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Genetic divergence study in rice (*Oryza sativa* L.)

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Abstract
The genetic improvement of any crop mainly depends on the amount of genetic variability present in the population. To explore this variability, an effort was made to classify, understand the diversity among 95 rice genotypes for 27 yield and yield contributing traits using Mahalanobis D^2 statistics. Analysis of variance revealed a wide and significant variation for all the 27 traits studied. Divergence studies through D^2 statistics indicated the presence of substantial diversity by forming large number of clusters (22 clusters at Shirgaon and 20 clusters at Karjat) with wide range of inter-cluster distances.

Keywords: Rice, yield, D^2

1. Introduction
India is the world's second largest rice producer and consumer next to China, about 90% of all rice grown in the world is produced and consumed in Asian region. In Maharashtra, the total area occupied by this crop was about 1.465 million hectares with annual production of 3.276 lakh tonnes and average productivity of the state was about 2.24 t/ha, (Anonymous, 2021) [1]. In Konkan region, rice occupies an area of about 0.387 million hectares with an annual production of around 1.031 million tonnes and average productivity of the konkan was about 2.66 t/ha. The area under rice in konkan region is 26.41% of the total area in Maharashtra (0.387 million hectares). (Anonymous, 2021) [1]. the landraces maintained by farmers are endowed with tremendous genetic variability, as they are not subjected to subtle selection over a long period of time. This aids in the adaptation of landraces to wide agro-ecological conditions. This rich variability of complex quantitative traits with respect to maturity, growing adaptation and their physicochemical and organoleptic properties still remains unexploited. Land-races are also important genetic resources for resistance to pests and diseases; they provide "adaptability genes" for specific environmental conditions. Incorporation of adaptability genes from landraces could ensure optimum grain yield for the region (Vijayakumar *et al.*, 2020) [15]. It is very difficult to judge whether observed variability is heritable or not. Heritability indicates the extent of transmissibility of a character into future generations. Genetic diversity is a ubiquitous feature of all species in nature. Genetic diversity is an inherited variation among and between populations, created, activated and maintained by evolution. It is a fundamental characteristic without which breeders are very limited and powerless in plant breeding. Genetic divergence among the genotypes plays an important role in the selection of parents having wider variability for different characters and ultimately for a rational use of genetic resources.

2. Material and Methods
The genetic divergence were estimated for 95 rice genotypes during first year at Shirgaon and second year at Karjat, respectively. The 95 genotypes were obtained from various sources as details given below.
The observations were made on 30 plants or parts of 30 plants, which were divided among 3 replications (10 plants in each replication) as per the guidelines of PPV & FR Authority (Anonymous, 2009) [2].
The data was recorded for all the characters whose mean values were subjected to analysis of variance to test the significance for each character as per the methodology proposed by Patterson and Williams (1976). Genetic divergence among the genotypes was estimated using Mahalanobis' D2 statistics (1936) and the germplasm was grouped into several clusters by Torcher's method as described by Rao (1952).

Table 1: Experimental material along with source

S N	Genotype	Source	SN	Genotype	Source
I	**Red kernel local lines**		**II**	**Restorer lines**	
1	MO-6	ARS, Moncomba	25	KJT-1R	ARS, Karjat
2	MO-8		26	KJT-2R	
3	MO-13		27	KJT-3R	
4	MO-17		28	KJT-4R	
5	MO-19		29	PR-114	IIRR, Hyderabad
6	Khara Rata	KRS, Panvel	30	RTN 11-2-1-3	ARS, Shirgaon
7	Mayekar Bhat	ARS, Karjat	31	PR-118	IIRR, Hyderabad
8	Munga	ARS, Shirgao ARS, Shirgaon	32	DRR-215	
9	Mahsad		33	RTN-69-1-1	ARS, Shirgaon
10	Waksal-207		34	NAUR-1	NAU, Navsari
11	Barmil		35	BL-184AR	ARS, Karjat
12	Jyoti		36	Gurjari	NAU, Navsari
13	Patani-6		37	DRR-50-12	IIRR, Hyderabad
14	Bhadas-79		38	DRR-363-5	
15	Pandy		39	DRR-50-13	
16	Dular		40	DRR-50-10	
17	Try-1		41	DRR-86-8	
18	Kochari		42	IR-63879-195-2-2-3-2	IRRI, Manila,
19	Lal Patani		43	RTN-27-1-1-2	ARS, Shirgaon
20	Dodak		44	RTN-214-1-1-1-2	
21	Karhad		45	VDN-9-10-1	ARS, Vadgaon
22	Ratnagiri 7		46	VDN-10-18	
23	Bela		47	RTN-35-1-1	ARS, Shirgaon
24	Valai		48	Sahyadri 5 R	
			49	HRTMS-61	
			50	CR-3993-2-24-45-2	IIRR, Hyderabad
III	Aromatic lines		IV	Lines responsive to biotic and abiotic stresses	
51	P Basmati	IARI, N. Delhi	70	RS-1113	IIRR, Hyderabad
52	S Basmati		71	RP Bio 197	
53	Kothambir Sal	ARS, Karjat	72	RP-BIO-226	
54	Chinoor	PDKV, Akola	73	Ajaya	
55	P Sugandha-1	IARI, N. Delhi	74	KJT 1	ARS, Karjat
56	P Sugandha-3		75	KJT 2	
57	P Sugandha-4		76	IR-64	IRRI, Manila
58	P Sugandha-5		77	MUDGO	
59	Bhadasbhog	IIRR, Hyderabad	78	MILYANG 46	
60	CR2713-180		79	PTB 33	RARS, Pattambi
61	Kalanamak		80	MTU1010	RARS, Maruteru
62	NDR6315		81	BG 367-2	IRRI, Manila
63	P Samruddhi	MPKV, Rahuri	82	MILYANG 63	
64	Indrayani	ARS, Vadgaon	83	FL 478	
65	Dhanesal	IIRR, Hyderabad	84	MUT NS 1	
66	Ambemohar	ARS, Vadgaon	85	RATHU HEENATI	
67	K Shatabdi	ARS, Karjat	86	SINNA SIVAPPU	
68	Bhogwati	ARS, Radhanagari	87	IRRI 190	
69	Sugandha	VNMKV, Parbhani	88	IRRI 193	
			89	ARC 10550	
			90	S MAHSURI	IIRR, Hyderabad
			91	IRRI 123	IRRI, Manila
			92	IRRI 104	
			93	IRRI 192	
			94	Sonsali	IIRR, Hyderabad
			95	TN-1	

Table 2: Observations recorded on 27 yield and yield contributing characters, including 14 measurable DUS descriptors along with abbreviations

SN	Character	Abbreviation	Remark
1	Days to 50% Flowering (Nos.)	DFF (Nos.)	Measurable DUS descriptor No. 20
2	Plant Height (cm)	PHT (cm)	Yield and yield contributing character
3	Stem Length Excluding Panicle (cm)	SLEP (cm)	Measurable DUS descriptor No. 29
4	Number of Tillers Plant^{-1}	TLPP (Nos.)	Yield and yield contributing character
5	Panicle Length of Main Axis (cm)	PLMA (cm)	Measurable DUS descriptor No. 33
6	Number of Spikelets Panicle^{-1}	SPP (Nos.)	Yield and yield contributing character
7	Fertility (%)	Fertility (%)	Yield and yield contributing character
8	Days to Maturity (Nos.)	DM (Days)	Measurable DUS descriptor No. 47
9	Test Weight of 1000 Grains (g)	TW (g)	Measurable DUS descriptor No. 50
10	Grain Length (mm)	GL (mm)	Measurable DUS descriptor No. 51
11	Grain Width (mm)	GW (mm)	Measurable DUS descriptor No. 52
12	Grain Yield Plant^{-1} (g)	GYPP(g)	Yield and yield contributing character
13	Straw Yield Plant^{-1} (g)	SYPP (g)	Yield and yield contributing character
14	Grain Yield/ Straw Yield Ratio	G/S	Yield and yield contributing character
15	Straw Yield/ Grain Yield Ratio	S/G	Yield and yield contributing character
16	Leaf Length (cm)	LL (cm)	Measurable DUS descriptor No. 16
17	Leaf Breadth (cm)	LB (cm)	Measurable DUS descriptor No. 17
18	Stem Thickness (cm)	ST (cm)	Measurable DUS descriptor No. 28
19	No. of Panicles Plant^{-1}	PPP (Nos.)	Measurable DUS descriptor No. 36
20	Decorticated Grain Length (mm)	DGL (mm)	Measurable DUS descriptor No. 54
21	Decorticated Grain Breath (mm)	DGB (mm)	Measurable DUS descriptor No. 55
22	DGL/DGB Ratio	L/B	Grain type determining character
23	Amylose Content (%)	AC (%)	Measurable DUS descriptor No. 59 and Biochemical Character
24	Zinc Content (ppm)	Zn (ppm)	Biochemical Character
25	Iron Content (ppm)	Fe (ppm)	Biochemical Character
26	Calcium Content (ppm)	Ca (ppm)	Biochemical Character
27	Alkali Spreading Value	ASV	Biochemical Character and cooking quality assessment Character

Results and Discussion

Genetic divergence

Genetic diversity is the most important tool in the hands of the plant breeder in choosing the right type of parents for hybridization program. The divergence can be studied by technique using D^2 statistics developed by Mahalanobis (1936) [8]. This is considered as the most effective method for qualifying the degree of genetic diversity among the genotypes included in the study. The present investigation aimed to estimate the magnitude of genetic divergence present in the 95 rice genotypes and to identify the diverse genotypes for future utilization breeding program. In the present investigation for the experiment conducted at ARS, Shiragon, the genotypes were grouped into 22 clusters on the basis of D^2 matrix which was based on D^2 values and Ward minimum variance. Cluster I comprised of maximum number of genotypes (57) followed by cluster IV with 32 genotypes. Remaining clusters constitutes of each one genotype only. Whereas for the experiment carried out at RARS, Karjat, the genotypes were grouped into 20 clusters on the basis of D^2 matrix which was based on D^2 values and Ward minimum variance Cluster I was largest out of the 20 clusters which comprises of 58 genotypes followed by cluster V with 14 genotypes and cluster X with 6 genotypes. Remaining clusters constitute of each one genotype only. The genotypes present in different clusters showed high degree of diversity than the genotypes present in the same cluster. The genotypes belonging to same cluster had an average smaller D^2 values than those belonging to different clusters For location I (Shirgaon) intra cluster D^2 values ranged from 0.00 (all clusters except cluster I and IV) to 723.08 (IV). Maximum intra cluster distance was observed in cluster IV (723.05) followed by cluster I (587.10). The inter-cluster D^2 values ranged from 147.10 (cluster II and III) to 3111.77 (clusters XIX and XX) indicating high diversity among the genotypes of these clusters. The highest inter cluster distance was observed between cluster XIX and XX (3111.77), followed by cluster XVIII and XX (3076.24), cluster XX and XXI (3018.86), cluster XXI and XXII (2771.82)**,** cluster X and cluster XXII (2405.44), cluster XIII and XX (2344.39). Cluster I comprises 57 genotypes. It was nearest to cluster VIII (766.88) indicating genotypes are closely related and was farthest from the cluster XXII (1624.67) implying these genotypes more diversely related conferring intermitting within these genotypes would be useful for crop improvement. For location II (Karjat), intra cluster D^2 values ranged from 0.00 (all clusters except cluster I, V and X) to 607.76 (cluster X). Maximum intra cluster distance was observed in cluster X (723.05) followed by cluster V (481.62) and cluster I (437.13). The inter-cluster D^2 values ranged from 232.11 (cluster IX and XI) to 2259.27 (clusters XIV and XX) indicating high diversity among the genotypes of these clusters. The highest inter cluster distance was observed between cluster XIV and XX (2259.27), followed by cluster VII and XX (1830.75), cluster XI and XIV (1730.06), cluster III and XX (1730.06)**,** cluster XVIII and cluster XX (1665.85), cluster IV and XIX (1557.16). Cluster I comprises 58 genotypes. It was nearest to cluster IV (552.11) indicating genotypes are closely related and was farthest from the cluster XX (1407.01) implying these genotypes more diversely related conferring intermitting within these genotypes would be useful for crop improvement. Similar divergence estimation based on D^2 distances was done by Shivani *et al.* (2018) [14], Kumari *et al.* (2013) [7], Bhargavi *et al.* (2022) [4] and Kushwaha *et al*. (2022) [9]. Cluster means with respect to 27 characters and 95 genotypes was evaluated with help D^2

values for the both the locations. A critical appraisal of the observations indicated that none of the clusters contained genotypes with all the desirable traits which could be directly selected and utilized. Therefore, hybridization between the selected genotypes from divergent clusters is essential to judiciously combine all the targeted traits. The promising landraces from these clusters with high mean values for different traits may be directly used for adaptation or may be used as parents in future hybridization, depending upon the objective of the breeding programme to derive superior transgressive segregants. The selection and choice of parents mainly depend upon contribution of characters towards divergence. The utility of D^2 statistics as a potential 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 total genetic divergence.

For ARS, Shirgaon location, out of the 27 characters studied, 13 characters namely leaf length, calcium content, number of panicles plant-, fertilitya%, zinc content, iron content, number of spikelets panicle-1, plant height, days to 50% flowering, grain width, amylose content, straw yield plant^{-1} and grain yield plant^{-1} together contributed maximum (92.69%) to the total genetic divergence. Whereas for RARS, Karjat location out of the 27 characters studied, 11 characters namely leaf length, calcium content, fertility, decorticated grain length, zinc content, iron content, number of spikelets panicle^{-1}, plant height, amylose content, days to 50% flowering and grain yield plant^{-1} together contributed maximum (98.99%) to the total genetic divergence (Table 5 to Table 10; Fig. 1 and Fig. 2). Thus, it is suggested that these traits should be given importance in further breeding programmes i.e., during hybridization and selection of segregating populations, using this particular set of landraces, so far not utilized in breeding programmes, which have potential for use in future rice improvement programmes aiming at the development of rice varieties or hybrids with high yield and better grain quality. These findings were in accordance with the finding of Guru *et al.*, (2017) [6], Shivani *et al*. (2018) [14], Kumari *et al*. (2013) [7], Bhargavi *et al*. (2022) [4] and Kushwaha *et al*. (2022) [9].

Table 3: Clustering pattern of 95 genotypes studied at ARS, Shirgaon Year *Kharif*, 2020 based on D^2 analysis

Cluster No.	No. of genotypes	Genotype number	Genotypes name
I	57	1, 2, 3, 4, 5, 7, 10, 11, 14, 15, 16, 21, 22, 25, 29, 30, 31, 32, 34, 35, 39, 41, 42, 47, 50, 52, 54, 55, 56, 57, 58, 59, 60, 63, 64, 70, 71, 72, 74, 76, 77, 78, 79, 80, 82, 83, 84, 85, 86, 87, 88, 89, 91, 92, 93, 94 and 95	MO-6, MO-8, MO-13, MO-17, MO-19, Mayekar Bhat, Waksal207, Barmil, Bhadas-79, Pandy, Dular, Karhad, Ratnagiri 7, KJT-1R, PR-114, RTN 11-2-1-3, PR-118, DRR-215, NAUR-1, BL-184AR, DRR-50-13, DRR-86-8, IR-63879-195-2-2-3-2, RTN-35-1-1, CR-3993-2-24-45-2, S Basmati, Chinoor, P Sugandha-1, P Sugandha-3, P Sugandha-4, P Sugandha-5, Bhadasbhog, CR2713-180, P Samruddhi, Indrayani, RS-1113, RP Bio 197, RP-BIO-226, KJT 1, IR-64, MUDGO, MILYANG 46, PTB 33, MTU1010,MILYANG 63, FL 478, MUT NS 1, RATHU HEENATI, SINNA SIVAPPU, IRRI 190, IRRI 193, ARC 10550, IRRI 123, IRRI 104, IRRI 192, Sonsali and TN-1
II	1	65	Dhanesal
III	1	46	VDN-10-18
IV	32	6, 8,9, 13, 18, 23, 24, 33, 37, 38, 40, 45, 49, 51, 61, 62, 66 and 73	Khara Rata, Munga, Mahsad, Patani-6, Kochari, Bela, Valai, RTN-69-1-1, DRR-50-12, DRR-363-5, DRR-50-10, VDN-9-10-1, HRTMS-61, P Basmati, Kalanamak, NDR6315, Ambemohar and Ajaya
V	1	67	K Shatabdi
VI	1	81	BG 367-2
VII	1	44	RTN-214-1-1-1-2
VIII	1	26	KJT-2R
IX	1	68	Bhogwati
X	1	48	Sahyadri 5 R
XI	1	27	KJT-3R
XII	1	19	Lal Patani
XIII	1	36	Gurjari
XIV	1	43	RTN-27-1-1-2
XV	1	12	Jyoti
XVI	1	90	S MAHSURI
XVII	1	75	KJT 2
XVIII	1	28	KJT-4R
XIX	1	20	Dodak
XX	1	53	Kothambir Sal
XXI	1	69	Sugandha
XXII	1	17	Try-1

Table 4: Clustering pattern of 95 genotypes studied at RARS, Karjat Year *Kharif*, 2021 [based] on D^2 analysis

Cluster No.	No. of genotypes	Genotype number	Genotypes name
I	58	1, 2, 3, 4, 5, 7, 8, 11, 14, 15, 16, 21, 22, 24, 25, 26, 29, 30, 32, 33, 35, 39, 40, 41, 42, 47, 50, 51, 52, 54, 55, 56, 57, 58, 59, 60, 63, 64, 67, 71, 72, 74, 76, 77, 78, 79, 80, 82, 84, 85,86, 87,88, 89, 91, 93, 94 and 95	MO-6, MO-8, MO-13, MO-17, MO-19, Mayekar Bhat, Munga, Barmil, Bhadas-79, Pandy, Dular, Karhad, Ratnagiri 7, Valai, KJT-1R, KJT-2R, PR-114, RTN 11-2-1-3, DRR-215, RTN-69-1-1, BL-184AR, DRR-50-13, DRR-50-10, DRR-86-8, IR-63879-195-2-2-3-2, RTN-35-1-1, CR-3993-2-24-45-2, P Basmati, S Basmati, Chinoor, P Sugandha-1, P Sugandha-3, P Sugandha-4, P Sugandha-5, Bhadasbhog, CR2713-180, P Samruddhi, Indrayani, K Shatabdi, RP Bio 197, RP-BIO-226, KJT 1, IR-64, MUDGO, MILYANG-46, PTB 33, MTU1010, MILYANG 63, MUT NS 1, RATHU HEENATI, SINNA SIVAPPU, IRRI 190, IRRI 193, ARC 10550, IRRI 123, IRRI 192,Sonsali and TN-1,
II	1	65	Dhanesal
III	1	75	KJT 2
IV	1	45	VDN-9-10-1
V	14	6, 9, 10, 13, 18, 23, 37, 38, 46, 49, 61, 62 and 73	Khara Rata, Mahsad, Waksal-207, Patani-6, Kochari, Bela, DRR-50-12,DRR-363-5, VDN-10-18, HRTMS-61, Kalanamak, NDR6315 and Ajaya
VI	1	68	Bhogwati
VII	1	20	Dodak
VIII	1	92	IRRI 104
IX	1	34	NAUR-1
X	6	43, 44, 53, 66, 70 and 90	RTN-27-1-1-2, RTN-214-1-1-1-2, Kothambir Sal, Ambemohar, RS-1113 and S MAHSURI
XI	1	19	Lal Patani
XII	1	81	BG 367-2
XIII	1	12	Jyoti
XIV	1	48	Sahyadri 5 R
XV	1	69	Sugandha
XVI	1	31	PR-118
XVII	1	36	Gurjari
XVIII	1	27	KJT-3R
XIX	1	28	KJT-4R
XX	1	17	Try-1

Table 5: Intra and Inter-cluster distances amonf cluster groups at ARS, Shirgaon (Year I, Loation I)

		CLUSTER DISTANCES																					
	SN	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI	XVII	XVIII	XIX	XX	XXI	XII
CLUSTER DISTANCES	I	587.1																					
	II	792.91	0																				
	III	783.45	147.1	0																			
	IV	899.78	532.08	493.74	723.08																		
	V	837.77	1361.03	1250.82	1217.24	0																	
	VI	934.32	911.79	1094.47	1247.34	1694.8	0																
	VII	781.98	1239.14	1240.97	1375.37	1114.04	558.98	0															
	VIII	766.88	914.47	979.18	1020.59	721.25	715.73	809.74	0														
	IX	774.98	913.59	977.29	1224.85	1050.38	363.17	355.94	555.95	0													
	X	790.25	1346.64	1338.69	1349.94	709.23	908.74	440.15	667.87	494.26	0												
	XI	781.14	732.49	685.19	992.05	1134.72	1159.31	1291.51	548.02	832.33	855.81	0											
	XII	772.3	1193.81	1243.27	1238.48	1236.06	1131.62	918.65	822.79	938.51	1392.91	1121.13	0										
	XIII	877.41	1889.74	1741.74	1592.49	1070.06	1743.98	1079.21	1219.09	1382.91	1087.56	1187.07	447.59	0									
	XIV	878.39	1175.54	1166.9	1224.34	894.77	1020.66	786.14	500.52	609.98	1086.32	1128.6	303.76	862.03	0								
	XV	863.62	1392.06	1308.11	1246.97	1296.68	1496.35	1004.64	1454.15	1678.79	1174.38	1647.2	1136.88	946.68	1536.24	0							
	XVI	828.35	1091.2	935.63	1086.17	1063.63	1066.52	728.41	1337.38	921.19	1291.48	1608.17	885.27	1136.78	1039.03	980.83	0						
	XVII	996.59	1502.02	1366.77	1437.69	1181.12	746.59	627.73	687.91	702.98	991.05	1238.45	840.82	985.25	634.92	1580.03	1164.32	0					
	XVIII	878.13	1413.75	1425.12	1614.92	1576.66	1333.07	1135.18	964.17	1144.34	1094.09	527.88	722.06	638.59	1140.08	1220.66	1733.74	1230.29	0				
	XIX	1157.8	1967.47	2089	1972.05	1985.19	1372.62	1115.92	1648.77	1781.66	1707.11	1927.18	882.02	950.9	1603.53	513.87	1267.51	1558.49	924.56	0			
	XX	1421.04	1002.5	935.07	1039.05	1019.8	1649.25	1500.74	1447.52	1380.77	1563.59	2060.97	1919.89	2344.39	1308.49	1948.56	1183.92	1398.47	3076.24	3111.2	0		
	XXI	1083.06	1450.02	1528.41	1635.36	1964.67	1736.59	1736.66	1812.48	2004.43	1773.37	1190.4	1341.19	1099.13	2163.85	864.77	1759.33	1727.15	670.28	719.58	3018.86	0	
	XXII	1624.67	1151.53	1255.29	1292.64	2140.34	1589.48	2172.29	1081.59	1816.52	2405.44	1536.41	1073.68	1962.01	954.21	2188.83	1865.41	1798.23	1905.07	2472.34	1923.25	2771.82	0

Table 6: Intra and Inter-cluster distances amonf cluster groups at RARS, Karjat (Year II, Loation II)

		CLUSTER DISTANCES																		
	SN	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI	XVII	XVIII	XIX	XX
CLUSTER DISTANCES	I	437.13																			
	II	595.43	0																		
	III	594.98	1025.04	0																	
	IV	552.11	452.62	553.16	0																
	V	647.61	392.85	950.07	500.98	481.62															
	VI	612.23	680.31	432.09	539.86	963.61	0														
	VII	695.5	1380.22	769.19	1063.29	1230.1	1197.97	0													
	VIII	572.67	1156.24	500.78	856.04	1128.59	781.82	255.97	0												
	IX	644.78	820.82	598.2	846.54	678.47	1075.02	641.68	633.82	0											
	X	742.24	784.04	666.01	486.15	835.42	658.73	1308.17	887.95	973.58	607.76										
	XI	729.07	1088.4	593.92	943.1	998.74	966.24	483.78	465.97	232.22	991.29	0									
	XII	712.72	729.94	403.26	450.59	991.15	250.75	1085.47	767.1	1089.3	869.28	1069.01	0								
	XIII	571.23	1030.61	881.02	772.34	755.71	1221.71	415.6	527.98	607.68	990.12	822.61	1249.35	0							
	XIV	603.46	1017.97	622.66	752.29	1050	433.15	997.82	737.58	1301.15	886.66	1277.62	650.09	695.64	0						
	XV	670.69	981.44	1112.44	1262.93	1074.67	1217.19	550.78	753.8	770.57	1573.92	969.79	1274.18	756.52	1064.4	0					
	XVI	596.78	731.47	766.29	1005.34	744.5	881.88	959.3	873.95	489.83	1147.64	901.38	1007.55	634.24	834.72	518.62	0				
	XVII	745.65	1501.01	611.12	1260.16	1201.56	1192.61	508.62	510.09	411.75	1190.68	326.25	1426.5	639.66	972.02	719.28	692.36	0			
	XVIII	577.86	591.03	796.05	896.08	778.06	664.83	929.11	1018.53	763.25	1280.21	968.59	778.12	937.06	681.26	366.2	461.56	894.16	0		
	XIX	816.95	1188.34	908.97	1557.16	1308.42	1065.3	541.86	728.18	722.05	1730.06	692.56	1108.87	976.38	1011.67	408.86	645.69	636.93	405.57	0	
	XX	1407.01	1086.44	1213.26	1152.83	1062.82	1830.75	1435.33	1437.53	617.68	1548.93	850.34	1355.28	1418.62	2259.3	1920.54	1469.58	1541.53	1665.85	1579.3	0

Table 7: Cluster means values of 22 (I to XXII) cluster groups for 27 different quantitaive characters at ARS, Shirgaon (Year I, Location I)

		CHARACTERS																									
	SN	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27
		DFF	PHT	SLEP	TLPP	PLMA	SPP	FERT	DM	TW	GL	GW	GYPP	SYPP	G/S	S/G	LL	LB	ST	PPP	DGL	DGB	L/B	AC	Zn	Fe	Cu	ASV
CLUSTER MEANS	I	89.95	115.89	89.24	11.78	26.74	125.00	87.00	119.95	21.81	9.60	2.85	17.09	23.43	0.74	1.38	47.62	1.13	0.75	10.78	6.94	2.44	2.90	22.59	12.34	13.55	51.53	4.70
	II	83.00	163.20	135.07	13.80	28.13	129.66	92.59	113.00	13.84	10.40	2.57	11.20	15.00	0.75	1.34	66.20	1.03	0.70	12.80	7.18	2.41	3.03	23.80	13.73	12.75	63.00	5.00
	III	99.00	129.53	103.20	12.20	26.33	164.44	89.33	129.00	13.70	9.36	2.58	14.97	19.40	0.77	1.30	67.23	1.10	0.87	11.20	6.87	2.04	3.37	27.64	13.65	18.30	59.10	5.00
	IV	95.74	148.79	120.94	11.15	27.86	153.67	87.06	125.74	22.46	8.79	3.09	16.70	23.21	0.72	1.41	61.12	1.04	0.76	10.15	6.11	2.52	2.51	24.67	12.50	11.44	51.69	4.63
	V	89.67	104.93	79.13	11.60	25.80	108.05	91.02	119.67	13.79	7.36	3.09	16.68	20.10	0.83	1.21	41.37	1.00	0.60	10.60	5.02	2.47	2.03	19.24	12.60	16.45	43.33	5.00
	VI	93.00	107.33	79.00	11.87	28.33	71.89	90.39	123.00	27.26	10.27	2.61	23.57	31.47	0.75	1.34	44.17	1.20	0.70	10.87	7.99	2.18	3.67	14.33	4.50	8.67	101.33	3.67
	VII	92.00	124.53	99.67	10.67	24.87	187.77	86.24	122.00	18.80	9.34	2.49	17.57	19.33	0.91	1.10	30.37	0.80	0.50	9.67	6.92	2.22	3.12	28.60	9.40	21.28	92.57	3.67
	VIII	85.67	132.47	104.47	10.40	28.00	140.80	84.25	115.67	21.20	10.16	2.70	21.70	31.03	0.70	1.43	43.40	0.90	0.60	9.40	7.03	2.28	3.08	27.39	1.09	11.50	72.57	5.00
	IX	92.00	107.67	81.27	12.53	26.40	105.63	90.30	122.00	22.53	11.06	2.30	17.99	27.67	0.65	1.54	38.40	0.90	0.70	11.53	8.04	1.87	4.30	21.26	15.82	18.25	102.00	5.00
	X	97.00	154.53	128.80	11.73	25.73	176.75	97.30	127.00	27.17	8.94	3.15	24.28	32.13	0.76	1.33	33.43	1.40	0.57	10.73	6.81	2.65	2.58	23.97	8.47	21.42	64.00	5.00
	XI	97.67	136.07	108.47	9.73	27.60	178.35	92.89	127.67	25.06	11.68	2.31	21.50	26.33	0.82	1.22	52.57	1.10	0.80	8.73	8.87	2.09	4.24	25.37	8.68	14.42	39.10	5.00
	XII	78.00	108.83	82.97	9.43	25.87	101.56	63.87	108.00	24.43	10.42	2.71	12.30	16.97	0.73	1.38	41.13	1.00	0.60	8.43	7.61	2.25	3.38	29.40	18.53	8.83	63.50	5.00
	XIII	96.00	114.73	92.33	9.87	22.40	170.51	68.21	126.00	26.91	9.39	3.24	23.07	24.70	0.94	1.07	32.97	1.10	0.77	8.87	7.23	2.67	2.70	24.36	17.83	10.10	28.67	3.67
	XIV	86.67	123.20	98.47	10.67	24.73	77.30	65.45	116.67	21.78	9.50	2.59	11.73	18.17	0.65	1.55	39.47	1.10	0.80	9.67	6.86	2.19	3.14	29.42	15.43	16.52	84.23	4.33
	XV	88.33	134.33	108.53	10.40	25.80	124.58	82.59	118.33	27.01	7.58	3.21	22.50	32.33	0.70	1.44	47.53	0.72	0.63	9.40	5.20	2.79	1.87	26.99	3.87	18.27	28.53	3.00
	XVI	102.67	81.33	57.33	10.27	24.00	144.82	81.42	132.67	11.98	7.75	2.23	14.61	19.30	0.76	1.32	40.30	1.00	0.60	9.27	5.49	1.87	2.94	18.50	18.55	10.45	71.67	3.67
	XVII	108.33	94.47	67.07	11.60	27.40	178.06	74.53	138.33	20.64	9.47	2.51	25.00	29.57	0.84	1.18	33.17	1.10	0.80	10.60	7.19	2.03	3.57	18.50	7.68	10.67	82.00	4.33
	XVIII	86.00	109.87	84.07	11.40	25.80	152.00	79.32	116.00	23.45	12.84	2.60	15.20	21.47	0.71	1.42	43.17	1.33	0.70	10.40	9.68	2.07	4.69	25.49	5.90	16.35	32.90	4.33
	XIX	78.33	94.57	68.10	10.47	26.47	55.32	77.84	108.33	26.61	9.89	2.51	16.26	20.21	0.81	1.24	36.17	0.95	0.53	9.47	7.04	2.18	3.24	27.24	2.03	8.33	38.33	3.00
	XX	106.33	162.47	135.53	12.53	26.93	106.35	87.51	136.33	12.06	5.99	3.26	12.34	18.10	0.68	1.48	53.60	0.80	0.77	11.53	4.03	2.87	1.41	21.47	19.13	13.27	79.10	5.00
	XXI	87.33	107.40	81.80	14.87	25.60	125.77	91.09	117.33	24.58	11.65	2.51	16.93	26.83	0.63	1.59	51.30	1.33	0.80	13.87	8.17	2.39	3.45	17.15	8.00	5.72	3.63	3.00
	XXII	93.67	173.60	142.87	10.50	30.73	97.08	57.54	123.67	23.76	10.16	3.50	11.73	14.35	0.81	1.23	62.93	1.10	0.83	9.50	6.98	3.10	2.25	17.72	2.15	5.53	68.47	3.00

Table 8: Cluster means values of 22 (I to XXII) cluster groups for 27 different quantitaive characters at RARS, Karjat (Year II, Location II)

		CHARACTERS																										
	SN	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27
		DFF	PHT	SLEP	TLPP	PLMA	SPP	FERT	DM	TW	GL	GW	GYPP	SYPP	G/S	S/G	LL	LB	ST	PPP	DGL	DGB	L/B	AC	Zn	Fe	Ca	ASV
CLUSTER MEANS	I	89.85	117.59	90.45	12.39	27.14	128.16	87.84	119.85	21.73	9.52	2.83	16.76	22.49	0.89	1.34	47.97	1.09	0.77	11.24	6.91	2.43	2.89	22.89	12.05	13.25	51.48	4.72
	II	82.33	164.39	135.30	14.78	29.09	128.93	92.90	112.33	13.36	10.44	2.34	10.99	14.61	0.75	1.33	66.35	1.11	0.78	13.78	7.15	2.39	3.05	23.26	13.98	12.87	63.23	5.00
	III	107.00	95.45	67.72	12.26	27.73	178.57	74.81	137.00	20.83	9.44	2.50	24.63	29.13	0.84	1.18	32.65	1.11	0.82	11.26	7.17	2.01	3.60	18.35	7.30	10.40	83.00	4.33
	IV	90.33	129.92	104.49	12.99	25.43	121.07	90.30	120.33	24.10	8.55	3.01	17.25	26.18	0.66	1.52	52.68	1.05	0.78	11.99	5.58	2.26	2.47	27.78	9.07	6.23	83.69	3.67
	V	93.55	152.27	123.89	11.34	28.38	150.98	86.08	123.55	21.99	8.99	3.12	16.26	21.43	0.77	1.32	63.14	1.06	0.80	10.08	6.22	2.55	2.52	25.66	12.62	13.75	50.53	4.81
	VI	91.33	108.95	81.55	13.56	27.40	104.90	90.66	121.33	22.05	11.10	2.07	17.78	27.28	0.66	1.54	38.60	0.97	0.77	12.56	8.01	1.85	4.33	20.72	16.07	18.37	102.23	5.00
	VII	74.33	90.72	63.68	11.14	27.04	55.50	77.84	104.33	26.76	9.85	2.51	16.28	20.17	0.81	1.23	36.26	0.94	0.52	9.52	7.08	2.17	3.26	27.39	2.02	8.48	38.66	3.00
	VIII	72.33	85.83	63.41	12.42	22.42	95.59	79.09	102.33	20.87	9.32	2.74	15.86	18.94	0.84	1.20	34.09	1.31	0.72	11.42	6.76	2.58	2.62	12.39	5.73	10.18	59.45	5.00
	IX	93.00	113.72	86.89	12.59	26.84	140.28	65.26	123.00	27.83	9.33	2.77	18.88	26.01	0.72	1.38	54.36	1.09	0.79	11.59	7.03	2.33	3.02	18.99	13.38	12.51	44.33	4.33
	X	93.06	125.49	98.67	12.18	26.82	127.62	83.29	123.06	15.05	7.96	2.56	14.31	18.95	0.75	1.35	43.15	0.95	0.69	11.18	5.68	2.23	2.64	22.14	17.06	13.81	83.70	4.11
	XI	76.00	105.09	78.66	10.10	26.44	101.74	63.88	106.00	24.59	10.66	2.71	12.33	16.93	0.73	1.38	41.22	0.99	0.58	8.48	7.65	2.25	3.40	29.55	18.52	8.98	63.75	5.00
	XII	92.00	108.57	79.78	12.66	28.79	72.40	90.67	122.00	27.44	10.24	2.60	23.26	31.09	0.75	1.33	43.71	1.27	0.78	11.66	7.97	2.16	3.70	14.52	4.46	8.74	102.68	3.67
	XIII	83.00	133.88	107.51	11.07	26.37	124.76	82.60	113.00	27.16	7.50	3.21	22.53	32.30	0.70	1.44	47.62	0.71	0.62	9.45	5.24	2.79	1.88	27.14	3.86	18.41	28.97	3.00
	XIV	95.67	154.59	128.42	12.12	26.17	177.17	97.16	125.67	26.76	8.93	3.20	23.93	32.33	0.74	1.36	33.45	1.19	0.61	11.12	6.85	2.67	2.57	23.57	8.53	21.39	64.15	5.00
	XV	86.67	107.85	81.67	15.48	26.19	125.04	91.03	116.67	24.10	11.69	2.28	16.73	26.44	0.63	1.58	51.08	1.39	0.86	14.48	8.14	2.37	3.46	16.62	8.25	5.83	3.86	3.00
	XVI	98.00	140.75	108.42	13.99	32.33	164.58	82.38	128.00	20.34	11.07	2.69	30.64	46.50	0.66	1.52	55.09	1.16	0.95	12.99	7.36	2.30	3.21	14.08	14.74	17.77	32.76	4.00
	XVII	95.00	114.16	91.95	10.25	22.21	170.94	68.06	125.00	26.50	9.38	3.28	22.93	27.51	0.83	1.20	33.08	0.98	0.83	9.25	7.26	2.69	2.70	23.99	17.92	10.10	28.84	3.67
	XVIII	96.33	136.03	108.09	10.12	27.95	178.78	92.74	126.33	24.65	11.67	2.35	21.90	27.36	0.80	1.25	52.52	0.82	0.84	9.12	8.91	2.11	4.22	24.98	8.75	14.39	39.25	5.00
	XIX	85.00	109.09	83.69	11.79	25.40	152.43	79.17	115.00	23.04	12.83	2.65	15.64	21.38	0.73	1.37	43.10	1.04	0.70	10.79	9.71	2.09	4.66	25.06	5.92	16.29	33.01	4.33
	XX	91.67	167.46	136.15	11.17	31.30	97.25	57.54	121.67	23.92	10.20	3.51	11.76	14.31	0.82	1.22	63.02	1.09	0.82	9.55	7.02	3.09	2.27	17.87	2.14	5.68	68.82	3.00

Table 9: Ranking and percent contribution of 27 characters towards total divergence (ARS, Shirgaon) based on Wilks'V test

SN	Character	Times ranked first	Per cent contribution
1	Days to 50% Flowering (Nos.)	25	0.56%
2	Plant Height (cm)	28	0.63%
3	Stem Length Excluding Panicle (cm)	0	0.00%
4	No. of Tillers Plant-1	2	0.04%
5	Panicle Length of Main Axis (cm)	0	0.00%
6	No. of Spikelets Panicle-1	47	1.05%
7	Fertility (%)	406	9.09%
8	Days to Maturity (Nos.)	73	1.63%
9	Test Weight of 1000 Grains (gm)	2	0.04%
10	Grain Length (mm)	0	0.00%
11	Grain Width (mm)	19	0.43%
12	Grain Yield Plant-1 (gm)	11	0.25%
13	Straw Yield Plant-1 (gm)	14	0.31%
14	Grain Yield/ Straw Yield Ratio	6	0.13%
15	Straw Yield/ Grain Yield Ratio	0	0.00%
16	Leaf Length (cm)	1161	26.00%
17	Leaf Breadth (cm)	0	0.00%
18	Stem Thickness (cm)	0	0.00%
19	No. of Panicles Plant-1	867	19.42%
20	Decorticated Grain Length (mm)	244	5.46%
21	Decorticated Grain Breath (mm)	0	0.00%
22	DGL/DGB Ratio	0	0.00%
23	Amylose Content (%)	15	0.34%
24	Zinc Content (ppm)	254	5.69%
25	Iron Content (ppm)	254	5.69%
26	Calcium Content (ppm)	1037	23.23%
27	Alkali Spreading Value	0	0.00%

Table 10: Ranking and percent contribution of 27 characters towards total divergence (RARS, Karjat) based on Wilks'V test

SN	Character	Times ranked first	Per cent contribution
1	Days to 50% Flowering (Nos.)	39	0.87%
2	Plant Height (cm)	62	1.39%
3	Stem Length Excluding Panicle (cm)	0	0.00%
4	No. of Tillers Plant-1	14	0.31%
5	Panicle Length of Main Axis (cm)	11	0.25%
6	No. of Spikelets Panicle-1	110	2.46%
7	Fertility (%)	651	14.58%
8	Days to Maturity (Nos.)	1	0.02%
9	Test Weight of 1000 Grains (gm)	12	0.27%
10	Grain Length (mm)	1	0.02%
11	Grain Width (mm)	0	0.00%
12	Grain Yield Plant-1 (gm)	33	0.74%
13	Straw Yield Plant-1 (gm)	6	0.13%
14	Grain Yield/ Straw Yield Ratio	0	0.00%
15	Straw Yield/ Grain Yield Ratio	0	0.00%
16	Leaf Length (cm)	1165	26.09%
17	Leaf Breadth (cm)	0	0.00%
18	Stem Thickness (cm)	0	0.00%
19	No. of Panicles Plant-1	0	0.00%
20	Decorticated Grain Length (mm)	445	9.97%
21	Decorticated Grain Breath (mm)	0	0.00%
22	DGL/DGB Ratio	0	0.00%
23	Amylose Content (%)	54	1.21%
24	Zinc Content (ppm)	405	9.07%
25	Iron Content (ppm)	281	6.29%
26	Calcium Content (ppm)	1175	26.32%
27	Alkali Spreading Value	0	0.00%

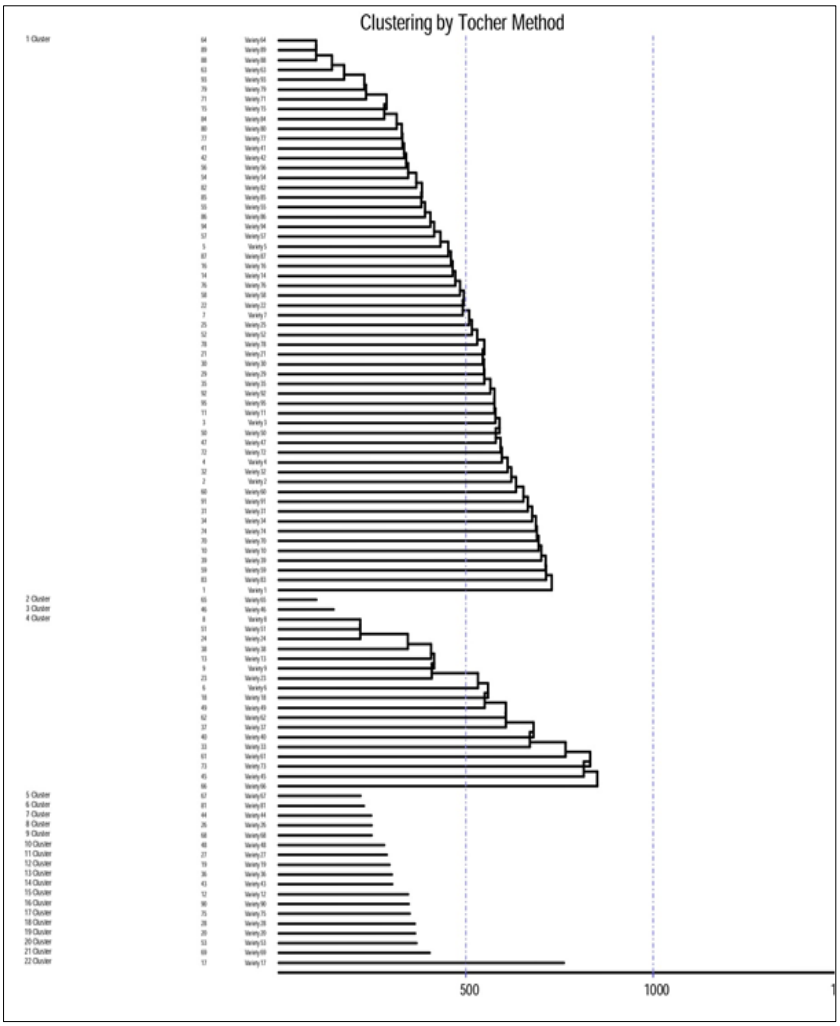

Fig1: Dendrogram showing clustering pattern of 27 rice genotypes in kharif-2020 (ARS, Shirgaon) using Torcher's method

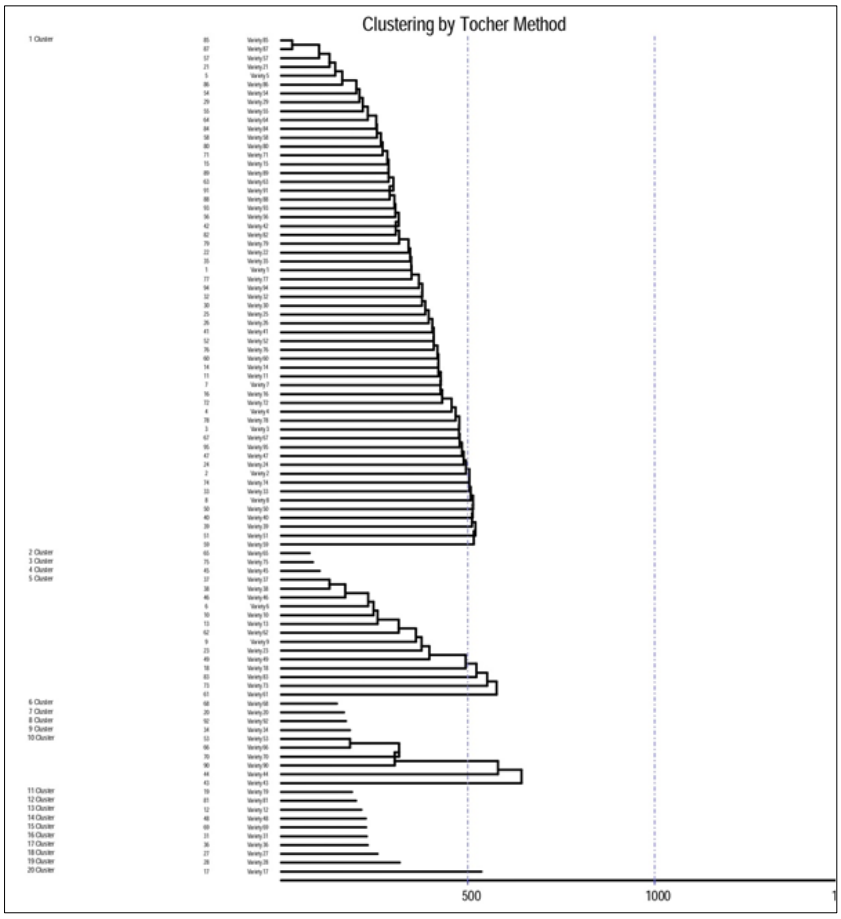

Fig 2: Dendrogram showing clustering pattern of 27 rice genotypes in kharif-2020 (RARS, Karjat) using Torcher's method

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