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Genetic variability and multivariate analysis in tall coconut germplasms

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Abstract

Coconut is a perennial plantation crop grown extensively throughout the tropics and sub-tropics. Exploitation of available genetic variability forms the primary step in any crop improvement program. In this study, 18 Tall coconut germplasms, comprising of 12 exotic and six indigenous populations maintained under AICRP on Palms – Crop Improvement trials at Coconut Research Station, TNAU, Aliyar Nagar were used. The experiments were laid in randomized block design with two replications. Observations were recorded on seven morphological traits *viz.*, palm height, palm girth, leaf length, petiole length, leaflet length, leaflet breadth and nut yield per palm per year for three years (from 2014 – 15, to 2016 – 2017). Analysis of the data revealed that the accession Seychelles recorded statistically significant mean value for nut yield. High heritability and genetic advance was recorded for nut yield indicating additive genetic control of the trait. In correlation studies, out of the six yield contributing traits, none showed significant correlation with nut yield. A total of three principal component axes explained the total variability. Cluster analysis showed that it would be advantageous to utilize the coconut genotypes in cluster I (Java, Federated Malay States), Cluster IV (Seychelles) and cluster V (Nadora Tall) in breeding programmes.

Keywords: Genetic variability, heritability, genetic advance, correlation, cluster analysis

Introduction

Coconut (*Cocos nucifera*) is an important plantation crop of various tropical and subtropical countries of the world. It is cultivated in almost 93 countries of the world with a total production of 67128 million nuts per year (APCC, 2015) [5]. In India, coconut is cultivated in an area of 20.82 Lakh ha with a production of 23,904 million nuts and productivity of 11,481 nuts / palm / year (Coconut Development Board, 2016) [7]. Currently, India ranks first as regards coconut production and productivity in the world. As a primary plantation crop and as home stead garden crop of the country, it serves as a source of multitude of agricultural commodities like refreshing drink for consumption, endosperm for direct use and oil extraction, fibre with commercial value, timber, shell for industrial use etc. and forms the basis for many food and industrial processes (Jones, 1990) [9]. Owing to its multifaceted economic uses, coconut palm is also referred to as “Tree of Life”, “Tree of wealth” and *Kalpatharu*. Coconut belongs to the genus *Cocos*, which is considered to be monotypic Beccari (1916) [4]. The palms are broadly classified in to two groups *viz.*, Talls and Dwarfs (Narayana and John, 1949) [13]. Tall coconut types are characterised by prominent bolls, tall stem, longer fronds and thicker endosperm. These are primarily cross pollinated because of non-overlapping of male and female phase in the inflorescence. The bolls in case of dwarf types are less prominent and the nuts are characterised by thin leathery endosperm. Dwarfs are predominantly self-pollinated (Liyanage, 1949) [10]. Because of cross pollination, Tall coconut palms are highly heterozygous and hence are store house of lot of genetic variability.

Evaluation and exploitation of existing genetic variability forms the preliminary step in any crop improvement programme. In perennial crops like coconut, initial selection is done predominantly based on available variability in mother palm and seedling features. The variability available for any trait in a population could be partitioned as heritable and non-heritable components by studying their genetic parameters, phenotypic and genotypic coefficients of variation, heritability and genetic advance. Selection of coconut based on available variability has been reported to enhance the performance in first generation to the tune of 25 – 35 per cent (Jack, 1930) [8]. Genetic diversity in any crop is the amount of genetic variability among the individuals of a variety or population of a species. Assessment of genetic diversity of a population is of paramount importance to decide on proper conservation and utilisation of germplasm. Grouping of genotypes is done through many statistical procedures. Multivariate analysis, which includes PCA, dendrogram and discriminant analysis can be used

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to unearth the relationship between variables and classify the genotypes. With this background, a study was undertaken to document the genetic diversity among the Tall coconut germplasm conserved at Coconut Research Station, Aliyarnagar, Tamil Nadu, under AICRP on Palms scheme and to study the extent of genetic variability in the germplasm which could enhance selection efficiency.

Materials and Methods

Experimental material, design and test location

The study was conducted at Coconut Research Station, Aliyarnagar, Tamil Nadu for three years (from 2014 – 15, to 2016 – 2017) and it involved eighteen Tall coconut germplasm, comprising of 12 exotic and 6 indigenous populations. The age of the palms studied were 23 to 25 years old. Four mother palms from each of the genotypes were selected after ascertaining the type identity and group uniformity through planting history and palm yield from previous years records. Observations on seven morphological traits viz., palm height, palm girth, leaf length, petiole length, leaflet length, leaflet breadth and nut yield per palm per year were recorded in the palms as suggested in coconut descriptor (IPGRI,1995) [5]. Considering the obvious limitation in laying out a replicated trial in perennial crops like coconut with wider crop geometry, the observations from four palms were treated as two replications in RBD with two palms per replication.

The means for all the characters were subjected to Analysis of Variance (ANOVA) on the basis of model proposed by Panse and Sukhatme (1969) [16]. The Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV) were analyzed by adopting the procedure suggested by Searle (1961) [19]. Heritability in broad sense h^2 (b) and genetic advance as per cent of mean were estimated by the formula suggested by Allard (1960) [1]. The above data analyses were performed using TNAUSTAT data analysis software. The principal component analysis was carried out as suggested by Rao (1952) [18], using Statistical Tools for Agricultural Research (STAR) 2.0.1 software.

Results and Discussion

A combined ANOVA was carried out for seven yield contributing quantitative traits in coconut which revealed significant difference among the genotypes for all the characters studied. The interaction between year and genotypes showed significant variation for five characters viz., leaf length, petiole length, leaf let length, leaflet breadth and nut yield, indicating the varying effects of environment (Table 1). Analysis of pooled means over three years was done to identify economically desirable coconut germplasm (Table 2). It revealed that the accession Seychelles recorded statistically significant mean value for nut yield, where as for other morphological traits, it showed non significant difference.

Table 1: Combined ANOVA for seven quantitative traits

Source	df	Palm height	Palm girth	Leaf length	Petiole length	Leaflet length	Leaflet width	Nut yield / palm / year
Replication	1	11819.67	15.58	356.96	126.56	0.34	0.03	171.96
Genotype	17	243356.93**	564.62**	10751.88**	10003.18**	565.57**	0.91**	5977.03**
Year	2	39315.11	291.64*	4006.35	10608.74**	532.32*	0.17	186.29
Year x Genotype	34	3016.14	103.36	8498.43**	6929.15**	102.67*	0.37*	838.04*
Pooled Error	51	22349.35	92.12	935.34	183.74	54.89	0.22	438.1

Table 2: Mean performance of eighteen coconut genotypes

Sl. No.	Genotypes	Palm height (cm)	Palm girth (cm)	Leaf length (cm)	Petiole length (cm)	Leaflet length (cm)	Leaflet width (cm)	Nut yield / palm / year
1	Zanzibar	1374.2	115.5	512.9	124.4	130.5	4.5	132.5
2	San Ramon	1161.3	105.5	564.5**	142.4	139.8**	4.8	99.1
3	Gonthombelli	1219.6	97.8	492.6	125.3	116.3	4.9	91.3
4	Java	1419.4	114.8	531.5	142.7	123.2	5.2	119.9
5	Federated Malay States	1389.7	120.3	527.8	143.8	128.3	5.2	118.5
6	British Solomon Islands	1380.3	102.4	543.6*	134.4	127.3	4.9	103.7
7	St. Vincent	1167.3	95.8	506.1	117.3	128.4	4.8	111.9
8	Arasampatti Tall	1373.7	106.2	455.1	107.6	110.5	4.0	89.3
9	Tiptur Tall	916.9	83.4	404.6	106.2	105.2	3.8	76.4
10	East Coast Tall	1214.8	98.3	441.2	116.8	108.9	4.1	136.5
11	Guam	732.8**	99.3	479.3	117.3	109.2	4.6	88.2
12	Ceylon Tall	1066.7	113.0	520.4	136.8	125.5	4.5	110.7
13	Jamaica	837.1*	102.8	454.5	130.1	113.3	4.5	125.2
14	Seychelles	969.0	92.4	494.5	128.3	124.3	4.6	217.7**
15	Laccadive ordinary	1056.4	111.8	517.8	138.0	122.1	4.7	154.8
16	Andaman giant	1303.6	117.3	538.9*	146.1	128.3	5.1	131.0
17	Cochin China	1142.7	110.7	507.4	137.0	125.2	4.8	120.8
18	Nadora Tall	1164.6	108.5	443.5	294.3**	135.4**	4.4	128.3

The feasibility of selection of desirable traits was assessed through genetic variability studies and it revealed that the PCV was higher than GCV for all the morphological traits. This indicated that expression of the traits studied was highly influenced by environment and this is in conformity with the results of Natarajan *et al.* (2010) [14], Manju and Gopimoni (2001) [11] and Suchithra and Paramaguru (2018) [21]. Though

genetic variability is an important parameter for the selection of a trait, it is necessary that the concerned character is also highly heritable. The heritability values hovered around medium to high for the seven traits studied. High heritability values were recorded by the traits plant height, leaf length, petiole length, leaf let length and nut yield whereas, petiole length and nut yield showed high genetic advance along with

high heritability indicating preponderance of additive gene action in the inheritance of the traits and hence selection will be effective and could serve as yardsticks for prepotency (Table 3). Natarajan *et al.*, (2010) [14]. Manju and Gopimony (2001) [11] and Selvaraju and Jayalekshmi (2011) [20] also

observed high heritability with genetic advance for nut yield. However, according to Falconer and Mackey (1996) [6], estimates of heritability are subject to environmental conditions and therefore are to be used with great care and caution in plant improvement programme.

Table 3: Genetic variability parameters for seven quantitative traits

Character	Mean	PCV (%)	GCV (%)	Heritability (%)	Genetic advance as percentage of mean (%)
Plant Height	1160.5 cm	19.16	15.33	64.01	25.27
Palm girth	105.3 cm	10.81	7.27	45.28	10.08
Leaf length	496.5 cm	8.91	8.12	83.02	15.24
Petiole length	138.3 cm	29.85	29.21	95.73	58.87
Leaf let length	122.3 cm	8.31	7.55	82.50	14.12
Leaf let breadth	4.6 cm	9.62	7.01	53.07	10.52
Nut Yield	119.7	28.20	24.37	74.65	43.37

Nut yield is a complex trait whose expression is influenced by panoply of various other quantitative traits. Hence, for selection of elite coconut germplasms with higher nut yield, better understanding of the relationship of various quantitative traits with nut yield is very important. The results of both genotypic and phenotypic correlations for seven morphological traits (Table 4) revealed that the magnitude of genotypic correlation was higher than that of the phenotypic correlation for all the seven characters. This indicated that, the correlation between the traits was purely dependant on genetic constitution with least environmental influence. Similar trends were observed in coconut by Augustine Jerard (2002) [3] and Suchithra and Paramaguru (2018) [21]. However, out of the six yield contributing traits, none showed significant correlation with nut yield and hence the characters considered for the study were not sufficient to identify a candidate trait for indirect selection.

Table 4: Genotypic and phenotypic correlation for seven quantitative traits

Characters		PH	GTH	LL	PL	LLL	LLB	NY
PH	G	1.000	0.598**	0.485*	0.119	0.458	0.443	-0.171
	P	1.000	0.523*	0.400	0.078	0.387	0.358	0.025
GTH	G		1.000	0.735**	0.401	0.813**	0.917**	0.154
	P		1.000	0.509*	0.229	0.364	0.411	0.061
LL	G			1.000	-0.083	0.724**	0.996**	0.169
	P			1.000	-0.043	0.688**	0.762**	0.107
PL	G				1.000	0.549*	0.136	0.167
	P				1.000	0.505*	0.057	0.141
LLL	G					1.000	0.649**	0.274
	P					1.000	0.548*	0.251
LLB	G						1.000	0.113
	P						1.000	0.175
NY	G							1.000
	P							1.000

(In the table PH = Plant Height, GTH = Palm girth, LL = Leaf length, PL = Petiole length, LLL = Leaflet length, LLB = Leaflet breadth, NY = Nut yield, G = Genotypic correlation, P = Phenotypic correlation)

The patterns and trends exhibited by the quantitative traits and the genotypes were assessed using principal component analysis (Table 5, Fig 1). Three major Eigen vectors with values greater than one explained around 81 percent of the total variability among the 18 coconut germplasms through three main principal components. Principal Component 1 vs Principal Component 2 biplot (PC1 vs PC2) showed that the genotypes are well dispersed along the vector plane indicating significant variation among the coconut germplasms (Fig 2). The first principal component explained 48% of the total

variability and the traits, leaf let length (-0.46), leaf let breadth (-0.46) and leaf length (-0.47) contributed the most to the PC1 in the negative direction. Second principal component accounted for 18% of the total variability and the traits nut yield (0.48) and petiole length (0.72) exerted maximum positive contribution to PC2. Third principal component explained 14% of the total variability and the major trait that contributed negatively was nut yield (-0.70) whereas, the traits petiole length (0.43) and plant height (0.40) contributed positively towards PC3 (Table5). Thus, the characters that came in different principal component axes have the tendency to remain together (Mohanlal *et al.* 2018) [12]. Similar variations in the contribution pattern towards principal components were also reported by Nazirul Islam *et al.* (2009) [15] in coconut.

Table 5: Eigen values, factor scores and contribution of principal component axes

Principal Components	PC 1	PC 2	PC 3
Eigen values	3.39	1.26	1.04
Percentage of Variance	0.48	0.18	0.14
Cumulative percentage	0.48	0.66	0.81
Plant height	-0.34	-0.23	0.40
Palm girth	-0.43	-0.03	0.21
Leaf length	-0.47	-0.28	-0.27
Petiole length	-0.18	0.72	0.43
Leaflet length	-0.46	0.28	0.02
Leaflet breadth	-0.46	-0.20	-0.23
Nut yield	-0.13	0.48	-0.70

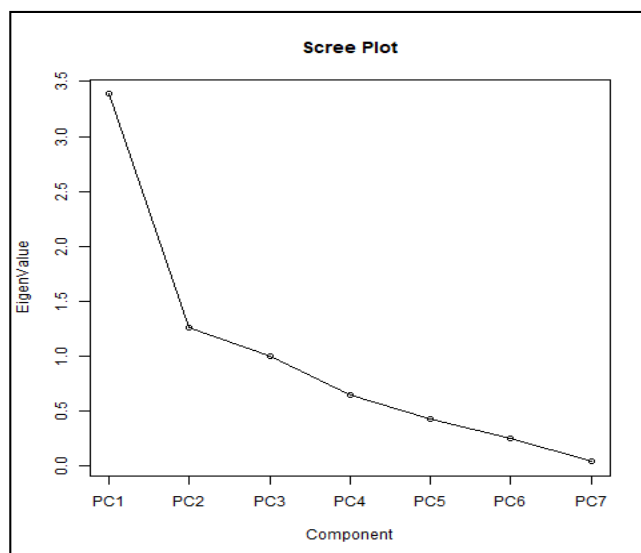


Fig 1: Scree plot showing eigen value variation

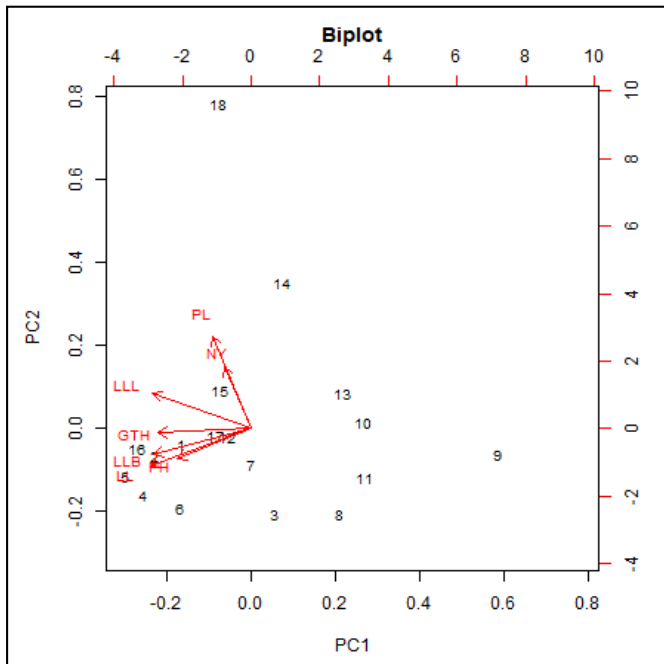


Fig 2: Distribution of various traits and genotypes across two components

Cluster analysis (Ward's method) was carried out using the seven morphological traits for grouping of coconut

germplasms (Table 6, Fig 3). A total of five clusters were formed where cluster II was the largest group with two sub clusters with eight genotypes. Cluster three consisted of two sub clusters with two genotypes each. Three genotypes were grouped under cluster I whereas; cluster IV and V was solitary clusters. The overall clustering pattern did not reflect the geographical diversity of the genotypes studied. This is in conformity with the reports of Perera *et al.*, 1998^[17], Teulat *et al.*, 2000^[22], Upadhyay *et al.*, 2002^[23]. According to the distance matrix (Euclidean), cluster I and cluster V has the maximum variation. Hence, it would be advantageous to utilize the coconut genotypes in cluster I (Java, Federated Malay States), Cluster IV (Seychelles) and cluster V (Nadora Tall) in breeding programmes.

Table 6: Composition of genotypes in clusters

Cluster no.	Cluster composition
1	Java, Federated Malay States, Andaman Giant
2	Zanzibar, Laccadive ordinary Tall, Ceylon tall, Cochinchina Tall, Gonthebili, St. Vincent, San Ramon, British Solomon States
3	Guam, Jamaica, Tiptur tall, Arasampatti tall, East Coast tall
4	Seychelles
5	Nadora tall

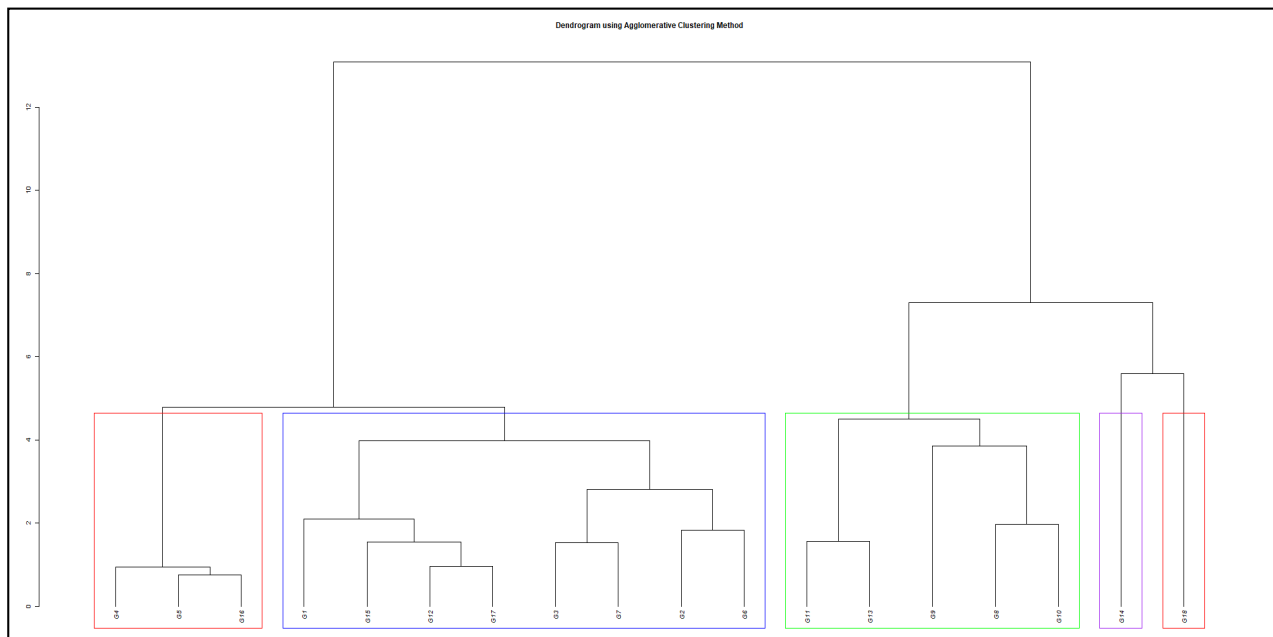


Fig 3: Grouping of eighteen coconut germplasms

Conclusion

High heritability and genetic advance for nut yield per palm per year indicates that additive gene action is operational in inheritance of the trait and hence selection based on the trait could yield better results. However, for indirect selection, apart from the traits included in the analysis, some more traits which could have strong correlation with yield are being studied. The principal component analysis revealed substantial variation among the genotypes and this needs to be validated at molecular level.

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