Received: 01 Sep 2021 | Revised: 13 Sep 2021 | Accepted: 28 Sep 2021

Electronic Journal of Plant Breeding

Research Article

Studies on genetic diversity in selected rice (*Oryza sativa* L.) landraces of Tamil Nadu

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Abstract
A total of 50 traditional rice landraces of Tamil Nadu were characterised for 12 biometric traits and the data were subjected to principal component analysis and cluster analysis to determine the contribution in variation, diversity level and the strength of association prevailing between grain yield and its related traits. Out of 12 Principal components, four exhibited more than 1.0 eigenvalues and contributed to 73.58 per cent of the total variability. PC1 alone accounts for about 39.15 per cent, while PC2, PC3, PC4 contributed 14.39, 11.00 and 9.04 per cent for total variability, respectively. Through agglomerative clustering, the landraces were grouped into five clusters. The landraces present in cluster I (G1, G18, G23, G26, G31, G32, G36, G39, G43, G44, G45) and cluster V (G30 and G45) were found to be with contrasting characters making them ideal parents for further utilization in rice breeding programmes.

Key words: Rice, Landraces, Principal Component Analysis, Cluster Analysis

INTRODUCTION

Rice is one of the major food crops is consumed by more than half of the world population (Jiang *et al.,* 2020). In India, rice is cultivated under a wide range of ecosystems. Because of the wide range of adaptability, India has a rich diversity and variability which can be utilized for the enhancement of rice. Tamil Nadu has long been known as a rice-growing region with exceptional biodiversity. There are extensive mentions of varieties of rice in various kinds of literature and technical texts (Balasubramanian *et al*., 2019). Tamil Nadu has long been home to a myriad of rice varieties, many of which have been lost due to the extensive cultivation of high yielding varieties. The indigenous crop varieties that farmers have traditionally grown and preserved possess a high degree of genetic diversity and can serve as potential genetic resources for enhancing yield, pest and disease resistance along with agronomic performance (Hosington *et al*., 1999).

The yield of major cereal crops like rice, wheat and maize have plateaued after considerable improvements during the green revolution (Brisson *et al*., 2010). In order to satisfy the needs of the growing population, new strategies are needed to assist breeding programs to further enhance crop productivity, particularly in view of the negative effects of climate change on food security and on the environmental sustainability of cropping systems (Bocchiola *et al*., 2015; Diffenbaugh and Giorgi, 2012). The knowledge of the accessible genetic variability and complex relationships between the traits of interest are essential for all the crop improvement techniques. Morphological characterization of existing traditional germplasm is essential for the creation of new improved rice varieties that can aid rice systems in achieving greater economic and environmental sustainability (Mongiano *et al.,* 2020).

Multivariate statistical tools include Principal Component Analysis (PCA), Cluster Analysis and Discriminate Analysis (Oyelola *et al.,* 2004). The variation in a dataset is described by a set of uncorrelated variables, each of which is a linear combination of the original variables. The first principal component (PC) accounts for the bulk of the total variance, while the others account for the remaining variation in the data (Lopez-Cortes *et al.,* 2020).

Cluster analysis is a statistical approach for converting numerous characteristics of objects into quantitative measures (similarity distance) and, as a result grouping them into clusters at relatively close distances (Endo *et al.,* 1990). The cluster analysis may be used to classify rice germplasm with comparable characteristics into a single category. These multivariate analyses help in determining the traits contributing to yield. Therefore, the aim of this study is to assess the genetic diversity among the selected rice landraces of Tamil Nadu.

MATERIALS AND METHODS

The present study was carried out at the Department of Rice, Tamil Nadu Agricultural University, Coimbatore, during *Rabi,* 2020. A total of 50 rice landraces were collected from the germplasm collection of the Department of Rice, Tamil Nadu Agricultural University (**Table 1**). The materials were evaluated under Randomized Complete Block Design (RCBD) with two replications. Each germplasm was grown in a plot size of 1.2 m^2 with a plant spacing of 20 x 20 cm. A random sample of five plants was observed for each trait under study. The biometrical traits *viz.,* days to 50% flowering, days to maturity, flag leaf length (cm), flag leaf width (cm), stem thickness (cm), plant height (cm), the number of productive tillers per plant, panicle length (cm), the number of spikelets per panicle, the number of grains per panicle, spikelet fertility (%) and single plant yield (g) were recorded as per the national guidelines by PPV & FRA (2007). The observations recorded on the 12 traits were statistically analysed using STAR 2.0.1 software. Pearson's correlation coefficients were computed to evaluate the relationship among the observed variables. The principal component analysis was computed using the equation: $PC1 = {}^{p}\Sigma_{1} ajXj$, where; PC = Principal component, a_iX_i = Linear coefficient – Eigenvectors (Shoba *et al*., 2019). Agglomerative clustering was performed following Ward's method based on euclidean distance (Shoba *et al.,* 2019).

RESULTS AND DISCUSSION

Pearson's correlation coefficient was calculated to detect the association among the observed biometrical traits (**Table 2**). A positive correlation was found among most of the traits. Single plant yield had a highly significant positive correlation with traits like the number of productive tillers, the number of spikelets per panicle, the number of grains per panicle, spikelet fertility. It also had a significant positive correlation with days to 50% flowering, days to maturity, flag leaf length, flag leaf width, stem thickness and plant height. There was also a significant correlation among the traits contributing to yield. Days to 50% flowering was highly significant and positively correlated to days to maturity, flag leaf width, plant height, the number of spikelets per panicle and the number of grains per panicle. The number of productive tillers per plant was found to be positively correlated to the number of spikelets per panicle, the number of grains per panicle and spikelet

Table 1. List of rice traditional landraces used in this study

Code	Germplasm	Code	Germplasm	Code	Germplasm
G1	*Sarapillisamba*	G18	*SwarnaMashuri*	G35	*VasanaiSeeraga Samba*
G2	*Rangoon Samba*	G19	*White Ponni*	G36	*Kullakaru*
G3	*Muthuvellai*	G20	*Kitchilli Samba*	G36	*Kullakaru*
G4	*Korangu Samba*	G21	*Salem Channa*	G37	*Kuzhiyadichan*
G5	*Chetty samba*	G22	*AtthurKichili Samba*	G38	*ThulasiVasanai Samba*
G6	*Chitthan Samba*	G23	*Seeraga Samba*	G39	*Thengai Poo Samba*
G7	*Karthigai samba*	G24	*ThooyaMalli*	G40	*MutrinaKannam*
G8	*Palkachaka*	G25	*Mappillai Samba*	G41	*Rajamudi*
G9	*Ghandhasala*	G26	*Poongar*	G42	T182 *(Sornavari)*
G10	*Varakkal*	G27	*ArcotKichilli*	G43	T396 *(Peria Samba)*
G11	*Murugankar*	G28	*ManjaPonni*	G44	T507 *(Vellai Samba)*
G12	*Karuthakar*	G29	*Ottadaiyan*	G45	T508 *(Thooyala)*
G13	*Ponmani Samba*	G30	*Kattuyanam*	G46	T71 *(VellaiGundu Samba*
G14	*Vadakathi Samba*	G31	*Illumpam Poo Samba*	G47	T73 *(Godumarai Samba)*
G15	*Sadai Samba*	G32	*AruvathamKuruvai*	G48	T146 *(Ayyan Samba)*
G16	*KattuPonni*	G33	*SivappuKavuni*	G49	T181 *(ArupathamVellai)*
G17	*KaruppuKavuni*	G34	*Milagu Samba*	G50	T256 *(Puthupatty Samba)*

Table 2. Correlation matrix (Pearson (n)) for the 12 traits

Traits	DFF	DM	FLL	FLW	ST	PH	NPT	PL	NSP	NGP	SF	SPY
DFF	1	0.853**	0.217	0.525**	0.350*	0.385**	0.065	0.260	0.418**	0.417**	0.207	0.352*
DM	0.853**	1	0.136	0.558**	0.418**	0.400**	0.117	0.230	0.483**	0.477**	0.234	0.312*
FLL	0.217	0.136	1	0.276	0.168	0.025	-0.110	0.336*	0.299	0.299*	0.127	0.284*
FLW	0.525**	0.558**	0.276	1	0.245	0.213	0.075	0.198	0.390**	0.379**	0.149	0.217
ST	0.350*	0.418**	0.168	0.245	1	0.480**	0.112	0.236	0.347	0.373**	0.258	0.301*
PH	0.385**	0.400**	0.025	0.213	0.480**	1	0.111	0.296*	0.136	0.175	0.239	0.296*
NPT	0.065	0.117	-0.110	0.075	0.112	0.111	1	-0.188	0.343	0.395**	0.448**	0.603**
PL	0.260	0.230	0.336*	0.198	0.236	0.296*	-0.188	1	0.405**	0.408**	0.217	0.271
NSP	0.418**	0.483**	0.299*	0.390**	0.347*	0.136	0.343*	0.405**	1	0.981**	0.443**	0.531**
NGP	0.417**	0.477**	0.299*	0.379**	0.373**	0.175	0.395**	0.408**	0.981**	1	0.602**	0.557**
SF	0.207	0.234	0.127	0.149	0.258	0.239	0.448**	0.217	0.443**	0.602**	1	0.397**
SPY	0.352*	0.312	0.284*	0.217	0.301*	0.296*	0.603**	0.271	0.531**	0.557**	0.397**	1

(**Note:** *Significant at 0.05, **Significant at 0.01, DFF- days to 50% flowering , DM- days to maturity , FLL- flag leaf length , FLW– flag leaf width , ST- stem thickness , PH– plant height , NPT- number of productive tillers per plant , PL- panicle length , NSP– number of spikelets per panicle , NGP– number of grains per panicle , SF – spikelet fertility percentage, SPY- single plant yield.

fertility percentage. The number of spikelets per panicle and the number of grains per panicle are found to be significantly positively correlated to all the observed traits except for flag leaf length. Sohrabi *et al*. (2012) reported similar results where the yield of the plant was correlated with 12 traits. Most of the quantitative characters like yield and yield contributing traits are highly influenced by the interaction between genotype and environment, which shows that correlation coefficient is helpful for breeders in selecting important traits (Ahmadikhah *et al*., 2008).

The relationship among the traits was further investigated using principal component analysis, to determine the strength and direction of correlation between the original traits and their corresponding principal components (PCs) (Mongiano *et al.,* 2020). The proportion of variance, cumulative proportion and eigenvalues were given in **Table 3**. Out of the 12 principal components obtained, four PCs had eigenvalues of more than 1 cumulatively contributed for 73.58 per cent of the total variation. This suggests that the identified characteristics within these axes had a significant impact on the germplasm's phenotype. This is in agreement with earlier reports by Sheela *et al*. (2020) in which 4 PCs of 24 genotypes for 10 traits contributed to 72.24 per cent of the total variability. The contribution of different morphological traits to the total variation in each principal component was given in **Table 4**. PC1 alone contribute to 39.15 per cent of the total variability. Total variation in each principal axis is determined by the number of variables. PC1 had

Table 3. Eigen values, % variance and cumulative eigen values of rice germplasm

Traits	Principal Component	Eigenvalue	Variability (%)	Cumulative %
DFF	PC1	4.70	39.15	39.15
DM	PC2	1.73	14.39	53.54
FLL	PC3	1.32	11.00	64.54
FLW	PC4	1.09	9.04	73.58
ST	PC5	0.78	6.48	80.06
PH	PC6	0.64	5.35	85.41
NPT	PC7	0.59	4.89	90.30
PL	PC8	0.51	4.21	94.51
NSP	PC9	0.34	2.81	97.32
NGP	PC10	0.19	1.62	98.94
SF	PC11	0.13	1.04	99.99
SPY	PC12	0.00	0.01	100.00

DFF- days to 50% flowering , DM- days to maturity , FLL- flag leaf length , FLW– flag leaf width , ST- stem thickness , PH– plant height , NPT- number of productive tillers per plant , PL- panicle length , NSP– number of spikelets per panicle , NGP– number of grains per panicle , SF – spikelet fertility percentage, SPY- single plant yield.

contribution from days to 50% flowering (0.707), days to maturity (0.737), flag leaf width (0.578), stem thickness (0.571), the number of spikelets per panicle (0.825), the number of grains per panicle (0.858), spikelet fertility percentage (0.582) and single plant yield (0.688). This shows that PC1 synthesised the direct relations between most of the traits and yield. In PC 2, which contributed to 14.49 per cent of total variability, the number of productive tillers per plant showed high factor loading (0.747). PC 3 was found to have 11 per cent of total variability with high factor loading for flag leaf length (0.630) and panicle length (0.497). Another 9.04 per cent of the total diversity was found to be present in PC4, in which plant height accounts for 0.567 factor loading. A similar type of performance was obtained by Sanni *et al.* (2012) and Guei *et al.* (2005). 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 (Nachimuthu *et al.*, 2014). The genotypes having more than one PC score were given in **Table 5**. The G41, G47, G19, G28, G30, G7, G17, G3, G32, G25, G27 were found to have high PC scores in more than one PC.

Scree plot was obtained by plotting the eigenvalues on the y axis and PC numbers on x axis. In the scree plot, the point where the slope of the curve levelled off (elbow) indicated the appropriate number of PCs to be considered (**Fig. 1**). Scree plot clearly showed that a maximum amount of variation was found in PC1, meaning the selection of germplasm and traits from PC1 would be useful. Shoba *et al.* (2019) and Nachimuthu *et al.*(2014) also reported similar results where PC1 contributed for the highest variability.

The biplot of PC1 against PC2 showed that the germplasm *viz*., G48, G49, G3 G37 were positively influenced by the traits as 50% flowering, days to maturity, flag leaf width,

Table 4. Principal component analysis (PCA) for 12 variables of rice germplasm

Traits	DFF	DM	FLL	FLW	ST	PH	NPT	PL	NSP	NGP	SF	SPY
PC1	0.707	0.737	0.383	0.578	0.571	0.478	0.394	0.486	0.825	0.858	0.582	0.688
PC2	-0.437	-0.398	-0.194	-0.357	-0.181	-0.263	0.747	-0.271	0.217	0.282	0.448	0.390
PC3	-0.250	-0.312	0.630	-0.036	-0.227	-0.441	-0.357	0.497	0.280	0.250	-0.005	-0.024
PC4	-0.256	-0.269	0.009	-0.427	0.421	0.567	-0.110	0.423	-0.160	-0.099	0.175	0.094

DFF- days to 50% flowering , DM- days to maturity , FLL- flag leaf length , FLW– flag leaf width , ST- stem thickness , PH– plant height , NPT- number of productive tillers per plant , PL- panicle length , NSP– number of spikelets per panicle , NGP– number of grains per panicle , SF – spikelet fertility percentage, SPY- single plant yield.

Table 5. Selection of Germplasm with more than 1.0 PC score

PC1		PC2		PC3		PC4	
Germplasm	PC score	Germplasm	PC score	Germplasm	PC score	Germplasm	PC score
G41	5.408	G32	3.411	G28	3.738	G30	2.486
G30	4.852	G47	3.258	G29	3.539	G7	2.175
G21	3.957	G43	2.355	G30	2.414	G17	1.787
G48	3.156	G19	2.161	G8	1.487	G41	1.785
G19	3.128	G5	2.074	G33	1.118	G3	1.598
G28	3.125	G39	1.915	G27	1.013	G32	1.484
G17	2.419	G44	1.618			G25	1.304
G40	2.197	G1	1.270			G27	1.139
G49	1.991	G26	1.199				
G47	1.973	G23	1.036				
G38	1.757						
G37	1.685						
G3	1.673						
G50	1.338						
G7	1.099						
G25	1.093						

panicle length, stem thickness (**Fig. 2**). Also, the biplot of PC1 against PC3 revealed that the genotypes G30, G28, G48 were positively influenced by important yield contributing traits as the number of spikelets per panicle, the number of grains per panicle, panicle length and flag leaf length (**Fig. 3**). G48 was found to be common in both biplots showing it was influenced by most of the traits. Similarly, Shoba *et al.*(2019) reported several aromatic rice genotypes positively influenced by yield contributing traits in PC1, PC2 and PC3.

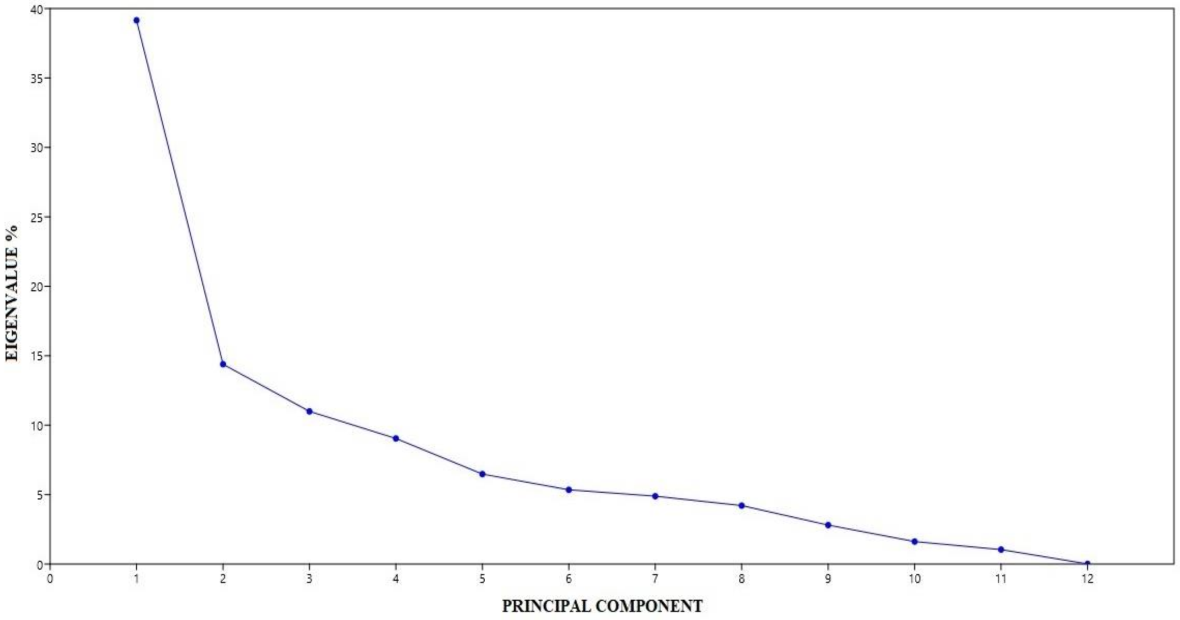

Fig. 1. Scree plot for different PCs

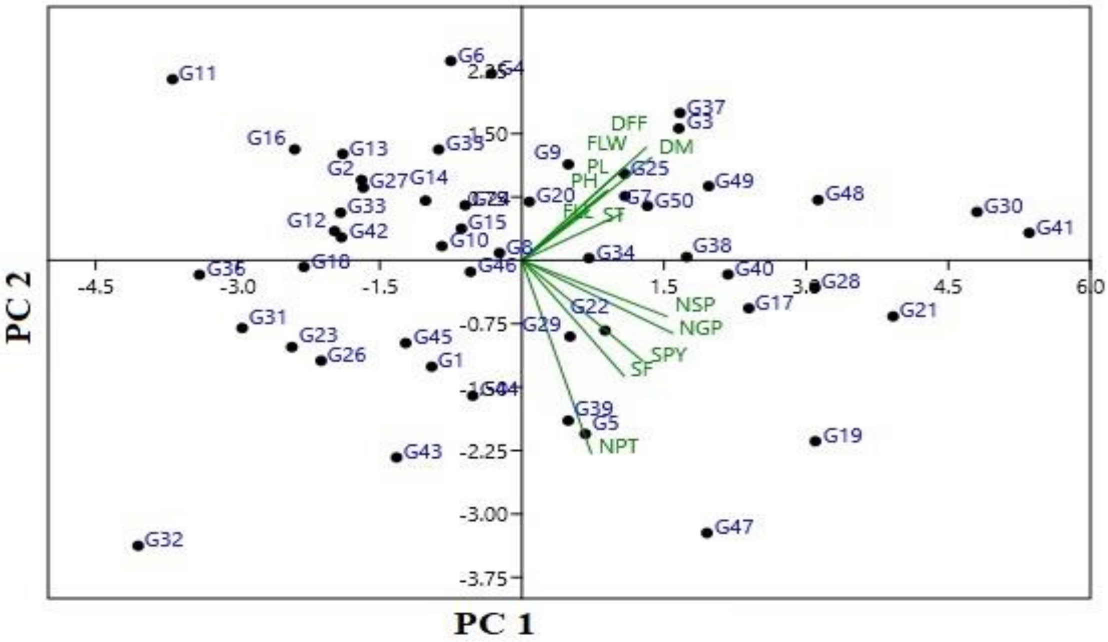

Fig. 2. The Biplot of germplasm for PC1 and PC2

DFF- days to 50% flowering , DM- days to maturity , FLL- flag leaf length , FLW– flag leaf width , ST- stem thickness , PH– plant height , NPT- number of productive tillers per plant , PL- panicle length , NSP– number of spikelets per panicle , NGP– number of grains per panicle , SF – spikelet fertility percentage, SPY- single plant yield. G1 to G50- Rice landraces

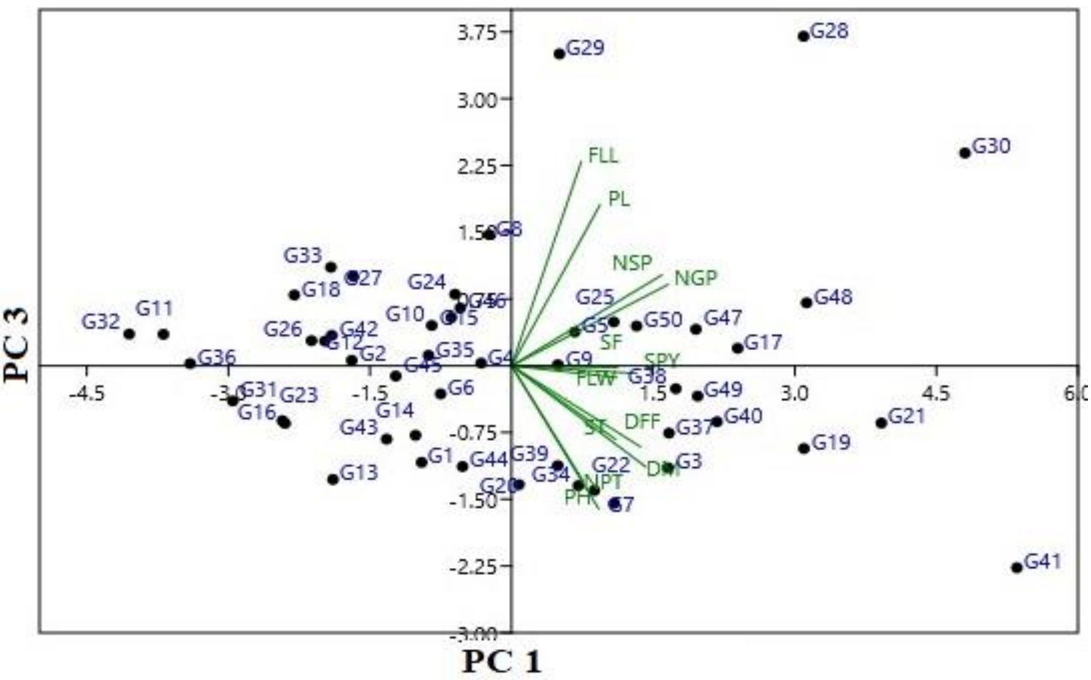

Fig. 3. The Biplot of germplasm for PC1 and PC3

DFF- days to 50% flowering , DM- days to maturity , FLL- flag leaf length , FLW– flag leaf width ,ST- stem thickness , PH– plant height, NPT- number of productive tillers per plant , PL- panicle length , NSP– number of spikelets per panicle , NGP– number of grains per panicle , SF – spikelet fertility percentage, SPY- single plant yield. G1 to G50- Rice landraces

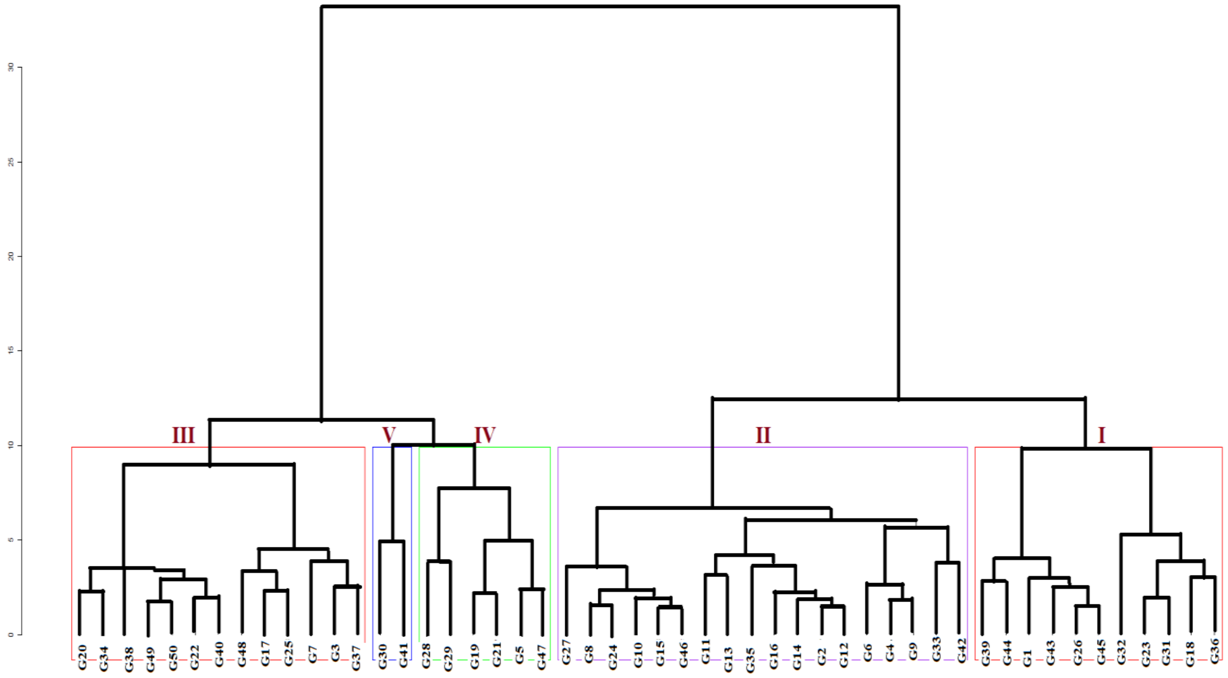

Fig. 4.Dendrogram using agglomerative clustering method in traditional rice germplasm

Table 6. Hierarchical cluster grouping in aromatic rice germplasm accessions

Cluster	Number of genotypes	Germplasm	Percentage of total germplasm
I	11	G1 G18 G23 G26 G31 G32 G36 G39 G43 G44 G45	22
II	18	G2 G4 G6 G8 G9 G10 G11 G12 G13 G14 G15 G16 G24 G27 G33 G35 G42 G4	30
III	13	G3 G7 G17 G20 G22 G25 G34 G37 G38 G40 G48 G49 G50	26
IV	6	G5 G19 G21 G28 G29 G47	12
V	2	G30 G41	4

Table 7. Cluster mean for different traits of the landraces

Cluster	DFF	DM	FLL	FLW	ST	PH	NPT	PL	NSP	NGP	SF	SPY
I	78.73	112.82	34.81	1.02	0.34	95.39	12.57	20.88	133.10	100.71	76.34	23.90
II	89.78	121.33	41.48	1.28	0.34	104.46	8.88	22.85	131.94	96.74	73.26	21.41
III	100.23	134.38	39.14	1.57	0.38	119.25	11.31	23.81	177.62	142.45	80.05	26.64
IV	92.67	125.33	43.12	1.38	0.36	96.81	12.93	23.84	244.84	201.81	82.57	30.97
V	103.00	136.50	52.35	1.51	0.71	136.2	12.35	26.28	242.08	204.08	84.47	32.87

DFF- days to 50% flowering (days), DM- days to maturity (days), FLL- flag leaf length (cm), FLW– flag leaf width (cm), ST- stem thickness (cm), PH– plant height (cm), NPT- number of productive tillers per plant (no.), PL- panicle length (cm), NSP– number of spikelets per panicle (no.), NGP– number of grains per panicle (no.), SF – spikelet fertility percentage (%), SPY- single plant yield (g)

Cluster analysis was performed to identify the grouping patterns among the landraces that were evaluated and to give phenotypic categorization (**Fig. 4**). The relationship among the 50 landraces of rice was revealed by agglomerative clustering analysis following the Euclidean distance method. The 50 landraces were grouped into five clusters (**Table 6**). Cluster II was the largest cluster with 18 landraces or 30 per cent of all genotypes. Cluster III was the second largest cluster with 13 germplasm followed by cluster I with 11 landraces. Cluster IV had four landraces and cluster V is the smallest with two germplasm. Cluster means for different traits of all the landraces were given in **Table 7**. Cluster I had a low mean for all the traits except for the number of productive tillers per plant, spikelet fertility percentage and single plant yield. Cluster II had a low mean value for stem thickness, the number of productive tillers per plant, the number of spikelets per panicle, the number of grains per panicle, spikelet fertility percentage and single plant yield. Cluster III had a high mean for flag leaf width. Cluster IV had a high mean for the number of productive tillers per plant and the number of spikelet per panicle. Cluster V had the highest mean for the following traits *viz*., days to 50% flowering, days to maturity, flag leaf length, stem thickness, plant height, the number of grains per panicle, spikelet fertility percentage and single plant yield. From this, it was concluded that cluster I was made of early maturing varieties having a low mean for yield contributing traits, whereas cluster V consisted of late maturing landraces with a high mean for yield contributing traits. This showed that the genotypes present in cluster I (G1, G18, G23, G26, G31, G32, G36, G39, G43, G44, G45) and cluster V (G30 and G45) were of contrasting characters making them ideal parents for the production of short duration rice with high yielding traits through recombination. A similar clustering pattern was previously recorded in several reports (Rahman *et al*., 2011; Hanyong *et al*., 2004 and Shoba *et al*., 2019). Selecting parents for hybridization from the diverse clusters (cluster I and cluster V) identified in this study may result in segregants with the much needed combinations of superior alleles for various traits like early flowering, high yield, increased number of tillers and quality grains (Anyaoha *et al*., 2018).

From this research, it was concluded that traits *viz*., days to 50% flowering, days to maturity, flag leaf length, the number of productive tillers per plant, plant height, the number of spikelets per panicle, the number of grains per panicle are all critical variables. In addition, the multivariate analysis indicates the appropriate use of several rice landraces as a part of future breeding programmes.

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