Research Article

Characterization of rice landraces of Tamil Nadu by multivariate analysis

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Abstract
The morphological characterization of plant is the basic criteria in order to provide fundamental information for plant breeding programme. The main objective of the present work was to characterize 56 landraces of rice including high yielding varieties of Tamil Nadu, based on six quantitative agro-morphological characters. Agro-morphological characters were analyzed using Multivariate statistical analysis. Multivariate analysis involves observation and analysis of more than one statistical variable at a time. Principal component analysis was utilized to examine the variation and to estimate the relative contribution of various traits for total variability. This analysis helps to enabled pattern of variation of the germplasm of landraces of rice. PCA showed the contribution of each character to the classification of the rice landraces into different cluster groups. The first three principal components explained about 76.13 % of the total variation among the six characters. In the current study, Component 1 had the contribution from all the traits which accounted 34.66 % of the total variability. Component 2 had the contribution from plant height and panicle length which accounted 27.99 % of the total variability with the Eigen value of 1.68. The remaining variability of 13.48 %, 9.47 %, 9.0 % and 5.41 % was consolidated in component 3, component 4, component 5 and component 6 by various traits. The cumulative variance of 94.59 % of total variation among six characters was explained by the first five axes. Thus the results of principal component analysis used in the study have revealed the high level of genetic variation and the traits contributing for the variation was identified. Hence this population panel can be utilized for trait improvement in breeding programs for the traits contributing for major variation.

Keywords
Rice land races, Genetic Variation, Principal Component Analysis

Introduction

Rice is a major agriculture crop in India grown under diverse ecological conditions, with varied phenology and yield (Rani and Maragatham, 2013). History shows that technological advancement and its applications in agricultural crop plants brought great respite at times when burgeoning population desperately needed security in food fronts (Shetty *et al.,* 2014). 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. Information on the genetic diversity and distance among the breeding lines and the correlation between genetic distances are important for determining breeding strategies, classifying the parental lines, defining heterotic groups, and predicting future hybrid performance (Acquaah, 2012).

The landraces are valuable as they possess treasure of genetic materials which may prove valuable in future crop development and improvement programs. Green revolution was considerably held to improve production of food grains in our country and its role in achieving status of self sufficiency in food grain is beyond any doubt (Srivastava and Jaffe, 1993). But high yielding varieties, which are the back bone of green revolution, have indirectly stimulated erosion of landraces and wild varieties of rice (Fowler and Moony 1990). Presently more than 90% of rice cultivation is being done using high yielding variety only. Obviously landraces are disappearing fast. Importance of landraces can never be denied in agriculture system, because improvement in existing variety depends upon desirable genes which are possibly present in landraces and wild varieties only (Holden *et al.,* 1993). Landraces offer a valuable gene pool for future breeding programme (Patra 2000). 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 (Nachimuthu *et al*., 2014).

Multivariate statistical tools include Principal Component Analysis (PCA), Cluster analysis and discriminate analysis (Maji *et al.* 2012). 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 (Oyelola, 2004). Principal components are generally estimated either from correlation matrix or covariance matrix.
When the variables are measured in different units, scale effects can influence the composition of

derived components. In such situations it becomes desirable to standardize the variables. In the present investigation correlation matrix was used to extract the principal components. It accomplishes this reduction by identifying directions (positive & negative), called principal components, along which the variation in the data is maximal (Singh and Narayanan, 2013). Thus the primary benefit of PCA arises from quantifying the importance of each dimension for describing the variability of a data set. Considering the importance of PCA, an investigation was carried out on rice germplasm with an objective to dissecting yield and quality related inters componential traits. The study is aimed to determine level of germplasm variation in *Oryza sativa* L. to identify and classify variation for grouping the accessions by taking into account several characteristics and relationship between them.

Materials and Methods
The present investigation was carried out using 55 traditional lowland and upland rice cultivars, collected from the Cauvery Delta Region, Gudalur, Coimbatore of Tamil Nadu during kharif season of 2015 (Table 1). For easy identification and retrieval, each accession was named as RG 1 to RG 56. A set of 56 genotypes were grown in Tamil Nadu Rice Research Institute, Tamil Nadu Agricultural University, Aduthurai, India during Rabi 2015. Six 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 traits *viz.,* days to 50% flowering, plant height, no. of productive tillers per plant, panicle length, no. of grains per panicle and single plant yield.

Data were statistically analyzed to identify groups among the traditional rice varieties that were genetically different or similar based on the six traits measured. In order to identify the patterns of variation, Principal component Analysis was conducted. Those PCs with Eigen values greater than one were selected as proposed by Jeffers (1967). Correlations between the original traits and the respective PCs were calculated and the principal component analysis (PCA) were done using SAS PC version 8 (SAS Institute, 1999). Data were processed using statistical program (Statistical analysis System). The principal component analysis was computed using the following equation:

PCA

$$PC1 = \sum_{1}^{p} a_j X_j$$

Where; PC = Principal component, a_{1j} = Linear coefficient – Eigen vectors

Results and Discussion
The mean performance and first order Statistical measures *i.e.* maximum, minimum, mean and Standard Deviation (SD) for the measured traits are presented in Table 2 and 3. The genotype RG29 (Illupaipu Samba) has taken the longest days (119 days) for days to 50 per cent flowering and RG 16 (TKM 9) had short duration (79 days) of 50 per cent flowering. The overall mean for flowering for the germplasm accessions was 94 days. Mean for productive tillers of 56 germplasm lines were 8.0 with the minimum and maximum value of 33.0 in the genotype RG30 (Karudan Samba) and in the genotype RG54 (Kakkarathan) respectively and the RG 54 also showed maximum single plant yield (59.65 g). The germplasm RG 43 (Nootripathu) showed minimum number of grains per plant and single plant yield (14.68 g). Maximum number of grains per plant recorded by the genotype Sivappukavuni (RG 32) with the mean value of 114.9. Mean height of 55 lines were 110.9 cm. The variation observed for this trait was 65.0 cm to 148.5 cm (Manulayan).

The trait panicle length had recorded the mean value of 25.32 cm with genotype RG35 (Kallurundaikar) recorded the lowest panicle length of 16.0 cm and the genotype RG25 (Jeeragasamba) had lengthier panicle of 31.0 cm. The trait single plant yield had recorded the overall mean of 26.56 g per plant. The genotype RG43 (Nootripathu) was recorded with the lowest single plant yield of 15.0g and the genotype RG54 (Kakkarathan) had the highest single plant yield (60.5g). The genotype RG29 has taken the longest days for flowering as well as maturity. The taller genotype is RG22 (Manulayan) where as RG18 (ADT 43) has short stature (65 cm). RG32 (Sivappukavuni) has more number of grains (114.9) but RG54 has higher single plant yield. Frequency distribution for different traits on 55 germplasm accessions revealed different patterns of distribution as shown on Figure 1-6.

Principal component analysis (PCA) was employed to reduce the complexity of the data set while retaining the variation within the data set as far as possible. The result of the PCA explained the genetic diversity of the rice collection. Proper values measure the importance and contribution of each component to 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 PCA resulted in six independent principal components that had a cumulative explained variance of 100%

(Table 4).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.

In this study, we chose to follow the criterion used by Clifford and Stephenson (1975) and supported by Guei *et al.* (2005), which suggested that the first three principal components are often the most important in reflecting the variation patterns among accessions and the characters associated with these are more useful in differentiating accessions. The first three component in PCA analysis contribute 76.13% of the variability with eigen values >1 & = 1 among total genotypic variability for six quantitative characters of 55 landraces including high yielding varieties are represented in Table 4 and Fig. 7 and 8, giving a clear idea of the structure underlying the variables analyzed. PC 4 to PC 6 possesses eigen value <1. PC1 with eigen value of 2.09 contribute 34.66% of the total variability, PC2 and PC 3 with eigen value of 1.68, 0.91contribute 27.99% and 13.48 % of the total variability respectively. PC4, PC 5 and PC 6 with eigen value < 1 possess < 10 %, contribution to the total genotypic variability.

Scree Plot: Scree plot explained the percentage of variance associated with each principal component obtained by drawing a graph between eigen values and principal component numbers. PC1 showed 34.66 % variability with eigen value 2.09 which then declined gradually. Nachimuthu *et al.*, 2014 also got highest variability in PC1 with eigen value more than 1.0. Semi curve line is obtained after five PC tended to become straight with little variance observed in each PC. From the graph, it is clear that the maximum variation was observed in PC1 in comparison to other PCs. So, selection of lines from this PC will be useful (Fig. 9). Those principal components having more than one eigen value that showed more variation among the rice genotypes for the selection of the diverse parents.

The different morphological traits contribute for total variation calculated for each component. The first principal component accounted for more than 30% of total variance. Variables highly and positively correlated were days to 50% flowering with loading of 0.487, panicle length (0.483) and number of grains per panicle (0.414). Second principal component PC2 accounted for more than 27% variation and identified yield component variables *i.e.* number of productive tillers and number of grains per panicle presenting negative contributions. The first, second and fifth component has phenological and yield related variables. Similar type of performance was

obtained by Kayode, 2008; O'Rourke and Hatcher, 2013; Sanni *et al.,* 2012 has obtained similar pattern for phenological variables in rice.

The second principal component PC2 accounted for 27.99 % variation and was associated with plant height (0.539) and panicle length (0.412). PC3 is related to days to 50 % flowering (0.541). PC 4 is related to panicle length (0.349), PC 5 is more related to days to 50 %flowering (0.347), single plant yield (0.309), number of grains per panicle and PC 5 is related plant height (0.689) and single plant yield (0.264) (Table 5).

In that, principal component analysis revealed that six quantitative characters *viz.,* days to 50% flowering, plant height, number of productive tillers, panicle length, number of grains per panicle, single plant yield significantly influenced the variation in these cultivars. The first three components in the PCA analysis with eigenvalues >1 and =1 contributed 76.13 per cent of the variability among genotypes evaluated for different agro-morphological traits. Similar type of performance was obtained by Varthini V *et al.,* 2014. Other PCs (4 - 6) had eigenvalues less than 1. 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.

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Table 1. List of various landraces of rice collected from various parts of Tamil Nadu

AC No.	Name of Germplasm	AC No.	Name of Germplasm
RG1	JAYA	RG29	ILLUPAIPU SAMBA
RG2	CHINNAPUNCHAI	RG30	KARUDAN SAMBA
RG3	VARISURIAN	RG31	SURA KURUVAI
RG4	THAICHING	RG32	SIVAPU KAVUNI
RG5	KURAKAT	RG33	KAIVARA SAMBA
RG6	IR 20 RED	RG34	NORUNGAN
RG7	ADUKAN	RG35	KALLURUNDAI KAR
RG8	KALYANI	RG36	WHITE PONNI
RG9	MANDAMARANELLU	RG37	SIVAPPUKURUVIKAR
RG10	KALAYA	RG38	KATTU PONNI
RG11	KOTHANDAN	RG39	KATTAI KAR
RG12	ATHIRA 1	RG40	POONGAR
RG13	CHINTHAMANI	RG41	PURPLE PUTTU
RG14	KADAI KANNAN	RG42	MURUNGAN KAR
RG15	KAYAMMA	RG43	NOOTRIPATHU
RG16	TKM 9	RG44	UPPUMILAGAI
RG17	ADT 45	RG45	VELLAICHITHIRAIKAR
RG18	ADT 43	RG46	SIVAPUCHITHIRAIKAR
RG19	ADT 41	RG47	KAVUNI
RG20	THONDI	RG48	BARMA KAVUNI
RG21	MALLAM PUNCHAN	RG49	VELLAI KAVUNI
RG22	MANULAYAN	RG50	KARUTHA KAR
RG23	MARANELLU	RG51	KALLUNDAI
RG24	GEB 24	RG52	MOHINI SAMBA
RG25	JEERAGASAMBA	RG53	SAYASREE
RG26	SWARNA	RG54	KAAKRATHAN
RG27	MAPPILAI SAMBA	RG55	BPT 5204
RG28	THANGAN KAR	RG56	MATTAIKAR

Table 2. Mean performance of traditional and promising rice varieties for biometrical traits

Sl. No.	GENOTYPES	DFF (days)	PH (cm)	NPT (no.)	PL (cm)	NG (no.)	SPY (g)
1	JAYA	90.50	80.50	21.50	24.70	108.50	20.29
2	CHINNAPUNCHAI	83.50	115.50	16.00	25.00	88.00	20.50
3	VARISURIAN	112.50*	110.00	15.00	29.30*	126.50*	16.93
4	THAICHING	83.00	105.00	19.00	24.70	112.50	15.16
5	KURAKAT	93.50	91.50	15.00	27.00	137.50*	22.51
6	IR 20 RED	112.50*	93.00	21.50	26.00	143.50*	47.64*
7	ADUKAN	91.00	75.00	17.00	25.30	91.50	20.59
8	KALYANI	94.00	80.50	15.50	24.10	106.00	28.68*
9	MANDAMARANELLU	88.50	120.50*	13.00	27.10	88.00	21.00
10	KALAYA	88.50	115.50	17.50	26.60	88.50	22.50
11	KOTHANDAN	99.00*	67.00	30.00*	19.00	96.00	36.68*
12	ATHIRA 1	88.50	91.00	21.00	25.50	107.50	53.81*
13	CHINTHAMANI	86.50	98.50	16.00	20.50	87.50	20.00
14	KADAI KANNAN	88.00	105.50	13.50	26.70	98.00	26.77
15	KAYAMMA	86.00	104.00	17.50	23.60	103.50	22.67
16	TKM 9	79.00	70.50	16.50	22.25	108.50	26.50
17	ADT (R) 45	82.50	65.50	11.50	19.50	102.50	35.76*
18	ADT 43	85.50	65.00	14.00	22.35	163.00*	38.79*
19	ADT 41	83.50	69.50	16.50	21.20	150.00	30.00
20	THONDI	86.00	120.00	22.50	23.50	119.00	23.65
21	MALLAM PUNCHAN	94.00	113.50	19.50	24.00	93.00	25.45
22	MANULAYAN	94.00	148.50*	12.00	25.85	97.50	20.77
23	MARANELLU	111.00*	126.50*	19.00	28.10*	100.50	18.38
24	GEB 24	105.50*	124.00*	20.50	30.25*	123.50*	23.00
25	JEERAGASAMBA	111.50*	135.00*	28.50*	30.85*	153.00*	23.61
26	SWARNA	101.00*	79.00	32.00*	22.25	142.50	26.60
27	MAPPILAI SAMBA	114.00*	130.50*	17.00	25.75	112.50	27.57
28	THANGAN KAR	92.50	127.00*	19.00	22.25	102.00	17.25
29	ILLUPAIPU SAMBA	119.00*	119.50*	13.50	20.75	109.00	18.85
30	KARUDAN SAMBA	113.50*	146.00*	8.00	28.75*	117.50	25.00
31	SURA KURUVAI	85.50	141.50*	11.00	27.25	105.50	23.69
32	SIVAPU KAVUNI	90.50	138.50*	28.00*	30.60*	**253.00***	31.37*
33	KAIVARA SAMBA	91.50	139.00*	20.00	29.05*	98.00	52.01*
34	NORUNGAN	87.00	100.50	12.50	25.60	123.50*	21.68
35	KALLURUNDAI KAR	88.50	81.50	13.50	15.50	133.50*	20.66
36	WHITE PONNI	107.00*	88.50	13.50	12.50	135.00*	30.00*
37	SIVAPPUKURUVIKAR	85.50	141.50*	11.00	27.25	105.50	23.69
38	KATTU PONNI	86.50	100.50	12.50	21.50	130.00*	21.88
39	KATTAI KAR	90.50	134.50*	20.50	30.50*	94.00	15.65
40	POONGAR	92.50	127.00	19.00	22.25	102.00	17.25
41	PURPLE PUTTU	81.50	115.50	11.50	26.25	106.50	19.57
42	MURUNGAN KAR	82.50	95.50	12.00	24.95	121.50*	15.43
43	NOOTRIPATHU	83.00	114.50	13.50	23.65	87.50	14.68
44	UPPUMILAGAI	115.50*	125.50*	11.50	26.25	96.50	26.65
45	VELLAICHITHIRAIKAR	92.50	108.50	23.00	17.85	99.00	22.50
46	SIVAPUCHITHIRAIKAR	82.50	90.50	18.50	16.10	104.00	19.76
47	KAVUNI	89.00	137.50*	14.00	25.75	113.50	20.80
48	BARMA KAVUNI	111.00*	136.50*	22.50	29.25	115.00	26.93
49	VELLAI KAVUNI	89.00	133.50*	15.50	27.75	123.50*	26.34
50	KARUTHA KAR	85.50	106.00	14.00	23.25	112.50	21.00
51	KALLUNDAI	110.50*	131.00*	13.60	27.10	100.00	21.58
52	MOHINI SAMBA	85.00	75.50	24.50*	18.10	88.50	25.78
53	SAYASREE	123.00*	130.50*	21.50	26.10	165.50*	52.55*
54	KAAKRATHAN	116.00*	128.50*	32.50*	30.50	156.00*	59.65*
55	KALLUNDAIKAR	88.50	81.50	13.50	15.50	133.50*	20.66
56	BPT 5204	106.00*	75.50	32.50*	21.25	95.50	39.88*
57	MATTAIKAR	85.00	82.50	11.00	19.60	108.50	20.16
	MEAN	94.54	107.97	17.64	24.28	115.51	26.12
	SEd	1.23	3.90	2.83	1.67	2.94	1.08
	CD (5%)	2.48	7.82	5.66	3.34	5.88	2.16

Table 3. Characteristic means and variations of 55 traditional rice varieties

Sl. No.	Characters	Germplasm Name	Minimum	Germplasm Name	Maximum	Mean	SD
1	Days to 50% flowering	RG 16	79.0	RG 29	119.0	93.9	11.3
2	Plant Height	RG 18	65.0	RG 22	148.5	110.9	24.2
3	No. of Productive tillers	RG 30	08.0	RG 54	33.0	19.1	7.1
4	Panicle length	RG 35	16.0	RG 25	31.0	25.3	4.2
5	No. of grains/ panicle	RG 43	88.0	RG 32	253.0	114.9	28.6
6	Single plant yield	RG 43	15.0	RG 54	60.5	26.6	11.3

Table 4. Computed eigenvalues of the different principal components with corresponding proportion and cumulative explained variance.

Components	Eigenvalue	Explained Variance	
		Percent	Cumulative
PC 1	2.09	34.66	34.66
PC 2	1.68	27.99	62.64
PC 3	0.91	13.48	76.12
PC 4	0.57	09.47	85.59
PC 5	0.54	09.00	94.59
PC 6	0.32	05.41	100

Table 5. Principal component analysis of six morphological characters for 55 landraces of rice
(Correlations between initial variables and PC: component loading)

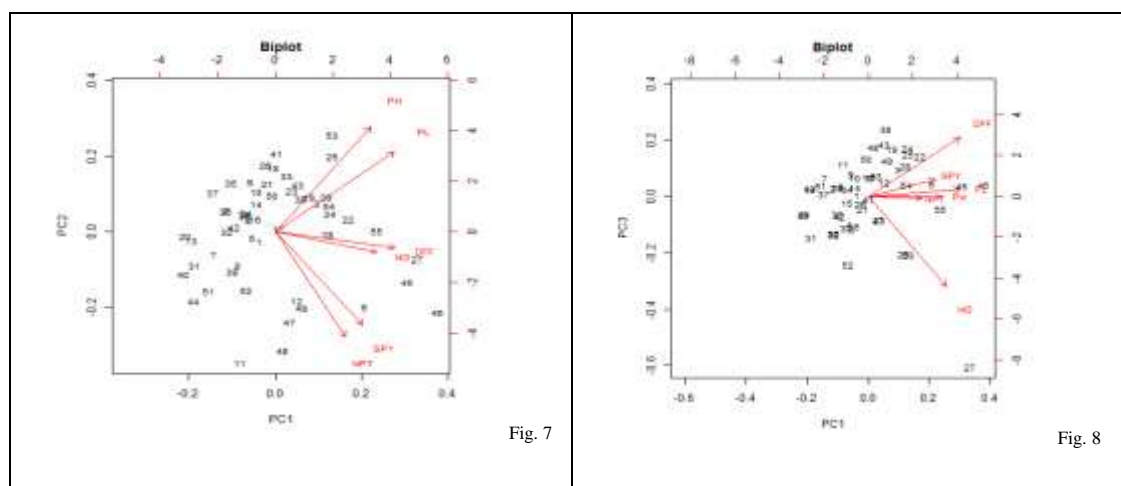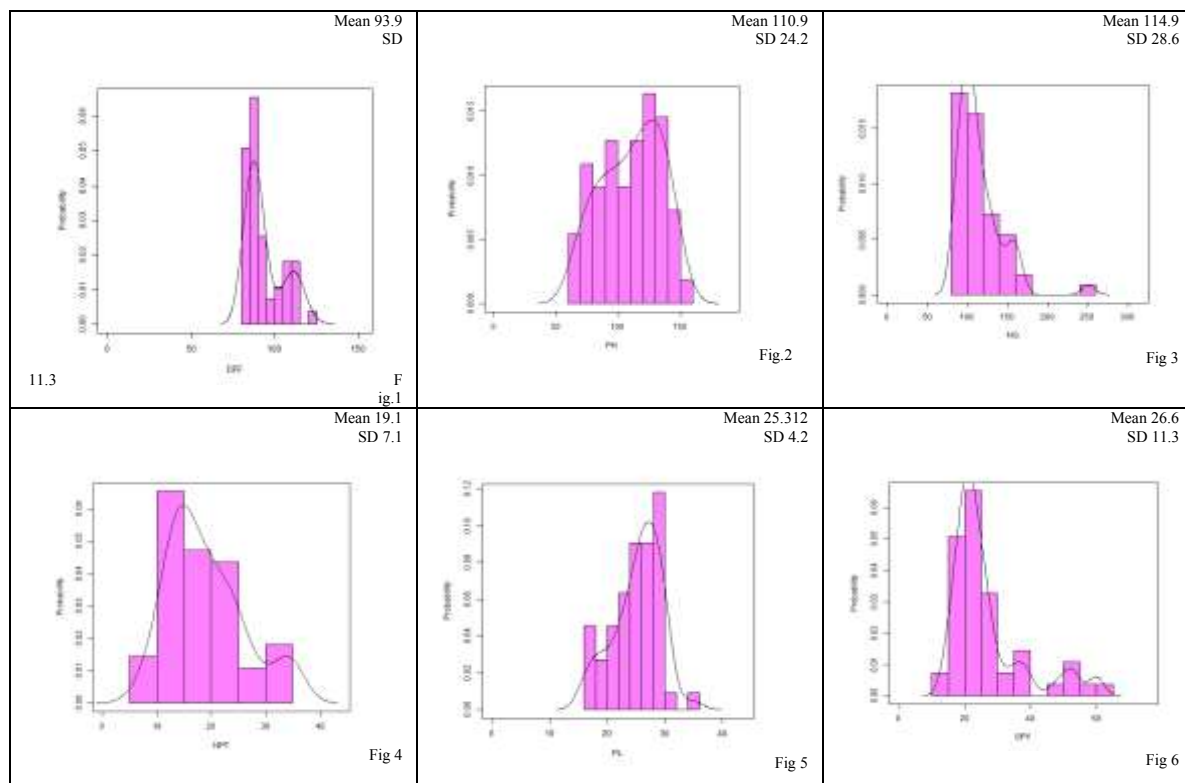| Variables	PC1	PC2	PC3	PC4	PC5	PC6
Days to 50% flowering	**0.487**	-0.081	**0.541**	-0.586	**0.347**	-0.025
Plant Height	0.387	**0.539**	-0.004	0.043	-0.289	**0.689**
No. of productive tillers	0.287	-0.541	-0.016	-0.157	-0.773	-0.052
Panicle length	0.483	0.412	0.061	0.349	-0.136	-0.673
No. of grains per panicle	0.414	-0.104	-0.825	-0.229	0.292	-0.019
Single plant yield	0.355	-0.479	0.154	**0.675**	0.309	0.264

Fig. 7 and 8 Distribution of genotypes across two components
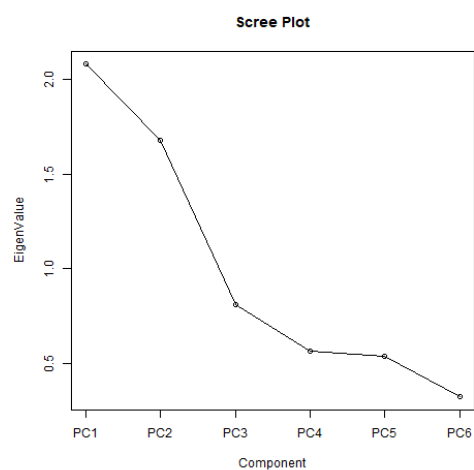
Fig. 9. Scree plot showing Eigen value variation