

Genetic divergence of rice varieties and hybrids for quality traits

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ABSTRACT

Genetic divergence of fifty one breeding lines/cultivars of rice was studied for fourteen physico-chemical quality characteristics of different duration groups viz., early, mid-early, medium, long duration.. The genotypes were grouped into thirteen clusters of which cluster III with seventeen varieties was the largest. The genetic diversity observed was not related to duration of groups and genotypes of same duration group were distributed in different clusters. Cluster VII and XII were identified as genetically most divergent which include the varieties and hybrids viz., MDU 5, TNRH 50 and PM 0200022. High inter-cluster distance was observed between cluster XII and other clusters. Since the cluster XII include a drought tolerant culture PM 0200022 and high inter cluster distance with other clusters, it could be utilized for developing drought tolerant varieties. Highest mean values for hulling, milling, kernel length, length/breadth ratio, kernel length after cooking, intermediate gelatinization temperature and intermediate amylose content with soft gel consistency were recorded in cluster IV. Considering the cluster distances and means, the present investigation revealed that due emphasis should be given on the members of cluster III comprising of medium duration cultures viz., AS 00044, AD 99218, CB 99019, CB 20090, CB 20035, AD 00194, Improved White Ponni, ADT (R) 46, ADT 38, long duration genotypes viz., TP 1038, KR 99001, CR 1009, Swarna, ADT 44, semidry group cultures viz., PM 01011, PM 01010, quality culture TP1028 for selection of parents for hybridization program which could result in varieties with good physicochemical quality traits in rice.

Key words: rice, genetic divergence, quality characteristics

Grain quality along with crop yield and resistance to pest and disease is one of the important criteria in most rice breeding programs; it has always been an important consideration in rice variety selection and development (Singh *et al.*, 2000). The physio-chemical characteristics of rice grain are important indicators of grain quality. It is mainly determined by combination of many physical as well as chemical characters. The physical quality characters include kernel size, shape, hulling, milling and head rice recovery. The chemical quality is determined by amylose content, gelatinisation temperature, gel consistency and cooking behaviour. Cooking quality is important character that determines consumer's preference. Surveys show that consumer acceptance of a variety depends primarily on its cooking and eating quality. Rice with soft to medium gel consistency, intermediate amylose content and intermediate gelatinization temperature is a preferred level for the consumers (Khush *et al.*, 1979).

Genetic diversity is an essential requirement of any crop improvement programme, because genetically diverse parent when crossed can bring together diversity of gene combination either to exploit heterosis or to obtain superior recombinants. The importance of information about the extent and magnitude of genetic divergence in rice and its utilization for the selection of desirable parents/donors either for exploitation of hybrid vigour or to get desirable recombination's, had been stressed by many workers (Anand and Murthy, 1968; Maurya and Singh, 1977).

In order to develop improved breeding lines having superior quality traits it is essential to have genetically diverse parental lines which can result into good genotype with improved quality. Hence, the present investigation was attempted to assess the physicochemical quality traits of genetically diverse breeding lines/cultivars in rice.

MATERIALS AND METHODS

The experimental materials consisted of 51 rice cultures and varieties of different groups *viz.*, 9 early duration varieties/cultures AD99110, AD00119, AD00141, AS00004, TP20001, TP1050, ADT43, ADT(R) 45, CO47, 6 mid early genotypes TP 1121, CB 98004, CB 20021, ASD 16, ADT 42, IR 64, 10 medium duration genotypes AS00044, AD99217, AD99218, CB99019, CB20090, CB20035, AD 00194, improved White Ponni, ADT(R) 46, ADT 38, 6 long duration genotypes TP 1038, KR 99001, AD99001, CR 1009, Swarna, ADT 44, 10 semidry varieties/cultures PM01011, PM01010, PM 0200022, CB(MAS1)20001, PMK 1, PMK 2, PMK(R)3, MDU5, TKM 11, TKM 12, 3 quality groups TP1021, TP1028, ACK99017, 6 hybrids TNRH31, TNRH50, TNRH 55, CORH2, ADRH15, ADTRH1 and one check variety BPT 5204 for comparing the quality traits. The grains of the above varieties were utilized for analyzing fourteen quality characters *viz.*, hulling, milling, head rice recovery, kernel length, kernel breadth, L/B ratio, kernel length after cooking, kernel breadth after cooking, linear elongation ratio, breadth wise elongation ratio, volume expansion, gelatinization temperature, gel consistency and amylose content.

The analysis was carried out in the rice quality lab Tamil Nadu Agricultural University, Coimbatore during 2004-2005. Size and shape classification was

done as per standard evaluation system. Amylose content was determined by the procedure of (Juliano, 1971). Based on amylose content milled rice was classified as waxy – 1-2% amylose, very low - amylose 2-9% amylose, low amylose– 9-20%, intermediate – 20-25% and high amylose– 25-33% (Juliano, 1972). Alkali spreading value was determined according to procedure of Little *et al.*, 1958 and classified as alkali spreading value 1-3 corresponds to high, 3-5 corresponds to intermediate and 6-7 corresponds to low gelatinization temperature. Elongation ratio was calculated by measuring the length of cooked and uncooked milled rice by scale. Volume of cooked and uncooked milled rice was measured by water displacement method. Gel consistency was analyzed based on the method described by Cagampang *et al.*, 1973. The genetic diversity between the genotypes was worked out using Mahalanobis 'D²' statistics as described (Rao, 1952). On the basis of magnitude of the D² values, grouping of genotypes into cluster distance was done using Tocher's method (Rao, 1952).

RESULTS AND DISCUSSION

The 51 rice varieties, cultures and hybrids were grouped into thirteen cluster based on relative magnitude D² estimate (Table 1). Among the different clusters, cluster III contained maximum of 17 genotypes followed by

Table 1. Distribution of 51 rice varieties, cultures and hybrids in different clusters

ClusterNo	No of genotypes	Name of the genotypes
I	16	AD99110, AD 00119, AD 00141, AS 00004, TP 20001, TP 1050, ADT 43, CO 47, TP 1121, CB 98004, CB 20021, ASD 16, ADT 42, IR 64, AD 99217, AD 99001
II	1	BPT 5204
III	17	AS 00044, AD 99218, CB 99019, CB 20090, CB 20035, AD 00194, Improved White ponni, ADT (R)46, ADT 38, TP 1038, KR 99001, CR 1009, Swarna, ADT 44, PM 01011, PM 01010, TP 1028
IV	2	TNRH 31, TNRH 55
V	2	PMK 1, TKM 11
VI	2	TP 1021, ACK 99017
VII	2	MDU 5, TNRH 50
VIII	2	PMK 2, TKM 12
IX	2	CORH 2, ADT (R) 45
X	1	ADTRH 15
XI	2	CB (MAS 1) 20001, ADTRH 1
XII	1	PM 0200022
XII	1	PMK (R) 3

cluster I contained 16 genotypes, clusters IV, V, VI, VII, VIII, IX and XI accommodated 2 genotypes each and the clusters II, X, XII and XIII contains one genotype each in a cluster (Table1).

All genotypes from early and mid early groups were grouped in cluster I indicating that based on early duration these genotypes may be clustered in the same cluster. The other genotypes from medium and long duration were grouped in cluster I may be due to high volume expansion. Cluster III included genotypes from medium, long duration, semidry and quality rice group shows that genotypes from different groups were clustered in same cluster thus the distribution of genotypes into different cluster was not associated with their duration groups. Clusters IV, IX, X contained hybrids while clusters V, VIII, XII, XIII had genotypes of semidry group. Quality genotypes were distributed in cluster VI (Roy *et al.*, 2005).

The inter-cluster distance analysis revealed the maximum divergence between cluster VII and cluster XII (Table 2). The varieties developed from the genotypes within the traits of compatibility of these cluster may produce high magnitude of heterosis for quality character with drought tolerance, since the genotypes of these cluster are belong to semidry group, it could be possible to get drought tolerant variety/hybrids. The inter cluster distance between the cluster XII and XIII, cluster IV and XII, cluster IX and XII, cluster V and XII, cluster XI and XII, cluster X and XII, cluster I and XII were also relatively higher as

compared to the other so the genotypes of these clusters merit due consideration for selection of parents for hybridization. Minimum inter-cluster distance D^2 (120.75) was observed between cluster IX and VII suggesting relatively close relationship between these two clusters. The results revealed that cluster XII had high intercluster distance with most of the cluster. Hence the semidry culture *viz.*, PM0200022 in cluster XII could be effectively utilized for hybridization programme.

Maximum intra-cluster distance (175.61) was observed in cluster III comprising of genotypes AS 00044, AD 99218, CB 99019, CB 20090, CB 20035, AD 00194, improved white ponni, ADT (R) 46, ADT (38) TP 1038, KR 99001, CR 1009, Swarna, ADT 44, PM 01011, PM 01010, TP1028 which is indicative of wide genetic divergence among the constituent genotypes. Genotypes within a cluster with high degree of divergence would produce more desirable breeding materials for achieving maximum genetic advance with regard to yield *per se* provided there is adequate complementation.

Therefore, due emphasis should be given on the members of the cluster III for selection of parents for hybridization programme. Since the cluster III includes medium, long duration, semidry and quality group genotypes, the high diversity between the genotypes would be useful for better parents of hybridization programme. The intra-cluster distance was also high.

Table 2. Estimate of average intra (diagonal and bold) and inter cluster D^2 for 13 cluster constructed from 51 rice genotypes

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII
I	158.37	203.91	174.48	197.93	154.67	136.93	195.21	204.90	155.25	178.39	200.88	420.56	212.49
II		0.000	190.14	217.33	161.30	172.90	223.64	165.17	147.01	142.56	209.59	371.18	324.57
III			175.61	189.94	168.31	143.33	190.19	209.37	175.82	180.30	193.12	387.06	221.88
IV				78.39	176.65	189.24	120.75	255.05	182.69	222.87	127.04	440.74	198.20
V					86.39	151.73	157.12	134.60	134.21	145.30	198.47	434.38	226.04
VI						92.20	192.35	182.85	151.02	159.49	188.78	360.72	197.74
VII							101.35	244.97	181.21	191.58	160.83	461.70	197.90
VIII								108.96	181.02	178.09	262.67	396.92	290.79
IX									109.15	150.43	185.97	438.52	265.87
X										144.30	216.29	421.09	274.64
XI											168.92	422.64	229.04
XII												0.00	448.77
XIII													0.00

Highest mean value for hulling (82.00), kernel length (6.25), L/B ratio (3.34), Kernel length after cooking (10.15) with intermediate gelatinization temperature (5.20), soft gel consistency (61.00) and intermediate amylose content (24.20) was recorded in cluster IV while cluster II included only one genotype BPT 5204 that had high head rice recovery (53.90), milling (86.20), low kernel breadth (1.9), kernel breadth after cooking (2.00) (Table 3). The result is in agreement with the previous findings (Chauhan and Singh, 2003). High volume expansion (5.6) was in cluster IX, good gel consistency (131.00) in cluster XIII. Average cluster mean of more than 70% hulling was observed in clusters III, IV, V, VIII, IX while the clusters II, IV, IX, X has recorded >50% of milling. Head rice recovery an important quality parameter which was >45% of average cluster mean was found in cluster II, X and XI.

As low values for kernel breadth, kernel breadth after cooking, high value for hulling (> 70%), milling (> 50%), head rice recovery (>45%), volume

expansion (> 4 times), intermediate gelatinization temperature and amylose content with soft to medium gel consistency, medium to long slender are the mandatory varietal requirements for quality breeding programme, such genotypes of any cluster can be utilized for quality improvement programme. The results revealed that the average cluster mean values for most of the quality parameters was found promising in clusters II, VI, IX, XI (Table 4). Among the above clusters, high cluster distance was observed between cluster VI and XI indicating that it could be possible to develop drought tolerant hybrids with desirable quality traits, since the cluster VI possessed genotypes of quality group viz., TP1021, ACK99017 and cluster XI has a drought tolerant culture CB(MAS1)20001.

Considering the cluster distances and means, the present investigation indicated that due emphasis should be given on the members of cluster III comprising of medium duration cultures viz., AS 00044, AD 99218, CB 99019, CB 20090, CB 20035, AD 00194, Improved White Ponni, ADT (R) 46, ADT 38,

Table 3. Mean values of physicochemical character in various clusters in rice

Character	Clusters												
	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII
Hulling (%)	66.52	59.10	102.12	82.00	79.85	67.66	72.95	75.95	70.60	61.97	73.65	52.50	54.70
Milling (%)	57.90	86.20	63.22	77.30	62.25	61.42	68.25	60.40	76.15	76.25	67.55	48.10	37.30
Head rice recovery	40.16	53.90	42.63	48.30	46.70	34.52	49.95	48.90	49.00	54.95	51.30	37.80	30.30
Kernel length (mm)	5.33	4.90	5.50	6.85	5.40	5.43	6.25	5.85	5.80	5.35	6.45	6.50	6.20
Kernel Breadth (mm)	2.14	1.90	2.15	2.05	2.05	2.06	1.90	2.35	2.20	1.95	2.00	2.00	2.30
L/B ratio	2.48	2.57	2.62	3.34	2.63	2.69	3.32	2.50	2.64	2.74	3.22	3.25	2.61
Kernel length after cooking	7.93	7.90	8.37	10.15	7.35	7.83	8.75	6.75	7.60	8.10	9.80	8.60	9.50
Kernel Breadth after cooking	2.69	2.00	2.44	2.80	2.85	2.18	2.80	2.65	2.85	2.65	2.50	2.40	3.00
Linear elongation ratio	1.49	1.61	1.54	1.48	1.53	1.50	1.33	1.71	1.31	1.83	1.43	1.63	1.59
Breadth wise elongation ratio	1.26	1.05	1.16	1.36	1.39	1.09	1.49	1.13	1.30	1.33	1.25	0.37	1.30
Volume expansion	5.06	4.10	4.07	4.55	3.20	5.20	3.45	3.50	5.60	5.05	4.10	2.5	4.20
Gelatinization temperature	1.78	1.00	1.95	5.20	5.25	1.41	5.70	5.45	1.60	1.45	1.30	1.60	6.00
Gel consistency	96.72	57.00	66.95	61.00	85.50	101.84	54.50	96.00	66.50	63.00	85.00	35.00	131.00
Amylose content	23.37	19.40	24.78	24.20	19.40	24.91	28.20	19.00	23.60	28.40	25.90	28.40	27.60

Table 4. Relative contributions of different quality characters to D² values in rice

Characters	Contribution (%)
Amylose content (%)	27.87
Breadth wise elongation ratio	11.64
Linear elongation ratio	11.24
Kernel Breadth (mm)	10.70
Kernel length after cooking (mm)	10.63
Gel consistency (mm)	7.20
Gelatinization temperature	5.72
Volume expansion	4.64
Kernel length (mm)	3.29
Kernel breadth after cooking (mm)	2.62
Hulling (Per cent)	2.35
L/B ratio	1.14
Head rice recovery	0.87
Milling (Per cent)	0.00

long duration genotypes *viz.*, TP 1038, KR 99001, CR 1009, Swarna, ADT 44, semidry group cultures *viz.*, PM 01011, PM 01010, quality culture TP1028 for selection of parents for hybridization program which could yields varieties with good physicochemical quality traits in rice.

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