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Research Article

Characterization of morpho-phenological traits in the traditional landraces of rice

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Abstract

The landraces of rice provide a wide range of genetic variations and environmental adaptation and act as excellent genetic resources for crop improvement. Natural germplasm that has been maintained through conservation is in desperate need of rigorous investigation in order to uncover new genes or alleles to introduce into rice breeding programmes. Given this context, an investigation was done to determine the degree of genetic divergence and variability across 31 rice landraces for various productivity, physiological, and grain quality traits. On evaluation of the mean performance of landraces and the influence of characters in genetic divergence resulted in the identification of better landraces *viz*., Vellaikuruvikar, Karupu Kavuni, Kichidi Samba and Athur Kichadi which are better for both grain yield and quality traits that can be used to create better recombinants, by hybridization. These gene pools could be used in selective breeding to significantly enhance the agronomic characters. Out of 20 traits that were investigated,15 traits *viz*., height of the plant, productive tillers per plant, length of panicle, spikelets per panicle, filled grains per panicle, grain yield per plant, seedling root to shoot ratio, harvest index, head rice recovery, length of the kernel, length to breadth ratio of kernel, breadth of kernel after cooking, length to breadth ratio of kernel after cooking, gelatinization temperature and aroma were noted for high heritability and genetic advancement suggesting that additive gene action predominates, there by opening up a wide range of opportunities for these traits to be improved through simple phenotypic selection.

Keywords: Rice, landraces, GCV, PCV, heritability, PCA

INTRODUCTION

Landraces offer a vast wealth of genetic resources for crop breeding and development programmes, making agro-morphological characterisation the most essential and valuable. Although the green revolution significantly increased food grain production and helped India to reach self-sufficiency (Srivastava and Jaffe, 1993), high yielding varieties, which are the foundation of the green revolution, have indirectly accelerated the extinction of rice landraces and wild varieties (Fowler and Moony 1990). Currently, only high yielding cultivars are used to cultivate more than 90% of the rice area, indicating clearly, that the landraces are vanishing quickly (Matson *et al*., 1997). It is impossible to ignore the significance of landraces and wild types in the agricultural system because they are the natural source of favourable genes for disease and pest tolerance. (Holden *et al.,* 1993).

Morphological characterization of natural plant genetic materials like landraces, wild relatives and their utilization in breeding programme are essential to avoid losing or extinction of these immense valuable resources. Hence, there is an urgent need to explore and conserve these landraces of rice (Sinha and Mishra, 2012). Landraces are the irreplaceable source of highly co-adapted germplasm, since they have high genetic variability and the best environmental adaptability (Lanteri and Barcaccia, 2006). The limited genetic base is typically cited as the primary cause of both the stagnation of genetic advancements in rice breeding programmes and the global increase in pest and disease susceptibilities in contemporary rice cultivars (Castro *et al.,* 1999). Since 1960s, improved rice cultivars have been successfully bred, which has increased rice output but forced many landrace varieties to be replaced by a small number of improved cultivars. Thus, the sustainability of rice landraces has been impacted by a gradual but continuing loss of genetic diversity (Chaudhary *et al.,* 2004). A key focus of current rice improvement efforts is maintaining rice landraces and using them for genetic improvement (Joshi and Witcombe, 2003).

Hence, the main objectives of the present study was to characterize the 31 traditional landraces collected from different parts of Southern India using IPGRI descriptors, (1983) for eight productive, two physiological and ten quality traits to provide useful information to facilitate the choice of genitors for rice breeding programmes.

MATERIALS AND METHODS

The present experiment was carried out at the Western farm of Pandit Jawaharlal Nehru College of Agriculture and Research Institute, Karaikal during the year 2017-2018 of *Rabi*. All landraces were transplanted and spaced at 30 × 20 cm apart in three replications using a randomised complete block design (RCBD) (**Table 1**).

Table 1. Details of landraces utilized for variability study

S.No.	Name	Source	Origin
1	Athur kichadi	Athirangam – Thiruthuraipoondi	Tamil Nadu
2	Bhutnath	PAJANCOA & RI - Karaikal	West Bengal
3	Garudan samba	Athirangam – Thiruthuraipoondi	Tamil Nadu
4	Illupai poo samba	Athirangam – Thiruthuraipoondi	Tamil Nadu
5	Jeeraga samba	Athirangam – Thiruthuraipoondi	Tamil Nadu
6	Kalanamaku	PAJANCOA & RI -Karaikal	Uttar Pradesh
7	Karupu kavuni	Athirangam – Thiruthuraipoondi	Tamil Nadu
8	Karuthakar	Athirangam – Thiruthuraipoondi	Tamil Nadu
9	Kullakar	Athirangam – Thiruthuraipoondi	Tamil Nadu
10	Kottara samba	Ulunthoor Pettai – Saradha Mut	Tamil Nadu
11	Kichili samba	Ulunthoor Pettai – Saradha Mut	Tamil Nadu
12	Kuzhiyadichan	Athirangam – Thiruthuraipoondi	Tamil Nadu
13	Kaivarai samba	Ulunthoor Pettai – Saradha Mut	Tamil Nadu
14	Kallurunadai	Athirangam – Thiruthuraipoondi	Tamil Nadu
15	Kantha sala	Ulunthoor Pettai – Saradha Mut	Tamil Nadu
16	Milagu samba	Athirangam – Thiruthuraipoondi	Tamil Nadu
17	Oswa kuthalai	PAJANCOA & RI -Karaikal	Andhra Pradesh
18	Panangattu kudavazhai	Ulunthoor Pettai – Saradha Mut	Tamil Nadu
19	Perunkar	Ulunthoor Pettai – Saradha Mut	Tamil Nadu
20	Pokkali	PAJANCOA & RI -Karaikal	Kerala
21	Sigappu kavuni	Athirangam – Thiruthuraipoondi	Tamil Nadu
22	Semuli samba	Athirangam – Thiruthuraipoondi	Tamil Nadu
23	Selam sanna	Athirangam – Thiruthuraipoondi	Tamil Nadu
24	Sandikar	Athirangam – Thiruthuraipoondi	Tamil Nadu
25	Suwarna masuri	Athirangam – Thiruthuraipoondi	Andhra Pradesh
26	Surakuruvai	Athirangam – Thiruthuraipoondi	Tamil Nadu
27	Singinikar	Athirangam – Thiruthuraipoondi	Tamil Nadu
28	Thengai poo samba	Athirangam – Thiruthuraipoondi	Tamil Nadu
29	Vadan samba	Athirangam – Thiruthuraipoondi	Tamil Nadu
30	Vasanai jeeraga samba	Athirangam – Thiruthuraipoondi	Tamil Nadu
31	Vellaikuruvikar	PAJANCOA & RI -Karaikal	Tamil Nadu

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Recommended agronomic practices for raising a healthy crop were followed throughout the experiment. Data were collected for productive, physiological and grain quality attributes. The productive traits observed were days to flowering, height of the plant, productive tillers per plant, length of panicle, spikelets per panicle, spikelets fertility percentage, filled grains per panicle, grain yield per plant. The physiological traits observed were the seedling root to shoot ratio and harvest index. The grain quality traits observed were hulling percentage, head rice recovery, length of the kernel, length to breadth ratio of kernel, breadth of the kernel, length of the kernel after cooking, breadth of kernel after cooking, length and breadth ratio of kernel after cooking, gelatinization temperature and aroma. The aroma was assessed as per the methodology of Bhonsle and Sellapan (2010).

In order to assess the variability criteria and diversity components, observations were made on five randomly chosen plants. The mean values were then used to perform statistical analysis, including analysis of variance, genotypic and phenotypic coefficients of variation, heritability, genetic advance as percentage of mean (Dutta *et al.,* 2013) and D^2 statistics using UPGMA (Mahalanobis, 1936) method and PCA (Rao, 1952) using statistical packages of IBM SPSS software.

RESULTS AND DISCUSSION

In this study, the variance analysis showed that there were substantial variations between all of the investigated landraces, showing that there was a lot of diversity. At a significance level of 0.01 probabililty, the analysis of variance revealed that the landraces varied significantly for each character (**Table 2**).

High estimates of phenotypic and genotypic coefficients of variation were observed for productive tillers / plant, spikelets / panicle, filled grains / panicle, grain yield/ plant, seedling root to shoot ratio, harvest index, head rice recovery, length of the kernel, length and breadth ratio of kernel, gelatinization temperature and aroma. Similar results were observed by Dutta *et al.* (2013) for productive tillers/ plant and grain yield /plant; Subbaiah *et al.* (2011) for filled grains/panicle; Bisne *et al.* (2009) for spikelets /panicle; Dhurai *et al.* (2014) and Roy *et al.* (2009) for seedling root to shoot ratio; and Shrivastava *et al.* (2014) for head rice recovery.

For the traits hulling percentage, breadth of kernel after cooking, and length and breadth ratio of kernel after cooking, a higher phenotypic coefficient of variation and a medium genotypic coefficient of variation were found. Asish *et al.* (2007) findings, in contrast, indicated

Table 2. Analysis of variance for 20 characters in 31 traditional landraces of rice

Source	Replication	Landraces	Error
Degrees of freedom	2	30	60
	Mean sum of squares		
Days to flowering	9.59	82.06**	3.41
Height of the Plant	721.87	2444.18**	321.76
Productive tillers/ plant	28.18	61.17**	20.05
Length of the panicle	3.40	28.92**	1.30
Spikelets/ panicle	250.74	5308.32**	132.31
Filled grains/ panicle	68.38	4915.30**	119.55
Spikelets fertility percentage	18.70	24.05**	8.23
Grain yield/ plant	2.53	255.03**	8.78
Root to shoot ratio	0.0016	0.51**	0.01
Harvest index	0.002	0.03**	0.002
Hulling percentage	241.29	507.15**	98.90
Head rice recovery	309.37	666.43**	102.64
Length of the Kernel	0.22	1.75**	0.10
Breadth of the Kernel	0.004	0.69**	0.17
Length and breadth ratio of Kernel	0.24	1.16**	0.08
Length of Kernel after cooking	0.21	2.85**	0.33
Breadth of the Kernel after cooking	0.48	1.76**	0.29
Length breadth ratio of Kernel after Cooking	0.15	0.71**	0.12
Gelatinization temperature	0.001	3.03**	0.01
Aroma	0.01	0.82**	0.01

**Significant at 1%

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a moderate coefficient of variation at phenotypic and genotypic levels. Height of the plant, length of panicle, length of kernel, and length of kernel after cooking all showed moderate phenotypic and genotypic coefficients of variation.

This agrees with Dhanwani *et al.* (2013) observations for height of plant, length of kernel, and length of kernel after cooking; and Dutta *et al.* (2013) observations for panicle length. For the traits, days to flowering and spikelet's fertility, low estimates of coefficients of variation at phenotypic and genotypic levels were found. For days to flowering, Vanisree *et al.* (2015) noted comparable outcomes.

All the characters under the study were found to have higher phenotypic coefficient of variation (PCV) than the genotypic coefficient of variation (GCV) (**Table 3**). It was observed that the difference between PCV and GCV was found to be meagre for the following traits *viz.,* days to flowering, plant height, length of the panicle, filled grains per panicle, spikelet fertility percentage, root to shoot ratio, length of the kernel, gelatinization temperature and aroma which indicating that the environment had less impact on how characters were expressed or that landraces were less sensitive to the environment, which is consistent with the findings of Sravan *et al*. (2012) and Karim *et al*. (2007).

The findings from our study are consistent with those from earlier research (Hossain *et al*., 2015), indicating that environmental influence does not significantly affect how phenotypic traits are expressed. It implies that traits that are less influenced by the environment (Karad *et al*., 2008) and that can be improved by selection based on phenotype rather than genotype. Studies also showed that in order to create high yielding varieties through hybridization and selection, landraces with high GCV of yield-attributing characteristics are crucial. High GCV alone would not indicate the true selection value and hence, heritability estimates may also be considered for an effective selection. High heritability represents

Table 3. Assessment of variability parameters for 20 different traits of 31 landraces

S. No.	Characters	Range	Variance		Co efficient of variation (%)		Heritability in broad sense (Percentage)	Genetic advance as percentage of mean
			Phenotypic	Genotypic	Phenotypic	Genotypic		
1.	Days to flowering	90.33 - 108.33	29.62	26.21	5.61	5.28	88.48	10.24
2.	Height of the Plant	69.47 - 185.00	804.31	763.80	19.33	18.83	94.96	37.81
3.	Productive tillers/ plant	7.67 - 25.80	31.09	27.42	30.61	28.74	88.17	55.60
4.	Length of panicle	13.50 – 26.40	10.51	9.20	14.57	13.63	87.54	26.28
5.	Spikelets/ panicle	28.40 - 221.13	1857.64	1725.33	35.20	33.92	92.88	67.34
6.	Filled grains/ panicle	25.60 - 214.90	1718.13	1598.59	35.76	34.49	93.04	68.54
7.	Spikelets fertility percentage	87.05 - 97.91	13.51	5.27	3.94	2.46	39.01	3.16
8.	Grain yield/ plant	11.96 - 38.14	90.86	82.02	42.39	40.39	90.34	78.89
9.	Root to shoot ratio	1.32 - 3.12	0.18	0.16	22.37	21.47	92.10	42.45
10.	Harvest index	0.28 - 0.68	0.01	0.01	25.69	23.87	86.35	45.71
11.	Hulling percentage	38.71 – 89.38	234.98	136.08	22.92	17.44	57.91	27.35
12.	Head rice recovery	33.18 - 82.57	290.57	187.92	30.56	24.57	64.67	40.71
13.	Length of the Kernel	4.63 – 8.06	0.65	0.55	12.23	11.23	84.36	21.25
14.	Breadth of the Kernel	1.45 - 3.55	0.34	0.17	23.56	16.64	49.85	24.20
15.	Length and breadth ratio of Kernel	1.91 - 5.01	0,44	0.36	23.03	20.82	81.71	38.77
16.	Length of Kernel after cooking	6.40 - 10.97	1.17	0.84	12.91	10.94	71.79	19.09
17.	Breadth of the Kernel after cooking	2.58 - 5.48	0.78	0.49	23.01	18.20	62.56	29.66
18.	Length breadth ratio of Kernel after Cooking	1.53 - 3.29	0.32	0.19	24.82	19.34	60.72	31.04
19.	Gelatinization temperature	1.71 - 4.71	1.02	1.01	27.84	27.65	98.62	56.57
20.	Aroma	1.00 - 3.00	0.27	0.26	26.80	26.41	97.08	53.61

the strong reflection of genotype on phenotype. Consequently, the superiority of the selected plants is transferred to the next generation. High genetic advance and heritability are indirect indicators of the relative importance of additive gene action on the corresponding traits (Johnson *et al.,* 1955). So, in addition to evaluating the effectiveness of phenotypic selection, studying heritability in conjunction with genetic advancement will become beneficial.

With this background, high heritability and genetic advance were observed for 15 characters *viz.,* height of the plant, productive tillers/ plant, length of panicle, spikelets/panicle, filled grains/panicle, grain yield/plant, seedling root to shoot ratio, harvest index, head rice recovery, length of kernel, length to breadth ratio of kernel, breadth of kernel after cooking, length to breadth ratio of kernel after cooking, gelatinization temperature and aroma, showing that additive gene activity is predominant and is anticipated to be responsive to direct selection. These findings are congruent with those of Yadav *et al.* (2009) for height of the plant; gelatinization temperature, productive tillers/plant, filled grains/panicle, length and breadth of kernel; breadth of kernel after cooking (Subbaiah *et al.,* 2011); productive tillers/ plant, spikelets/ panicle (Nandan *et al.,* 2010); productive tillers/plant, length of panicle and spikelets/panicle (Kumar *et al.,* 2014); grain yield/ plant (Dhanwani *et al.,* 2013); seedling root to shoot ratio (Haider *et al*., 2012); harvest index (Kumar *et al.,* 2015); head rice recovery (Asish *et al.,* 2007); and length to breadth ratio of kernel after cooking (Manonmani *et al*., 2010).

Days to flowering and length of kernel after cooking showed high heritabilities with modest genetic advance, showing a preponderance of non-additive gene action as reported earlier by Ketan and Sarkar (2014), Kumar *et al.* (2015), and Madakemohekar *et al.* (2014). Such a phenomenon indicates that the interplay of hereditary and environmental factors largely control these features. Purely genotype-based selection is not feasible in this situation.

For hulling percentage and breadth of kernel, moderate heritability and high genetic advance were found. This is in contrast to Madakemohekar *et al.* (2014) findings, which showed high heritability with low genetic advance. The outcome of Karim *et al.* (2007), which demonstrated that selection for such a characteristic could not bring about desired modifications over the population mean, is extremely consistent with this. Spikelet fertility as a percentage was shown to have moderate heritability and low genetic advancement. The findings of Karim *et al.* (2007), which revealed modest heritability and genetic advance as percentage of mean, disagree with this.

Therefore, it is inferred that the 15 characters, exhibited higher heritability and genetic advance have additive gene action and can respond very well to selection. Therefore, the pedigree method of breeding may be used to improve these traits genetically. Both additive and non-additive gene action affected the remaining five characteristics. As a result, heterosis breeding is necessary to improve these traits, and pedigree breeding may be pursued after one or two rounds of recurrent selection.

According to the UPGMA method of divergence, 31 landraces were grouped into ten Clusters (**Table 4**). Among these Clusters, I comprised of 10 landraces. The landraces with different geographical origins fell with the same Cluster. These revealed that landraces of the same states were grouped into different Clusters. The Clustering pattern of landraces suggested that genetic variety may not always be correlated with geographic diversity, because Cluster I had landraces with origins in Tamil Nadu, West Bengal, and Andhra Pradesh, Both Fatema *et al.* (2011) and Sandhya *et al*. (2012) also reported evidences of genetic divergence that did not match to regional diversity (Dhurai *et al.,* 2014). Such a convergence of landraces from several geographic regions into a single Cluster may have resulted via differential selection or genetic drift under diverse environmental conditions within the same geographical origin (Bansal *et al.,* 1999). Therefore, changes in adaptability, selection criteria, selection pressure, and environmental variables could account for the type of genetic diversity reported among landraces with the same geographic origin (Maurya and Singh, 1977).

Cluster II consisted of three landraces *viz.,* Kantha Sala, Panangattu Kudavazhai and Sigappu Kavuni. These three landraces had similar characters such as medium bold, light red coloured grain. Cluster III consisted of two landraces *viz.,* Semuli Samba and Kalanamak. These two landraces contained closely related traits for height of the plant and productive tillers/plant. Kottara Samba, Kuzhiyadichan, Vasanai Jeeraga Samba, and Perunkar were similar in terms of high spikelet fertility percentage, panicle length, number of grains per panicle and medium slender grains. Hence, these landraces were grouped in Cluster IV. Cluster X consists of only one genotype *viz.,* Pokkali (from Kerala). Geographical obstacles that hinder the gene flow of intense natural or human selection for various adaptive gene complexes cause solitary Clusters to emerge.

Cluster V had three landraces namely, Sandikar, Kaivarai Samba and Surakuruvai. Kichidi Samba, Athur Kichadi, in Cluster VI. Cluster VII had Kullakar, Suwarna Masuri. Cluster VIII Jeeraga Samba, Vadan Samba ; Illupai Poo Samba and Karuthakar in Cluster IX. Higher degree of divergence between Clusters II and IX indicated a large diversity between these Clusters that may be exploited in the hybridization programme for the improvement of rice, according to the relative divergence of each Cluster from other Clusters. Wide diversity that appears to be

Table 4. Distribution of landraces to different Clusters using Tocher's method

S.No.	Total number of landraces	Landraces	Origin
I	10	Salem Samba	Tamil Nadu
		Thengai Poo Samba	Tamil Nadu
		Vellai Kuruvikar	Tamil Nadu
		Bhutnath	West Bengal
		Karudan Samba	Tamil Nadu
		Milagu Samba	Tamil Nadu
		Singinikar	Tamil Nadu
		Oswa Kuthalai	Andhra Pradesh
		Karupa Kavani	Tamil Nadu
		Kallurundai	Tamil Nadu
II	3	Kantha Sala	Tamil Nadu
		Panangatti Kudavazhai	Tamil Nadu
		Sigappu Kavuni	Tamil Nadu
III	2	Kalanamaku	Uttar Pradesh
		Semmuli Samba	Tamil Nadu
IV	4	Kottara Samba	Tamil Nadu
		Kuzhiyadichan	Tamil Nadu
		Vasanai Jeeraga Samba	Tamil Nadu
		Perunkar	Tamil Nadu
V	3	Sandikar	Tamil Nadu
		Kaivarai Samba	Tamil Nadu
		Surakuruvai	Tamil Nadu
VI	2	Kichidi Samba	Tamil Nadu
		Athur Kichadi	Tamil Nadu
VII	2	Kullakar	Tamil Nadu
		Suwarna Masuri	Andhra Pradesh
VIII	2	Jeeraga Samba	Tamil Nadu
		Vadan Samba	Tamil Nadu
IX	2	Illupai Poo Samba	Tamil Nadu
		Karuthakar	Tamil Nadu
X	1	Pokkali	Kerala

produced by very diverse landraces aids in subsequent selection for genetic improvement (Garg *et al.,* 2011). High heterosis or favourable transgressive segregants may results by hybridization from the landraces within the range of compatibility of those Clusters, which would be advantageous for genetic improvement.

The landracess *viz.,* Selam Samba, Thengai Poo Samba, Vellaikuruvikar, Bhutnath, Karudan Samba, Milagu Samba, Singinikar, Oswa Kuthalai, Karupu Kavuni and Kallurundai in Cluster I, exhibited maximum intra-Cluster distance, indicating the existence of wide genetic divergence among the constituent landraces in it (**Table 5**). The high degree of divergence among the landraces within a Cluster would produce more segregating breeding materials and selection within such Cluster may be executed based on the maximum mean value for the desirable characters.

Among the different traits examined, the gelatinization temperature contributed the largest to genetic diversity followed by grain yield/plant, aroma, root to shoot ratio, height of the plant, length of kernel and length to breadth ratio of kernel. In the present study, among ten Clusters, Cluster IX was found to be superior since it recorded the highest Cluster mean value for the traits *viz.,* length of panicle, length of kernel after cooking, length of kernel, gelatinization temperature and length to breadth ratio after cooking and Cluster X for hulling percentage and head rice recovery. However, Cluster VII was superior

Table 5. Average intra and inter Cluster by D^2 values

Cluster Number	I	II	III	IV	V	VI	VII	VIII	IX	X
I	333.64 (18.26)	937.38 (30.61)	783.18 (27.98)	357.95 (18.91)	640.41 (25.30)	332.67 (18.23)	505.57 (22.48)	641.76 (25.33)	474.49 (21.78)	408.89 (20.22)
II		246.96 (15.71)	341.71 (18.48)	944.64 (30.73)	234.96 (15.32)	684.77 (26.16)	1046.56 (32.35)	447.33 (21.15)	1300.08 (36.05)	732.58 (27.06)
III			118.21 (10.87)	735.79 (27.12)	248.79 (15.77)	687.62 (26.22)	774.10 (27.82)	267.93 (16.36)	860.96 (29.34)	481.07 (21.93)
IV				327.91 (18.10)	658.63 (25.66)	323.45 (17.98)	634.80 (25.19)	572.04 (23.91)	319.16 (17.86)	480.82 (21.92)
V					175.49 (13.24)	515.67 (22.70)	697.98 (26.41)	369.12 (19.21)	907.27 (30.12)	494.39 (22.23)
VI						177.59 (13.32)	486.55 (22.05)	489.16 (22.11)	555.08 (23.56)	512.41 (22.63)
VII							235.12 (15.33)	686.44 (26.20)	678.91 (26.05)	568.84 (23.85)
VIII								271.58 (16.48)	684.29 (26.15)	644.95 (25.39)
IX									297.90 (17.26)	544.99 (23.34)
X										0.00 (0.00)

Intra Cluster divergence: diagonal values; Inter Cluster divergence: off – diagonal values D values : values in parenthesis

for grain yield/ plant and harvest index while, Cluster VIII for spikelets/panicle, filled grains/panicle and breadth of kernel; Cluster V for days to flowering and Cluster VI for productive tillers/ plant and aroma; Cluster IV for height of the plant and length to breadth ratio, Cluster III for spikelet fertility percentage, Cluster II for breadth of kernel after cooking and Cluster I for root to shoot ratio. Thus involving the landraces of these Clusters, as parents would throw a wide range of variability which could be selected for these characters.

The genetic diversity among landraces was also convincingly demonstrated using principal component analysis (PCA) (**Table 6**). It assesses the significant characters that have a stronger influence on the total variables, and each appropriate vector's coefficient indicates the extent to which each original variable contributes to each major component (Sanni *et al.,* 2008).

The 31 landraces of rice were subjected to principal component analysis according to Rao (1952) and a principal component matrix was derived for 20 characters as given in **Table 6**. The first 13 components explained 97.88 percentage of the total variation, of which, the first component, explained 25.00 percentage of variance and the second component to 13 components explained 13.90, 10.27, 9.52, 8.68, 6.20, 6.11, 5.69, 3.92, 3.47, 2.09, 1.79 and 1.23 percentage of the variance respectively. The graphical distribution of landraces using the first two principal components, which together accumulated to 38.90 percentage of the overall variability (**Fig. 1**).

The values of principal components score 1 and principal component score 2 are presented in **Table 7**. The graph was drawn by plotting PC 1 values on X axis and PC 2 on Y axis for each of the 31 landraces. The relative contribution of each characters towards genetic divergence was derived from the loading coefficients (or) component coefficients of first two principal components PC 1 and PC 2. Among the component coefficients, of the first 13 components for the 20 characters (**Table 6**), spikelets/ panicle and filled grains/panicle recorded the highest coefficients of (0.37) followed by length of panicle (0.36), height of the plant (0.34), head rice recovery (-0.29), days to flowering (0.27), productive tillers /plant (0.26), hulling percentage (-0.23), harvest index (-0.20), gelatinization temperature (-0.19) and spikelet fertility percentage (0.18) as reflected in the first component (PC 1). In the second principal component (PC 2), the maximum coefficient was observed for grain yield/ plant (-0.44), followed by harvest index (-0.41), length to breadth ratio of kernel (0.34), productive tillers / plant (-0.32), length to breadth ratio of kernel after cooking (-0.27), kernel breadth (-0.25), days to flowering (-0.22), kernel breadth after cooking (0.22), length of kernel after cooking (-0.21), height of the plant (-0.17), aroma (-0.17) and filled grains / panicle (0.15).

The variation present in the rice germplasm is usefully revealed by the principal component analysis and D^2 analysis (Roy *et al.,* 2013). The relative distribution of landraces showed broad parallelism between groupings obtained by D^2 analysis and principal component analysis when the first two or three principal components

Table 6. Principal component matrix for 20 characters of 31 landraces

S.No.	Characters	Common components coefficients												
		PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	PC12	PC13
1	Days to flowering	0.27	-0.22	-0.29	-0.10	-0.10	0.11	0.19	0.30	0.06	-0.09	-0.17	0.10	0.38
2	Height of the Plant (cm)	0.34	-0.17	-0.01	0.04	0.07	0.05	-0.08	0.28	-0.18	-0.48	-0.08	-0.01	-0.02
3	Productive tillers/ plant	0.26	-0.32	-0.05	0.05	0.02	-0.20	0.33	0.13	0.12	0.04	-0.22	0.08	-0.72
4	Length of panicle	0.36	-0.05	0.09	0.14	0.07	0.02	-0.15	0.35	-0.08	-0.06	0.27	0.11	0.21
5	Spikelets/ panicle	0.37	0.14	0.13	0.02	-0.08	-0.08	-0.10	0.09	-0.12	0.49	0.00	-0.09	0.05
6	Filled grains/ panicle	0.37	0.15	0.14	0.02	-0.06	-0.05	-0.12	0.05	-0.02	0.48	-0.05	-0.07	-0.05
7	Spikelets fertility percentage	0.18	0.03	0.02	0.07	0.13	0.35	-0.24	-0.09	0.85	-0.05	-0.02	0.05	-0.03
8	Root to shoot ratio	-0.14	0.14	-0.06	-0.16	-0.16	0.46	-0.47	0.18	-0.27	0.03	-0.45	0.26	-0.27
9	Harvest index	-0.20	-0.41	-0.18	0.02	-0.18	-0.22	-0.24	0.04	0.07	0.13	-0.20	-0.09	0.22
10	Hulling percentage	-0.23	-0.10	0.15	-0.21	0.39	0.01	0.08	0.40	0.11	0.28	-0.07	0.21	0.21
11	Head rice recovery	-0.29	-0.01	0.16	-0.18	0.35	0.03	0.17	0.36	0.04	0.12	0.05	-0.06	-0.14
12	Length of the Kernel	0.00	0.11	0.39	-0.22	-0.41	-0.09	0.33	0.05	0.13	-0.13	-0.40	-0.03	0.21
13	Breadth of the Kernel	0.17	-0.25	0.20	-0.48	-0.01	0.18	-0.01	-0.22	0.03	0.03	-0.11	-0.37	0.06
14	Length and breadth ratio of Kernel	-0.12	0.34	-0.01	0.38	-0.24	-0.26	0.03	0.25	0.24	-0.01	-0.22	0.12	0.05
15	Length of Kernel after cooking	-0.07	-0.21	0.41	-0.16	-0.42	-0.03	-0.08	0.01	0.08	-0.01	0.37	0.40	-0.13
16	Breadth of the Kernel after cooking	0.04	0.22	-0.28	-0.47	-0.24	-0.12	-0.04	0.22	0.10	-0.09	0.41	0.09	-0.11
17	Length breadth ratio of Kernel after Cooking	-0.04	-0.27	0.48	0.36	0.03	0.15	-0.04	-0.03	-0.11	-0.08	0.06	0.14	0.06
18	Gelatinization temperature	-0.19	-0.01	0.03	0.22	-0.32	0.40	0.13	0.39	0.02	0.03	0.21	-0.60	-0.13
19	Aroma	0.00	-0.17	-0.30	0.13	-0.18	0.43	0.43	-0.16	-0.06	0.33	0.09	0.34	0.10
20	Grain yield per plant (g)	-0.15	-0.44	-0.16	0.05	-0.16	-0.24	-0.34	0.08	0.11	0.18	0.03	-0.11	-0.03
Eigen Values		5.00	2.78	2.05	1.90	1.74	1.24	1.22	1.14	0.78	0.69	0.42	0.36	0.25
Percentage of Variance		25.00	13.90	10.27	9.52	8.68	6.20	6.11	5.69	3.92	3.47	2.09	1.79	1.23
Cumulative percentage		25.00	38.90	49.17	58.70	67.38	73.58	79.68	85.37	89.29	92.76	94.85	96.64	97.88

accounted for more than 80 percentage of the total variance (Hoque *et al.,* 2015). The reason for the first two principal components accounting for minimum variations was the reduced correlations between the variables under study. The basic criteria for principal component analysis revealed that the variables should be highly correlated. The first two components in the current study contributed the least variation, because majority of the productive and quality characters did not significantly affect grain yield.

Based on the variability and genetic divergence studies, the landraces of two Clusters were distinct and better performing *viz*., Vellaikuruvikar, Karupu Kavuni, Kichidi Samba and Athur Kichadi those of which can be used in hybridization programmes to produce superior recombinations. In general, the phenological traits and yield components of the landraces varied greatly. These gene pools could be used in selective breeding to significantly enhance agronomic traits. Genotype exchange between farmers, selection practices and local environmental adaptation can generate novel adapted allele combinations, which can be used in breeding programmes to reinitiate the process. The improvement of national and international germplasm should benefit greatly from the diversity offered by this mostly untapped collection of rice landraces.

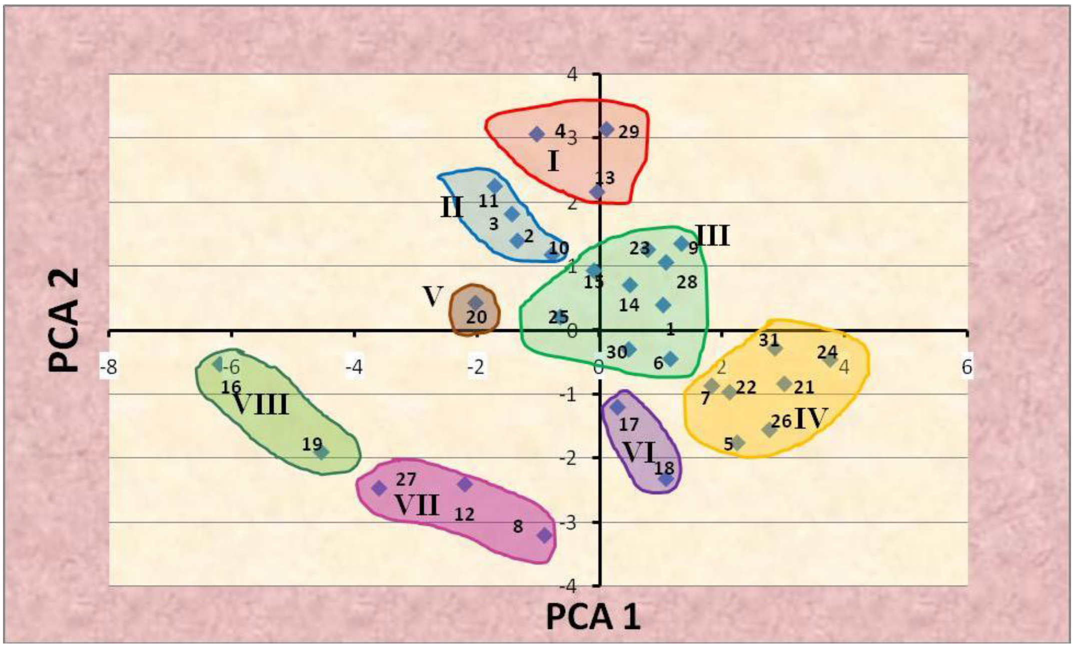

Fig. 1. Scatter diagram for distribution of 31 rice landraces based on principal component scores

1. Athur Kichadi
2. Selam Samba
3. Thengai Poo Samba
4. Vellai Kuruvikar
5. Karudan Samba
6. Milagu Samba
7. Singinikar
8. Oswa Kuthalai
9. Kantha Sala
10. Kuzhiyadichan
11. Jeeraga samba
12. Sandikar
13. Kalanamaku
14. Karupa Kavani
15. Illupai Poo Samba
16.Kullakar
17. Kottara Samba
18.Kichidi Samba
19.Suwarna Masuri
20. Pokkali
21.Panangattu Kudavazhai
22. Kaivarai Samba
23.Jeeraga Samba
24. Vadan Samba
25. Kallurundai
26. Sigappu kavuni
27. Karuthakar
28. Semuli samba
29. Bhutnath
30. Surakuruvai
31.Perunkar

Table 7. Principal component scores for 31 landraces

S.No.	Landraces	PC1	PC2
1	Athur Kichadi	1.04	0.40
2	Selam Samba	-1.34	1.40
3	Thengai Poo Samba	-1.43	1.82
4	Vellai Kuruvikar	-1.02	3.07
5	Karudan Samba	2.24	-1.76
6	Milagu Samba	1.16	-0.44
7	Singinikar	1.83	-0.86
8	Oswa Kuthalai	-3.59	-2.46
9	Kantha Sala	1.34	1.36
10	Kuzhiyadichan	-0.78	1.19
11	Vasanai Jeeraga Samba	-1.71	2.26
12	Sandikar	-2.19	-2.40
13	Kalanamaku	-0.04	2.17
14	Karupa Kavani	0.50	0.71
15	Illupai Poo Samba	-0.09	0.94
16	Kullakar	-6.19	-0.52
17	Kottara Samba	1.09	-2.32

Table 7. Continued..

S.No.	Landraces	PC1	PC2
18	Kichidi Samba	0.29	-1.20
19	Suwarna Masuri	-4.53	-1.90
20	Pokkali	-2.02	0.43
21	Panangattu Kudavazhai	3.02	-0.83
22	Kaivarai Samba	2.12	-0.96
23	Jeeraga Samba	0.79	1.27
24	Vadan Samba	3.76	-0.45
25	Kallurundai	-0.64	0.21
26	Sigappu Kavuni	2.77	-1.55
27	Karuthakar	-0.90	-3.20
28	Semmuli Samba	1.08	1.07
29	Bhutnath	0.11	3.15
30	Surakuruvai	0.48	-0.30
31	Perunkar	2.86	-0.28

REFERENCES

Asish, K. B., Kalaiyarasi, R. and Thiyagarajan, K. 2007. Genetic parameter studies on quality traits in rice. *Madras Agric. J.,* **94** (1-6) : 109-113.

Bansal, V. K., Saini, R. G., Rani, N. S. and Kaur, A. 1999. Genetic divergence in quality rice. *Oryza*, **36**(1) : 20-30.

Bisne, A., Sarawgi, K. and Verulkar, S. B. 2009. Study of heritability, Genetic advance and variability for yield contributing characters in rice. *Bangladesh J. Agril. Res.,* **34**(2) : 175-179. [Cross Ref]

Bose, L. K., Das, S., Pradhan, S. K., Subudhi, H., Singh, S. and Singh, O. 2007. Genetic variability of quality characters and grain yield in lowland rice landraces of Eastern India, *Korean Journal of Breeding Science*, **39**: 39–44.

Castro, E. da M. de, Vieria, N.R. de A., Rabelo, R.R., Silva, S.A. da. Qualidade de grãos em arroz. Santo Antônio de Goiás: Embrapa Arroz e Feijão, 1999. 30p.

Chaudhary, P, Gauchan, D, Rana, R.B, Sthapit, B.R. and Jarvis, D.I. 2004. Potential loss of rice landraces from a Terai community in Nepal: a case study from Kachorwa, Bara. Plant Genetic Resource Newsletter, **137**: 14 –21.

Dhanwani, R. K., Sarawgi, A. K., Solanki, A. and Tiwari, J. K. 2013. Genetic variability analysis for various yield attributing and quality traits in rice (*Oryza sativa* L.). *The Bioscan*., **8(**4) : 1403- 1407.

Dhurai, S. Y., Bhati, P. K. and Saroj, S. K. 2014. Studies on genetic variability for yield and quality characters in rice (*Oryza sativa* L.) under integrated fertilizer management. *The Bioscan.,* **9**(2): 745-748.

Dutta, P., Dutta, P. N. and Borua, P. K. 2013. Morphological traits as selection indices in Rice: A Statistical View. *Univ. J. Agric. Res*., **1**(3) : 85-96. [Cross Ref]

Fatema, K., Rasul, M. G., Mian, M. A. K. and Rahman, M. M. 2011. Genetic variability for grain quality traits in aromatic rice (*Oryza sativa* L). *Bangladesh J. Pl. Breed. Genet.,* **24**(2) : 19-24. [Cross Ref]

Fowler, C. and Mooney, P. 1990. Shattering: Food, Politics and Loss of Genetic diversity. University of Arizona Press. Tucson.

Garg, P., Pandey, D. P. and Kaushik, R. P. 2011. Genetic divergence for yield and quality traits in rice (*Oryza sativa L.*). *J. Rice Res*., **4**(1 & 2) : 1-5.

Gauchan, D., Smale, M. and Chaudhary, P. 2005. Market-based incentives for conserving diversity on farms: the case study of rice landraces in central Tarai, Nepal. *Genetic Resources and Crop Evolution* **52**: 293 –303. [Cross Ref]

Holden, J., Peacock., J. and Williams, T. 1993. Gens, Crops and the Environment. Cambridge University Press, Cambridge.

Hoque, A., Begum, S. N., Robin, A. H. K. and Hassan, L. 2015. Partitioning of rice (*Oryza sativa* L.) landraces based on morphometric diversity. *American J. Experiment. Agric.,* **7**(4) : 242-250. [Cross Ref]

Hossain, S., Haque, M. and Rahman, J. Genetic variability, correlation and path coefcient analysis of morphological traits in some extinct local Aman rice (*Oryza sativa* L), Rice Research: Open Access, 2015. [Cross Ref]

Johnson, H. W., Robinson, H. F. and Coinstock, R.E. 1955. Estimates of genetic and environmental variability in soybeans. *Agro. J.,* **47** : 314-18. [Cross Ref]

Joshi, K.D. and Witcombe, J.R. 2003. The impact of participatory plant breeding (PPB) on landrace diversity: a case study for high-altitude rice in Nepal. *Euphytica* **134**: 117 – 125. [Cross Ref]

Karad, S. and Pol, K. 2008. Character association, genetic variability and path coefcient analysis in rice (*Oryza sativa* L.), *International Journal of Agricultural Sciences*, **4**: 663–666.

Karim, D., Sarkar, S. U., Siddiqe, M. N. A., Miah, M. A. K. and Hasnat, M. Z. 2007. Variability and genetic parameter analysis in aromatic rice. *Int. J. Sust. Crop prod.*, **2**(5) : 15-18.

Ketan, R. and Sarkar, G. 2014. Studies on variability, heritability, genetic advance and path analysis in some indigenous Aman rice (*Oryza sativa* L.). *J. Crop and Weed.,* **10**(2) : 308-315.

Kumar, R., Suresh, G. B., Lavanya, G. R., Rai, S. K., Sandhya, L. and Devi, B. 2014. Genetic variability and character association among biometrical traits in F_2 generation of some rice crosses. *Int. J. Food. Agric. and Veter. Sci.*, **4** (1) : 155-159.

Kumar, V., Kumar, N., Suresh, B. G. 2015. Systematic evaluation of exotic rice germplasm for yield component characters and its grain yield. *Int. J. Res. Studies in Biosci.,* **3**(3) : 53-56.

Lanteri, S. and Barcaccia, G. 2006. Molecular marker based analysis for crop germplasm preservation. In: Ruane, J. Sonnino, A. (Ed.). The role of biotechnology in exploring and protecting agricultural genetic resources. Rome: FAO, p.55-66.

Madakemohekar, A. H., Bornare, S. S. and Chavan, A. S. 2014. Genetic variabiity and character association for quality Traits in recombinant inbred lines derived from inter Sub-specific crosses of rice (*Oryza sativa* L.). *Bangladesh J. Bot.* **43**(1) : 97-99. [Cross Ref]

Manonmani, S., Malarvizhi, D., Robin, S., Umadevi, M., Ameenal, M., Pushpam, R., Sundaram, K. M. and Thiyagarajan, K. 2010. Breeding three line rice hybrids with good grain quality. *Electronic Journal of Plant Breeding*, **1**(4) : 1265- 1269.

Matson, A.P., Parton, W.J., Power, A.G., Swift, M.J. 1997. Agricultural intensification and ecosystem properties. *Science*, **277**:504-509. [Cross Ref]

Maurya, D. M. and Singh, P. 1977. Singh. Genetic divergence in rice. *Indian J. Genet. and Pl.*

Nandan, R. Sweta and Singh, S. K. 2010. Character association and path analysis in rice (*Oryza sativa* L.) landraces. *World J. Agric. Sci.,* **6** **(**2) : 201-206.

Rao, C. R. 1952. Advanced statistical methods in biometrical research. John Wiley and Sons. Inc., New York, pp: 390.

Roy, R., Mazumder, P. B. and Sharma, G. D. 2009. Proline, catalase and root traits as indices of drought resistance in bold grained rice (*Oryza sativa*) landraces. *African J. Bio.,* **8** (23) : 6521-6528.

Roy, S., Rathi, R. S., Misra, A. K. and Bhatt, B. P. 2013. Phenotypic characterization of indigenous rice (*Oryza sativa* L.) germplasm collected from the state of Nagaland, India. *Pl. Genet. Res.,* **12**(1) : 58-66. [Cross Ref]

Sandhya, G., Babu, S. and Kumar, R. 2014. Genetic variability, interrelationship and path analysis for yield improvement of rice landraces. *The Bioscan*., **9**(3) : 1161-1164.

Sanni, K.A., Fawole, I., Guei, R.G., Ojo, D.K. and Somado, E.A. 2008. Geographical patterns of phenotypic diversity in Oryza sativa landraces of Côte d'Ivoire, *Euphytica*, **160**: 389-400. [Cross Ref]

Shrivastava, I. C., Nagarajan, P., Thiyagarajan, K., Bharathi, M. and Rabindran, R. 2011. Genetic parameters of variability, correlation and path-coefficient studies for grain yield and other yield attributes among rice blast disease resistant landraces of rice (*Oryza sativa L.*). *African J. Biot*., **10**(17) : 3322-3334. [Cross Ref]

Shrivastava, A., Mishra, D. K., Kouter, G. K. and Singh, S. K. 2014. Heritability genetic advance estimation from parental lines of hybrid rice. *Int. J. Sci. Res.,* **3**(7) : 11-13. [Cross Ref]

Sinha, A.K. and Mishra, P.K. 2012. Agronomic evalution of landraces of rice (*Oryza sativa*) of Bankura District of West Bengal, *Columban Journal of Life Science*,**13** (1&2) : 35-38.

Sravan, T., Rangare, N. R., Suresh, B. G. and kumar, S. R. 2012. Genetic variability and character association in rainfed upland rice (*Oryza sativa* .L). *Journal of Rice Research.*, **5**(1 and 2) : 24-29.

Srivastava, J.P. and Jaffe, S. 1993. Best practices for Moving seed Technology: New Approaches to Doing Business. World Bank Technical Paper No-213. The World bank. Washington, DC.

Subbaiah, P. V., Sekhar, M. R., Reddy, K. H. P. and Reddy, N. P. E. 2011. Variability and genetic parameters for grain yield and its components and kernel quality attriburtes in CMS based rice hybrids *(Oryza sativa L.). Int. J. App. Bio. Pharm. Tech.*, **2**(3) : 603-609.

Vanisree, S., Anjali, K., Damodar Raju, Ch., Surender Raju, Ch. and Sreedhar, M. 2013. Variability, heritability and association analysis in scented rice. *J. Bio. Sci. Opinion*., **1**(4) : 1-20. [Cross Ref]

Yadav, P., Rangare, N. R., Anurag, P. J. and Chaurasia, A. K. 2009. Quantitative analysis of rice (*Oryza sativa*. L.). in Allahabad Agro Climate Zone. *J. Rice Res.,* **3**(1) : 16-18.

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