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Research Article

Assessment of genetic diversity in aromatic rice (*Oryza sativa* L.) germplasm using PCA and cluster analysis

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Abstract

A total of 67 aromatic rice germplasm lines were evaluated for nine traits by PCA and cluster analysis for determining the pattern of variation, relationship among individuals and their characteristics. Out of nine PCs, four exhibited more than 1.0 eigen values and showed 70.14 per cent total variability among the characters. PC1 showed high proportion of total variation 25.9 per cent and PC2, PC3 and PC4 contributed 16.96 per cent, 15.06 per cent and 12.22 per cent of the total variance, respectively. Highest positive eigen vector was observed in grain width (0.46) followed by plant height (0.34) in PC1 indicated the large effect in the overall variation of the genotypes. From the cluster analysis, clusters I, II and III had desirable mean values for days to 50 per cent flowering, plant height, number of productive tillers/plant, grain length, grain width, 100 grain weight, panicle length and single plant yield. The genotypes in these clusters would be utilized for aromatic rice improvement breeding.

Key words

Aromatic rice, Genetic diversity, PCA, Cluster analysis

Introduction

Rice is vital to the lives of billions of people around the world. It is the staple food for 2.5 billion people and covering 9% of the earth's arable land (International year of rice, 2004). It provides 21% of global human per capita energy and 15% of per capita protein (International Rice Research Institute, 2002). Calories in rice are largely important among the poor, where it accounts for 50-80% of daily caloric intake (International Rice Research Institute, 2001). Rice is grown in all the continents, except Antarctica occupying 165 million hectare area and producing 720 million tonnes (Anonymous, 2012). In India, it accounts for more than 43% of food grain production. It is grown in 44.8 million hectare under 4 major ecosystems: irrigated, rainfed lowland, rainfed upland and flood-prone with average annual production of 100 million tonnes (Sohgaura *et al.* 2015). Preference for quality rice has expanded from Southeast Asia to Europe, Africa and United States of America.

Aromatic or scented rice have long been highly regarded in Indian society not only because of their excellent quality but also because they are considered auspicious. Aromatic rice is known for its nut-like aroma and taste, which is caused by the chemical compound 2-acetyl-1-pyrroline (Ghareyazie *et al.* 1997). Many scented varieties

of rice have been cultivated in the Indian sub-continent and Basmati distinguishes itself from all other aromatic rice due to its unique aromatic characteristics together with silky texture of its long grain. Aromatic rice have been traditionally cultivated in northern India, confined mainly to Punjab, Haryana, Western Uttar Pradesh and adjoining districts of Rajasthan.

Over the past few years, there has been a noteworthy increase in India's foreign exchange earnings from export of Basmati rice. The incorporation of basmati quality in the high yielding background has been the most challenging one. It might be due to its complex nature with respect to its constitution and inheritance pattern of component indices (Yumnam *et al.* 2015). Hence, greater genetic variation with greater diversity in rice gene pool is necessary for utilization in breeding programmes (Sivaranjani *et al.* 2010). Genetic diversity serves as a way for populations to adapt to changing environments.

With more deviation, it is more likely that some individuals in a population will possess variations of alleles that are suited for the environment. Genetic distance estimates for population grouping can be estimated by different methods as it is critical to realize the usable

variability existing in the population (Nachimuthu *et al.* 2014) and one of the approaches is multivariate analysis. Multivariate statistical tools include Principal Component Analysis (PCA), cluster analysis and discriminate analysis (Oyelola, 2012) and PCA may be used to reveal patterns and eliminate redundancy in data sets as variations routinely occur in crop species for yield and grain quality (Maji *et al.* 2012). Principal components (PCs) are generally estimated either from correlation matrix or covariance matrix. Correlation matrix was used to extract the principal components in the present study. The primary benefit of PCA is to quantify the significance of each dimension for relating the variability of a data set.

Cluster analysis is a powerful tool for determining clustering patterns as a way to establish relationships between genetic divergence as well as it is a measure of estimating the cophenetic correlation coefficient. Cophenetic correlation coefficient is a measure of how realistically a dendrogram preserves the pair wise distances between the original unmodeled data points. Hence, the present investigation was carried out on rice aromatic germplasm with an objective of dissecting yield and quality related traits and to identify maximum variability into total variability for grouping the aromatic germplasm accessions by taking into account of several characteristics and relationship between them.

Materials and Methods

A total of sixty seven aromatic rice germplasm accessions collected from different sources were used for study (Table 1). The experiment was carried out at Department of Rice, TNAU during 2013-14. Each germplasm line was sown in plot size of 0.96 m² with spacing of 20 x 20 cm. The experiment was conducted by adopting Randomized Block Design (RBD) replicated twice. Ten randomly selected plants were taken for observations for each replication. Biometrical observations on days to 50% flowering, number of productive tillers per plant, plant height (cm), panicle length (cm), grain length(mm), grain width(mm), hundred grain weight(g) single plant yield(g) and presence of aroma were recorded. Grain length and grain width were measured using vernier caliper. Presence of aroma was also observed by sensory evaluation method suggested by Sood and Siddiq (1978).

In order to classify the patterns of variation, PCA was performed. Those PCs with Eigen values greater than one were selected as proposed by Jeffers (1967). Correlations between the original

traits and the respective Principal Components (PCs) were calculated. Statistical analysis was carried out using the software STAR 2.0. The principal component analysis was computed using the following equation: $PC1 = \sum a_i X_i$ where, $a_i X_i$ = Linear coefficient – Eigen vectors. Cluster analysis was performed using agglomerative clustering method adopting Euclidean distance measure.

Results and Discussion

PCA is a powerful tool in modern data analysis because it is a well known multivariate statistical technique which is used to identify the minimum number of components, which can explain maximum variability out of the total variability (Anderson, 1972 and Morrison, 1978) and also to rank genotypes on the basis of PC scores. In the present study, PCA was performed using yield and quality related traits in 67 aromatic rice germplasm accessions. The proportion of variance, cumulative proportion and eigen values are given in Table 2. Out of nine PCs, four exhibited more than 1.0 eigen values and exhibited 70.14 % total variability among the characters studied. The principal components having more than one eigen value showed more variation among the aromatic rice germplasm accessions for the selection of the diverse parents. Among the four principal components, PC1 shared high proportion of total variation 25.9% and the rest of the three principal components *viz.*, PC2, PC3 and PC4 contributed 16.96%, 15.06% and 12.22% of the total variance respectively. Ashfaq *et al.* (2012) resulted PC1 with 33% and PC2 (14.3%), PC3 (11.4%) and PC4 (9%) variability in forty rice genotypes. Maji and Shaibu (2012) reported that PCA resulted in the first two components with eigen value greater than 1 accounting for 78% of the total variation on sixteen agro-morphological data on twenty three rice germplasm lines. Ahmed *et al.* (2016) studied that PCA showed that first five components with vector values > 1 contributed 82.90% of the total variations in 31 rice germplasm lines. Gour *et al.* (2017) reported that out of thirty three traits studied in 83 rice genotypes which include traditional land races, fourteen PCs exhibited more than 0.5 eigen values and showed about 92.75% total variability among the characters studied. Pachauri *et al.* (2017) studied one hundred twenty four rice germplasm accessions on the basis of nineteen morphological and eleven agronomical traits. From their studies, PC1 expressed 37.12% variability, while PC2, PC3 and PC4 recorded 13.56, 11.04 and 10.76% variability respectively and the traits such as number of effective tillers and 100 grain weight were the principal discriminatory traits.

Scree plot explained the percentage of variance associated with each PC obtained by drawing a graph between eigen values and PC numbers. In the present study, PC1 showed 25.9 % variability with eigen value 2.33 which then declined gradually (Fig 1.). Semi curve line is obtained after PC3 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. Hence, selection of lines from this PC would be useful for further breeding programs. Nachimuthu *et al.* 2014 reported the highest variability in PC1 with eigen value more than 1.0 in 192 rice genotypes comprising traditional landraces and exotic genotypes.

An eigenvector or characteristic vector of a linear transformation is a non zero vector that changes by only a scalar factor when that linear transformation is applied to it. Eigen value or characteristic value is associated with the eigenvector. To determine the critical limit for the coefficients of the proper vectors, coefficients with greater than 0.3 having large effect to be considered in the overall variation present in the genotypes (Raji, 2002). Eigen vectors of the PCs for different traits are presented in Table 3. The results showed that grain width had highest positive value (0.46) followed by plant height (0.34) in PC1. Plant height recorded highest positive value (0.59) followed by panicle length (0.57), days to 50% flowering (0.43) and presence of aroma (0.33) in PC3.

In the present investigation, the first two PCs (PC1 and PC2) were plotted against each other in biplot to observe the relation among the aromatic rice germplasm lines based on the observed yield and quality attributing characters (Fig.2). Genotypes *viz.*, CANP 496, CANP 295, CANP 510, CANP 265, CANP 90, CANP 91, CANP 168, CANP 325, CANP 318, CANP 355, CANP 108, CANP 51, CANP 307, CANP 132, CANP 302, CANP 58 and CANP 85 formed a group in right top corner of the biplot showed positive values of both the PCs and the character plant height placed in the same quadrant influencing of the character on the grain yield. In Fig. 3, PC1 and PC3 were plotted against each other in biplot. Genotypes *viz.*, CANP 58, CANP 307, CANP 422, CANP 17, CANP 510, CANP 427, CANP 108, CANP 404, CANP 302, CANP 51, CANP 403, CANP 355, CANP 91, CANP 325, CANP 121 and CANP 139 formed a group in right top corner of the biplot showed positive values of both the PCs and the characters days to 50% flowering, plant height and grain width positioned in the same quadrant influencing on the grain yield. Ashfaq *et al.* 2012 reported that

highest variability was observed in plant height, tillers per plant and panicle length in 40 rice varieties.

In the present study, 67 aromatic rice germplasms were grouped into five clusters based on average linkage distance method of hierarchical clustering as shown in the diagram (Figure 4 and Table 4). Five major groups were formed as Clusters *viz.*, I, II, III, IV and V consisting of 9, 31, 13, 11 and 3 genotypes respectively. Cluster means of different traits of aromatic rice germplasm accessions are given in Table 5. Cluster I had highest mean value for the traits *viz.*, number of productive tillers/plant (23 No.), grain length (7.7mm), grain width (1.7 mm), 100 grain weight (2.4 g) and single plant yield (3.72g). Cluster III had low mean value for days to 50% flowering (85) and highest mean value for panicle length (25.1 cm). Cluster II had low mean value for plant height (109.1cm). Hence, the genotypes belongs to these clusters can be utilized for the future breeding programs. Same clustering pattern was previously recorded in several reports (Rahman *et al.* (2011); Suh *et al.* (1997) and Han-yong *et al.* (2004)).

A dendrogram is the graphical representation of a cophenetic matrix and hence dendrograms can be compared to one another by comparing their cophenetic matrices (Lapointe *et al.* 1995). The cophenetic correlation coefficient has been widely used in numerical phenetic studies, both as a measure of degree of fit of a classification to a set of data and as a criterion for evaluating the efficiency of various clustering techniques (Farris *et al.* 1969). The magnitude of this value should be very close to 1 for a high-quality solution. In the present study, cophenetic correlation coefficient was 0.74 which indicated the more efficiency of the clustering pattern. Huang *et al.* (2010) reported that the cophenetic correlation coefficient ($r=0.918$, 0.878 and 0.924 respectively) showed a highly accurate dendrogram represented the genetic distance among 36 rice entries.

A total of sixty seven aromatic rice germplasms were taken for assessing genetic diversity using PCA and cluster analysis for nine yield and quality contributing characters. PCA was utilized to study the variation and to estimate the relative contribution of various traits for total variability. The PC1 showed 25.9%, variability and PC2, PC3 and PC4 exhibited 16.96%, 15.06% and 12.22% variability respectively. It is concluded that PCA highlighted the characters with maximum variability in the present study. Eigen vectors with more than 0.3 value was observed in grain width and plant height in PC1 and also plant height,



panicle length, days to 50% flowering and presence of aroma in PC3. In conclusion, these traits had large effects in the overall variation present in the genotypes and selection of these traits would be useful for further breeding programs.

From the biplot, genotypes viz., CANP 496, CANP 295, CANP 510, CANP 265, CANP 90, CANP 91, CANP 168, CANP 325, CANP 318, CANP 355, CANP 108, CANP 51, CANP 307, CANP 132, CANP 302, CANP 58, CANP 85, CANP 422, CANP 17, CANP 427, CANP 404, CANP 403, CANP 121 and CANP 139 showed positive values for the characters viz., days to 50% flowering, plant height and grain width in biplots for PC1, PC2 and PC3 indicated that these characters are highly influencing on yield. From the cluster analysis, clusters I, II and III had desirable mean values for days to 50% flowering, plant height, number of productive tillers/plant, grain length, grain width, 100 grain weight, panicle length, and single plant yield. The genotypes belongs to these clusters can be utilized for the aromatic rice improvement programs.

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Table 1. Details of aromatic rice germplasm accessions used in the study

Sl. No.	Accession No.	Designation	Source
1	CANP252	Pusa Basmati 1121	IARI/DRR
2	CANP199	Ranbir Basmati	J&K/IARI
3	CANP551	IET 22787 (RP 4594-121-148-24-11)	DRR
4	CANP375	Basmati 5874	PU/DRR
5	CANP140	Laldhan	PANTNAGAR
6	CANP90	Kanak Jeer	UP/DRR
7	CANP210	Basmati 564	J&K/IARI
8	CANP168	Shyamjeera	RPR
9	CANP520	UPR 3565-10-1-1	PANTNAGAR
10	CANP413	Hung-mi-hsiang-ma-tsan	CHINA/DRR
11	CANP206	Domsaih	IRAN/DRR
12	CANP212	Chimbalate Basmati	J&K/IARI
13	CANP255	Yamini (Basmati CSR 30)	CSSRI/DRR
14	CANP344	Basmati Type 3	PU/DRR
15	CANP463	IR 62873-227-1-16	IRRI/DRR
16	CANP465	IR 62873-238-2-3	IRRI/DRR
17	CANP444	IR 841-85-1-1-2	IRRI/DRR
18	CANP383	Basmati 11	PU/DRR
19	CANP251	Pusa Basmati 1	IARI/DRR
20	CANP554	Bas 867	US PATENTED LINE
21	CANP250	Mahisugandha	KOTA/DRR
22	CANP535	IR 75428-6-3	IRRI/DRR
23	CANP246	Taroari Basmati	PU/DRR
24	CANP385	Basmati 138	PU/DRR
25	CANP446	Kalimooch (Raipur)	RPR/DRR
26	CANP260	Basmati Bahar	PU/DRR
27	CANP471	Hasan Serai	IRAN/DRR
28	CANP440	HBC 46	HA/DRR
29	CANP129	Haryana Basmati 1	HA/NAGINA
30	CANP496	JGL 1798 (Jagithyal Sannalu)	DRR
31	CANP309	Improved Pusa Basmati 1	IARI/DRR
32	CANP500	Kasturi	DRR
33	CANP549	IET 18033 (RP 3644-9-5-3-2)	DRR
34	CANP139	Improved Sarbati	PANTNAGAR
35	CANP151	Basmati 386	LUDHIANA
36	CANP521	UPR 2828-7-2-1	PANTNAGAR
37	CANP327	Karnal Local	PU/DRR
38	CANP355	Basmati Mahan	DRR
39	CANP162	Banspatri	RPR
40	CANP347	Basmati 410	PU/DRR
41	CANP353	Basmati 370	PU/DRR
42	CANP132	Bindli	NAGINA
43	CANP354	Basmati 6141	PU/DRR
44	CANP410	Daw Leuang	THAILAND/DRR
45	CANP404	Binirhen	PHILIPPINES/DRR
46	CANP412	Guinata	PHILIPPINES/DRR
47	CANP123	Co ACC 167 (T167)	COIMBATORE
48	CANP242	Basmati 217	PU/DRR
49	CANP15	RAU 3043	BI/DRR
50	CANP422	Longku Labat	INDONESIA/DRR
51	CANP318	PDKV Shriram	MH/DRR
52	CANP58	Kapoor kranti	RPR/DRR
53	CANP325	Dhanaprasad	DRR
54	CANP91	Bhanta Phool A	UP/DRR
55	CANP295	Tarunbhog	RPR/DRR
56	CANP302	Neelabati	DRR
57	CANP307	Kalikhasa	AS/DRR
58	CANP510	Kh.sakani	DRR
59	CANP17	Maguraphulla	DRR
60	CANP427	Niaw Hawm Mali	THAILAND/DRR
61	CANP256	Vasumati	DRR
62	CANP85	Adam Chini B	UP/DRR
63	CANP51	Kanika bhog	DRR
64	CANP121	KDML 105	THAILAND/CBT
65	CANP108	Kamini Joha	AS/DRR
66	CANP265	Lectimachi	DRR
67	CANP403	Ayepyaung	MYANMAR/DRR

(Note: IARI-Indian Agricultural Research Institute, New Delhi, DRR-Directorate of Rice Research, Hyderabad, J&K-Jammu and Kashmir, PU-Punjab, RPR-Raipur, CSSRI-Central Soil Salinity Research Institute, Karnal, MH-Maharashtra, UP-Uttar Pradesh, AS-Assam, BI-Bikaner)



Table 2. Proportion of variance, cumulative proportion and eigen values of aromatic rice germplasm accessions

Statistics	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9
Proportion of Variance	25.9	16.96	15.06	12.22	10.65	8.93	6.02	2.71	1.56
Cumulative Proportion	25.9	42.86	57.92	70.14	80.78	89.72	95.73	98.44	100
EigenValues	2.33	1.52	1.35	1.09	0.95	0.80	0.54	0.24	0.14

Table 3. Contribution of different traits towards total variance in aromatic rice germplasm

Traits	Eigen Vectors								
	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9
Days to 50% flowering	0.18	-0.06	0.43	-0.62	0.29	-0.11	0.53	0.13	0.04
Number of productive tillers/plant	-0.24	0.16	-0.08	0.44	0.61	-0.51	0.19	0.19	0.07
Plant height (cm)	0.34	0.05	0.59	0.28	0.01	-0.28	-0.17	-0.57	-0.14
Panicle length (cm)	-0.20	-0.07	0.57	0.46	-0.21	0.37	0.22	0.42	0.08
Grain length(mm)	-0.54	-0.35	0.04	-0.05	-0.11	-0.08	0.19	-0.49	0.54
Grain width (mm)	0.46	-0.46	-0.01	0.06	-0.04	-0.26	-0.29	0.34	0.55
Hundred grain weight(g)	-0.20	-0.73	0.00	0.01	0.00	-0.20	-0.03	0.09	-0.61
Single plant yield(g)	0.25	-0.30	-0.13	0.19	0.59	0.62	0.08	-0.25	0.04
Presence of aroma	-0.38	0.06	0.33	-0.30	0.37	0.13	-0.69	0.12	0.05

Table 4. Hierarchical cluster grouping in aromatic rice germplasm accessions

Clusters	Frequency	Cluster Memberships
I	9	CANP252, CANP344, CANP251, CANP246, CANP151, CANP327, CANP353 CANP354, CANP412
II	31	CANP199, CANP551, CANP210, CANP168, CANP520, CANP206, CANP212, CANP255, CANP463, CANP465, CANP383, CANP554, CANP535, CANP385, CANP446, CANP471, CANP440, CANP129, CANP309, CANP500, CANP549, CANP139, CANP521, CANP162, CANP347, CANP242, CANP15, CANP318, CANP325 CANP91, CANP256
III	13	CANP375, CANP140, CANP90, CANP413, CANP444, CANP260, CANP496, CANP132, CANP410, CANP123, CANP422, CANP510, CANP265
IV	11	CANP250, CANP295, CANP302, CANP307, CANP17, CANP427, CANP85, CANP51, CANP121, CANP108, CANP403
V	3	CANP355, CANP404, CANP58

Cophenetic correlation coefficient: 0.74



Table 5. Cluster means of different traits of aromatic rice germplasm accessions

Traits	Cluster	Minimum	Maximum	Mean	StdDev
Days to 50% flowering	1	80	94	86	4.6
	2	78	104	88	7.3
	3	65	98	85	9.0
	4	91	99	94	2.4
	5	86	103	95	8.5
Number of productive tillers/plant	1	19	26	23	3.2
	2	11	21	13	2.6
	3	11	15	13	1.1
	4	12	19	13	2.0
	5	13	23	17	5.5
Plant height(cm)	1	93.6	133.1	114.5	13.3
	2	72.0	148.0	109.1	18.4
	3	71.1	146.1	114.3	21.4
	4	100.8	153.0	134.8	13.3
	5	126.8	167.3	146.3	20.3
Panicle length (cm)	1	21.7	25.5	23.9	1.3
	2	17.3	26.8	23.4	2.4
	3	19.1	24.1	21.8	1.4
	4	19.6	25.8	22.6	2.1
	5	24.6	25.6	25.1	0.5
Grain length (mm)	1	6.0	9.0	7.7	0.9
	2	5.5	9.3	7.5	0.9
	3	4.3	7.5	5.8	1.0
	4	4.0	7.9	5.5	1.6
	5	4.3	7.7	6.4	1.8
Grain width (mm)	1	1.5	2.0	1.7	0.2
	2	1.3	2.0	1.8	0.2
	3	1.7	2.7	2.2	0.3
	4	1.7	3.0	2.2	0.4
	5	1.6	2.2	1.8	0.3
100 grain weight(g)	1	2.1	3.1	2.4	0.3
	2	1.0	3.0	2.2	0.4
	3	1.3	3.4	2.2	0.6
	4	0.9	3.8	2.0	0.9
	5	1.1	2.3	1.6	0.6
Single plant yield(g)	1	1.92	5.87	3.72	1.4
	2	0.95	8.87	2.61	1.7
	3	0.90	8.46	4.10	2.5
	4	1.76	6.49	4.46	1.4
	5	0.83	5.95	2.60	2.9

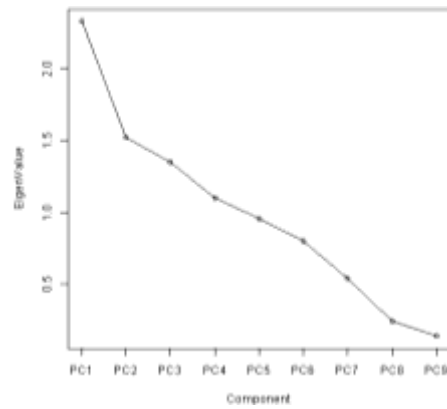


Fig. 1. Scree plot for different PCs in aromatic rice germplasm accessions

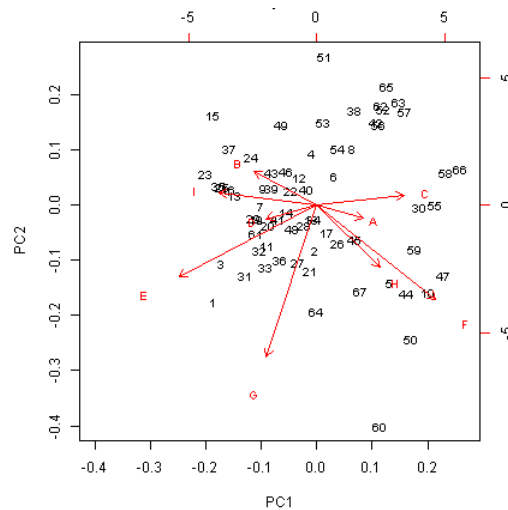


Fig. 2. The Biplot of aromatic rice germplasm accessions for PC1 and PC2

(**Note:** A- days to 50% flowering; B- number of productive tillers per plant; C-plant height (cm); D-panicle length (cm); E- grain length(mm); F-grain width(mm); G-hundred grain weight(g); H-single plant yield(g) and I-Presence of aroma. 1 to 67-Aromatic rice germplasm accessions)

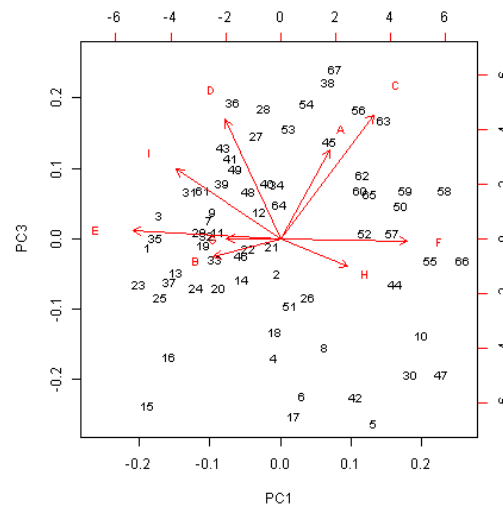


Fig. 3. The Biplot of aromatic rice germplasm accessions for PC1 and PC3

(**Note:** A- days to 50% flowering; B- number of productive tillers per plant; C-plant height (cm); D-panicle length (cm); E- grain length(mm); F-grain width(mm); G-hundred grain weight(g); H-single plant yield(g) and I-Presence of aroma. 1 to 67-Aromatic rice germplasm accessions)

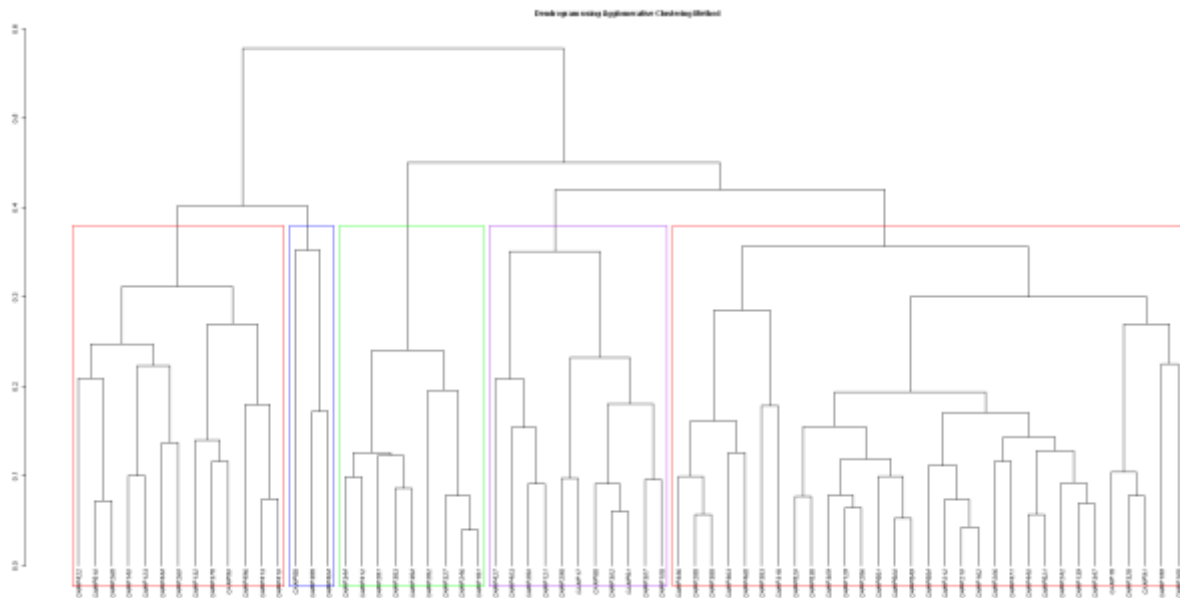


Fig. 4. Dendrogram using agglomerative clustering method in aromatic rice germplasm accessions

