

¹GENETIC CONTROL OF HUSKED NUT WEIGHT IN COCONUT (*Cocos nucifera*)

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ABSTRACT

The genetic control of husked nut weight in Coconut (*Cocos nucifera*) was investigated using a full-diallel cross including eight parents. The parents were a selected sample of palms which gave an annual mean yield of 23 kg of copra per palm with 713 gm of husked nut weight over five years. An average of five progenies per cross planted in a fully randomised design were evaluated for five years. Husked nut weight of five nuts per palm was recorded at each pick.

Analysis of variance of mean husked nut weight confirmed the presence of additive and non additive genetic variance. The non additive genetic component was found to be higher in magnitude than the additive component. The heritability expressed as the ratio of the genetic variance to the total phenotypic variance was 0.45. Of the dominance components, directional dominance was non significant. Neither the presence of heterosis nor inbreeding depression was consistent among the selfed and crossed progenies elucidating the fact that not only crossing but selfing could also improve the trait, depending on the genetic constitution of the individual. Reciprocal differences were evident in the crosses suggesting the importance of the direction of cross.

INTRODUCTION

With the exception of a few progeny tests, mass selection based on the phenotype followed by hybridisation is the rule in most coconut improvement programmes (Liyanage 1967). The theory on quantitative genetics highlights the risk of this procedure unless the heritability of the character of interest is very high where a high score for a character of interest in an individual actually mirrors its genotype (Falconer 1981). Therefore accurate estimates of the heritability of characters used as selection criteria is imperative before embarking on any major selection procedure. Liyanage and Sakai (1961) using the progenies of 9 high yielding palms estimated the heritability of the husked nut weight of coconut as 0.95 and concluded

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that mass selection for copra/nut ought to be very effective. Bourdeix (1988) estimated the heritability of copra/nut (estimated as 32% of the husked nut weight) in the range of 0.73 using parent-offspring regression with data extracted from parents and progeny planted in two separate blocks and for varying periods. However, an estimate of heritability of a character depends on the method of partitioning of the genetic and environmental components of variation and therefore the attempt of comparing the estimates obtained in two different situations is worthless. Furthermore the above procedures do not provide any information on the type of gene action controlling the yield characters in coconut which is a necessary pre-requisite in planning the breeding procedures.

The objective of the present study is to determine the type of gene action responsible for the husked nut weight in coconut and estimate the heritability of the above character. Diallel cross analysis was introduced as one of the strategic methods of determining the genetic control of quantitative traits and one that partition the genetic and environmental components of variation most efficiently (Mather and Jinks, 1982).

MATERIAL AND METHODS

The selection of parent palms for the diallel crossing programme was based on the nut yield/palm/year and mean husked nut weight for a period of five years after attaining yield stability. Yield data of the selected palms appear in Table 5. The pollinations were carried out in all possible combinations among the best 8 palms and the progeny was transplanted at Pothukulama Research Station in December 1964 in a fully randomized design with 10 plants per family (CRI, 1965). Although all progenies derived from 8 x 8 diallel crosses were planted originally, high casualty rates in the field resulted in only 40 progeny families surviving which could provide data for the present analysis. Average weight of 5 husked nuts were recorded at each pick for 5 years (1976 - 1980). An analysis of variance was carried out to test for differences between the reciprocal families for parents which they were available.

The loss of many families over time and the reduction in family size of others resulted in the situation that data could be used only as a half diallel with selfs. A maximum of 5 individuals per family was used in the analysis. The half diallel analysis of the mean husked nut weight over a 5 year period was carried out according to the method of Jones (1965). The general combining ability (G.C.A.) and specific combining ability (S.C.A.) effects were further analysed equating the additive component to G.C.A. and the sum of the dominance components to the S.C.A. effect.

RESULTS AND DISCUSSION

The analysis of variance between and within the reciprocal families revealed

significant differences between the reciprocal crosses (Table 1) indicating the importance of the direction of a cross. A possible reason for the above occurrence is the influence of the maternal parent in contributing more alleles to the triploid state of the endosperm.

Table 1. *Analysis of variance of reciprocal families.*

Source	df	SS	MS	P
Between reciprocal families	10	0.9292	0.0929	0.01**
Within families	375	12.6258	0.033	

The variance for husked nut weight between the families as partitioned by the half diallel analysis is summarised in Table 2. The additive component (a) was highly significant, of the dominance components (b₁) was not significant indicating the absence of directional dominance among the loci controlling nut weight. The significance of the (b₂) item indicated that there were differences between parents with respect to the relative proportions of dominant and recessive alleles at these loci, while residual dominance (b₃) was also significant.

Table 2. *Results of half diallel analysis of mean husked nut weight (a = additive, b₁ = directional dominance, b₂ = mean dominance b₃ = residual dominance).*

Source	df	SS	MS	P
a	6	1.625	0.270	0.0001***
b ₁	1	0.014	0.014	ns
b ₂	6	0.880	0.146	0.0001***
b ₃	14	1.175	0.084	0.01**
within family error	545	16.022	0.029	

The mean squares of (a) was equated to mean squares of general combining ability whilst the pooled mean squares (b₁) (b₂) and (b₃) was equated to the mean squares of the specific combining ability. The components general combining ability (σ^2_{gca}), specific combining ability (σ^2_{sca}) and the environmental component (σ^2_e) appearing in Table 3 were computed from the relevant mean squares. The variance component analysis revealed that additive genetic variation was available for selection but the non additive component was also of significant importance in controlling the husked nut weight. The ratio of the genetic variance to the total variance was 0.45. The value estimated by Liyanage and Sakai (1961) for heritability of husked nut weight using data from half sib families appear to be too high due to the reason that

dominance variance was assumed to be negligible.

The means of selfed and crossed progenies of the seven parents averaged over the five year period is shown in Table 4. A higher progeny mean was observed (586 gm) in the selfed families than in the crossed families (553 gm). However certain individuals produced improved progenies when crossed than selfed, elucidating the fact that either the presence of heterosis or the inbreeding depression was determined by the genetical constitution of the individual. Moreover the extent of inbreeding depression is controlled by the triploid nature of this tissue and the flow of genes brought by the pollen restores heterozygosity limiting inbreeding depression.

Table 3. *Results of the general and specific combining ability variance and heritability.*

Source	df	MS	EMS
GCA	6	0.2708	$\sigma_o^2 + 5 \sigma_{sca}^2 + 35 \sigma_{gca}^2$
SCA	21	0.0997	$\sigma_o^2 + 5 \sigma_{sca}^2$
within error	545	0.029	σ_o^2
$\sigma_{gca}^2 = 0.004$		$\sigma_{sca}^2 = 0.014$	$h^2 = 0.45$

Table 4. *Husked nut weight means of half diallel families averaged over 5 years (1976-1980) (kg).*

Parent	418	283	183	96	69	337	78
418	0.5657						
283	0.6126	0.6053					
183	0.6328	0.3840	0.5084				
96	0.6050	0.3660	0.4350	0.5914			
69	0.5706	0.4961	0.5175	0.5634	0.6134		
337	0.6236	0.5794	0.6133	0.6012	0.6470	0.6316	
78	0.5995	0.5681	0.4783	0.5935	0.4913	0.6468	0.5860

A comparison of the performance of the diallel parents on which the selection was carried out and the progeny performance (both self and crossed) are shown in Table 5. (total copra for the present experiment was calculated using the mean number of nuts/palm/year multiplied by the estimated copra/nut). The parent No 337 with an intermediate husked nut weight has produced the progeny with the highest husked nut weight and total copra exhibiting its general combining ability. Eventhough, parent no 78 with the highest husked nut weight (768 gm ; Table 5) showed low general combining ability, this palm produced the best progeny when crossed to palm 337 elucidating the importance of specific combining ability in controlling the husked nut weight (Table 4).

Table 5. *Details of parental performance (which the selection was based) and diallel progeny (selfed and crossed) performance.*

Parent	Parent		Progeny	
	Mean husked wt/nut gm	Total copra kg	Mean husked wt/nut gm	Total copra kg
418	736	23.78	601	13.07
283	690	22.90	515	8.24
183	745	27.65	509	12.86
96	613	21.70	536	13.21
69	709	23.31	557	12.47
337	713	22.50	620	15.87
78	768	20.64	566	11.41

CONCLUSION

The heritability of husked nut weight in coconut is estimated to be 0.45 suggesting that the improvement in the trait through mass selection is limited. The importance of both additive and non-additive genetic variance is evident in controlling the character indicating the possibility of not only crossing among individuals but also selfing the selected individuals for improving the character. A top cross or a test cross progeny testing method which would provide estimates of the general combining ability is suggested as a useful tool in determining the best parents for a crossing programme.

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