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Genetic Variability Studies for the Quantitative Traits in Coconut var.WCT

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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. Twenty five West Coast Tall (WCT) coconut palms were used to carry out this study. Observations were recorded on three vegetative characters, five floral characters and twelve yield related characters. Analysis of the data revealed a significant degree of variability among the population for most of the studied traits. Moderate degree of Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV) were exhibited by nut water weight, number of female flowers, shell thickness and dehusked nut weight High heritability and genetic advance was recorded for water weight and dehusked nut weight indicating additive genetic control of the trait. Therefore, these specific traits should receive significant attention and emphasis in a coconut breeding program aimed at improving yield.

Keywords: Coconut, variability, heritability, genetic advance

1. Introduction
Cocos nucifera L. belongs to the monocotyledon family Arecaceae (Palmae) and represents the sole species within the *Cocos* genus. This species is diploid, characterized by having 2n = 32 chromosomes. It holds significant importance as a versatile palm tree, widely cultivated in the humid tropics and often referred to as Kalpavriksha, meaning the "tree of heaven" due to its provision of essential life necessities (Kanimozhi *et al.*, 2018) [1].

Coconut cultivation spansmore than 90 countries, with Indonesia leading as the top global producer at 17.33 million tonnes, followed closely by the Philippines at 14.77 million tonnes, India at 13.27 million tonnes, Sri Lanka at 2.47 million tonnes, and Brazil at 2.33 million tonnes. Within India, Karnataka takes the top spot in coconut production with 4,210.87 tonnes, followed by Tamil Nadu at 3,751.26 tonnes, Kerala at 3,307.78 tonnes, and Andhra Pradesh at 1,127.27 tonnes (https://nhb.gov.in/Statistics.aspx). Despite ranking third in coconut production globally, India has witnessed a decline in production in recent years, with production volumes measured in metric tons, were 16.41 in 2018, 14.68 in 2019, 14.01 in 2020, 14.3 in 2021, and 13.27 in 2022. In recent times, a reduction has been noticed in coconut production in India. It is because of the unforeseen fluctuations in climatic conditions, global warming, tsunamis, floods, insects and pest attacks, aged plants, phytosanitary threats, infectious diseases such as lethal yellowing, lethal diseases, cadang-cadang. Apart from the external threats, the availability of healthy and elite planting material has become scarce as seeds are the only mode of propagation.

Coconut cultivars are typically categorized into two main types: Tall and Dwarf. The Tall variety primarily undergoes cross-pollination, while the Dwarf type, with a few exceptions, tends to self-pollinate. Given the cross-pollination nature of the Tall coconut type, mass selection serves as the fundamental method for coconut breeding. Coconut farmers and breeders traditionally rely on methods like mother palm selection followed by seedling selection Manju and Gopimony 2001) [2]. Coconut cultivars in India exhibit a diverse spectrum of genetic variation. Therefore, studies focused on assessing variability play a pivotal role in crop improvement programs.

Enhancing genetic traits, whether quantitative or qualitative, relies on the extent and type of variability within the population. Character selection can only occur when genetic variation is present. In general, the variability within a population can be divided into heritable and non-heritable components, which can be effectively discerned through genetic parameters such as

phenotypic and genotypic coefficients of variation, heritability, and genetic advance. These parameters serve as the basis for making selections in the breeding process.

The heritability estimate offers insight into how much a specific trait can be passed from parents to offspring, while genetic advance indicates the extent of improvement achieved in a trait after a single round of selection. When there is both a high heritability estimate and high genetic advance, it presents the ideal scenario for selection (Syukur et al. 2012) [3].

Several researchers have previously examined coconut genetic diversity through a morphological approach (N'cho et al. 1993) [4]. However, the conventional approach of seed-based planting fails to produce a sufficient quantity of high-quality seedlings, resulting in a heightened need for superior planting material. This was carried out to fulfill the increased demand for exceptional seedlings, through the selection of superior mother palms by assessing the genetic parameters for breeding programmes and in vitro studies.

2. Materials and Methods
The morphological characterization study was conducted at the Coconut Research Station in Aliyar Nagar, Coimbatore, Tamil Nadu. The experimental material consisted of 25 coconut palms (WCT palms). These palms were selected from among the 25-year-old WCT (West Coast Tall) palms during the period from 2021 to 2023. The selection was likely based on their annual yield per palm. The selected coconut palms were grown with a spacing of 25 feet × 25 feet. They were also maintained under well-irrigated conditions following a standard package of practices. Detailed morphological observations encompassing vegetative, floral and fruit characteristics were documented for each of the 25 selected palms among 50 palms, and this data was collected in triplicate for accuracy and reliability.

2.1 Vegetative characters
The height of the palm was determined annually by measuring from the stem's base to the top crown region using a graduated meter tape. The stem grith at a height of one meter above the collar region was measured and expressed in centimeters. The total number of fully opened leaves on the crown per palm were counted and recorded.

2.2 Floral characters
The monthly count of produced inflorescences was tallied, leading to the calculation of the total inflorescences produced over the course of a year. The length of each fully opened inflorescence was measured from its base to the tip, and the resulting average values were expressed in centimeters. The number of spikes per inflorescence was also counted and their mean values were recorded. The length of each spikes, measured from its base to the tip, was averaged and expressed in centimeters. Finally, the count of female flowers within each inflorescence was recorded, and the mean values were documented.

2.3 Yield and fruit characters
The parameters analyzed for this study includes number of nuts per palm per year, total number of nuts in each bunch, fruit weight, fruit length, fruit breadth, dehusked fruit weight, weight of broken nut, weight of water, weight of kernel, kernel thickness, husk thickness and shell thickness were

recorded. The number of nuts per palm in each harvest was documented, and the total number of nuts per palm per year was determined. For each harvest, the total number of nuts in each bunch was summed, and the average number of nuts per bunch was calculated. The nut's length was determined and the resulting mean values were expressed in centimeters. Similarly, the nut's breadth was measured with a scale and recoreded mean values in centimeters. The whole nut weight was determined by weighing harvested nuts, and the resulting mean values were expressed in grams. For dehusked nuts, the nuts were first dehusked, and the mean weight was expressed in grams. The thickness of the husk at the widest portion of the nuts was measured and mean values were obtained in centimeters. The weight of broken nuts was recorded by splitting them into two halves, and the mean values were expressed in grams. These broken nuts were subsequently deshelled, and the kernel thickness was measured, with mean values expressed in centimeters. The weight of the kernel was recorded, and the mean values were expressed in grams. Additionally, the water weight was recorded by collecting the water, and the mean values were expressed in grams. The shell thickness was measured and mean values were expressed in centimeters.

The data collected were subsequently utilized for statistical analysis using SPSS software, with mean values serving as the basis for this analysis. The phenotypic and genotypic coefficient of variation (GCV) was computed following (Burton's 1952) [5] recommendations by estimating variance components. Both PCV and GCV values were then categorized into high, medium, and low groups, as proposed by (Sivasubramanian and Madhava Menon 1973) [6]. Heritability (h^2) in a broad sense was computed according to (Lush 1949) [7] and expressed as a percentage. The heritability percentage was categorized in line with the guidelines (Robinson et al. 1949) [8]. Genetic advance was determined, and the genetic advance as a percentage of the mean was classified using the method outlined by Johnson et al. (1955) [9].

3. Result and Discussion
In any crop improvement program, assessing the extent of variability is crucial. The study by (Harland 1957) [10] highlighted that the limited transfer of yield from parent palms to their offspring could be attributed to the type of genetic variation present. Therefore, it is essential to estimate variability, heritability, and genetic advancement for traits that significantly influence productivity. This aids in focusing selection efforts on these key traits and ensuring their consistent performance. In this current study, we examined variability parameters such as PCV, GCV, heritability, and genetic advance using morphological traits to understand the diversity for its application in selection of superior palms for breeding programme and in vitro studies within the WCT populations at CRS, Aliyar Nagar, TNAU, Coimbatore.

Significant variations were detected across all the recorded traits, and these variations hold great significance for plant breeders. Effective selection depends on the extent of variability within the breeding population. The assessment of variability within the population was conducted through measurements of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, and genetic gain for individual quantitative characteristics.

Table 1: Genetic parameters for quantitative traits in the WCT population

Parameters	Mean	Range		GCV (%)	PCV (%)	h² (%)	GAM (%)
		Min	Min				
Plant height (cm)	1051.55	946	1168.67	4.7	4.8	99.0	10
Stem grith (cm)	110.33	98.67	117.17	3.6	3.9	82.4	6.7
No. of leaves on crown	33.0	30.0	39.0	5.0	6.0	69.6	8.6
No. of inflorescence	16.05	15.17	17.17	3.5	3.9	80.0	6.5
Length of inflorescence (cm)	148.0	134.0	161.1	4.7	4.9	93.7	9.5
No. of spikes/inflorescence	36.13	31.17	39.67	6.1	6.7	83.4	11.5
Length of spikes (cm)	32.19	28.67	37.17	7.6	7.9	91.5	15
No. of female flowers	18.0	14.0	22.0	8.9	13.2	45.5	12.4
No. of nuts /bunch	13.87	11.67	16.17	7.0	7.5	88.5	13.6
Nut yield / year	134.35	117.17	145.67	4.4	4.6	88.2	8.5
Fruit weight(g)	1269	1097	1456.33	6.6	6.7	99.0	13.7
Fruit length (cm)	22.05	19.17	24.75	6.1	6.3	93.6	12.2
Fruit breadth (cm)	12.72	10.67	15.17	9.2	9.6	91.8	18.3
De-husked nut weight (g)	596	450	751	11.6	11.7	98.0	23.9
Husk thickness (cm)	2.15	2	2.3	2.5	4.2	35.3	3.0
Broken nut weight (g)	447	393	529	6.7	6.8	94.7	13.4
Water weight (g)	153	95	204	17.6	18.2	93.5	35.1
Kernel weight (g)	276	233	325.33	8.7	9.1	92.0	17.4
Kernel thickness (cm)	1.09	1	1.30	4.9	6.5	58.1	7.8
Shell thickness (cm)	0.23	0.20	0.30	9.2	13.1	49.5	13.4

*GV- Genetic variance, PV- Phenotypic variance, GCV- Genetic coefficient of variation
PCV- Phenotypic coefficient of variation, h²- Heritability, GAM- Genetic advance as per mean

In this study, traits including water weight (18.2%), the number of female flowers (13.2%), shell thickness (13.1%), and de-husked nut weight (11.7%) exhibited a moderate PCV (ranging from 10-20%) within the WCT population (Table.1). Conversely, all other traits displayed a lower PCV (<10%). As indicated by (Sivakumar *et al.* 2020) [11] traits such as petiole length, leaf length, leaflet length, leaflet breadth, leaf count, annual leaf production, fruit length, fruit breadth, and kernel thickness exhibited low PCV values, suggesting that these traits were less susceptible to random ecological influences.

Moderate GCV values (10-20%) were observed for the traits water weight (17.6%) and de-husked nut weight (11.6%), while all other characteristics exhibited low GCV (<10%). When considering water content, fruit weight, de-husked nut weight, fruit length, and fruit breadth, the difference between GCV and PCV was minimal, indicating the reliability of these traits for selection indices. Significant phenotypic and genotypic variances were noted for fruit weight, de-husked nut weight, plant height, and broken nut weight, signifying their substantial variation. In contrast, husk thickness, shell thickness, kernel thickness, and the number of inflorescences displayed comparatively lower variance values. The presence of elevated genotypic and phenotypic variances in the former group suggests that these traits exhibit greater viability compared to the other traits studied across different coconut genotypes. Consequently, selecting for these specific characteristics is expected to yield more efficient results.Similar findings have been documented by previous studies, including those conducted by Balakrishnan *et al.* (1991), Renuga (1999), Augustine Jerard (2002), Suchithra and Paramaguru (2018), and Sivakumar *et al.* (2020) [12, 13, 14, 15, 11].

Heritability and genetic advance estimates convey the extent of character inheritance from parents to offspring. Heritability values for different traits provide insights into their impact on overall yield, with those showing high heritability being favorable for selection due to their resilience to environmental influences (Lush 1940) [16]. Genetic advance, a key breeding parameter, helps quantify the anticipated genetic changes resulting from selection. The combination of high heritability and significant genetic gain serves as a reliable indicator of the accuracy of heritable variation (Johnson *et al.* 1955) [9].

The study by (Panse 1957) [17] observed that nut yield, whole nut weight, and dehusked nut weight exhibited high heritability and genetic advance. High heritability for husked nut weight and suggested that selecting seedlings should be heritability-based traits such as the number of nuts per year and husked nut weight was reported (Liyanage and Sakai 1960) [18]. Similarly, (Sankaran *et al*. 2015) [19] found that fruit weight, dehusked fruit weight, kernel weight, shell weight, and plant height, all of which directly impact coconut yield, displayed high heritability and substantial genetic advance.

In our current study, husk thickness (35.3%), the number of female flowers (45.5%), shell thickness (49.5%), and kernel thickness (58.1%) displayed moderate heritability (30-60%), while all other traits exhibited high heritability (>60%). Notably, water weight and de-husked nut weight showed both high heritability and genetic advance as a percentage of the mean. Similarly, (Selvaraju and Jayalekshmi 2011) [20] found high heritability and genetic advance for whole nut weight, de-husked nut weight, and the annual number of nuts per palm. High heritability (>60%) was discovered by (Sudha *et al*. 2019) [21] in plant girth, number of leaves, leaf length, spikes-bearing portion length, spikes length, female flowers per inflorescence, inflorescence length, and total bunch count, indicating minimal influence from environmental factors.

A significant level of variability in coconut traits such as nut yield, whole nut weight, dehusked nut weight, and copra weight (Natarajan *et al*. 2010) [22]. The heritability values for the seven traits studied varied between medium and high. Notably, traits like plant height, leaf length, petiole length, leaflet length, and nut yield exhibited high heritability values, indicating a substantial genetic component. Furthermore, the petiole length and nut yield displayed both high genetic advance and high heritability, suggesting a prevalence of

additive gene action in the inheritance of these traits (Subramanian 2019) [23]. Consequently, the prospects for effective selection in these traits are favorable. Similarly, high genetic advance for copra yield, de-husked nut weight, nut yield, and whole nut weight was reported by (Ganesamoorthy *et al*. 2002) [24].

Therefore, characters displaying a significant genetic coefficient of variation, along with high heritability and substantial genetic advance as a percentage of the mean, suggest that the traits such as weight of water, dehusked nut weight, fruit breadth and kernel weight are likely to be passed on to offspring. Hence, phenotypic selection based on these traits is expected to be highly effective.

4. Conclusion
This study can be concluded that the presence of only a narrow range of differences between phenotypic and genotypic coefficient of variation. High heritability (>60%) was recorded for all the traits except husk thickness, number of female flowers, shell thickness and kernel thickness which exhibited moderate heritability. High heritability and genetic advance was noted in the traits water weight and dehusked nut weight. Hence selection for these traits may be rewarding.

5. Acknowledgement

6. Competing Interests
Authors have declared that no competing interests exist.

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