

Evaluation of grain yield, quality and nutrients content in rice (*Oryza sativa* L.)

Abstract

Developing rice varieties with higher yield and good cooking quality along with high micronutrients is one of the priorities of current rice research. Four rice genotypes (two parents Samba Mahsuri, Chittimutyalu and two selected derivatives of Samba Mahsuri and Chittimutyalu viz., BPCM1, BPCM2) were evaluated during two wet seasons for their yield, grain quality and nutritional properties. Both the lines (BPCM1 and BPCM2) have shown higher yield advantage (4.5% and 8.8%) than the Samba Mahsuri. These lines have shown acceptable grain quality (AC-23.3, 25% and GC 21.5, 23.7) as well as high zinc-20.6, 24 ppm, moderate iron- 3.6, 4.3 ppm and protein-7.1%, 6.9%, content in polished rice respectively. 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 four genotypes were profiled with eighteen polymorphic RM markers.

Keywords: Rice, Zinc, Iron, Quality, Biofortification.

INTRODUCTION

Rice (*Oryza sativa* L.) is the most important cereal crop and primary energy source for two thirds of the world's population. 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 (DES, DACFW 2017). Majority of rice consumers preferred polished rice for consumption and it is a poor source of micronutrients especially iron and zinc (Bouis and Welch, 2010). 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 (Welch and Graham, 2004). Rice biofortification is one of the enormous strategies to overcome malnutrition deficiency in rice consuming populations especially zinc and iron (Babu, 2013).

The genetic biofortification strategy uses plant breeding approaches to produce staple food crops with higher micronutrient content in edible parts (Harvest Plus 2014). It offers a sustainable solution to malnutrition problems by exploring natural genetic variation to develop micronutrient-dense crop varieties (Bouis 2003; Pfeiffer and McClafferty 2008). Breeding and adoption of rice cultivars with enhanced grain zinc content along with high yield potential has become a priority objective of the 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 (Hub, 2011).

The need for expansion of rice grain micronutrients depends not only on cultural practices and but 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 (Swamy *et al.*, 2016). Development and evaluation of potential rice genotypes with good cooking quality and desirable grain nutritional properties could be great advantage to solve malnutrition disabilities in humans (Gregorio, 2002). With an objective of combining higher yield and micronutrient content, an attempt has been made to evaluate two selected derivatives of Samba Mahsuri and Chittimutyalu for grain yield, grain quality and micronutrient content in polished rice.

MATERIALS AND METHODS

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 (Sundaram *et al.*, 2008). 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 and two promising lines were identified viz., BPCM1 and BPCM2. The two promising derivatives (BPCM1 & BPCM2) along

with two parents (Samba Mahsuri and Chittimutyalu) were evaluated in the farm of ICAR-Indian Institute of Rice Research, Hyderabad for two successive seasons Khari-2013 and 2014.

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. Before planting, soil pH was in the range of 8.53 to 8.58 and soil iron and zinc in the samples were 2.75 to 3.48 and 3.56 to 3.67 ppm respectively. The experiment was laid out in a Randomized Block Design (RBD) with three replications. Genotypes were grown in five meters apart maintaining 20 X15 cm row to plant spacing of individual genotype and all the recommended cultural practices for rice were followed.

Grain quality analysis

Genotypes were analyzed in triplicate for different agronomic and grain quality characteristics like; duration (day), plant height (cm), number of panicles per plant, panicle length (cm), number of filled grains/panicle, seed yield (kg/ha) (Yoshida. 1981). After harvesting approximately 250 grams of fresh paddy seed was collected from 4 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 %, milling %, grain dimensions, linear elongation on cooking, and biochemical characters were studied (Azam *et al.*, 2017).

Grain nutritional analysis:

For the nutritional content estimation, dried seed from each genotype was dehusked and polished separately using non-ferrous and non-zinc dehusker and polisher (*Krishi International*) to avoid metal contamination as described in (Babu *et al.*, 2014). Total crude protein content was determined by micro kjeldahl method using Elite EX, Kelplus automatic nitrogen 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 (Bressani *et al.*, 1971). Five grams of brown and polished rice

samples from each line were separately subjected to energy dispersive X-ray fluorescent spectrophotometer (ED-XRF) for iron and zinc estimation. (Sanjeeva rao *et al.*, 2014).

Genotyping with SSR markers

Tissue samples of 15 days old seedlings were used for DNA isolation using CTAB method (Zheng *et al.*, 1995). 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 standard protocols (Balaji *et al.*, 2012).

Statistical Analysis

The data was collected in triplicate and the mean score were subjected to analysis variance (ANOVA) at 5% level of significance as described by Obi (2002) to ascertain if there is significant difference among the different parameters between the rice genotypes. Other yielded related parameters were analyzed using SPAR 2.0 software (Sangeetha *et al.*, 2000)

RESULTS AND DISCUSSION

Grain Yield:

Increase in grain yield potential is the major goal of the rice breeders' research programs. Genetic variation of the genotype, soil and environmental conditions plays an important role on rice grain yields and micronutrient level (Welch and Graham, 2004; Wissuwa *et al.*, 2008). Rice grain yield per hectare was significantly influenced by the number of panicle-bearing tillers produced per plant, length of the panicle, number of filled grains per panicle, and 1000 grain weight (Bai *et al.*, 2012). 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 seed yield and grain micronutrients of two selected derivatives was found highly significant. BPCM1 is a semi-dwarf stature genotype with short bold grains (Fig.1) and 97days 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 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 have shown desirable growth of plant height with 89.7 and 98.2 cm, respectively. Semi dwarf or Medium plant height is a desirable feature for higher yield production (Ramalingam *et al.*, (1993).

Grain Quality:

Improvement of rice grain quality is an important challenge for the consumer's preference (Shobha Rani *et al.*, 2006). Quality wise BPCM1, BPCM2, Samba Mahsuri and Chittimutyalu showed intermediate amylose content (23.3%, 25%, 24.7% & 25%), medium gel consistency (21.5, 23.7, 35.5 & 24) and alkali spreading value (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 measurements of quality viz., AC and GC (amylose content and gel consistency) indicate the rice grain cooking quality properties (Pandey, 2012). These four genotypes have shown intermediate amylose (20-25%) content, similar observations were recorded by Kumar and Khush 1986. Amylose content determines the firmness and sticky nature of cooked rice while rice with high 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 (Juliano *et al.*, 1964; Kaw and Cruz, 1990; Tang *et al.*, 1989). Grain quality parameters of all the genotypes have shown desirable physical, chemical properties. Grain quality traits and genetic parameters of the four genotypes were given in the table 2.

Grain nutrients:

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 (Mahender *et al.*, 2016). Mohanty *et al.*, 2011 reported that the crude protein content of two cultivars viz., ARC 10063 and ARC 10075 was 16.41 and 15.27% from brown rice respectively. Loss of iron content is more than zinc during grain polishing. Therefore polished grain contains lesser minerals than unpolished grain (Pulagam *et al.*, 2015). 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 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 by Juliano 1993. 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 (Babu *et al.*, 2014).

Genetic parameters

The study of genetic parameters is important to know the amount of variability present in the genetic material, which in turn necessary for further improvement. Similarity has observed

between the phenotypic coefficients of variation (PCV) and genotypic coefficient of variation (GCV) for all the characters studied. However, the difference between PCV and 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 (Poehlman and sleeper, 1995). 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. Similar observations were recorded by Dabholkar, 1992.

The genotypic and phenotypic correlation coefficients for the yield and yield attributing traits are presented in table 4. 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 (%), alkali spreading value, amylose content and volume expansion ratio (mm). This trait also exhibited negative non-significant relation with L/B ratio, gel consistency, elongation ratio, water uptake and kernel length after cooking (table 5). All the nutritional traits were significantly and positively correlated with each other except protein with iron content in unpolished rice (table 6). Similar observations were recorded by Devi *et al.*, 2008.

Genotyping with SSR markers

DNA finger printing using molecular markers allows precise and rapid identification of cultivars and also it is a prerequisite for new varietal release in India. Utilization of simple sequence repeats markers (SSR) in rice (RM microsatellite marker) for characterization, finger printing

and mapping is well proved strategy (McCouch *et al.*, 1997). 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.

Conclusion

The present study indicated the derived lines of Samba Mahsuri and Chittimutyalu viz., BPCM1 and BPCM2 found to be promising recombinants with higher grain yield, good quality and desirable zinc content in polished grains. During two years evaluation, BPCM2 and BPCM1 have shown promising grain yield advantage over 4.5% and 8.8% Samba Mahsuri along with high zinc content (20.5ppm and 24ppm) in polished rice. Additionally, the cooking quality parameters were also similar to the Samba Mahsuri. These promising lines would be considerable value for breeders the development of high yielding cultivars with high zinc in polished rice and for their release as varieties.

REFERENCES

- Azam MM, Ram T, and Babu VR, A Guide to Rice Quality Trait Analysis. ICAR-IIRR Technical Bulletin No.96. ICAR-Indian Institute of Rice Research, Rajendranagar, Hyderabad-500 030, TS, India. 2017; pp 80.
- Babu VR. Importance and advantages of rice biofortification with iron and zinc. J SAT Agric Res 2013; 11: 1–6.
- Babu VR, Neeraja CN, Sanjeeva Rao D, Sundaram RM, Longvah T, Usharani G, Padmavathi G, Balachandran SM, Nirmala Devi G, Bhadana VP, Suneetha K, Rao KV, Surekha K, Sarla N, Brajendra P, Raghuveer Rao P, Girish C, Shashidhar HE, Bijan A and Viraktamath BC. *Biofortification in rice, Bulletin*, Directorate of Rice Research. 2014; 1-98.
- Balaji Suresh P, Srikanth B, Hemanth Kishore V, Subhakara Rao I, Vemireddy LN, Dharika N. Fine mapping of *Rf3* and *Rf4* fertility restorer loci of WA-CMS of rice (*Oryza sativa* L.) and validation of the developed marker system for identification of restorer lines. *Euphytica*. 2012; 187: 421–435.

- 246 Bai X, Wu B, Xing Y. Yield-related QTLs and their applications in rice genetic improvement. *J*
247 *Integr Plant Biol.* 2012; 54(5): 300–311.
248
- 249 Bouis HE. Micronutrient fortification of plants through plant breeding: can it improve nutrition
250 in man at low cost?. *Precede Nutri Soc.* 2003; 62:403–411
251
- 252 Bouis HE, Welch RM. Biofortification is a sustainable agricultural strategy for reducing
253 micronutrient malnutrition in the global south. *Crop Sci.* 2010; 50: S-20-S-32.
254 doi:10.2135/cropsci 2009.09.0531.
255
- 256 Bressani R, Elias LG, Juliano BO. Evaluation of the protein quality of milled rices differing in
257 protein content. *Journal of Agricultural and Food Chemistry.* 1971; 19: 1028-1034.
258 <http://dx.doi.org/10.1021/jf60177a043>
259
- 260 Dabholkar AR. Elements of biometrical genetics. 1992; Concept publishing company, New
261 delhi, india.
262
- 263 Devi Th. P, Durai A, Singh Th. A, Gupta S, Mitra J, Pattanayak A, Sarma BK, Das A.
264 Preliminary studies on physical and nutritional qualities of some indigenous and important
265 rice cultivars of north eastern hill region of India. *Journal of Food Quality.* 2008; 31: 686-
266 700. <http://dx.doi.org/10.1111/j.1745-4557.2008.00228.x>
267
- 268 DES, DACFW, Rice statistics, Directorate of Economics & Statistics. 2016; Department of
269 Agriculture, Cooperation and Farmers welfare, Government of India.
270
- 271 Fan CH, Xing YZ, Mao HL, Lu TT, Han B, Xu CG. GS3, a major QTL for grain length and
272 weight and minor QTL for grain width and thickness in rice, encodes a putative
273 transmembrane protein. *Theor Appl Genet.* 2006; 112:1164–1171. PMID: 16453132
274
- 275 Gregorio GB. Progress in breeding for trace minerals in staple crops. *J. Nutr.* 2002; 132, 500–
276 502.
277
- 278 Hub B. Definition and Significance of Genetic Variability. *Crop Res.* 2011; 32 (1): 69-71.
279
- 280 Hammoud SAA. Genetic behavior of some agronomic characters in two rice crosses. *Egypt. J.*
281 *Agric. Res.* 2005; 83 (5): 305-322.
282
- 283 Juliano B. *Rice in Human Nutrition.* Rome: Food and Agriculture Organization of the United
284 Nations and International Rice Research Institute. 1993.
285
- 286 Juliano BO, Bautista GM, Lugay JC, Reyes AC. Studies on physicochemical properties in rice. *J*
287 *Agric Food Chem.* 1964; 12:31–8.
288
- 289 Kaw RN, Cruz NM. Interrelations among physicochemical grain quality characters in
290 rice. *J Genet Breed.* 1990; 44:139–41

- Kumar I, Khush GS. Genetics of amylose content in rice. *J Genet.* 1986; 65:1-11.
- Mahender, Anumalla, Annamalai Anandan, Sharat Kumar Pradhan, Elssa Pandit. Rice Grain Nutritional Traits and Their Enhancement Using Relevant Genes and QTLs through Advanced Approaches. SpringerPlus. 2016; 1–18.
- McCouch SR, Chen X, Panaud O, Temnykh S, Xu Y, Cho YG, Huang N, Ishii T and Blair M. Microsatellite marker development, mapping and applications in rice genetics and breeding. *Plant Molecular Biology.* 1997; 35: 89–99.
- Mohanty A, Marndi BC, Sharma S, Das A. Biochemical characterization of two high protein rice cultivars from Assam rice collections. *Oryza.* 2011; 48(2):171–174.
- Obi I.U. Statistical Methods of Detecting Differences between Treatment Means and Research Methodology Issues in Laboratory and Field Experiments. 2002; Second Edition. Ap Express publication, Nsukka, Nigeria.
- Pandey Manish K. Different Isoforms of Starch-Synthesizing Enzymes Controlling Amylose and Amylopectin Content in Rice (*Oryza Sativa* L.). *Biotechnology Advances.* 2012; 30(6):1697–1706. Retrieved (<http://dx.doi.org/10.1016/j.biotechadv.2012.08.011>).
- Pfeiffer WH, McClafferty B. Biofortification: breeding micronutrient-dense crops. In: Kang MS, Priyadarshan PM (eds) *Breeding major food staples.* 2008; Blackwell Publishing Ltd, Oxford, pp 61–91.
- Pulagam MB, Praveen V, Sai Sravanthi M, Sanjeeva Rao D, Surekha K, Sundaram RM, Ravindra Babu V, Neeraja CN. Association of OsYSL9 gene with high iron and zinc content in rice grains and identification of elite rice lines. *IJTA,* 2015; 33:3031-3036.
- Poehlman JM, Sleeper DA. *Breeding field crops.* 1995; 4th Edn. Panima publishing corporation, New Delhi.
- Ramalingam J, Vivekanandan P, Vanniarajan C. Combining ability analysis in lowland early rice. *Crop Res.* 1993; 6(2): 228-233.
- Sangeetha ahuja, Malhotra PK, Bhatia VK, Rajendra Prasad. *Statistical Package for agricultural Research.* 2000; (SPAR 2.0).
- Sanjeeva Rao D, Madhu Bp, Swarnalatha P, Suneetha K, Bhadana VP, Varaprasad GS, Surekha K, Neeraja CN, and Ravindra BV. Assessment of grain zinc and iron variability in rice germplasm using Energy Dispersive X-ray Fluorescence Spectrophotometer (ED-XRF). *Journal of Rice Research.* 2014; 7: 45-52.

- Shobha Rani N, Pandey MK, Prasad GSV, Sudharshan I. Historical significance, grain quality features and precision breeding for improvement of export quality basmati varieties in India. *Indian J Crop Sci.* 2006; 1: 29–41.
- Sundaram RM, Vishnupriya MR, Biradar SK, Laha GS, Reddy GA, Rani NS, Sarma NP, Sonti RV. Marker assisted introgression of bacterial blight resistance in Samba Mahsuri, an elite indica rice variety. *Euphytica*. 2008; 160: 411-422. doi 10.1007/s10681-007-9564-6.
- Swamy BPM, Rahman MA, Inabangan-Asilo MA, Amparado A, Manito C, Chadha-mohanty, P. Advances in breeding for high grain zinc in rice. *Rice*. 2016; 9: 49. doi:10.1186/s12284-016-0122-5.
- Tang SX, Khush GS, Juliano BO. Variation and correlation of four cooking and eating indices of rices. *Phillipp J Crop Sci.* 1989; 14: 45–9
- Welch RM, Graham RD. Breeding for micronutrients in staple food crops from a human nutrition perspective. *J. Exp. Bot.* 2004; 55, 353–364. doi:10.1093/jxb/erh064
- Wissuwa M, Ismail AM, Graham RD. Rice grain zinc concentrations as affected by genotype, native soil-zinc availability, and zinc fertilization. *Plant Soil*. 2008; 306: 37–48. doi:10.1007/s11104-007-9368-4
- Yoshida S. Growth and Development of the Rice Plant. *Fundamentals of Rice Crop Science*. 1981; 1–61.
- Yoshida S. Rice. In: Potential productivity of field crops under different environments. Smith WH, Banta SJ (Eds). International Institute of Rice Research, Los Banos, the Philippines. 1983; 103-127 p.
- Zhao DL, Atlin GN, Amante M, Cruz MTS, Kumar A. Developing aerobic rice cultivars for water short irrigated and drought-prone rainfed areas in the tropics. *Crop Sci*. 2010; 50: 2268–2276.
- Zheng K, Huang N, Bennett J, Khush GS. PCR-based marker assisted selection in rice breeding. *IRRI Discussion Paper Series*, 1995; No.12. International Rice Research Institute, Manila, the Philippines.



Fig 1 Panicle and paddy images. A=*Samba Mahsuri*, B= *BPCM1*, C=*BPCM2* and D= *Chittimutyalu*

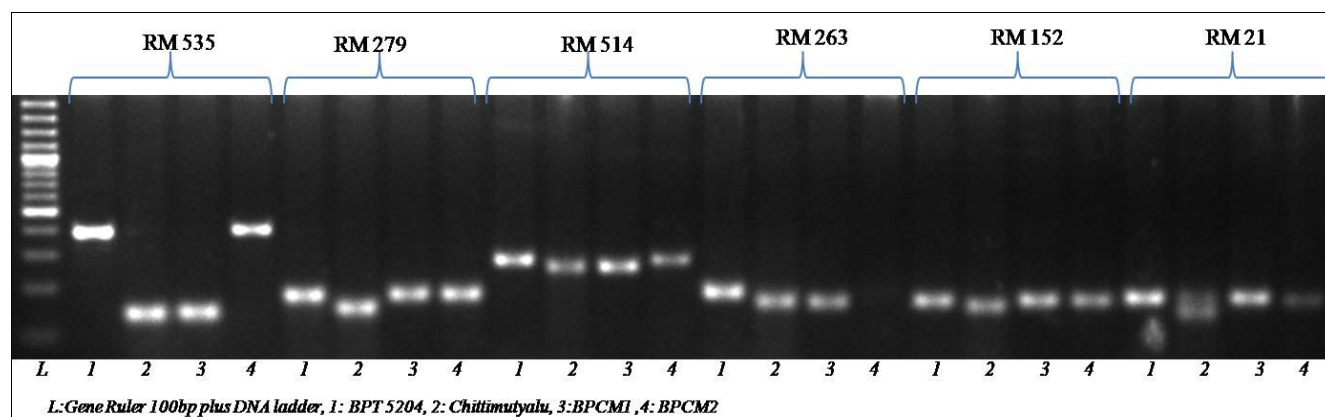


Fig 2 DNA fingerprinting between the genotypes with RM markers

396

Table 1. Mean values of yield components and genetic parameters.

SI NO	Character	BPCM-1	BPCM-2	Samba Mahsuri	Chittimutyalu	C.D. for Treatments (5%) Level of Significance	SE m for Treatments	Phenotypic Coefficient of Variation (PCV)	Genotypic Coefficient of Variation (GCV)	Heritability
1	Y1	89.7	98.2	81.7	132	3.38	0.75	22.06	22.04	0.99
2	Y2	14.5	17.2	12	19	1.84	0.41	19.73	19.38	0.97
3	Y3	23.3	26.9	23.3	30.2	2.31	0.51	12.91	12.6	0.95
4	Y4	163.7	240.2	158.5	265.7	15.26	3.39	26.17	26.07	0.99
5	Y5	45	38.2	31.2	13.7	2.17	0.48	42.1	42.05	0.99
6	Y6	118.7	202	127.3	252	17.25	3.83	36.36	36.23	0.99
7	Y7	72.5	84.1	80.3	94.9	2.25	0.5	11.22	11.18	0.99
8	Y8	4959.8	5165.7	4746.1	3891.7	538.55	119.68	12.2	11.65	0.91
9	Y9	5607.2	5478.4	5893	7448.4	968.47	215.21	15.33	14.5	0.89
10	Y10	88.5	94.4	80.6	52.3	10.96	2.44	23.81	23.4	0.97
11	Y11	19.9	23.9	22.6	16.5	1.65	0.37	15.77	15.57	0.97
12	Y12	97	97.8	116.2	103.7	1.06	0.24	8.54	8.53	0.99
13	Y13	126.7	127.5	144.3	129.2	2.19	0.49	6.3	6.28	0.99

397

398 Y1-Plant Height (cm), Y2-Productive tillers per hill, Y3-Panicle Length (cm), Y4-Total grains per panicle, Y5-Unfilled grains per panicle, Y6-
 399 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
 400 to 50% flowering and Y13-Days to maturity.

401

402

403

404

405

406

Table 2. Mean values of cocking quality and genetic parameters

Sl NO	Character	BPCM-1	BPCM-2	Samba Mahsuri	Chittimutyalu	C.D. for Treatments (5%) Level of Significance	SE m for Treatments	Phenotypic Coefficient of Variation (PCV)	Genotypic Coefficient of Variation (GCV)	Heritability
1	Q 1	66	68.7	72.3	69.6	5.08	1.13	4.11	3.4	0.68
2	Q 2	59.9	62.8	66.7	62.3	5.9	1.31	4.95	3.97	0.64
3	Q 3	53.7	64.7	65.2	63.9	13.34	2.97	10.05	7.42	0.55
4	Q 4	3.9	4.9	5	4.7	0.54	0.12	11.2	10.59	0.89
5	Q 5	1.8	1.9	1.8	2.1	0.16	0.04	7.29	6.78	0.86
6	Q 6	2.1	2.6	2.7	2.2	0.15	0.03	11.88	11.72	0.97
7	Q 7	10.8	10.2	1	9.1	1.45	0.32	58.97	58.68	0.99
8	Q 8	5.5	6.1	4.2	5.2	0.71	0.16	15.54	14.94	0.92
9	Q 9	21.5	23.7	35.5	24	5.23	1.16	24.52	23.71	0.93
10	Q 10	23.3	25	24.7	25	0.37	0.08	3.38	3.34	0.98
11	Q 11	1.8	2.2	2.1	1.8	0.05	0.01	10.18	10.15	0.99
12	Q 12	117.8	186.9	178.6	123.5	9.15	2.03	23.83	23.75	0.99
13	Q 13	8.3	11.6	10.5	8.5	0.36	0.08	16.38	16.34	0.99
14	Q 14	5.6	5.1	4.7	5.6	0.75	0.17	9.07	7.88	0.75

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 (GC). Q10-Amylose content (AC) %, Q11-Elongation ratio, Q12-Water uptake, Q13-Kernel Length after cocking (mm) and Q14-Volume Expansion Ratio (mm)

Table 3. Mean values of nutritional content in grains and genetic parameters

SI NO	Character	BPCM-1	BPCM-2	Samba Mahsuri	Chittimutyalu	C.D. for Treatments (5%) Level of Significance	SE m for Treatments	Phenotypic Coefficient of Variation (PCV)	Genotypic Coefficient of Variation (GCV)	Heritability
1	N 1	7.1	6.9	6.5	7.3	0.65	0.14	5.61	4.79	0.73
2	N 2	29.6	33.5	16	34.9	4.45	0.99	30.53	30.14	0.97
3	N 3	20.6	24	10.1	28.5	5.19	1.15	38.19	37.37	0.96
4	N 4	14.1	16	10.4	15.4	3.2	0.71	18.69	17.24	0.85
5	N 5	3.6	4.3	2	4.4	1.73	0.38	33.62	29.97	0.79

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)

438
439
440

Table 4. Correlations matrix for yield characters

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

441 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. Correlations matrix for quality parameters

		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)

Table 6 Correlations matrix for nutritional content

		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)

Table 7. Allele size with compared to 100 ladder (in bp)

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