



Research Article

Estimates of Components of Variances for Bunch Traits in Date Palm Crosses (*Phoenix dactylifera* L)

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ABSTRACT

A field experiment was carried out at Nigeria institute for Oil Palm Research date palm Research substation Dutse, Jigawa state during 2004-2005 flowering season. Biparental progenies derived from 60 crosses replicated twice were subjected to analysis of variance using nested design for the purpose of estimating additives, genetic and dominance components of variances of the seven bunch traits. Significant variation was observed for the traits studied. The male components of variances (σ^2_m) for all the traits were negative, indicating that the estimates were not different from zero or were very small. Positive estimates were recorded for females within male variance (σ^2_{tm}), while Non-significant negative additive variances (σ^2_A) were obtained for all the traits. Dominance variance (σ^2_D) showed significant positive values for number of fruits, spikelets, aborted fruits and unfertilized florets. Positive estimates were recorded for environmental variance (σ^2_e), genotypic variance (σ^2_g) and phenotypic variance (σ^2_{ph}). In all cases phenotypic variance was much larger than the genotypic variance. Low environmental variance were obtained for the traits indicating that the environmental condition where the experiment was carried out is homogenous and the material could perform considerably well under similar environmental conditions. The means performance of the males indicates that variability exists between the males; Males 6R3 and 1R7 are good combiners with female 12R3 for number of fruits while males 1R12 and 5R2 are good combiners with female 12R3 for number of fruits. Female 2R8 is poor general combiners for number of fruits. Males 1R12 and 5R2 are good combiners with female 1R27 for weight of fruit while male 6R3 and 1R7 are good combiners with female 12R3 for fruit weight. Recurrent and backcross selection are recommended for further date palm improvement programs.

INTRODUCTION

Improvement of any trait or character can only be achieved if there exist a large amount of genetic variability in the reference population the breeder intends to work with. To know level of variability existing among the traits, additive variance (σ^2_A), dominance variance (σ^2_D), genetic variance (σ^2_g), phenotypic variance (σ^2_p) and environmental variance (σ^2_e) with their standard errors have to be computed. Variation within date fruits evaluated would be attributed to be genotypic differences between the male and female plants, since the date palm is dioeciously and highly heterozygous (Zaid and de Wet, 1999). Nested design was used in this experiment because the prime objective of the study was to partition contributions by the males and females towards the variation in the bunch traits, in controlled crosses of date palm so as to obtain estimates of components of variances and also is appropriate for estimate of variance in a reference population (Hallauer and Miranda, 1989). According to Otegbeye (1989), additive variance is the major cause of similarity between parent and their progeny. Therefore additive genetic variance is the ultimate determinant of the degree of progress that can be made from a breeding scheme. It is well known that the pollen affects the size of the fruit and seed (Zaid and de Wet, 1999). This effect was verified by Nixon Carpenter (1978) in USA.

MATERIALS AND METHODS

The experiment was carried out at Nigeria institute for Oil Palm Research date Palm substation Dutse, Jigawa during 2004-2005 flowering season. It lies on latitude $10^0 14'N$ and longitude $4^0 25'E$. The vegetation is Sudan savannah, with an annual rainfall of about 600mm. The soil is sandy loam in nature and the soil height is at sea level, with an average temperature of $32.4^{\circ}C$.

5 male palms were randomly selected from the gene pool (GP) at the Dutse substation. 3 male palms from gene pool III field and 2 from the nationally coordinated research project (NCRP) field. Ten female palms were randomly selected from the gene pool at Dutse substation, 9 from gene pool III and one from gene pool IV.

They are: 19R1 GPIII, 1R12 GPIII, 6R3 GPIII, 5R2 NCRP, 1R7NCRP and Open pollinated. Ten female palms were randomly selected from the gene pool at Dutse Substation, nine from gene pool III and one from gene pool IV. They are:

12R3 GPIII, 6R5 GPIII, 2R8GPIII, 1R11 GPIII, 7R14 GPIII, 2R15 GPIII, 5R16 GPIII, 1R27 GPIII, 3R3 GPIII and 5R5 GPIV.

Nested design I was mating design used for the crosses. Twelve inflorescences (spathe) were chosen, six as

crosses and six as replicates, the extra one was cut up. One variety of pollen was used in pollinating two female inflorescences (spathes) making a total of 10 pollinated spathes using controlled pollination technique while the remaining two spathes (inflorescences) were open pollinated either by wind or insects and they served as control.

Data collected for the seven bunch traits were as follows:

Number of fruits, number of spikelet, number of aborted fruits, number of unfertilized florets, weight of bunch stalk, weight of fruits and total weight of bunch. Nested design 1 of Comstock and Robinson (1948) was used for the analysis of variance for the bunch traits studied. Design I is appropriate for the estimate of components of variances in a reference population (Hallauer and Miranda, 1986).

RESULTS AND DISCUSSION

Mean Performance

The mean, standard error of the mean range and coefficient of variation for seven bunch traits are shown in Table 1. A wide range within each trait observed. In all cases, the mean were very much larger than their respective standard errors. The coefficients of variation (C.V) for the different traits range from 16.9% for total weight of bunch to 32.4% for number of unfertilized floret. The traits which show highest mean performance are number of fruits, number of aborted fruit and number of unfertilized florets. The coefficient of variation expresses the experimental error as percentage of mean, thus the higher the C.V value the lower the reliability of the experiment. The coefficient of variation (C.V) indicates the degree of precision with which the treatments are compared and is good index of reliability of any experiment. It expresses the experimental error as percentage of mean, thus the higher the coefficient of variation (C.V) value the lower the reliability of the experiment (Gomez and Gomez, 1984). The coefficient of variation (C.V) varies greatly with the type of experiment, the crop and the character measured. For date palm, it was established that coefficient of variation (C.V) of about 13.7-18.6 is assume to be high, if it is assumed that environment variation was to be similar then the palm to palm variation within the population may be attributed to genotypic differences between the males and females. Since date palm is dioecious and heterozygous, an individual male palm can be genotypically unique. Duncan multiple range test was used to compare mean performance of the males and also to determine whether significant differences exist among the males for the seven bunch traits studied (Table 2). For number of fruits and number of spikelets there were no significant differences among the males, but significant differences exist among the males for the rest of the traits.

Table 1: Mean, Standard Error (SE), Range and Coefficient of variation (C.V) for Bunch Traits Studied

Traits	Mean \pm SE	Range	C.V (%)
No of fruits	96.350 \pm 20.986	700.0 – 1200.0	23.8
No of spikelets	67.817 \pm 1.099	40.0 – 80.0	17.8
No of aborted fruits	90.750 \pm 2.370	60.0 – 200.0	28.6
No of unfertilized florets	131.375 \pm 3.883	80.0 – 200.0	32.4
Weight of fruits	0.431 \pm 0.026	0.20 – 0.50	21.2
Weight of bunch stalk	4.728 \pm 0.077	3.00 – 6.00	17.8
Total weight of bunch	5.136 \pm 0.079	3.00 – 6.00	16.9

Table 2: Mean performance for bunch traits

Male	No of fruits	No of spikelets	No of aborted fruits	No of unfertilized florets	Weights of fruits	Weights of bunch stalks	Total weight of bunch
19R1 GP III	935.0	66.650	86.350bc	134.70ab	0.3885b	4.3305b	4.719b
1R12 GPIII	924.0	66.650	102.750 ab	118.25b	0.4545a	4.4085ab	4.863ab
6R3 GPIII	918.75	67.050	77.80c	155.65a	0.4505ab	4.940a	5.3655a
5R2 NCRP	1014.10	71.250	83.450c	118.30b	0.4360ab	4.887ab	5.323a
1R7 NCRP	965.20	66.850	84.100c	12500b	0.4465ab	4.981a	5.4265a
Control	1043.45	68.430	110.05a	136.35ab	0.411ab	4.823ab	5.121ab

Means sharing similar letter(s) do not differ significantly at $p = 0.05$

Variability among males and females within males

The mean squares from the analysis of variance for bunch traits are shown in Table 3. The results show a highly significant difference ($p=0.01$) for most traits in females

within males and a highly significant difference for number of aborted fruits in males. A significant difference ($p=0.05$) was also observed for weight of bunch stalk in the males, while the other traits for males show non-significant differences.

Table 3: Mean squares for bunch traits

Source	df	No of fruit	No of spikelets	No of aborted fruit	No of unfertilized florets	Weight of fruit	Weight of bunch stalk	Total weight of bunch
Rep	1	16008.300	30.0	30	364.008	0.001	0.119	0.231
Male	5	53296.160	65.733	3204.26 0	4035.775	0.014	1.613*	1.683
Female/male	54	274495.25 0**	763.22 8**	4235.05 9	62884.82 9**	0.094	6.29 5**	7.017
Error	59	52847.775	145.102	673.796	1809.839	0.008	0.712	0.749

*Significant differences at 5% level of probability

** Significant differences at 1% level of probability

Through selection of outstanding males and females, significant improvement could be achieved (Abubakar, 1984). According to Osuhor and Samarawira (1981), most of the Nigerian date palms compare favorably in fruit characteristics with leading world varieties like the deglet noor. It is obvious from these results that with careful planning, significant improvement could be achieved by selection and hybridization of those traits with significant means squares.

Estimates of components of variance

Estimates of male variance (σ^2_m), female within male variance ($\sigma^2_{f/m}$) with their respective standard errors and level of significance for the seven bunch traits are shown in Table 4. The male components of variances for all traits were negative. Highly significant differences ($p=0.01$) were observed for the male components of variances for

number of unfertilized floret, weight of fruit and total weight of bunch. While significant differences ($p=0.05$) were observed for number of fruits, number of spikelets, number of aborted fruits and weight of bunch stalk. The estimates for female within male components of variance ($\sigma^2_{f/m}$) were all positive and non-significant for all traits except number of aborted fruits which is significant at 5%

probability level ($p=0.05$). The standard errors for all traits were lower than the estimates and the estimates were more than twice larger than their respective standard errors. F-tests were used to determine if the variation among males and females within males were significantly different from zero.

Table 4: Estimates of male variance and female within male variance for bunch traits.

Traits	$\sigma^2_m \pm SE$	$\sigma^2_{F/m} \pm SE$
No of fruits	-11059.955 \pm 2828.937*	110823.738 \pm 26374.975
No of spikelets	-34.875 \pm 40.747*	309.063 \pm 73.410
No of aborted fruits	-56.039 \pm 287.717*	1825.631 \pm 413.609*
No of unfertilized florets	-2942.454 \pm 3368.251**	30537.495 \pm 5944.418
Weight of fruits	-0.004 \pm 0.005**	0.043 \pm 0.009
Weights of bunch stalk	-0.234 \pm 0.347*	2.792 \pm 0.599
Total weight of bunch	-0.267 \pm 0.386**	3.415 \pm 0.667

*Significant differences at 5% level of probability

** Significant differences at 1% level of probability

According to Silva (1974), since variance by definition is either zero or larger than zero, the negative estimates of male variance (σ^2_m) with respect to their standard errors must either be estimates of true zero value or they reflect some deficiency in the model. Furthermore, it can be observed from Table 4, that the variance estimates for females within males were far higher than the variance

estimates of the male parent used. In order to derive male lines that approach the females in genetic composition, it will be necessary to back cross selected males to selected females, and it will take about four backcrosses to reconstitute about 97% of the recurrent genotype of the female parent among the male segregate.

Table 5: Estimates of additive genetic variance and dominance variance for bunch traits.

Traits	$\sigma^2_A \pm SE$	$\sigma^2_D \pm SE$
No of fruits	-44239.82 \pm 420.664	487534.78 \pm 1396.474
No of spikelets	-139.500 \pm 23.624	1375.752 \pm 74.182
No of aborted fruits	-224.156 \pm 29.994	7526.68 \pm 173.513
No of unfertilized florets	-11769.816 \pm 216.978	133919.80 \pm 713.901
Weight of fruits	-0.016 \pm 0.253	0.188 \pm 0.867
Weights of bunch stalk	- 0.936 \pm 1.935	12.104 \pm 6.958
Total weight of bunch	-1.064 \pm 2.067	14.728 \pm 7.675

The estimates for additive genetic variance (σ^2_A) for seven bunch traits were all negative (Table 5). The standard errors for all the traits were much lower than the estimates, except in weight of fruit, weight of bunch stalk and total weight of fruit which are more than the estimates. Obilana *et al.* (1979) advanced some reasons for such results with negative estimates which include inadequate sampling and sample size, assortative mating and linkage. The estimates for dominance variance (σ^2_D) for the seven bunch traits are all positive (Table 5). The standard error was much lower than the estimates except for weight of fruits which is slightly larger than the estimate. The result shows that dominance variance (σ^2_D) is the major component of the total genetic variance (σ^2_g). Al- Juburi (1993), recorded higher estimates of

dominance variance (σ^2_D) than additive genetic variance (σ^2_g) for some of the traits he studied. In these studies, lines with unknown gene frequencies were used. However, the high degree of dominance could be due to inadequate sampling and sample size, assortative mating and linkage. The low samples in this study could be the reason for the bias towards the dominance variance. Also the restricted area of sampling the palm which served as male and female and the fact that the locations of the original parent palms were unknown may explain the variation observed in this study. This is in agreement with the work (Hallauer and Miranda, 1984 and Silva, 1974).

The estimates of environment variance (σ^2_e), total genetic variance (σ^2_g) and phenotypic variance ((σ^2_p) for

the seven bunch traits are presented in Table 6. The total genetic variances for the same traits were high and their respective standard errors are much lower than the estimates except for weight of fruit. High estimates were recorded for number of fruits, number of aborted fruits, number of unfertilized florets and number of spikelets. Low values were recorded for total weight of bunch stalk and total weight of bunch. The estimates for phenotypic variance (σ^2_p) for bunch traits are positive and the standard errors were much lower than the estimates, with the exception of weight of fruit which has standard error

many times larger than the estimates ($\sigma^2_p=0.180\pm 0.424$). The highest values were recorded for number of fruits, number of unfertilized florets, number of aborted fruits and number of spikelets respectively. Low values were recorded for weight of bunch stalk ($\sigma^2_p=11.919\pm 3.452$) and total weight of bunch ($\sigma^2_p=14.376\pm 3.792$). The lowest value was recorded for weight of fruits. The estimate of environmental variance (σ^2_e) shown in Table 6 are all positive, the estimates are lower than the total genetic variance (σ^2_g).

Table 6: Estimates of environmental variance, genotypic variance and phenotypic variance for bunch traits

Traits	$\sigma^2_e \pm SE$	$\sigma^2_g \pm SE$	$\sigma^2_p \pm SE$
No of fruits	52847.775 \pm 9569.225	443294.960 \pm 665.804	496142.735 \pm 704.374
No of spikelets	145.102 \pm 26.273	1236.252 \pm 35.160	1381.354 \pm 37.167
No of aborted fruits	673.797 \pm 112.005	7302.524 \pm 85.455	7976.321 \pm 89.310
No of unfertilized florets	1809.839 \pm 327.710	122150.00 \pm 349.500	123959.839 \pm 352.079
Weight of fruits	0.008 \pm 0.001	0.172 \pm 0.415	0.180 \pm 0.424
Weights of bunch stalk	0.749 \pm 0.136	11.170 \pm 3.342	11.919 \pm 3.452
Total weight of bunch	0.712 \pm 0.129	13.664 \pm 3.697	14.376 \pm 3.792

The very low estimates of environmental variance (σ^2_e) in comparison to the total genetic variance (σ^2_g) for bunch traits, presented in Table 6, indicates that the environmental factors have little effect on performance of the date palm. This is in agreement with the findings of Osuhor and Samarawira (1981); Osuhor (1983), Abubakar (1984); Abubakar and Samarawira (1989) and Zaid and Wet (1999). The phenotypic variance (σ^2_p), were mainly genetic in nature due to low estimates of environmental variance (σ^2_e) for the entire traits. For each trait, the genetic variance (σ^2_g) was many times more than the environmental variance. So we can conveniently say that most of the variance observed within the date fruits evaluated would be attributed to the genotypic differences between the male and female palms, since the date palm tree is dioecious and highly heterozygous.

CONCLUSION

From the crosses it was observed that males 6R3 and 1R7 are good combiners with female 12R3 for number of fruits while males 1R12 and 5R2 are good combiners with female 1R27 for number of fruits. Female 2R8 is a poor general combiner for number of fruits. Males 1R12 and 5R2 are good combiners with female 1R27 for weight of fruit while males 6R3 and 1R7 are good combiners with female 12R3 for fruit weight.

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