWC
X	IR 106516-1-2-2-2	Fertile grains, total number of spikelets, PDI, 1000 grain weight
XIII	IR 107891-B-B-664-3-1	Panicle length
XII	IR 14L155	Biological yield
VII	IR 107891-B-B-845-1-1	H.I. %, Proline content
XVIII	IR 107891-B-B-447-3-1	grain yield per plant, Leaf area, root biomass, lateness in flowering and maturity

Table 12. Selection of parents based on D² values, clusters mean and mean performance of genotypes under drought stress condition

V	IR107891-B-B-111-2-1	1000 grain weight, root biomass
IX	IR14L157	Panicle length, biological yield, harvest index and grain yield per plant.
VIII	IR 13L378	Effective Tillers per hill
X	IR 95817-5-1-1-2	Plant height, fertile grains per panicle, total spikelets per panicle, RWC, leaf area and proline content
XI	Sabour Deep	PDI, CI
VII	IR 107891-B-B-447-3-1	Lateness in flowering and maturity
IV	IR 107891-B-B-1253-1-1	Earliness in flowering and maturity, low spikelet sterility (%)
V	IR107891-B-B-111-2-1	1000 grain weight, root biomass

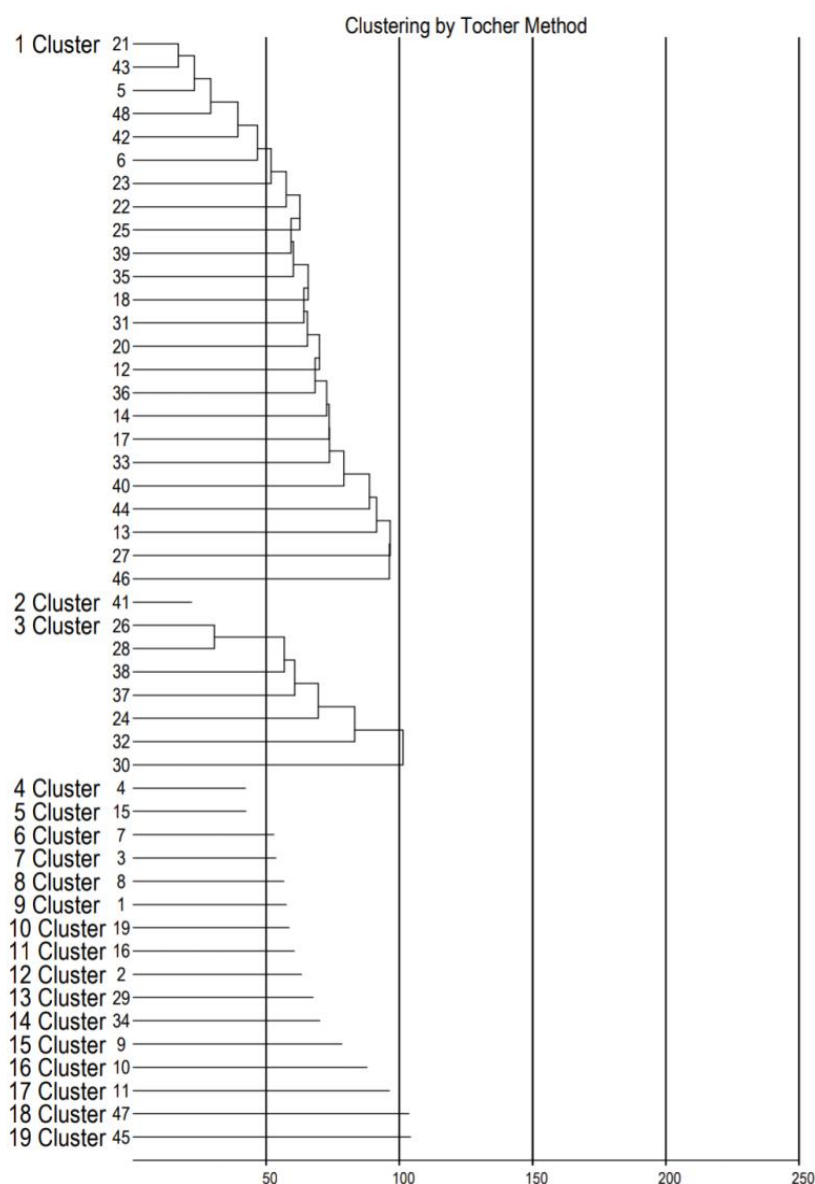


Fig. 1. Cluster analysis diagram under irrigated condition

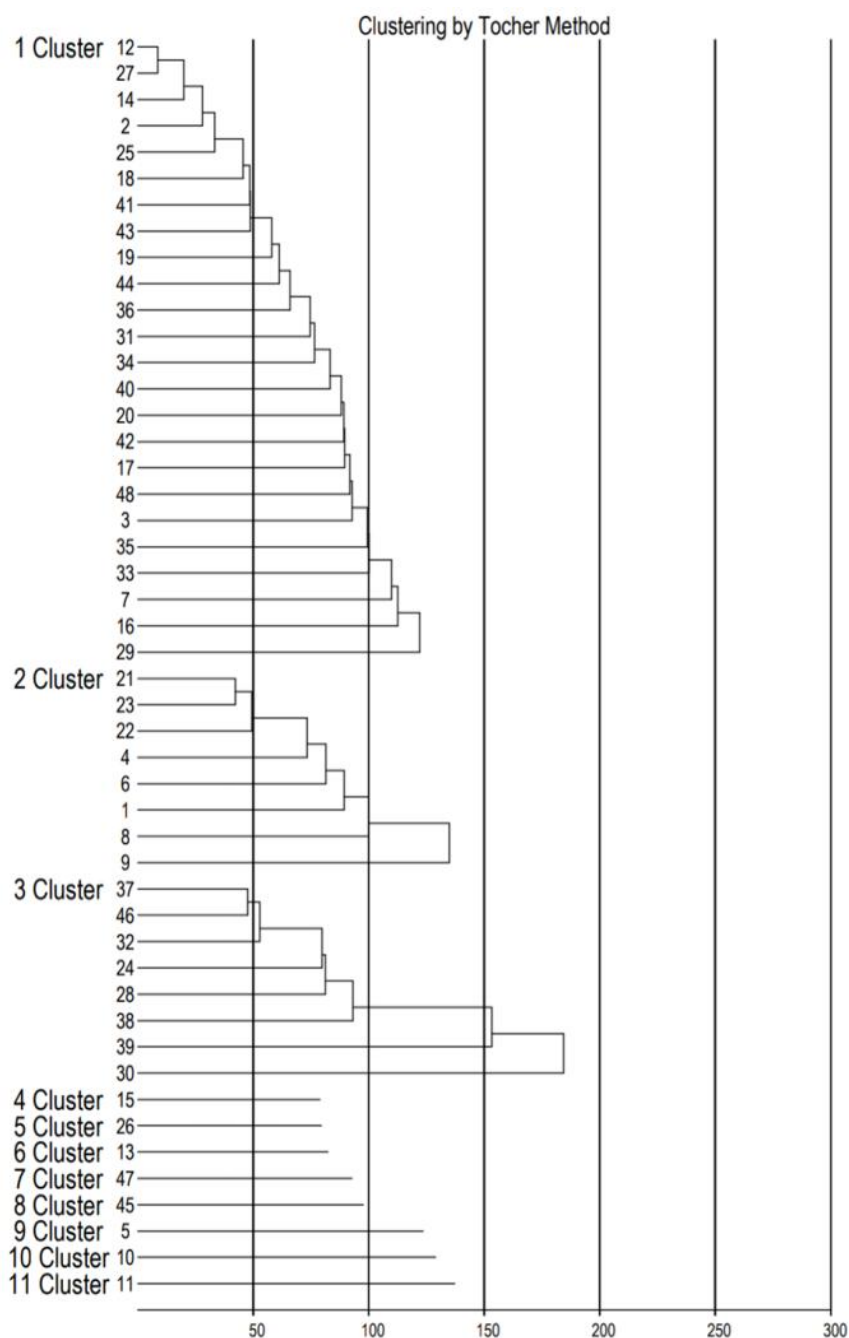


Fig. 1. Cluster analysis diagram under stress condition

4. CONCLUSION

Diverse germplasm lines possess desirable characters which may be used in future breeding programme to get maximum spectrum of variability for wide range of characters and broaden the genetic base of cultivars. The

criteria used for selection of genotype as parents for crop improvement program was using D^2 analysis in the inter cluster distance. Those genotypes with the maximum cluster distance are genetically more divergent. The hybridisation programme involving genotype of cluster XVIII (IR 107891-B-B-447-3-1) and cluster XIX (IR

13L378) under irrigated condition and the genotypes of cluster IX (IR 14L157) and X (IR 95817-5-1-1-2) under drought stress condition could be undertaken to isolate high yielding segregants, since these genotypes have high yielding potential, effective tillers per hill, relative water content, leaf area, root biomass, panicle length, biological yield, harvest index, plant height, number of fertile grains per panicle, total number of grains per panicle, leaf area and proline content with more genetic distances. These parents could be selected for hybridisation on the basis of their large inter-cluster distance for isolating useful recombinants in the segregating generations.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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