

Original Research Article

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Genetic Diversity for Yield Components, Physical and Biochemical Quality Parameters in Colored Rice (*Oryza sativa* L.)

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ABSTRACT

An investigation was carried out with twenty six colored rice (*Oryza sativa* L.) genotypes to study the genetic divergence using D² statistics. Based on 26 yield and quality traits, these genotypes were grouped into six clusters. Among these six clusters, cluster I possessed more number of genotypes (11) followed by cluster II with 8 genotypes and cluster III with 3 genotypes. Cluster II recorded maximum intra cluster distance, while highest inter cluster distance was observed between cluster V and cluster VI. Cluster II had highest mean value for grain yield/plant whereas the genotypes grouped in cluster III exhibited highest mean value for panicle length, number of filled grains/panicle and total number of grains/panicle. Cluster V was characterized by highest mean value for ear bearing tillers/plant and test weight among yield components and total starch content, Zn content & slowly digestible starch among quality parameters. Cluster VI manifested highest mean value for most of physic-chemical and biochemical quality traits studied viz., water uptake, volume expansion ratio, length/breadth ratio, total phenol content, total antioxidant activity, flavonoid content and Fe content. Hybridization among genotypes from cluster V and VI, cluster I and VI followed by cluster II and VI which had maximum inter cluster distances may result in maximum genetic improvement of yield and desirable quality traits of colored rice.

Keywords

Colored rice,
Quality parameters,
Clusters, D2
analysis

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Introduction

As the consumers become more health conscious and aware of the benefits of functional foods, diets containing bio-active compounds (secondary metabolites) such as antioxidants have received greater attention. Pigmented rice has been categorized as one of

the potent functional foods since it contains high amounts of phenolic compounds (Yawadio *et al.*, 2007). Owing to several health promoting impacts associated with anthocyanins, such as anti-oxidative, anti-inflammatory and anti-carcinogenic effects, coloured rice is considered as a functional food and food ingredient in many Asian

countries. The success of any plant breeding programme largely depends on the existence of diversity among the genotypes (Allard, 1960). This helps in the choice of parents for hybridization in yield improvement programmes. Hence, estimation of genetic diversity for yield components and quality parameters among genotypes is important for planning the future hybridization programme. Mahalanobis' D^2 statistic has proved to be powerful technique for estimating genetic divergence among the genotypes. Hence, the present investigation was carried out to ascertain the value and magnitude of genetic diversity between 26 colored rice genotypes.

Materials and Methods

Twenty six rice genotypes comprising of varieties developed at Agricultural Research Station, Bapatla and varieties received from ARS Pattambi, Kerala (Table 1) were used in the present study. Among the 26 genotypes seven had light brown pericarp color and nine genotypes possess red pericarp color. The remaining ten genotypes had black pericarp color. BPT 5204, a popular high yielding genotype with excellent cooking quality traits is used as check variety in the present study. The present investigation was carried out during *khari*, 2017 at Agricultural College Farm, Bapatla. These genotypes were evaluated in randomized block design with three replications under direct sowing by following manual dibbling method. Each genotype was sown in 10 rows of 3m length. Observations were recorded on ten plants selected at random per genotype per replication for 9 yield components and 6 physico-chemical quality traits *viz.*, days to 50% flowering, panicle length (cm), plant height (cm), ear bearing tillers per plant, grain yield per plant (g), test weight (g), number of filled grains per panicle, total number of grains per panicle, fertility (%), solid loss, water uptake, volume expansion ratio, alkali

spreading value, length/breadth ratio and amylose content (%). However, days to 50% flowering and test weight (g) were recorded on plot basis along with quality parameters. The polished rice was used for estimation of solid loss, water uptake, volume expansion ratio, length/breadth ratio, alkali spreading value and amylose content by following standard procedures delineated by Sidhu *et al.*, (1975), Directorate of Rice Research (2006), Little *et al.*, (1958) and Juliano (1971). Each sample per genotype per replication was dehusked and utilized for estimation of 11 nutritional and bio-chemical quality parameters *viz.*, total starch content (%), protein Content (%), Zn content (ppm), iron content (ppm), total phenol content (mg/100 g), total antioxidant activity (mg AAE/100 g), total flavonoid content (mg/100 g), glycemic index (%), slowly digestible starch (%), rapidly digestible starch (%) and resistant starch (%) by following standard procedures delineated by Hodge, J.E and Hofrieter (1962), Lowry *et al.*, 1951, DRR (2006), Malik C.P and Singh M.B.(1980), Pathirana *et al.*, (2005), Swain *et al.*, (1959), Goni *et al.*, (1997) Englyst *et al.*, (1999), Goni *et al.*, (1996) respectively. Genetic divergence analysis was done following the D^2 statistics proposed by Mahalanobis (1936).

Results and Discussion

The analysis of variance showed significant differences for all characters studied except for solid loss, volume expansion ratio and length/breadth ratio indicating wide variability among the genotypes under study. The twenty six genotypes were grouped in to six different clusters based on the relative magnitude of D^2 values. Among six clusters, cluster I had maximum number of genotypes (11) followed by cluster II with 8 genotypes and cluster III with 3 genotypes (Table 2). The clusters V and VI are solitary clusters with nil intra-cluster D^2 values. The distribution of

genotypes in cluster I indicated that different colored genotypes from different geographical regions grouped in single cluster. Ramesh *et al.*, (2007) Dushyantha (2008) and Eswar *et al.*, (2017) also reported similar findings. Character wise percent contribution towards genetic divergence by all the 26 characters is presented in Table 3. In D² analysis, resistant starch (71.38%) contributed maximum genetic divergence followed by slowly digestible starch (18.15%) and flavonoid content (4.0%).

These results of the present study indicate that the variation observed between different colored genotypes is mainly due to biochemical quality parameters

The magnitude of intra cluster distance measures the extent of genetic diversity between the genotypes of same cluster while the inter cluster distance measures the extent of genetic diversity between two clusters. The maximum inter cluster distance was observed between cluster V and cluster VI (826253.6) followed by cluster I and cluster VI (654680.6) (Table 4). Highest intra cluster distance was observed in cluster II followed by cluster III and cluster I. The maximum intra cluster distance observed in cluster II (14919.71) suggest the presence of wide genetic diversity among the genotypes *viz.*, BPT 3111, BPT 3138, BPT 3143, BPT 3143, BPT 3137, BPT 3136, BPT 3142, BPT 3145 grouped in this cluster. The genotypes of this cluster include both black and red pericarp colored genotypes. Cluster distances showed wide range among the genotypes studied indicating that the variation may be due to the diverse material included in the present study. For a successful breeding programme, selection of genetically diverse parents is an important pre-requisite to get the desirable recombinants. Similar findings were previously reported by Sandhya *et al.*, (2007), Parimalan *et al.*, (2008) and Eswar *et al.*, (2017).

The genotypes grouped in cluster I manifested highest mean value for days to 50 % flowering while the genotypes of cluster II had highest mean value for grain yield/plant (Table 5). Cluster III was characterized by highest mean value for panicle length, number of filled grains/panicle, total number of grains/panicle and fertility (%) among yield components.

Among quality parameters, the genotypes of cluster III recorded high protein content and resistant starch suggesting that the genotypes grouped in this cluster are nutritionally superior with high protein content and resistant starch. Patindol *et al.*, (2010) and Odenigbo *et al.*, (2013) reported that high RS content will manifest lower GI and hence, the genotypes grouped in this cluster may be suitable for diabetic diet as they possess more resistant starch. Cluster IV had highest mean value for plant height while cluster V was characterized by highest mean value for ear bearing tillers/plant and test weight among yield components and total starch content, Zn content & slowly digestible starch among quality parameters. Cluster VI manifested highest mean value for most of physico-chemical and biochemical quality traits studied *viz.*, water uptake, volume expansion ratio, length/breadth ratio, total phenol content, total antioxidant activity, flavonoid content and Fe content suggesting that this genotype had good cooking quality with more cooked rice volume. The genotype BPT 3140 also recorded high Fe content and anti-oxidant activity also hence, may be used in hybridization programme to get segregants possessing desirable nutritional traits.

Choice of particular cluster and selection of particular genotype from selected cluster are the two important points to be considered before initiating the crossing programme. The hybrids between varieties of diverse clusters will express high heterosis and give more useful segregants (Table 6).

Table.1 Details of the pedigree and pericarp colour of the genotypes used in the present study

S. No.	Designation	Cross combination	Pericarp colour
1.	BPT 5204	GEB 24/TN1/ Mahsuri	Light brown pericarp
2.	BPT 2270	BPT 5204/CRM 1523	
3.	BPT 2295	BPT 1768/ NLR 33641	
4.	BPT 2595	Mutant of BPT 2270	
5.	BPT 2782	NLR 145/ MTU 2077	
6.	BPT 2660	BPT 1768/ NLR 145	
7.	BPT 2776	BPT 2231/ NLR 145	
8.	Matta Triveni	Re-selection from Triveni	Red pericarp
9.	Annapurna	PTB 10/TN 1	
10.	Aathira	BR 51-46-1/C.2332-2-2	
11.	Harsha	M 210/ PTB 28	
12.	Jyothi	PTB 10/ IR 8	
13.	Samyuktha	Pureline selection from culture C3-2	
14.	BPT 3111	Swarna/ IRGC 18195// MTU 1081	
15.	BPT 2858	RP Bio 226 [*] 1/IRGC 48493	Black pericarp
16.	BPT 3139	Cult. 01120305/ cult. 0910025-7	
17.	BPT 3137	RP Bio 226 [*] 1/ IRGC 48493	
18.	BPT 3145	RP Bio 226/ IRGC26940// MTU 1081	
19.	BPT 3138	RP Bio 226 [*] 1/IRGC 18195	
20.	BPT 3136	RP Bio 226 [*] 1/IRGC 18195	
21.	BPT 3140	Swarna/IRGC 18195 /MTU 1081	
22.	BPT 3141	RP Bio 226 [*] 1/ IRGC 30938	
23.	BPT 3142	RP Bio 226/ IRGC 26940// MTU 1081	
24.	BPT 3143	RP Bio 226 [*] 1/ RGC 48493	
25.	BPT 2848	RP Bio 226 [*] 1/IRGC 48493	
26.	BPT 3144	RP Bio 226 [*] 1/IRGC 48493	

Table.2 Clustering pattern of colored rice (*Oryza sativa* L.) genotypes by Tocher's method

Cluster No.	No. of Genotypes	Designation of the Genotypes
I	11	BPT 2295, BPT 2782, BPT 2270, BPT 5204, BPT 2595, Samyuktha, Annapurna, Harsha, BPT 2660, BPT 2776, BPT 3139
II	8	BPT 3111, BPT 3138, BPT 3143, BPT 3143, BPT 3137, BPT 3136, BPT 3142, BPT 3145
III	3	BPT 3141, BPT 2848, BPT 2858
IV	2	Jyothi, BPT 3144,
V	1	Aathira
VI	1	BPT 3140

Table.3 Contribution of different characters towards genetic divergence among colored rice (*Oryza sativa* L.) genotypes

Character	Percent contribution towards divergence
Days to 50% flowering	0.01
Panicle length (cm)	0.01
Plant height (cm)	0.01
Ear bearing tillers per plant	0.01
Grain Yield per plant (g)	0.01
Test Weight (g)	0.01
Number of filled grains per panicle	0.01
Total number of grains per panicle	0.01
Fertility %	0.01
Solid Loss	0.01
Water Uptake	1.85
Volume Expansion Ratio	0.01
Alkali Spreading Value	0.01
Length/Breadth ratio	0.01
Amylose Content (%)	0.01
Protein Content (%)	0.01
Total Starch Content (%)	0.31
Total Phenol Content (mg/100g)	0.62
Total antioxidant Activity (mg AAE/100g)	0.31
Flavonoid content (mg/100g)	4.00
Zn content (ppm)	1.54
Iron content (ppm)	0.01
Glycemic Index	0.31
Slowly Digestible Starch (%)	18.15
Rapidly Digestible Starch (%)	1.54
Resistant Starch (%)	71.38

Table.4 Average intra and inter cluster D^2 values among six clusters in 26 colored rice (*Oryza sativa* L.) genotypes

Cluster No.	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	9457.74	44831.25	332166.00	151487.60	26774.73	654680.60
Cluster II		14919.71	174391.30	51429.46	81783.85	412625.40
Cluster III			12937.84	45563.13	46392.50	64390.78
Cluster IV				6151.04	233436.80	186465.70
Cluster V					0.00	826253.60
Cluster VI						0.00

Diagonal bold values indicate intra cluster distances

Table.5 Mean values of six clusters for yield components and quality parameters in colored rice (*Oryza sativa* L.) genotypes

Character/ cluster No.	Days to 50% Floweri ng	Panicle Length (cm)	Plant Height (cm)	Ear Bearing Tillers/ Plant	Grain Yield/ Plant (g)	Test Weight (g)	No.of Filled Grains/ Panicle	Total No. of Grains/ Panicle	Fertility %	Solid Loss	Water Uptake	Volume Expansi on Ratio	Alkali Spreading Value	Leng th/Br eadth Ratio	Amylose Content (%)
Cluster I	112.67	25.84	109.19	15.27	37.90	18.06	244.33	268.09	91.09	1.48	73.27	2.28	3.61	2.84	22.73
Cluster II	101.38	28.51	112.85	13.92	45.68	19.60	292.50	315.58	92.19	1.54	53.50	2.17	3.35	2.78	21.87
Cluster III	104.22	29.38	112.29	14.44	41.10	16.16	333.89	356.67	93.39	2.25	65.00	2.12	3.44	3.10	22.27
Cluster IV	102.50	27.61	118.47	14.33	43.75	17.90	247.83	277.67	89.88	1.35	56.50	1.82	3.08	2.78	21.44
Cluster V	98.33	25.19	101.93	15.67	36.13	22.79	312.33	362.67	86.41	0.80	52.00	2.00	2.00	2.26	24.24
Cluster VI	103.33	24.92	116.07	14.67	39.10	18.83	279.33	306.67	90.99	0.60	111.67	3.00	4.00	3.51	22.17

Bold figures are indicated maximum and minimum mean values for each character

Character/ cluster No.	Protein Content (%)	Total Starch Content(%)	Total Phenol Content(mg/100g)	Total Antioxidant Activity(mg AAE/100g)	Flavanoid Content (mg/100g)	Zn Content	Fe Content	Glycemic Index	Slowly Digestible Starch	Rapidly Digestible Starch	Resistant Starch
Cluster I	8.89	68.90	65.29	59.72	172.74	18.13	9.69	57.55	37.73	59.83	2.44
Cluster II	11.66	76.65	96.49	88.43	430.73	25.27	10.69	61.01	35.04	62.88	2.30
Cluster III	13.24	59.19	160.54	89.22	580.13	24.83	12.80	60.39	36.12	59.03	2.67
Cluster IV	12.80	69.96	128.07	99.05	554.09	19.40	10.95	62.49	32.88	62.79	1.83
Cluster V	8.21	87.57	56.36	105.13	303.80	25.90	10.70	57.12	39.40	58.48	2.12
Cluster VI	10.95	66.13	214.34	108.83	590.12	24.30	13.40	69.25	30.89	67.55	1.56

Bold figures are indicated maximum and minimum mean values for each character

Table.6 Contribution of different characters towards genetic divergence among 26 genotypes of colored rice (*Oryza sativa* L.)

Character	Percent contribution towards divergence
Days to 50% flowering	0.01
Panicle length (cm)	0.01
Plant height (cm)	0.01
Ear bearing tillers per plant	0.01
Grain Yield per plant (g)	0.01
Test Weight (g)	0.01
Number of filled grains per panicle	0.01
Total number of grains per panicle	0.01
Fertility %	0.01
Solid Loss	0.01
Water Uptake	1.85
Volume Expansion Ratio	0.01
Alkali Spreading Value	0.01
Length/Breadth ratio	0.01
Amylose Content (%)	0.01
Protein Content (%)	0.01
Total Starch Content (%)	0.31
Total Phenol Content (mg/100g)	0.62
Total antioxidant Activity (mg AAE/100g)	0.31
Flavonoid content (mg/100g)	4.00
Zn content (ppm)	1.54
Iron content (ppm)	0.01
Glycemic Index	0.31
Slowly Digestible Starch (%)	18.15
Rapidly Digestible Starch (%)	1.54
Resistant Starch (%)	71.38

Maximum grain yield was recorded in cluster II and the genotypes in cluster VI had high mean values for most of the bio-chemical quality parameters. Cluster II recorded maximum intra cluster distance while highest inter cluster distance was observed between cluster V and cluster VI.

Hence, it may be concluded that hybridization among genotypes from cluster V and VI, cluster I and VI followed by cluster II and VI with high inter cluster distances may result in maximum genetic improvement and the

segregants possessing high grain yield coupled with desirable physico-chemical and biochemical quality parameters may be isolated in future segregating generations.

Results of the present study indicated maximum inter cluster distance between cluster V & VI and high intra cluster distance in cluster II & III hence, the genotypes from these clusters may be identified for hybridization programme to incorporate high grain yield and superior quality characters in the segregating generations.

Conflicts of Interest

The authors Sri Devi, P., Krishna Veni, B and Sandeep Raja, D declare that they have no conflicts of interest.

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