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Studies of Genetic divergence in cultivated rice germplam under irrigated condition

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ABSTRACT
A statistical study for analyzing genetic divergence is one of the basic things. In this study the sixty three rice germplasm were taken for the genetic divergence analysis using D^2test. Eighteen yield and quality attributing characters were taken in this study. Based on the different characters, genotypes were differentiated into eight clusters and cluster VII was the Largent group occupied by the sixteen genotypes. Keeping the view of quality characteristics except kernel elongation ratio all characters were found highly significant variations. On the basis of mean performance with genetic diversity and cluster pattern the following genotypes viz. Sarju-52, ND Usar Dhan-3, Narendra-80 of cluster IV, MTU-7029. Sambha Mahsuri of cluster VI, Pusa Basmati-1, Taraori Basmati of cluster II and Malviya-36, Kanakjeer and Super Basmati of cluster VIII clarified that the promising combinations would be highly useful for further breeding Programme in future.
Keywords: *Divergence, rice,Cluster, yield and quality characters*

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INTRODUCTION
Identification of genetically closed and diverse type plants can be achieved by the grouping of the germplasm and D^2 statistic (4) is one of the wonderful techniques to estimate the genetic diversity and yield and yields components.Rice (*Oryza sativa* L.) constitutes a principal source of calories in Africa; it is a staple food crop in Côte d'Ivoire, Gambia, Guinea, Guinea-Bissau, Liberia, Madagascar, Mauritania, Senegal and Sierra Leone, Nigeria, among others (12). Its adoption as a principal staple food is increasingly spreading to other parts of Africa; however, self-sufficiency in rice production is declining as demand increases.However, in case of the rice genetic diversity such type of experiments has also been done for the selection of desirable parents for exploitation of hybrid vigour(1,2,5,11,10). The present investigation was undertaken to assess the nature and magnitude of genetic divergence and characters contributing the genetic divergence in 63 rice genotypes under irrigated condition. These genotypes included basmati, non-basmati, short grain aromatic, upland, land races, bold grain and long grain. The region of taking such huge type cultivars for avoiding the close proximity and exploiting the heterosis for future breeding programme for the development of high yielding rice cultivars.

MATERIAL AND METHODS
A set of 63 rice genotypes including basmati, non-basmati, short grain, long grain, elite breeding lines and landraces were evaluated for the phenotypic diversity using yield and yield related components.These genotypes were evaluated in the field in randomized complete block design with three replications. Three rows of individual genotypes were planted at a spacing of 20x15cm. Transplanting was done after the well establish nursery

of 25 days old. Recommended dose of fertilizers were applied to raise the good crop. Weeding was carried out manually as per need. Harvesting was done above the soil level at the physiological maturity after the removing off types plant.

For yield and yield components randomly five plants were selected form the middle row form each plot. Data were recorded on five competitive plants per genotype from middle row for yield and yield components such days to fifty per cent flowering (DFF), Days to maturity (DM), Plant height (Ph), Number of tiller/plant (NoT), panicle length (PL), number of filled grain/panicle (FG/PL), spikelet fertility (SF%), 100 grain weight (test Weight) and yield per plant(Y/P).

Quality traits were also analyzed form the collected seed samples like hulling percent recovery (HR), milling percent recovery (MR), head rice recovery (HRR), kernel length before cooking (KL), kernel breadth before cooking (KB), kernel length breadth ratio(L/B ratio), kernel length after cooking(KLAC), kernel elongation ratio (KE) and amylose content(AC).

The data were subjected to D^2 statistic (4) to measure the genetic divergence amongst the test entries. The grouping of genotypes in various clusters was done by the Tocher's method (7).

RESULT AND DISCUSSION

Genetic diversity is one of the important and useful tools to analyze the correlation between the genotypes for future breeding programme to bread high yielding cultivars and hybrid vigor. In present study most of the characters were analyzed except kernel elongation for the purpose of genetic divergence. All the genotypes were grouped into eight clusters/category using D^2 values are presented in Table 1.

Almost all of the clusters are included by the genotypes based on the observation and data analysis with respect to agronomic and quality traits. Among all the clusters, cluster VII carried a maximum of 16 genotypes VII, followed by cluster III (10 genotypes) and cluster IV (9 genotypes), while clusters II have minimum of 2 genotypes. Other rest of the clusters *viz.* cluster I, cluster V, cluster vi and cluster VIII having 6, 8, 5, and 7 genotypes respectively. The cluster composition of the different rice genotypes under this study indicates that most of the cultivars of same centers have close proximity and narrow genetic base. In case of cluster IV, Narendra-80, Narendra Usar Dhan-3, Narendra Usar Dhan-2, Sarju-52 are the cultivar of same center and have close proximity. However, the cultivar of GBPUA&T, Pant Nagar, like Pant Dhan-10 of cluster III is highly diverse from the other cultivar of the Pant Nagar of cluster VII (Pant Sugandh Dhan-17, Pant Sugandh Dhan-6).

Keeping the view of diversity analysis among the genotypes, intra-cluster distance related to the eighteen desirable characters was also estimated using D^2 is presented in the Table 3. The intra-cluster analysis revealed that cluster VII, cluster III, cluster V and cluster VI had high intra-cluster values. The maximum inter-cluster distance was also recorded between clusters II and VI and found to be 55.80, followed by the between clusters II and IV with value of 50.25 and cluster II and V (45.43). However, on other hand the distance between clusters IV and VIII was observed as minimum with value of 8.89.

Table 1. Cluster composition of different rice genotypes

Cluster Number	No of genotypes	Name of genotypes in each cluster
I	6	Rupali,Pant-12, Anjali, CR 2340-3, Barni Deep, Birsa Dhan 101
II	2	Pusa Basmati-1,Taraori Basmati
III	10	Pant Dhan-10, Type-3, Basmati-370 , Manhar, Naveen, CR-2340-7, BAU-170-90, IR-64, Kalanamak, Sulk Samrat
IV	9	Vishnuprag , Pant Dhan-4, Narendra-80, Narendra Usar-3, HUR 3022, Narendra Usar-2, Jaya, Sarju-52, Vandana
V	8	Pant Dhan-11, Annada , Gautam, IDR-763, Heera , Pusa-44, Kallinga-1, IR 68897B
VI	5	MTU-7029, BPT- 5204, Badshabhog , Tulsiparsad , Pusa Sugandh-2
VII	16	CR 2340-1, Pant Sugandh Dhan-17, Pusa Sugandh-3, Pant Dhan-6, Krishna Hansa , HUBR 2-1, NDR-118, Narendra-359, Narendra2026, Narendra-97, CR2340-5, Pusa Sugandh-4, Khilish , BVD 109, IR 58025B , Pusa 6B
VIII	7	Kanak Jeer , GR-32, Malviya-36, Maleshiya, Lalmati , Sona Choor , Super Basmati
Total	63	

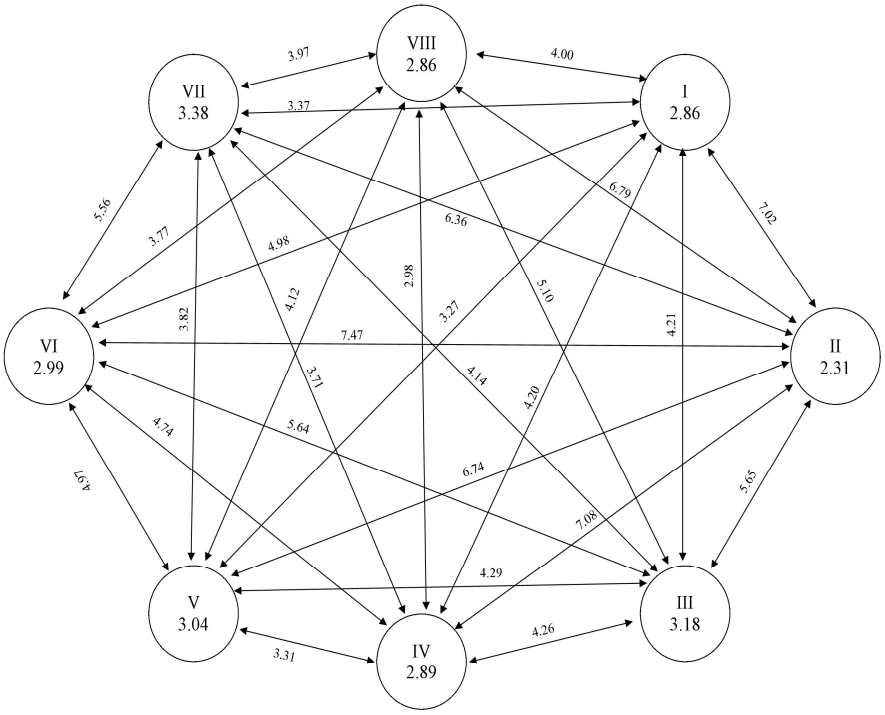

Fig. 1. Mutual relationship among clusters based on statistical distance (= $\sqrt{D^2}$) in rice genotypes

Table 2. Cluster means for eighteen characters of rice genotypes

Clusters	Characters																	
	DF	DM	PH	NET	PL	NSP	NGP	1000GW	GY	HR	MR	HRR	KL	KB	L/B ratio	KLAC	KE	AC
I	83.01	113.54	106.70	10.24	25.58	243.38	195.21	18.33	23.38	79.03	67.87	53.81	6.23	1.90	3.30	11.23	1.82	20.54
II	117.55	150.21	88.26	7.30	26.31	162.75	113.76	18.30	26.64	79.80	68.81	54.90	7.39	1.40	5.28	12.48	1.69	24.28
III	101.18	126.85	119.73	8.95	27.21	173.42	143.49	23.05	28.18	73.94	62.44	52.15	7.10	1.92	3.72	11.69	1.65	22.18
IV	98.33	128.45	125.92	8.63	26.05	174.56	140.98	20.94	27.36	80.99	71.05	58.94	6.16	2.12	2.93	9.60	1.56	21.69
V	80.84	111.17	91.36	10.37	22.81	167.16	146.20	21.93	24.43	79.96	68.53	56.82	6.02	1.86	3.26	9.77	1.63	21.69

VI	112.43	144.31	105.02	10.21	22.42	256.68	217.64	18.15	35.38	76.88	67.03	56.74	5.00*	1.77	2.83	8.15	1.63	22.22
VII	88.76	118.85	108.98	10.91	27.18	239.85	203.85	22.08	27.45	80.55	70.61	59.67	7.30	2.00	3.68	12.19	1.68	22.60
VIII	104.63	135.21	126.22	9.01	26.14	235.68	204.07	17.72	21.42	80.51	71.03	59.38	5.73	1.88	3.08	8.95	1.56	22.38
Mean	95.10	124.84	111.60	9.76	25.80	209.51	175.40	20.78	26.71	79.03	68.56	57.04	6.49	1.93	3.41	10.67	1.65	22.09
SEm±	2.69	3.57	2.97	1.73	1.73	4.22	4.06	0.59	0.91	2.50	2.21	1.94	0.30	0.08	0.22	0.40	0.03	0.77
CV%	4.90	4.96	4.61	6.56	6.10	3.48	4.01	4.96	5.87	5.47	5.59	5.90	8.01	7.33	10.97	6.56	10.69	6.06

The underlined figures indicate maximum (double) and minimum (single) values

Table 3. Intra and Inter-Cluster D^2 and D values of 63 genotypes for 18 characters in rice

Characters	I	II	III	IV	V	VI	VII	VIII
V III	16.056 (4.01)	46.19 (6.79)	26.08 (5.11)	8.89 (2.98)	16.98 (4.12)	14.19 (3.77)	15.80 (3.98)	**8.17 (2.86)**
VII	11.38 (3.37)	40.45 (6.36)	17.11 (4.14)	13.75 (3.71)	14.59 (3.82)	30.95 (5.56)	**11.44 (3.38)**	
VI	24.75 (4.97)	55.80 (7.47)	31.91 (5.65)	22.43 (4.74)	24.70 (4.97)	**8.98 (2.99)**		
V	10.69 (3.27)	45.43 (6.74)	18.37 (4.29)	10.98 (3.31)	**9.25 (3.04)**			
IV	17.67 (4.20)	50.25 (7.09)	18.19 (4.27)	**8.33 (2.89)**				
III	17.72 (4.21)	31.98 (5.66)	**10.08 (3.18)**					
II	49.24 (7.02)	**5.33 (2.31)**						
I	**8.17 (2.86)**							

The bold figures indicate intra-cluster D^2 values and values in parentheses are D-values

Table 2 represents the cluster mean of the different trait under the respective study. It is evident from Table 2 and Figure 1 that all the minimum and maximum cluster mean values were distributed in relatively distant clusters. In the case of days to fifty percent flowering and days to maturity cluster V showed minimum value followed by the cluster I and cluster

VII while cluster II showed the maximum value of days to fifty percent flowering followed by cluster VI and cluster VIII with over all days to fifty percent flowering of 95.10. The another useful trait that is plant height was also recorded between range from 88.26 to 126.22 cm which is followed by cluster II and cluster VIII respectively. The number of productive tillers is one of the yield attributing traits ranging from 7.30 to 10.91 with mean value of 9.76. The panicle length which bears the grain was range from 22.42 cm to 27.21 cm with an average panicle length of 25.80 cm. The number of spikelet per plant represent the yield was ranging from 162.75 to 256.68 with an average spikelet par panicle of 235.68. The 1000 grain weight also consider as test weight was recorded as minimum in cluster VI (18.15 gm) and maximum in cluster III (23.03gm) with mean test weight of 20.78gm. The single plant yield also consider as grain yield was found to be 21.42 gm in cluster VIII was a minimum single plant yield while maximum single plant was recorded as 35.38 gm under cluster VI with average single plant yield of 26.71 gm.

The maximum cluster mean was observed in the clusters VI for GY,NGP andNSP, in cluster III for PL and GW,in cluster V for earliness, in cluster II for dwarfness, kernel length, L/B ratio,KLAC and AC, in cluster IV for HR, MR and KB, in cluster VII for HRR and in cluster I for KE.Dispersion pattern of genotypes over large number of clusters with a maximum of 16 genotypes in cluster VII to 2 genotypes in cluster II indicated the presence of high degree of genetic divergence and genetic heterogeneity among the genotypes.

The quality attributing train were also recorded and presented as cluster-wise are given in Table 2. Hulling recovery percentage also known as de-husking was carried out from all the samples was computed with mean value of 79.03 % with a range of 79.03 to 80.99. The milling rice recovery percentage was recorded minimum 62.44% from cluster III and maximum 71.05% from the cluster IV with an average milling rice recovery of 68.56%. The head rice recovery percentage were also recorded after the removal of broken rice was ranged from 52.15 to 59.67 % followed by the cluster III and VII respectively with mean head rice recovery of 57.04%. The kernel length and breadth were also recoded from all the samples before cooking and after cooking. The value of kernel length before cooking ranged from 5.00 to 7.39 mm with average kernel length of 6.49 mm while kernel breadth before cooking was computed as 1.40 mm minimum and 2.12 mm maximum with mean value of 1.93 mm. L/B ratio is one of the important rice grain quality attributing trait were also recorded from the each sample of milled rice. L/B ratio was recorded as minimum 2.83 mm and maximum 5.28 mm with mean L/B ratio of 3.41 mm. The kernel elongation after cooking increased the value of rice was also recorded with minimum of 8.15 mm followed by the cluster II and maximum 12.48 mm followed by the cluster VI with mean value of 10.67 mm. Amylose content is the another important biochemical parameter in the case of rice grain quality was also be considered and computed from each sample with mean amylose content of 22.09. The minimum amylose content was recorded as 20.54 of cluster I and maximum 24.28 from cluster II.

A critical examination of the nature of clusters revealed that the genotypes together in a cluster were related by pedigree as in cluster II and cluster V, or originated in the same ecological regions as in cluster VIII, or similarities in their morphological characters, as seen in most of the clusters. Similar results were reported by several workers (9,3,6,8).

The different clustering patterns of the genotypes are meaningful in respect to diversity patters that may confer the sources of genes for yield and quality components. These highly diverse genotypes may be helpful as parents in crossing programme to incorporate the characters for which they have better values over others.

Considering mean performance, genetic distance and clustering pattern a hybridization prorgamme may be initiated involving genotypes 'Pusa Basmati' and Taraori Basmati of cluster II, Sarju-52, Narendra Usar-3 and Narendra-80 of cluster IV, Badshabhog, MTU-7029 and BPT-5204 of cluster VI and Malviya-36, Kanakjeer and Super Basmati of cluster VIII for combining high yielding and quality traits which are likely to produce superior segregants for high grain yield along with better grains qualities.

REFERENCES

1. Arunachalam V (1981) Genetic distance in plant breeding. *Indian J. Genet.* 41: 226-236.
2. Das GR and DN Borthakur (1973) Genetic divergence in rice. *Indian J. Genet.* 33: 436-443.
3. Gahalain SS (2006) Genetic divergence in rice (*Oryza sativa* L.) genotypes grown in Kumaon

Himalaya. *Indian J. Genet.* 66(1): 37-38.
4. Mahalanobis PC (1936) On the generalized distance in statistics. *Proc. Nat. Inst. Sci.* India B 2: 49-55.
5. Murty BR and V Arunachalam (1966) The nature of divergence in relation to breeding system in some crop plants. *Indian J. Genet.* 26A: 188-198.
6. Ramya K and Senthilkumar (2008) Genetic divergence in rice (*Oryza sativa* L.). *Crop Improvement.* 35 (2): 119-121.
7. Rao CR (1952) Advanced statistical methods in biometrical research, John Wiley and Sons Inc., New York.
8. Raut KR, PN Harer and PS Yadav (2009) Genetic divergence in rice (Oryza sativa L.). *Journal of Maharashtra Agricultural University.* 34 (2): 172-174.
9. Sardana S, DN Borthakur and TN Lakhanpal (1997) Genetic divergence in rice germplasm of Tripura. *Oryza* 34(3): 201-208.
10. Sharma MK, RK Agrawal and AK Richaria (1997).Genetic diversity in rice under rainfed upland and irrigated ecosystems. *Oryza* 34: 19-24.
11. Singh RS (1981) Genetic divergence in indigenous varieties of rice grown in Mirzapur district, U.P., *India. Int. Rice. Res. Newsl.* 6: 3-4.
12. Malton, P., T. Randolph and R. Guei (1998). Impact of Rice Research in West Africa. In: Impact of Rice Research. Thailand Development Research, International Rice Research Institute (IRRI), Manila, Philippines (Prabhu L. Pingali, Mahabub Hossain, ed.) pp. 383 -404