

## Genetic diversity studies of promising rice varieties of eastern India based on quality characters

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### ABSTRACT

Forty one promising rice varieties of eastern India were evaluated for physico- chemical and cooking characters to study the diversity pattern among the genotypes. The genotypes were grouped into ten clusters. Maximum 11 genotypes were grouped in cluster IV followed by ten in cluster I. The clusters VI, VIII, IX and X are represented by single genotype namely Gayatri, Hanseswari, Satyakrishna and Saket-4 respectively indicating high degree of heterogeneity among the genotypes. The intra cluster distance is highest in cluster IV ( $D=13.41$ ) followed by cluster V (10.16), cluster II (10.05) and lowest in cluster VII ( $D=7.31$ ). The coefficient of variation was highest in water uptake (10.1) and volume expansion ratio (6.97) and lowest in hulling% (1.26). The cluster mean for Kernel length and Kernel length after cooking were highest in cluster V. Highest cluster mean was reported in cluster VI for Hulling% and Kernel breadth. Percentage of contribution towards total divergence is highest in alkali spreading value (33.05) and lowest in milling recovery (0.0). Alkali spreading value, kernel length after cooking, amylose content and kernel breadth together accounted for 83.78 percent to the total divergence. So these characters should be considered during hybridization programme.

**Key words:** genetic diversity, quality characters, rice varieties, eastern india

Rice is the staple food of India and occupies 44.6 million ha. In eastern India it is 26.8 million ha. But due to regular flood, cyclone and drought, the production is very low. In order to meet the food requirement of the increasing population, development of high yielding varieties is essential. Breeders mostly focus on high yield. The consumers prefer quality rice. Hence breeders should give due importance to the quality traits in their breeding programme besides yield.

Genetic divergence is an efficient tool for an efficient choice of parents for hybridization programme. Such study also selects the genetically divergent parents to obtain desirable combinations in the segregating generations. Because cross between genetically divergent parents are likely to produce high heterotic effects. Information on the nature and degree of genetic divergence would help the plant breeder in choosing the right parents for the breeding programme (Vivekananda and Subramaniam, 1993). Keeping this in view, 41 promising rice genotypes of eastern India are analyzed for quality characters to study the clustering pattern so as to be utilized in the hybridization programme.

### MATERIALS AND METHODS

Forty one promising rice varieties of eastern India were transplanted at Central Rice Research Institute, Cuttack farm during 2007 wet season to evaluate the physico-chemical and cooking characters. The experiment was laid out in randomized block design with three replications. The spacing was 15x 20 cm. The recommended agronomic practices were followed. The seeds were stored for three months after harvest. The samples were analyzed for quality characters at 14% moisture content. The characters like hulling (%), milling (%), head rice recovery (HRR%), kernel length (KL), kernel breadth (KB), length breadth ratio (L/B), water uptake (WU), volume expansion ratio (VER), elongation ratio (ER), amylose content (AC%) etc. were analyzed based on standard methods like of Govindswami and Ghosh, (1969), Juliano (1971) and little *et al* (1958). Multivariate analysis of genetic divergence among varieties was done using Mahalanobis  $D^2$  statistics (1936) and grouping of varieties into clusters by Tochers method (Rao, 1952), (Arunachalam, 1981). Nayak *et al*, (2004) studied

genetic diversity analysis in scented rice.

## RESULTS AND DISCUSSION

Analysis of variance showed significant differences among the genotypes for 12 quality characters and indicated very high variability. Based on  $D^2$  value, 41 rice genotypes were grouped in to 10 clusters (Table 1). Maximum 11 genotypes were grouped in cluster IV. Cluster I consists of ten genotypes having medium slender grains. The clusters VI, VIII, IX, and X are represented by single genotypes viz. Gayatri, Hanseswari, Satyakrishna and Saket-4 respectively indicating high degree of heterogeneity.

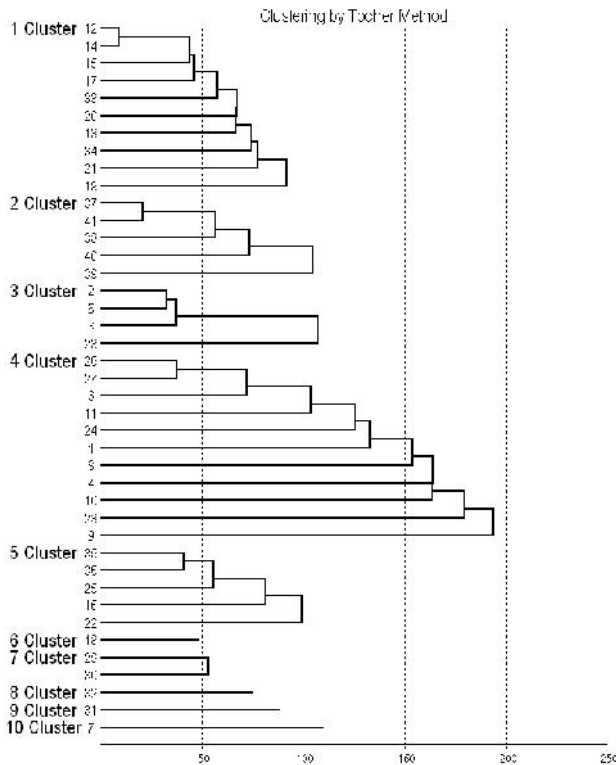
Cluster V is represented by five genotypes having long slender grains. All upland varieties like Vandana, Vanaprava, Heera, Kalyani-2 and Kalinga-3 are in cluster II. Nua Kalajeera and Nua Dhusara are the pure line selections in cluster VII. Gayatri and Savitri are in different clusters although, these are sister selections. But these were in one cluster based on morphological diversity studies.(Subudhi *et al.*, 2008). The hybrid varieties namely Ajay and Rajlakshmi are in cluster V. The dendrogram is given in (Fig. 1).

The inter cluster distance is higher than intra cluster distance indicating wide genetic diversity among the genotypes (Table 2). The highest intra cluster distance is observed in cluster IV ( $D=13.41$ ) followed by cluster II ( $D= 10.05$ ), cluster V( $D=10.16$ ), cluster III ( $D=9.78$ ) and cluster I ( $D= 9.07$ ).The intra cluster distance of cluster VI, VIII ,IX and X are zero as these clusters are represented by single genotype.

The inter cluster distance is highest in all except cluster I. Highest inter cluster distance is observed between clusters V and VII = 35.94 followed by VII and IX = 31.29, III and IX = 30.64, II and VII = 31.81 indicating very wide genetic variability and diversity among the varieties within these groups. Similarly minimum inter cluster distance is observed in VI and VIII = 9.71, I and X = 13.43, II & IX = 14.46 etc. These varieties are genetically very close. Hybridization among these varieties will not give encouraging result. Cluster mean and coefficient of variation were presented in (Table 3). The coefficient of variation is highest in water uptake (10.1) and VER(6.97) and lowest coefficient of variation was reported in Hulling percentage(1.26). The cluster I with ten genotypes exhibited highest mean value for head rice recovery percentage (64.1).Cluster II with five genotypes exhibited lowest mean value for hulling recovery (74.7), alkali spreading value (3.45) water uptake (151.0) and elongation ratio (1.5). Cluster III with four genotypes exhibited highest mean value for water uptake (278.75). Cluster IV is having highest mean value for milling recovery (72.36) although it contains eleven genotypes. Cluster V exhibited highest mean value for kernel length (7.2) and kernel length after cooking (11.25). Highest cluster mean for hulling recovery (80.0) and kernel breadth (2.72) was observed in cluster VI. Cluster VII, with two genotypes exhibited highest cluster mean for elongation ratio (2.04) and volume expansion ratio (5.2) and lowest cluster mean for kernel length (3.9), amylose content (22.2). Cluster VIII is having lowest cluster mean for head rice recovery (46.0). Cluster IX ,with one genotype exhibits

**Table 1 Clustering pattern of 41 rice genotypes of eastern India based on  $D^2$  statistics**

Clusters	Number of genotypes	Name of cultivars and serial number
I	10	CR1014(12), Padmini (14), Utkalprava (15), Panidhan (17), Chandan (33), Durga (20), Pooja (13), Chandrama (34), Sarala (21), Tulsi (19)
II	5	Kalinga-3 (37), Vanaprava (41), Vandana (38), Heera (40), Kalyani-2 (39)
III	4	Indira(2), Tara(5), Shaktiman (3), Savitri(23)
IV	11	Ketekijoha (26), BPT-5204 (27), Tapaswini (6), Naveen (11), Kshira (1), Varshadhan (24), Radhi(4), Ratna(8), Supriya (10), Lalat (28), Udaya (9)
V	5	Ajay (35), Rajlakshmi (36), Geetanjali (25), Lunishree (16), Samalei (22)
VI	1	Gayatri (18)
VII	2	Nuakalajeera (29), Nuadhusara (30)
VIII	1	Hanseswari (32)
IX	1	Satyakrishana (31)
X	1	Saket-4 (7)



**Fig. 1.** Clustering of forty one rice varieties by Tocher method based on quality characters

highest mean value for length breadth ratio (3.52) and lowest value for kernel breadth (1.75). Cluster X is having highest mean value for alkali spreading value (7.0) and lowest mean value for volume expansion ratio (3.45).

Contribution of different quality characters to total divergence is presented in (Table 4). The alkali

spreading value was having maximum contribution value i.e 33.05 followed by amylose content (21.71), KLAC (15.24), KB (13.78) and lowest value is observed in hulling (%) and milling (%) i.e zero. Hence alkali spreading value, amylose content, kernel length after cooking and kernel breadth together contributed 83.78 percent towards total divergence. Therefore hence these characters should be given importance during hybridization and selection of segregating populations.

It is assumed that maximum amount of heterosis will be manifested in cross combinations involving the parents belonging to most divergent clusters. But for a plant breeder, the objective is not only high heterosis but other quality characters also. The greater the distance between two clusters, the wider the genetic diversity between the genotypes. Mian and Bhal (1989) reported that parents separated by D<sup>2</sup> value of medium magnitude generally showed good results. Keeping this in view, it is indicated from the study that hybridization between the genotypes of the cluster I and IX (Satyakrishna), cluster I and V, cluster VII (Nua kalajeera and Nuadhusara) with IX (Satyakrishna) would produce encouraging results as cluster I is having highest cluster mean for head rice recovery and cluster IX the highest L/B ratio and lowest KB. Similarly cluster V is haung the highest in cluster mean value for kernel length and KL after cooking. Cluster VII is having highest value for VER and ER and cluster IX is lowest for KB and highest for L/B ratio. The genotypes of these clusters may be used as parents selected for future breeding programme.

**Table 2. Intra and Inter cluster average of quality characters in 41 rice genotypes of eastern India**

	I	II	III	IV	V	VI	VII	VIII	IX	X
I	9.07		14.08	16.36	19.54	14.47	21.24	16.15	21.73	13.43
II		(10.05)	28.26	15.06	17.49	21.42	31.81	21.84	14.46	25.38
III			(9.78)	23.13	23.91	15.04	25.96	15.35	30.64	14.7
IV				(13.41)	17.73	16.43	26.5	19.64	16.15	22.09
V					(10.16)	22.15	35.94	22.81	16.44	17.44
VI						(0.00)	24.07	9.71	26.08	21.74
VII							(7.31)	28.65	31.29	29.25
VIII								(0.00)	29.4	21.72
IX									(0.00)	23.93
X										(0.00)

**Table 3. Cluster mean of different quality characters in 41 rice genotypes of eastern India**

Cluster	Hull(%)	Mill(%)	HRR(%)	KL(mm)	KB(mm)	L/B	ASV	WU	KLAC	VER	ER	AC(%)
I	78.6	70.7	64.1**	5.59	2.08	2.72	5.56	178.75	9.34	3.87	1.65	23.25
II	74.7*	68.4	48.5	6.36	2.19	2.92	3.45*	151.0*	9.55	4.01	1.5*	25.09**
111	79.0	71.25	62.88	5.6	2.44	2.3	6.75	278.75**	9.86	3.81	1.76	24.0
IV	79.2	72.36**	60.94	5.86	2.18	2.72	4.0	162.73	9.92	3.84	1.70	23.36
V	79.7	71.60	59.98	7.2**	2.07	3.5	5.17	199.5	11.25**	3.95	1.58	24.59
VI	80.0**	71.5	61.0	4.97	2.72**	1.83*	5.0	185.0	9.0	4.13	1.81	24.4
VII	75.8	67.45*	63.3	3.9*	1.97	1.99	4.8	205.5	8.05*	5.2**	2.04**	22.2*
VIII	79.2	69.2	46.0*	5.43	2.68	2.03	5.1	155.0	8.4	3.6	1.55	23.9
IX	77	71.0	63.65	6.5	1.75*	3.52**	3.9	161.5	11.1	4.75	1.7	24.95
X	78.0	72.0	64.0	6.37	1.85	3.46	7.0**	244.5	10.7	3.45*	1.68	24.8
Mean	78.3	70.9	60.14	5.89	2.16	2.76	4.88	185.38	9.78	3.95	1.66	23.8
CV(%)	1.26	4.57	2.73	2.26	2.21	3.29	2.78	10.1	2.03	6.97	2.19	2.25
SEM $\pm$	0.70	2.29	1.58	0.09	0.03	0.06	0.09	13.24	0.14	0.19	0.025	0.38

\*,\*\* represent lowest and highest value for different characters

NB: HRR=Head rice recovery, KL=Kernel length, KB =Kernel breadth, WU=Water uptake, KLAC=Kernel length after cooking, VER=Volume expansion ratio, ER=Elongation ratio, AC= Amylose content.

**Table 4. Percentage of contribution of quality characters towards total divergence**

Characters	Time ranked	Contribution (%)
Hulling(%)	0	0.00
Milling(%)	0	0.00
Head rice recovery(%)	8	0.98
Kernel length	18	2.2
Kernel breadth	113	13.78
Length/breadth	88	10.73
Alkali spreading value	171	33.05
Water uptake	16	1.95
Kernel length after cooking	125	15.24
Volume expansion ratio	2	0.24
Elongation ratio	1	0.12
Amylose content(%)	178	21.71

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