Genetic variability of fresh fruit bunch yield in Deli/*dura* x *tenera* breeding populations of oil palm (*Elaeis guineensis* Jacq.) in Nigeria

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Received 5 December 2007; received in revised form 6 October 2008; accepted 9 October 2008.

Abstract

A study was conducted to assess the extent of genetic variability, broad-sense heritability, and correlation between yield and yield components in three Deli/*dura* x *tenera* (DxT) breeding populations. Populations 1, 2, and 3 were made up of 14 Deli x *tenera* progenies, 16 *dura* x *tenera* progenies, and 21 Deli/*dura* x *tenera* progenies respectively. The combined analysis of variance for number of bunches (BN), average bunch weight (ABW), and fresh fruit bunch yield (FFB) revealed significant genotypic differences. The phenotypic coefficient of variation, however, was generally greater than the genotypic coefficient of variation, implying the influence of genotype x environment interaction in the expression of these traits. Broad-sense heritability estimates for the three traits varied considerably from population to population. Estimates of heritability were high in population 1 (78, 88.6, and 70.7 respectively for BN, ABW, and FFB yield). The corresponding figures were 27.5, 41.5, and 24.3 for population 2, and 5.3, 32.7, and 20.5 for population 3. High genotypic coefficient of variation (31.4, 27.4, and 26.5), heritability, and genetic advance as percent of mean (57.2, 52.7, and 45.9) for the three bunch yield traits in population 1 imply the potential for improvement of these traits through selection. On the whole, population 1 is an appropriate starting point for the next cycle of breeding and selection. Highly significant positive ($p < 0.01$) relationships were noted between FFB and BN suggesting that BN is a major yield contributing component. Strong negative correlations between BN and ABW (–0.220**, –0.260**, and –0.368**), however, denote that selection for high BN may result in lower ABW and vice-versa, which would hinder the exploitation of high heritabilities. Accordingly, any form of selection that takes into account the additive genetic variation may neglect other pathways, such as heterosis which can be identified by progeny testing only.

Keywords: Deli/*dura* x *tenera*, Heritability, Phenotypic coefficient of variation, Genotypic coefficient of variation, Genetic gain.

Introduction

Oil palm (*Elaeis guineensis* Jacq.) is a major crop that ranks second in the world market as a producer of vegetable fats and oils (Wahid et al., 2004). In Nigeria, oil palm accounts for over 70% of the total vegetable oils consumed with an estimated annual production of 1.3 million tonnes from an area of about 2.5 million ha (Ruma, 2007). Improving the productivity of Nigerian oil palm plantations, therefore, assumes significance. Modified reciprocal recurrent selection (RRS) breeding strategy was adopted by the Nigerian Institute for Oil Palm Research (NIFOR) in the past towards this goal (Okwuagwu, 1996). Fresh fruit bunch yield (FFB), a product of the number of bunches (BN) and average bunch weight (ABW), is a major determinant of oil palm productivity (Broekmanns, 1957). Clearly, selection for FFB components would rapidly advance the oil palm breeding programme. The success of this, however, would depend on the nature and extent of available heritable variations in the populations and the traits of interest.

Information on genetic variability in populations will aid

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oil palm breeders in deciding whether to continue making selections on the parents in breeding cycles if there is adequate variability. If not, it may be essential to introgress genes from new germplasm sources into existing populations, to broaden their genetic base. Genetic variation for the different oil yield components of this crop has been estimated previously (Okwuagwu and Tai, 1995; Rafii et al., 2002; Musa et al., 2004). In particular, high heritability estimates associated with high genetic advance for FFB yield were reported by Okwuagwu and Tai (1995) and Okoye (2007). There is, however, need to estimate genetic variability, heritability, relative genetic gains, and correlation among the fresh fruit bunch yield traits of different breeding populations. Hence a study was undertaken with the objective of estimating the genetic traits of three second cycle oil palm breeding populations maintained by the Nigerian Institute for Oil Palm Research (NIFOR) to obtain information necessary for advancing the breeding populations into the next generation.

Materials and Methods

Three distinct breeding populations from the NIFOR second cycle modified reciprocal recurrent selection breeding programme were evaluated. The second cycle breeding populations were derived from the first cycle recombinant progenies (Okwuagwu, 1989). Five Deli *dura*, eight *dura* and 13 *tenera* parents were selected for the second cycle breeding programme based on their combining ability for major yield traits. All the populations were progeny trials laid out in a randomized complete block design (RCBD) with a planting space of 9 m equi-triangular and were managed as described by Utulu (1989). Population 1 consisted of 14 Deli x *tenera* progenies planted in 1987 with six replicates of 16 palms each per plot. Population 2 comprised 16 *dura* x *tenera* progenies planted in 1987 in four replicates of 16 palms per plot and population 3 comprised 21 Deli/*dura* x *tenera* progenies planted in 1993 in three replicates of 16 palms per plot. The NIFOR elite high yielding *tenera* hybrid planting material (extension work seed) was used as a control in each trial so that meaningful comparisons could be made between the progenies grown in all the trials.

The experiment was conducted at the main station of NIFOR at Benin City (Edo State, Nigeria; 06°312 N; 05°402 E; 149.4 m above sea level). This region has a humid, tropical climate with a total annual rainfall of 1595 to1958 mm and a mean annual temperature of 31.8 to 32°C. Populations 1 and 2 were planted on the Alagba series while population 3 was planted on the Orlu series (Dystric Nitosol) of acid sand soil (FAO-UNESCO, 1990; Ogunkunle et al., 1999). Depending on the series, pH, N, P, base saturation, and effective cation exchange capacity (ECEC) were 5.8 to 4.9, 0.09 to 0.08 %, 8.15 to 6.42 ppm, 86 to 69 % and 2.27 to 1.30 cmole kg^{-1}, respectively. Nutrients were applied at the rate of 0.5, 0.25, 0.75, and 0.2 kg N,P,K, and Mg sourced from a compound fertilizer (12:12:17:2) after transplanting. In addition, empty fruit bunch (25.5 to 203 kg $palm^{-1}$), pruned fronds and palm trunks (45.2 to 320 kg $palm^{-1}$), and fronds (90 kg $palm^{-1}$) at replanting were subsequently applied to the field as a substitute for inorganic fertilizers (Omoti, 1989).

Data on the number of bunches (BN) and fresh fruit bunch (FFB) yield (kg $palm^{-1}$ $year^{-1}$) were recorded every year. Average bunch weight (ABW) was obtained as the ratio of FFB to BN. Six year (1999–2004) juvenile yield data for population 3 and seven year (1999–2005) mature yield data for populations 1 and 2 were used. The procedure adopted for the yield analysis followed the methods of Okwuagwu and Tai (1995). Individual yield records on bunch number, annual fresh fruit bunch yield, and average bunch weight were calculated for populations 1, 2, and 3 respectively. Progeny means for each replicate was used in a factor analysis for each component of variance. The component of variance was derived from the combined analysis of 6 and 7 year data in three factor (genotype, year, and replicate) ANOVA. A random effect model was assumed for all sources of variations, with M_g, M_y, M_{rg}, M_{gy}, M_{ry} and M_{rgy} as the mean squares for genotypes, years, replicate x genotype interactions, genotype x year interactions, replicate x year interactions, and replicate x genotype x year interactions, respectively. Broad sense heritability was estimated as the ratio of the genotypic variance (σ_g^2) and phenotypic variance (σ_p^2). The analysis of variance and variance components were computed using the GLM and VARCOMP procedures of SAS (SAS

Inst., 2000). Genotypic and phenotypic variance and broad sense heritability (H_{bs}) were calculated as explained below:

Genotypic variance,

$$\sigma_g^2 = \frac{M_g - M_{gy} - M_{rg} + M_{rgy}}{y} \quad \text{(Eq. 1)}$$

Phenotypic variance,

$$\sigma_p^2 = \frac{M_{gy} + M_{rg} - M_{rgy}}{r} \quad \text{(Eq. 2)}$$

$$H_{bs} = \sigma_g^2 / \sigma_p^2 \times 100 \quad \text{(Eq. 3)}$$

The response of the FFB yield and its components to selection and the magnitude of variation responsive to selection was calculated according to the method of Burton and De Vane (1953).

$$\text{PCV (\%)} = \frac{\sqrt{\sigma_p^2}}{\bar{X}} \times 100 \quad \text{(Eq. 4)}$$

$$\text{GCV (\%)} = \frac{\sqrt{\sigma_g^2}}{\bar{X}} \times 100 \quad \text{(Eq. 5)}$$

Where $\bar{X}$ is the mean of each trait while PCV and GCV are phenotypic and genotypic coefficients of variation respectively.

Expected genetic advance (Gs) under selection for each trait was calculated according to Allard (1980) as follows:

$$Gs = (K)(\sigma_p)(H) \quad \text{(Eq. 6)}$$

where K is the selection differential, which varied with selection intensity (5% intensity was used at which K = 2.06). σ_p is the phenotypic standard deviation and H is the heritability in a broad sense. In order to determine the relationships between the examined traits and fresh fruit bunch (FFB) yield, correlation coefficients were calculated with SPSS software package version 12.0.1 (SPSS Inc. 2004).

Results and Discussion

A combined analysis of variance over years for BN, ABW, and FFB yield data from 51 oil palm progenies that constituted the three populations are presented in Table 1. The analysis of variance revealed that progenies and years were significantly different for all traits studied in the three populations. Replication effect also was consistently significant in this trial. The observed variability among progenies and years is pertinent for the effective selection of superior oil palm genotypes with increased fresh fruit bunch yield. Rafii et al. (2001) also reported similar observations. Furthermore, progeny, year, and progeny x year interaction effects for all traits were significant. Such variations would affect the genotypic variance and hence heritability estimates. These results also signify that some degree of selection for wide adaptability in all traits measured in this study occurred in the genetic material grown at Benin City, Nigeria, which is consistent with the observations of Rafii et al. (2002).

The experimental coefficient of variation (CV) for populations 1 and 2 with respect to BN (24.3 and 29.4%), ABW (16.1 and 19.1%), and FFB (24.4 and 28.1% respectively) were within the acceptable levels for valid statistical comparison of bunch yield traits. In general, CV higher than 20% is considered to be high; however, for a perennial tree crop like oil palm, CV values of 20-30% for bunch yield traits have been reported as tolerable (Hartley, 1988). Nonetheless, the CV values obtained in the present study for population 3 were too high (36.8 to 49.8%), presumably because of the inherent variability in juvenile fresh fruit bunch yield of oil palm (Okwuagwu and Okoye, 2006). The inconsistent CV values reported in many studies might be due to the genotypic differences and variable environments in which the trials were carried out.

The analysis of genetic variability given in Table 2 reveals that mean bunch number (BN) in populations 1 and 2 were similar (3.17 and 3.28 bunches per annum respectively). Also, the average bunch weight of population 2 (12.80 kg) was higher than population 1 (ll.93 kg). In all cases, the genotypic coefficient of variation (GCV) was less than its corresponding estimates of phenotypic coefficient (PCV), indicating a significant role of environment in the expression of these traits. This is consistent with earlier reports of Kushairi et al. (1999)

Table 1. Combined analyses of variance for number of bunches (BN), average bunch weight (ABW), and fresh fruit bunch yield (FFB) in three second cycle Deli x *tenera* oil palm breeding populations in Edo state, Nigeria.

Sources of variation	d.f.	Mean squares		
		BN	ABW	FFB
Population 1				
Replication	5	2.632***	25.290***	548.819***
Progeny	14	8.645***	81.843***	871.042***
Progeny x Rep.	70	1.126***	7.128***	140.234***
Year	6	80.284***	71.667***	9082.392***
Rep. x Year	30	3.223***	4.845ns	467.933***
Prog. x Year	84	1.150***	4.686ns	165.894***
Rep. x Prog. x Year	420	0.593	3.714	78.139
C.V. (%)		24.3	16.1	24.4
Population 2				
Replication	3	9.123***	50.563***	1611.042***
Progeny	16	3.812***	46.098***	497.930***
Prog. x Rep.	48	1.969***	17.869***	311.129***
Year	6	65.303***	93.522***	5702.985***
Rep. x Year	18	3.262***	7.830ns	485.109***
Prog. x Year	96	1.261*	8.658**	131.043ns
Rep. x Prog. x Year	288	0.937	5.967	123.116
C.V. (%)		29.4	19.1	28.1
Population 3				
Replication	2	36.384**	3.558ns	808.801**
Progeny	21	8.008**	12.472**	392.999***
Prog. x Rep.	42	7.919**	8.330ns	257.030**
Year	5	201.004***	395.392***	3762.096***
Rep. x Year	10	18.518***	5.576ns	204.400ns
Prog. x Year	105	3.901ns	4.227ns	141.550ns
Rep. x Prog. x Year	175	4.619	6.105	139.493
C.V. (%)		35.9	21.8	37.8

Populations 1, 2, and 3 are 14 Deli x *tenera* progenies, 16 *dura* x *tenera* progenies, and 21 Deli/*dura* x *tenera* progenies respectively; d.f. = degrees of freedom; *,**,*** Significant at p=5%, 1%, and 0.01% respectively; ns = not significant; CV= coefficient of variation.

and Musa et al. (2004). Notwithstanding the environmental influence on FFB yield, the multiplicative relationship between this trait and its two components (BN and ABW) could explain a wide range of phenotypic variability. GCV values differed from population to population. High estimates of GCV observed for all traits of population 1 suggest higher selection progress in this population. The low GCV values in populations 2 and 3 imply reduced genetic variability. This could be attributed to the effect of continuous selection of the parent trees with emphasis on FFB yield traits. Introgression of new genes from oil palm germplasm will broaden the genetic base of these populations.

High broad sense heritabilities were obtained for BN, ABW, and FFB yield in population 1 (78, 88.6, and 70.7). Similar findings were reported by Musa et al. (2004) from their study on D x P populations. The high heritability in population 1 could be attributed to high genetic variability and diversity of parents. According to Pradeepkumar et al. (2001), high heritability in broad sense does not always entail better selection due to the occurrence of non-additive variance. Consequently, genetic advance as percentage of the mean becomes a useful indicator of the progress that can be expected as a result of exercising selection on a particular population for specific traits (Kalia et al., 2005). The highest

Table 2. Genetic variability parameters for bunch yield components in the Nigerian Institute for Oil Palm Research (NIFOR) second cycle oil palm breeding populations in Edo state, Nigeria.

Traits	Population	Mean±SE	Range	GV	PV	GCV (%)	PCV (%)	H_{bs} (%)	GA as % of mean
Number of bunches	1	3.17±0.128	2.21-3.90	0.995	1.275	31.4	35.6	78.0	57.2
	2	3.29±0.242	2.46-3.76	0.217	0.790	14.2	23.0	27.5	15.3
	3	4.32±0.716	3.07-5.89	0.134	2.534	8.5	35.9	5.3	4.0
Average bunch weight (kg palm^{-1} year^{-1})	1	11.93±0.321	10.01-14.58	10.535	11.885	27.4	28.9	88.6	52.7
	2	12.80±0.611	10.87-15.56	3.648	8.788	14.9	17.7	41.5	19.8
	3	6.72±0.824	5.17-8.28	1.003	3.153	14.9	21.8	32.7	17.4
Fresh fruit bunch yield (kg palm^{-1} year^{-1})	1	36.18±1.473	27.37-43.43	91.865	129.863	26.5	31.5	70.7	45.9
	2	39.50±2.774	31.94-48.56	25.553	105.317	12.8	22.6	24.3	13.0
	3	24.59±3.937	15.69-33.23	22.319	108.681	19.2	37.8	20.5	17.9

Populations 1, 2, and 3 are 14 Deli x *tenera* progenies, 16 *dura* x *tenera* progenies, and 21 Deli/*dura* x *tenera* progenies respectively; GV=Genotypic variance; PV= Phenotypic variance; GCV= genotypic coefficients of variation; PCV= phenotypic coefficients of variation; GA=genetic advance.

genetic advance in this study was predicted for the FFB yield traits in population 1. High heritability accompanied by high genetic advance for BN, ABW, and FFB yield in this population is suggestive of additive gene action, and their possible improvement through selection. Selection for bunch yield should, however, be based on progeny testing for general and specific combining abilities of parents because of the significant negative correlation between BN and ABW, which hinders exploitation of high heritability estimates for bunch yield and its components (Okwuagwu and Tai, 1995).

The correlation coefficients for bunch yield traits revealed significant and negative relationships between BN and ABW in all populations studied (Table 3). Implicit in this is that selection of genotypes for high BN would result in palms that produce relatively lower ABW. This phenomenon would then limit exploitation of high heritability of the two bunch yield traits when selection is applied to both. Similar observations were reported by Kushairi et al. (1999) also. FFB yield exhibited significant positive correlations with BN and ABW in the populations studied. These results suggested that any positive increase in BN and ABW will accelerate the improvement in FFB yield. The high correlation coefficient between FFB yield and BN indicates that BN is a critical determinant of FFB yield. Therefore, selection for BN could suffice for the improvement of FFB yield in oil palm.

Table 3. Correlations among bunch yield traits in the Nigerian Institute for Oil Palm Research (NIFOR) second cycle oil palm breeding populations in Edo state, Nigeria.

Traits	Fresh fruit bunch yield	Average bunch weight
Bunch number	0.860** a	–0.220** a
	0.795** b	–0.260** b
	0.676** c	–0.368** c
Fresh fruit bunch yield		0.180** a
		0.240** b
		0.223** c

** Correlation is significant at $p= 0.01$; a, b, c are correlation coefficients for populations 1, 2, and 3 respectively.

In the light of the high estimates of genotypic coefficient of variation, heritability, and genetic advance recorded for the three bunch yield traits in population 1, it could be inferred that this population would be the most appropriate as a starting point in the next cycle of breeding and selection programme while BN with the highest correlation coefficient with FFB yield offers the greatest scope for FFB yield improvement in the oil palm.

Acknowledgements

We wish to express our gratitude to Mr. Sam Ofodile of the biometric unit of IITA Ibadan for his assistance in the statistical analyses of the data.

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