



Evaluation of Grain Yield, Quality and Nutrients Content in Four Rice (*Oryza sativa* L.) Genotypes

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Authors' contributions

This work was carried out in collaboration between all authors. All authors read and approved the final manuscript.

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ABSTRACT

Aims: The main objective of the study is to combining the higher yield and micronutrient content along with good grain cooking quality in polished rice.

Study Place and Duration of Study: The experiment was conducted in the farm of Indian Institute of Rice Research, Hyderabad, India. The duration of the study was two successive wet seasons 2013 and 2014.

Methodology: The experiment was conducted in a randomized complete block design (RCBD). Four rice accessions consist of two parent lines (Samba Mahsuri and Chittimutyalu) and two derivatives (BPCM1 and BPCM2) were grown under normal agronomical conditions, evaluated for their yield, grain quality and nutritional properties. The four genotypes were profiled with RM markers.

Results: Both the derivative lines BPCM1 and BPCM2 have shown higher yield advantage (4.5% and 8.8%) than the parent Samba Mahsuri along with quality parameters like amylose content

(23.3%, 25%) and gel consistency (21.5, 23.7) as well as high zinc content (20.6 ppm, 24 ppm) moderate iron content (3.6 ppm, 4.3 ppm) in polished rice. High heritability (0.91%) was found for the all traits studied. The association of grain yield is significant with harvest index, test weight and straw yield. Grain zinc content was significantly and positively associated with iron content and negatively associated with total protein. The experiment result indicates that, the micronutrient enhancement could be possible along with grain yield and cooking quality.

Keywords: Biofortification; iron; quality; rice; zinc.

1. INTRODUCTION

Rice (*Oryza sativa* L.) is the most important cereal crop and primary energy source for two thirds of the world's population [1]. Rice occupies a unique position in many nations because for its importance in traditional diets and the main source of income of many peoples in the world. Moreover, India ranks first in the world in area of rice cultivation with 43.49 million hectares and second in production with 104.41 million tons [2]. Majority of rice consumers preferred polished rice for consumption and it is a poor source of micronutrients especially iron and zinc [3]. Plant based foods are significant sources of zinc for humans and mal-nutrition is a severe health problem affecting nearly three billion people across the world [4]. Rice biofortification is one of the enormous strategies to overcome malnutrition deficiency in rice consuming populations especially zinc and iron [5].

The genetic biofortification strategy uses plant breeding approaches to produce staple food crops with higher micronutrient content in edible parts [6]. It offers a sustainable solution to malnutrition problems by exploring natural genetic variation to develop micronutrient-dense crop varieties [7,8]. Breeding and adoption of rice cultivars with enhanced grain zinc content along with high yield potential has become a priority for breeders. Variability is the difference in individual genotypes (and thus traits) within a population and the rate at which a certain genotype can change in response to environmental or genetic factors [9]. The need for expansion of rice grain micronutrients depends not only on cultural practices and also on their inbuilt genetic variability. Hence, a successful breeding programme will depend on the genetic diversity of a crop for achieving the goals of improving the high yielding rice varieties along with improved grain micronutrients [10]. Development and evaluation of potential rice genotypes with good cooking quality and desirable grain nutritional properties could be a great advantage in solving malnutrition disabilities in humans [11]. There are

several studies on grain yield and nutritional content using brown rice and in this study we used polished rice for the evaluation of grain yield, quality and nutrients content in four rice (*Oryza sativa* L.) genotypes.

2. MATERIALS AND METHODS

2.1 Location of the Study

The experimental area was located at 17.53°N latitude and 78.27°E longitude, 545 m altitude, with mean temperature of 31.2°C and mean annual precipitation of 988.3 mm. In the wet seasons of 2013 and 2014 the soil pH before planting was 8.53 and 8.58 and during the crop period iron and zinc content in soil ranged from 2.75 to 3.48 and 3.56 to 3.67 ppm, respectively. The experiment was laid out in a randomized complete block design (RCBD) in the field. Twenty six day seedlings were transplanted in the experimental field. Twenty two meters square area was used for growing sixty plants (four rows consisting fifteen plants per row) from each genotype by maintaining 20x15 cm spacing. Two lines gap was maintained between the genotypes and replications for varietal purity. The recommended cultural methods were used in the study of rice cultivation [12]. The fertilizers, nitrogen (N), phosphorus (P) and potassium (K) were applied to the experimental plot as per the recommended doses per hectare (NPK ratio is 5:3:2) [13].

2.2 Plant Material

“Samba Mahsuri” (BPT 5204) was released in 1986 from the cross combination of GEB 24 / TN1 / Mahsuri. It is a medium slender grain *indica* rice variety, very popular with farmers and consumers across India because of its high yield and excellent cooking quality [14]. However, this variety contains low level of micronutrients especially iron and zinc in the polished grain. “Chittimutyalu” is a land race that is being cultivated in some regions of southern India. Its grain is short bold, poses aroma and contains

higher zinc and iron content. Hence, a cross was made between “Samba Mahsuri” and “Chittimutyalu” as per Mc Couch emasculation and pollination method and two promising lines were identified named as “BPCM1” and “BPCM2”. These two derivatives (BPCM1 & BPCM2) along with two parents (Samba Mahsuri and Chittimutyalu) were evaluated in the farm of (Indian Council for Agricultural Research) ICAR-Indian Institute of Rice Research, Hyderabad.

2.3 Vegetative, Yield and Grain Quality Parameters

Individual genotypes were analyzed separately for different agronomic and grain quality characteristics like; crop duration (days), plant height (cm), number of panicles per plant, panicle length (cm), number of filled grains per panicle, grain yield (kg/ha) [15]. After harvesting approximately 250 grams of fresh paddy seeds were collected from four genotypes for analysis. For maintaining varietal purity, discolored, damaged, unfilled, different sized and shaped grains were removed. To define the grain quality, nearly 16 characters like hulling percent, milling percent, grain dimensions, linear elongation on cooking, and biochemical characters were studied [16].

2.4 Grain Nutritional Content Analysis

For the nutritional content estimation, dried seeds from each genotype were dehusked and polished separately using non-ferrous and non-zinc dehusker and polisher (*Krishi International*) to avoid metal contamination [17]. Total crude protein content was determined by micro kjeldahl method using Elite EX, Kelplus automatic nitrogen (N₂) analyzer of Pelican Equipments. One hundred milligram sample was mixed with catalyst mixture (copper sulphate: potassium sulphate: selenium: 10:50:1) and digested with 10 ml concentrated sulphuric acid. The digest was distilled and ammonia released was captured in 4% boric acid solution. Then it was titrated with 0.1 N HCl. The resulting N₂ content was multiplied by a factor 5.95 to convert into crude protein content [18]. Five grams of brown and polished rice samples from each line were separated and subjected to energy dispersive X-ray fluorescent spectrophotometer (ED-XRF) for iron and zinc estimation [19].

2.5 Genotyping with SSR Markers

Tissue samples of 15 days old seedlings were used for DNA isolation using CTAB method [20].

Randomly selected 24 microsatellite markers were used to identify polymorphism between “Samba Mahsuri” and “Chittimutyalu” and two selected derivatives (BPCM1 and BPCM2). PCR amplification of the rice microsatellite (RM) markers, gel electrophoresis and documentation were carried out as per following protocols. The veriti PCR system (M/s Applied Bio systems, USA) was used for PCR amplification with following buffer composition; about 3 µl of template DNA (30 ng/µl), 1.5 µl of 10 X PCR buffer (GeNei), 1 µl of forward and reverse primer each (5 pM/µl), 1 µl of dNTPs (2.5 mM Conc) and 0.5 µl of Taq polymerase (GeNei,1U) and the final reaction volume was made up to 12 µl with nuclease free water. Template DNA was initially denatured at 95°C for five minutes. Followed by 30 seconds of denaturation at 95°C, 30 seconds of annealing at 58°C and 1 min of elongation at 72°C for 35 cycles was done and final elongation at 72°C for 7 min. The Amplified products were separated in 3% Agarose gel electrophoresis (at 120 V for 2 hour) contain ethidium bromide and documented (UV transilluminator) [21].

2.6 Statistical Analysis

The four genotypes of two years RCBD mean data were subjected to analysis of variance (ANOVA), heritability, PCV and GCV were analyzed using SPAR 2.0 software [22].

3. RESULTS AND DISCUSSION

3.1 Grain Yield

Increase in grain yield potential is the major goal of the rice breeders' research programs. A considerable variation was observed among the four rice genotypes for yield and yield contributing traits and results were presented in Table 1. The variation in grain yield of two selected derivatives was found highly significant. BPCM1 is a semi-dwarf stature genotype with short bold grains (Fig. 1) and 97 days to 50% flowering duration, whereas BPCM2 is a semi-dwarf stature genotype with, medium slender grains and had 97 days 50% flowering duration. “Samba Mahsuri” is a semi-dwarf, medium slender grains and 116 days 50% flowering duration, whereas “Chittimutyalu” is a medium tall stature genotype with short bold grains and had 103 days 50% flowering duration with. Based on overall mean yield BPCM2 ranked first with 5165.7 kg/ha, BPCM1 ranked second with 4959.8 kg/ha and has similar yield as that of



Fig. 1 Panicle and paddy images

A=Samba Mahsuri, B= BPCM1, C=BPCM2 and D= Chittimutyalu

“Samba Mahsuri” whereas “Chittimutyalu” showed lower yield 3891.7 kg/ha than “Samba Mahsuri” 4746.1 kg/ha. BPCM1 and BPCM2 recorded significant yield advantage 4.5% and 8.8% over parents during the last two years of testing respectively. The mean values of plant height varied from 89.7 cm to 131 cm among four genotypes. “Samba Mahsuri” being shorter (81.7 cm) and “Chittimutyalu” showed taller plant height (132 cm). The two promising lines BPCM1 and BPCM2 show desirable plant height with 89.7 and 98.2 cm, respectively. Semi dwarf or Medium plant height is a desirable feature for higher yield production [23].

3.2 Grain Quality

The four genotypes BPCM1, BPCM2, “Samba Mahsuri” and “Chittimutyalu” showed intermediate amylose content (AC) 23.3%, 25%, 24.7% & 25%, medium gel consistency (GC) 21.5, 23.7, 35.5 & 24 and Intermediate Gelatinization Temperature (70°C-74°C) or alkali spreading value score (ASV) 5.5, 6.1, 4.2 & 5.2 respectively. Desirable head rice recovery (53.7%) showed by BPCM1, high by “Samba Mahsuri” (65.2%), good by BPCM2 (64.7%) and “Chittimutyalu” (63.9%). The aroma content of grains was medium scented (MS) for BPCM1, strongly scented (SS) for “Chittimutyalu” and non-scented (NS) for BCPM2 and “Samba

Mahsuri”. Two main quality measurements, amylose content and gel consistency (AC and GC) used to indicate the cooking quality property of rice grain [24]. These four genotypes have shown intermediate amylose (20-25%) content and previously similar observations were noticed [25]. Amylose content determines the firmness and sticky nature of cooked rice while rice with high Gelatinization Temperature (GT) requires higher temperature, more water and time to cook than those with low or intermediate GT. As the GT is directly correlated to the time required to cook rice, therefore, rice with intermediate GT are preferred over those with high or low-GT. These two properties have highest effect on cooked rice grain quality and thus play major role in influencing consumer's preference. In several studies, both AC and GT were found highly associated with eating and cooking properties of rice [26,27]. Grain quality parameters of all the genotypes have shown desirable physical, chemical properties (Table 2).

3.3 Grain Nutrient Content

In our study, a significant level of variation was observed for all the nutrient composition studied among the four cultivars. The grain nutritional and genetic components of different characters studied are given in Table 3. The two years overall mean values of protein content in the

Table 1. Mean values of yield components and genetic parameters of four genotypes of rice (*Oryza sativa* L.).

SI No	Yield component	Rice genotypes				CD	SE	Coefficient of Variations		Heritability
		BPCM-1	BPCM-2	SM	CTM			PCV	GCV	
1	Plant Height (cm)	89.7	98.2	81.7	132	3.38	0.75	22.06	22.04	0.99
2	Productive tillers per hill	14.5	17.2	12	19	1.84	0.41	19.73	19.38	0.97
3	Panicle Length (cm)	23.3	26.9	23.3	30.2	2.31	0.51	12.91	12.6	0.95
4	Total grains per panicle	163.7	240.2	158.5	265.7	15.26	3.39	26.17	26.07	0.99
5	Unfilled grains per panicle	45	38.2	31.2	13.7	2.17	0.48	42.1	42.05	0.99
6	Filled grains per panicle	118.7	202	127.3	252	17.25	3.83	36.36	36.23	0.99
7	Spikelet sterility percentage	72.5	84.1	80.3	94.9	2.25	0.5	11.22	11.18	0.99
8	Seed Yield Kg/ha	4959.8	5165.7	4746.1	3891.7	538.55	119.68	12.2	11.65	0.91
9	Straw Yield Kg/ha	5607.2	5478.4	5893	7448.4	968.47	215.21	15.33	14.5	0.89
10	Harvest index	88.5	94.4	80.6	52.3	10.96	2.44	23.81	23.4	0.97
11	Test weight	19.9	23.9	22.6	16.5	1.65	0.37	15.77	15.57	0.97
12	Days to 50 percent flowering	97	97.8	116.2	103.7	1.06	0.24	8.54	8.53	0.99
13	Days to maturity	126.7	127.5	144.3	129.2	2.19	0.49	6.3	6.28	0.99

SM-Samba Mahsuri, CTM-Chittimutyalu, CD- Critical difference for Treatments (5%) Level of Significance, SE-Standard Error mean for Treatments, PCV-Phenotypic Coefficient of Variation, GCV-Genotypic Coefficient of Variation, Kg/ha- kilograms per hectore

Table 2. Mean values of grain quality and genetic parameters of four genotypes of rice (*Oryza sativa* L.)

SI No	Grain quality component	Rice genotypes				CD	SE	Coefficient of Variations		Heritability
		BPCM-1	BPCM-2	SM	CTM			PCV	GCV	
1	Hulling percent	66	68.7	72.3	69.6	5.08	1.13	4.11	3.4	0.68
2	Milling percent	59.9	62.8	66.7	62.3	5.9	1.31	4.95	3.97	0.64
3	Head rice recovery percent	53.7	64.7	65.2	63.9	13.34	2.97	10.05	7.42	0.55
4	Kernel length (mm)	3.9	4.9	5	4.7	0.54	0.12	11.2	10.59	0.89
5	Kernel breadth (mm)	1.8	1.9	1.8	2.1	0.16	0.04	7.29	6.78	0.86
6	Length / Breadth Ratio (mm)	2.1	2.6	2.7	2.2	0.15	0.03	11.88	11.72	0.97
7	Grain chalk percent	10.8	10.2	1	9.1	1.45	0.32	58.97	58.68	0.99
8	Alkali spreading value	5.5	6.1	4.2	5.2	0.71	0.16	15.54	14.94	0.92
9	Gel consistency (mm)	21.5	23.7	35.5	24	5.23	1.16	24.52	23.71	0.93
10	Amylose content percent	23.3	25	24.7	25	0.37	0.08	3.38	3.34	0.98
11	Elongation ratio	1.8	2.2	2.1	1.8	0.05	0.01	10.18	10.15	0.99
12	Water uptake (ml)	117.8	186.9	178.6	123.5	9.15	2.03	23.83	23.75	0.99
13	Kernel length after cooking (mm)	8.3	11.6	10.5	8.5	0.36	0.08	16.38	16.34	0.99
14	Volume expansion ratio (mm)	5.6	5.1	4.7	5.6	0.75	0.17	9.07	7.88	0.75

SM-Samba Mahsuri, CTM-Chittimutyalu, CD- Critical difference for Treatments (5%) Level of Significance, SE-Standard Error mean for Treatments, PCV-Phenotypic Coefficient of Variation, GCV-Genotypic Coefficient of Variation

Table 3. Mean values of nutritional content and genetic parameters of four genotypes of rice (*Oryza sativa* L.)

SI No	Nutritional content	Rice genotypes				CD	SE	Coefficient of Variations		Heritability
		BPCM-1	BPCM-2	SM	CTM			PCV	GCV	
1	Polished rice Protein percentage	7.1	6.9	6.5	7.3	0.65	0.14	5.61	4.79	0.73
2	Zinc before polish (ppm)	29.6	33.5	16	34.9	4.45	0.99	30.53	30.14	0.97
3	Zn after polish (ppm)	20.6	24	10.1	28.5	5.19	1.15	38.19	37.37	0.96
4	Fe before polish (ppm)	14.1	16	10.4	15.4	3.2	0.71	18.69	17.24	0.85
5	Fe after polish (ppm)	3.6	4.3	2	4.4	1.73	0.38	33.62	29.97	0.79

SM-Samba Mahsuri, CTM-Chittimutyalu, CD- Critical difference for Treatments (5%) Level of Significance, SE-Standard Error mean for Treatments, PCV-Phenotypic Coefficient of Variation, GCV-Genotypic Coefficient of Variation

Table 4. Correlation matrix of yield characters for four genotypes of rice (*Oryza sativa* L.)

		Y1	Y2	Y3	Y4	Y5	Y6	Y7	Y8	Y9	Y10	Y11	Y12	Y13
Y1	G	1	0.91**	0.97**	0.88*	-0.8	0.92**	0.87*	-0.84*	0.90**	-0.82*	-0.77	-0.26	-0.46
	P		0.89*	0.95**	0.88*	-0.8	0.92**	0.87*	-0.79	0.86*	-0.81*	-0.76	-0.25	-0.45
Y2	G		1	0.97**	0.96**	-0.52	0.93**	0.75	-0.5	0.58	-0.48	-0.52	-0.58	-0.73
	P			0.90**	0.95**	-0.51	0.92**	0.73*	-0.46	0.59	-0.49	-0.48	-0.57	-0.71
Y3	G			1	0.99**	-0.78	0.99**	0.94**	-0.73	0.81*	-0.72	-0.54	-0.25	-0.44
	P				0.96**	-0.77	0.98**	0.92**	-0.64	0.74	-0.66	-0.55	-0.24	-0.42
Y4	G				1	-0.64	0.99**	0.87*	-0.52	0.61	-0.51	-0.37	-0.36	-0.51
	P					-0.64	0.99**	0.87*	-0.48	0.6	-0.51	-0.36	-0.35	-0.5
Y5	G					1	-0.76	-0.92**	0.96**	-0.97**	0.95**	0.65	-0.37	-0.16
	P						-0.76	-0.92**	0.90*	-0.93**	0.93**	0.64	-0.37	-0.17
Y6	G						1	0.94**	-0.65	0.73	-0.64	-0.46	-0.23	-0.4
	P							0.94**	-0.6	0.71	-0.63	-0.45	-0.22	-0.39
Y7	G							1	-0.79	0.85*	-0.79	-0.47	0.12	-0.07
	P								-0.74	0.81*	-0.77	-0.47	0.12	-0.06
Y8	G								1	-0.99**	0.99**	0.90**	-0.27	-0.05
	P									-0.91**	0.98**	0.84*	-0.25	-0.04
Y9	G									1	-0.99**	-0.91**	0.18	-0.05
	P										-0.97**	-0.81*	0.18	-0.03
Y10	G										1	0.89*	-0.27	-0.05
	P											0.83*	-0.27	-0.06
Y11	G											1	0.11	0.3
	P												0.11	0.3
Y12	G												1	0.98**
	P													0.97**
Y13	G													1
	P													

G=Genotypic Correlations Matrix, P= Phenotypic Correlations Matrix; *Significant at $p < 0.05$, ** Significant at $p < 0.01$;

Y1-Plant Height (cm), Y2-Productive tillers per hill, Y3-Panicle Length (cm), Y4-Total grains per panicle, Y5-Unfilled grains per panicle, Y6-Filled grains per panicle, Y7-Spikelet sterility %, Y8-Seed Yield Kg/ha, Y9-Straw Yield Kg/ha, Y10-Harvest index, Y11-Test weight, Y12- Days to 50% flowering and Y13-Days to maturity.

Table 5. Correlation matrix of quality parameters for four genotypes of rice (*Oryza sativa* L.)

		Q1	Q2	Q3	Q4	Q5	Q6	Q7	Q8	Q9	Q10	Q11	Q12	Q13	Q14
Q1	G	1	0.99**	0.94**	0.86*	-0.03	0.86*	-0.99**	-0.89*	0.94**	0.72*	0.57	0.63	0.48	-0.99**
	P		0.95**	0.79	0.85*	0.13	0.76	-0.79	-0.64	0.87*	0.66	0.5	0.56	0.43	-0.51
Q2	G		1	0.73	0.85*	-0.28	0.99**	-0.99**	-0.86*	0.99**	0.61	0.72	0.78	0.62	-0.99**
	P			0.79	0.8	-0.1	0.84*	-0.82*	-0.66	0.90*	0.53	0.62	0.65	0.53	-0.61
Q3	G			1	0.99**	0.43	0.84*	-0.64	-0.29	0.64	0.99**	0.73	0.81*	0.74	-0.94**
	P				0.89*	0.35	0.66	-0.42	-0.28	0.5	0.84*	0.58	0.61	0.57	-0.37
Q4	G				1	0.19	0.84*	-0.59	-0.34	0.61	0.93**	0.76	0.81*	0.75	-0.88*
	P					0.26	0.82*	-0.54	-0.26	0.63	0.91**	0.74	0.78	0.72	-0.57
Q5	G					1	-0.37	0.36	0.18	-0.42	0.59	-0.38	-0.34	-0.3	0.53
	P						-0.35	0.33	0.24	-0.29	0.58	-0.35	-0.3	-0.28	0.52
Q6	G						1	-0.77	-0.45	0.83*	0.54	0.92**	0.94**	0.86*	-0.99**
	P							-0.75	-0.43	0.8	0.54	0.91**	0.93**	0.85*	-0.88*
Q7	G							1	0.94**	-0.99**	-0.27	-0.44	-0.49	-0.32	0.83*
	P								0.89*	-0.98**	-0.26	-0.43	-0.48	-0.31	0.76
Q8	G								1	-0.94**	-0.09	-0.04	-0.1	0.1	0.52
	P									-0.82*	-0.05	-0.04	-0.09	0.09	0.46
Q9	G									1	0.31	0.53	0.57	0.41	-0.97**
	P										0.32	0.51	0.56	0.39	-0.74
Q10	G										1	0.51	0.56	0.54	-0.43
	P											0.51	0.56	0.54	-0.32
Q11	G											1	0.99**	0.99**	-0.98**
	P												0.99**	0.99**	-0.81*
Q12	G												1	0.98**	-0.99**
	P													0.98**	-0.82*
Q13	G													1	-0.89*
	P														-0.74
Q14	G														1
	P														

G=Genotypic Correlations Matrix, P= Phenotypic Correlations Matrix; *Significant at $p<0.05$, ** Significant at $p<0.01$

Q1-Hulling %, Q2-Milling %, Q3-Head Rice Recovery %, Q4-Kernel Length (mm), Q5-Kernel Breadth (mm), Q6-L/B Ratio (mm), Q7-Grain Chalk (%), Q8-Alkali spreading value, Q9-Gel Consistency. Q10-Amylose content %, Q11-Elongation ratio, Q12-Water uptake, Q13-Kernel Length after cooking (mm) and Q14-Volume Expansion Ratio (mm)

polished rice were 7.1% (BPCM1), 6.9% (BPCM2), 6.5% (Samba Mahsuri) and 7.3% (Chittimutyalu). Similar observations on mean crude protein content of the varieties estimated using Kjeldhal method was in the range of 6 to 8% were reported. [28]. The polished grains zinc content was 20.6 ppm (BPCM1), 24 ppm (BPCM2), 10.1 ppm (Samba Mahsuri) and 28.5 ppm (Chittimutyalu). The iron content values of the BPCM1, BPCM2, Samba Mahsuri and Chittimutyalu were 3.6 ppm, 4.3 ppm, 2.0 ppm and 4.4 ppm respectively in the polished rice. During polishing, 28.5% zinc and 75% iron content was lost from these accessions grains. Several thousands of rice germplasm lines have been screened for iron and zinc content in brown and polished grain across the world and many promising donors were identified and 90% of iron and 40% of zinc was lost during polishing [17]. The nutritional quality of rice depends on the protein content and other micronutrients such as zinc and iron. Among cereals, rice is the poor sources of protein as well as iron and zinc [29]. The crude protein content of two cultivars viz., "ARC 10063" and "ARC 10075" was 16.41 and 15.27% from brown rice respectively [30]. Loss of iron content is more than zinc during grain polishing. Therefore polished grain contains lesser minerals than unpolished grain [31].

3.4 Genetic Parameters

The heritability for all the traits ranged from 0.55 to 0.99 percent with a mean value of 0.91. Highest heritability was observed for the days to maturity, days to 50% flowering, spikelet sterility, filled grains per panicle, unfilled grains per panicle, total grains per panicle, plant height, kernel length after cooking, water uptake, elongation ratio and grain chalkiness. Several similar observations were reported previously. The difference between Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV) slightly varies for the characters such as head rice recovery, volume expansion ratio, grain iron content after polishing. This indicates low environmental influence and predominance of genetic factors controlling variability for these traits by [32,33].

Genotypic correlation coefficients in general were higher than phenotypic correlation coefficients (Table-4, 5 and 6) indicating strong inherent association between the traits. Filled grains per panicle exhibited positive significant genotypic and phenotypic correlation with plant height, productive tillers per plant, panicle length, and

total grains per panicle. Similarly significant positive correlation by seed yield per hectare has exhibited with harvest index and test weight indicating that it is one of the selection attribute for yield improvement. Seed yield per hectare exhibited significant negative correlation with straw yield kg/ha. For grain quality parameters wise, grain chalkiness had significant positive correlation with alkali spreading value and significant negative correlation with gel consistency. Kernel breadth has shown positive non-significant association with grain chalk percent, alkali spreading value, amylose content and volume expansion ratio (mm). This trait also exhibited negative non-significant relation with Length/Breadth ratio, gel consistency, elongation ratio, water uptake and kernel length after cooking (Table 5 above). All the nutritional traits were significantly and positively correlated with each other except protein with iron content in unpolished rice (Table 6). These observations were matching with previous report on nutritional aspects on indigenous rice cultivars [34].

Table 6. Correlation matrix of nutritional content for four genotypes of rice (*Oryza sativa* L.)

		N1	N2	N3	N4	N5
N1	G	1	0.95**	0.97**	0.8	0.94**
	P		0.85*	0.89*	0.79	0.8
N2	G		1	0.98**	0.99**	0.99**
	P			0.98**	0.97**	0.92**
N3	G			1	0.95**	0.99**
	P				0.93**	0.90*
N4	G				1	0.99**
	P					0.89*
N5	G					1
	P					

G=Genotypic Correlations Matrix, P= Phenotypic Correlations Matrix; *Significant at $p < 0.05$, ** Significant at $p < 0.01$

N1-Protein % in Polished Rice, N2-Zn Before Polish (ppm), N3-Zn After Polish (ppm), N4-Fe Before Polish (ppm) and N5-Fe After Polish (ppm)

3.5 Genotyping with SSR Markers

DNA finger printing was performed using 24 SSR markers for four genotypes viz. "Samba Mahsuri", BPCM1, BPCM2 and "Chittimutyalu". Among 24 RM markers, 18 markers have shown polymorphism and RM535 marker has shown very distinct polymorphism between the genotypes (Fig. 2). The polymorphic markers and allele sizes of the four genotypes with comparing 100 base pair gene ladder was given in the Table 7.

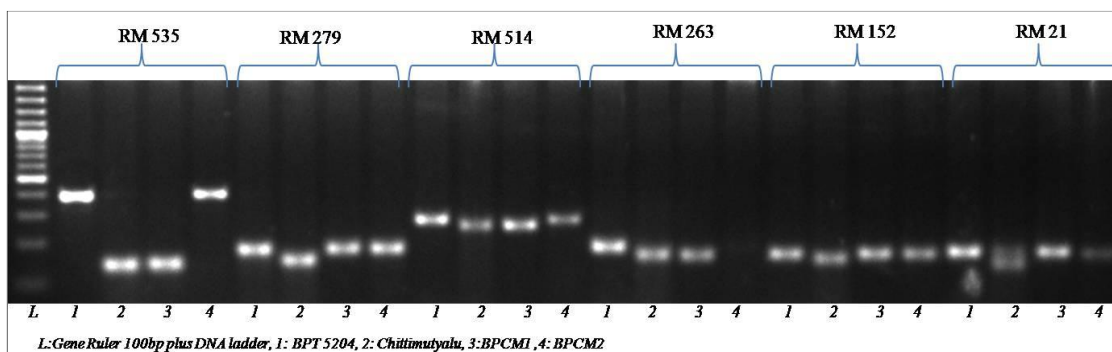


Fig. 2. DNA fingerprinting between the genotypes with RM markers

Table 7. Allele sizes compared with 100 base pair ladder for four genotypes of rice (*Oryza sativa* L.)

SL No	Primer ID	Chromosome number	BPCM1	BPCM2	Samba Mahsuri	Chittimutyalu
1	RM1	1	110	110	110	80
2	RM5	1	110	110	110	120
3	RM535	2	140	400	400	140
4	RM279	2	190	190	190	160
5	RM263	2	170	190	190	170
6	RM12469	2	180	160	180	160
7	RM13347	2	180	160	180	160
8	RM514	3	270	295	295	270
9	RM85	3	110	110	110	90
10	RM1359	4	110	110	110	120
11	RM169	5	170	170	190	170
12	RM190	6	140	140	140	150
13	RM152	8	170	170	170	160
14	RM22885	8	120	120	120	100
15	RM160	9	140	140	140	150
16	RM24829	9	180	180	180	200
17	RM3912	9	190	210	190	210
18	RM21	11	175	175	175	140

4. CONCLUSION

The present study indicated that, the two derived lines BPCM1 and BPCM2 from the parents “Samba Mahsuri” and “Chittimutyalu” found to be promising recombinants for combining higher grain yield, good quality and desirable nutrient content in polished rice. Overall, the resource generated in this study can be used to identify and development of high yielding rice genotypes with good grain and nutritional quality in polished rice and for their release as varieties.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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