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Research Article

Genetic variability and diversity of grain nutritional and quality traits of unexplored traditional rice landraces for developing biofortified varieties

M. Parikh*[1], Sanjeeva Rao Durbha[2], Parmeshwar K. Sahu[1], Ritu R. Saxena[1], Bhawana Sharma[1] and Deepak Sharma*[1]

[1]Department of Genetics and Plant Breeding, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya (IGKV), Raipur-492012 (C.G.), India
[2]ICAR-Indian Institute of Rice Research, Rajendranagar, Hyderabad-500030, India
***E-Mail:** manglachaudhary@rediffmail.com, deepak1962@igkv.ac.in

Abstract
Characterization of grain nutritional and quality traits was done in a total of 192 exotic and indigenous rice genotypes were genetically characterized for 16 grain nutritional and quality traits. Substantial genetic variability was observed for all the traits. The coefficient of variation was maximum for flavonoid content (87.10%) and minimum for kernel breadth (11.90%). The estimated coefficient of skewness and kurtosis indicated the presence of genetic interaction among the traits. Based on grain shape 4, 37, 31, 65 and 55 rice genotypes were classified as short slender, short bold, medium slender, long slender and long bold respectively. Further, kernel length was negatively associated with zinc, iron, phenolics and flavonoid contents. Amylose content was positively associated with protein, phenolics and flavonoid contents suggesting that such relationship could serve as grain indices for indirect selection of genotypes. Four genotypes- *Oryza officinalis, Oryza latifolia,* IC435559 and IC135877 were identified as donors for zinc and iron contents. The genotypes- IC74637, IC301547, IC301589 and IC301625 were identified as potential donors for both phenolics and flavonoid. Five genotypes *viz*., IC379109, IC331668, Mancha (M:1028), Dubraj (D:1251) and Laxmibhog (L:708) were identified for grain yield, quality and nutritional traits. The identified donors will be useful to develop nutrient dense biofortified varieties.

Keywords: Rice landraces, diversity, variability, grain nutritional and quality traits, photochemical

INTRODUCTION

Rice (*Oryza sativa* L.) is the major staple food for almost three billion people across the globe. However, in rice, the availability of calories manifolds higher than nutrients, like vitamins and minerals. In the last decade, demand for nutrient dense rice has increased (Zhou *et al*., 2018, Sahu *et al.,* 2014). Hence, in addition to yield and cooking quality, nutritional quality of grain is also important. Thus, developing rice varieties with higher grain nutritional and quality traits becomes a prime goal at global level (Asante, 2017).

Rice genetic resources or germplasm plays crucial role to meet the challenges of food and nutritional security. India possesses rich genetic diversity of rice germplasm due to varied eco-geographical conditions and is almost represent significant proportion of the global diversity. Since several centuries, the Chhattisgarh state is renowned as “rice bowl of India” due to the availability of vast diversity of rice landraces having unique characters such as biotic and abiotic resistance, medicinal and nutritional values, typical grain colouration, aroma, etc. Moreover, Chhattisgarh state noted maximum acreage and productivity of rice due to suitable agro-climatic conditions and soil types (Sahu *et al*., 2017). Considering the importance of this germplasm, Indira Gandhi Krishi Vishwavidyalaya has been conserving as well as maintaining about 23,250 rice accessions that were collected from different districts of the state (Sao *et al.,* 2021, Sahu *et al*., 2017).

The nutrient rich rice genotypes can be incorporated into functional foods (Shen *et al*., 2009). In addition, phytochemicals such as phenolics, flavonoids, gamma oryzanols, tocopherols etc. provide potential health benefits to cardiovascular, reproductive and nervous systems as well as possess anti-oxidative, anti-cancer, anti-diabetic, anti-obesity, anti-microbial properties (Bahare *et al*., 2020). In lieu with the demand for nutrient dense rice, it is highly essential to explore the available diversity for one or more nutrients in the germplasm followed by the identification of the superior donors to develop superior segregants with maximum heterosis (Descalsota-Empleo *et al*., 2019). Statistical parameters are often used to extract the basic information about the desirable traits of interest and their relationship along with the identification of donor parents. The association studies between the nutritional and grain quality characteristics could serve as indices for indirect selection of rice genotypes with high nutritional parameters (Shen *et al*., 2009).

Therefore, in this study, grain quality and nutritional traits were analysed in 192 diverse rice germplasm to identify desirable genotypes foruse as donors in future breeding programmes to develop the high yielding and nutritionally enriched varieties. In addition, associations were determined among these traits using descriptive statistics.

MATERIALS AND METHODS

Experimental materials: The research materials comprised of a panel of 192 diverse rice genotypes (**Table 1**) including 186 test genotypes and 6 checks *viz*., Aruna (red rice variety of Kerala), Krishnanjana (red rice variety of Kerala), Dubraj Selection -1 (Aromatic rice variety), Badshahbhog Selection-1 (Aromatic rice variety), Jaldubi (Submergence tolerant rice variety) and IGKV R-1 (Rajeshwari) (High yielding rice variety) (**Table** 1). All these accessions were procured from R.H. Richharia rice germplasm section of IGKV, Raipur.

The experiment was conducted at Research Farm, IGKV, Raipur, during wet (*Kharif)* season 2018 by following the augmented block design (Federer, 1956). All the genotypes (186 test genotypes and 6 checks) were grown in six blocks (37 genotypes per block). Recommended package of practices were followed to raise the crop. After harvesting, all the genotypes were properly cleaned, dried under shade till the moisture content decreased to the recommended 12-14% and were stored at room temperature for four months prior to the grain quality and nutritional analysis.

A total of 10 grain quality parameters *viz.,* kernel length, kernel breadth, kernel length breadth ratio, elongation ratio, hulling %, milling %, head rice recovery %, alkali spreading value (gelatinization temperature), gel consistency and amylose content were recorded (DRR, 2014).

A total of six nutritional parameters were recorded from all the rice samples. Protein content (Lowry method, 1951) was estimated in brown rice powder. Iron and zinc contents were estimated in brown rice using ED-XRF spectrometry (Energy dispersive X-ray fluorescence) (Sanjeeva Rao *et al*., 2020). Total phenolic content equivalent to µg of gallic acid (Bao *et al*., 2005), flavonoid content equivalent to µg of quercetin (Jia *et al*., 1999) and γ-oryzanol content (Bucci *et al*., 2003) were estimated in rice bran.

Mean data of all the observations were subjected to statistical analysis by XLSTAT v 19.03 for descriptive statistics. Histogram and correlation plots were drawn using ggplot2 and performance analytics packages R version 4.0.2. IASRI online software was used for augmented block design (Federer, 1956). PAST v 3.14 software was used for principal component analysis (PCA) by following the correlation based method.

RESULTS AND DISCUSSION

Rice is the major staple food and dietary source of nutrition of the Asian Countries. Biofortification through conventional breeding strategy has been considered as the best tool to develop nutritionally improved rice genotypes. The pre-requisite of biofortification programme is the availability of significant diversity and variability of the target trait(s) in the gene pool. Hence, the present set of 192 diverse rice genotypes were screened for important grain cooking and nutritional quality aspects.

Analysis of Variance (ANOVA) revealed significant differences among the genotypes for all the 16 grain quality and nutritional traits. The block effect was non-significant for most of the traits indicating that their role is negligible in expression of the traits (**Table 1**). The block effects were significant for H% and KL.

The mean, maximum, minimum, standard deviation, coefficient of variation, standard error of the mean and kurtosis for all the analysed traits are presented in **Table 2**. The relatively higher coefficient of variation% (CV%) for the traits is due to the inclusion of diverse panel of rice genotypes from indigenous, exotic and pigmented landraces along with the wild species. The observed variation is similar to some of the reported findings for GC and AC (Sahu *et al.,* 2017), for AC, GC, zinc content (ZnC) and iron content (FeC) (Umarani *et al*., 2016), for Phenolic content (PhC),

Table 1. Analysis of variance (ANOVA) for grain quality and nutritional traits

Traits	Source of variation					CD at 1% between genotype and check
	Block	Test Treatments	Checks	Treatments vs Checks	Error	
Degree of freedom	5	191	5	1	25	
Kernel Length (KL) mm	0.72*	0.48*	2.04**	2.73**	0.23	1.56
Kernel Breadth (KB) mm	0.01	0.08**	.73**	0.38**	0.01	0.37
KLBC	0.01	0.20**	1.3**	6.53**	0.01	0.35
Elongation ratio (ER)	0.01	0.04**	0.21**	0.03**	0.01**	0.04
Hulling percent (HRR%)	0.06	37.16**	24.37**	5.6	6.49	8.28
Milling percent (M%)	0.02	52.23*	30.43	16.9	18.43	13.96
Head Rice Recovery (HRR%)	6.23	105.69**	62.18	120.53	34.28	19.04
Gel Consistency (GC)	0.01	681.32**	1598.05**	79.26	27.27	16.98
Alkali Spreading value (ASV)	0.01	1.81**	11.95**	0.21	0.31	1.81
Amylose Content (AC%)	0.04	52.67**	146.55**	215.01**	2.46	5.1
Protein Content (PC%)	0.01	7.05**	24.54**	423.45**	0.56	2.45
Iron content (Fe) in ppm	0.01	5.86**	35.03**	51.78**	0.01	0.01
Zinc content (Zn) in ppm	0.01	18.75**	18.8**	24.85**	0.01	0.03
Phenolic content (PhC) (µg /100g)	3.71	519956.73**	687206.91**	519.47	53698.85	753.58
Flavonoid content (FC) (µg /100 g)	115732.12**	114516.10**	106457.56**	889777.36**	90867.88	980.24
Oryzanol content (OC) (µg /100 g)	0.06	291.17**	2183.35**	11284.63**	7.731	8.68

** Significant at 1% level of significance / * Significant at 5% level of significance

Flavonoid content (FC) and Oryzanol content (OC) (Sanghamitra *et al*., 2018) and for Protein content (PC) (Prasad *et al*., 2021) in rice genotypes. Genotypes with intermediate values of AC, GC and ASV are always considered best in cooking quality (Nandedkar *et al*., 2020).

The accession IC388737 recorded highest ZnC (36.6ppm). Similarly, *Oryza officinalis* for highest FeC (25.04 ppm) and Kanak jira for highest PC (15.49%). The highest PhC, FC and OC were observed in IC206322 (3161.20 µgGAE /100g), Guinata (14469.16 µgQE/100g) and Makado dhan (95.5 µg/100mg) respectively. Utilization of these promising donors in breeding programmes would be helpful to develop new rice lines with better nutrient content.

Frequency distribution of grain quality and nutrition traits
The graphical representation of the frequency of distribution indicates that KLBR and HRR% traits alone were closer to normal distribution (**Fig. 1**). The statistical analysis of the data for the kurtosis (**Table 2**) gives information regarding the nature of gene action (Fisher *et al*., 1932) and the number of genes that control the traits (Robson, 1956). Negative kurtosis value was observed for KLBC (-0.18), HRR% (-0.85), ASV (-0.78), PhC (-0.03) and FC (-0.29). Positive kurtosis value was noted for KL (0.42), KB (1.30), ER (0.57), H% (2.79), M% (1.51), GC (0.05), AC% (1.97), PC% (0.62), FeC (12.66), ZnC (0.12), and γ-oryzanol (0.95). Kurtosis value and graphical distribution through histogram for FeC followed the leptokurtic configuration which indicates that it is controlled by fewer number of genes, whereas KB, M% and AC followed the platykurtic configuration which indicates that these traits are controlled by more number of genes. Mesokurtic and leptokurtic configuration observed for grain quality characters like H%, M% and for grain cooking characters like KLAC, ASV and GC (Sahu *et al*., 2017). For the given trait, the positive and negative or close to zero kurtosis represent the presence and absence of gene interaction respectively (Nachimuthu *et al*., 2014).

Correlation estimates showed the possibility of improvement of a character through selection for other character. The significant positive correlation of KLBR (0.75) with KL and the significant negative association between KB and KLBR (-0.50) imply that varieties with larger kernel length can provide higher KLBR (**Fig. 2**). As expected, negative association was observed between KL and HRR% since kernels with smaller length yield more unbroken grains than longer kernels during milling (Shivani *et al*., 2007). Positive significant association between physical quality traits such as H% with M% (0.74) and HRR% (0.0.36) means that selection of one trait can lead to simultaneous improvement in three quality traits. Like Singh *et al*. (2020), M% showed highly significant positive correlation with HRR% (0.45) and significant negative correlation with AC (−0.06).

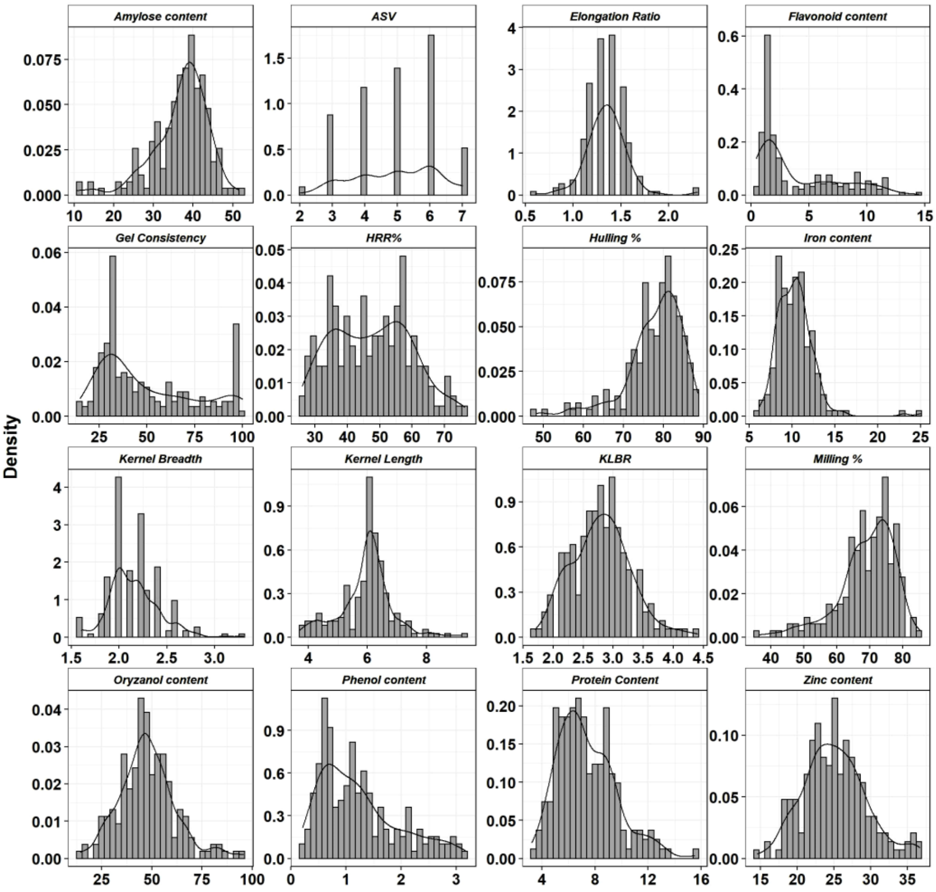

Fig. 1. Distribution of various quality and nutritional traits in the germplasm

Table 2. Descriptive statistical parameters for grain quality and nutritional traits in 192 rice genotypes

Statistic	Mean	Minimum	Maximum	Standard deviation	Coefficient of variation	Standard error of the mean	Kurtosis
Kernel Length (KL) mm	6.45	3.7	9.2	0.66	12.8	0.05	0.42
Kernel Breadth (KB) mm	2.45	1.6	3.3	0.26	11.9	0.02	1.3
KLBC	3.05	1.7	4.4	0.4	16.8	0.03	-0.18
Elongation ratio (ER)	1.45	0.6	2.3	0.2	13	0.01	0.57
Hulling percent (HRR%)	68.36	48.08	88.65	7.04	13	0.51	2.79
Milling percent (M%)	60.94	36.3	85.59	8.61	12.5	0.62	1.51
Head Rice Recovery (HRR%)	51.15	26.02	76.29	11.94	25.2	0.86	-0.85
Gel Consistency (GC)	57.5	15	100	0.26	20.9	0.02	0.05
Alkali Spreading value (ASV)	4	2	7	24.88	50.2	1.8	-0.78
Amylose Content (AC%)	36.9	10.67	51.65	6.95	18.8	0.09	1.97
Protein Content (PC%)	7.37	3.25	15.49	2.17	29.4	0.5	0.62
Iron content (Fe) in ppm	25.11	14.58	36.68	4.26	17	0.16	12.66
Zinc content (Zn) in ppm	10.39	6.12	25.04	2.25	21.7	0.31	0.12
Phenolic content (PhC) (µg /100g)	1226.34	211.56	3161.2	708.97	57.8	0.16	-0.03
Flavonoid content (FC) (µg /100 g)	3985.79	463.32	14469.16	3472.32	87.1	51.3	-0.29
Oryzanol content (OC) (µg /100 g)	47.77	14.63	95.49	13.95	29.2	251.25	0.95

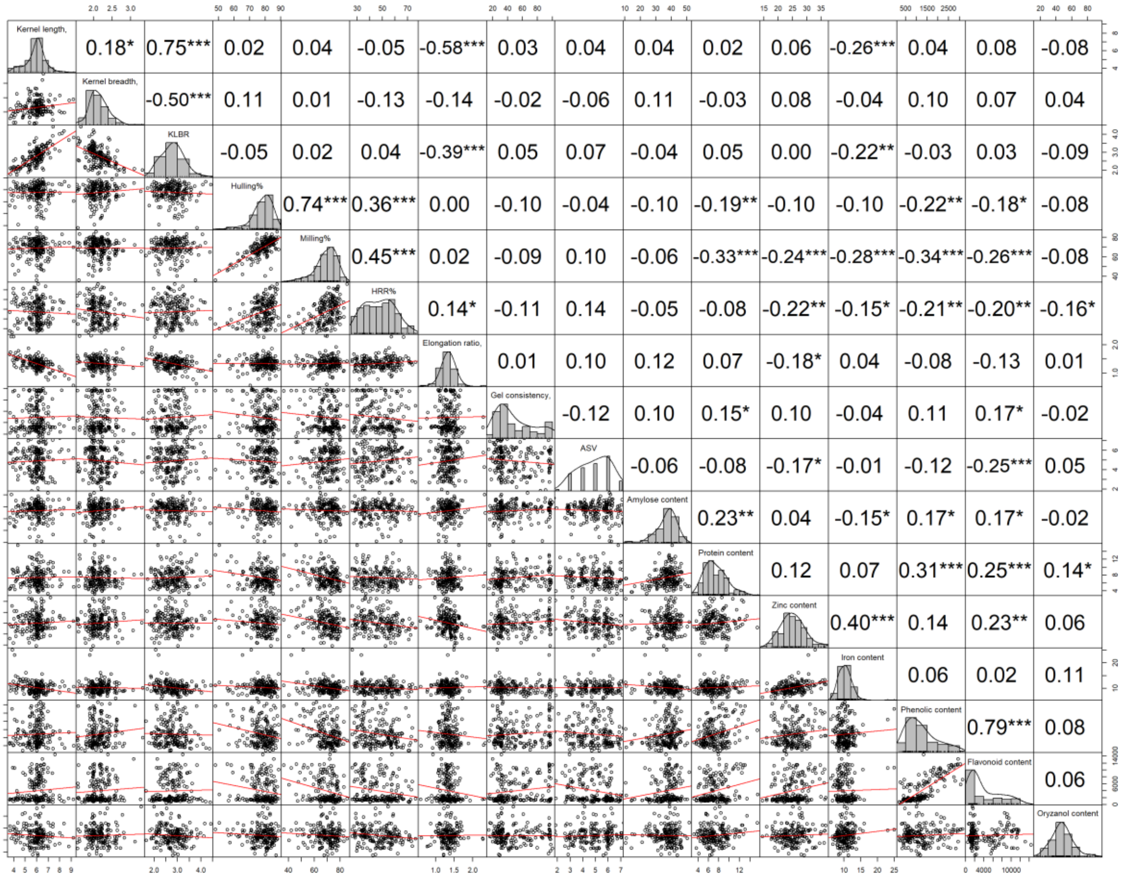

Fig. 2. Correlation between quality and grain nutritional traits.

The symbols "***", "**" and "*" represent significant at probability level at 0.001, 0.01 and 0.05 respectively.

Significant negative association of M% with PC, ZnC, FeC, PC and FC indicates increase in M% leads to nutrient loss. This relationship holds good because it is well known that majority of the nutrients are distributed more in the aleurone layer of brown rice and their content reduces due to loss of this layer during milling (Maganti *et al*., 2019). Higher ZnC and FeC were observed in wild rice which is frequently poor in yield (Anuradha *et al*., 2012). In general, zinc and iron are negatively correlated with yield (Sanjeeva Rao *et al*., 2020). As reported by Khatun *et al*. (2003), non-significant positive association (0.10) was observed between GC and AC and it indicates that higher AC may lead to the recovery of genotypes with soft GC. Compared with genotypes with low AC, genotypes having higher AC result in less hard and shorter gel length due to retrogradation behaviour of amylose during cooling of the gel (Rani *et al*., 2006).

A highly significant positive association was observed between AC and PC (0.23). Further, PC also noted strong positive correlation with PhC (0.31) as well as FC (0.25) and a weak association with OC. ZnC was found to be positively correlated with FeC (0.40) and FC (0.232) and weakly associated with PhC (0.136). This is in line with the findings of Heydari *et al*. (2019) and contrary to the findings of Pathak *et al*. (2017). Positive correlation between grain zinc and iron content indicates common mechanisms for their uptake, translocation and loading and suggests that there is scope for simultaneous improvement of both traits.

Principal component analysis revealed six major PCs having more than 1 eigen value and more than 5% variability. First two PCs contributed about 33.32% of the total variation present among the genotypes for the studied traits indicating the availability of substantial variations (**Table 3**). PCA factor loading indicated the dominance of milling percentage, head rice recovery (%), phenolic contents and flavonoid contents in PC1 while the traits kernel length, kernel length breadth ratio, elongation ratio contributed more towards PC2 (**Table 3**). This indicated the major role of milling percentage, head rice recovery (%), phenolic contents, flavonoid contents, kernel length, kernel length breadth ratio and elongation ratio in classifying the 192 genotypes in five major groups as indicated in the PCA scatter diagram (**Fig. 3**). The outcome of the PCA is further supported by the cluster analysis which also grouped the 192 genotypes into

Table 3. Contribution of first six principal component axes to variation in rice germplasm

Parameters	PC 1	PC 2	PC 3	PC 4	PC 5	PC 6
Kernel length	0.035	0.601	0.031	-0.118	-0.169	0.023
Kernel breadth	0.059	-0.071	0.439	-0.429	-0.477	-0.061
Kernel length breadth ratio	-0.006	0.573	-0.263	0.195	0.166	0.056
Hulling percentage	-0.351	0.034	0.379	-0.183	0.313	0.164
Milling percentage	-0.436	0.081	0.317	-0.040	0.181	0.138
Head rice recovery percentage	-0.329	0.008	0.151	0.211	0.271	0.201
Elongation ratio	-0.089	-0.457	0.001	0.384	0.037	-0.038
Gel consistency	0.150	0.049	0.107	0.177	0.189	-0.451
Alkali spreading value	-0.157	0.000	-0.259	0.130	-0.342	0.402
Amylose content	0.135	-0.005	0.307	0.309	-0.209	-0.176
Protein content	0.282	-0.012	0.048	0.297	0.070	0.166
Zinc content	0.260	0.006	-0.055	-0.387	0.348	-0.079
Iron content	0.165	-0.256	-0.284	-0.348	0.339	0.129
Phenolic content	0.398	0.033	0.296	0.132	0.082	0.344
Flavonoid content	0.394	0.084	0.340	0.092	0.207	0.238
Oryzanol content	0.113	-0.112	-0.089	-0.088	-0.156	0.533
Eigen values	3.04	2.28	1.58	1.48	1.19	1.07
Variance (%)	19.06	14.26	9.93	9.30	7.48	6.74
Cumulative variance (%)	19.06	33.32	43.25	52.55	60.03	66.77

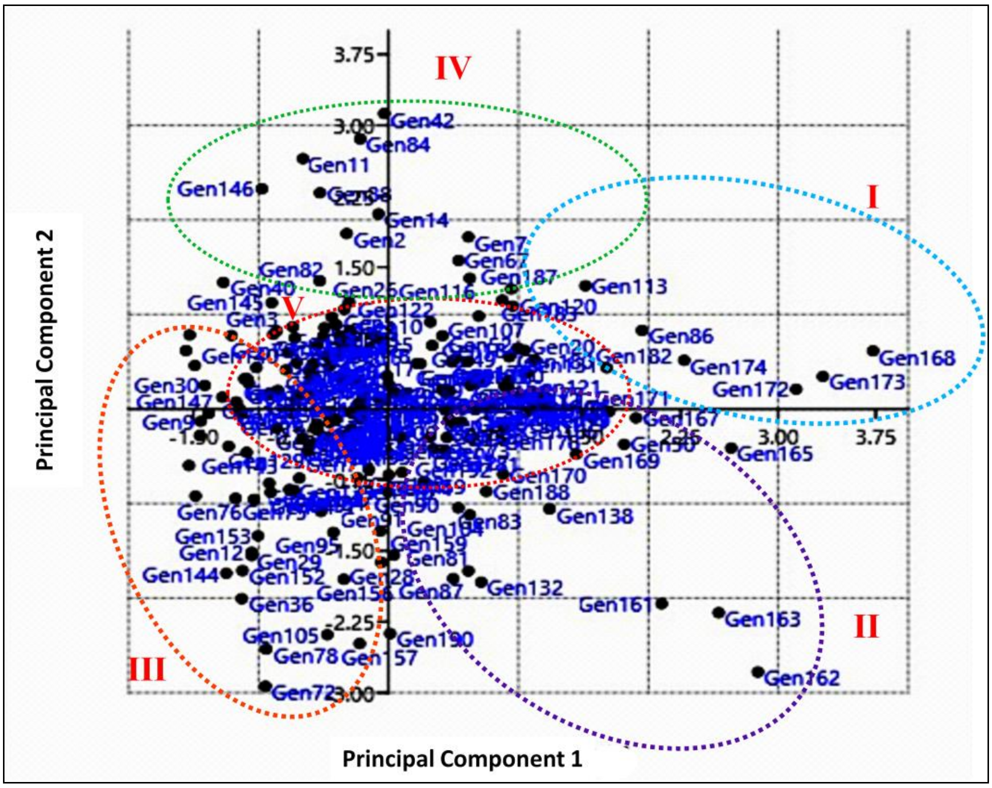

Fig. 3. PCA Scatter diagram showing the grouping pattern of 192 rice genotypes

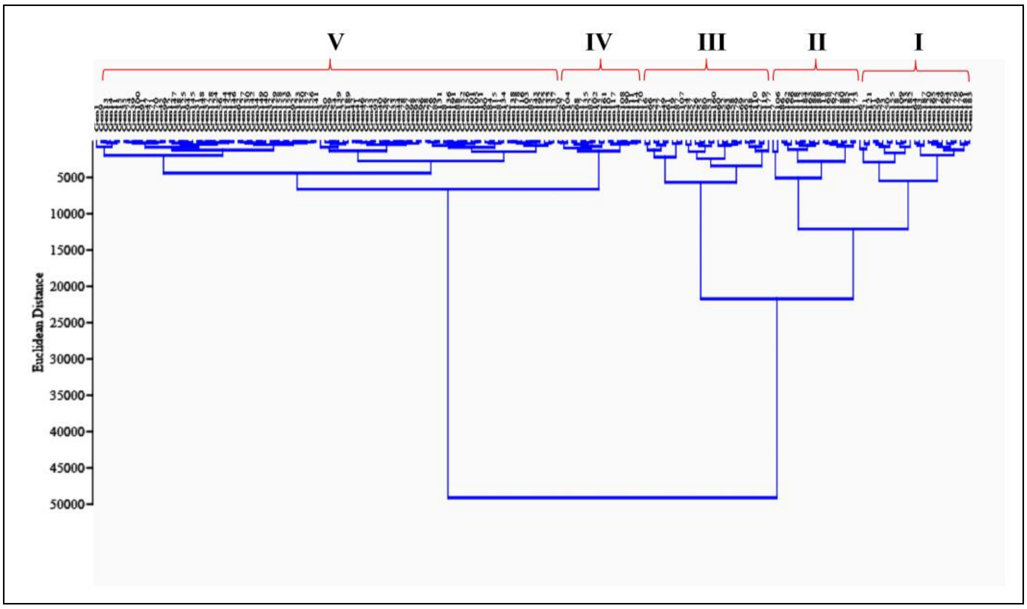

Fig. 4. Euclidean distance based cluster diagram of 192 rice genotypes

five major clusters (**Fig. 4**). PCA scatter diagram and cluster diagram revealed that genotypes of cluster I, II and II are distantly related with the genotypes of cluster IV and V. This indicated the usefulness of genotypes of cluster I and II in crossing with the genotypes of cluster V for getting the better transgressive segregants for grain quality and nutritional traits. Similar studies were done by Nachimuthu *et al.* (2014) and Gour *et al.* (2017).

Promising genotypes identified for grain nutritional and quality traits: Of the 192 genotypes, majority have long slender (65) followed by long bold (55), short bold (37), medium slender grains (31) and only four genotypes have short slender grains. The highest and least kernel length (KL) values were recorded for Improved Dokra-dokri and Khera ghul followed by Tarunbhog, respectively. Seventy-six genotypes have desired HRR% (76%) and 147 noted recorded desired M% (65%). Only 22 genotypes with KL >6.6 mm showed the desired HRR% of ≥45% while 52 genotypes with KL <6.6 mm noted desired HRR% of ≥55% (**Table 4**).

Although Improved Dokra-dokri was observed to register highest KL, none of the long slender or long bold grain genotypes recorded the desired KLAC of 12mm. In the case of ER, nine genotypes registered desired ER of ≥1.7. Notably, Badshahbhog and selection of Badshahbhog showed >2 ER which indicate their basmati type feature. In this study the genotypes, IC435559, IC301559, IC301558, IC388737 and Ateya showed highest ZnC of 36ppm in brown rice. However, upon polishing, only three genotypes, IC435559, IC301559 and IC301558 registered ZnC of 27.6, 32.6 and 28.2 ppm respectively which compares well with the international biofortification target value of ≥28 ppm. Apart from these, 20 genotypes recorded zinc content ≥28 ppm in polished rice and among these, only three genotypes- Khatiya pati, IC124525 and Angur guchcha recorded YP equal to or above that of the mega variety, Swarna. One genotype, *Oryza officinalis,* recorded highest FeC (25.04 ppm) in brown rice, however, only 6.7 ppm remained in the polished rice. Twenty-two genotypes recorded PC ≥10%, however, only 10 genotypes (**Table 5**) recorded YP similar to above that of Swarna. Few rice landraces *viz.,* Kanak jira, IC301555 and IC301622 was observed to have high protein contents above 10%, however, their YP of 15.49%, 13.11% and 12.75% respectively was less than that of Swarna.

The total PhC and FC in bran ranged from 211.56 to 3161.20 (µgGAE /100g) and 463.32 to 14469.16 (µgQE/100g) respectively. IC206322 and Guinata registered highest PhC and FC respectively. OC ranged from 14.6 to 95.5 (Makado dhan) µg/100mg of bran. Generally, OC ranged from 1 to 2 % in rice bran oil (Patel and Naik, 2004). In addition, few rice genotypes were found promising for multiples desirable traits *viz.,* grain quality, grain nutritional and grain yield (**Table 5**). Next to yield, grain type or shape plays major role in the selection of rice variety and their subsequent popularity across the stake holders of rice. The consumer preference for grain shape differs widely according to different geographical locations and customs. Among the white rice, maximum grain length was recorded for the genotype Improved Dokra-dokri whereas minimum grain length was recorded for Khera ghul and Tarunbhog. The presence of diverse grain shapes in experimental material provides more flexibility to develop rice varieties that cater to wide preferences.

Table 4. Promising rice genotypes for grain quality and nutritional traits

S. No.	Trait	Desired value with units (Genotype number)	Name of genotypes
1	HRR%	45% (22) For genotypes with KL >6.6 mm	Dubraj (Red rice), Shri kamal (S:660 I), Luchai (L:246) CR 3856-44-22-2-1-10-1-5 (IR 73963-86-1-5-2-2/CR2324-1), Dubraj 11 (CGR: 12230), Parmal (CGR: 15971), Hawm Jan (Indonesia), Guinata (Thailand), OR 2573-11 (Birupa/ IR 76561-AC-8-8), Lalbasmati (Jammu & Kashmir), Chhattisgarh Zinc Rice-1, IGKV R1 (Rajeshwari), Binirhen (Phillipines), Aruna, Umariya chudi (U: 229), Khatiya pati (CGR : 14230), Hasan Serai (Iran), IC124346, Chhatri (C:54 I), Dokra dokri (CGR : 12126), R 1661-1372-1-601-1 and Kankadiya (K:18 II)
2	HRR%	55% (52) For genotypes with KL <6.6 mm	Maharaji (M:504), Dubraj (D:1251), IC 331668, Kalikhasa (Assam), Kamini Joha (Assam), Mokdo (M:550), Bongcay (Vietnam), Umari (CGR:17451), Selection of Badshahbhog (CGR: 17760), Newara (CGR: 4053), IC 116076 (CGR: 10007), NiiawHawm (Pant nagar), Lonkti monchhi (CGR : 16804), Lua Nhe Den (Thailand), Muchchhan moti (IC 387442), Damrubaba-3 (Farmer's variety), BanthaLuchai (B:2733), Javaphool (J:333), IC390299, Mancha (M:1028) IC41843 (Black rice), IC206615, IC296890, Loktimachhi, IC435091, CR 3969-24-1-2-1-1 (IR 73907-753-2-3/ Pratiksya), IC 460160, Adhan chilpa (A: 701), Laxmibhog (L: 708), Jaldubi, Baihaguda (Red rice), IC 379122, Kodha Phool (Farmer's variety), Dondagi (CGR: 12135), Luchai (L:1099) Badshahbhog (CGR: 10919), Sonagathi (Breeding line), Improved Chepti gurmatiya, Satha Dhan (CGR: 394), Swarna sub-1, Nagbel (CGR: 4003), IC 389838, OR 2487-13 (OR 2076-2/Ashoka228), Dawleuang (China), IC 459147, Jaigundi (J:248), Jira Dhan (J:53), Swarna, IC 388204, CR 3504-12-2-1-1-1-1 (IR 36/Birupa), Bisni and Chhatri (CGR: 669)
3	KLAC	Above 12.00 mm	NONE FOR BASMATI
	ER	Above 1.7 (9)	Selection of Badshahbhog (CGR: 17760), Badshahbhog (CGR: 10919), Swarna, Badshahbhog Selection-1, IC 460160, YNP 7060 (NPG 6/NPG 15), Tarunbhog, Goindi (Farmer's variety) and Keraghul (K:2034)
4	AC%	20 to 25% (7)	CR 3561-3-2-1-1-1-1 (Surendra/Annapurna), Banspatri (B:728), R 1700-2247-1-2313-1, Loktimachhi, *O. latifolia* Swarna sub-1 and IC : 206866
5	PC%	≥10% (28)	Kanak jira, Jaldubi, *O. nivara* (IC301555), *O. nivara* (IC301622), Krishnanjana, *O. sativa* var. *fatua* (IC301558), *O. nivara* (IC301589), Dubraj Selection-1, *O. nivara* (IC301584), Muchchhan moti (IC387442), *O. nivara* (IC301625), IC277830, NPT 14-10 (NPT 29/R 296), Katarni bhog (K: 415 II), Hawm Jan (Indonesia), Sugarkand (CGR: 17213), *O. nivara* (IC 301559), Madhuraj-55, Sonagathi (Breeding line), Aruna, PA 6444, Mokdo (M:550), Badshahbhog Selection-1, Fundri (F:28), Karhani (K : 1276), CR 3856-29-14-2-1-1-7-1 (IR 73963-86-1-5-2-2/CR 2324-1), Ayepyaung (Myanmar) and IC133146
6	ZnC	≥28.0 ppm (20) in polished rice	*O. nivara* (IC301559), *O. nivara* (IC301622), *O. sativa* var. *fatua* (IC 301558), Kanji Local (CGR: 174), IC 435559 Lalmati, IC 135877, Khatiya pati (CGR: 14230), Binirhen (Phillipines), Satha Dhan (CGR: 394), Chanda (IC287), IC 124525, Fara (CGR: 113), *O. nivara* (IC 301547), BanthaLuchai (B:2733), Kekai (K:927 II), IC 449793, Ateya (CGR : 2), Angur guchcha (CGR: 1803) and *O. nivara* (IC 301626)

Maharaji and Dubraj are famous landraces of Chhattisgarh. Maharaji is famous for its medicinal properties *viz.,* post-natal tonic for women (based on farmer's perception) whereas Dubraj is famous for its aromatic short slender grains and cooking quality parameters. Landraces having good grain quality features will be utilized as donors in breeding to develop rice varieties having medicinal properties along with cooking quality.

In the present study, IC435559, IC301559, IC301558, IC388737 and Ateya genotypes showed highest ZnC of 36ppm in brown rice. However, only three genotypes, IC435559, IC301559 and IC301558, noted ≥28 ppm in polished rice. One genotype, *Oryza officinalis,* noted highest iron content (25.04 ppm) in brown rice, however, only 6.7 ppm remained with the polished rice. IC206322 and Guinata noted highest PhC and FC respectively.

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Table 5. Promising top ten rice genotypes containing various desirable traits

S. No.	Genotype	Traits	Name of traits
1	IC 379109	Yield + Nutritional traits	YP, ZnC, FC,ASV, OC
2	IC 331668	Yield + Nutritional traits	YP, HRR, FC, OC
3	Mancha (M:1028)	Yield + Grain Quality + Nutritional traits	YP, HRR, GC, ASV, AC, ZnC, FC, PhC, FC, OC
4	Dubraj (D:1251)	Yield + Grain Quality + Nutritional traits	YP, HRR, ASV, ZnC, PhC
5	Laxmibhog (L:708)	Yield + Grain Quality	YP, HRR, GC, ASV, PhC, FC, OC
6	Piso (CGR: 16109)	Yield + Nutritional traits	YP, ZnC, OC
7	Sonagathi	Yield + Nutritional traits	YP, PC, ZnC, FC
8	Katarnibhog (K:415)	Nutritional traits	PC, ZnC, FC, PhC, FC, OC
9	Kanakjira	Nutritional traits	PC, ZnC, FC, PhC, OC
10	*O. sativa* var *fatua* (IC 301558)	Nutritional traits	PC, ZnC, FC, PhC, FC, OC

Generally, OC ranges from 1 to 2 % in rice bran oil (Patel and Naik, 2004). In this study, highest OC was found in Makado dhan. These landraces having high anti-oxidant properties can be employed in breeding programmes to develop natural energy boosters from rice varieties.

In addition, few rice genotypes were found promising for multiples desirable traits. Two genotypes, *O. officinalis*, *O. latifolia* and IC 460160 with short KL (<4.0 mm) and low KLBR (< 1.9) noted higher level of ZnC (> 25ppm), FeC (>15 ppm), PhC (> 2000 microgram GAE/100g) and FC (> 10000 microgram QAE/100g). Generally, it is rare to get genotypes having promising yield as well as one or multiple nutrients and hence, the above two genotypes are recommended for scale-up studies.

Current study was undertaken to decipher the potential of indigenous and exotic rice genotypes based on their grain quality and nutritional traits. Presence of wide diversity for nutritional and quality traits rice genotypes opens the possibilities to further enhance these traits with the help of traditional and modern breeding programmes. Understanding the relationship among grain characteristics could serve as grain indices for indirect selection of genotypes with high zinc, iron, phenolics and flavonoid. Superior genotypes *viz., Oryza officinalis, Oryza latifolia,* IC435559 , IC135877 ,IC74637, IC301547, IC301589 and IC301625 , IC379109, IC331668, Mancha (M:1028), Dubraj (D:1251) and Laxmibhog (L:708) were identified promising for various grain nutritional and quality traits have enormous potential to enhance the nutritional and quality status thus can be exploited in the development of develop biofortified rice varieties after further validation to combat the malnutrition without any additional cost.

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