

Characterization of rice (*Oryza sativa* L.) landraces and cultivars using agro morphological traits

M Jegadeeswaran^{1,2*}, A Manivannan^{1,2}, S Mohan^{1,3}, G Pavithradevi¹, AP Salini¹, CR Anandakumar¹ and M Maheswaran¹

¹TNAU, Coimbatore, Tamil Nadu, India

²Central Institute for Cotton Research (Regional Station), Coimbatore, Tamil Nadu, India

³Faculty of Agriculture and Animal Husbandry, GRI, Gandhigram, Tamil Nadu, India

*Corresponding author e-mail: jegades@gmail.com

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ABSTRACT

A set of 152 rice genotypes comprising of landraces, traditional varieties, exotic lines, cultures and released varieties collected from nine different states of India as well as from nine countries were evaluated for 12 agromorphological traits by principal component analysis for determining the pattern of genetic diversity and relationship among individuals. The largest variation was observed for the trait single plant yield with CV of 39.52% followed by single panicle sterile seed (35.41%) and single panicle fertile seed (29.34%). The trait panicle length exhibited the least variation with the CV of 14.86%. Principal component analysis revealed four significant principal components and accounted for a cumulative variation of 74.90%. The first principal component accounted for 34.97%, second for 19.56%, third for 10.55% and fourth for 9.81% of total variation. Biplot exhibited convex of the hull which was occupied by the genotypes namely TKM3, ADT 47, CO 39, Nootripathu, Veeradangan, Cult 3000 and T1035 as these genotypes were exhibited highest level of variation. They can be used as diverse parents in crossing programme. Traits namely culm thickness, panicle length, days to heading, flag leaf length, plant height, width of flag leaf were discriminated the genotypes in higher degree. Cluster analysis identified five distinct groups among 152 genotypes which can be utilized for the trait improvement breeding programme.

Key words: Rice, principal component analysis, genetic diversity, clustering, characterization

Rice (*Oryza sativa* L.) is the major staple food for the most of the people in South East Asia in order to cater the need of burgeoning population, production level has to be increased tremendously. Local landraces are best adapted to their native environment and harbour many agronomical genes that can be utilized in the development of high yielding cultivars with tolerance to biotic and abiotic stresses (Lisa *et al.* 2011; Zhao *et al.* 2011). Landraces are considered as intermediate between cultivated varieties and their wild progenitors (Pusadee *et al.* 2009). These landraces are in extinction stage due to lack of adequate research attention. Characterization of landraces for the desired traits can

lead to identification of new sources of tolerance to biotic and abiotic stresses in rice (Wang *et al.* 2007).

The principal component analysis (PCA) is one of the most successful techniques that have been used in germplasm characterization which involves cumbersome data. The purpose of PCA is to reduce the large dimensionality of the data space (*i.e.*, observed variables) to the smaller intrinsic dimensionality of feature space (*i.e.*, independent variables), which are needed to describe the data economically when there is a strong correlation between observed variables. Principal component analysis (PCA) is a classical

statistical method based on linear transform which has been widely used in data analysis and comparison. Principal component analysis is based on the statistical representation of a random variable which involves the calculation of the eigen value decomposition of a data covariance matrix or singular value decomposition of a data matrix, usually after mean-centering the data for each attribute. It is the simplest of the true eigenvector based multivariate analyses. Often, its operation can be thought of as revealing the internal structure of the data in a way which best explains the variance in the data (Lenord and Peter 2009). The present study was aimed to understand the diversity present among the rice accessions using different agro morphological traits which will lead to understand relationship among the different genetic groups.

The germplasm collection of 152 rice accessions used in this study involving landraces and varieties collected from nine different states of India as well as from nine countries namely China, Columbia, India, Indonesia, Japan, Philippines, Srilanka, Taiwan and USA. It consisted of 38 landraces, 19 cultures, 12 exotic collections and 83 varieties. A set of 152 genotypes were grown in Paddy Breeding Station, Department of Rice, Tamil Nadu Agricultural University, Coimbatore, India during *Rabi* 2013. This area is situated at latitude of 11°N and longitude of 77°E with clay soil of pH 7.8. These genotypes were transplanted 20 days after sowing as two seedlings per hill in augmented design with a spacing of 20 x 20 cm. Each plot per accession consisted of five rows each of 2 m long and at a distance of 40 cm between the plots. Normal cultural practices were followed as per standard recommendation.

Principal component analyses (PCA) based on twelve quantitative traits was performed to find out the relative importance of different traits in capturing the genetic variation. The factors of these traits were used to determine the contribution of each factor towards variation. The standardized values were used to perform PCA using PAST 3 (Hammer *et al.* 2001). A scree plot was drawn from the eigen values associated with a component or factor in descending order versus the number of the component or factor. Scree plot used for visually assess which components or factors explain most of the variability in the data.

The genetic diversity maintained in a species is considered as a function of its ecological and evolutionary history (Hamrick and Godt 1996). The high genetic diversity among rice landraces and cultivars have been described in relation to agro-morphological traits (Singh and Singh 2009; Borkakati *et al.* 2000; Jegadeeswaran *et al.* 2014), morpho-physiological characters (Vairavan *et al.* 1973), enzymatic characters (Glaszmann *et al.* 1989), and molecular markers (Nachimuthu *et al.* 2015; Sarma and Bahar 2005; Bhuyan *et al.* 2007). The high genetic diversity among rice varieties in India is due to combined effect of wide eco-geographical conditions, diverse agro-ecosystems associated with various rice farming practices and diverse human cultural preferences.

In the present study, 152 accessions exhibited significantly varying performance for the twelve agro morphological traits (Table 1, Fig 1a & 1b). These traits namely culm thickness, heading date, plant height, flag leaf length, flag leaf width, panicle length, productive tillers, single panicle fertile seed, single panicle sterile seed, single panicle total seed, 1000 seed weight and single plant yield were observed. The largest variation was observed for the trait single plant yield with CV of 39.52% followed by single panicle sterile seed (35.41%) and single panicle fertile seed (29.34%). The trait panicle length exhibited the least variation with the CV of 14.86%. The genotype HKR47 recorded highest yield with mean of 31.71g and Cult14106 observed with lowest low (3.69g). The overall mean of germplasm accessions was 16.95g. The skewness and kurtosis coefficients were 0.09 and -0.64 respectively with the variation of 39.52%. Single panicle sterile seed was highest in T2684 (96) and lowest in TN1 (12) with overall mean of 40.44. Positive skewness (0.65) and heavy tailed kurtosis (1.65) was observed for this character with a variation of 35.41%. The genotype TKM3 recorded highest mean of 260 for the trait single panicle fertile seed and Cult3000 was observed with lowest value 40. The overall mean of germplasm accessions was 138.42. The skewness and kurtosis coefficients for this character were 0.36 and 0.45 respectively with the variation of 29.34 per cent. Mean length of flag leaf was 27.91 cm with the minimum and maximum value of 14.15 cm in the genotype CO39 and 54.60 cm in Cult14106, respectively. It also showed higher coefficient of variation of 27.91 per cent with positive skewness (0.83) and kurtosis (0.40). The trait

Table 1. Variation in quantitative traits of rice genotypes

Variables	Mean	Min	Genotype	Max	Genotype	SD	CV (%)	Skewness	Excess Kurtosis
CD	4.38	2.66	Nootripathu	7.85	Cult14106	1.04	23.73	0.84	0.67
HD	100.69	68.00	CO39	185.00	Chethuvali, ASD9	25.03	24.86	1.09	0.61
PH	111.68	62.80	CO39	192.80	T1904	26.06	23.34	0.65	-0.23
FLL	30.44	14.15	CO39	54.60	Cult14106	8.50	27.91	0.83	0.40
FLW	1.10	0.65	TKM5	2.00	WGL14	0.21	18.96	1.01	1.99
PL	22.90	14.50	CO39	32.20	T1035	3.40	14.86	0.25	-0.10
PT	13.94	5.10	Uplri	23.80	T1915	3.52	25.27	0.47	0.02
SPFS	138.42	40.00	Cult3000	260.00	TKM3	40.62	29.34	0.36	0.15
SPSS	40.44	12.00	TN1	96.00	T2684	14.32	35.41	0.65	1.63
SPTS	178.86	89.50	Dular	313.00	TKM3	45.64	25.51	0.28	-0.28
SW	19.85	11.50	Whitesannam	27.60	Karanellu	3.60	18.16	-0.41	-0.68
SPY	16.95	3.69	Cult14106	31.71	HKR47	6.70	39.52	0.09	-0.64

CD: Culm diameter; HD: Heading date; PH: Plant height; FLL: Flag leaf length; FLW: Flag leaf width; PL: Panicle length; PT: productive tillers; SPFS: Single panicle fertile seed; SPSS: Single panicle sterile seed; SPTS: Single panicle total seed; SW: 1000 seed weight; SPY: Single plant yield

single panicle total seed was observed highest in TKM3 (313) and lowest in Dular (89.50) with overall mean of 178.9. Positive skewness (0.28) and light tailed kurtosis (-0.28) distribution was observed for the single panicle total seed with the variation of 25.51%. The larger variation was observed for number of productive tillers with coefficient of variation of 25.27 per cent. The genotype T1915 recorded maximum number of productive tillers per plant (23.8) and the genotype Uplri had registered less number of productive tillers (5). The overall mean was 13.94 productive tillers per plant. The skewness and kurtosis coefficients were 0.47 and 0.02 respectively which shows right skewed and platykurtic distribution. The genotype Chethuvali ASD9 had taken

the longest duration for heading (185 days) and CO39 had shortest (68 days). The overall mean for heading for the germplasm accessions was 101days. The skewness and kurtosis coefficients were 1.09 and 0.61 respectively with the variation of 24.86 per cent. Overall mean for culm thickness of 152 germplasm lines were 4.38 cm with the minimum and maximum value of 2.66 cm in the genotype Nootripathu, CO39 and 7.85cm in Cult14106 respectively. It also showed higher coefficient of variation of 23.73 per cent with positive skewness (0.84) and kurtosis (0.67). The genotype T1904 was the tallest with mean height of 192.8cm and CO39 was shortest (62.8cm) with mean plant height of 111.68 cm was observed among the germplasm accession. A total

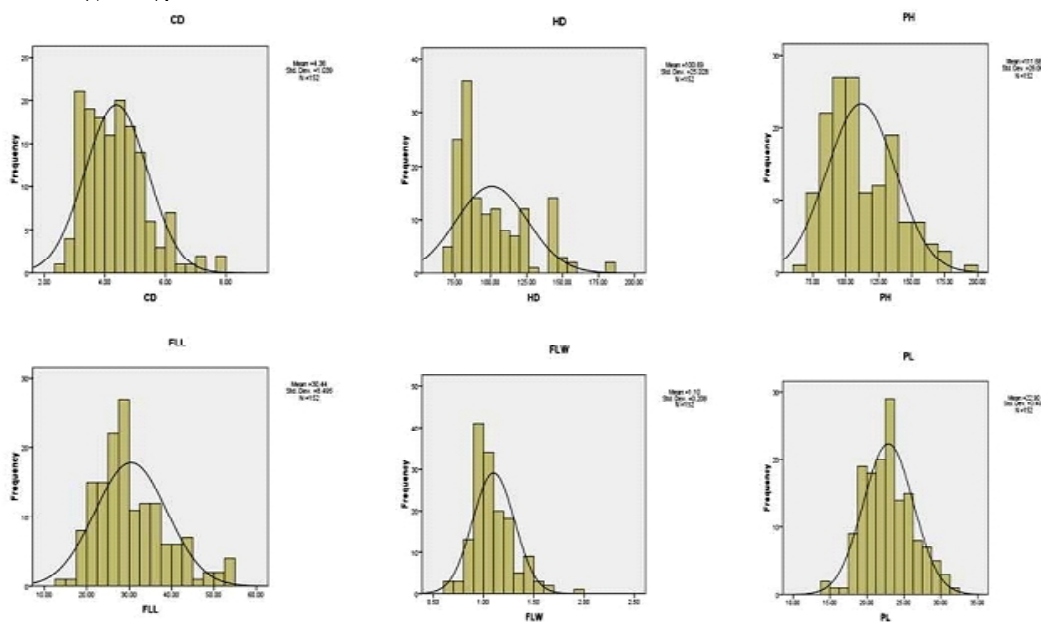


Fig. 1a. Frequency distribution of different quantitative traits

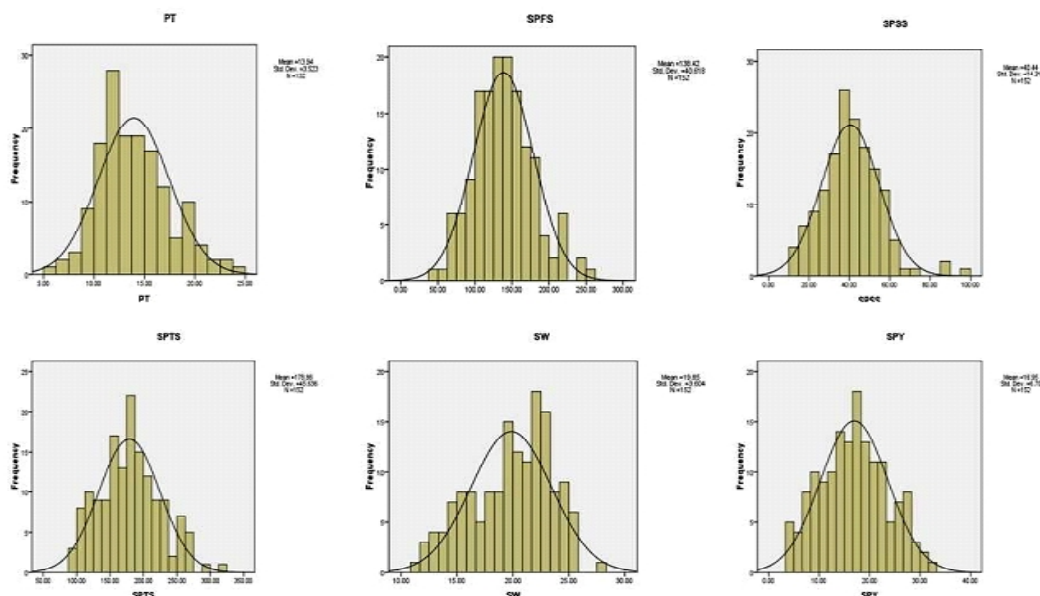


Fig. 1b. Frequency distribution of different quantitative traits

variation of 23.34 per cent with positive skewness (0.65) and negative kurtosis (-0.23) was observed. The trait flag leaf width was recorded the overall mean of 1.1 cm; the genotype WGL14 was broader (2cm) and TKM5 was narrow (0.65). It showed a variation of 18.96% with positive skewness (1.01) and kurtosis (1.99). The genotype Karanellu was heavy (27.6g) and whitesannam was lighter (11.5g) for the trait 1000 seed weight. Overall mean of 1000 seed weight was 19.85g with variation of 18.16 per cent. Left handed skewness (-0.41) and low tailed kurtosis (-0.68) distribution was observed. The genotype T1035 possessed long panicle (32.2cm) and CO39 was with smallest (14.5 cm) with overall mean of 22.9 cm. A total variation of 14.86 per cent with positive skewness (0.25) and negative kurtosis (-0.10) was observed.

Four significant principal components were identified and accounted for a cumulative variation of 74.90%. The first principal component accounted for 34.97 %, second for 19.56%, third for 10.55% and fourth for 9.81% of total variation (Table 2). The scores of quantitative traits were taken into account and subjected to PCA using PAST 3. Eigenvectors and principal components based on non-rotated loadings were estimated for all the traits (Table 2; Fig 2 & 3). First principal component (PC1) was correlated with culm thickness (0.43), panicle length (0.4), days to heading (0.39), flag leaf length (0.38), plant height (0.35) and

width of flag leaf (0.34). Second principal component (PC2) was associated single panicle, total seed (0.58) and single panicle fertile seed (0.57). Third principal component (PC3) was related with productive tillers (0.64) and single plant yield (0.55). Fourth principal

Table 2. Eigen value and percent of total variation and component matrix for the principal component axes

PC	PC 1	PC 2	PC 3	PC 4
Eigen value	4.20	2.35	1.27	1.18
% variance	34.97	19.56	10.55	9.81
Cumulative %	34.97	54.53	65.08	74.90
	Component Matrix			
	PC 1	PC 2	PC 3	PC 4
CD	0.425	-0.058	0.039	-0.081
HD	0.394	-0.021	0.075	-0.248
PH	0.348	-0.232	0.128	0.157
FLL	0.383	-0.186	0.122	0.050
FLW	0.341	0.073	0.139	0.051
PL	0.403	-0.077	0.083	0.141
PT	-0.161	0.149	0.640	-0.235
SPFS	0.090	0.573	-0.070	0.267
SPSS	0.239	0.226	-0.414	-0.294
SPTS	0.155	0.581	-0.193	0.145
SW	-0.046	-0.212	-0.084	0.776
SPY	0.028	0.334	0.552	0.213

CD: Culm diameter; HD: Heading date; PH: Plant height; FLL: Flag leaf length; FLW: Flag leaf width; PL: Panicle length; PT: productive tillers; SPFS: Single panicle fertile seed; SPSS: Single panicle sterile seed; SPTS: Single panicle total seed; SW: 1000 seed weight; SPY: Single plant yield

Component Plot in Rotated Space

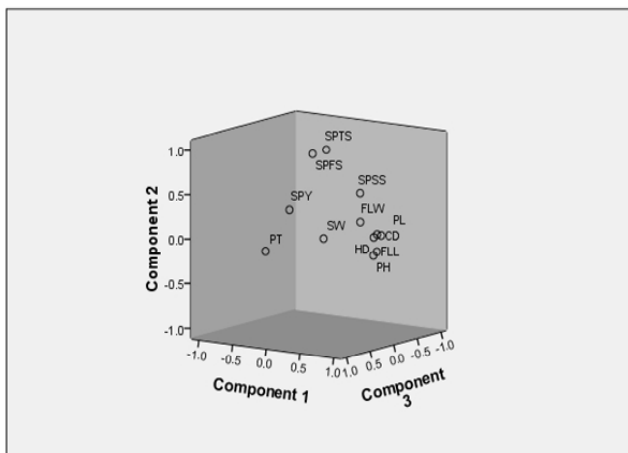


Fig. 2. Component plots for the twelve quantitative traits in Rice accessions

component (PC4) was associated with 1000 seed weight (0.78). Nachimuthu *et al.* (2014) also obtained 80% variability contributed by five principal components in 192 germplams using 12 agro morphological traits.

A scatter plot was drawn using PC1 and PC2 factor scores and clear pattern of grouping of genotypes was observed in the factor plane (Fig 4). Convex of the hull was occupied by the genotypes namely TKM3, ADT 47, CO 39, Nootripathu, Veeradangan, Cult3000 and TJ035 as these genotypes were placed in the highest point on the hull. These genotypes were exhibited the highest level of variation. They can be used as diverse parents in crossing programme for exploitation of heterosis. A vector line drawn from the origin to the

Scree Plot

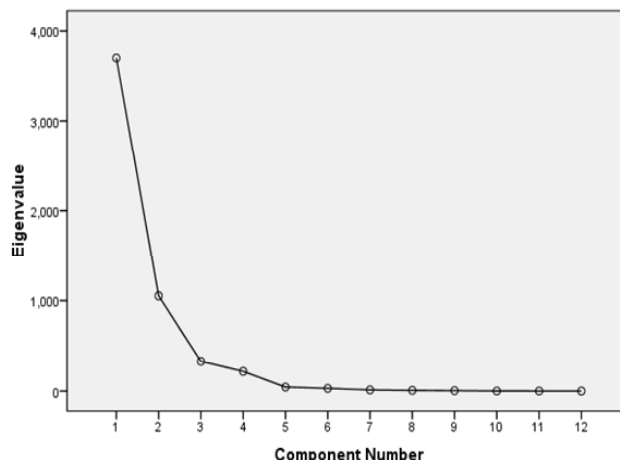


Fig. 3. Scree plot showing the eigen value variation for twelve quantitative traits in rice

place where traits have been mapped. Based on the length of the vector, the traits namely culm thickness, panicle length, days to heading, flag leaf length, plant height, width of flag leaf were possessing lengthy vector (these traits would be used as salient descriptor for characterization), single panicle total seed and single panicle fertile seed were medium in length, productive tiller, 1000 seed weight and single plant yield were short.

Pearson correlation coefficient was worked out for 12 different morphological traits, among the inter correlation, 40 were showed significance (Table 3). The trait culm thickness positively and significantly correlated with heading date, plant height, flag leaf length, flag leaf width, panicle length and single panicle

Table 3. Correlation among twelve agromorphological traits

	CD	HD	PH	FLL	FLW	PL	PT	SPFS	SPSS	SPTS	SW	SPY
CD	1.00											
HD	0.77**	1.00										
PH	0.56**	0.49**	1.00									
FLL	0.65**	0.55**	0.68**	1.00								
FLW	0.57**	0.50**	0.34**	0.45**	1.00							
PL	0.64**	0.57**	0.62**	0.68**	0.52**	1.00						
PT	-0.25**	-0.13	-0.24**	-0.15	-0.22**	-0.25**	1.00					
SPFS	0.06	0.07	-0.12	-0.03	0.17*	0.07	0.05	1.00				
SPSS	0.36**	0.36**	0.16*	0.19*	0.23**	0.29**	-0.25**	0.20*	1.00			
SPTS	0.18	0.17*	-0.06	0.03	0.23**	0.16	-0.03	0.95**	0.49**	1.00		
SW	-0.08	-0.20*	0.11	0.03	-0.10	0.04	-0.19*	-0.09	-0.26**	-0.16*	1.00	
SPY	0.01	-0.02	0.01	-0.11	0.22**	0.08	0.30**	0.34**	-0.01	0.30**	-0.06	1.00

*Significance at 5%, ** Significance at 1%

CD: Culm diameter; HD: Heading date; PH: Plant height; FLL: Flag leaf length; FLW: Flag leaf width; PL: Panicle length; PT: productive tillers; SPFS: Single panicle fertile seed; SPSS: Single panicle sterile seed; SPTS: Single panicle total seed; SW: 1000 seed weight; SPY: Single plant yield

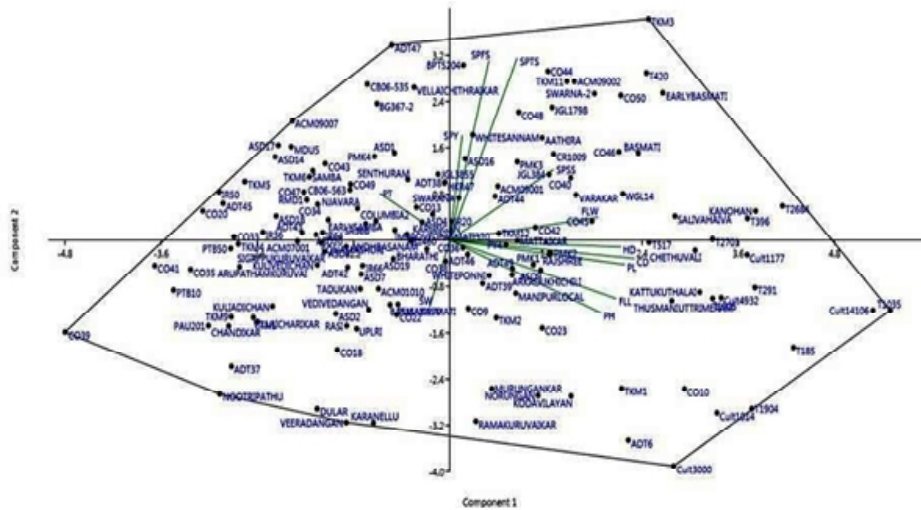


Fig. 4. Distribution of genotypes across the two components

sterile seed. However, it had significant negative correlation with productive tillers. The trait heading date significantly positively correlated with plant height, flag leaf length, flag leaf width, panicle length and single panicle sterile seed. But negatively correlated with 1000 seed weight. Plant height was positively and significantly correlated with flag leaf length, flag leaf width, panicle length and single panicle sterile seed. It was negatively correlated with productive tillers. Flag leaf length was significantly and positively correlated with flag leaf width, panicle length and single panicle sterile seed. Flag leaf width was negatively correlated with productive tillers, but in contrast it was positively associated with panicle length, single panicle fertile seed, single panicle sterile seed, single panicle total seed and single plant yield. Panicle length was positively correlated with single panicle sterile seed and negatively associated with productive tillers. Productive tiller was positively and significantly associated with single plant yield, it was negatively correlated with single panicle sterile seed. Single panicle fertile seed was positively and significantly associated with single panicle sterile seed, single panicle total seed and single plant yield. Single panicle sterile seed was positively and significantly associated with single panicle total seed, but negatively correlated with 100 seed weight. Single panicle total seed was positively and significantly associated with single plant yield and negatively correlated with 1000 seed weight.

The factors corresponding to four PCs were subjected to cluster analysis based on Euclidean

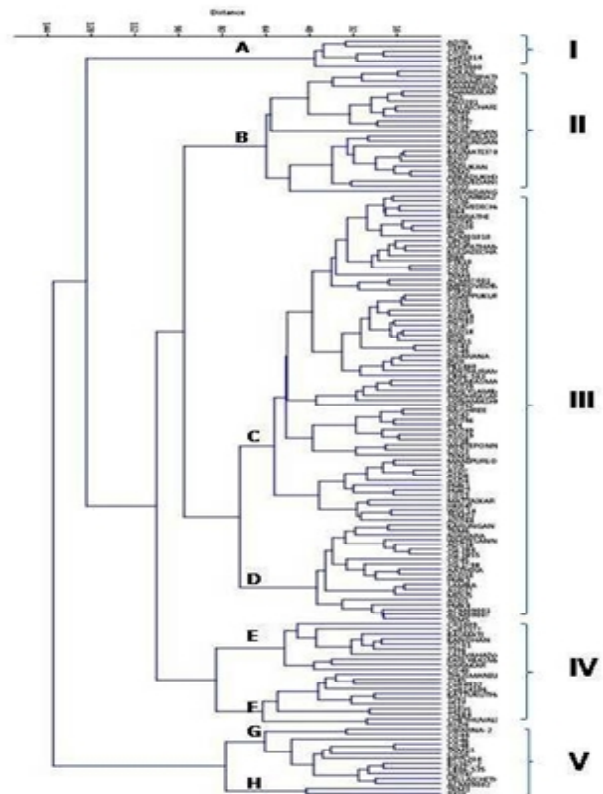


Fig. 5. Dendrogram based on morphological traits in Rice accessions

Table 4. Grouping of genotypes based on agro morphological traits

Group	Sub group	Genotypes	Salient characters
1	1	ADT6, T1904, CO10, Culture 1014, Culture 3000 and T1915	Higher plant height, flag leaf length and Panicle length Lower in single panicle. fertile seed, single panicle total seed and single plant yield
2	1	Dular, Nootripathu, Karanellu, Rama Kuruvaikar, Chandikar, TN1, Villaicharikar, TKM9, ADT37, CO39, CO41, Murungan Kar, Norungan, Kodavilayan, Basmati370, TKM2, ASD2, CO18, CO22, Rasi, Vedivedangan and Veeradangan	Higher productive tillers and 1000 seed weight. Lower culm thickness, heading date, flag leaf width, panicle length and single plant sterile seed
	1	Columiba 2, CO36, Kulivedichan, IR64, Bharathi, ADT45, ASD20, IR36, ACM01010, Uplri, Arupathamkuruvai, Kuliadichan, IR66, PTB10, CO33, CO35, TKM4, ACM07001, Improved Basmati370 and PTB50	Lower plant height and flag leaf length
	2	SR36B, CO34, Sigappukuruvai Kar, CO20, ASD14, ASD18, IR50, RMD1, CO43, CO49, CO47, PB1460, Swarana, IR20, Senthuram and CB06-563	
3	3	Pusa Basmati, ADT39, Early Samba, Andhra Sanam, Sonamashuri and ADT42	
	4	TKM1, CO23, White Ponni, CO38, ASD19, ADT49, PY4, ADT46, Rajshree and CO42	
	5	ASD4, ASD8, ASD7, Manipur local, CO9, PMK1, PMK2, Mattaikar, CO13, HKR47, TKM12, WGL14 and ADT44	
	6	Karungan, Njavara, White Sannam, TKM6, JGL1798, ADT38, JGL384, JGL3855, CO45, PTB51, MDU5, Samba, ASD16, PMK3, ASD1, ASD17, PMK4, ACM09001, ACM09007 and TKM5	
4	1	T2701, Kanohan, Basmati, CR1009, Culture 1177, Salivahaiva, Early Basmati, T396, Varakar and CO40	Higher culm thickness, heading date, flag leaf width and single panicle sterile seed
	2	Thusmani uttrimeram, T185, Culture 4932, Culture 14106, Kattu Kuthalai, T291, T517, T1035, T2684, Chethuvali and ASD9	Lower productive tiller
5	1	Swargathara, Vellaichithrai Kar, BG367-2, ACM09002, ADT43, ADT47, BPT5204, CO44, CO46, CO48, CO50, TKM11 and CB06-535	Higher single panicle total seed, single panicle fertile seed and single plant yield
	2	TKM3 and T420	

distances and grouped by unweighted paired group method using arithmetic average (UPGMA) using DARwin 5. The dendrogram depicted five distinct clusters (Table 4; Fig. 5). Group 1 consisted of 6 genotypes with characteristics of higher plant height, flag leaf length and panicle length. Group 2 had 22 genotypes with higher productive tillers and 1000 seed weight. A set of 88 genotypes were present in group 3. Group 4 had 21 genotypes with higher culm thickness, heading date, flag leaf width and single panicle sterile seed. Group 5 consisted of 15 genotypes with higher single panicle total seed, single panicle fertile seed and single plant yield.

The indigenous rice varieties cultivated by farmers in traditional tracts may contain huge agronomical genes that can serve as a source of germplasm to use in varietal improvement programmes. Landraces around centre of diversity and domestication are key natural resources important for maintaining the

future food security in the current scenario of climate change (Pusadee *et al.* 2009). Conserving the existing various farmers varieties and landraces are greater priorities. Once the characterization has been done, it is very easy to maintain these landraces without any change in their genetic structure and also useful for plant varietal production in the era of intellectual property rights (IPR).

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