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Research Article

Assessment of genetic variability for growth, floral, yield and its component traits in coconut (*Cocos nucifera* L.)

V. Sivakumar*[1], A. Subramanian[2], S. Geethanjali[2], S. Praneetha[4] and H. P. Maheswarappa[5]

[1]Coconut Research Station (AICRP on Palms), Aliyarnagar – 642 101,
[2]ADAC & RI, TNAU, Tiruchirappali
[3]Department of Genetics and Plant Breeding, CPBG, TNAU, Coimbatore
[4]Coconut Research Station, Tamil Nadu Agricultural University, Aliyarnagar – 642 101, Coimbatore, Tamil Nadu, India
[5]AICRP on Palms, IACR-CPCRI, Kasaragod
***E-Mail:**shivafruitscience@gmail.com

Abstract

Genetic variability, heritability and genetic advance analysis of growth, floral, yield and yield attributing traits were studied in four dwarf x tall coconut hybrids, one tall x dwarf hybrid along with two tall varieties as checks. The palms were raised in four replications in randomised block design with six palms per replication. The age of the palm was nine years. Observations on morphological features were recorded in all the palms and the datas were subjected to statistical analysis. It revealed high to moderate degree of variability among the genotypes for most of the traits studied. The genetic variability studies indicated that the number of nuts per palm, whole nut weight, de-husked nut weight and tender nut water content evidenced high degree for phenotypic coefficient of variation and genotypic coefficient of variation. Superior level of heritability was recorded for palm height, leaflet breadth, the number of leaves, nut yield, fruit length, fruit breadth, tender nut water content, whole nut weight, de-husked nut weight and copra outturn thus indicating the prominence of genetic influence in inheritance of these traits. Genetic advance expressed on per cent mean was high in palm height, nut yield, tender nut water content, whole nut weight, de-husked nut weight and copra outturn. Therefore, the above traits could be given due weightage in coconut breeding programmes.

Key words

Coconut, hybrids, variability, heritability, genetic advance

INTRODUCTION

Coconut (*Cocos nucifera* L.) is generally known as 'tree of heaven' because of its diverse economic uses and importance in nourishing the life of the people who grows coconut (Kanimozhi *et al.,* 2018). In India, coconut cultivation is spread over an area of 2,150 thousand hectares with a total production of 21,288 million nuts and productivity of 9,897 nuts per ha. Tamil Nadu is one of the leading producers of coconut in India with an area of 4.37 thousand hectares, production of 5,370 million nuts and a productivity of 12,291 nuts per ha (CDB 2018-19). It belongs to the monotypic genus *Cocos* and family Arecaceae. It is a cross pollinated crop with wide variability for most of the morphological characters. Variability always provides more possibility of selecting desired types (Vavilov, 1951). Before planning any breeding programme, the estimation of genetic variability in genotypes and study of inter relationship between traits is essential. Genetic improvement for quantitative and qualitative characters depends on the nature and amount of variability present in the population. Coconut cultivars in India possesses a wide range of genetic variability. The analysis of genetic variation or diversity in coconut has been attempted for many years using morphological traits (Meunier *et al.*,1992). The variability available in the population classified into heritable and non heritable components, using genetic parameters, phenotypic and genotypic coefficients of variation, heritability and genetic advance based on which the selection can be effectively carried out. The desirable traits having high heritability provides greater chances of improvement through selection or hybridization. Keeping the above points in view, this study was carried out involving five coconut hybrid combinations, along two tall cultivars as checks, to assess the variability, heritability and genetic advance.

MATERIAL AND METHODS

The experiment was laid out in randomized block design (RBD) with four replications maintaining six palms per replication. The investigational hybrid combinations consisted of five location specific cross combinations *viz*., Chowghat Orange Dwarf x Arasampatti Tall (COD x ALR), Arasampatti Tall x Malayan Green Dwarf (ALR x MGD), Malayan Green Dwarf x Arasampatti Tall (MGD x ALR), Chowghat Orange Dwarf x West Coast Tall (COD x WCT) and Kenthali Dwarf x Arasampatti Tall (KTD x ALR), and two tall varieties *i.e.* West Coat Tall and Kalpatharu as checks. The seedlings were planted in Coconut Research Station Aliyarnagar farm during 2012 with a spacing of 7.5 x 7.5 m under irrigated conditions and were maintained duly following the standard package of practices as recommended by Tami Nadu Agricultural University. Presently the palms are eight years old.

Observations on quantitative traits like palm height, palm girth, petiole length, leaf length, leaflet length, leaflet breadth, total number of leaves, annual leaf production, the number of spikes per spathe, the number of female flowers per spathe, nut yield per palm per year, fruit length, fruit breadth, tender water content, whole nut weight, de-husked nut weight, kernel thickness and copra outturn were recorded in six palms per replication in each hybrid combination and the mean data used for the statistical analysis. The mean values were used for analysis of variance (ANOVA) following the procedures prescribed by (Panse and Sukhatme 1985). The phenotypic and genotypic variances were calculated by using the respective mean sum of square from variance table (Lush, 1940). The Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV) were calculated as per the formula proposed by Burton (1954). Based on PCV and GCV, the genotypes were classified into three range of variations such as low (less than 10 %), medium (10-20 %) and high (more than 20 %) as suggested by Sivasubramanian and Madhava Menon (1973). Heritability in the broad sense was estimated as per the formula suggested by Lush (1940) and expressed in per cent. The range of heritability was categorized as low (0-30 %), medium (31-60 %) and high (more than 60 %) as proposed by Johnson *et al.* (1955). Genetic advance was calculated as per formula proposed by Johnson *et al.* (1955) and characters were classified in to high (more than 20 %), medium (10 - 20 %) and low (less than 10 %) as per procedure recommended by Johnson *et al.* (1955). The nut yield per palm was recorded periodically at each harvest and the data from July 2017 to June 2019 was used and pooled to get nut yield per palm per year. Copra content per nut was recorded by depiction of random sample of six nuts per each entry in each replication during June, 2019. Copra output per palm was calculated based on the copra content per nut in each treatment (Ramanandam *et al.,*2018).

RESULTS AND DISCUSSION

Greater variability in the initial breeding material guarantees better chances of selection, which is the basis of any breeding program. The primary objective of hybridization

Table 1. ANOVA for quantitative traits

Source of Variation	Df	Mean sum of squares								
		Palm height	Palm girth	Petiole length	Leaf length	Leaflet length	Leaflet breadth	Total leaves	Annual leaf production	No of spikes / spathe
Genotypes	6	12028.75**	4817.43**	277.00**	907.86**	85.18**	0.43**	25.75**	1.32**	62.39**
Error	27	1757.44	2957.50	113.85	803.60	62.38	0.05	4.15	0.51	20.69

**Significant at 1% level

Table 1 (contd.) ....

Source of Variation	df	Mean sum of squares								
		No. female flowers /spathe	Nut yield / palm/year	Fruit length	Fruit breadth	Tender nut water content	Whole nut weight	De-husked nut weight	Kernel thickness	Copra output per palm
Treatment	6	69.56**	2330.91**	20.83**	3.23**	17331.83**	895398.17**	178570.81**	0.02**	4884.83**
Error	27	41.50	57.33	1.91	0.55	127.15	10711.87	2228.48	0.01	644.47

**Significant at 1% level

is to create and conserve the genetic variability in plant species to make it available to the present and future generations. In the present experiment, the ANOVA indicated the significance of mean squares for all the characters studied (**Tables 1 and 2**). This suggested the existence of variability for all the traits which can be further utilized for future breeding purposes in coconut. The high degree of variability in coconut for nut yield, whole nut weight, dehusked nut weight and copra weight was reported by Natarajan *et al.,* (2010).

Variability, heritability and genetic advance in coconut hybrids :The extent of variation as explained by PCV(%) and GCV (%), heritability(%) and genetic advance as per cent mean (%) are presented in **Table 2**. The data on the variability parameters, revealed that GCV was high for annual nut yield (41.76 %), tender nut water content (22.79 %), whole nut weight (30.70%) and de-husked nut weight (30.54) and its value was medium for palm height (19.39 %), palm girth (18.96%), the number of spikelets per spathe (10.73%), the number of buttons per spathe (14.59 %) and copra outturn (17.62%). However, PCV was greater than GCV for most of the characters. This indicated the preponderance of environmental effect in inheritance of the traits (Manju and Gopimony, 2001). Wide difference was observed between PCV and GCV for the characters palm girth and the number of buttons per spathe indicated the drastic influence of environment on their expression. In case of tender nut water content, whole nut weight and de-husked nut weight, the difference between GCV and PCV was narrow suggesting that these traits could be reliable on the selection indices. Similar results have also been reported by Balakrishnan *et al.*, (1991) and Renuga (1999), Augustine Jerard (2002) and Suchithra and Paramaguru (2018).

Table 2. Genetic variability for quantitative traits

S. No.	Parameters	Mean	GCV (%)	PCV (%)	Heritability (%)	Genetic advance as per cent of mean (%)
1	Palm height (cm)	261.37	19.39	25.16	60.10	30.77
2	Palm girth (cm)	113.75	18.96	51.43	13.59	14.39
3	Petiole length (cm)	152.03	4.20	8.18	26.37	4.44
4	Leaf length (cm)	532.96	0.96	5.40	3.13	0.35
5	leaf let length (cm)	120.35	1.98	6.86	8.38	1.18
6	leaf let breadth (cm)	4.75	6.47	8.02	65.07	10.75
7	No. of leaves (number)	26.69	8.71	11.58	61.56	13.49
8	Annual leaf production (number)	10.60	4.23	7.97	28.08	4.61
9	No. of spikelet's / spathe (number)	30.08	10.73	18.55	33.50	12.80
10	No. of buttons / spathe (number)	18.16	14.59	38.36	14.46	11.43
11	Nut yield (number/year)	57.09	41.76	43.82	90.84	81.99
12	Fruit length (cm)	21.87	9.95	11.78	71.30	17.30
13	Fruit breadth (cm)	14.45	5.66	7.63	62.03	8.65
14	Tender nut water content (ml)	287.75	22.79	23.13	97.13	46.27
15	Whole nut weight (g)	1531.75	30.70	31.44	95.38	61.77
16	De-husked nut weight (g)	687.43	30.54	31.31	95.19	61.39
17	Kernel thickness (cm)	1.26	4.20	9.39	19.77	3.87
18	Copra outturn (Kg/Palm)	184.75	17.62	22.35	62.19	28.63

Low PCV was recorded for petiole length (8.18%), leaf length (5.40%), leaf let length (6.86%), leaflet breadth (8.02%), the number of leaves (11.58%), annual leaf production (7.97%), fruit length (11.78%), fruit breadth (7.63%) and kernel thickness (9.39%) signifying that these traits were not as much vulnerable for chance ecological impacts. Parallel results were also reported by Patil *et al.,* (1993) Renuga (1999) and Augustine Jerard (2002). The selection of high performing genotypes or hybrids is based on the heritability estimates on phenotypic performance. The heritable variation may be effectively used with better accuracy when studied in combination with genetic advance (Burton, 1952; Swarup and Chaugale, 1962). Johnson *et al.*, (1955) recommended that heritability and genetic advance when considered collectively were more useful for predicting the significant effect of selecting the best individuals than heritability or genetic advance considered separately. In the present study, high heritability was observed for palm height (60.10%), leaflet breadth (65.07%), the number of leaves (61.56%), nut yield (90.84%), fruit length (71.30%), fruit breadth (62.03%), tender nut water content (97.13%), whole nut weight (95.38%), de-husked nut weight (95.19%) and copra output (62.19%). Among the above traits, except leaflet breadth, the number of leaves, fruit length and fruit breadth, all the other traits recorded high genetic advance which indicated that their inheritance could be under the influence of additive gene action (Panse, 1959) and hence the selection based on these traits could be effective for crop improvement (Sreeja *et al.,*2014).

Similar high heritability has been reported for the number of leaves per palm (Liyanage and Sakai, 1960); the number of bunches per palm, nuts per bunch and kernel weight and shell weight (Patil *et al*., 1993) and dehusked nut weight (Liyanage and Sakai 1960). Selvaraju and Jayalekshmi (2011) reported high heritability in coconut varieties along with high genetic advance for whole nut weight, de-husked nut weight, the number of nuts per palm per year. High heritability estimates for all the characters indicates high degree of inheritance of these characters in further generations. (Ganesamoorthy *et. al.,* 2002) reported a high genetic advance for copra yield, de-husked nut weight, nut yield and whole nut weight. Moderate heritability was recorded in the number of spikelet's per inflorescence (33.50%) while the traits palm girth (13.59%), petiole length (26.37%), leaf length (3.13%), leaf let length (8.38%), annual leaf production (28.08%), the number buttons per inflorescence (14.46%) and kernel thickness (19.77%) recorded a low level of heritability. This indicates that, the above parameters are highly influenced by environmental factors (Sreeja *et al.,* 2014). Thus it could be concluded that, the tender nut water content, whole nut weight and de-husked nut weight which recorded a favourable GCV, PCV, high heritability along with the high genetic advance can be relied as efficient selection parameters for coconut crop improvement.

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