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Rice Diversity Panel Evaluated for Agro-Morphological Diversity by Multivariate Analysis

N. Vishnu Varthini[1*], D. Sudhakar[2], M. Raveendran[2], S. Rajeswari[1], S. Manonmani[1], Shalini Tannidi[1], P. Balaji Aravindhan[1], Govindaraj Ponniah[1], Karthika Gunasekaran[1] and S. Robin[1]

[1]Centre for Plant Breeding and genetics, [2]Centre for Plant Molecular Biology and Biotechnology, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India
**Corresponding author*

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A B S T R A C T

Genetic diversity assessment for agro morphological traits in a population can be estimated by different methods such as univariate and multivariate analysis. Multivariate analysis is utilized for analyzing more than one variable at once. A diversed collection of 192 genotypes with traditional landraces and exotic genotypes from 12 countries was evaluated for 12 agro- morphological traits by multivariate analysis which reveals the pattern of genetic diversity and relationship among individuals. Twelve quantitative characters i.e. plant height, leaf length, number of productive tillers, panicle length, number of filled grains, spikelet fertility, days to 50% flowering; days to harvest maturity, grain length, grain width, grain length width ratio, and single plant yield were measured. Multivariate techniques such as UPGMA cluster analysis, principal component analysis and canonical vector analysis was utilized to examine the variation and to estimate the relative contribution of various traits for total variability. Analysis by UPGMA method had clustered 192 genotypes into seven clusters. Principal component analysis had shown the genetic diversity of the population panel. The cumulative variance of 80.56% of total variation among 12 characters was explained by the first five axes. Canonical discriminant analysis indicated that the first two functions accounted for more than 86% of total variance and the traits such as days to 50% flowering, maturity, grain characters, panicle length and plant height were identified as principal discriminatory characters. These analyses have indicated the presence of variation in the population panel which can be utilized for various crop improvement programs.

Introduction

Rice is an indispensable staple food for half of the world's population. In countries where rice is used as staple food, the per capita consumption is very high ranging from 62 to 190 kg/year (Kaiyang *et al.*, 2008). It has the second largest production after wheat with over 503 million tonnes recorded in 2013. While the demand for rice is rising up steadily with steep increase in human population, the land area available for rice production is shrinking due to rapid urbanization and changing life style. New rice cultivars that combine high yield potential, resistance to both biotic and abiotic stress and good grain quality are urgently needed to meet future consumer demands.

Genetic diversity represents the heritable variation within and between populations of organisms. The success of plant breeding depends on the availability of genetic variation, knowledge about desired traits, and efficient selection strategies that make it possible to exploit existing genetic resource. The pool of genetic variation within an inter-mating population is the basis for selection as well as for plant improvement.

Before exploiting a population for trait improvement, it is necessary to understand the magnitude of variability in the population which is fundamental for genetic improvement in all crop species. To develop segregating population, genetic distance estimates form the basis for selecting parental combinations with sufficient genetic diversity and for classifying germplasm into heterotic groups for hybrid crop breeding. Population Grouping can be based on geographical origin, agro-morphological traits, pedigree information, or molecular marker data (Liakat Ali *et al.*, 2011).

Genetic distance estimates for population grouping can be estimated by different methods as it is crucial to understand the usable variability existing in the population panel. One of the approaches is to apply multivariate analysis. Cluster analysis can group cultivars and meaningful information of genetic distance between genotypes and clusters can be obtained. Genotypically distant parents are able to produce higher heterosis (Mian, 1989; Ghaderi *et al.*, 1979). It is assumed that the maximum amount of heterosis is manifested in cross combination involving genotypes from the most divergent cluster (Firoz *et al.*, 2008).

Statistical method of classification is usually by multivariate methods as it has extensive use in summarizing and describing the inherent variation among crop genotypes. Multivariate statistical tools include principal component analysis (PCA), Cluster analysis and discriminate analysis (Oyelola, 2004).

Principal component analysis (PCA) can be used to uncover similarities between variable and classify the cases (genotypes), while cluster analysis on the other hand is concerned with classifying previously unclassified materials (Kaufman and Rouseeuw, 2009). Canonical discriminant analyses were used to determine the relative contribution and linear associations among the traits.

It can separate among-population effects from within population effects by maximizing discrimination among populations when tested against the variation within populations (Riggs, 1973; Tai, 1989).

Multivariate analysis has been used in various crops *i.e.*, Rice (Sanni *et al.*, 2012, Chakravorthy *et al.*, 2013), soybean (Bhawana Sharma and Brijvirsingh, 2012), coconut (Odewale *et al.*, 2012), safflower, sorghum and oil palm to study the pattern of variation. The study aimed to determine level of germplasm variation and identify and classify variation for grouping the accessions by taking into account several characteristics and relationship between them.

Materials and Methods

Experimental material

The germplasm collection consisting of 192 rice accessions was used in this study, which consist of land races and varieties collected from nine different states of India as well as from different countries (Table 1). It has 82 landraces from different agro climatic zones of Tamil Nadu and two landraces from Orissa. 62 exotic genotypes from Argentina, Bangladesh, Brazil, Bulgaria, China,

Colombia, Indonesia, Philippines, Taiwan, Uruguay, Venezuela and United States and 46 varieties and improved genotypes from different states of India constitute the population panel of 192 genotypes. For easy identification and retrieval, each accession was named as RG 1 to RG 192.

Experimental site

A set of 192 genotypes were grown in Paddy Breeding Station, Department of Rice, Tamil Nadu Agricultural University, India during Rabi 2013. This area is situated at latitude of 11ºN and longitude of 77 ºE with clayey soil of pH 7.8.

Methods

One hundred and ninety two genotypes were transplanted 21 days after sowing as two seedlings per hill in randomized complete block design with a spacing of 20 X 20 cm.

Each plot per accession consisted of four rows each 0.8 by 3.6 m long at a distance of 40 cm between the plots. Normal cultural practices were followed as per standard recommendation.

Twelve quantitative characters were measured according to methods in the descriptors for rice *O. sativa* (IRRI, 1980). Variables considered in the descriptive and multivariate analyses were morphological (plant height, leaf length, number of productive tillers, panicle length, number of filled grains, spikelet fertility), phenological (days to 50% flowering and days to harvest maturity from the day of seeding), and grain traits (grain length, grain width, grain length width ratio, and single plant yield).

Statistical analysis

The observations recorded on 12 traits were statistically analyzed in SPSS16.0 to cluster the genotypes based on genetic similarity. Unweighted pair group method of average linkage (UPGMA) constructed by SPSS16.0 was used to classify the accessions into clusters. The PCA analysis reduces the dimensions of a multivariate data to a few principal axes, generates an Eigen vector for each axis and produces component scores for the characters (Sneath and Sokal, 1973; Ariyo and Odulaja, 1991). Canonical discriminate analysis measure the axis along which variation between entries were maximum (Rezai and Frey, 1990; Ariyo, 1993).

Results and Discussion

The maximum, minimum, sum, mean, standard deviation (SD) and coefficient of variation (CV) for the measured traits are presented in table 2. The largest variation was observed for number of productive tillers with CV of 28.03 % followed by number of filled grains per panicle (CV= 27), single plant yield (23.19), leaf length (23.02), grain length width ratio (22.16). Days to maturity has shown the least variation with the CV of 9.74%.

The genotype RG1 has taken the longest days for flowering as well as maturity. The taller genotype is RG20 whereas RG111 has short stature. RG183 has more number of productive tillers but RG164 has higher single plant yield.

Spikelet fertility ranges from 95.7% in RG131 to 54.2 in RG25. The accession with longest grain was RG57 (10.5) and largest grain width in RG160 (3.7) which is a bold grain type. The slim grain type with lesser grain width was RG95 (1.5) and shortest grain was RG111 (5.8).

Cluster analysis

Analysis by UPGMA method has clustered 192 genotypes into seven clusters (Table 1).

Landraces has diffused across the different clusters. 72 % of the landraces (62 landraces) has amalgamated in cluster 2. Cluster 1,3,4,5 and 7 has the remaining landraces. Cluster 1 has two landraces RG1 (Mapillai samba) and RG 106 (Katta samba). Cluster 7 has one landrace RG164 (Thillainayagam). Cluster 3 has 7 landraces (RG4, RG12, RG33, RG42, RG50, RG110andRG120). Nine landraces (RG32, RG73, RG97, RG109, RG155, RG163, RG168, RG179 and RG192) spread across cluster 4. Cluster 5 has three landraces (RG24, RG25 and RG44).

The population panel has 61 exotic genotypes which has been clustered in group 2 (22 genotypes), group 4(29 genotypes) and each 2 genotypes in cluster 5 and 6. This panel also has 47 improved genotypes and varieties from different states of India. Majority of the improved genotypes and varieties (51%) has clustered in group 4. Remaining improved genotypes and varieties has dispersed in cluster 2 (13 genotypes), cluster 3(8 genotypes), cluster 5(1genotype) and cluster 6 (1 genotype).

Principal component analysis

Principal component analysis has shown the genetic diversity of the population panel. The cumulative variance of 80.56% by the first five axes with Eigen value of > 1.0 (Figure 1 and 2) indicates that the identified traits within the axes exhibited great influence on the phenotype of population panel (Table 3 and 4).

The different morphological traits contribute for total variation calculated for each component. For Component 1 which has the contribution of Days to 50% flowering (loadings -0.87), leaf length (0.78), plant height (0.765), panicle length (0.637), days to maturity (0.853) and number of filled grains (0.352) for 28.46 % of the total variability. For component 2, grain width (0.886) and grain length width ratio (0.951) has contributed 16.8 % of total variability. Similarly spikelet fertility (0.771) and single plant yield (0.542), grain length (0.81), number of productive tillers (0.846) has contributed for the total variation of 14.4%, 11.7% and 9.3% from component 3, component 4 and component 5 respectively.

Canonical Discriminant analysis

Canonical discriminant analysis simultaneously examines the differences in the morphological variables and indicates the relative contribution of each variable to accession discrimination (Vaylay and van Santen, 2002).

Quantitative variables were considered as independent and the clusters identified by cluster analysis as dependent variables. The first four Discriminant functions were statistically significant according to the chi-square test at a probability of 0.01. Proper values and the distribution of their variances indicated that the first two functions accounted for more than 86% of total variance. Wilks' lambda coefficients for these two functions were precisely the lowest, indicating an almost perfect discrimination regarding the remaining functions. The significant ($p< 0.001$) canonical correlation between the accessions and the first canonical variate (canonical correlation = 0.851) and second canonical variate (canonical correlation = 0.748) indicates that the canonical variates can explain the differentiation of the accessions.

The standardized canonical discriminant coefficients can be used to rank the importance of each variable. A high standardized discriminant function coefficient for a trait might mean that the variable has greater discriminating ability. The first

canonical Discriminant function is dominated by plant height, days to 50% flowering and days to maturity (Table 5). Number of filled grains per panicle, panicle length spikelet fertility and grain length contribute for second canonical Discriminant function. It is therefore evident in the canonical discrimination that the composition of the accessions differs chiefly in days to 50% flowering, maturity, grain characters, panicle length and plant height. Centroids are discriminant score for each group when the variable means (rather than individual values for each case) are entered into the function. The Proximity of group centroids indicates the errors in classification. The distance between group centroids for different clusters is far away which indicates the precision of classification level (Figure 3).

Fig.1 Scattered Diagram of first two components explaining the diversity of genotypes

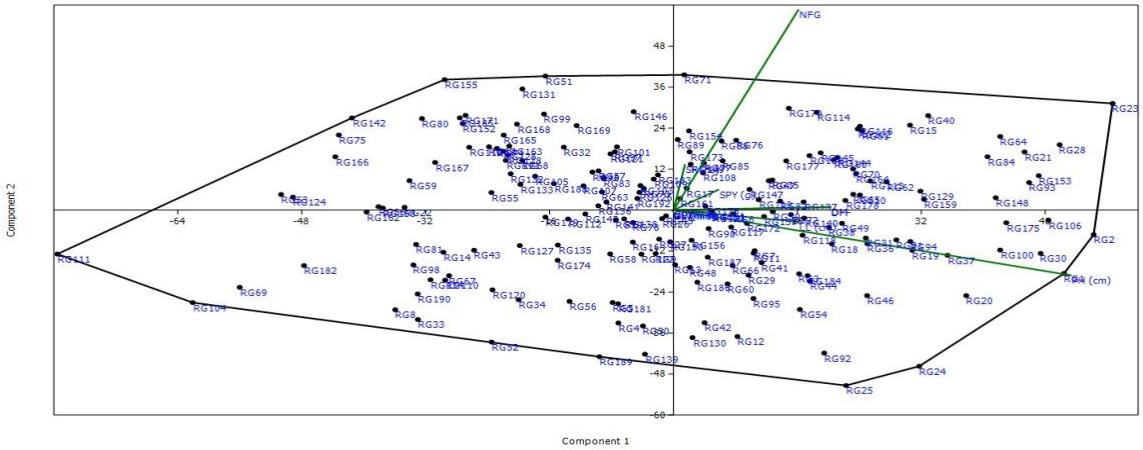

Fig.2 Eigen value for the corresponding principal components

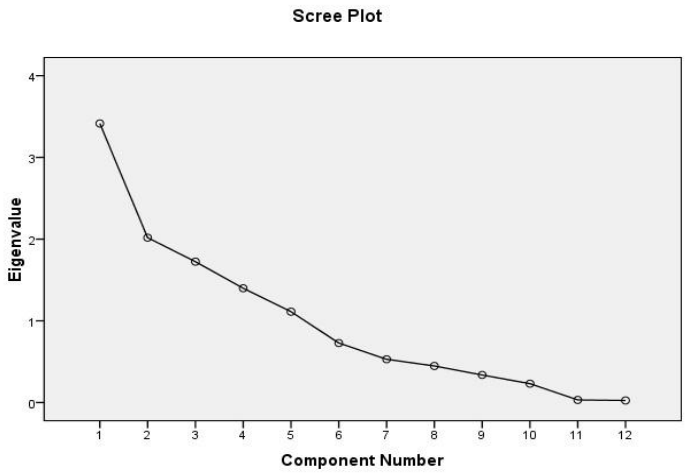

Fig.3 Group centroids for different clusters is far away which indicates the precision of classification level

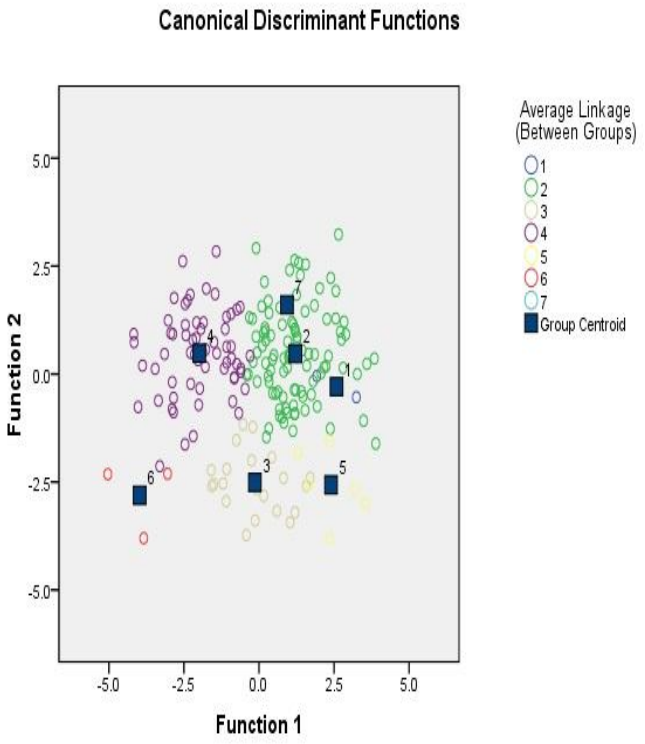

Table.1 Genotypes information with clustering pattern

G.	Genotypes	Parentage	Origin	Cluste
RG1	Mapillai samba	Landrace	Tamil Nadu, India	1
RG10	Katta samba	Landrace	Tamil Nadu, India	1
RG2	CK 275	CO50 X KAVUNI	Tamil Nadu, India	2
RG3	Senkar	Landrace	Tamil Nadu, India	2
RG6	CHIR 5	Improved chinsurah	West Bengal	2
RG7	Kudaivazhai	Landrace	Tamil Nadu, India	2
RG9	Kuruvaikalanjiyam	Landrace	Tamil Nadu, India	2
RG10	Nava konmani	Landrace	Tamil Nadu, India	2
RG11	CHIR 10	Improved chinsurah	West Bengal	2
RG13	CHIR 2	Improved chinsurah	West Bengal	2
RG15	Palkachaka	Landrace	Tamil Nadu, India	2
RG16	Thooyala	Landrace	Tamil Nadu, India	2
RG17	Chivapuchithiraikar	Landrace	Tamil Nadu, India	2
RG18	CHIR 11	Improved chinsurah	West Bengal	2
RG19	Koolavalai	Landrace	Tamil Nadu, India	2
RG20	Kalvalai	Landrace	Tamil Nadu, India	2

RG21	Mohini samba	Landrace	Tamil Nadu, India	2
RG23	Koombalai	Landrace	Tamil Nadu, India	2
RG26	Rascadam	Landrace	Tamil Nadu, India	2
RG27	Muzhikaruppan	Landrace	Tamil Nadu, India	2
RG28	Kaatukuthalam	Landrace	Tamil Nadu, India	2
RG29	Vellaikattai	Landrace	Tamil Nadu, India	2
RG30	Poongar	Landrace	Tamil Nadu, India	2
RG31	Chinthamani	Landrace	Tamil Nadu, India	2
RG35	CK 143	CO50 X KAVUNI	Tamil Nadu, India	2
RG36	Kattikar	Landrace	Tamil Nadu, India	2
RG37	Shenmolagai	Landrace	Tamil Nadu, India	2
RG38	Velli samba	Landrace	Tamil Nadu, India	2
RG39	Kaatuponni	Landrace	Tamil Nadu, India	2
RG40	kakarathan	Landrace	Tamil Nadu, India	2
RG41	Godavari samba	Landrace	Tamil Nadu, India	2
RG45	RPHP 105	Moirangphou	MANIPUR	2
RG47	Machakantha	Landrace	Orissa, India	2
RG48	Kalarkar	Landrace	Tamil Nadu, India	2
RG49	Valanchennai	Landrace	Tamil Nadu, India	2
RG58	Kodaikuluthan	Landrace	Tamil Nadu, India	2
RG60	Rama kuruvaikar	Landrace	Tamil Nadu, India	2
RG61	Kallundai	Landrace	Tamil Nadu, India	2
RG62	Purple puttu	Landrace	Tamil Nadu, India	2
RG63	IG 71(EC 728651-	TEPI BORO::IRGC 27519-1	IRRI, Philippines	2
RG64	Ottadaiyan	Landrace	Tamil Nadu, India	2
RG65	IG 56 (EC 728700-	BICO BRANCO	Brazil	2
RG66	Jeevan samba	Landrace	Tamil Nadu, India	2
RG70	Karthi samba	Landrace	Tamil Nadu, India	2
RG72	Aarkadukichili	Landrace	Tamil Nadu, India	2
RG76	Mattakuruvai	Landrace	Tamil Nadu, India	2
RG77	Karuthakar	Landrace	Tamil Nadu, India	2
RG78	RPHP 165	Tilakkachari	West Bengal	2
RG79	Manavari	Landrace	Tamil Nadu, India	2
RG82	Thooyamalli	Landrace	Tamil Nadu, India	2
RG84	Velsamba	Landrace	Tamil Nadu, India	2
RG85	RPHP 104	Kasturi (IET 8580)	UTTARKHAND	2
RG88	Saranga	Landrace	Tamil Nadu, India	2
RG90	IG 61(EC 728731-	CRIOLLO LA FRIA	Venezuela	2
RG91	IG 23(EC 729391-	MAHA PANNITHI::IRGC 51021-	IRRI, Philippines	2
RG93	uppumolagai	Landrace	Tamil Nadu, India	2
RG94	Karthigai samba	Landrace	Tamil Nadu, India	2
RG95	Jeeraga samba	Landrace	Tamil Nadu, India	2
RG10	IG 7(EC 729598-	VARY MAINTY::1RGC 69910-1	IRRI, Philippines	2
RG10	Varakkal	Landrace	Tamil Nadu, India	2

RG10	Mattaikar	Landrace	Tamil Nadu, India	2
RG10	Red sirumani	Landrace	Tamil Nadu, India	2
RG11	IG 45(EC 728768-	FORTUNA	Puerto Rico	2
RG11	RPHP 159	RadhuniPagal	BANGLADESH	2
RG11	RPHP 27	Azucena	HARYANA	2
RG11	IG 65(EC 729024-	GODA HEENAT1::IRGC 31393-1	IRRI, Philippines	2
RG11	Ponmani samba	Landrace	Tamil Nadu, India	2
RG11	Ganthasala	Landrace	Tamil Nadu, India	2
RG12	Kaliyan samba	Landrace	Tamil Nadu, India	2
RG12	IG 2(EC 729808-	BLUEBONNET 50::IRGC 1811-1	IRRI, Philippines	2
RG12	Kallimadayan	Landrace	Tamil Nadu, India	2
RG12	IG 38(EC 728742 -	DELREX	UNITED STATES	2
RG13	IG 37(EC 728715-	CENIT	ARGENTINA	2
RG13	Sigappukuruvikar	Landrace	Tamil Nadu, India	2
RG14	Raja mannar	Landrace	Tamil Nadu, India	2
RG14	IG 46(IC 471826-	BABER	INDIA	2
RG14	Chetty samba	Landrace	Tamil Nadu, India	2
RG14	IG 60(EC 728730-	CREOLE	Belize	2
RG14	IG 58(EC 728725-	CI 11011	UNITED STATES	2
RG14	Chinnaadukunel	Landrace	Tamil Nadu, India	2
RG15	IG 14(IC 517381-	MALACHAN::IRGC 54748-1	IRRI, Philippines	2
RG15	IG 32(EC 728838-	NOVA	United States	2
RG15	Sembilipiriyan	Landrace	Tamil Nadu, India	2
RG15	IG 12(EC 729626-	SHESTAK::IRGC 32351-1	IRRI, Philippines	2
RG15	Karungan	Landrace	Tamil Nadu, India	2
RG15	Sembala	Landrace	Tamil Nadu, India	2
RG16	IG 72(EC 728650-	TD 25::IRGC 9146-1	IRRI, Philippines	2
RG16	Panamarasamba	Landrace	Tamil Nadu, India	2
RG17	RPHP 42	Shalimar Rice -1	JAMMU and	2
RG17	IG 25(EC 729728-	LOHAMBITRO 224::GERVEX	IRRI, Philippines	2
RG17	IG 73(EC 728627-	MAKALIOKA 34::1RGC 6087-1	IRRI, Philippines	2
RG17	Vellaikudaivazhai	Landrace	Tamil Nadu, India	2
RG17	Kodai	Landrace	Tamil Nadu, India	2
RG17	Kallundaikar	Landrace	Tamil Nadu, India	2
RG17	IG 17(EC 728900-	SIGADIS	INDONESIA	2
RG18	IG 59(EC 728729-	COPPOCINA	BULGARIA	2
RG18	IG 18(EC 728892-	SERATOES HARI	INDONESIA	2
RG18	IG 28(EC 728920-	TIA BURA	INDONESIA	2
RG18	Vadakathi samba	Landrace	Tamil Nadu, India	2
RG4	Murugankar	Landrace	Tamil Nadu, India	3
RG5	CHIR 6	Improved chinsurah	West Bengal	3
RG8	CHIR 8	Improved chinsurah	West Bengal	3
RG12	Vellaichithiraikar	Landrace	Tamil Nadu, India	3
RG33	Malayalathan samba	Landrace	Tamil Nadu, India	3

RG34	RPHP 125	NDR 2026 (RICHA)	UTTAR	3
RG42	Earapalli samba	Landrace	Tamil Nadu, India	3
RG43	RPHP 129	Kamad	JAMMU and	3
RG50	Sornavari	Landrace	Tamil Nadu, India	3
RG52	ARB 58	Variety	Karnataka	3
RG56	RPHP 59	Taroari Basmati/karnal local	HARYANA	3
RG67	RPHP 106	akutphou	MANIPUR	3
RG11	Norungan	Landrace	Tamil Nadu, India	3
RG12	Thattan samba	Landrace	Tamil Nadu, India	3
RG12	IG 10(EC 729686-	HASAN SERALIRGC 79564-C1	IRRI, Philippines	3
RG13	IG 39(EC 728779-	HONDURAS	HONDURAS	3
RG13	IG 9(EC 729682-	GEMJYA JYANAM::IRGC	IRRI, Philippines	3
RG13	RPHP 138	EDAVANKUDI POKKALI	Kerala, India	3
RG18	IG 52(EC 728756-	DOURADO AGULHA	BRAZIL	3
RG18	IG 41(EC 728800-	KANIRANGA	Indonesia	3
RG19	IG 26(IC 0590943-	BASMATI 370::IRGC 3750-1	IRRI, Philippines	3
RG14	Jothi	variety	Kerala, India	4
RG22	IR 36	IR 1561 X IR 24 X Oryzanivara x	IRRI, Philippines	4
RG32	Thogai samba	Landrace	Tamil Nadu, India	4
RG51	RPHP 134	NJAVARA	Kerala	4
RG53	IR 68144-2B-2-2-3-1-	IR 72 X ZAWA BONDAY	IRRI, Philippines	4
RG55	IG 67(EC 729050-	IR 77384-12-35-3-12-l-B::IRGC	IRRI, Philippines	4
RG57	RPHP 103	Pant sugandhdhan -17	UTTARKHAND	4
RG59	RPHP 68	Subhdra	Orissa, India	4
RG68	IG 63(EC 728711-	CAAWA/FORTUNA	IRRI, Philippines	4
RG71	IG 27(IC 0590934-	ARC 11345::IRGC 21336-1	IRRI, Philippines	4
RG73	Kunthali	Landrace	Tamil Nadu, India	4
RG74	ARB 65	Variety	Karnataka	4
RG75	IG 21(EC 729334-	HONGJEONG::IRGC 73052-1	IRRI, Philippines	4
RG80	IG 66 (EC 729047-	IR 71137-243-2-2-3-3::IRGC	IRRI, Philippines	4
RG81	CB-07-701-252	Improved line	Tamil Nadu, India	4
RG83	RPHP 93	Type-3 (Dehradooni Basmati)	UTTARKHAND	4
RG86	RPHP 102	Kanchana	Kerala, India	4
RG87	IG 40 (EC 728740-	DEE GEO WOO GEN	TAIWAN	4
RG89	IR 83294-66-2-2-3-2	DAESANBYEO X IR65564-44-5-	IRRI, Philippines	4
RG96	RP-BIO-226	IMPROVED SAMBHA	ANDHRA	4
RG97	Varigarudan samba	Landrace	Tamil Nadu, India	4
RG98	IG 5(EC 729642-	IR 65907-116-1-B::C1	IRRI, Philippines	4
RG99	IG 31(EC 728844-	ORYZICA LLANOS 5	Colombia	4
RG10	RPHP 52	SEBATI	Orissa, India	4
RG10	IG 6(EC 729592-	SOM CAU 70 A::1RGC 8227-1	IRRI, Philippines	4
RG10	RH2-SM-1-2-1	SWARNA X MOROBERAKAN	Tamil Nadu, India	4
RG10	Vadivel	Landrace	Tamil Nadu, India	4
RG11	IG 35(EC 728858-	PATE BLANC MN 1	Cote D'Ivoire	4

RG11	IG 43(EC 728788-	IR-44595	IRRI, Philippines	4
RG12	IG 74(EC 728622-	KINANDANG PATONG::IRGC	IRRI, Philippines	4
RG12	IG 29(EC 728925-	TOX 782-20-1	NIGERIA	4
RG12	RPHP 55	Kalinga -3	Orissa	4
RG12	IG 75(EC 728587-	AEDAL::IRGC 55441-1	IRRI, Philippines	4
RG13	RPHP 90	182(M)	Andhra Pradesh	4
RG13	IG 33(EC 728938-	WC 3397	JAMAICA	4
RG13	IG 42(EC 728798-	KALUBALA VEE	SRILANKA	4
RG13	RPHP 161	ChampaKhushi		4
RG13	IG 8(EC 729601-	XI YOU ZHAN::1RGC 78574-1	IRRI, Philippines	4
RG14	IG 44(EC 728762-	EDITH	UNITED STATES	4
RG14	Sasyasree	TKM 6 x IR 8	West Bengal	4
RG14	IR 75862-206	IR 75083 X IR 65600 -81-5-3-2	IRRI, Philippines	4
RG14	RH2-SM-2-23	SWARNA X MOROBERAKAN	Tamil Nadu, India	4
RG15	RPHP 47	Pathara (CO-18 x Hema)	India	4
RG15	IG 48(EC 729203-	DINOLORES::IRGC 67431-1	IRRI, Philippines	4
RG15	Sonamahsuri	Landrace	Tamil Nadu, India	4
RG15	IG 13(EC 729640-	CURINCA::C1	IRRI, Philippines	4
RG16	IR 64	IR-5857-33-2-1 x IR-2061-465-1-	IRRI, Philippines	4
RG16	Mikuruvai	Landrace	Tamil Nadu, India	4
RG16	ARB 64	Variety	Karnataka	4
RG16	RPHP 140	VYTILLA ANAKONDAN	Kerala	4
RG16	IG 70(EC 729045-	IR43::1RGC 117005-1	IRRI, Philippines	4
RG16	Haladichudi	Landrace	Orissa, India	4
RG16	IG 24(EC 728751-	DNJ 140	BANGLADESH	4
RG17	RPHP 44	BR- 2655	KARNATAKA	4
RG17	IG 51(EC 728772-	GOGO LEMPUK	Indonesia	4
RG17	Avasara samba	Landrace	Tamil Nadu, India	4
RG18	ARB 59	Variety	Karnataka	4
RG18	RPHP 163	Seeta sail	West Bengal	4
RG18	RPHP 36	TKM-9	Tamil Nadu, India	4
RG18	RPHP 80	24(K)	Andhra Pradesh	4
RG19	IG 15(EC 728910-	SZE GUEN ZIM	CHINA	4
RG19	Nootripathu	Landrace	Tamil Nadu, India	4
RG24	Tadukan	Landrace	Tamil Nadu, India	5
RG25	Sornakuruvai	Landrace	Tamil Nadu, India	5
RG44	Mangam samba	Landrace	Tamil Nadu, India	5
RG46	IG 4 (EC 729639-	TD2: :IRGC 9148-1	IRRI, Philippines	5
RG54	PTB 19	Variety	Kerala, India	5
RG92	IG 49(EC 729102-	MENAKELY ::IRGC 69963-1	IRRI, Philippines	5
RG69	RPHP 48	Bindli	UTTARKHAND	6
RG10	IG 53(EC 728752-	CAROLINA RINALDO	URUGUAY	6
RG11	IG 20(EC 729293-	CHIGYUNGDO::IRGC 55466-1	IRRI, Philippines	6
RG16	Thillainayagam	Landrace	Tamil Nadu, India	7

Table.2 Characteristic means and variations of 192 accessions panel

					MIN		MAX	
Variable	Sum	Mean	SD	CV	Value	Accessions	Value	Accessions
DFF	16380.1	85.31	11.07	12.97	66.0	RG69	123.0	RG1
LL (cm)	7227.7	37.64	8.67	23.02	20.8	RG104	62.4	RG106
PH (cm)	22231.6	115.79	21.79	18.82	51.0	RG111	162.3	RG20
NPT	2547.95	13.27	3.72	28.03	5.0	RG147	26.5	RG183
PL (cm)	4237.2	22.07	2.74	12.42	11.6	RG111	31.1	RG85
DM	22556.5	117.48	11.44	9.74	94.0	RG43, RG59	155.0	RG1
NFG	13201.1	68.76	18.56	27.00	26.6	RG189	112.0	RG23
SF (%)	15907.25	82.85	6.93	8.37	54.2	RG25	95.7	RG131
GL (mm)	1592.5	8.29	0.89	10.68	5.8	RG111	10.5	RG57
GW(mm)	483.785	2.52	0.49	19.49	1.5	RG95	3.7	RG160
GLWR	661.4	3.44	0.76	22.16	1.8	RG122	5.6	RG47
SPY (g)	4832.88	25.17	5.84	23.19	12.0	RG104	55.5	RG164

Table.3 Eigen value and percent of total variation and component matrix for the principal component axes

PC	1	2	3	4	5
Eigen values	3.415	2.017	1.724	1.399	1.112
% of Variance	28.459	16.810	14.369	11.658	9.267
Cumulative %	28.459	45.269	59.638	71.296	80.563
Component Matrix					
DFF	**0.87**	0.047	-0.222	-0.276	-0.125
LL (cm)	**0.78**	-0.297	-0.062	-0.063	0.108
PH (cm)	**0.765**	-0.11	-0.025	0.267	0.214
NPT	-0.056	0.179	0.284	-0.194	**0.846**
PL (cm)	**0.637**	0.134	-0.084	0.524	-0.029
DM	**0.853**	0.034	-0.219	-0.279	-0.116
NFG	**0.352**	0.258	0.711	0.003	-0.326
SF (%)	0.03	0.233	**0.771**	-0.003	-0.294
GL (mm)	-0.147	0.232	-0.256	**0.81**	-0.031
GW(mm)	-0.089	**-0.886**	0.154	0.323	-0.047
GLWR	0.024	**0.951**	-0.228	0.098	0.034
SPY (g)	0.416	0.012	**0.542**	0.295	0.335

Table.4 Discriminant functions that distinguish between clusters of rice accessions

		Variance %						
Function	Eigen Value	Proportion	Cumulative	Canonical	Wilks'	Chi-	df	Sig.
1	2.622	58.4	58.4	0.851	0.071	480.035	72	<0.0001
2	1.266	28.2	86.7	0.748	0.257	246.429	55	<0.0001
3	0.295	6.6	93.2	0.477	0.583	97.926	40	<0.0001
4	0.213	4.7	98	0.419	0.755	51.029	27	0.003
5	0.063	1.4	99.4	0.243	0.916	15.995	16	0.453
6	0.028	0.6	100	0.164	0.973	4.947	7	0.666

Table.5 Canonical discriminant coefficient showing the contribution of each character for the variation

	1	2
DFF	0.269	-0.022
LL (cm)	0.093	0.028
PH (cm)	0.928	-0.228
NPT	0.023	-0.117
PL (cm)	0.035	0.39
DM	-0.139	0.079
NFG	-0.245	0.744
SF (%)	0.188	0.344
GL (mm)	0.078	-0.281
GW(mm)	-0.158	0.194
GLWR	-0.155	0.094
SPY (g)	0.032	0.133
canonical correlation	0.851	0.748
level of significance	0.01	0.01
Variance accounted for	58.4	28.2
Cumulative variance	58.4	86.7

Multivariate analysis i.e. UPGMA cluster analysis, principal component analysis and canonical Discriminant analysis used to study genetic variability has revealed wide genetic variation among rice germplasm accessions. According to Aliyu *et al.*, (2000) cluster analysis has the singular efficacy and ability to identify crop accessions with highest level of similarity using the dendrogram. Cluster analysis has revealed seven groups and the genotypes were distributed across all the clusters. Though origin has significant role in clustering i.e. most of the landraces from Tamil Nadu has been confined to cluster 2, > 50 % of exotic lines has assigned to cluster 4, phenology has played prominent role in clustering along with morphological and grain traits. Cluster 1 has two landraces RG1 (mapillai samba) and RG 106 (Katta samba) which are the late maturing genotypes and duration of 50% flowering was123 and 119 respectively. Genotypes with early 50% flowering duration and maturity period have been grouped in cluster 6 (RG69, RG111, RG104). These genotypes have short stature and lesser leaf length. Cluster 7 has one landrace RG164 (Thillainayagam) which has higher single plant yield, medium height, lengthier leaf and panicles. Cluster 5 has 6 genotypes (RG24, RG25, RG44, RG46, RG54 and RG92) which are taller plant types with less spikelet fertility and higher leaf length. Cluster 3 has 21 genotypes that are having lesser number of filled grains per panicle, spikelet fertility and single plant yield as it has clustered mainly based on grain (yield) traits. The second largest cluster 4 has 62 genotypes with half of the exotic lines has medium grain length, width and grain length width ratio and it has short to medium stature genotypes. The largest cluster 2 with 97 genotypes is dominated by landraces. It is characterized with the genotypes of median performance for all measured traits.

Similar type of clustering based on phenology and morphological characteristics was reported by Sanni *et al.*, (2012) in 434

landraces of rice collected from African continent. In his study, the late maturing landraces has clustered in 4, 5 and 6 clusters and early maturing accessions in cluster 2 and the total number of tillers was lowest in cluster 7 and cluster 3 has classified based on grain characteristics. Clustering analysis in coconut by Odewale *et al.,* (2012), tall cultivars were grouped in one cluster and dwarf cultivars in another cluster. Worede *et al.,* (2014) has also reported clustering based on flowering, plant type and yield traits in 24 rice genotypes for 17 traits.

Principal Component Analysis measures the importance and contribution of each component to total variance. It can be used for measurement of independent impact of a particular trait to the total variance whereas each coefficient of proper vectors indicates the degree of contribution of every original variable with which each principal component is associated. The higher the coefficients, regardless of the sign, the more effective they will be in discriminating between accessions. There are no inferential tests to prove significance of proper values and the coefficients (Sanni *et al.,* 2012). The current study was based on the Proportion of Variance Criterion by O'Rourke and Hatcher (2013). According to this criterion, Five principal components with cumulative variance of 80.6% was extracted which gives the clear idea of structure underlying the variables analyzed.

Total variation in each principal axis is determined by number of variables. In the current study, Component 1 has the contribution from Days to 50% flowering, leaf length, plant height, panicle length, days to maturity and number of filled grains for 28.46 % of the total variability. The first component has phenological and yield related variables. Similar type of performance was obtained by Sanni *et al.,* (2012) and Sanni *et al.,* (2008). Guei *et al.,* (2005) has obtained similar pattern for phenological variables in rice

Takeda (1990) reported that grain size that may be indicated by weight, volume, or length is one of the most important agronomic traits in rice. In current study also, grain width and grain length width ratio has contributed 16.8 % of total variability in component 2. The remaining variability of 14.4%, 11.7% and 9.3% was consolidated in component 3, component 4 and component 5 by various traits such as spikelet fertility, single plant yield, grain length and number of productive tillers.. Rai *et al.,* (2013) has also reported similar results that grain characteristics along with panicle density, leaf length and plant height contributes for phenotypic diversity in a study involving Indian landraces of aromatic and non-aromatic accessions. Caldo *et al.,* (1996) has reported similar results that the traits such as maturity, heading, plant height, culm length, leaf length, and tillering ability were found to be the major factors contributing to the variation of parental lines of modern Philippine rice cultivars. Thus, the prominent characters coming together in a particular principal component by contributing towards variability has the tendency to hang together offer opportunity for its utilization in crop breeding (Chakravorty *et al.,* 2013).

Dissimilarity estimated by multivariate criterion is useful to determine the traits causing the dissimilarity to arise and the relative contributions of various characters to the total variability in the germplasm (Ariyo, 1993). The canonical Discriminant analysis in current study has shown that the days to 50% flowering, maturity, grain characters, panicle length and plant height contributes for the total variability which is consistent with the results obtained by Sanni *et al.,* (2012) as the first and second canonical discriminant function is dominated by the loadings from number of days to 50% heading and maturity,

grain width, plant height, tiller number, and grain length.

Principal component analysis and canonical vector analysis has identified few characters that plays prominent role in classifying the variation existing in the germplasm set. Both the analysis identified days to 50% flowering, days to maturity plant height, number of filled grains, spikelet fertility, panicle length and grain length in different principal components and vectors are the most important for classifying the variation. Thus the results of principal component analysis and canonical vector analysis confirmed the result of cluster analysis. Sanni *et al.,* (2008, 2012) has also reported similar results with these multivariate analyses. Hence the three multivariate techniques used in the study has revealed the high level of genetic variation existing in the population panel and explains the traits contributing for this diversity.

As rice has enormous genetic diversity, its utilization primarily depends on the way of identifying variation in a population. Multivariate analysis employed in this study has clearly depicted the diversity and contributing characters of the population. Hence the results will be of greater benefit to identify parents for improving various morphological traits analyzed in this study.

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