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

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**Abstract**

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 diversified 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.

**Keywords**

Rice, Genetic variation, Agro morphological traits, Multivariate analysis, UPGMA, Principal component analysis, Canonical vector analysis.

**Article Info**

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**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.
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, RG110 and RG120). 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                | Cluster |
|------|-----------------|-------------------|-----------------------|---------|
| 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  | Kuruvaikalaniyam| 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       |
| Code | Variety | Breed | Location | Origin |
|------|---------|-------|----------|--------|
| 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 | Landrace | 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 | Kaatupponni | Landrace | Tamil Nadu, India | 2 |
| RG40 | kakerathan | Landrace | Tamil Nadu, India | 2 |
| RG41 | Godavari samba | Landrace | Tamil Nadu, India | 2 |
| RG45 | RPHP 105 | Landrace | 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 kuruvaiyar | Landrace | Tamil Nadu, India | 2 |
| RG61 | Kallundai | Landrace | Tamil Nadu, India | 2 |
| RG62 | Purple puttu | Landrace | Tamil Nadu, India | 2 |
| RG63 | IG 71(EC 728651-1) | Landrace | IRRI, Philippines | 2 |
| RG64 | Ottadaiyan | Landrace | Tamil Nadu, India | 2 |
| RG65 | IG 56 (EC 728700-1) | Landrace | 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 | Mattakuruvaikar | Landrace | Tamil Nadu, India | 2 |
| RG77 | Karuthakar | Landrace | Tamil Nadu, India | 2 |
| RG78 | RPHP 165 | Landrace | 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 | Landrace | Kasturi (IET 8580) | UTTARKHAND | 2 |
| RG88 | Saranga | Landrace | Tamil Nadu, India | 2 |
| RG90 | IG 61(EC 728731-1) | Landrace | CRIOLLO LA FRIA | Venezuela | 2 |
| RG91 | IG 23(EC 729391-1) | Landrace | MAHA PANNITHI::IRGC 51021 | IRRI, Philippines | 2 |
| RG93 | uppumologai | 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 729598-1) | Landrace | VARY MAINTY::IRGC 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  | Chinnadukunel      | 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 KASHMIR | 2 |
| RG17  | IG 25(EC 729728-  | LOHAMBITRO 224::GERVEX | IRRI, Philippines | 2 |
| RG17  | IG 73(EC 728627-  | MAKALIOKA 34::IRGC 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 |
| ID  | Name                        | Type                  | Origin/Region            | Latitude | Longitude |
|-----|-----------------------------|-----------------------|--------------------------|----------|-----------|
| RG34| RPHP 125                    | Landrace              | Tamil Nadu, India        | 3        |
| RG42| Earapalli samba             | Landrace              | Tamil Nadu, India        | 3        |
| RG43| RPHP 129                    | Kamad                 | JAMMU and Kashmir        | 3        |
| RG50| Sornavari                   | Landrace              | Tamil Nadu, India        | 3        |
| RG52| ARB 58                      | Variety               | Karnataka                | 3        |
| RG56| RPHP 59                     | Tarotari Basmati/karnal local | HARYANA          | 3        |
| RG67| RPHP 106                    | akutphou              | MANIPUR                  | 3        |
| RG11| Norungan                    | Landrace              | Tamil Nadu, India        | 3        |
| RG12| IG 10(ERC 729686)           | HASAN SERALIRGC 79564-C1 | IRRI, Philippines       | 3        |
| RG13| IG 39(ERC 728779)           | HONDURAS              | HONDURAS                 | 3        |
| RG13| IG 9(ERC 729682)            | GEMJYA JYANAM::IRGC   | IRRI, Philippines        | 3        |
| RG13| RPHP 138                    | EDAVANKUDI POKKALI    | Kerala                   | 3        |
| RG18| IG 52(ERC 728756)           | DOURADO AGULHA        | BRAZIL                   | 3        |
| RG18| IG 41(ERC 728800)           | KANIRANGA             | Indonesia                | 3        |
| RG19| IG 26(ERC 0590943)          | BASMATI 370::IRGC 3750-1 | IRRI, Philippines     | 3        |
| RG14| Jothi                       | variety               | Kerala                   | 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-2-2-3-1-1       | IR 72 X ZAWA BONDAY   | IRRI, Philippines        | 4        |
| RG55| IG 67(ERC 729050)           | IR 77384-12-35-3-12-1-B::IRGC | IRRI, Philippines   | 4        |
| RG57| RPHP 103                    | Pant sugandhdhan -17  | UTTARKHAND               | 4        |
| RG59| RPHP 68                     | Subhdra               | Orissa                   | 4        |
| RG68| IG 63(ERC 728711)           | CAAWA/FORTUNA         | IRRI, Philippines        | 4        |
| RG71| IG 27(ERC 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(ERC 729334)           | HONGJEONG::IRGC 73052-1 | IRRI, Philippines   | 4        |
| RG80| IG 66(ERC 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                   | 4        |
| RG87| IG 40(ERC 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(ERC 729642)            | IR 65907-116-1-B::C1  | IRRI, Philippines        | 4        |
| RG99| IG 31(ERC 728844)           | ORÝZICA LLANOS 5      | Colombia                  | 4        |
| RG10| RPHP 52                     | SEBATI                | Orissa                   | 4        |
| RG10| IG 6(ERC 729592)            | SOM CAU 70 A::IRGC 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(ERC 728858)           | PATE BLANC MN 1       | Cote D'Ivoire            | 4        |
| RG11 | IG 43(EC 728788-1) | KALINGA -3 | IRRI, Philippines |
|------|--------------------|-------------|-------------------|
| RG12 | IG 74(EC 728622-1) | KINANDANG PATONG::IRGC | IRRI, Philippines |
| RG12 | IG 29(EC 728925-1) | TOX 782-20-1 | NIGERIA |
| RG12 | RPHP 55 | | Orissa |
| RG12 | IG 75(EC 728587-1) | AEDAL::IRGC 55441-1 | IRRI, Philippines |
| RG13 | RPHP 90 | 182(M) | Andhra Pradesh |
| RG13 | IG 33(EC 728938-1) | WC 3397 | JAMAICA |
| RG13 | IG 42(EC 728798-1) | KALUBALA VEE | SRILANKA |
| RG13 | RPHP 161 | ChampaKhushi | |
| RG13 | IG 8(EC 729601-1) | XI YOU ZHAN::IRGC 78574-1 | IRRI, Philippines |
| RG14 | IG 44(EC 728762-1) | EDITH | UNITED STATES |
| RG14 | Sasyasree | TKM 6 x IR 8 | West Bengal |
| RG14 | IR 75862-206 | IR 75083 X IR 65600 -81-5-3-2 | IRRI, Philippines |
| RG14 | RH2-SM-2-23 | SWARNA X MOROBERAKAN | Tamil Nadu, India |
| RG15 | RPHP 47 | Pathara (CO-18 x Hema) | India |
| RG15 | IG 48(EC 729203-1) | DINOLORES::IRGC 67431-1 | IRRI, Philippines |
| RG15 | Sonamahsuri | Landrace | Tamil Nadu, India |
| RG15 | IG 13(EC 729640-1) | CURINCA::C1 | IRRI, Philippines |
| RG16 | IR 64 | IR-5857-33-2-1 x IR-2061-465-1-1 | IRRI, Philippines |
| RG16 | Mikuruvai | Landrace | Tamil Nadu, India |
| RG16 | ARB 64 | Variety | Karnataka |
| RG16 | RPHP 140 | VYTILLA ANAKONDAN | Kerala |
| RG16 | IG 70(EC 729045-1) | IR43::IRGC 117005-1 | IRRI, Philippines |
| RG16 | Haladichudi | Landrace | Orissa, India |
| RG16 | IG 24(EC 728751-1) | DNJ 140 | BANGLADESH |
| RG17 | RPHP 44 | BR- 2655 | KARNATAKA |
| RG17 | IG 51(EC 728772-1) | GOGO LEMPUK | Indonesia |
| RG17 | Avasara samba | Landrace | Tamil Nadu, India |
| RG18 | ARB 59 | Variety | Karnataka |
| RG18 | RPHP 163 | Seeta sail | West Bengal |
| RG18 | RPHP 36 | TKM-9 | Tamil Nadu, India |
| RG18 | RPHP 80 | 24(K) | Andhra Pradesh |
| RG19 | IG 15(EC 728910-1) | SZE GUEN ZIM | CHINA |
| RG19 | Nootripathu | Landrace | Tamil Nadu, India |
| RG24 | Tadukan | Landrace | Tamil Nadu, India |
| RG25 | Sornakuruvi | Landrace | Tamil Nadu, India |
| RG44 | Mangam samba | Landrace | Tamil Nadu, India |
| RG46 | IG 4 (EC 729639-1) | TD2: :IRGC 9148-1 | IRRI, Philippines |
| RG54 | PTB 19 | Variety | Kerala, India |
| RG92 | IG 49(EC 729102-1) | MENAKELY ::IRGC 69963-1 | IRRI, Philippines |
| RG69 | RPHP 48 | Bindli | UTTARKHAND |
| RG10 | IG 53(EC 728752-1) | CAROLINA RINALDO | URUGUAY |
| RG11 | IG 20(EC 729293-1) | CHIGYUNGDO::IRGC 55466-1 | IRRI, Philippines |
| RG16 | Thillainayagam | Landrace | Tamil Nadu, India |
### Table 2: Characteristic means and variations of 192 accessions panel

| Variable | Sum | Mean | SD  | CV | Value | Accessions | Value | Accessions |
|----------|-----|------|-----|----|-------|------------|-------|------------|
| DFF (cm) | 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

| Function | Eigen Value | Variance % Proportion | Cumulative | Canonical | Wilks’ Chisq | 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   |
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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