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Genetic Diversity Studies of Popular Rice Varieties based on Grain Quality Characters

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A B S T R A C T

One hundred rice genotypes released for different ecologies such as upland, irrigated, lowland, and saline in different states of India were evaluated for 12 quality characters like Hulling (%), Milling (%), Head rice recovery(%), Kernel length(cm), Kernel breadth(cm), Length breadth ratio, Volume expansion ratio, Elongation ratio and Amylose content(%) etc to study the magnitude of genetic diversity among the genotypes and major traits contributing to variation. Based on Mahalanobis D^2 value, 100 genotypes are grouped in to 12 clusters. The single genotype having independent cluster are WITA-8, WGL32183, Konark, Purnendu, VLD-61, PusaSugandh-3 and Improved Lalat. Maximum 55 genotypes are in cluster 1. Maximum inter cluster divergence was observed between cluster 3 and 11(667.36) followed by cluster 8 and 11(615.50), cluster 7and 11(604.87). Lowest inter cluster distance was observed between cluster 2and 3(10.68).Intra cluster distance (D) ranged from 48.77(cluster 5) to 100.4(cluster 8). These are more diverse and can be used in hybridisation programme for development of effective hybrids. The inter cluster distance is higher than intra cluster distance indicating wide genetic diversity among the genotypes.

Introduction

Rice is the staple food for more than half of the world population and number one human food crop in the world.(Itani, 2002). Rice occupies a pivotal role in Indian food and livelihood security. India is the second most populous nation and stand first in areas and second in production followed by China. In India, 44.6Mha are in rice cultivation. It is grown in all continent and in all agro-climatic zones. These wide adaptations lead to evolution of thousands of varieties having diverse cooking and eating characters. Before 2000AD, there is demand for increase in production and productivity to meet the food requirement of the growing population. There after, India became self sufficient and surplus country so far as rice is concerned. People became more concerned about quality rather than quantity. Previously breed varieties are mostly bold grain, which people do not like. India has released 705 varieties without testing quality characters (Thongbam *et al.*, 2010). Now quality characters are considered during the varietal development and release.

Quality is very important determinant of market price, consumer acceptance and end users. Consumers preference depend on appearance, milling and cooking process, grain shape and size. Grain quality in rice is determined by grain appearance nutritional value, cooking and eating quality (Juliano *et al.,* 1990).Good grain quality fetches high market price. So demand for better grain quality is increasing day by day in developing and developed countries. Now quality is an important breeding objective in all rice breeding programme. Sobha Rani *et al.*, (2008) studied the quality characters of 78 varieties of India. There after 28 land races of Assam were evaluated by Das and Borah, (2008). Realising the importance, Bhonsle and Sellapan (2010) evaluated 22 traditional varieties of Goa for their physico-chemical characters. Vanaja and Babu (2006) studied 56 high yielding varieties of Kerala. Shrivastava *et al*., (2012) also evaluated 12 genotypes of Faizabad. Subudhi *et al*., (2012) evaluated 42 released varieties of Odisha for their quality characters and their variations. It is evident that there is no systematic study of grain quality characters for released varieties in India. Now attempts have been made to evaluate the released varieties for their quality characters to find out better donors for hybridisation, popularisation and development of database. In the preliminary study, 100 genotypes of different states and for different ecologies were evaluated to find out better donors for hybridisation and analysis of their diversity.

Materials and Methods

The experiment was conducted in the farm of National Rice Research Institute, Cuttack during Kharif 2017.One hundred released rice varieties for different states in India of different ecologies viz., upland (17), medium (50) and lowland (30), saline (3)were transplanted in randomised block design with two replications. 25 days old seedlings were transplanted with spacing 15x20cm. The recommended dose of N:P:K(80:40:40) were applied. All the agronomic practices were followed to raise good crop.

Methods

After 3 months of harvest, Samples were cleaned thoroughly using winnower to remove chaff and other foreign matters and dried up to 12-14%moisture content. Analysis of all quality traits were done in two replications.

Physical properties

Kernel length, kernel breadth, and kernel length breadth ratio were measured by dial micrometer(Ramiah,1969).Hulling (%) and Milling (%) were done by using standard rice huller (SatakeThuza) and rice polisher (Satake TMO5A) respectively. After cleaning and weighing the dehusked kernel(brown rice), Hulling (%) was calculated. Dehusked kernel were polished to remove bran and Milling (%) was calculated. Head rice recovery (%) were calculated (Govindswamy and Ghosh, 1969).

Chemical properties: Alkali spreading value was analysed following Little *et al*., (1958). Amylase content was calculated (Juliano, 1971).

Cooking characters: Water uptake and Volume expansion ratio were done (Anonymous, 2004), (Beachell and Stanse, 1963). Similarly kernel length after cooking were measured following Azeez and Shafi (1966). All the pooled data were analysed statistically (Gomez and Gomez, 1984).

Results and Discussion

Based Mahalanobis D^2 value, 100 genotypes are grouped in to 12 clusters (Fig-1)

maximum 55 genotypes are in cluster 1 followed by 19 genotypes (cluster-4), 12genotypes (cluster-8), 4 genotypes (cluster-5), 3genotypes (cluster-11). But the cluster viz., 2,3,6,7,9,10,and 12 are represented by single genotype. The single genotype viz., WITA-8, WGL32183, Konark, Purnendu, VLD-61, Pusasugandh-3 and Improved Lalat are more diverse and can be used in hybridisation for effective result.

The inter cluster distance is higher than intra cluster distance indicating wide genetic diversity among the genotypes. The highest intra cluster distance is observed in cluster 8 (100.04) followed by 11(86.66), cluster IV(69.94), cluster-1(57.2). The intra cluster distance is zero in cluster -7, 9,10 and 12 as these clusters are represented by single genotype.

The inter cluster distance is lowest between cluster-2 and 3(10.68) followed by cluster 3 and 7(49.75), cluster2 and 7 (59.73).Highest inter cluster distance was observed in cluster-3 and 11(667.36) followed by cluster 8 and 11(615.50), cluster 7 and 11(604.87), cluster 2 and 11(598.87), cluster 7 and 10(584). Hybridisation between the genotypes having low inter cluster distance are not effective whereas hybridisation between highest cluster mean can provide very good result (Fig-2).

Cluster mean

Cluster mean for hulling (%) is highest in cluster 12(81.0) and lowest incluster 5(76.6). For Milling (%), cluster 6 is having maximum value (72.0) and cluster 3 is having minimum value (65.5). For HRR (%), highest mean value is in cluster 8 (61.5) and lowest in cluster 6(42.5). Highest mean value for kernel length is observed in cluster 11(6.67) and lowest value in cluster 9(5.46). Cluster 2 (1.93) and cluster 4 (2.32) are having lowest and highest cluster mean for kernel breadth. For L/B ratio, cluster 1 (2.49) and cluster 3 (3.17) are having lowest and highest value respectively. Cluster mean for water uptake is highest in cluster 11 (317) and lowest in cluster 7 (95).

Table.1 Eigen value, contribution of variability, factor for principal component axis

Characters	Vector-1	Vector-2	Vector-3
Eigen value	3.47	2.69	1.41
Variability%	28.91	22.45	11.79
Cumulative %	28.91	51.37	63.16
Hull(%)	0.009	0.070	0.003
Mill(%)	-0.014	0.188	-0.066
HRR(%)	0.044	0.234	-0.021
KL(mm)	-0.067	-0.239	0.380
KB(mm)	-0.010	0.473	-0.414
L/B	-0.017	-0.220	0.211
ASV	-0.398	0.592	0.615
WU	-0.858	-0.297	-0.240
VER	-0.191	-0.069	0.073
KLAC	0.126	-0.279	0.369
ER	0.202	-0.33	0.191
AC(%)	0.056	-0.224	-0.136

Table.2 Cluster Mean value of 12 quality characters for 100 rice genotypes

Cluster mean												
Cluster no.	Hull(%)	Mill(%)	HRR(%)	KL	KB	L/B	ASV	WU	VER	KLAC	ER	AC(%)
1	78.15	70.76	58.90	5.65	2.29	2.49*	4.54	131.82	3.96	9.84	1.75	23.90
2	78.25	66.00	52.75	5.75	1.93*	2.99	3.0*	115.00	4.00	10.30	1.79	26.01
3	78.75	65.50	56.50	6.18	1.95	3.17**	3.25	95.00	4.25	10.40	1.68*	27.05
4	78.02	71.53	59.21	5.91	2.32**	2.63	6.92	251.71	3.95	10.46	1.78	23.61
5	76.63*	69.56	57.29	5.62	2.22	2.53	3.38	241.88	4.25	10.31	1.85	25.43
6	79.00	72.00**	42.50*	6.58	2.18	3.02	5.00	122.50	3.88	11.55	1.76	23.20
7	77.00	64.50*	55.00	5.60	2.09	2.65	5.25	95.00*	3.88	11.10	1.99	27.90**
8	78.67	70.02	61.50**	5.84	2.27	2.61	3.46	122.96	3.95	10.99	1.89	23.87
9	78.00	69.00	53.00	5.46*	2.15	2.52	6.75	172.50	3.88	9.30*	1.70	25.95
10	79.00	67.00	54.00	6.24	2.10	2.98	5.25	310.00	4.00	10.90	1.75	21.00*
11	78.42	67.17	54.75	6.67**	2.15	3.16	7.08**	317.00**	4.33**	13.13**	2.01**	25.73
12	81.25**	70.50	54.00	6.58	2.14	3.08	5.00	135.00	3.88*	9.60	1.80	24.85

*,** stands for minimum and maximum value

Table.3 Intra and inter Cluster distances of D^2 value in 100 genotypes for 12 quality characters

	cl1	**cl2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**
cl1	**(57.2)**	76.67	90.89	255.04	183.21	80.17	88.87	94.47	95.10	392.22	497.03	120.81
cl2		**(0.0)**	10.68	476.65	201.39	89.09	59,73	78.22	158.45	475.42	598.87	113.54
3			**(0.00)**	429.99	265.59	105.50	49.75	86.91	186.14	583.80	667.36	111.64
4				**(69.94)**	150.15	234.43	380.83	374.79	100.61	108.06	144.25	307.39
5					**(48.77)**	210.63	294.34	247.53	126.87	136.44	244.96	262.77
6						**(0.00)**	101.85	126.85	85.16	341.17	420.96	102.17
7							**(0.00)**	95.12	144.09	584.0	604.87	128.76
8								**(100.04)**	193.71	511.39	615.50	162.14
9									**(0.00)**	216.83	266.85	138.77
10										**(0.00)**	101.03	437.72
11											**(86.66)**	520.52
12												**(0.00)**

Fig.1 Clustering of 100 genotypes in to 12 groups based on 12 quality characters

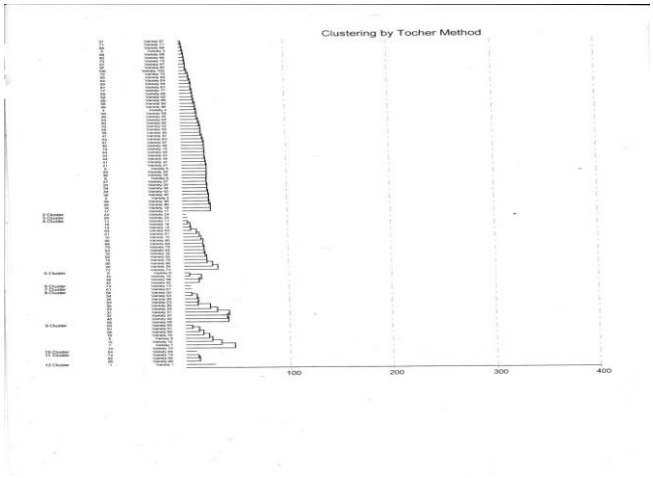
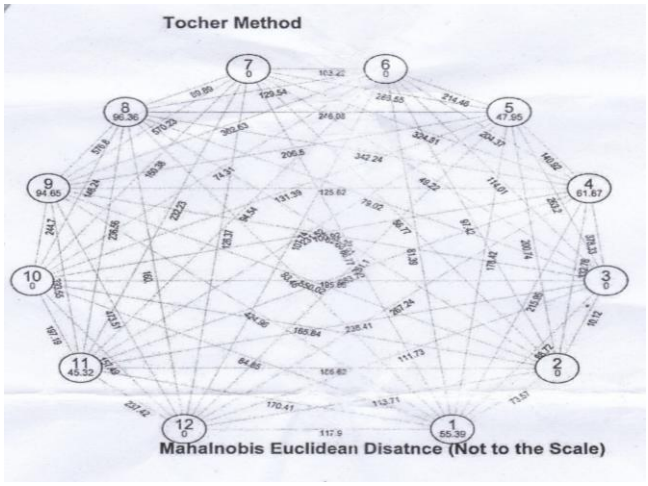


Fig.2 Euclidean distance among 12 clusters



Mean value for Volume expansion ratio is lowest in cluster 12(3.88) and highest in cluster 11(4.33). Cluster mean for KLAC is highest in cluster 11(13.13) and lowest in cluster 9(9.3).Amylose content is highest in cluster 7 (27.9) and lowest in cluster 10(21.0). PCA revealed that three most important components having Eigen value 3.47, 2.69 and 1.41 respectively which accounts for 63.16% of the total variance for all the characters. Percentage of variance for the 3 factors are 28.91, 22.45 and 11.79 which together account for 63.16% of the variability of the genotypes used for diversity analysis (table-1).

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