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GENOTYPE x ENVIRONMENT INTERACTION AND STABILITY ANALYSES IN OIL PALM (*Elaeis guineensis* Jacq.) PROGENIES OVER SIX LOCATIONS

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Genotype and environment (G x E) interaction was estimated in 40 oil palm dura x pisifera *progenies, evaluated at six locations for yield and its components. The presence of G x E interaction was detected for yield and its components. The G x E variance component was relatively small and ranged from 3.53% to 4.12%. The result showed that fresh fruit bunch (FFB) yield had a larger G x E variance component (σ^2_{gl}) than genetic variance component (σ^2_g), indicating that this character was very sensitive to the environment. The joint regression analysis showed that the linear regressions accounted for a small proportion of the total G x E interaction. This suggests that a non-linear component part of G x E interaction for the characters played an important role.*

The combined use of all the stability determination methods could provide a better interpretation of individual stability of genotypes. Combined use of 10 stability statistics for FFB yield indicated that progenies DP8 and DP21 were highly stable genotypes, which also produced above average FFB yield. On the other hand, progenies DP7 and DP30 were the most unstable genotypes as indicated by all the stability parameters.

Keywords:

Genotype x environment interaction, stability statistics, G x E variance and genetic variance.

INTRODUCTION

Multilocation trials play an important role in breeding programmes in evaluating the adaptability of new varieties in various environments. Often, the genotypic performance depends on the environment, leading to changes in relative phenotypic values for a number of genotypes in diverse environments. This difference is considered as an interaction between G x E. Several methods of estimating the relative stability of performance of genotypes across environments, such as joint regression analysis (Eberhart and Russell, 1966), genotype grouping techniques (Francis and Kannenberg, 1978; Rajanaidu *et al.,* 1993; Yong *et al.,* 1993) and rank sum method (Kang, 1988a; Kang *et al.,* 1990) are available.

G x E interaction has in recent years gained importance in oil palm breeding programmes. Several researchers studied G x E interaction in oil palm and found that genotypes respond to the environment in different ways. Rosenquist (1985) and Rajanaidu *et al.* (1986) reported the absence of G x E interaction for yield in their progenies studied. However, significant G x E interaction was reported by Obisesan and

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Fatunla (1983), Ong *et al.* (1986), Lee *et al.* (1988), Rajanaidu *et al.* (1992) and, Yong and Chan (1990) in other progenies.

In the present study, 40 oil palm progenies derived from crosses between D x P were tested at six different locations. The objectives of this study were to understand the G x E interaction in an oil palm population and to identify and select for high yielding and stable oil palm genotypes using several methods of stability analysis.

MATERIALS AND METHODS

Genotypes

Forty D x P progenies were tested in each of six locations. The North Carolina Mating Design I (NCMI) described by Comstock and Robinson (1948; 1952) was used to develop the progenies for G x E interaction studies.

Fifteen *pisifera* palms of AVROS, Serdang S27B, Serdang 29/36, Lever Nigeria and Lever Cameroon were chosen to be the male and each of them was mated initially to four Deli *dura* palms designated as females. Forty full-sib families were developed from crosses between each *pisifera* parent to two to four *duras* for this study (*Table 1*).

Locations and Experimental Design

Six locations were used for testing the progenies, namely Kluang (Johor), Kudat (Sabah), Beaufort (Sabah), Teluk Intan (Perak), Carey Island (Selangor) and Kepong (Selangor). All the locations differed in terms of soil physical and chemical properties and climate (specifically rainfall). The soil types ranged from coastal clay to riverine alluvium and the rainfall in these sites ranged from 1800 to 3500 mm yr^{-1}. The Kudat area has a distinct dry period with only 102 rainy days.

The progenies were arranged in a completely randomized design (CRD) with two replications at each location and five palms were planted for each progeny and replication. The planting density varied from 136 to 148 palms ha^{-1}.

Data Collection

Yield data were collected in all six locations. The FFB yield was harvested from 37 months after planting. Four years of yield data were collected from 1985 to 1988 for Kudat, Beaufort, Teluk Intan, Carey Island and Kepong, and from 1986 to 1989 for Kluang. Each palm was inspected every 10 days and any ripe fruit bunch present was harvested and weighed using a simple spring balance. The weight of bunch(es) and the number of bunches (BNO) were recorded for each palm, and the average bunch weight (ABWT) was derived by dividing FFB by BNO.

General Statistics

Genotype means for each location and across locations, and location means were computed. From the computation, the simple statistics for each character, *i.e.*, mean, minimum and maximum values, and the least significant difference (LSD) was obtained. For location means, the Duncan new multiple range test (DNMRT) was carried out.

The analysis of variance for each of the characters under study in the 40 D x P progenies for each location and pooled data over locations was computed using individual palms data. A random model was used.

Stability of Genotypes

The analyses of variance is useful for estimating genetic and environment variances as well as for detecting the G x E effect. They could not be used to determine the stability of individual genotypes. Several techniques were used to measure the stability of the individual genotypes.

Genotype-grouping Techniques

Two types of genotype-grouping techniques have been reported. They are:

i) Mean against coefficient of variation (CV) as proposed by Francis and Kannenberg (1978); and
ii) Mean against standard deviation (SD) as used by Yong *et al.* (1993).

These techniques are essentially descriptive or illustrative where the genotypes are grouped by plotting their respective CV or SD against their means for each of the characters. Four quadrants are formed by the intersecting lines drawn to represent the overall CV and SD and grand mean (over all locations) for a particular

TABLE 1. PEDIGREE OF THE 40 FULL-SIB PROGENIES INVOLVED IN THE STUDY

No.	ϕCode No.	Pro-geny	Parents		♂ Code	Grandparents		ϕCode No.	Grandparents		ϕCode No.
			Female (a&b)	Male (c&d)		(a)	(b)		(c)	(d)	
1	MS1741	DP 1	0.117/1725	0.108/9681	1	ZG.14 4/3	ZE.14 26/6	HE.1172	ZE.30.1	29.36	P.903(TxP)
2	MS1746	DP 2	0.103/8659	0.108/9681	1	413.7	4/3.7	65/SBS/26	ZE.30.1	29.36	P.903(TxP)
3	MS1749	DP 3	0.117/1532	0.108/9681	1	ZG.14 4/3	ZE.14 4/3	HE.1163	ZE.30.1	29.36	P.903(TxP)
4	MS1752	DP 4	0.104/8745	0.108/9681	1	4/3.7	4/3.7	65/SBS/65	ZE.30.1	29.36	P.903(TxP)
5	MS1743	DP 5	0.80/470	0.107/9379	2	42.1	42.1	A(63/E4)	ZE.39.15	29.63	P.900(TxP)
6	MS1745	DP 6	0.117/1626	0.107/9379	2	ZG.14 4/3	ZE.12/17	HE.1163	ZE.39.15	29.63	P.900(TxP)
7	MS1744	DP 7	0.105/8997	0.116/1400	3	4/47.2	KB. BLK1/3	S.71	KB.AVROS4/6	19/29.36	65/E11(TxP)
8	MS1753	DP 8	0.80/905	0.116/1400	3	0.3/1.7	0.3/1.7	J(62/E28)	KB.AVROS4/6	19/29/36	65/E11(TxP)
9	MS1759	DP 9	0.104/8745	0.116/1062	4	4/3.7	4.37	65/SBS/26	HE.ZE.23.13	27B	P.908(TxP)
10	MS1773	DP10	0.102/8303	0.116/1062	4	UR(D)6b	UR(D)6b	NA	HE.ZE.23.13	27B	P.908(TxP)
11	MS1774	DP11	0.102/8282	0.116/1062	4	ZE.33.18	ZE.50.14	P.911	HE.ZE.23.13	27B	P.908(TxP)
12	MS1804	DP12	0.105/8997	0.110/9786	5	4/47.2	KB BLK1/3	3.71	ZE.33.5	ZE.23.15	P.913(TxT)
13	MS1828	DP13	0.117/1496	0.110/9786	5	ZG.14 6/16	ZG.12 6/14	HE.1175	ZE.33.5	ZE.23.15	P.913(TxT)
14	MS1778	DP14	0.80/867	0.108/9676	6	0.3/2.4	0.3/2.4	O(63/E21)	ZE.39.17	29.36	P.902(TxP)
15	MS1826	DP15	0.85/4401	0.108/9676	6	HE.505	HE.752	P.804	ZE.39.17	29.36	P.902(TxP)
16	MS1823	DP16	0.82/2316	0.109/191	7	UR(D)26	UR(D)9a	NA	LN(T)2	LN(T)2	NA(TxT)
17	MS1827	DP17	0.85/4401	0.109/191	7	HE.505	HE.752	P.804	LN(T)2	LN(T)2	NA(TxT)
18	MS1855	DP18	0.80/905	0.108/9680	8	0.3/1.7	0.3/1.7	J(62/E28)	ZE.30.1	29.36	P.903(TxP)
19	MS1860	DP19	0.105/9011	0.108/9680	8	UR(D)9a	UR(D)9a	NA	ZE.30.1	29.36	P.903(TxP)

TABLE 1. Continued

No.	ϕCode No.	Pro-geny	Parents		♂ Code	Grandparents		ϕCode No.	Grandparents		ϕCode No.
			Female (a&b)	Male (c&d)		(a)	(b)		(c)	(d)	
20	MS1868	DP20	0.80/26	0.108/9680	8	0.3/12.3	4/4.9	D(64/E2)	ZE.30.1	29.36	P.903(TxP)
21	MS1864	DP21	0.102/8282	0.107/9527	9	ZE.33.18	ZE.50.14	NA	ZE.30.1	29.36	P.899(TxP)
22	MS1891	DP22	0.85/4315	0.107/9527	9	20A/68JL(D)8b	0.3/1.7 JL(D)8b	62/E.12	ZE.30.1	29.36	P.899(TxP)
23	MS1897	DP23	0.105/9011	0.107/9527	9	UR(D)9a	UR(D)9a	P.911	ZE.30.1	29.36	P.899(TxP)
24	MS1921	DP24	0.103/8659	0.109/6	10	4/3.7	4/3.7	65/SBS/26	20A/43	AVROS KB4/4	65/E90(TxT)
25	MS1925	DP25	0.85/897	0.109/6	10	ANON	ANON	ANON	20A/43	AVROS KB4/4	65/E90(TxT)
26	MS1934	DP26	0.85/4315	0.109/6	10	20A/68	0.3/1.7	62/E.12	20A/43	AVROS KB4/4	65/E90(TxT)
27	MS1867	DP27	0.104/8745	0.116/1325	11	4/3.7	4/3.7	65/SBS/26	HE.ZB.14/20	AVROS KB4/26	65 E135(TxP)
28	MS1870	DP28	0.80/4320	0.116/1325	11	ANON	ANON	ANON	HE.ZB.14/20	AVROS KB4/26	65/E135(TxP)
29	MS1985	DP29	0.117/1488	0.116/1198	12	ZG.12 19/16	ZG.14 2/5	HE.1138	HE.ZB.14/20	AVROS KB4/12	65/E134(TxP)
30	MS1987	DP30	0.105/8914	0.116/1198	12	JL(D)1a	JL(D)1a	NA	HE.ZB.14/20	AVROS KB4/12	65/E134(TxP)
31	MS1979	DP31	0.117/1488	0.107/9413	13	ZG.12 19/16	ZG.14 2/5	HE.1138	C.96	AVROS KB4/18	65/E131(TxP)
32	MS2005	DP32	0.117/1488	0.107/9413	13	ZG.12 19/16	ZG.14 2/5	HE.1138	C.96	AVROS KB4/18	65/E131(TxP)
33	MS2075	DP33	0.80/295	0.107/9413	13	4/42.1 M.7	4/42.1 M.7	A(63/E4)	C.96	AVROS KB4/18	65/E131(TxP)
34	MS1998	DP34	0.117/1644	0.107/9607	14	ZG.12 19/18	ZG.14/18	HE.1107	C.81	29.36	P.891(TxP)
35	MS2049	DP35	0.117/1487	0.107/9607	14	ZG.12 4/6	ZG.12 4/12	HE.1125	C.81	29.36	P.891(TxP)
36	MS2050	DP36	0.117/1487	0.101/9607	14	ZG.12 4/6	ZG.12 4/12	HE.1125	C.81	29.36	P.891(TxP)
37	MS2071	DP37	0.117/1631	0.107/9607	14	ZG.12 19/18	ZG.13/19	HE.1126	C.81	29.36	P.891(TxP)
38	MS1996	DP38	0.80/883	0.109/208	15	0.3/1.7	0.3/1.7	J(62/E28)	LC(T)4	LC(T)4	NA(TxT)
39	MS1997	DP39	0.117/1644	0.109/208	15	ZG.12 19/18	ZG.14/18	HE.1107	LC(T)4	LC(T)4	NA(TxT)
40	MS2072	DP40	0.117/1631	0.109/208	15	ZG.12 19/18	ZG.13/19	HE.1126	LC(T)4	LC(T)4	NA(TxT)

Notes: ϕ crossing code; ♂ *pisifera* code.

NA - data not available.

character. Stability is then defined according to the relationship of the genotypes to these four general combinations of CV or SD and grand mean:

i) Low CV or SD and high mean (highly stable);
ii) Low CV or SD and low mean (stable);
iii) High CV or SD and high mean (unstable); and
iv) High CV or SD and low mean (highly unstable).

G x E Variance Component Analyses

According to Shukla (1972), the values of stability variance (σ^2_i) and stability variance following removal of heterogeneity due to the linear effect of a covariate (s_i^2) are computed from the following equations:

The ecovalence sum of square, for each genotype was divided by (g - 1) (l - 1)/g to estimate W_i mean square (Kang and Miller, 1984). The values of σ^2_i, s^2_i and W_i were computed by Interactive BASIC programme for calculating the stability parameters developed by Kang (1988b).

The palms within genotype mean squares were used for testing the stability variance (σ^2_i), stability variance after removal of covariate effect (s^2_i) and ecovalence mean square (W_iMS). Highly significant or significant values of those parameters imply that the genotype was highly unstable or unstable, respectively.

Joint Regression Analysis

The method of joint regression analysis after Eberhart and Russell (1966) was chosen to interpret the G x E interaction to have an insight

$$\sigma^2_i = \frac{1}{(l-1)(g-1)(g-2)} \times [g(g-1)\Sigma_j(\mu_{ij}-\mu_{i\cdot})^2 - \Sigma_i \Sigma_j (\mu_{ij}-\mu_{i\cdot})^2]$$

where $\mu_{ij} = Y_{ij} - Y_{\cdot j}$

$\mu_{i\cdot} = \Sigma_j \mu_{ij} / l$

l = number of locations.

g = number of genotypes.

Y_{ij} = trait value of i^th^ genotype in j^th^ location, and

$Y_{\cdot j}$ = mean of all genotypes in j th location.

$$s_i^2 = \frac{g}{(g-2)(l-2)} [S_i - \Sigma_i S_i/g(g-1)]$$

where $S_i = \Sigma^s_{j=1}(\mu_{ij} - \mu_{i\cdot} - b_i Z_j)^2$

$b_i = \Sigma_j(\mu_{ij} - \mu_{i\cdot}) Z_j / \Sigma_j Z_j^2$

Z_j = a covariate for the j th location.

Ecovalence was calculated for each genotype according to Wricke (1962):

$$W_i = \Sigma_j(\mu_{ij})^2 - 1/l\,(Y_{i\cdot} - Y_{\cdot\cdot}/g)^2$$

where $Y_{i\cdot}$ = sum of the i th genotype over all locations.

$Y_{\cdot\cdot}$ = grand sum.

into the stability of the 40 genotypes for the selected characters under study.

The model according to Eberhart and Russell (1966) is defined by the following form:

$$Y_{ij} = \mu_i + \beta_i I_j + \delta_{ij}$$

where Y_{ij} = genotype mean of the i^{th} genotype at the j^{th} location.

μ_i = the mean of the i^{th} genotype over all locations.

β_i = the regression coefficient.

I_j = the environment index obtained as the mean of all genotypes at the j^{th} location minus the grand mean.

δ_{ij} = the deviation from regression of the i^{th} genotype at the j^{th} location.

The regression coefficient was estimated as follows:

$$b_i = \Sigma_j Y_{ij} I_j / \Sigma_j I_j^2$$

The deviation from regression ($s^2 d_i$) was computed using the following equation:

$$s^2 d_i = [\Sigma \delta^2_{ij} / (l - 2)] - S^2_e / r$$

where S^2_e = the estimate of the pooled error.

r = number of replications.

l = number of locations.

Table 2 shows the analysis of variance for the model. In this model, the sum of squares due to environment and G x E are partitioned into environment (linear), G x E (linear) and deviation from regression.

Following this model, a stable genotype has a regression coefficient of $b_i = 1.0$ and deviation from the regression as small as possible ($s^2 d_i = 0$).

Huhn's Non-parametric Stability Statistic

The stability statistic, S_i^3 as proposed by Huhn (1979), is based on the yield rank and stability

TABLE 2. ANALYSIS OF VARIANCE WHEN STABILITY PARAMETERS ARE ESTIMATED

Source	df	SS	MS
Total	gl-1	$\Sigma_i \Sigma_j Y^2_{ij}$ – C.F.	
Genotype (G)	g-1	$1/l \, \Sigma_i Y^2_{i.}$ – C.F.	
Environment (Env) + G x Env	g (l-1)	$\Sigma_i \Sigma_j Y_{ij}^2 - \Sigma Y^2_{i.}/l$	MS1
Env (linear)	1	$1/g \, (\Sigma_j Y_{.j} I_j)^2 / \Sigma_j I_j^2$	
G x Env (linear)	g-1	$\Sigma_i [(\Sigma_j Y_{ij} I_j)^2 / \Sigma_j I^2_j]$ – Env (linear) SS	MS2
Pooled deviation	g(l-2)	$\Sigma_i \Sigma_j \delta^2_{ij}$	MS3
Pooled error	l (r-1)(g-1)		

Notes: C.F. - correction factor.
g - number of genotypes.
l - number of locations.
r - number of replications.
I_j - environmental index in j^{th} location.

of the genotype in each environment as expressed below:

$$S_i^3 = \frac{\sum_j (r_{ij} - r_i)^2}{r_i}$$

where r_{ij} is the rank of the ith genotype in the jth environment and r_i is the mean of ranks over all environments for ith genotype. The genotype with the smallest value is given the rank of 1 and the highest is given a rank of 40.

Lin and Binns' Superiority Measure

Lin and Binns (1988) developed a superiority measure (P_i) for genotypes from genotype x location data. The P_i is defined as the distance mean square between the genotype response and the maximum response averaged over all the locations, and is computed as follows:

$$P_i = \sum_{j=1}^{n} (X_{ij} - M_j)^2 / 2l$$

where X_{ij} is the mean of the ith genotype grown in the jth location, M_j is the maximum response among all genotypes in the jth location, and l is the number of locations. In the same manner as S^3_i, the smallest value of P_i indicated the most stable genotype.

Kang's Rank Sum Method

Two stability statistics, rank sum (RS) and modified rank sum (MRS), were developed by Kang (1988a) and Kang *et al.* (1990), respectively. The RS is derived from the sum of character mean rank and Shukla's stability variance (σ^2_i) rank. In this method, ranks are assigned for the mean character with the genotype having the highest mean receiving the rank of 1. Similarly, ranks are assigned for stability variance, with the lowest estimated value receiving the rank of 1. The lowest RS value is regarded as the most desirable and represented the most stable genotype.

The MRS does take into account the significance levels of stability variance, which are not considered in RS method. The MRS method assigns a stability rating of zero for a non-significant σ^2_i, 10 for significant at the 5% probability level, and 20 for σ^2_i significant at the 1% probability level in the present study. This rating is added to the yield rank of a genotype and the lowest MRS value is regarded as the most desirable genotype.

RESULTS AND DISCUSSION

Performance of the D x P Progenies and Genetic Variation

The performance and genetic variation of the D x P progenies at each location for FFB yield, BNO and ABWT are shown in *Tables 3* to *7*. Results of the evaluation at each location showed that Carey Island (184.63 kg palm^{-1} yr^{-1}) was the most favourable environment for FFB yield, whereas Kudat (86.06 kg palm^{-1} yr^{-1}) was the least. The DNMRT determined that the FFB yield means at Teluk Intan and Carey Island were not significantly different, but were significantly different compared to the other envi-

TABLE 3. LOCATION MEANS FOR YIELD AND ITS COMPONENTS

	Character		
Location	**(FFB, kg palm^{-1} yr^{-1})**	**BNO**	**(ABWT, kg)**
Kudat	86.06d	8.82f	9.97b
Beaufort	142.65b	11.67d	12.17a
Teluk Intan	177.86a	14.51c	12.53a
Carey Island	184.63a	20.23a	9.31c
Kepong	135.58b	17.49b	7.82d
Kluang	96.22c	9.75e	9.89b
Mean	137.17	13.74	10.28

Note: means with the same letter in the same column are not significantly different at $P \leq 0.05$ with DNMRT.

TABLE 4. PROGENY MEANS FOR FFB (kg palm^{-1} yr^{-1}) YIELD IN INDIVIDUAL LOCATIONS

No.	Progeny code	*Pisifera*	Kudat	Beaufort	Teluk Intan	Carey Island	Kepong	Kluang	Progeny mean
1	DP 1	1	75.94	172.88	163.27	144.64	132.88	90.91	130.09
2	DP 2	1	86.59	137.65	189.90	171.55	141.81	97.15	137.44
3	DP 3	1	88.67	123.35	175.71	180.28	133.25	108.42	134.95
4	DP 4	1	91.40	146.33	163.91	171.33	131.80	78.32	130.51
5	DP 5	2	77.30	130.98	169.82	160.01	149.04	94.23	130.23
6	DP 6	2	102.80	145.34	159.88	174.21	116.57	109.74	134.76
7	DP 7	3	85.53	88.53	182.69	221.10	135.09	114.93	138.02
8	DP 8	3	87.60	173.94	188.46	190.92	141.45	106.63	148.16
9	DP 9	4	83.72	159.69	174.40	173.28	129.61	100.14	136.81
10	DP10	4	86.42	166.33	195.83	176.95	157.07	103.70	147.72
11	DP11	4	84.82	143.70	197.60	184.20	128.62	104.65	140.60
12	DP12	5	86.77	144.07	181.47	209.51	127.13	90.81	139.96
13	DP13	5	84.66	116.67	162.85	188.38	119.01	94.85	127.74
14	DP14	6	66.41	114.75	153.88	164.92	146.76	78.85	120.93
15	DP15	6	99.97	132.66	170.05	178.87	139.61	80.01	133.53
16	DP16	7	90.80	187.59	171.74	196.07	161.49	93.13	150.14
17	DP17	7	81.79	154.95	176.08	169.46	119.93	103.84	134.34
18	DP18	8	82.73	154.15	180.23	170.85	140.37	84.54	135.48
19	DP19	8	100.13	196.88	171.85	222.19	130.87	127.19	158.18
20	DP20	8	88.68	126.89	160.42	193.17	144.93	105.96	136.68
21	DP21	9	100.01	186.15	185.63	181.29	130.49	101.96	147.59
22	DP22	9	86.13	138.21	154.43	187.32	142.43	135.11	140.60
23	DP23	9	113.79	138.80	209.73	235.02	141.59	123.77	160.45
24	DP24	10	72.98	143.32	214.16	187.46	125.55	114.67	143.02
25	DP25	10	82.12	160.71	205.70	184.32	127.75	125.68	147.71
26	DP26	10	97.88	132.88	208.21	225.40	130.09	87.47	146.99
27	DP27	11	90.65	150.30	178.12	174.58	126.14	95.80	135.93
28	DP28	11	94.13	126.51	187.68	199.46	121.28	78.13	134.56
29	DP29	12	67.25	145.83	178.95	182.12	132.80	106.21	135.53
30	DP30	12	75.33	67.77	146.44	181.54	128.95	78.77	113.13
31	DP31	13	96.42	137.70	194.19	199.03	125.28	92.46	140.85
32	DP32	13	72.15	124.99	189.54	177.74	133.95	54.50	125.48
33	DP33	13	84.82	138.46	203.29	224.28	136.27	87.93	145.84
34	DP34	14	81.89	144.78	156.12	188.24	151.32	107.37	138.29
35	DP35	14	74.72	125.35	193.61	165.81	146.86	90.59	132.82
36	DP36	14	82.66	154.82	166.13	168.73	142.37	66.86	130.26
37	DP37	14	68.46	150.39	173.28	169.84	126.21	64.76	125.49
38	DP38	15	101.97	150.58	154.36	166.07	147.39	93.67	135.67
39	DP39	15	75.36	137.78	169.80	179.07	140.47	95.90	133.06
40	DP40	15	90.87	133.32	155.14	166.13	138.57	79.05	127.18
Location mean			86.06	142.65	177.86	184.63	135.58	96.22	137.17
Min.			66.41	67.77	146.44	144.64	116.57	54.50	113.13
Max.			113.79	196.88	214.16	235.02	161.49	135.11	160.45
LSD ($P \leq 0.05$)			27.89	61.31	34.73	38.69	25.14	42.83	35.79

TABLE 5. MEAN SQUARES OF FULL-SIB ANOVA AND VARIANCE COMPONENTS FOR FFB YIELD IN INDIVIDUAL LOCATIONS

Source	df	Kudat	Beaufort	Teluk Intan	Carey Island	Kepong	Kluang
Progeny (G)	39	1 108.95	5 758.80**	2 983.10**	3 682.96**	1 025.33	2 865.12**
Replication (R)	1	2 095.33	107 572.02**	14 673.73**	3 131.83	5 598.06	22 395.61
G x R	39	944.65	4 565.86	1 446.49	1 720.10	742.08	2 160.52
@ within palms		882.07 (318)	3410.87 (318)	1 495.39 (314)	1 228.76 (301)	1 952.97 (307)	1 575.38 (308)
σ^2_g		16.53 (1.80)+	120.01 (2.80)	156.48 (9.10)	208.81 (13.47)	29.51 (1.47)	73.09 (3.90)
σ^2_r		5.79 (0.63)	518.14 (12.10)	67.35 (3.92)	7.51 (0.48)	25.29 (1.26)	104.95 (5.60)
σ^2_{gr}		12.59 (1.37)	232.39 (5.43)	0.00 (0.00)	104.54 (6.75)	0.00 (0.00)	121.40 (6.47)
σ^2_w		882.07 (96.19)	3 410.87 (79.67)	1 495.39 (86.98)	1 228.76 (79.29)	1 952.97 (97.27)	1 575.38 (84.03)

Notes: ** Significant at $P \leq 0.01$; @ ( ) df for within palms; ( )+ variance component as percentage of total variance. Harmonic means for palms in progeny/rep (n') = 4.97, 4.97, 4.91, 4.70, 4.78 and 4.82 for Kudat, Beaufort, Teluk Intan, Carey Island, Kepong and Kluang , respectively. Negative estimate for which the most reasonable value is zero.

ronments (*Table 3*). The results of progeny mean over locations showed that DP23 had the highest FFB yield (160.45 kg palm^{-1} yr^{-1}), whereas progeny DP30 had the lowest (113.13 kg palm^{-1} yr^{-1}) (*Table 4*). The ANOVA for individual locations showed differences between progenies at Beaufort, Teluk Intan, Carey Island and Kluang but not at Kudat and Kepong (*Table 5*). The genetic variance (σ_g^2) as a proportion of all components, was much smaller than σ_w^2 and ranged from 1.47% (Kepong) to 13.47% (Carey Island).

BNO was highest at Carey Island, followed by Kepong, Teluk Intan, Beaufort, Kluang and Kudat (*Table 3*). The mean BNO at each environment was different. Statistical analysis using DNMRT supported these results by detecting significant differences among locations. The progeny means over all locations ranged from 12.16 (DP30) to 18.24 bunches (DP19) (*Table 6*). The progenies were significantly different in all locations except at Kepong. The genetic variance was the second largest as compared to other components at all locations except at Kudat. The σ_g^2 ranged from 3.19% to 25.74%, indicating that the environment had a major role in determining BNO of oil palm for these progenies (*Table 7*).

In the present study, a large variation among the genotypes was detected in the D x P progenies. Differences in the performance of genotypes might have been due to differences in the environmental factors, especially rainfall intensity, soil fertility, genetical differences and G x E interaction. Higher FFB yield and BNO were obtained at Carey Island and Teluk Intan than at the other locations mainly due to the very fertile and well drained soils and good rainfall amounting to 150 mm mth^{-1}. The lowest FFB yield and BNO at Kudat could be due to the dry season (about 2 mth yr^{-1}) and relatively lower yield at Kluang was due to poor soil texture (laterite soils). The results reported here are comparable to the studies by Lee and Donough (1993) and Tarmizi *et al.* (1992), where coastal soils (such as Carey Island and Teluk Intan) could support a better yield production than inland soil (such as Kluang).

The weight of bunches was higher at Teluk Intan compared to other locations. Mean ABWT

TABLE 6. PROGENY MEANS FOR BNO IN INDIVIDUAL LOCATIONS

No.	Progeny code	*Pisifera*	Kudat	Beaufort	Teluk Intan	Carey Island	Kepong	Kluang	Progeny mean
1	DP 1	1	7.33	12.66	12.47	15.83	17.42	8.12	12.31
2	DP 2	1	8.87	11.37	15.45	18.25	18.88	9.87	13.78
3	DP 3	1	9.65	10.30	15.00	20.25	16.51	11.08	13.80
4	DP 4	1	8.93	11.95	13.82	17.88	17.83	7.14	12.93
5	DP 5	2	8.01	10.16	12.82	17.44	19.05	8.55	12.67
6	DP 6	2	9.50	10.87	12.82	17.78	15.55	8.83	12.56
7	DP 7	3	9.15	8.57	15.15	26.59	18.06	11.68	14.87
8	DP 8	3	10.31	14.96	15.64	23.54	18.67	10.75	15.65
9	DP 9	4	7.99	11.60	12.48	15.82	17.37	8.38	12.27
10	DP10	4	9.00	13.68	16.21	22.12	19.33	11.82	15.36
11	DP11	4	8.61	11.47	16.21	19.92	17.65	9.37	13.87
12	DP12	5	9.41	11.48	14.31	21.99	15.97	10.34	13.92
13	DP13	5	8.35	10.14	13.38	21.28	14.63	9.16	12.82
14	DP14	6	6.60	9.70	13.96	18.89	18.19	8.54	12.65
15	DP15	6	9.83	12.30	12.30	18.33	17.82	8.25	12.86
16	DP16	7	9.41	14.51	14.73	21.28	19.71	9.92	14.93
17	DP17	7	7.74	11.32	15.47	17.85	15.24	10.18	12.97
18	DP18	8	8.24	12.40	15.63	19.78	18.05	9.68	13.96
19	DP19	8	12.25	18.97	17.56	27.30	16.07	17.32	18.24
20	DP20	8	8.26	9.98	12.51	20.74	18.85	10.50	13.47
21	DP21	9	9.62	13.77	14.75	19.90	16.12	8.26	13.74
22	DP22	9	8.64	11.20	12.01	20.20	18.01	11.82	13.65
23	DP23	9	12.01	13.13	18.58	25.23	18.21	14.59	16.96
24	DP24	10	8.03	12.23	16.93	22.96	14.03	12.55	14.45
25	DP25	10	8.90	12.96	18.33	24.32	17.03	12.92	15.74
26	DP26	10	10.28	9.97	15.59	19.56	16.10	7.34	13.14
27	DP27	11	8.28	12.26	15.83	21.84	16.77	10.20	14.20
28	DP28	11	8.64	9.92	14.83	19.27	16.83	7.15	12.77
29	DP29	12	7.68	11.18	13.18	18.47	17.30	7.79	12.60
30	DP30	12	7.33	6.47	13.87	18.62	17.88	8.81	12.16
31	DP31	13	9.33	11.09	14.70	22.56	16.48	9.35	13.92
32	DP32	13	7.95	10.98	14.82	17.76	17.31	6.66	12.58
33	DP33	13	8.45	12.12	14.55	22.08	18.23	10.04	14.25
34	DP34	14	8.95	12.23	12.13	19.25	17.33	10.48	13.40
35	DP35	14	7.39	11.62	15.22	19.25	18.89	8.63	13.50
36	DP36	14	8.23	12.00	13.13	17.35	19.63	8.23	13.10
37	DP37	14	6.90	10.92	15.10	19.09	18.41	6.88	12.88
38	DP38	15	11.08	11.82	12.24	18.38	17.85	11.50	13.81
39	DP39	15	8.33	12.55	13.72	21.60	18.61	9.51	14.05
40	DP40	15	9.31	10.14	12.90	18.56	17.81	7.64	12.73
Location mean			8.82	11.67	14.51	20.23	17.49	9.75	13.74
Min.			6.60	6.47	12.01	15.82	14.03	6.66	12.16
Max.			12.25	18.97	18.58	27.30	19.71	17.32	18.24
LSD ($P \leq 0.05$)			3.04	4.27	3.17	3.57	3.38	2.98	3.79

TABLE 7. MEAN SQUARES OF FULL-SIB ANOVA AND VARIANCE COMPONENTS FOR BNO IN INDIVIDUAL LOCATIONS

Source	df	Kudat	Beaufort	Teluk Intan	Carey Island	Kepong	Kluang
Progeny (G)	39	14.74**	38.24**	27.81**	66.85**	16.76	44.98**
Replication (R)	1	63.76**	292.30**	29.30	19.28	0.98	91.35**
G x R	39	11.23	22.19	12.07	14.65	13.39	10.44
@ within palms		8.88 (318)	19.99 (318)	11.76 (314)	14.84 (301)	27.26 (307)	9.49 (308)
σ^2_g		0.35 (3.51)+	1.61 (6.88)	1.60 (11.84)	0.49 (3.19)	1.64 (5.67)	3.58 (25.74)
σ^2_r		0.26 (2.61)	1.36 (5.81)	0.09 (0.67)	0.03 (0.20)	0.00 (0.00)	0.42 (3.02)
σ^2_{gr}		0.47 (4.72)	0.44 (1.88)	0.06 (0.04)	0.00 (0.00)	0.00 (0.00)	0.42 (3.02)
σ^2_w		8.88 (89.16)	19.99 (85.43)	11.76 (87.05)	14.84 (96.61)	27.26 (94.33)	9.49 (68.22)

Notes: **significant at $P \leq 0.01$; @ ( ) df for within palms; ( )+ variance component as percentage of total variance. Harmonic means for palms in progeny/rep (n') = 4.97, 4.97, 4.91, 4.70, 4.78 and 4.82 for Kudat, Beaufort, Teluk Intan, Carey Island, Kepong and Kluang , respectively. Negative estimate for which the most reasonable value is zero.

for the D x P progenies at each location ranged from 7.82 (Kepong) to 12.53 kg (Teluk Intan) (*Table 3*). The ABWT mean over all locations for the individual progenies ranged from 8.80 to 11.50 kg (*Table 8*). The ANOVA results showed that the progeny item was highly significant at Beaufort, Teluk Intan, Carey Island and Kluang but not at Kudat and Kepong (*Table 9*). The genotype variance (σ_g^2) was higher than σ_r^2 and σ_{gr}^2 at Teluk Intan, Carey Island and Kluang. However, the lack of σ_g^2 at Kudat and Kepong could be due to the higher level of σ_w^2. The variation in yield and its components appeared to be influenced, at least partly, by the genotype. However, the magnitude of genetic variance was not consistent from one environment to another, implying that the performance of genotypes was influenced by environmental effects. At individual locations, the results indicated that the genotype item was significant for yield and its components at all environments except at Kudat and Kepong for FFB yield and ABWT, and at Kepong for BNO only. These findings also showed that performance of genotypes was greatly influenced by environmental factors. The results obtained by several workers (Ataga, 1993; Corley *et al.*, 1993; Lee *et al.*, 1988) also indicated similar trends.

Table 10 presents ANOVA of FFB yield, BNO and ABWT for full-sib analyses over the environments. Differences between locations and progenies were highly significant and these results were expected because of the choice of diverse environments and genotypes. The progeny x location interaction was highly significant for yield and its components. This indicated the presence of G x E interaction and showed that the oil palm progenies were sensitive to the environments since they responded differently to changes in the set of environments. The second order interactions between replications in location and progeny were highly significantly different for FFB yield and ABWT but not for BNO. The components of G x E interaction ($\sigma_{gl}^2 + \sigma_{g}^2{}_{(r/l)}$) was relatively small, 4.65%, 5.20% and 3.53% of the phenotypic variance ($\sigma_g^2 + \sigma_{gl}^2 + \sigma_{g}^2{}_{(r/l)} + \sigma_w^2$) for FFB yield, BNO and ABWT, respectively. Only FFB yield had a larger progeny x location variance (σ_{gl}^2) as compared to the

TABLE 8. PROGENY MEANS FOR ABWT (kg) IN INDIVIDUAL LOCATIONS

No.	Progeny code	*Pisifera*	Kudat	Beaufort	Teluk Intan	Carey Island	Kepong	Kluang	Progeny mean
1	DP 1	1	10.74	13.28	13.32	9.15	7.80	11.48	10.96
2	DP 2	1	9.87	11.83	12.36	9.51	7.50	9.81	10.15
3	DP 3	1	9.94	11.68	12.14	9.11	7.54	9.69	10.02
4	DP 4	1	10.62	12.68	12.23	9.88	7.54	10.76	10.62
5	DP 5	2	10.08	12.72	13.43	9.31	7.79	10.85	10.70
6	DP 6	2	10.93	13.52	12.66	10.34	7.63	12.11	11.20
7	DP 7	3	10.21	10.56	12.07	8.39	7.56	9.66	9.74
8	DP 8	3	8.45	11.55	12.75	8.13	7.56	9.86	9.72
9	DP 9	4	10.66	13.73	14.50	11.19	7.26	11.65	11.50
10	DP10	4	9.73	11.89	12.09	7.95	8.25	8.75	9.78
11	DP11	4	9.84	12.80	12.44	9.70	7.04	11.22	10.51
12	DP12	5	9.28	12.20	13.14	9.68	7.97	8.66	10.16
13	DP13	5	10.16	11.60	12.15	8.93	8.28	9.91	10.17
14	DP14	6	9.25	11.61	11.69	9.26	8.29	9.06	9.86
15	DP15	6	10.84	12.32	13.99	9.85	7.99	9.16	10.69
16	DP16	7	9.84	12.49	11.96	9.26	8.48	9.05	10.18
17	DP17	7	10.67	13.31	11.45	9.56	7.69	10.01	10.45
18	DP18	8	10.37	12.32	12.19	8.67	7.72	8.39	9.94
19	DP19	8	8.75	10.52	9.75	8.31	8.20	7.24	8.80
20	DP20	8	10.22	12.71	13.16	9.42	7.64	9.75	10.48
21	DP21	9	10.34	13.80	12.67	9.53	7.86	11.82	11.00
22	DP22	9	10.00	12.10	12.83	9.50	8.03	11.56	10.67
23	DP23	9	10.04	10.47	11.39	9.44	7.83	8.28	9.57
24	DP24	10	8.94	11.83	12.60	8.19	8.77	9.14	9.91
25	DP25	10	9.64	12.16	11.35	7.64	7.30	9.93	9.67
26	DP26	10	9.69	12.92	13.28	11.59	8.13	11.58	11.20
27	DP27	11	11.19	12.22	11.59	8.10	7.53	9.13	9.96
28	DP28	11	11.36	12.26	12.76	10.30	7.07	10.81	10.76
29	DP29	12	8.79	12.52	13.69	9.65	8.18	13.31	11.07
30	DP30	12	10.21	9.63	10.75	10.00	7.41	9.11	9.52
31	DP31	13	11.14	12.54	13.35	8.91	7.29	9.91	10.52
32	DP32	13	9.10	10.87	12.84	9.95	8.10	8.35	9.87
33	DP33	13	10.36	11.29	14.30	10.22	8.37	8.84	10.56
34	DP34	14	9.16	11.82	13.07	9.81	8.72	10.32	10.48
35	DP35	14	10.06	10.98	12.90	8.60	7.86	10.57	10.16
36	DP36	14	10.14	13.20	12.91	9.78	7.23	8.17	10.24
37	DP37	14	9.25	13.72	11.46	9.14	6.99	9.59	10.02
38	DP38	15	9.63	12.86	12.70	9.11	8.57	8.14	10.17
39	DP39	15	9.52	11.07	12.75	8.29	7.57	10.05	9.87
40	DP40	15	9.73	13.05	12.49	8.85	8.08	9.96	10.36
Location mean			9.97	12.17	12.53	9.31	7.82	9.89	10.28
Min.			8.45	9.63	9.75	7.64	6.99	7.24	8.80
Max.			11.36	13.80	14.50	11.59	8.77	13.31	11.50
LSD ($P \leq 0.05$)			2.32	2.11	2.03	1.78	1.52	2.54	1.62

TABLE 9. MEAN SQUARES OF FULL-SIB ANOVA AND VARIANCE COMPONENTS FOR ABWT IN INDIVIDUAL LOCATIONS

Source	df	Kudat	Beaufort	Teluk Intan	Carey Island	Kepong	Kluang
Progeny (G)	39	4.84	9.64**	8.47**	6.69**	2.01	15.96**
Replication (R)	1	12.33	96.08**	10.76	0.46	21.34**	37.98**
G x R	39	4.84	5.42	4.92	3.64	2.73	7.63
@ within palms		6.40	5.81	4.30	2.85	3.32	5.57
		(318)	(318)	(314)	(301)	(307)	(308)
σ^2_g		0.00	0.42	0.36	0.32	0.00	0.86
		(0.00)$^+$	(6.28)	(7.47)	(9.58)	(0.00)	(12.25)
σ^2_r		0.04	0.46	0.03	0.00	0.10	0.16
		(0.62)	(6.88)	(0.62)	(0.00)	(2.93)	(2.28)
σ^2_{gr}		0.03	0.00	0.13	0.17	0.00	0.43
		(0.46)	(0.00)	(2.70)	(5.09)	(0.00)	(6.13)
σ^2_w		6.40	5.81	4.30	2.85	3.32	5.57
		(98.92)	(86.84)	(89.21)	(85.33)	(97.07)	(79.34)

Notes: **significant at $P \leq 0.01$; @ ( ) df for within palms. ( )$^+$ variance component as percentage of total variance. Harmonic means for palms in progeny/rep (n') = 4.97, 4.97, 4.91, 4.70, 4.78 and 4.82 for Kudat, Beaufort, Teluk Intan, Carey Island, Kepong and Kluang , respectively. Negative estimate for which the most reasonable value is zero.

TABLE 10. MEAN SQUARES AND VARIANCE COMPONENTS OVER LOCATIONS FOR FFB YIELD, BNO AND ABWT

Source	df	FFB	BNO	ABWT
Progeny (G)	39	5 136.06**	96.41**	17.24**
Location (L)	5	639 948.25**	7 882.22**	1 234.28**
Rep in location (R/L)	6	25 545.66**	81.75**	29.49**
G x L	195	2 453.68**	22.87**	6.07**
G x R/L	234	1 929.93**	14.00	5.15**
@ within palms	1 866	1 762.78	15.34	4.73
σ^2_g		45.99	1.26	0.19
		(1.28)$^+$	(3.32)	(2.28)
σ_l^2		1 579.77	20.06	3.10
		(43.90)	(52.90)	(37.21)
$\sigma^2_{r/l}$		121.48	0.35	0.13
		(3.38)	(0.92)	(1.56)
σ^2_{gl}		53.88	0.91	0.09
		(1.50)	(2.40)	(1.08)
$\sigma^2_{g(r/l)}$		34.39	0.00	0.09
		(0.96)	(0.00)	(1.08)
σ^2_w		1 762.78	15.34	4.73
		(48.99)	(40.45)	(56.78)
G x E (%)		4.65	5.20	3.53
$\sigma^2_{gl} / \sigma^2_g$ (%)		117.16	72.22	47.37

Notes: **significant at $P \leq 0.01$; ( )$^+$ variance component as percentage of total variance. Harmonic means for palms in progeny/rep (n') = 4.86. Negative estimate for which the most reasonable value is zero.

genotype variance (σ_g^2), indicating that it was more sensitive to environmental changes than BNO and ABWT.

The data pooled over locations showed a highly significant environmental item, suggesting that the soil type, rainfall distribution and other common factors accounted for a large proportion of the variation. The location variance component (σ^2_l) was the highest for BNO, and the second highest for FFB yield and ABWT. However, σ^2_l is not under genetic control, unlike σ^2_g, σ^2_{gl}, σ^2_{rg}, $\sigma^2_{g(r/l)}$ and σ^2_w. Therefore, it was not of interest. The G x E interaction was detected by ANOVA for yield and its components. Previous studies have also reported the presence of G x E interaction in oil palm populations for these characters (Ataga, 1993; Hutomo and Pamin, 1992; Lee *et al.*, 1988; Ong *et al.*, 1986; Rajanaidu *et al.*, 1993).

Stability Analyses

In the present study, several methods were used to estimate the stability of each full-sib progeny, namely genotype-grouping techniques (mean against CV_i and mean against SD_i), G x E variance components analysis (σ^2_i, σ^2_i and W_iMS statistics), joint regression analysis (JR), non-parametric statistic (S^3_i), superiority measure statistic (P_i) and rank sum methods (RS_i and MRS_i). The stability statistics were computed only if the progeny x location interaction item was significant.

FFB

According to the genotype-grouping techniques using mean against CV_i (Francis and Kannenberg, 1978), DP8, DP11, DP16, DP21, DP22, DP23, DP31 and DP34 were found to be highly stable for FFB yield, whereas five of the above genotypes (DP8, DP11, DP21, DP22 and DP34) remained highly stable using mean against SD_i (*Figure 1*). On the other hand, out of 40 genotypes, 12 genotypes were identified to be highly unstable by following mean against CV_i. However, some genotypes (eight) were highly unstable using mean versus SD_i (*Figure 1*).

Highly significant σ^2_i value (implying highly unstable) was obtained for DP7, DP19 and DP30, and significant σ_i^2 value (implying unstable) was obtained for DP1, DP22 and DP26 (*Table 11*). Other 34 genotypes were considered to be stable across locations. After removal of the influence of environmental index (covariate), s^2_i was computed. The genotypes classified as highly unstable over locations were DP1, DP7, DP19 and DP30, while the genotypes DP16 and DP23 were unstable. Except for DP1, the highly unstable genotypes were the same as those identified by the σ^2_i statistic (*Table 11*). According to ecovalence mean square (W_iMS), three genotypes (DP7, DP19 and DP30) were also found inconsistent across locations (*Table 11*).

The ANOVA for regression of FFB yield is in *Table 12*. Genotypes, environments (Env. + G x Env.), environment (linear) and pooled deviation were highly significantly different for the character while G x E (linear) was not significant. This result showed that in FFB yield, a significant part of the G x E interaction was largely accounted for by a non-linear relationship between the genotypic and environment values.

In the stability analyses, the regression of genotype means on the environmental index resulted in regression coefficients ranging from 0.69 to 1.40 (*Table 13*). According to Eberhart and Russell (1966), a large variation in b_i values indicates large differences in the genotypic response to different environments. Only six genotypes had deviation mean square from regression (s^2d_i) that differed significantly from zero for FFB yield. The coefficient of determination (r^2_i) which is the proportion of total variation explained by the regression ranged from 0.67 to 0.98.

Using Eberhart and Russell's graphical presentation, it could be classified that genotypes DP8, DP10, DP21 and DP25 were highly stable over a range of environments for FFB yield (*Figure 2*). Three genotypes in the group (DP16, DP19 and DP23) had deviation mean square from regression values significantly different from zero, indicating that the genotypes were inconsistent in their linear response to environments.

According Huhn's non-parametric stability statistic (S_i^3), DP2, DP8, DP10, DP21, DP23 and DP39 were classified as highly stable genotypes for FFB yield, while the stable ones were DP3, DP4, DP9, DP11, DP12, DP15, DP16, DP18, DP19, DP20, DP25, DP27, DP29, DP33 and DP34 (*Table 14*). When using Lin and Binns' superiority measure statistic (P_i), seven geno-

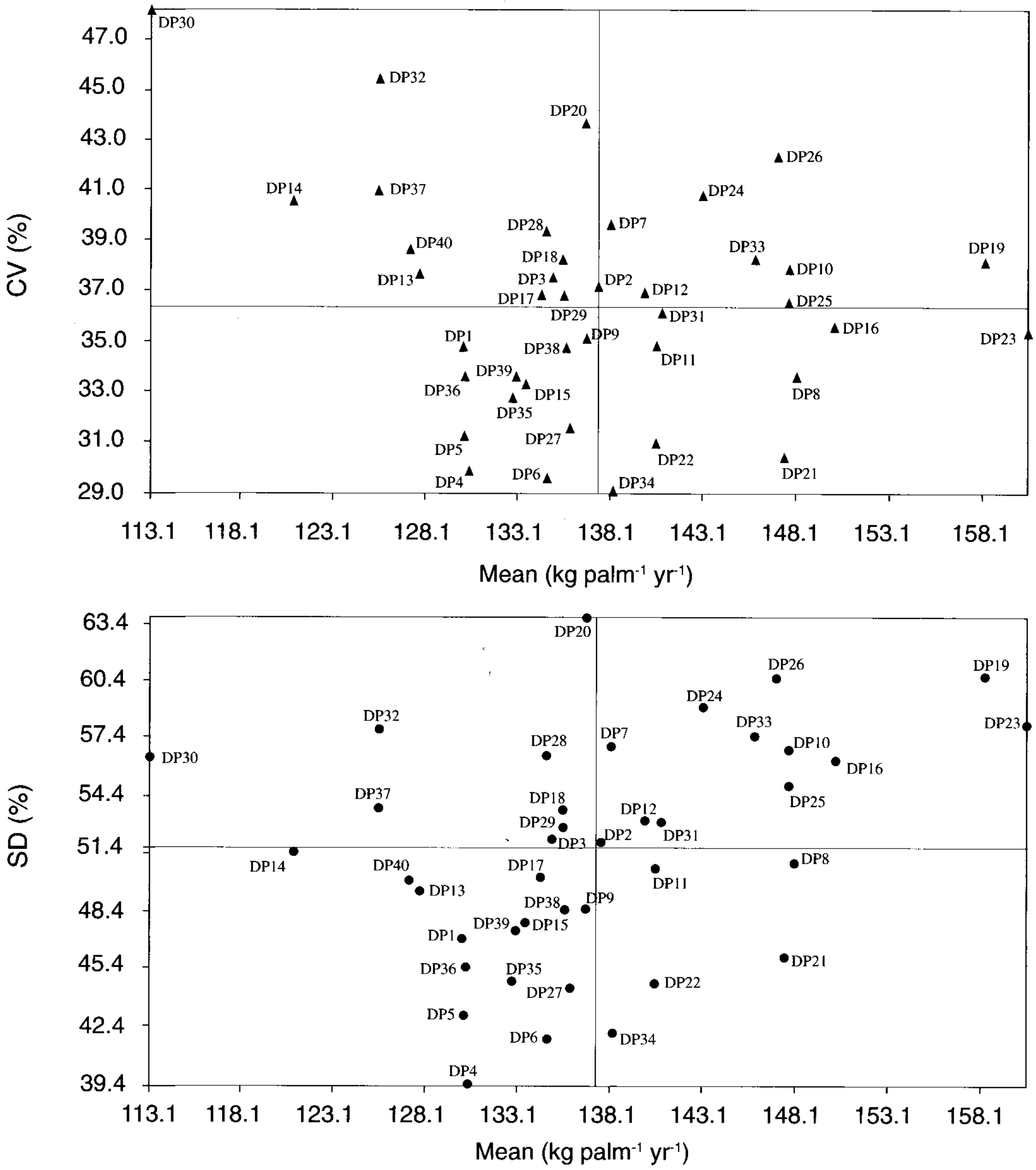

Figure 1. Plot of mean against CV (top) and mean against SD (bottom) of individual genotypes for FFB yield.

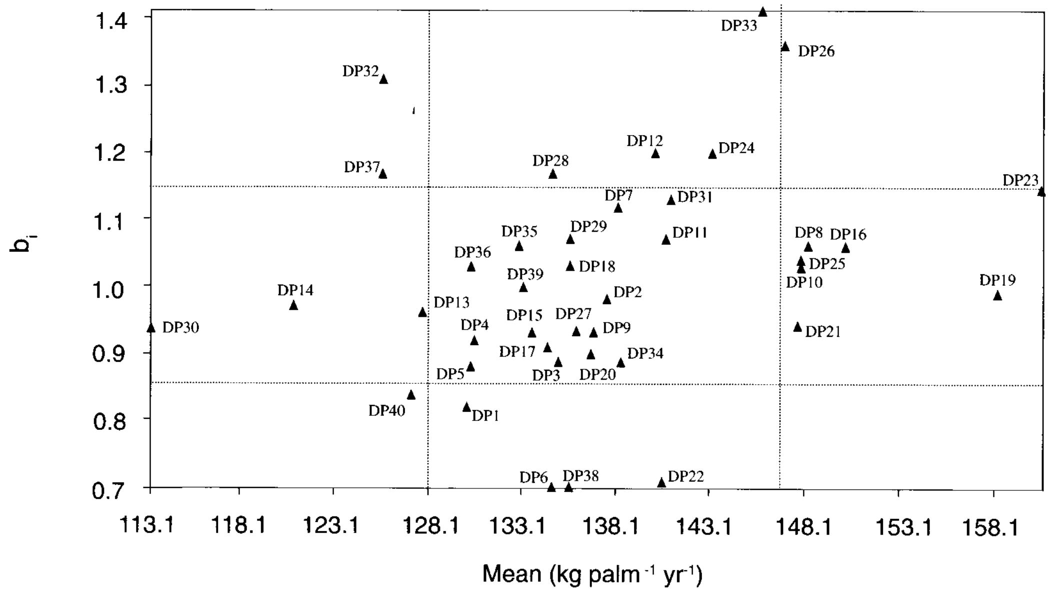

Figure 2. Plots of genotype mean against their respective regression coefficients (b_i) for FFB yield [vertical dotted line:grand mean ± SD, horizontal dotted lines: (b=1) ± SD].

TABLE 11. STABILITY VARIANCE (σ_i^2, s_i^2) AND ECOVALENCE MEAN SQUARE (W$_i$MS) STATISTICS FOR INDIVIDUAL GENOTYPES

No.	Progeny code	*Pisifera*	FFB			BNO			ABWT		
			σ_i^2	s_i^2	W$_i$MS	σ_i^2	s_i^2	W$_i$MS	σ_i^2	s_i^2	W$_i$MS
1	DP1	1	5 183.24*	5 708.75**	5 112.60*	33.98*	33.90*	33.69	4.40	3.87	4.45
2	DP2	1	713.90	889.09	756.44	13.37	15.58	13.61	0.23	0.30	0.38
3	DP3	1	1 014.10	952.08	1 050.91	10.75	11.15	11.06	0.10	0.05	0.25
4	DP4	1	924.15	1 010.75	963.28	17.71	21.58	17.84	2.39	3.02	2.48
5	DP5	2	1 532.14	1 584.65	1 555.60	20.92	26.20	20.97	1.91	1.22	2.02
6	DP6	2	2 450.38	990.18	2 450.17	11.92	2.26	12.20	7.48	9.17	7.44
7	DP7	3	9 403.95**	11 520.82**	9 222.47**	95.86**	77.60**	93.98*	4.09	4.12	4.14
8	DP8	3	1 062.44	1 295.35	1 098.00	11.67	12.84	11.96	4.53	5.29	4.57
9	DP9	4	932.93	1 061.05	971.83	26.26	21.92	26.27	9.74	6.34	9.64
10	DP10	4	1 558.59	1 956.10	1 581.36	4.62	4.62	5.09	4.24	5.25	4.29
11	DP11	4	838.04	978.03	879.39	5.83	7.20	6.27	5.24	5.90	5.26
12	DP12	5	1 343.39	961.74	1 371.71	11.72	14.76	12.01	4.81	5.73	4.84
13	DP13	5	1 283.19	1 562.46	1 313.06	16.58	20.60	16.74	1.46	0.63	1.58
14	DP14	6	1 925.57	2 378.81	1 836.89	10.90	9.23	11.21	2.68	1.40	2.76
15	DP15	6	1 136.43	1 281.99	1 170.09	19.92	20.71	20.00	5.48	5.76	5.50
16	DP16	7	3 788.69	4 704.11*	3 753.99	11.91	14.14	12.19	2.98	3.19	3.06
17	DP17	7	1 282.77	1 420.89	1 312.65	18.83	17.72	18.94	5.75	7.19	5.76
18	DP18	8	920.77	1 158.09	959.99	4.20	5.30	4.68	4.53	5.59	4.57
19	DP19	8	5 905.31**	7 388.80**	5 816.05**	126.67**	148.90*	123.99**	13.87*	7.28	13.67*
20	DP20	8	1 598.87	1 738.46	1 620.61	18.65	20.83	18.76	10.01	0.08	1.14
21	DP21	9	3 141.10	3 847.87	3 123.08	18.41	20.88	18.52	6.93	7.90	6.90

TABLE 11. Continued

No.	Progeny code	*Pisifera*	FFB			BNO			ABWT		
			σ_i^2	s_i^2	W_iMS	σ_i^2	s_i^2	W_iMS	σ_i^2	s_i^2	W_iMS
22	DP22	9	4 160.14*	3 336.92	4 115.86	21.93	26.44	21.95	4.04	4.98	4.09
23	DP23	9	3 849.44	4 442.97*	3 813.17	31.96	40.06*	31.72	7.62	5.02	7.58
24	DP24	10	3 479.52	3 622.41	3 452.79	63.00**	78.78**	61.96**	6.18	7.55	6.17
25	DP25	10	2 756.79	3 444.80	2 748.68	38.95*	45.19*	38.53*	4.60	5.77	4.64
26	DP26	10	4 734.36*	3 354.74	4 675.28*	24.33	30.34	24.29	8.62	10.78*	8.56
27	DP27	11	469.66	478.41	520.51	8.57	9.05	8.93	7.80	9.78	7.76
28	DP28	11	2 250.34	2 246.85	2 255.29	10.95	12.75	11.26	5.97	7.39	5.97
29	DP29	12	882.72	1 039.80	922.92	4.30	5.45	4.78	23.00**	28.68**	22.57**
30	DP30	12	7 302.79**	9 043.98**	7 177.51**	36.87*	42.33*	36.51*	15.01**	7.92	14.78**
31	DP31	13	1 253.79	1 293.61	1 284.39	13.88	13.97	14.11	4.49	3.24	4.53
32	DP32	13	3 234.53	2 156.27	3 214.10	17.49	21.92	17.63	8.79	10.25	8.72
33	DP33	13	3 730.50	1 301.76	3 697.30	5.32	1.44	5.77	11.73*	14.68**	11.59*
34	DP34	14	1 720.50	1 871.80	1 739.34	13.25	12.08	13.50	4.07	4.44	4.12
35	DP35	14	2 136.24	2 622.55	2 144.12	12.39	12.51	12.66	4.83	5.87	4.86
36	DP36	14	2 335.23	2 920.42	2 337.98	30.03	37.37*	29.85	9.57	8.86	9.48
37	DP37	14	1 714.20	1 585.10	1 732.96	20.89	17.11	20.94	9.02	9.79	8.94
38	DP38	15	2 689.88	1 399.37	2 683.49	33.92*	18.50	33.63	8.49	10.54*	8.43
39	DP39	15	256.98	333.54	313.31	8.08	5.25	8.46	3.11	3.92	3.18
40	DP40	15	1 315.14	1 046.85	1 344.19	12.25	15.39	12.52	2.07	2.30	2.18
	σ^2_w		1 762.78	1 762.78	1 762.78	15.34	15.34	15.34	4.73	4.73	4.73

Notes: * significant at $P \leq 0.05$; ** significant at $P \leq 0.01$.

types (DP8, DP10, DP16, DP19, DP21, DP23 and DP25) were considered to be highly stable and another 14 genotypes were found to be stable over a range of environments (*Table 14*).

Seven genotypes were classified to be highly stable for FFB yield, namely DP2, DP8, DP9, DP10, DP11, DP27 and DP31 according to the rank sum stability statistic (RS_i), and genotypes, DP8, DP10, DP16, DP21, DP23, DP25 and DP33 by following the modified rank sum stability statistic (MRS_i). Only two genotypes (DP8 and DP10) were judged as highly stable using both the stability statistics (*Table 15*). With the exception of DP19 and DP26, all the top nine genotypes, based on mean FFB yield which was associated with non-significant stability variances, qualified for high stability according to the MRS_i method. Another 17 genotypes were found to be stable according to the RS_i statistic. However, only 14 genotypes were stable using the MRS_i statistic (*Table 15*).

BNO

According to genotype-grouping techniques, out of 40 genotypes, 12 genotypes using the mean against CV_i method and five genotypes using the mean against SD_i method were judged to be highly stable. The genotypes, DP2, DP12, DP18, DP21 and DP38 were shown to be stable by both the techniques (*Figure 3*).

Following the σ_i^2 statistic, three genotypes (DP7, DP19 and DP24) were found to be highly unstable and another four genotypes (DP1, DP25, DP30 and DP38) were unstable across the six locations (*Table 11*). However, after the covariate, s_i^2 was computed, two genotypes (DP7 and DP24) remained highly unstable over the

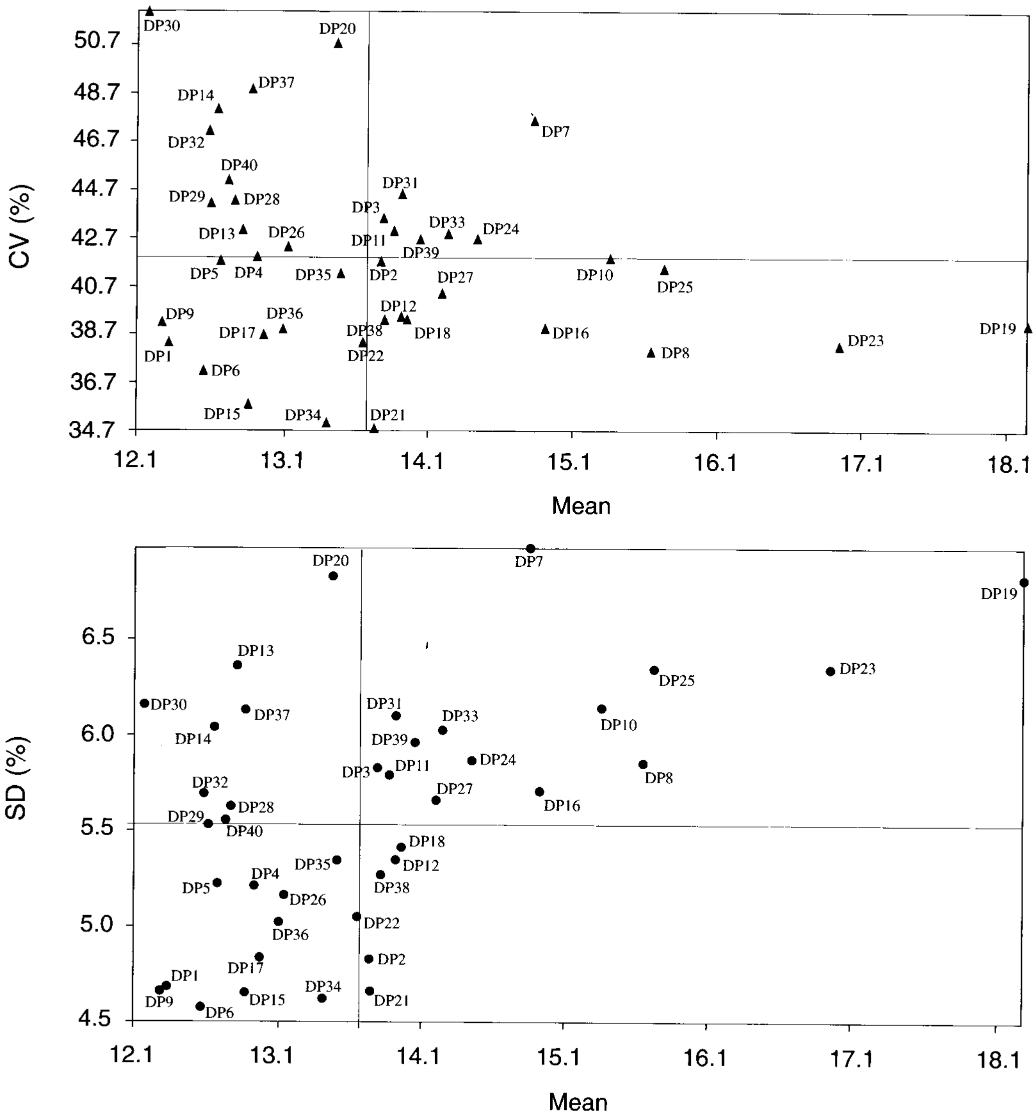

Figure 3. Plots of mean against CV (top) and mean against SD (bottom) of individual genotypes for BNO.

environments. On the other hand, DP1, DP19, DP23, DP25, DP30 and DP36 were found to be *unstable*. The number of genotypes classified as very sensitive or sensitive to the environmental changes increased from seven to eight by applying the σ_i^2 and s_i^2 statistics, respectively. When using the ecovalence mean square (W_iMS), only two genotypes, (DP19 and DP24) were found to be highly unstable, whereas DP7, DP25 and DP30 were unstable (*Table 11*).

The ANOVA for regression of BNO showed that a significant part of the GxE interaction was largely accounted for by the non-linear relationship between genotypic and environmental values (*Table 12.*) The regression coefficients (b_i) and coefficient of determination (r_i^2) ranged from 0.70 to 1.19 and 0.53 to 0.99, respectively (*Table 13*). Only six genotypes had a deviation mean square from regression (s^2d_i) that differed significantly from zero.

The ideal genotype as proposed by Eberhart and Russell (1966) would have a high mean performance over a range of environments, regression coefficient of one and deviation mean square (s^2d_i) of zero. According to joint regression analysis, DP8 and DP10 were classified as to be highly stable genotypes over the environments because their regression coefficients were close to unity (b=1), s^2d_i=0 and high bunch number (*Table 13* and *Figure 4*). The genotypes, DP23 and DP25 had high BNO and their regression coefficients were nearly equal to one. They were considered to be unstable because the second stability parameter (s^2d_i) was significantly different from zero.

Following Huhn's non-parametric stability statistic (S_i^3), eight genotypes (DP8, DP10, DP11, DP16, DP18, DP23, DP29 and DP33) were regarded as highly stable, while another 12 genotypes were considred to be stable (*Table 14*). According to Lin and Binns' superiority measure statistic (P_i), genotypes with high stability were DP8, DP10, DP16, DP19, DP23 and DP25. Of these six, four genotypes were highly stable by both the techniques.

After Kang's RS stability methods were computed, eight genotypes (DP8, DP10, DP11, DP16, DP18, DP27, DP33 and DP39) were found to be highly stable by following the RS_i statistic, while seven genotypes (DP8, DP10, DP16, DP23, DP27, DP33 and DP39) were classified to be highly stable according to the MRS_i statistic (*Table 15*). Of the above genotypes, six genotypes were common using both the statistics.

ABWT

By using genotype-grouping techniques, DP5, DP22, DP26, DP28, DP33 and DP34 were judged to be highly stable by following the mean against CV_i method and out of the above six genotypes, three genotypes (DP22, DP33 and DP34) also were found to be highly stable by following the mean against SD_i method (*Figure 5*). Highly unstable progenies were DP3, DP7, DP8, DP12, DP14, DP18, DP25, DP30, DP32, DP35, DP36, DP37 and DP39 using the mean againt CV_i method, while using the mean against SD_i method, the number of genotypes was reduced

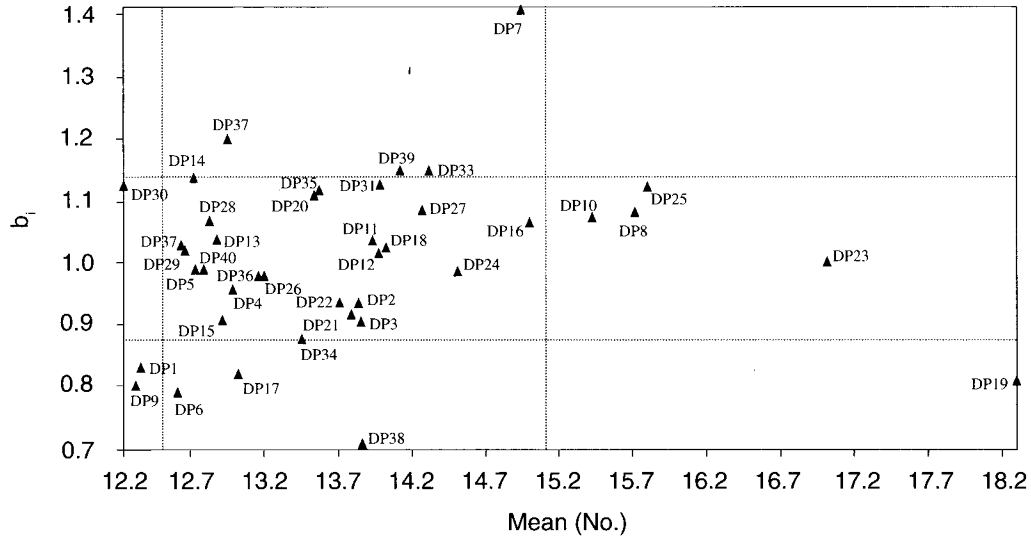

Figure 4. Plots of genotype mean against their respective regression coefficients (b_i) for BNO [vertical dotted line:grand mean ± SD, horizontal dotted lines: (b=1) ± SD].

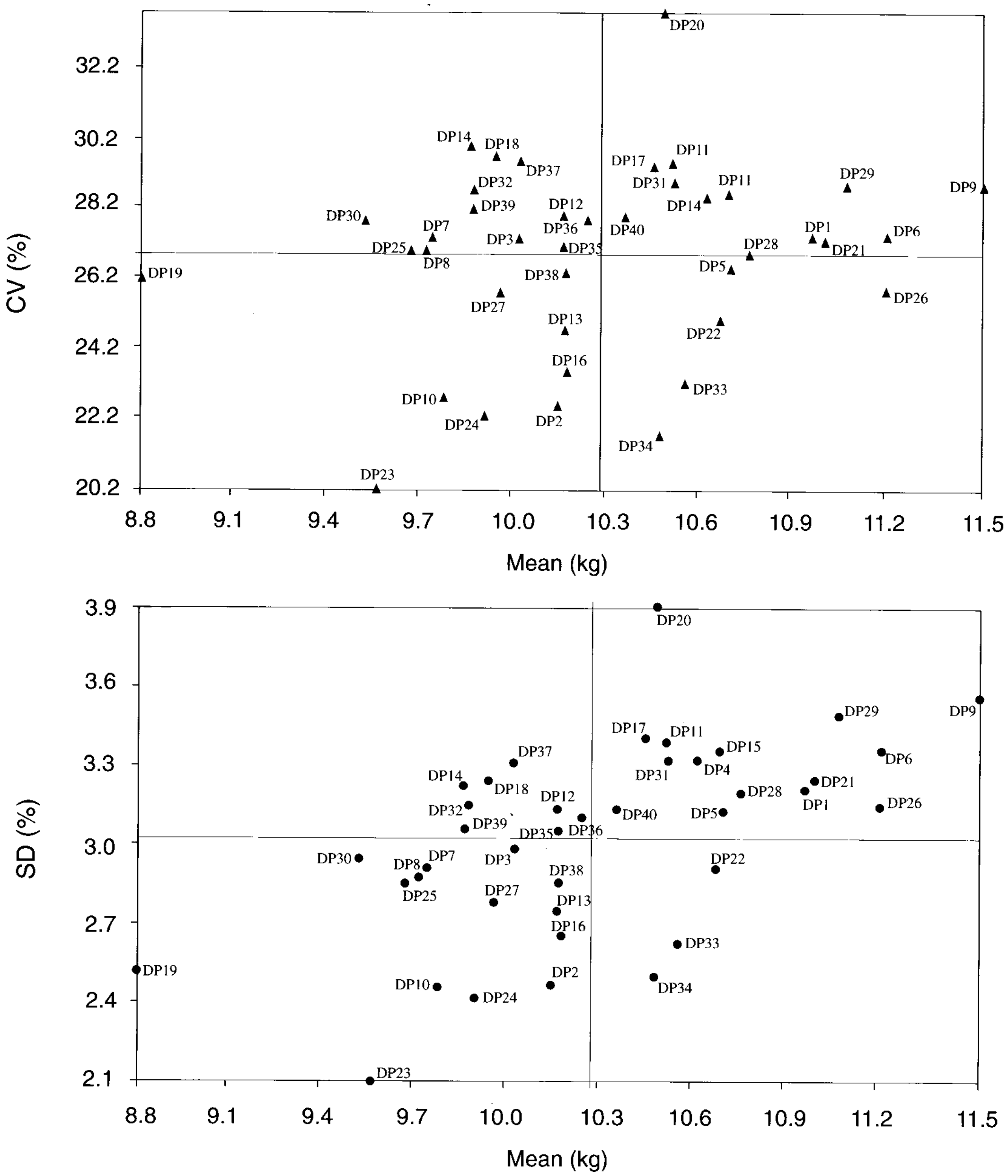

Figure 5. Plots of mean against CV (top) and mean against SD (bottom) of individual genotypes for ABWT.

from 13 to eight genotypes (DP12, DP14, DP18, DP32, DP35, DP36, DP37 and DP39).

Highly significant σ_i^2 and W_iMS values (implying highly unstable) were obtained in ABWT for DP29 and DP30, while unstable genotypes were DP19 and DP33 (*Table 11*). Two genotypes (DP29 and DP33) were found to be highly unstable and another two, DP26 and DP38, found to be sensitive to the environment according to the s_i^2 statistic. Only genotype DP29 was judged to be highly unstable according to the three statistics σ_i^2, s_i^2 and W_iMS (*Table 11*).

The ANOVA for regression of ABWT showed that genotypes, environments (Env + G x Env.), environment (linear) and pooled deviation were highly significantly different (*Table 12*). This finding showed that the character G x E interaction component was largely accounted for by a non-linear relationship between genotypic and environment values.

The stability analysis results showed, the regression coefficients (b_i) and coefficient of determination (r_i^2) ranging from 0.48 to 1.38 and 0.54 to 1.00, respectively. Two genotypes (DP29 and DP33) had s^2d_i values significantly deviated from zero (*Table 13*). Using Eberhart and Russell's graphical presentations, it could be classified that genotypes DP4, DP5, DP6, DP15, DP21, DP22, DP26 and DP28 were the ideal genotypes which performed consistently over different environments (*Figure 6*). The genotypes had high

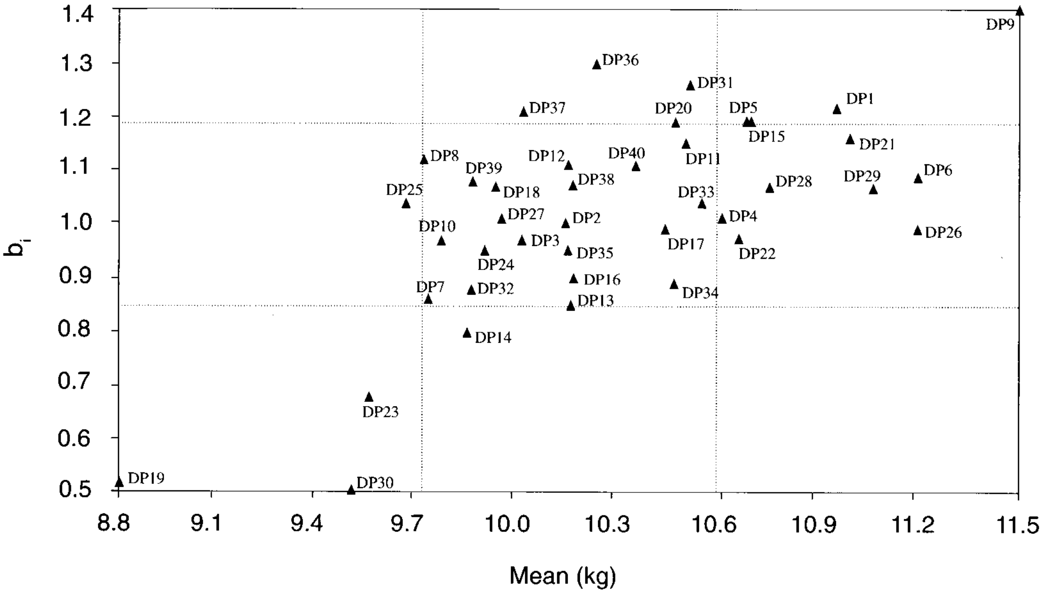

Figure 6. Plots of genotype mean against their respective regression coefficients (b_i) for ABWT [vertical dotted line:grand mean ± SD, horizontal dotted lines: (b=1) ± SD].

bunch weight, b_i was close to one and s^2d_i was not significantly different from zero.

According to Huhn's non-parametric stability statistic (S_i^3), the genotypes which displayed high stability were DP1, DP2, DP3, DP5, DP20, DP21 and DP22, whereas 14 others were considered to be stable (*Table 14*). For selection based on Lin and Binns' superiority measure statistic (P_i), six genotypes (DP1, DP6, DP9, DP21, DP26 and DP29) were found to be highly stable, whereas the stable ones were DP2, DP4, DP5, DP11, DP13, DP15, DP17, DP20, DP22, DP28, DP31, DP33, DP34, DP35 and DP40 (*Table 14*). The genotypes, DP1 and DP21, were judged to be highly stable to environmental changes by both S_i^3 and P_i.

The genotypes identified for high stability in ABWT by following the RS_i statistic were DP1, DP4, DP5, DP20, DP22 and DP40, while 15 genotypes were found to be stable. By using the MRS_i, eight genotypes (DP1, DP5, DP6, DP9, DP15, DP21, DP26 and DP28) were classified as highly stable, and 13 others were judged as stable (*Table 15*).

Combined Use of the Stability Statistics

In a plant breeding programme, it is desirable to identify promising genotypes which may provide maximum yield over a range of environments and show consistent performance. Selection based on mean yield alone may not always be adequate when G x E interaction is sig-

TABLE 12. ANALYSIS OF VARIANCE FOR REGRESSION OF FFB YIELD, BNO AND ABWT

Source	df	FFB	BNO	ABWT
Genotype (G)	39	5 136.06**	96.41**	17.24**
Environment (Env.) + (G x Env)	200	18 391.04**	219.36**	36.77**
Env. (Linear)	1	3 199 741.50**	39 411.08**	6 191.48**
G x Env. (Linear)	39	2 074.00	17.65	4.75
Pooled deviation	160	2 484.88**	23.58**	6.11**
Rep in Env. (R/E)	6	25 545.66**	81.75**	29.49**
G x R/E	234	1 929.93**	14.00	5.15**
Pooled error	1 866	1 762.78	15.34	4.73

Note: ** significant at P ≤ 0.01.

TABLE 13. REGRESSION COEFFICIENT (b_i), DEVIATION MEAN SQUARES (s^2d_i) AND COEFFICIENT OF DETERMINATION (r_i^2) FOR FFB YIELD, BNO AND ABWT

No.	Progeny code	*Pisifera*	FFB			BNO			ABWT		
			b_i	s^2d_i	r^2_i	b_i	s^2d_i	r^2_i	b_i	s^2d_i	r^2_i
1	DP 1	1	0.81	4 602.93*	0.70	0.82	25.39	0.83	1.20	1.46	0.97
2	DP 2	1	0.97	27.65	0.95	0.93	7.65	0.93	0.98	0.00	0.99
3	DP 3	1	0.88	87.82	0.94	0.90	3.21	0.95	0.95	0.00	0.99
4	DP 4	1	0.91	141.54	0.94	0.95	13.64	0.91	0.99	0.64	0.93
5	DP 5	2	0.87	688.27	0.91	0.98	17.74	0.90	1.17	0.00	0.98
6	DP 6	2	0.69	122.35	0.90	0.78	0.00	0.98	1.07	6.55	0.83
7	DP 7	3	1.11	10 136.78**	0.69	1.40	65.63**	0.87	0.84	1.69	0.87
8	DP 8	3	1.05	411.95	0.94	1.08	5.47	0.96	1.10	2.82	0.90
9	DP 9	4	0.92	189.48	0.94	0.79	13.92	0.88	1.38	3.87	0.92
10	DP10	4	1.02	1 039.65	0.91	1.07	0.00	0.98	0.95	2.76	0.87
11	DP11	4	1.06	111.72	0.96	1.03	0.00	0.97	1.13	3.37	0.90
12	DP12	5	1.19	95.76	0.97	1.01	6.89	0.94	1.09	3.24	0.89
13	DP13	5	0.95	667.54	0.92	1.03	12.35	0.93	0.83	0.00	0.97
14	DP14	6	0.96	1 443.29	0.89	1.13	1.57	0.97	0.78	0.00	0.94
15	DP15	6	0.92	400.39	0.93	0.90	10.08	0.92	1.17	3.29	0.90
16	DP16	7	1.05	3 649.38*	0.83	1.06	6.75	0.95	0.88	0.84	0.90
17	DP17	7	0.90	531.74	0.92	0.81	6.88	0.92	0.97	4.61	0.84
18	DP18	8	1.02	281.68	0.95	1.02	0.00	0.97	1.05	3.10	0.89
19	DP19	8	0.98	6 198.43**	0.73	0.81	134.81**	0.53	0.50	4.74	0.58
20	DP20	8	0.89	835.51	0.90	1.10	12.47	0.94	1.17	0.00	1.00

TABLE 13. Continued

No.	Progeny code	*Pisifera*	FFB			BNO			ABWT		
			b_i	s^2d_i	r^2_i	b_i	s^2d_i	r^2_i	b_i	s^2d_i	r^2_i
21	DP21	9	0.93	2 836.72	0.82	0.91	13.13	0.91	1.14	5.28	0.87
22	DP22	9	0.70	2 353.13	0.75	0.93	17.91	0.89	0.95	2.51	0.88
23	DP23	9	1.14	3 323.32*	0.86	1.00	30.70*	0.87	0.66	2.59	0.77
24	DP24	10	1.19	2 624.80	0.89	0.98	67.69**	0.76	0.93	4.98	0.82
25	DP25	10	1.03	2 454.20	0.86	1.12	35.76*	0.88	1.02	3.28	0.88
26	DP26	10	1.35	2 370.40	0.92	0.97	21.53	0.89	0.97	8.01	0.78
27	DP27	11	0.92	0.00	0.97	1.08	1.60	0.97	0.99	7.10	0.80
28	DP28	11	1.16	1 335.65	0.92	1.06	4.91	0.96	1.05	4.79	0.86
29	DP29	12	1.06	170.33	0.96	1.01	0.00	0.98	1.05	24.99**	0.61
30	DP30	12	0.93	7 777.12**	0.67	1.12	32.40*	0.86	0.48	5.31	0.54
31	DP31	13	1.12	411.09	0.95	1.12	6.10	0.95	1.24	0.86	0.95
32	DP32	13	1.30	1 230.88	0.94	1.02	13.78	0.92	0.86	7.48	0.74
33	DP33	13	1.40	419.43	0.97	1.14	0.00	0.99	1.02	11.70**	0.74
34	DP34	14	0.88	960.63	0.89	0.87	4.53	0.94	0.87	2.01	0.87
35	DP35	14	1.05	1 674.28	0.90	1.11	4.90	0.96	0.93	3.36	0.85
36	DP36	14	1.02	1 954.47	0.88	0.97	28.62	0.86	1.28	6.18	0.88
37	DP37	14	1.16	686.72	0.95	1.19	9.32	0.95	1.19	7.05	0.85
38	DP38	15	0.69	510.75	0.87	0.70	10.42	0.87	1.05	7.80	0.81
39	DP39	15	0.99	0.00	0.98	1.14	0.00	0.98	1.06	1.50	0.91
40	DP40	15	0.83	176.02	0.93	0.98	7.43	0.94	1.09	0.00	0.95

Notes: * significant different from 0.00 at $P \leq 0.05$; ** significant different from 0.00 at $P \leq 0.01$.
Negative estimate for which the most reasonable value is zero.

TABLE 14. SUPERIORITY MEASURE (P_i) AND NON-PARAMETRIC STABILITY (S_i^3) STATISTICS FOR INDIVIDUAL GENOTYPES

No.	Progeny code	*Pisifera*	P_i			S_i^3		
			FFB	BNO	ABWT	FFB	BNO	ABWT
1.	DP 1	1	1 294.93	26.90	1.02**	47.60	61.57	11.23**
2.	DP 2	1	891.11*	18.09	2.41*	14.02**	17.71*	7.70**
3.	DP 3	1	1 001.87	16.14*	2.74	20.68*	24.15*	3.72**
4.	DP 4	1	1 145.39	23.24	1.49*	29.28*	24.88*	16.61*
5.	DP 5	2	1 257.75	25.28	1.35*	46.91	50.90	8.38**
6.	DP 6	2	1 006.90	23.86	0.66**	57.42	40.60	17.03*
7.	DP 7	3	1 235.56	13.71*	3.56	33.61	31.23	23.80*
8.	DP 8	3	419.18**	7.24**	3.49	2.67**	1.29**	34.13
9.	DP 9	4	826.60*	27.24	0.47**	15.22*	24.18*	28.50*
10.	DP10	4	533.05**	8.45**	3.87	13.51**	2.63**	39.35
11.	DP11	4	711.04*	16.42*	1.54*	14.76*	9.40**	31.84
12.	DP12	5	698.46*	14.44*	2.89	19.23*	22.56*	24.68*
13.	DP13	5	1 292.97	20.74	2.56*	39.81	27.84*	21.66*
14.	DP14	6	1 743.34	24.11	3.41	97.36	38.09	36.22
15.	DP15	6	1 077.37	21.34	1.96*	25.11*	41.75	13.40*
16.	DP16	7	474.48**	11.15**	2.84	18.83*	9.52**	27.98*
17.	DP17	7	936.28*	20.73	2.18*	38.47	41.47	26.85*
18.	DP18	8	921.92*	15.47*	3.53	19.45*	10.38**	23.95*
19.	DP19	8	261.80**	1.19**	7.34	20.58*	27.76*	95.91
20.	DP20	8	941.04*	18.66	1.91*	27.89*	37.51	7.40**
21.	DP21	9	505.48**	16.53	0.97**	14.30**	29.90	10.58**
22.	DP22	9	867.79*	16.68*	1.29*	33.40	32.35	8.00**
23.	DP23	9	326.46**	4.01**	4.44	10.47**	2.33**	40.60
24.	DP24	10	708.80*	11.65*	3.52	48.13	47.11	53.24
25.	DP25	10	515.05**	6.90**	3.73	28.85*	17.78*	36.82
26.	DP26	10	644.38*	22.20	0.70**	37.76	55.00	14.20*
27.	DP27	11	870.99*	13.12*	3.52	15.60*	17.23*	54.61
28.	DP28	11	1 013.98	23.77	1.35*	56.91	26.67*	34.27
29.	DP29	12	872.38*	23.78	0.99**	23.35*	6.18**	31.78
30.	DP30	12	2 485.64	29.48	4.57	38.55	29.98	67.47
31.	DP31	13	719.02*	15.17*	1.99*	32.69	20.68*	33.89
32.	DP32	13	1 503.80	25.57	3.68	48.82	28.51	54.39
33.	DP33	13	612.31*	13.34*	2.45*	22.72*	6.40**	37.87
34.	DP34	14	846.83	17.93	1.91*	31.98*	26.00*	31.12
35.	DP35	14	1 170.95	19.16	2.46*	58.81	28.09	24.37*
36.	DP36	14	1 205.25	23.01	3.04	44.04	52.58	44.76
37.	DP37	14	1 360.79	23.64	3.06	43.71	48.87	61.01
38.	DP38	15	1 044.14	17.47*	3.34	54.21	39.43	44.75
39.	DP39	15	1 003.93	14.57*	3.07	12.89**	13.58	26.16*
40.	DP40	15	1 371.87	24.38	2.21*	37.49	39.43	16.60*
	Mean		958.02	17.92	2.59	32.43	27.84	30.67
	SD		413.28	6.65	1.33	19.09	15.54	18.91

Notes: *mean - SD < P_i or S_i^3 ≤ mean (stable).
**P_i or S_i^3 ≤ mean - SD (highly stable).

TABLE 15. MEAN RANK, STABILITY VARIANCE RANK (σ^2_i), RANK SUM (RS_i) AND MODIFIED RANK SUM (MRS_i) STATISTICS FOR FFB YIELD, BNO AND ABWT

			FFB				BNO				ABWT			
No.	Progeny code	*Pisifera*	Mean rank	σ^2_i Rank	RS_i	MRS_i	Mean rank	σ^2_i Rank	RS_i	MRS_i	Mean rank	σ^2_i Rank	RS_i	MRS_i
1	DP 1	1	34.0	37.0*	71.0	44.0	38.0	35.0*	73.0	48.0	6.0	15.0	21.0^{++}	6.0^{++}
2	DP 2	1	17.0	3.0	20.0^{++}	17.0^{+}	18.0	18.0	36.0^{+}	18.0^{+}	25.0	2.0	27.0^{+}	25.0
3	DP 3	1	24.0	9.0	33.0^{+}	24.0	17.0	8.0	25.0^{+}	17.0^{+}	26.5	1.0	27.5^{+}	26.5
4	DP 4	1	31.0	7.0	38.0^{+}	31.0	27.0	22.0	49.0	27.0	11.0	7.0	18.0^{++}	11.0^{+}
5	DP 5	2	33.0	17.0	50.0	33.0	33.0	28.0	61.0	33.0	8.0	5.0	13.0^{++}	8.0^{++}
6	DP 6	2	25.0	26.0	51.0	25.0	37.0	14.0	51.0	37.0	2.5	28.0	30.5^{+}	2.5^{++}
7	DP 7	3	16.0	40.0**	56.0	36.0	7.0	39.0**	46.0	27.0	35.0	13.0	48.0	35.0
8	DP 8	3	4.0	10.0	14.0^{++}	4.0^{++}	4.0	11.0	15.0^{++}	4.0^{++}	36.0	17.5	53.5	36.0
9	DP 9	4	18.0	8.0	26.0^{++}	18.0^{+}	39.0	31.0	70.0	39.0	1.0	36.0	37.0^{+}	1.0^{++}
10	DP10	4	5.0	18.0	23.0^{++}	5.0^{++}	5.0	3.0	8.0^{++}	5.0^{++}	34.0	14.0	48.0	34.0
11	DP11	4	12.5	4.0	16.5^{++}	12.5^{+}	15.0	5.0	20.0^{++}	15.0^{+}	14.0	22.0	36.0^{+}	14.0^{+}
12	DP12	5	14.0	16.0	30.0^{+}	14.0^{+}	13.5	12.0	25.5^{+}	13.5^{+}	23.5	20.0	43.5	23.5
13	DP13	5	35.0	14.0	49.0	35.0	30.0	20.0	50.0	30.0	21.5	4.0	25.5^{+}	21.5^{+}
14	DP14	6	39.0	22.0	61.0	39.0	34.0	9.0	43.0	34.0	33.0	8.0	41.0^{+}	33.0
15	DP15	6	28.0	11.0	39.0^{+}	28.0	29.0	26.0	55.0	29.0	9.0	23.0	32.0^{+}	9.0^{++}
16	DP16	7	3.0	33.0	36.0^{+}	3.0^{++}	6.0	13.0	19.0^{++}	6.0^{++}	20.0	9.0	29.0^{+}	20.0^{+}
17	DP17	7	27.0	13.0	40.0^{+}	27.0	26.0	25.0	51.0	26.0	17.0	24.0	41.0^{+}	17.0^{+}
18	DP18	8	23.0	6.0	29.0^{+}	23.0	12.0	1.0	13.0^{++}	12.0^{+}	29.0	17.5	46.5	29.0
19	DP19	8	2.0	38.0**	40.0^{+}	22.0^{+}	1.0	40.0**	41.0^{+}	21.0^{+}	40.0	38.0*	78.0	50.0
20	DP20	8	19.0	19.0	38.0^{+}	19.0^{+}	22.0	24.0	46.0	22.0^{+}	15.5	3.0	18.5^{++}	15.5^{+}

TABLE 15. Continued

			FFB				**BNO**				**ABWT**			
No.	**Progeny code**	***Pisifera***	**Mean rank**	**σ^2_i Rank**	**RS$_i$**	**MRS$_i$**	**Mean rank**	**σ^2_i Rank**	**RS$_i$**	**MRS$_i$**	**Mean rank**	**σ^2_i Rank**	**RS$_i$**	**MRS$_i$**
21	DP21	9	7.0	29.0	36.0^{+}	7.0^{++}	19.0	23.0	42.0	19.0^{+}	5.0	27.0	32.0^{+}	5.0^{++}
22	DP22	9	12.5	35.0*	47.5	22.5^{+}	20.0	29.0	49.0	20.0^{+}	10.0	11.0	21.0^{++}	10.0^{+}
23	DP23	9	1.0	34.0	35.0	1.0^{++}	2.0	33.0	35.0^{+}	2.0^{++}	38.0	29.0	67.0	38.0
24	DP24	10	10.0	31.0	41.0^{+}	10.0^{+}	8.0	38.0**	46.0	28.0	30.0	26.0	56.0	30.0
25	DP25	10	6.0	28.0	34.0^{+}	6.0^{++}	3.0	37.0*	40.0^{+}	13.0^{+}	37.0	19.0	56.0	37.0
26	DP26	10	8.0	36.0*	44.0^{+}	18.0^{+}	24.0	30.0	54.0	24.0	2.5	32.0	34.5^{+}	2.5^{++}
27	DP27	11	20.0	2.0	22.0^{++}	20.0^{+}	10.0	7.0	17.0^{++}	10.0^{++}	28.0	30.0	58.0	28.0
28	DP28	11	26.0	24.0	50.0	26.0	31.0	10.0	41.0^{+}	31.0	7.0	25.0	32.0^{+}	7.0^{++}
29	DP29	12	22.0	5.0	27.0^{+}	22.0^{+}	35.0	2.0	37.0^{+}	35.0	4.0	40.0**	44.0	24.0
30	DP30	12	40.0	39.0**	79.0	60.0	40.0	36.0*	76.0	50.0	39.0	39.0**	78.0	59.0
31	DP31	13	11.0	12.0	23.0^{++}	11.0^{+}	13.5	19.0	32.5^{+}	13.5^{+}	13.0	16.0	29.0^{+}	13.0^{+}
32	DP32	13	38.0	30.0	68.0	38.0	36.0	21.0	57.0	36.5	31.5	33.0	64.5	31.5
33	DP33	13	9.0	32.0	41.0^{+}	9.0^{++}	9.0	4.0	13.0^{++}	9.0^{++}	12.0	37.0*	49.0	22.0^{+}
34	DP34	14	15.0	21.0	36.0^{+}	15.0^{+}	23.0	17.0	40.0^{+}	23.0^{+}	15.5	12.0	27.5^{+}	15.5^{+}
35	DP35	14	30.0	23.0	53.0	30.0	21.0	16.0	37.0^{+}	21.0^{+}	23.5	21.0	44.5	23.5
36	DP36	14	32.0	25.0	57.0	32.0	25.0	32.0	57.0	25.0	19.0	35.0	54.0	19.0^{+}
37	DP37	14	37.0	20.0	57.0	37.0	28.0	27.0	55.0	28.0	26.5	34.0	60.5	26.5
38	DP38	15	21.0	27.0	48.0	21.0^{+}	16.0	34.0*	50.0	26.0	21.5	31.0	52.5	21.5^{+}
39	DP39	15	29.0	1.0	30.0^{+}	29.0	11.0	6.0	17.0^{++}	11.0^{++}	31.5	10.0	41.5	31.5
40	DP40	15	36.0	15.0	51.0	36.0	32.0	15.0	47.0	32.0	18.0	6.0	24.00^{++}	18.0^{+}
	Mean		-	-	41.0	22.7	-	-	41.0	23.0			41.0	22.0
	SD		-	-	14.9	12.8	-	-	17.0	11.5			16.2	12.9

Notes: * stability rating 10 plus mean rank for MRS$_i$ statistic; ** stability rating 20 plus mean rank for MRS$_i$ statistic.

$^{+}$ Mean - SD < RS$_i$ or MRS$_i$ values ≤ mean.

$^{++}$ RS$_i$ or MRS$_i$ values ≤ mean - SD.

TABLE 16. STABILITY OF INDIVIDUAL GENOTYPES AS DEFINED BY VARIOUS METHODS FOR FFB YIELD

No.	Progeny code	*Pisifera*	Mean *vs.* CV	Mean *vs.* SD	σ^2_i	s^2_i	W_iMS	JR	S_i^3	P_i	RS_i	MRS_i	Total
1	DP 1	1	+	+									2
2	DP 2	1			+	+	+	+	++	+	++	+	10
3	DP 3	1			+	+	+	+	+		+		6
4	DP 4	1	+	+	+	+	+	+	+		+		8
5	DP 5	2	+	+	+	+	+	+					6
6	DP 6	2	+	+	+	+	+						5
7	DP 7	3											0
8	DP 8	3	++	++	+	+	+	++	++	++	++	++	17
9	DP 9	4	+	+	+	+	+	+	+	+	++	+	11
10	DP10	4			+	+	+	++	++	++	++	++	13
11	DP11	4	++	++	+	+	+	+	+	+	++	+	13
12	DP12	5			+	+	+		++	+	+	+	8
13	DP13	5		+	+	+	+	+					5
14	DP14	6		+	+	+	+						4
15	DP15	6	+	+	+	+	+	+	+		+		8
16	DP16	7	++		+		+		+	++	+	++	10
17	DP17	7		+	+	+	+	+		+	+		7
18	DP18	8			+	+	+	+	+	+	+		7
19	DP19	8							+	++	+	+	5
20	DP20	8			+	+	+	+	+	+	+	+	8
21	DP21	9	++	++	+	+	+	++	++	++	+	++	16
22	DP22	9	++	++		+	+			+		+	8
23	DP23	9	++		+		+		++	++		++	10
24	DP24	10			+	+	+			+	+	+	6
25	DP25	10			+	+	+	++	+	++	+	++	11
26	DP26	10				+				+	+	+	4
27	DP27	11	+	+	+	+	+	+	+	+	++	+	11
28	DP28	11			+	+	+	+					4
29	DP29	12			+	+	+	+	+	+	+	+	8
30	DP30	12											0
31	DP31	13	++		+	+	+	+		+	++	+	10
32	DP32	13			+	+	+						3
33	DP33	13			+	+	+		+	+	+	++	8
34	DP34	14	++	++	+	+	+	+	+		+	+	11
35	DP35	14	+	+	+	+	+	+					6
36	DP36	14	+	+	+	+	+	+					6
37	DP37	14			+	+	+						3
38	DP38	15	+	+	+	+	+					+	6
39	DP39	15	+	+	+	+	+	+	++		+		9
40	DP40	15		+	+	+	+						4

Notes: + stable; ++ highly stable.

TABLE 17. STABILITY OF INDIVIDUAL GENOTYPES AS DEFINED BY VARIOUS METHODS FOR BNO

No.	Progeny code	*Pisifera*	Mean *vs.* CV	Mean *vs.* SD	σ^2_i	s^2_i	W_iMS	JR	S_i^3	P_i	RS_i	MRS_i	Total
1	DP 1	1	+	+			+						3
2	DP 2	1	++	++	+	+	+	+	+		+	+	11
3	DP 3	1			+	+	+	+	+	+	+	+	8
4	DP 4	1		+	+	+	+	+	+				6
5	DP 5	2	+	+	+	+	+	+					6
6	DP 6	2	+	+	+	+	+						5
7	DP 7	3								+			1
8	DP 8	3	++		+	+	+	++	++	++	++	++	15
9	DP 9	4	+	+	+	+	+		+				6
10	DP10	4	++		+	+	+	++	++	++	++	++	15
11	DP11	4			+	+	+	+	++	+	++	+	10
12	DP12	5	++	++	+	+	+	+	+	+	+	+	12
13	DP13	5		+	+	+	+	+	+				6
14	DP14	6			+	+	+	+					4
15	DP15	6	+		+	+	+	+					5
16	DP16	7	++		+	+	+	+	++	++	++	++	14
17	DP17	7	+	+	+	+	+						5
18	DP18	8	++	++	+	+	+	+	++	+	++	+	14
19	DP19	8	++	+					+	++	+	+	8
20	DP20	8			+	+	+	+				+	5
21	DP21	9	++	++	+	+	+	+				+	9
22	DP22	9	+	+	+	+	+	+		+		+	8
23	DP23	9	++		+		+		++	++	+	++	11
24	DP24	10								+			1
25	DP25	10	++						+	++	+	+	7
26	DP26	10		+	+	+	+	+					5
27	DP27	11	++		+	+	+	+	+	+	++	++	12
28	DP28	11			+	+	+	+	+		+		6
29	DP29	12		+	+	+	+	+	++		+		8
30	DP30	12											0
31	DP31	13			+	+	+	+	+	+	+	+	8
32	DP32	13			+	+	+	+					4
33	DP33	13			+	+	+		++	+	++	++	10
34	DP34	14	+	+	+	+	+		+		+	+	8
35	DP35	14	+	+	+	+	+	+			+	+	8
36	DP36	14	+	+	+		+	+					5
37	DP37	14			+	+	+						3
38	DP38	15	++	++		+	+			+			7
39	DP39	15			+	+	+			+	++	++	8
40	DP40	15		+	+	+	+	+					5

Notes: + stable; ++ highly stable.

TABLE 18. STABILITY OF INDIVIDUAL GENOTYPES AS DEFINED BY VARIOUS METHODS FOR ABWT

No.	Progeny code	*Pisifera*	Mean *vs.* CV	Mean *vs.* SD	σ^2_i	s^2_i	W_iMS	JR	S_i^3	P_i	RS_i	MRS_i	Total
1	DP 1	1			+	+	+		++	++	++	++	11
2	DP 2	1	+	+	+	+	+	+	++	+	+		10
3	DP 3	1		+	+	+	+	+	++		+		8
4	DP 4	1			+	+	+	++	+	+	++	+	10
5	DP 5	2	++		+	+	+	++	++	+	++	++	14
6	DP 6	2			+	+	+	++	+	++	+	++	11
7	DP 7	3		+	+	+	+	+	+				6
8	DP 8	3	+	+	+	+	+						5
9	DP 9	4			+	+	+		+	++	+	++	9
10	DP10	4	+	+	+	+	+	+					6
11	DP11	4			+	+	+	+		+	+	+	7
12	DP12	5			+	+	+	+	+				5
13	DP13	5	+	+	+	+	+	+	+	+	+	+	10
14	DP14	6			+	+	+				+		4
15	DP15	6			+	+	+	++	+	+	+	++	10
16	DP16	7	+	+	+	+	+	+	+		+	+	9
17	DP17	7			+	+	+	+	+	+	+	+	8
18	DP18	8			+	+	+	+	+				5
19	DP19	8	+	+		+							3
20	DP20	8			+	+	+	+	++	+	++	+	10
21	DP21	9			+	+	+	++	++	++	+	++	12
22	DP22	9	++	++	+	+	+	++	++	+	++	+	15
23	DP23	9	+	+	+	+	+						5
24	DP24	10	+	+	+	+	+	+					6
25	DP25	10	+	+	+	+	+						5
26	DP26	10	++		+		+	++	+	++	+	++	12
27	DP27	11	+	+	+	+	+	+					6
28	DP28	11	++		+	+	+	++		+	+	++	11
29	DP29	12								++			2
30	DP30	12		+		+							2
31	DP31	13			+	+	+			+	+	+	6
32	DP32	13			+	+	+	+					4
33	DP33	13	++	++						+		+	6
34	DP34	14	++	++	+	+	+	+		+	+	+	11
35	DP35	14			+	+	+	+	+	+			6
36	DP36	14	+		+	+	+					+	5
37	DP37	14			+	+	+						3
38	DP38	15		+	+		+	+				+	5
39	DP39	15			+	+	+	+	+				5
40	DP40	15			+	+	+	+	+	+	++	+	9

Notes: + stable; ++ highly stable.

nificant. *Tables 16* to *18* give the summary of the stability studies for each trait.

Seventeen genotypes produced above average FFB yield over a range of environments, but of these only 12 (DP2, DP8, DP9, DP10, DP11, DP16, DP21, DP23, DP25, DP27, DP31 and DP34) were rated highly stable (scored 10 and above) by the combined use of all the stability statistics (*Table 16*). The stability parameters differed in some cases in identifying the stable genotypes. For instance, only three genotypes were identified stable or highly stable by all the stability statistics. It is worthwhile to note that DP7 which produced high FFB yield, was rated as unstable by all the stability methods. Hence, this study shows that high yielding genotypes may not necessarily be highly stable over the environments.

With regards to bunch production, the top five genotypes were DP8, DP10, DP19, DP23 and DP25, but only two (DP8 and DP10) were found to be highly stable (*Table 17*). For ABWT, 13 genotypes were considered to be highly stable (DP1, DP2, DP4, DP5, DP6, DP13, DP15, DP20, DP21, DP22, DP26, DP28 and DP34) and only two genotypes (DP2 and DP13) produced ABWT lower than the genotype means over locations (*Table 18*).

CONCLUSION

Significant differences for the environment, genotype and genotype x location interaction items were observed in FFB yield, BNO and ABWT. There was a marked influence of environment on the magnitude of the genetic variance. The σ^2_{gl} component was larger in magnitude than the σ^2_g component for FFB yield in contrast to BNO and ABWT, indicating that FFB yield was more sensitive to the environmental fluctuations than the BNO and ABWT characters. By the combined use of 10 stability statistics, the genotypes DP2, DP8, DP10 and DP11, were found to be highly stable for FFB yield and BNO. These superior genotypes identified in this study are useful for future breeding programmes to develop high yielding planting materials with stable performance.

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