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ST Binisundar
Assistant Professor,
Horticulture, TNAU,
Coimbatore, Tamil Nadu, India

G Ashokkumar
Assistant Professor,
Horticulture, TNAU,
Coimbatore, Tamil Nadu, India

P Rajarathinam
Associate Professor (Agronomy),
Tamil Nadu Rice Research
Institute, Aduthurai, Tamil
Nadu, India

A Jaya Jasmine
Professor and Head,
Horticultural Research station,
Pechiparai, Kanyakumari, Tamil
Nadu, India

S Vasanth
Ph.D., Scholar (Horticulture),
HC&RI TNAU, Coimbatore,
Tamil Nadu, India

Corresponding Author:
ST Binisundar
Assistant Professor,
Horticulture, TNAU,
Coimbatore, Tamil Nadu, India

Studies on genetic variability, principal component analysis and cluster analysis for clove accession

ST Binisundar, G Ashokkumar, P Rajarathinam, A Jaya Jasmine and S Vasanth

Abstract

In this study, the mean performance of various clove accessions, as well as a local check, was assessed in terms of tree characteristics and bud yield. The results indicate that the accessions exhibit significant variation in their tree characteristics, comprising an average height of 9.02 metres for the trees, an average stem girth of 38.76 centimetres, an average leaf length of 10.16 cm, an average leaf breadth of 6.09 cm, and an average number of branches per tree of roughly 13.28. Furthermore, an average dry bud yield of 0.99 kg per tree was shown for the accessions; values ranged from 0.66 kg to 1.67 kg per tree. On the other hand, the local check showed particular features: an average of 10 branches per tree; a dry bud yield of 0.71 kg per tree; a tree height of 12.34 metres; a stem girth of 40.99 cm; a leaf length of 11.67 cm; a leaf breadth of 4.89 cm. With regard to tree growth and bud yield, these results give a thorough understanding of the differences in performance between various accessions and the local check. The genetic divergence study produced seven unique clusters, the biggest of which, Cluster II, showed strong genetic similarity among genotypes SA-8, SA-10, SA-12, SA-7, SA-5, SA-4, SA-6, SA-9, SA-2, and SA-14. The formation of these clusters provides valuable insights into the genetic relationships and diversity among the evaluated genotypes. The study also explores genetic variability, principal component analysis, cluster analysis, shedding light on the diverse facets of clove cultivation and breeding strategies.

Keywords: Clove, accessions, variability, principal component analysis, cluster analysis

Introduction

Clove, (*Syzygium aromaticum*) (Synonym: *Eugenia caryophyllata*), tropical evergreen tree of size (8-12 m) belongs to the family Myrtaceae which is native to Moluccas islands or often called spice island of east Indonesia and its small reddish brown flower buds used as a spice. Cloves are available throughout the year owing to different harvest seasons across various countries. A wide range of bioactive compounds, including some potent antioxidants and antimicrobials, are present in cloves. The clove tree is frequently cultivated in coastal areas at maximum altitudes of 200 m above the sea level. The trees are evergreen with large leaves and crimson flowers grouped in terminal clusters. The major component of clove taste is imparted by the chemical eugenol. Nowadays, the larger producer countries of clove are Indonesia, India, Malaysia, Sri Lanka, Madagascar and Tanzania. Chemical and pharmacological basis of clove the dried flower bud of *Syzygium aromaticum* dominated by eugenol, fixed oil dominated by oleic and linoleic acids; terpenoids dominated by oleonolic and masilinic acids, flavonoids and phenolic acids, as well as highly water-soluble tannins with a great deal of structural diversity. Additionally, the essential oil of clove has anaesthetic and antimicrobial qualities, and is used to prevent halitosis and ameliorate dental pain. Eugenol, chemically known as 4 - ally - 2 - methoxyphenol, is the principal active component of clove oil well invested for its pharmacological effects with respect to the anti-arthritis [1]. Clove and its compounds in noncytotoxic concentration exhibited immunomodulatory and anti-inflammatory actions on cytokine production by murine macrophages [2]. Higher levels of variety are linked to a better likelihood of discovering features of agronomic importance for any crop. Little is known about the many kinds and varieties of cloves found in India. To determine the diversity of clove, look at its morphological features in the wild [3].

Materials and Methods

The experiment was conducted from 2018 to 2022 at the Horticultural Research Station at Pechiparai, Kanyakumari districts, Tamil Nadu in randomized block design with three

replications to find out the genetic diversity of the clove accessions. Number of treatments/genotypes are 24 genotypes with line planting in separate blocks. The experimental plot size and spacing is 6m x 6m. The Characters observed for the attributes, the observations were recorded *viz.*, Tree height, stem girth, leaf length, leaf breadth, number of branches per tree, dry bud yield [4]. The Biometrical studies such as Genetic variability, Principal component analysis (PCA), cluster analysis, correlation analysis, path analysis and D² analysis for the clove accessions.

Results and Discussion

Mean performance of clove accessions

The mean performance of the various accessions and the local check in terms of tree characteristics and bud yield is as follows: The tree heights of the accessions range from 4.74 to 12.65 metres, with an average of 9.02 metres. The average stem girth is 38.76 cm, with a range of 15.73 cm to 50.19 cm. 10.16 cm is the average length of a leaf, while 6.09 cm is the average width. There are between 10 to 17 branches on average per tree, with a mean of 13.28. The accessions show an average dry bud yield per tree of 0.99 kg, with values ranging from 0.66 kg to 1.67 kg per tree. In contrast, the local check features a tree height of 12.34 metres, a stem girth of 40.99 cm, leaf length and width of 11.67 and 4.89 cm, respectively, and a dry bud yield of 0.71 kg per tree in Table 1 and Figure 1, with an average of 10 branches per tree. These results provide insights into the performance variations across different accessions and the local check in terms of tree growth and bud yield [5].

Genetic variability

Significant levels of genetic variation within the population under study are shown by the investigation of genetic variability in several tree features. Tree height, stem girth, leaf length, leaf breadth, number of leaf branches, and dry bud yield per tree are among the features that show substantial phenotypic and genetic coefficients of variation (PCV and GCV, respectively). Moreover, these characteristics exhibit high heritability in the broad sense (h^2), suggesting that genetic factors account for a significant amount of the observed variance. Particularly noteworthy is the genetic advance expressed as a percentage of the mean (%), which indicates the possibility for genetic improvement. Table 2 and Figure 2 reveal that stem girth and dry bud output per tree have the greatest values, at 58.39% and 56.00%, respectively. The results of this study indicate that there exists a significant potential for selective breeding and genetic enhancement of these traits, rendering them advantageous objectives for breeding initiatives that seek to augment tree productivity and performance [6].

Principal component analysis

The results of the Principal Component Analysis (PCA) are presented in the table, which shows the loadings of the original variables on the first six principal components (PC1 to PC6). PC1 has the highest loadings for Tree height, Stem girth, and Leaf breadth, indicating that it explains a significant portion of the variance in these variables. PC2 is strongly loaded with Leaf length and Dry bud yield per tree. PC3, PC4, and PC5 capture additional variance with different combinations of variables. The eigenvalues indicate the amount of variance explained by each principal component, with PC1 explaining the most variance. The % total variance and % cumulative variance columns provide insight into the cumulative explained variance by the principal components, with PC1 accounting for 47.82% of the total variance, and the first two components (PC1 and PC2) together explaining 72.53% of the variance in table 3 and screen plots and biplots in figure 4. These results suggest that the data can be effectively reduced and analysed using these principal components, with PC1 and PC2 being particularly important for capturing the underlying patterns in the original variables [7].

Cluster analysis

The clustering analysis has resulted in the formation of five distinct clusters with varying frequencies of observations. Cluster I contain 3 instances, including SA-1, SA-2, and Local check. Cluster II comprises 2 observations, represented by SA-3 and SA-13. Cluster III is the most populated cluster, consisting of 11 observations: SA-4, SA-5, SA-6, SA-7, SA-8, SA-9, SA-10, SA-11, SA-12, SA-14, and SA-16. Cluster IV contains 4 instances, namely SA-15, SA-17, SA-18, and SA-19. Finally, Cluster V encompasses 5 observations, including SA-20, SA-21, SA-22, SA-23, and SA-24. These clusters help organize and group similar data points, providing valuable insights into the underlying patterns or similarities within the dataset. The table provides the cluster means for various variables, shedding light on the central tendencies within each cluster. For tree height (m), Cluster 1 has a mean of 12.11, Cluster 2 has 11.09, Cluster 3 has 10.06, Cluster 4 has 8.26, and Cluster 5 has 5.78. In terms of stem girth (cm), Cluster 1 has a mean of 43.35, Cluster 2 has 50.16, Cluster 3 has 42.64, Cluster 4 has 31.89, and Cluster 5 has 20.65. For leaf length (cm), Cluster 1 has a mean of 12.13, Cluster 2 has 14.57, Cluster 3 has 9.52, Cluster 4 has 10.74, and Cluster 5 has 10.79. Leaf breadth (cm) reveals Cluster 1 with a mean of 6.23, Cluster 2 with 7.30, Cluster 3 with 6.43, Cluster 4 with 4.62, and Cluster 5 with 5.54. Lastly, the number of branches per tree shows Cluster 1 with a mean of 11.67, Cluster 2 with 16.00, Cluster 3 with 13.64, Cluster 4 with 11.50, and Cluster 5 with 11.80 in table 4 and 5, dendrogram in figure 4. These cluster means offer valuable insights into the variations and tendencies within each cluster for the respective variables [8, 9, 10].

Table 1: Performance of clove accessions

Sl. No	Accessions	Tree height (m)	Stem girth (cm)	Leaf length (cm)	Leaf breadth (cm)	No of branches (Nos.)	Dry bud yield kg/tree
1.	SA- 1	12.65	39.98	12.85	6.33	12	0.66
2.	SA -2	11.34	49.07	11.86	7.46	13	0.72
3.	SA -3	12.49	50.14	12.98	7.97	17	1.67
4.	SA -4	9.58	40.19	11.63	6.85	15	0.78
5.	SA -5	10.37	39.75	11.08	6.63	13	0.86
6.	SA -6	10.89	49.18	11.83	6.86	15	0.97
7.	SA -7	10.15	45.85	9.97	7.74	14	1.08
8.	SA -8	9.78	46.27	8.82	6.75	13	0.85
9.	SA -9	10.78	44.82	8.06	5.26	12	0.81
10.	SA -10	10.25	47.64	8.63	6.53	14	0.77
11.	SA -11	10.26	34.16	6.60	7.09	14	0.73
12.	SA -12	9.52	43.67	10.25	6.93	14	0.99
13.	SA -13	9.68	50.19	16.16	6.64	15	1.64
14.	SA -14	9.41	41.73	8.93	5.06	12	1.05
15.	SA- 15	8.72	34.75	10.16	5.23	13	1.32
16.	SA-16	9.68	35.81	8.89	5.06	14	0.96
17.	SA -17	8.95	31.70	12.27	4.15	12	1.05
18.	SA -18	8.11	30.85	10.92	3.97	10	1.18
19.	SA -19	7.26	30.27	9.60	5.15	11	1.09
20.	SA -20	6.58	28.49	11.16	6.23	13	1.02
21.	SA -21	6.68	25.86	8.04	6.09	14	0.87
22.	SA -22	5.48	15.73	10.61	6.15	11	1.12
23.	SA -23	5.42	15.92	12.10	4.12	11	0.98
24.	SA -24	4.74	17.25	12.06	5.13	10	0.93
25.	Local check	12.34	40.99	11.67	4.89	10	0.71
	Mean	9.24	37.21	10.68	6.01	12.88	0.99
	SEd	0.18	0.76	0.19	1.14	0.34	0.02
	CD (P = 0.05)	0.37	1.54	0.3	2.30	0.46	0.04

Table 2: Variability parameters for clove accessions

Characters	GCV	PCV	Heritability in broad sense h^2 (%)	Genetic advance as percentage of mean (%)
Tree height	24.15	24.37	98.26	49.33
Stem girth	28.61	28.89	98.11	58.39
Leaf length	18.23	18.64	95.66	36.74
Leaf breadth	19.50	19.87	96.31	39.42
Number of leaf branches	12.84	13.36	92.34	25.42
Dry bud yield per tree	27.65	28.13	96.64	56.00

Table 3: Principal component analysis for clove accessions

Variables	PC1	PC2	PC3	PC4	PC5	PC6
Tree height	-0.4723	-0.2263	0.5044	-0.1973	-0.0073	-0.6575
Stem girth	-0.5330	-0.1071	0.2890	-0.2753	0.1530	0.7224
Leaf length	-0.0978	0.6380	0.4972	0.5462	-0.1818	0.0702
Leaf breadth	-0.4776	-0.0587	-0.3982	0.5430	0.5502	-0.1113
Number of leaf branches	-0.4940	0.1084	-0.4641	-0.0316	-0.7262	-0.0210
Dry bud yield per tree	-0.1060	0.7177	-0.2022	-0.5396	0.3368	-0.1679
Eigenvalues	2.8693	1.4824	0.8649	0.4993	0.1813	0.1028
% total variance	47.82	24.71	14.42	8.32	3.02	1.71
% cumulative variance	47.82	24.71	14.42	8.32	3.02	1.71

Table 4: Clustering in clove accessions

Cluster	Frequency	Cluster Membership
I	3	SA-1, SA-2, Local check
II	2	SA-3, SA-13
III	11	SA-4, SA-5, SA-6, SA-7, SA-8, SA-9, SA-10, SA-11, SA-12, SA-14, SA-16
IV	4	SA-15, SA-17, SA-18, SA-19
V	5	SA-20, SA-21, SA-22, SA-23, SA-24

Table 5: Cluster mean for characters in clove accessions

Variables	Cluster	Min	Max	Mean	Std Dev
Tree height (m)	1	11.34	12.65	12.11	0.68
	2	9.68	12.49	11.09	1.99
	3	9.41	10.89	10.06	0.51
	4	7.28	8.95	8.26	0.76
	5	4.74	6.68	5.78	0.83
Stem girth (cm)	1	39.98	49.07	43.35	4.98
	2	50.14	50.19	50.16	0.04
	3	34.16	49.18	42.64	4.80
	4	30.27	34.75	31.89	1.99
	5	15.73	28.49	20.65	6.06
Leaf length (cm)	1	11.67	12.85	12.13	0.63
	2	12.98	16.16	14.57	2.25
	3	6.60	11.83	9.52	1.60
	4	9.60	12.27	10.74	1.16
	5	8.04	12.10	10.79	1.66
Leaf breadth (cm)	1	4.89	7.46	6.23	1.29
	2	6.64	7.97	7.30	0.94
	3	5.06	7.74	6.43	0.90
	4	3.97	5.23	4.62	0.66
	5	4.12	6.23	5.54	0.91
Number of branches per tree	1	10.00	13.00	11.67	1.53
	2	15.00	17.00	16.00	1.41
	3	12.00	15.00	13.64	1.03
	4	10.00	13.00	11.50	1.29
	5	10.00	14.00	11.80	1.64
Dry bud yield per tree (kg)	1	0.66	0.72	0.70	0.03
	2	1.64	1.67	1.65	0.02
	3	0.73	1.08	0.90	0.12
	4	1.05	1.32	1.16	0.12
	5	0.87	1.12	0.98	0.09

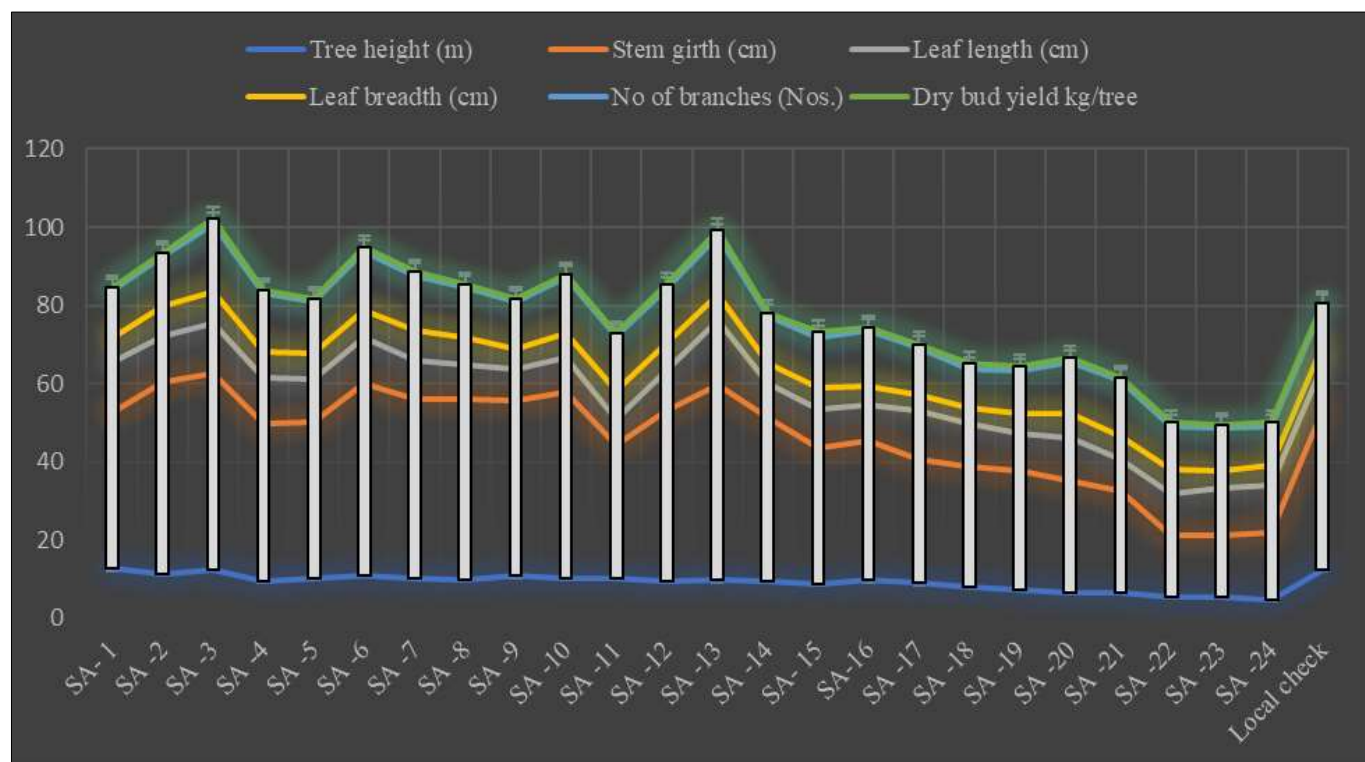


Fig 1: Graphical representation of Mean performance for clove accessions

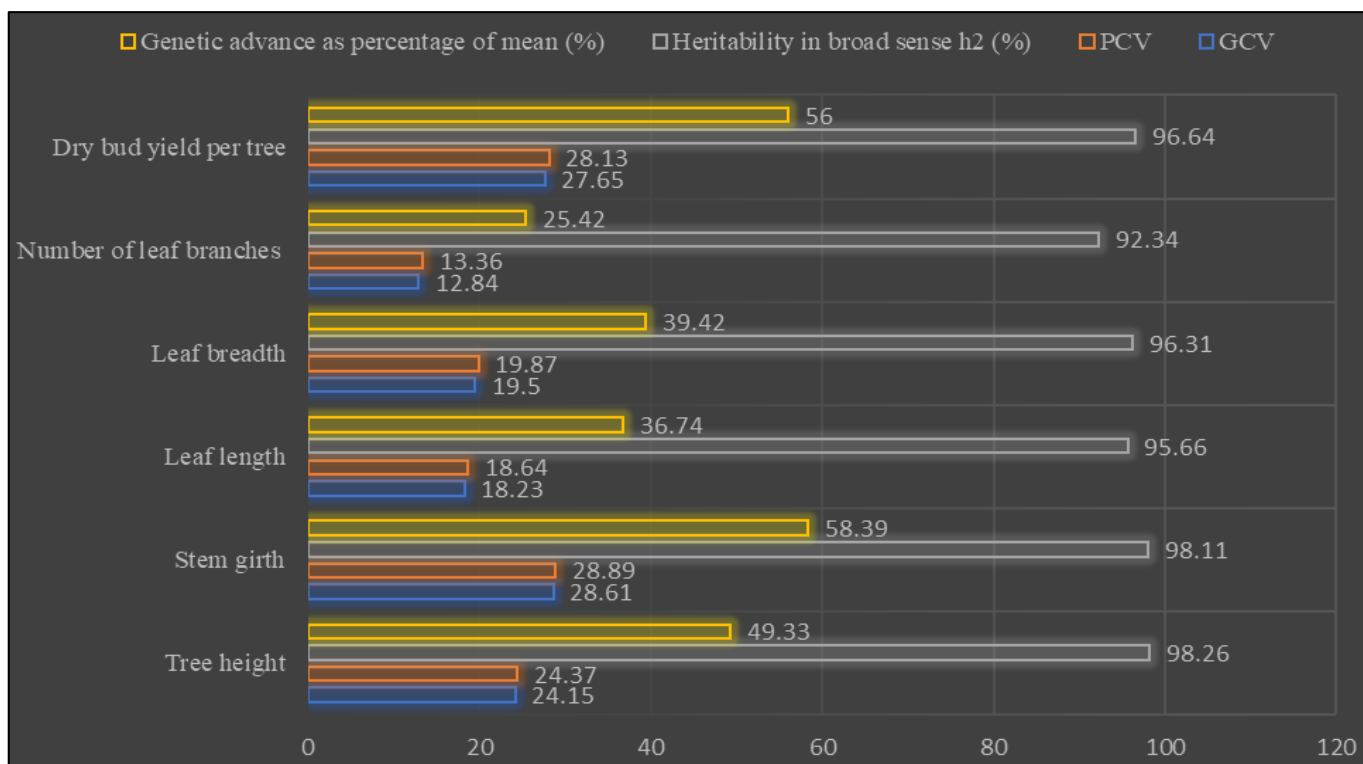
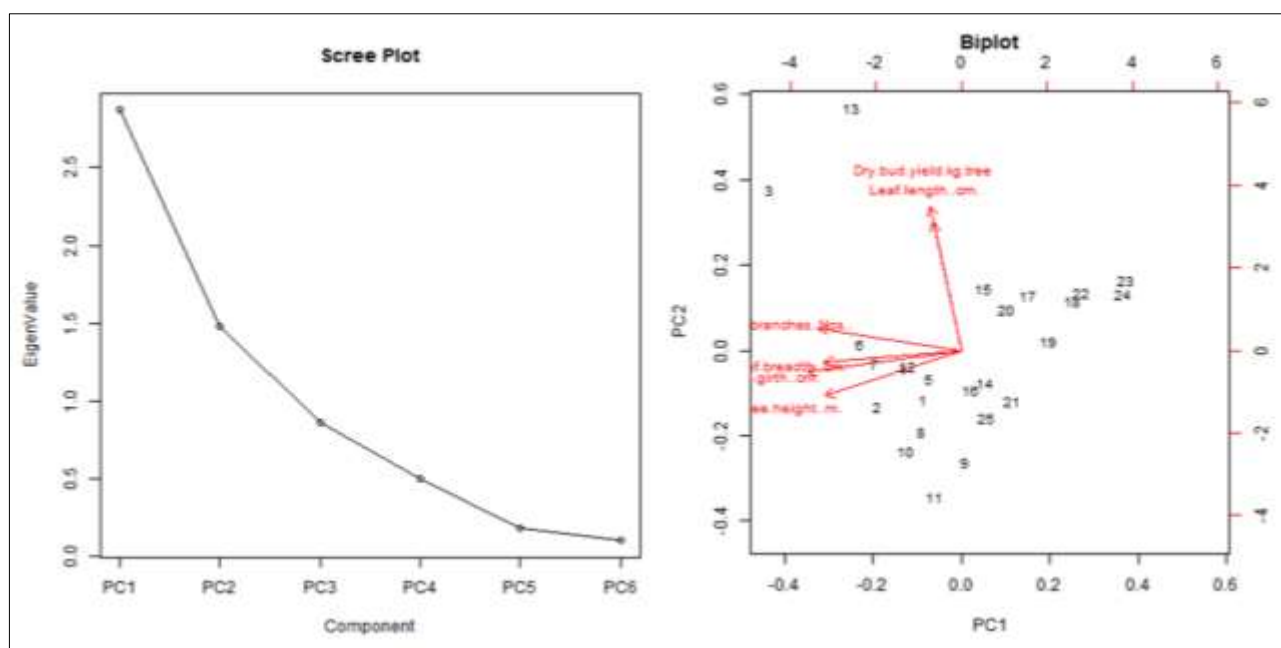


Fig 2: Graphical representation of genetic variability for clove accessions



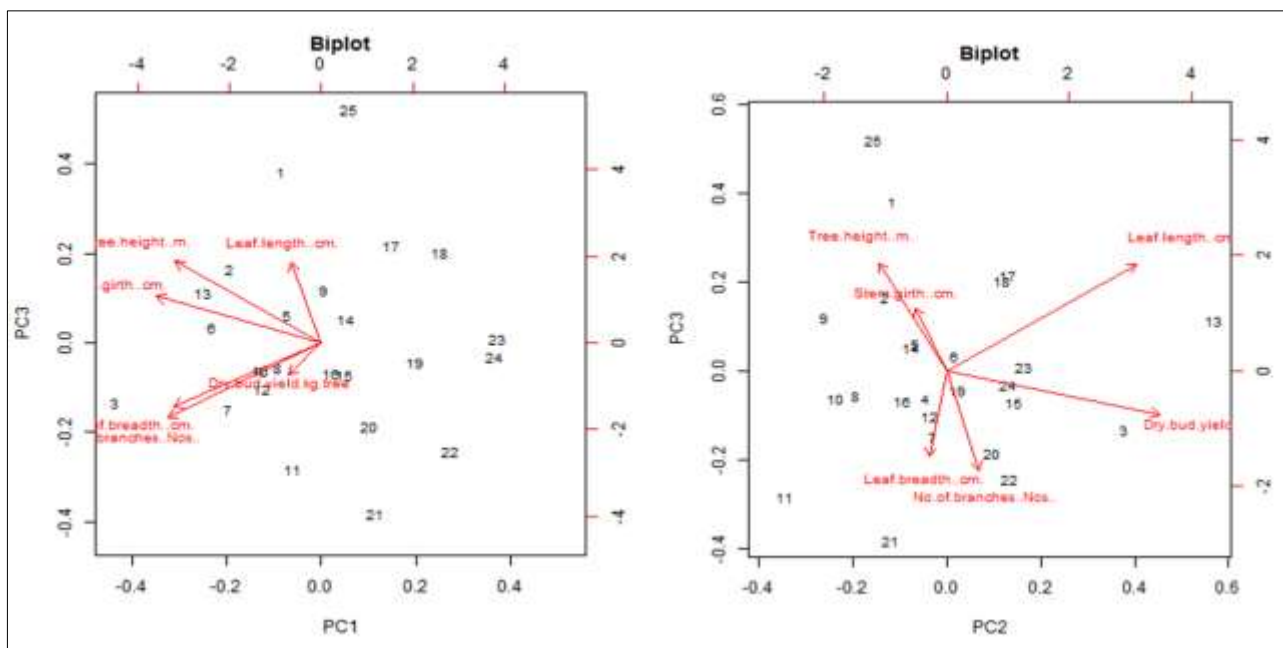


Fig 3: Screen plots and Biplots for clove accessions

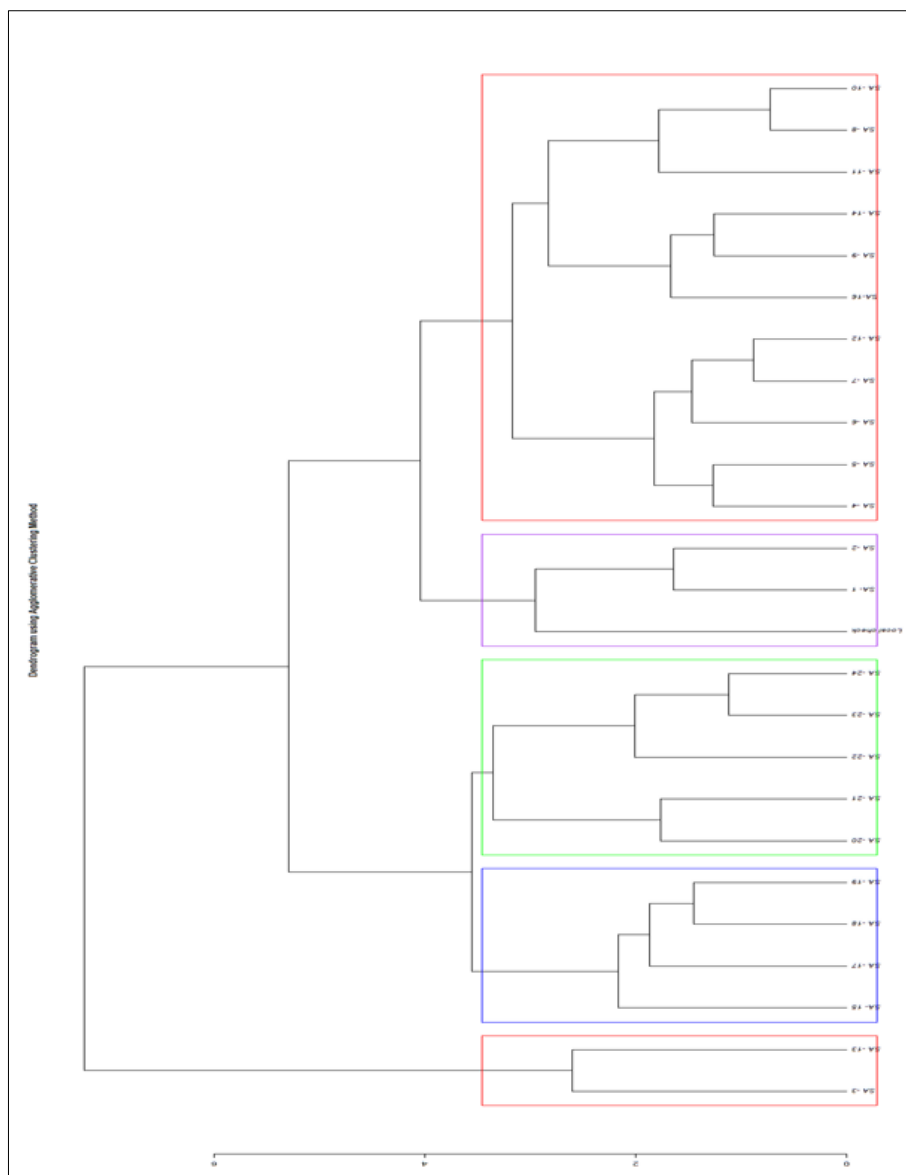


Fig 4: Dendrogram using agglomerative clustering for clove accessions

Conclusion

In conclusion, the comprehensive analysis of various aspects of the studied population, including mean performance, genetic variability, principal component analysis, cluster analysis, provides valuable insights into the characteristics, genetic diversity, relationships, and factors influencing tree growth and bud yield. The diverse range of tree characteristics, such as tree height, stem girth, leaf length, leaf breadth, and the number of branches, shows considerable variation across different genotypes. Genetic variability analysis emphasizes the potential for selective breeding and genetic improvement, with stem girth and dry bud yield showing promising opportunities for enhancement. Principal component analysis allows for data reduction and captures underlying patterns. Cluster analysis forms distinct groups of genotypes based on genetic similarity.

Acknowledgement

This is to verify that there are no conflicts of interest in the research article that both authors have submitted since all of the data that was collected, aggregated, analysed, reviewed, developed a methodology for, and deduced the results and recommendations from were reliable.

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