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Genetic divergence analysis in indigenous rice (*Oryza sativa* L.) germplasm of bastar

Vipin Kumar Pandey and Sonali Kar

Abstract
The way of life in Bastar continues to be dictated by ritual. Even today, agricultural practices are traditional. Use of wooden ploughs is massive while the number of iron ploughs is stumpy. The same is true of improved rice cultivation. The number of rice varieties and hybrids are truncated while the local landraces and germplasm are privileges. The usage of traditional agricultural implements has lowered the production of agriculture but the sustainability is maintained and crop biodiversity protected. The *kharif* crops grown here are paddy, millets, urad, arhar, jowar and maize. Sustainable agriculture, in terms of food security, rural occupation, and environmentally sustainable technologies such as soil conservation, sustainable natural resource management and biodiversity protection, are essential for holistic rural development.
The research was carried out S.G. College of Agriculture and Research Station, Jagdalpur, Chhattisgarh. The materials was used ninety four local landraces of rice and three standard checks during *Kharif* 2016 in RBD Design, 16 qualitative and 20 quantitative characters observations was recorded. Analysis of variance showed significantly differences for all characters; out of 20, only seven principal components (PCs) exhibited more than 1.00 eigen value, and showed 77.42% variability among the traits studied. The PC1 was related to quality characters while PC2, PC3, PC4, PC5, PC6 and PC7 associated with quantitative traits.

Keywords: Genetic variability, bastar rice research, genetic divergence analysis, paddy diversity in bastar

Introduction
Rice (*Oryza sativa* L.) (2n =24) is the most significant food crops in the world and feeds over half of the over-all population. Rice has played a central role in human nutrition and culture for the past 10,000 years. However, increase in global population, projected to be 9.2 billion by 2030, predicted increase in water scarcity and decrease in arable land, the constant battle against new emerging pathogens and pests and reduced quality due to possible adverse effects from climate change will pose greater challenges for rice breeders and agricultural Scientists (Khush, 2005) [5]. The total area under rice cultivation is globally estimated to be 162 million hectares with annual global production for 2016 at 745.5 million tonnes (495.2 million tonnes, milled basis) (Anonymous, 2016). Rice is life, for most people living in Asia
Rice is one of the most important staple foods for more than half of the world's population and influences the livelihoods and economies of several billion people. (Pandey and Kar, 2017) [8] Being staple food, improving productivity and quality traits of rice always remains crucial. The quality of rice is a complex trait involving many physicochemical properties, and thus it has been a challenge to accurately evaluate quality for selection in rice breeding programs. To accomplish this, crop improvement programmes should necessarily aim at broadening the genetic base of the breeding stock (Vanaja and Babu, 2004) [12]. India has tremendous biodiversity for the landraces of rice. The number of landraces cultivated locally is rapidly replaced by improved varieties, which is causing narrowing of genetic base (Guei, 2000) [4]. Thus, reduced genetic variability underscores the need to collect landraces for ex-situ conservation and to characterize them for future rice breeding programmes based on agro-morphological traits because the evaluation of phenotypic diversity usually reveals important traits of interest to plant breeders. India is a primary centre of origin of rice and has many local landraces available in the remote tribal areas. Most of the land races are not in cultivation while many are lost and few are still cultivated by resource-poor traditional farmers in areas practising subsistence farming. They constitute an excellent reservoir of variability for several traits, resistance to biotic and abiotic stresses, quality and yield traits (Tanksley and Mc-couch, 1997) [11].
Keeping in view the above facts, the present investigation was undertaken to study the nature and degree of genetic divergence among the rice land races grown in Bastar plateau zone of

Chhattisgarh, India which is a hot spot of biodiversity. Outcomes of investigation can be exploited in future for varietal improvement programme of rice.

Materials and Methods

The experiment was carried out at Research cum Instructional Farm, S.G. College of Agriculture and Research Station, Kumhrawand, Jagdalpur, Bastar, Chhattisgarh, India. The experimental materials comprised of ninety-four local landraces of rice and three popular standard checks. The experimental materials were received from rice breeding section of S.G. College of Agriculture and Research Station, Jagdalpur, Bastar, Chhattisgarh. The experiment was conducted during *Kharif* 2016 in an RBD Design to assess the genetic divergence among the ninety-four local landraces of rice (*Oryza sativa* L.) and three popular standard checks namely MTU-1010, Danteshwari and CR-40 (Table 1). The observations on various agro-morphological characters including qualitative and quantitative characters of rice were recorded *viz.* harvest index, grain yield/plant, days to 50% flowering, days to maturity, flag leaf length, flag leaf width, plant height, panicle length, number of effective tillers/plant, total number of grain /panicle, spikelet fertility, test weight, total number of filled grains/panicle, days to first heading, grain breadth, grain length, grain length breadth ratio, kernel breadth, kernel length, kernel length breadth ratio, grain shape, kernel shape. The list of characters along with descriptor is mentioned in (Table 2). The data recorded on ninety-four local landraces of rice and three popular standard checks for different quantitative characters and quality characters were subjected to the statistical analysis *viz.* analysis of variance, Genetic divergence: Principal Component Analysis.

Table 1: List of ninety-four local landraces of rice and three popular standard checks used in the present study.

Entry No.	Genotypes Name	Entry No.	Genotypes Name
1	Rago vati	20	Narial
2	Hiran bako	21	Noni dhan
3	Band kari	22	Kal tut masilo
4	Bakti chudi	23	Kari chudi
5	Ram jeera	24	Bghal mijo
6	Bans koria	25	Bhuku kuda
7	Baria dhan	26	Koog dhan
8	Mayur funda	27	Kapoor sai
9	Lokti machhi	28	Baku dhan
10	Pat dhan	29	Bhata dubraj
11	Surmatia	30	Sagi pareta
12	Sendur senga	31	Haldi ghati
13	Tiki chudi	32	Tama koni
14	Anjani	33	Bhasam patti
15	Kadam phool	34	Dumar phool
16	Sona sari	35	Bode bargi
17	Chepti gurmutiya	36	Kava padi
18	Bhata mokdo	37	Koorlu mundi
19	Kukda mor	38	Anga dhan

Table: Continued…….

Entry No.	Genotypes Name	Entry No.	Genotypes Name
39	Lankeshri	67	Hisya dhan
40	Rami gali	68	Chagdi kaj
41	Bhata gada khuta	69	Dokra mecha
42	Rai kera	70	Barha sal
43	Kurli kabri	71	Kala umari
44	Alti mijo	72	Kakda kdo
45	Alam dhan	73	Bargi dhan
46	Ghaghar dhan	74	Koosum jhopa
47	Mudria	75	Bas koriya
48	Kari khuji	76	Manki dhan
49	Dumar phool	77	Bhata kanai
50	Pharsa phool	78	Bhalu dubraj
51	Hathi panjra	79	Baso mati
52	Karmari bhog	80	Rang gada khuta
53	Godavari	81	Ghdva phool
54	Kari gudi	82	Son pari
55	Dogar kanri	83	Mundra chudi
56	Bhanvar gedi	84	Mehar dhan
57	Machi dhan	85	Kormel
58	Dhabda dhan	86	Gogal sathka
59	Kura dhan	87	Dogar kabri
60	Bhans path	88	Lal makdo
61	Barangi	89	Moha dhan
62	Goyadi	90	Laycha
63	Ram bhog	91	Godandi

64	Aajan dhan	92	Hare krishna
65	Masur lochia	93	Tagan dhan
66	Aasan chudi	94	Machhali poti
CH1	MTU1010	CH3	CR40
CH2	Danteshwari		

Note: CH=check variety.

Table 2: Description of agro-morphological characters.

S. No.	Characters	Growth stage	Categories or type	Symbols
1.	Basal leaf sheath Colour	Vegetative	Green	1
			Light purple	2
			Purple lines	3
			Uniform purple	4
2.	Auricle colour	Late vegetative	Absent (no auricles)	1
			Whitish	2
			Yellowish green	3
			Purple	4
			Light purple	5
			Purple lines	6
3.	Leaf blade Colour	Late vegetative	Pale green	1
			Green	2
			Dark green	3
			Purple tips	4
			Purple margin	5
			Purple blotch	6
			Purple	7
4.	Ligule shape	Late vegetative	Acute to acuminate	1
			2-cleft	2
			Truncate	3
5.	Flag leaf angle	Reproductive	Erect	1
			Semi-erect	3
			Horizontal	5
			Drooping	7
6.	Plant height (cm)	Reproductive	Very short (<91 cm)	1
			Short (91-110 cm)	3
			Medium (111-130 cm)	5
			Long (131-150 cm)	7
			Very long (>150 cm)	9
7.	Flag leaf length (cm)	Reproductive	Short (<30 cm)	3
			Med. (30-45 cm)	5
			Long (>45 cm)	7
8.	Flag leaf width (cm)	Reproductive	Narrow (<1 cm)	3
			blade Medium (1-2 cm)	5
			Broad (>2 cm)	7
9.	Date to 50% Flowering	Reproductive	Very early (<71 days)	1
			Early (71-90 days)	3
			Medium (91-110 days)	5
			Late (111-130 days)	7
			Very late (> 131 days)	9

Table 2: Continued……….

S. No	Characters	Growth stage	Categories or type	Symbols
10.	Stigma Colour	Reproductive	White	1
			Light green	2
			Yellow	3
			Light purple	4
			Purple	5
11.	Apiculus Colour	At dough stage	White	1
			Straw	2
			Brown	3
			Red	4
			Red apex	5
			Purple	6
			Purple apex	7
12.	Awning	Flowering to maturity	Absent	0
			Present	1
13.	Awn Colour	At maturity	Straw	1
			Gold	2

			Brown	3
			Red	4
			Purple	5
			Black	6
14.	Awn length	At maturity	None (awnless)	0
			Very short (<5 mm)	1
			Short (~8 mm)	3
			Intermediate (~15 mm)	5
			Long (~30 mm)	7
			Very long (>40 mm)	9
15.	Date to maturity (days)	Maturity	Very early (<100 days)	1
			Early (101-120 days)	3
			Medium (121-140 days)	5
			Late (141-160 days)	7
			Very late (>160 days)	9
16.	Panicle length (cm)	Maturity	Very short (<16cm)	1
			Short (16-20 cm)	3
			Medium (21-25cm)	5
			Long (26-30 cm)	7
			Very long (>30 cm)	9

Result and Discussion

The outcomes of analysis of variance showed that the mean sum of squares due to the genotypes were highly significant for various quantitative and quality characters studied i.e. days to 50% flowering, days to maturity, days to first heading, number of effective tillers per plant, plant height (cm), flag leaf length, flag leaf width, panicle length (cm), total number of grains per panicle, number of filled spikelets per panicle, spikelet fertility percentage (%),test weight (g), grain yield per plant (g), harvest index (%), grain length (mm), grain breadth (mm), grain length: breadth ratio, kernel length (mm), kernel breadth (mm), kernel length: breadth ratio (Pandey and Kar, 2018) [9]. The analysis of variance for quality and quantitative character and morphological variation is presented in (Table 3, Table 4 and fig.1 to 6) respectively.

In the present study, PCA was performed for twenty agro morphological traits in local landraces of rice. As per the criteria set by (Brejda *et al*., 2000) [3] the PC with eigen values >1 and which explained at least 5% of the variation in the data were considered in the present study. The PC with higher eigen values and variables which had high factor loading was considered as best representative of system attributes. Out of 20, only seven principal components (PCs) exhibited more than 1.00 eigen value, and showed about 77.42% variability among the traits studied. So, these 7 PCs were given due importance for further explanation. The PC1 showed 20.76% while, PC2, PC3, PC4, PC5, PC6 and PC7 exhibited 16.47%, 12.51%, 10.18%, 7.17%, 5.83% and 5.49% variability respectively among the genotypes for the traits under study (Table 5). The first PC accounts for as much of the variability in the data as possible, and each succeeding component accounts for as much of the remaining variability as possible. Component matrix revealed that the PC1 was mostly related to quality characters while PC2, PC3, PC4, PC5, PC6 and PC7 mostly associated with yield related traits. So, a good breeding programme can be initiated by selecting the genotypes from PC1 for quality aspect and for yield related traits genotypes from PC2, PC3, PC4, PC5 and PC6 can be selected. Top 10 principal component scores (PC scores) for all the genotypes were estimated in seven principal components. These scores can be utilized to propose precise selection indices whose intensity can be decided by variability explained by each of the principal component. High PC score for a particular accession in a particular component denotes high values for the variables in that particular accession. So, genotypes showing top scores in their respective components can be selected for breeding programmes in association with the traits showing high factor loadings in their respective components. These results are in agreement with the findings of earlier workers (Sinha and Mishra, 2013; Nachimuthu *et al*., 2014; Musyoki *et al*., 2015; Baloch *et al*., 2016) [10, 7, 6, 2].

Fig 1: Basal leaf sheath colour

Fig 2: Ligule shape.

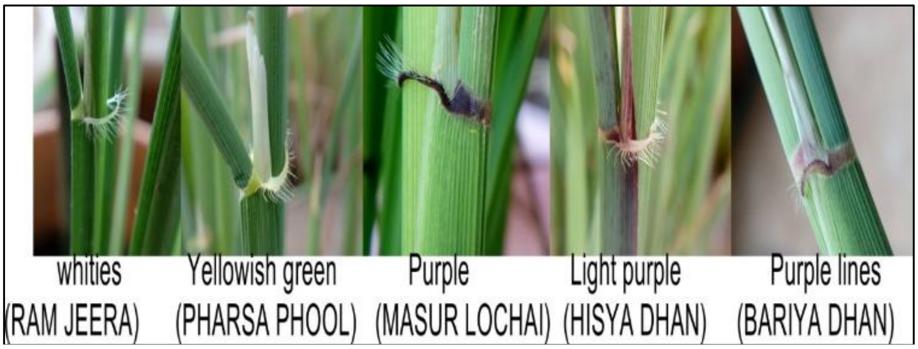

Fig 3: Auricle

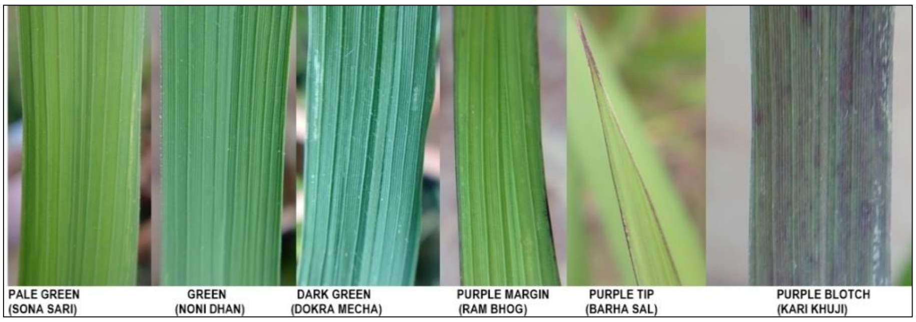

Fig 4: Leaf blade colour

Fig 5: Flag leaf angle.

Fig 6: Apiculus colour.

Table 3: Analysis of variance for quality traits related to yield.

Source of Variation	Degree of Freedom	Mean squares					
		GB	GL	GLBR	KB	KL	KLBR
RSS	1	164.42	614.24	148.09	98.04	392.66	102.95
TMSS	96	0.28	2.11	0.58	0.20	1.54	0.55
ErSS	96	0.10	0.07	0.13	0.07	0.02	0.10
F cal.		2.82**	32.07**	4.36**	2.81**	77.62**	5.38**

*= significant at 5%, **= significant at 1% p value of 0.1 level of significance DFn 96 and DFd 96 p=1.0000 p value of 0.5 level of significance DFn 96 and DFd 96 p=0.9996 GB=grain breadth, GL= grain length, GLGR=grain length breadth ratio, KB=kernel breadth, KL=kernel length, KLBR= kernel length breadth ratio.

Table 4: Analysis of variance for quantitative traits.

SOV	DF	Mean squares						
		TNFGP	TNGP	SF	PH	NETH	PL	GYP
RSS	1	5041.86	23289.56	14163.08	9.93	0.4250	9.84	7.56
TMSS	96	1212.23	1536.46	38.61	487.63	4.86	8.26	55.13
Er.SS	96	344.12	1.17	0.69	13.82	0.35	1.57	8.43
F cal.		3.52**	1308.13**	56.19**	35.28**	13.74**	5.25**	6.54**

Table: 4 continued………

SOV	DF	Mean squares						
		HI	TW	FLL	FLW	DTF	DTFH	DTM
RSS	1	6203.14	6931.30	3.54	0.003	424.58	19002.06	0.05
TMSS	96	120.20	60.11	52.74	0.871	175.09	113.42	177.03
ErSS	96	1.91	1.74	7.22	0.006	52.14	2.61	13.46
F cal.		63.03**	34.50**	7.30**	153.594**	3.36**	43.43**	13.15**

*= significant at 5%, **= significant at 1% p value of 0.1 level of significance DFn 96 and DFd 96 p=1.0000 p value of 0.5 level of significance DFn 96 and DFd 96 p=0.9996

HI=Harvest Index, GYP=grain yield/plant, DTF= days to 50% flowering, DTM =days to maturity, FLL=flag leaf length, FLW=flag leaf width, PH= plant height, PL=panicle length, NETH= number of effective tillers/plant, TNGP= total number of grain /panicle, SF spikelet fertility, TW=test weight, TNFGP=total number of filled grains/panicle, DTFH=days to first heading.

Table 5: Principal component analysis of 20 agro-morphological traits for 97 genotypes of rice.

	Components						
	PC1	PC2	PC3	PC4	PC5	PC6	PC7
TNFGP	-0.056	0.209	0.473	-0.218	0.060	-0.326	-0.052
TNGP	-0.083	0.228	0.455	-0.144	0.065	-0.261	-0.228
SF	0.085	-0.003	0.085	-0.202	0.161	-0.329	0.616
PH	0.191	0.240	0.058	-0.166	0.390	0.191	0.165
NETH	0.086	-0.110	0.264	-0.057	-0.339	0.403	0.370
PL	0.021	0.075	0.092	-0.120	0.605	0.254	-0.076
GYP	0.102	0.277	0.185	-0.354	-0.289	0.207	-0.005
HI	0.027	-0.013	-0.031	-0.383	-0.370	-0.035	-0.384
TW	0.009	0.402	-0.346	-0.134	0.001	0.015	0.041
FLL	-0.042	-0.004	0.204	-0.128	0.056	0.612	-0.094
FLW	-0.055	0.208	-0.100	-0.122	-0.252	0.016	0.420
DTF	0.124	0.369	0.082	0.423	-0.052	0.061	-0.018
DTFH	0.123	0.338	0.094	0.430	-0.030	0.085	-0.095
DTM	0.154	0.210	0.247	0.327	-0.198	-0.084	0.083
GB	-0.319	0.311	-0.222	-0.053	0.027	0.065	-0.007
GL	0.342	0.182	-0.253	-0.082	0.015	-0.003	0.032
GLBR	0.446	-0.099	-0.042	-0.011	0.025	-0.057	0.002
KB	-0.360	0.268	-0.199	-0.065	-0.028	-0.016	0.020
KL	0.342	0.190	-0.201	-0.187	-0.033	-0.087	-0.174
KLBR	0.451	-0.075	-0.043	-0.071	-0.003	-0.035	-0.116
Eigenvalue	4.151	3.295	2.502	2.037	1.433	1.165	1.097
Variability (%)	20.755	16.474	12.511	10.184	7.166	5.826	5.487
Cumulative %	20.755	37.230	49.741	59.925	67.090	72.916	78.403

HI=Harvest Index, GYP=grain yield/plant, DTF= days to 50%flowering, DTM =days to maturity, FLL=flag leaf length, FLW=flag leaf width, PH= plant height, PL=panicle length, NETH= no. of effective tillers/plant, TNGP= total no. of grain /panicle, SF spikelet fertility, TW=test weight, TNFGP=total no. of filled grains/panicle, DTFH=date of first heading, GB=grain breadth, GL= grain length, GLGR=grain length breadth ratio, KB=kernel breadth, KL=kernel length, KLBR= kernel length breadth ratio.

Note: Values in bold represent highly weighted factors in respective PC.

Conclusion

Component matrix revealed that the PC1 was mostly related to quality characters while PC2, PC3, PC4, PC5, PC6 and PC7 mostly associated with yield related traits. So, a good breeding programme can be initiated by selecting the genotypes from PC1 for quality aspect and for yield related traits genotypes from PC2, PC3, PC4, PC5 and PC6 can be selected.

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