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Heritability of Fresh Fruit Bunch Yield and Its Components in the Oil Palm (*Elaeis guineensis*, Jacq.)

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Summary. Single-plant heritability estimates of 38.9%, 31.5% and 42.3% were obtained for number of bunches (NB), fresh fruit bunch yield (FFB) and mean bunch weight (MBW) respectively. Hybrid (family) mean heritability estimates for these traits were 88.9%, 90.5% and 96% respectively. Repeatability estimates for these traits were 33%, 11% and 8% for NB, FFB and MBW respectively. Evaluation of hybrid family mean for yield components appears feasible at the third or fourth year of data collection. Phenotypic and genotypic correlations between NB and FFB were 0.80 and 0.61 respectively; between NB and MBW, –0.41 and –0.16 respectively; and between FFB and MBW, 0.66 and 0.60 respectively. The hypothesis that increased FFB can be obtained by hybridization between parents with high NB and heavy MBW is supported by this correlation set.

Key words: Genotypic correlation – Phenotypic correlation – Clones – Repeatability – Selection – *Elaeis guineensis*

Introduction

Fresh fruit-bunch (FFB) yield in the oil palm (*Elaeis guineensis*, Jacq.) is a product of number of bunches (NB) and mean bunch weight (MBW). NB generally declines with age of palms, while MBW generally increases with age (Sparnaaij 1963; Hartley 1977). Negative and significant phenotypic and genotypic correlations have been reported between NB and MBW (Ooi et al. 1973; Van der Vossen 1974; Tan and Rajanatnam 1978).

Broekmans (1957) and Sparnaaij (1960) claimed that MBW is generally less affected by environmental factors than NB. Knowledge of the degree of inheritance of each character is fundamental to the planning of an effective breeding programme aimed at improving FFB and its components in the oil palm. Heritability estimates are most useful in their predictive role in assessing reliabilities of phenotypic values as a guide to the breeding value of an individual.

Many attempts have been made by previous workers to establish a relationship between early and mature production patterns in the oil palm. Blaak (1965) obtained a positive correlation between FFB within the first 4 years and 11–16 years of production. Also Obasola and Nampoothiri (1978) reported a positive association between the first 6 and 7 years of FFB and the average of 19th to the 22nd year. In addition to establishing the relationship between early and mature yields, repeatability estimates help to ascertain how many repeated measurements of a trait will be adequate for obtaining enough information to determine when to start data evaluation to make decision on such cultivars/crosses.

The objectives of this study were to quantify the genetic and environmental components of NB, MBW and FFB in a population of 49 oil palm hybrids and to establish the inter-relationships among these characters.

Materials and Methods

Forty nine *dura*×*pisifera* hybrids (full-sib families) planted at the Nigerian Institute for Oil Palm Research (NIFOR), in Benin City were used for this study. Nursery plantings were carried out in 1951 while field planting took place in 1952. A 7×7 quadruple lattice design with 4 replicates was used. There were 16 plants per plot, 7 plots per block and 7 blocks per replicate. The spacing between plants was 8.8 meters triangular. Data were collected on FFB, NB and MBW from 1956 when the palms came into bearing to 1969.

Dura and *pisifera* are two true-breeding fruit forms of the oil palm. Dura palms are thick shelled while pisifera lack shells. The hybrid between *dura*×*pisifera* is referred to as *tenera* and are thin shelled. Pisifera palms usually serve as the male because the absence of shell leads to very low fruit production. The total number of parents used in making crosses was 60. However only 10 parents were evaluated in at least three crosses and data for the remainder are not presented.

The experiment was analysed as a quadruple lattice (Goulden 1960) and then as a randomized complete block.

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Table 1. Quandruple lattice analyses of variance for FFB and its components

Source	d.f.	Mean Squares		
		NB	FFB (kg/plot)	MBW (kg/plot)
Years (Y)	13	240,709**	22,104,528**	3,987.65**
Replicates (R)	3	4,197**	936,021*	28.50**
Blocks / R	24	13,156**	1,695,187**	92.61**
Hybrid families	48	13,987**	1,006,352**	112.52**
H×Y	624	1,552**	94,924**	4.46**
Blocks / R×Y	312	63	3,955	0.32
Error	1,719	344	34,644	1.77

* Significant at 0.05 level of probability

** Significant at 0.01 level of probability

Table 2. Heritability (H), Repeatability (R) and Percent gain in estimate of precision expected from additional measurements (Gp) of NB, FFB and MBW

	i/Gp					ii/Gp					iii/Gp				
	H	R	2nd	3rd	4th	H	R	2nd	3rd	4th	H	R	2nd	3rd	4th
NB	38.9	0.33	34	11	5	27.83	0.16	42	14	7	23.41	0.044	48	16	8
FFB	31.4	0.11	45	14	8	23.89	0.08	46	15	8	21.13	0.04	48	16	8
MBW	42.3	0.08	46	15	8	38.30	0.07	47	15	8	38.60	0.03	49	15	9

i, ii, iii = estimates derived from data collected over five, ten and fourteen years, respectively

Broadsense heritability on single-plant basis was computed as

$$H=\delta^2_g/\delta^2_g+\delta^2_{gy}+\delta^2_e$$

while broadsense heritability on family-mean basis as

$$H=\delta^2_g/\delta^2_g+\sigma_{gy/m}+\sigma^2_{e/rm}$$

Repeatability estimates were computed (i) for the first five years data (ii) the first ten years data and (iii) for the entire 14 year period (Falconer 1960; Hansche and Brooks 1964) as

$$R=\sigma^2_g/\sigma^2_g+\sigma^2_{gy}+\sigma^2_y+\sigma^2_e$$

where

σ^2_g = genotypic variance
σ^2_{gy} = interaction variance due to genotype × year
σ^2_y = variance due to year
σ^2_e = error variance
m = number of years
r = number of replicates.

Gain in precision (Gp) of estimates to be expected from repeated measurement over years is computed as:

$$Gp=1-[1+R(y-1)]/y$$

where R is the repeated estimate of a specific trait while y represents the number of repeated measurements (Falconer 1960; Hansche and Brooks 1964).

Precision of the quadruple lattice design over a randomized complete block design was computed as outlined by Goulden (1960).

The genotypic and phenotypic correlations between each pair of traits were calculated using covariance analysis (Johnson et al. 1957).

Results

There were significant year, hybrid and hybrid × year effects (Table 1). Single plant heritability estimates for the first 5 years were 38.9%, 31.5% and 42.3% for NB, FFB and MBW respectively. The corresponding repeatability estimates were 33%, 11% and 8% respectively (Table 2). Heritability and repeatability estimates were highest for all traits during the first 5 years (Table 2). The lower heritability and repeatability estimates for the 10 year and 14 year record are attributable to the larger year and g × e variance components as compared to the first 5 years. Broadsense hybrid (family) mean heritability estimates for these

Table 3. Phenotypic (upper value) and genotypic (lower value) correlation coefficients among FFB and its components

	FFB	MBW
NB	0.80** 0.61**	-0.41 -0.16
FFB		0.66** 0.60**

** Significantly different from 0.0 at 0.01 level of probability

Table 4. Parents evaluated in at least three crosses

Parent[a]	Number of hybrid families in which evaluated	Mean performance for each trait		
		NB/plot	MBW kg/bunch	FFB kg/plot
1.465	3	107	10.7	1,016.0
5.1296	3	103	11.5	1,125.1
1.864	4	103	10.9	1,021.7
2.3242	4	133	10.3	1,157.5
2.3570	4	111	9.9	1,012.1
5.1081	3	92	10.8	946.2
2.1834	3	99	11.7	945.2
1.314	9	106	10.9	1,009.0
1.1375	3	111	10.2	940.4
1.474	3	105	11.0	1,155.5
x̄ of the experiments		104	11.0	1,012.3
Range of the experiment		75 – 143	7.1 – 12.1	635 – 1,259
Hybrid 21 (2.3242 × 1.314)		143	8.6	1,236.7
Hybrid 23 (5.1296 × 1.474)		91	11.5	1,048.0
Hybrid 1 (1.465 × 1.1375)		111	8.2	917.8

[a] Code number refers to NIFOR nomenclature. The figure before decimal point represents the field in NIFOR where the palm is planted. Figures after the decimal point indicate the number of that palm within the field

traits were 88.9%, 90.5% and 96% for NB, FFB and MBW over the 14 year period.

Blocks/replicate and replicate mean squares were also highly significant. The relative efficiencies of the quadruple lattice design and analyses compared to a randomized complete block in this investigation were 1.13, 1.23 and 1.27 for NB, FFB and MBW respectively.

NB and MBW were both positively and significantly correlated with FFB (Table 3). NB and MBW are not correlated.

The performance of ten parents that were involved in more than three crosses are presented in Table 4. NB and FFB are expressed on per plot basis while MBW was on an individual palm basis. Data from three hybrid families (hybrids 1, 21, 23) are presented to illustrate whether crosses between parents with high NB and heavy MBW will produce high FFB. While the yield of hybrid 21 was above the average performance of both parents the yield of hybrid 23 was below that of the average of the two parents (Table 4).

Discussion

From parent-offspring regression, Van der Vossen (1974) obtained narrow-sense heritability estimates of 51.2%, 9.1% and 20.6% for number of bunches (NB) fresh fruit bunch yield (FFB) and mean bunch weight (MBW) respectively. Blaak (1965), using parent offspring regression, had earlier obtained narrow-sense heritability estimates of 36% and 41% for FFB and MBW respectively. Our broad sense heritability estimates of 38.9%, 31.5% and 42.3% for NB, FFB and MBW respectively, include non-additive genetic variance. Frey and Horner (1955) have also pointed out that heritability estimates from parent/offspring regression tend to be lower than those from component of variance analysis. Heritability estimates from parent-offspring regression may be biased by genotype × environmental interaction, particularly when they are grown at different times. The parents of the hybrids were collected from within and outside Nigeria to ensure high variability. This may also account for the high heritability estimates obtained in this study. The heritability estimates were also biased upwards by our inability to separate location, hybrid × location, and year × location × hybrid effects.

The availability of tissue culture technique for clonal propagation of outstanding oil palm trees (Jones 1974) has increased the value of data collection on individual trees. Since the same trees were evaluated from year-to-year, data taken on each trait are repeated measurements on the same individual. Repeatability and single-plant heritability estimates were highest for all traits during the first five years. Lower estimates were obtained for the 10-year and 14-year periods. In the 3 sets of analyses substantial gains in precision were made at the second and third repeated measurements which means that 3 to 4 years of bunch production will provide sufficient information for effecting meaningful, valid and reliable evaluation of oil palm families for NB, FFB and MBW. This means that the generation interval for oil palm breeding could be as short as 6–7 years after transplanting to the field.

The fact that NB and MBW have significant genotypic correlation with FFB suggests that simultaneous selection for high NB and MBW could produce high FFB. This expectation is justified by the absence of negative correlation between MBW and NB. Adams (1967) had earlier suggested that there is no true genetic correlation between yield components. In the present study, parents were not evaluated per se. Their potential for NB and MBW was inferred from their hybrid progeny in 3 or more crosses. It should be noted that pisifera parents for all practical purposes can only be evaluated in crosses since absence of shell results in near sterility. The sterility results from the invasion of developing fruits by ants and pathogens. The shells protect the tenera and dura fruit forms from invading organisms. The FFB yield of crosses between parents with potential for high NB and high MBW could be high or low as judged by hybrid families 1, 21 and 23.

From the present study it can be concluded that the variability among the hybrid families is highly heritable, as judged by heritability estimates, and this variability can be exploited to produce high-yielding crosses. Individual palm selection and their clonal propagation will preserve unique genetic combinations that will be expected to considerably exceed family means. The positive association between NB and MBW with FFB and the lack of correlation between NB and MBW implies that simultaneous selection for the high NB and MBW will result in improved fresh fruit bunch yield. The repeatability estimates reveal that prolonging yield evaluation beyond 4 years of data collection is wasteful of resources and prolongs the breeding cycle.

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