

INDEX SELECTION UTILIZING PLOT AND FAMILY INFORMATION IN OIL PALM

Keywords : Oil palm ortet selection; Selection index; Plot and family information.

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Index selection utilizing plot and family (full-sib and half-sib) information has been demonstrated in selecting palms for cloning in a progeny-test trial on hybrids of Deli dura (D) x Dumpy-AVROS pisifera (P).

Inclusion of plot information did not significantly improve the precision or efficiency of the single trait indices for five traits; oil yield (Y), bunch number (BNo), height increment (HINC), kernel to fruit ratio (KF) and mesocarp to fruit ratio (MF); or of the multiple trait indices involving the first three traits. Inclusion of family information greatly improved the precision for the traits Y, KF and MF, which were poorly heritable but improved it to a lesser degree for the more heritable traits, BNo and HINC.

Although the inclusion of information from plot, family and correlated traits in an index would greatly improve the selection efficiency (by as much as 60%) over mass selection for Y, the expected quantum improvement was only about 13% of the trial mean.

The expected selection response from the multiple trait indices involving Y and HINC as objective traits indicated that it was possible to achieve significant reduction in height increment without sacrificing the efficiency of selection for yield in this Deli D x Dumpy-AVROS P population.

INTRODUCTION

The selection index method has received much attention in plant breeding ever since it was proposed by Smith (1936). Except for a few cases (Moreno-Gonzalez and Hallauer, 1982; Burdon, 1982), most of the reports dealt with multi-trait selection using information only from the individual plants for selection (Baker, 1986). In animal breeding, selection index methodology commonly incorporates information from other sources, particularly relatives, into the index (Henderson, 1963; Ronningen and Van Vleck, 1985). In tree crop breeding and in oil palm breeding, in lieu of selection index methodology and progeny-testing, the common practice is to select individuals on the basis of their family means and their deviations from the block or trial means, also often using knowledge or observations on the performance of their relatives. Selection index methodology can incorporate all these information in a more objective and useful manner.

This paper examines the use of this approach in a progeny-test trial on *dura* (D) x *pisifera* (P) hybrids with the objective of selecting palms for cloning or ortet selection (The approach can be used to select parent palms for further breeding as well).

MATERIALS AND METHODS

Data

The hybrid trial progeny-tested four Dumpy-AVROS Ps (Soh *et al.*, 1981) randomly mated to three Deli Ds (Rosenquist, 1986) each in a nested design. The trial was planted on coastal soil as randomized blocks with three replications in plots of 20 palms spaced 9.1m triangularly. The following traits were studied on individual palms:

1. Palm oil yield (Y): Average yield of oil in kg per palm per annum for the first four years of harvesting.
2. Bunch number (BNo) : Total number of bunches per palm per annum averaged over the first four years of harvesting.
3. Kernel to fruit ratio (KF) : Kernel weight as percentage of fruit weight, determined from 3-4 bunches sampled over the first four years of harvesting.

vesting.

4. Mesocarp to fruit ratio (MF) : Mesocarp weight as percentage of fruit weight, determined from 3-4 bunches sampled over the first four years of harvesting.

5. Height increment (HINC) : Annual palm height increment in dm averaged over the first four years of height measurement.

ANALYSES

Estimation of Variance - Covariance Components

Male (*pisifera*, Δ_m^2), female (*dura*, Δ_f^2), random plot error (Δ_p^2) and random tree error (Δ_w^2) components of variance were obtained from the analysis of variance for a nested mating design (Becker, 1975), with the following genetic model:

$$\Delta_m^2 = 1/4 (1 + F_m) \Delta_A^2 + 1/16 (1 + F_m)^2 \Delta_{AA}^2 + \dots$$

$$\Delta_f^2 = 1/4 (1 + F_f) \Delta_A^2 + 1/4(1 + F_m)(1 + F_f) \Delta_D^2 + \dots$$

where F_m and F_f are the respective inbreeding coefficients of the parents, and Δ_A^2 , the additive genetic variance in the hybrid population, which was estimated by:

$$1/2 \left[\frac{4\Delta_m^2}{(1+0.1875)} + 4\Delta_f^2 \right] \text{ as } F_m = 0.1875 \text{ (Soh, 1992)}$$

$$F_f = 0$$

Although the estimation would be biased by the inclusion of non-additive genetic variances, this is not a disadvantage as in selecting plants for cloning non-additive effects also come into play. Negative components were assumed to be zero.

Covariance components were obtained in a similar manner except that negative components were not assumed to be zero.

SELECTION INDEX ANALYSES

Single trait

y and α vectors

The selection index approach of White and Hodge (1989) was followed. Let *y* be a vector for

predicting the genetic worth of a palm in an AxE family containing the individual observation, the AxE plot and full-sib family means, and means of two families AxF and AxG related to AxE as half-sibs.

i.e.

$$y = \begin{bmatrix} y_{ijAEIm} \\ \bar{y}_{ijAEI} \\ \bar{y}_{i.AE} \\ \bar{y}_{i.AF} \\ \bar{y}_{i.AG} \end{bmatrix} = \begin{bmatrix} \text{individual observation} \\ \text{plot mean} \\ \text{full-sib family mean} \\ \text{half-sib family mean 1} \\ \text{half-sib family mean 2} \end{bmatrix}$$

The model for an individual tree observation is:

$$y_{ijklm} = u + E_i + B_{ij} + f_k + fe_{ik} + m_l + me_{il} + fm_{kl} + fme_{ikl} + p_{ijkl} + w_{ijklm}$$

where u = general mean

E_i = fixed effect of the i th test environment

B_{ij} = fixed effect of the j th block in i th test

f_k = random effect of k th female
 $E(f_k) = 0, \text{Var}(f_k) = \Delta^2_f$

fe_{ik} = random effect of the k th female in i th test
 $E(fe_{ik}) = 0, \text{Var}(fe_{ik}) = \Delta^2_{fe}$

m_l = random effect of the l th male
 $E(m_l) = 0, \text{Var}(m_l) = \Delta^2_m$

me_{il} = random effect of l th male in i th test.
 $E(me_{il}) = 0, \text{Var}(me_{il}) = \Delta^2_{me}$

fm_{kl} = random interaction effect of the kl th full-sib family
 $E(fm_{kl}) = 0, \text{Var}(fm_{kl}) = \Delta^2_d$

fme_{ikl} = random interaction effect of kl th family in i th test.
 $E(fme_{ikl}) = 0, \text{Var}(fme_{ikl}) = \Delta^2_{dc}$

p_{ijkl} = random plot error of kl th family in j th block of i th test
 $E(p_{ijkl}) = 0, \text{Var}(p_{ijkl}) = \Delta^2_p$

w_{ijklm} = random tree error of m th tree in $ijkl$ th plot
 $E(w_{ijklm}) = 0, \text{Var}(w_{ijklm}) = \Delta^2_w$

The covariances between all pairs of effects are assumed to be zero.

As the analysis is based on one test environment, the model for an individual tree observation becomes:

$$y_{ijklm} = u + E_i + B_{ij} + f^*_k + m^*_l + p_{ijkl} + w_{ijklm}$$

where $f^*_k = f_k + fe_{ik} + fm_{kl} + fme_{ikl}$

$$m^*_l = m_l + me_{il}$$

The expected values of the various observations or fixed effects, *i.e.* α vector are:

$$\alpha = \begin{bmatrix} E(y_{ijAEIm}) \\ E(\bar{y}_{ijAEI}) \\ E(\bar{y}_{i.AE}) \\ E(\bar{y}_{i.AF}) \\ E(\bar{y}_{i.AG}) \end{bmatrix} = \begin{bmatrix} E(\bar{y}_{ij..}) \\ E(\bar{y}_{ij..}) \\ E(\bar{y}_{i..}) \\ E(\bar{y}_{i..}) \\ E(\bar{y}_{i..}) \end{bmatrix} = \begin{bmatrix} (\bar{y}_{ij..}) \\ (\bar{y}_{ij..}) \\ (\bar{y}_{i..}) \\ (\bar{y}_{i..}) \\ (\bar{y}_{i..}) \end{bmatrix} = \begin{bmatrix} \text{block mean} \\ \text{block mean} \\ \text{trial mean} \\ \text{trial mean} \\ \text{trial mean} \end{bmatrix}$$

V matrix : Variance and Covariance of Observations

$$\text{Var}(\text{individual mean}) = \text{Var}(\bar{y}_{ijklm}) = \Delta^2_{f^*} + \Delta^2_{m^*} + \Delta^2_p + \Delta^2_w$$

$$\text{Var}(\text{plot mean}) = \text{Var}(\bar{y}_{ijkl}) = \Delta^2_{f^*} + \Delta^2_{m^*} + \Delta^2_p + \Delta^2_w/n$$

where n = palms per plot

$$\text{Var}(\text{full-sib mean}) = \text{Var}(\bar{y}_{i.kl}) = \Delta^2_{f^*} + \Delta^2_{m^*} + \Delta^2_p/b + \Delta^2_w/bn$$

where b = number of replicates

$$\text{Cov}(\text{individual, plot}) = \text{Cov}(y_{ijklm}, \bar{y}_{ijkl}) = \text{Var}(\bar{y}_{ijkl})$$

$$\text{Cov}(\text{individual, full-sib}) = \text{Cov}(y_{ijklm}, \bar{y}_{i.kl}) = \text{Var}(\bar{y}_{i.kl})$$

$$\text{Cov}(\text{individual, half-sib}) = \text{Cov}(y_{ijklm}, \bar{y}_{i.kl'}) = \Delta^2_{m^*}$$

$$\text{Cov}(\text{plot, full-sib}) = \text{Cov}(\bar{y}_{ijkl}, \bar{y}_{i.kl}) = \text{Var}(\bar{y}_{i.kl})$$

$$\text{Cov}(\text{plot, half-sib}) = \text{Cov}(\bar{y}_{ijkl}, \bar{y}_{i.kl'}) = \Delta^2_{m^*}$$

$$\text{Cov}(\text{full-sib/half-sib, half-sib}) = \text{Cov}(\bar{y}_{i.kl}, \bar{y}_{i.kl'}) = \Delta^2_{m^*}$$

The V matrix becomes:

$$\begin{bmatrix} \text{Var}(y_{ijklm}) & \text{Cov}(y_{ijklm}, \bar{y}_{ijkl}) & \text{Cov}(y_{ijklm}, \bar{y}_{i.kl}) \\ & \text{Cov}(y_{ijklm}, \bar{y}_{i.kl'}) & \text{Cov}(y_{ijklm}, \bar{y}_{i.kl'}) \\ \text{Cov}(y_{ijklm}, \bar{y}_{ijkl}) & \text{Var}(\bar{y}_{ijkl}) & \text{Cov}(\bar{y}_{ijkl}, \bar{y}_{i.kl}) \\ & \text{Cov}(\bar{y}_{ijkl}, \bar{y}_{i.kl'}) & \text{Cov}(\bar{y}_{ijkl}, \bar{y}_{i.kl'}) \\ \text{Cov}(y_{ijklm}, \bar{y}_{i.kl}) & \text{Cov}(\bar{y}_{ijkl}, \bar{y}_{i.kl}) & \text{Var}(\bar{y}_{i.kl}) \\ & \text{Cov}(\bar{y}_{i.kl}, \bar{y}_{i.kl'}) & \text{Cov}(\bar{y}_{i.kl}, \bar{y}_{i.kl'}) \\ \text{Cov}(y_{ijklm}, \bar{y}_{i.kl'}) & \text{Cov}(\bar{y}_{ijkl}, \bar{y}_{i.kl'}) & \text{Cov}(\bar{y}_{i.kl}, \bar{y}_{i.kl'}) \\ & \text{Var}(\bar{y}_{i.kl'}) & \text{Cov}(\bar{y}_{i.kl}, \bar{y}_{i.kl'}) \\ \text{Cov}(y_{ijklm}, \bar{y}_{i.kl'}) & \text{Cov}(\bar{y}_{ijkl}, \bar{y}_{i.kl'}) & \text{Cov}(\bar{y}_{i.kl}, \bar{y}_{i.kl'}) \\ & \text{Cov}(\bar{y}_{i.kl}, \bar{y}_{i.kl'}) & \text{Var}(\bar{y}_{i.kl'}) \end{bmatrix}$$

C matrix : Covariance Between Observation and Genetic Value

i. The genetic value of an individual in the k th full-sib family:

$$g_{ijklm} = f_k + m_j + d_{ijklm}$$

where d_{ijklm} = random genetic effect of the m th individual in the j th block of the k th family in the i th test, $E(d_{ijklm}) = 0$, $Var(d_{ijklm}) = 1/2 \Delta_A^2$

$$Var(g_{ijklm}) = Var(f_k) + Var(m_j) + Var(d_{ijklm}) = \Delta_A^2$$

ii. Covariance between an individual tree observation and its genetic value:

$$Cov(y_{ijklm}, g_{ijklm}) = \Delta_A^2$$

iii. Covariance between the individual tree's plot mean and its genetic value:

$$Cov(\bar{y}_{ijkl}, g_{ijklm}) = 1/2 \Delta_A^2 (1+1/n)$$

iv. Covariance between the individual tree's full-sib family mean and its genetic value:

$$Cov(\bar{y}_{i.kl}, g_{ijklm}) = 1/2 \Delta_A^2 (1+1/bn)$$

v. Covariance between the individual tree's half-sib family mean and its genetic value.

$$Cov(\bar{y}_{i.kl}, g_{ijklm}) = 1/4 (1+F_m) \Delta_A^2 = \Delta_{m^*}^2$$

as only the paternal half-sib relationship was involved.

i.e.

$$C = \begin{bmatrix} Cov(y_{ijklm}, g_{ijklm}) \\ Cov(\bar{y}_{ijkl}, g_{ijklm}) \\ Cov(\bar{y}_{i.kl}, g_{ijklm}) \\ Cov(\bar{y}_{i.kl}, g_{ijklm}) \\ Cov(\bar{y}_{i.kl}, g_{ijklm}) \end{bmatrix} = \begin{bmatrix} \Delta_A^2 \\ \Delta_A^2 (1+1/n) \\ \Delta_A^2 (1+1/bn) \\ \Delta_{m^*}^2 \\ \Delta_{m^*}^2 \end{bmatrix}$$

Selection index equation and solution

The genetic worth function of each candidate:

$$w = a'g,$$

where g = vector of genetic values
 a = the relative economic value of each trait.

The selection index function pertaining to the observation on each candidate:

$$I = b'(y-\alpha)$$

where b' = vector of index coefficients
 y = vector of observed values
 α = vector of fixed effects.

By maximizing the correlation between the genetic worth and the index, *i.e.* $Corr(w, I)$:

$$Vb = Ca$$

The solution :

$$b = V^{-1}Ca$$

where $a = 1$ or -1 since we are interested in only one trait.

The error variance of prediction is given by:

$$Var(w-\hat{w}) = a'[G-CV^{-1}C]a,$$

where G = genetic variance-covariance of traits predicted = Δ_A^2 , since only one trait is predicted.

The correlation between true and predicted genetic worth, which measures the precision of an index, is given by:

$$Corr.(w, \hat{w}) = [a'CV^{-1}Ca/a'Ga]^{1/2}$$

The expected genetic progress is given by:

$$\Delta g = i[a'CV^{-1}Ca]^{1/2}$$

where i = selection intensity = 2.06 (for 5%)

The following variant indices of the above were also constructed:

i) Data from individual, plot and its full-sib family mean.

ii) Data from individual and its full-sib family mean.

These indices were constructed for each of the five single traits; Y, BNo, HINC, KF and MF. For those traits in which the $\Delta^2_{m^*}$ or Δ^2_p were assumed to be zero, the respective information (i.e. plot, half-sib), in the indices was ignored.

The expected genetic progress from these variant indices was compared with the first which used individual, plot, full-sib family and half-sib family information and to the expected progress from mass selection based on only the individual's records.

i.e. $\Delta g = ih \Delta^2_A$
 where h = square root of heritability.

Multiple traits

Oil yield (Y), BNo and HINC were selected to illustrate the multiple trait index case. Only individual, plot and full-sib family information were used.

The elements for the y and α vectors were as before but combined into a single column matrix.

The V, C and G matrices were arranged in the following simplified illustration to avoid excessive use of notation:

V =	Variance-covariance of individual observations	Variance-covariance of individual observations & plot means	Variance-covariance of individual observations and full-sib family means
	Variance-covariance of individual observations & plot means	Variance-covariance of plot means	Variance-covariance of plot mean & full-sib family means
	Variance-covariance of individual observations & full-sib family means	Variance-covariance of plot means & full-sib family means	Variance-covariance of full-sib family means

The only additional items which needed to be calculated were:

The covariance between measurements of u and v for traits u and v on an individual tree:

$Cov(u_{ijAEIm}, v_{ijAEIm}) = \Delta_{f^*,uv} + \Delta_{m^*,uv} + \Delta_{p,uv} + \Delta_{w,uv}$
 where; $\Delta_{f^*,uv}$, $\Delta_{m^*,uv}$, $\Delta_{p,uv}$ and $\Delta_{w,uv}$ are the corresponding covariance components.

The covariance between a measurement of trait u on an individual and its plot mean for trait v:

$Cov(u_{ijAEIm}, \bar{v}_{ijAEI}) = \Delta_{f^*,uv} + \Delta_{m^*,uv} + \Delta_{p,uv} + \Delta_{w,uv}/n$

The covariance between a measurement of trait u on an individual and its family mean for trait v, $Cov(u_{ijAEIm}, \bar{v}_{iAEI})$
 = $Cov(\bar{u}_{ijAEI}, \bar{v}_{iAEI})$, covariance between a plot mean of trait u and its family mean of trait v
 = $Cov(u_{iAEI}, v_{iAEI})$, covariance between family means for traits u and v

= $\Delta_{f^*,uv} + \Delta_{m^*,uv} + \Delta_{p,uv} \Delta_{p,uv}/b + \Delta_{w,uv}/bn$ Again, to simplify illustration:

C =	Covariance between individual observation and the individual's breeding value
	Covariance between plot mean and the individual's breeding value
	Covariance between family mean and the individual's breeding value

The following additional items needed to be calculated:

The covariance between the measurement on an individual for trait u and the breeding value for trait v:

$Cov(y^u_{ijAEIm}, g^v_{ijAEIm}) = \Delta_{A,uv}$
 where $\Delta_{A,uv}$ = covariance of additive effects.

The covariance between the plot mean for trait u, and the breeding value of an individual for trait v.

$Cov(\bar{y}^u_{ijAEI}, g^v_{ijAEIm}) = 1/2 \Delta_{A,uv} (1+1/n)$

The covariance between the family mean for trait u, and the breeding value of an individual for trait v.

$Cov(\bar{y}^u_{iAEI}, g^v_{ijAEIm}) = 1/2 \Delta_{A,uv} (1+1/bn)$

G =	Covariance between individual observation and the individual's breeding value	i.e. top part of C
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The predicted genetic gain for each of the traits in the index when selection is based on the index values is given by :

$$\Delta g = i. [C'V^{-1}Ca / (a'CV^{-1}Ca)^{1/2}]$$

The formula for $\text{Corr}(w, \hat{w})$ remains as for single-trait indices.

A total of six multiple trait indices was constructed with three sets of relative economic values:

$$a' = [1 \ 0 \ 0], a' = [1 \ 1 \ -1], a' = [1 \ 0 \ -1]$$

for the traits Y, BNo and HINC in order of the elements where a trait assigned 0 became a selection (supporting) trait instead of an objective (primary) trait; and with and without inclusion of plot data.

RESULTS AND DISCUSSION

Heritability and genetic correlations

Heritability (h^2) estimates obtained in this Deli D x Dumpy-AVROS P population (Table 1) although likely to underestimate non-additive genetic effects, were higher for Y and particularly BNo and HINC than the corresponding broad-sense heritability estimates obtained for the Deli D x AVROS P population (Soh and Chow 1989, Soh *et al.*, 1992). This perhaps reflected the relatively more outbred nature of the Dumpy-AVROS Ps (Soh, 1992) and the segregation of the lower BNo and HINC genes from the Dumpy ancestor. In contrast, the h^2 values for KF and MF were very much lower in the former than the latter populations. This might reflect the selection for these traits in the breeding history of the Dumpy-AVROS P parental population.

The genetic correlations obtained here (Table 2) for Y and BNo were high and almost identical with those obtained for the Deli D x AVROS P population. In the latter population HINC was moderately positively correlated to Y but here HINC was negatively correlated to Y and BNo although of a lower order. Again this perhaps

reflected the segregation out of HINC genes with respect to Y and BNo genes indicating that it is possible to select palms with high oil yield and low height increment.

Single-trait indices

Index coefficients (b) for the various information sources, $\text{Corr}(w, \hat{w})$, Δg (absolute units), $\Delta g\%^d$ (expressed over Δg by mass selection) and $\Delta g\%^e$ (expressed over trial mean) for the 11 selection indices involving the five single traits are shown in Table 3.

For single trait prediction, $\text{Corr}(w\hat{w})$ and Δg are both measures of precision or efficiency of an index. As can be seen from the results for each trait, $\text{Corr}(w\hat{w})$ increased or decreased correspondingly with Δg . In fact $\text{Corr}(w\hat{w})$ can be interpreted as a standardized gain, *i.e.* gain per unit of selection intensity (i) and per unit of genetic variance (Δ) of the target trait:

$$\text{Corr}(w\hat{w}) = \text{gain}_{gt} / (i. \Delta_{gt}) \text{ (White and Hodge, 1991)}$$

Inclusion of plot information did not significantly improve the precision [$\text{Corr}(w\hat{w})$ or Δg] of the index for any of the traits except perhaps HINC (Table 3 : Index Nos; 2 vs 3, 5 vs 6, 9 vs 10). The relatively higher plot variance (Δ_p^2) of about 15 % of the phenotypic variance [$\text{Var}(y_{ijklm})$] would explain this (Table 1).

As expected, inclusion of full-sib family information improved the precision of indices for the poorly heritable traits; Y, KF and MF every appreciably (Index Nos. 3, 13 and 16). For the more heritable traits, BNo and HINC, the improvements were still significant although were not as great, again as expected (Index Nos. 6 and 10).

Inclusion of half-sib family information (Index Nos. 8, 12 and 15) in addition to full-sib family information was only useful for MF, which might be explained by its very low heritability (0.07).

Multiple-trait indices

The three sets of economic values were chosen to reflect three cases of likely interest to the breeder (Table 3).

i. $a' = 1\ 0\ 0$ (Index Nos. 17 and 20), where Y was the objective trait, while BNo and HINC were the supporting selection traits.

ii. $a' = 1\ 1\ -1$ (Index Nos. 18 and 21), where all three were the objective traits.

iii. $a' = 1\ 0\ -1$ (Index Nos. 19 and 22), where Y and HINC were the objective traits and BNo the selection trait.

As in the single-trait indices, judging from the corresponding $\text{Corr.}(w\hat{w})$'s there appeared to be little advantage in including plot information (Index Nos. 17 vs 20, 18 vs 21 and 19 vs 22).

As was evident from all three cases inclusion of BNo and HINC, whether as objective or selection traits, gave better expected response to selection for Y than single trait index selection on Y alone. This was probably due to the contribution of BNo, which was highly heritable and had a high positive genetic correlation to Y. Case (ii), *i.e.* Index Nos. 18 and 21, gave relatively lower Δg 's than Case (i), *i.e.* Index Nos. 17 and 20 for Y and HINC, and a relatively higher Δg for BNo. The higher Δg 's for BNo probably reflected the effects of a positive selection pressure on BNo being an objective trait in Case (ii). The lower Δg 's for Y and HINC in Case (ii) despite positive selection pressures on them might have been the consequence of a negative genetic correlation between Y and HINC.

Incidentally, Δg 's for BNo and HINC in Case (i) and BNo in Case (iii) were correlated responses to selection. Case (ii) would be of comparatively lesser interest to breeders as it would involve achieving an increase in yield from an increased number of bunches and a lesser reduction of palm height. This would result in a relatively higher harvesting cost. Case (i) would be of more interest because of the very high Δg in Y but the response in height reduction was poorest. Case (iii) would be of considerable interest as it would achieve a very high expected response to Y without the need to harvest more bunches, and at a lower height.

Despite the much expected increase in selection efficiency of about 50%-60% ($\Delta g\%^d$) over mass selection for Y utilizing information from plot,

family and correlated traits, and the fact that the Dumpy-AVROS P parents were relatively more outbred than the AVROS P parents; the maximum expected response in Y ($\Delta g\%^e$) was only about 13%, which was similar to the average figure obtained from Deli D x AVROS P population using family and individual selection (Soh, 1986). Apparently genetic variability for Y in Deli D x Dumpy-AVROS P, despite the relatively more outbred Ps was still rather restricted. However, there would be an important advantage in selecting from the Deli D x Dumpy AVROS P population in that one could achieve a substantial response in HINC reduction without compromising selection efficiency for high Y. This would not be possible with the Deli D x AVROS P population.

It can be argued that since all the estimates and predictions were based on data obtained from one trial in one location, they were likely to be biased by the effects of genotype-environment interaction. The results obtained would then only be applicable to similar materials planted in similar conditions. However results from a Deli D x AVROS P trial (Rosenquist, 1982), in which the AVROS P was closely related to Dumpy-AVROS P (Soh, 1992), and which was replicated in Malaysia and Papua New Guinea, showed that genotype x location effects were not important. So the results obtained here may have wider applicability.

Finally, utilizing plot, family and also other (White and Hodge, 1992) sources of information in the form of a selection index is a useful approach in plant selection and will probably be of wider applicability in oil palm breeding, as well as in selecting palms for cloning.

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TABLE 1. MEANS AND VARIANCES FOR THE VARIOUS TRAITS IN THE HYBRID PROGENY-TEST TRIAL

Trait ⁺	Mean	Δ^2_f	$\Delta^2 A_f$	$\Delta^2_{m^*}$	$\Delta^2 A_m$	Δ^2_p	Δ^2_w	h^2	Δ^2_A	Var(y_{ijklm})	Var(\bar{y}_{ijkl})	Var($\bar{y}_{i.kl}$)
Y	44.65	7.57	30.28	0	0	3.28	58.00	0.22	15.14	68.86	14.68	9.94
BNo	20.78	6.04	24.16	0	0	0.67	12.10	0.64	12.08	18.81	7.51	6.53
HINC	4.63	0.16	0.65	0.13	0.42	0.17	0.65	0.49	0.54	1.11	0.50	0.36
KF	7.33	0.27	1.09	0.14	0.47	0	3.05	0.22	0.78	3.46	0.61	0.48
MF	8.23	0.08	0.31	0.69	2.32	0	19.07	0.07	1.32	19.84	2.03	1.19

⁺ Y	= total oil yield (kg p ⁻¹ yr ⁻¹)	Δ^2_f	= variance of female parent effects
BNo	= total bunch number (no.p ⁻¹ yr ⁻¹)	$\Delta^2_{m^*}$	= variance of male parent effects
HINC	= average annual height increment (dm p ⁻¹ yr ⁻¹)	Δ^2_p	= variance of plot effects
KF	= kernel to fruit ratio (%)	Δ^2_w	= within plot variance
MF	= mesocarp to fruit ratio (%)	Var (y_{ijklm})	= variance of individual observations
$\Delta^2 A_f$	= additive genetic variance estimate from female component of variance	Var (\bar{y}_{ijkl})	= variance of a plot mean
	= 4 Δ^2_f (female parents assumed non-inbred)	Var ($\bar{y}_{i.kl}$)	= Variance of a full-sib family mean
$\Delta^2 A_m$	= additive genetic variance estimate from male component of variance	h^2	= heritability
	= 4 $\Delta^2_{m^*} + (1+F)$ where F = inbreeding coefficient of male parents		
	= 0.1875		
$\Delta^2 A_A$	= 1/2 ($\Delta^2 A_f + \Delta^2 A_m$)		

TABLE 2. COVARIANCES AND GENETIC CORRELATIONS AMONG TOTAL BUNCH NUMBER (BNo), AVERAGE HEIGHT INCREMENT (HINC) AND TOTAL OIL YIELD (Y) IN THE HYBRID PROGENY-TEST TRIAL

Traits*	Δ_f	ΔA_f	Δ_{m^*}	ΔA_m	Δ_p	Δ_w	Δ_A	r_A
Y and BNo	6.11	24.43	-2.04	-6.89	1.42	14.55	8.77	0.64
Y and HINC	-0.62	-2.48	0.21	0.71	0.26	1.24	-0.89	-0.31
B.No. and HINC	-0.29	-1.14	0.29	0.97	0.09	0.12	-0.09	-0.03

Δf^*	= female (<i>dura</i>) component of covariance
Δm^*	= male (<i>pisifera</i>) component of covariance
Δp	= plot component of covariance
Δw	= tree component of covariance
ΔA	= covariance of genetic effects
r_A	= genetic correlation

⁺ Y	= total oil yield (kg p ⁻¹ yr ⁻¹)
BNo	= total bunch number (no. p ⁻¹ yr ⁻¹)
HINC	= average annual height increment (dm p ⁻¹ yr ⁻¹)

TABLE 3. ESTIMATED INDEX COEFFICIENTS(b), CORRELATIONS BETWEEN THE INDEX AND AGGREGATE GENETIC WORTHS [Corr(w̄w)] AND SELECTION GAINS (Δg) FOR THE VARIOUS TRAITS IN THE HYBRID PROGENY-TEST TRIAL.

Index No.	Traits ^a	Relative economic values	Individual observation	Index Coefficients (b)				Δ g				
				Plot mean	Full-sib family mean	Half-sib family mean	Half-sib family mean	Corr (w̄w)	Trait units	% ^d	% ^c	
1	Y	1 ^b	1							3.76	100.0	8.4
2	Y	1	0.1305	-0.0602	0.7080			0.68		5.44	144.7	12.2
3	Y	1	0.1256		0.6527			0.68		5.43	144.6	12.2
4	BN ₀	1 ^b	1							5.74	100.0	27.6
5	BN ₀	1	0.4992	-0.2274	0.6737			0.85		6.08	106.0	29.3
6	BN ₀	1	0.4811		0.4644			0.85		6.07	105.8	29.2
7	HINC	-1 ^b	1							-1.05	100.0	22.7
8	HINC	-1	-0.4117	0.3271	-0.6284	-0.0748		0.77		-1.16	110.6	25.1
9	HINC	-1	-0.4117	0.3271	-0.6811			0.77		-1.15	109.9	24.9
10	HINC	-1	-0.3506		-0.4151			0.75		-1.13	107.7	24.5
11	KF	1 ^b	1							0.86	100.0	11.7
12	KF	1	0.1273		0.6791	0.0434		0.70		1.27	147.7	17.3
13	KF	1	0.1273		0.7093			0.70		1.27	147.3	17.3
14	MF	1 ^b	1							0.61	100.0	0.7
15	MF	1	0.0345		0.2101	0.2776		0.66		1.55	255.3	1.9
16	MF	1	0.0345		0.5325			0.55		1.31	214.9	1.6
17	Y + BN ₀ + HINC	1	0.0805	-0.0563	0.6341					5.98	159.2	13.4
		0	0.2745	-0.0997	0.0258			0.75		4.39 ^c	76.5	21.1
		0	-0.8847	0.6259	-0.4824					-0.55 ^c	52.7	12.0
18	Y + BN ₀ + HINC	1	0.0324	-0.1029	0.7281					5.62	149.5	12.6
		1	0.8403	-0.2287	0.5469			0.82		5.57 ^c	97.0	26.8
		-1	-1.3779	0.9788	-1.3225					-0.44 ^c	42.3	9.6

19	Y	1	0.1023	-0.0645	0.6494	0.77	5.90	157.1	13.2
	+ BNo	0	0.2565	-0.0952	0.0285		4.03 ^c	70.2	19.4
	+ HINC	-1	-1.3344	0.9749	-1.1226		-0.72 ^c	68.2	15.5
20	Y	1	0.0750		0.5833	0.74	5.96	158.6	13.3
	+ BNo	0	0.2678		-0.0672		4.39 ^c	76.4	21.1
	+ HINC	0	-0.7818		0.0406		-0.54 ^c	51.4	11.7
21	Y	1	0.0223		0.6353	0.82	5.60	148.9	12.5
	+ BNo	1	0.8240		0.3345		5.56 ^c	96.9	26.8
	+ HINC	-1	-1.2250		-0.4966		-0.43 ^c	41.4	9.4
22	Y	1	0.0957		0.5914	0.77	5.88	156.6	13.2
	+ BNo	0	0.2513		-0.0615		4.04 ^c	70.4	19.4
	+ HINC	-1	-1.1679		-0.3143		0.70 ^c	66.5	15.1

^a Y = oil yield in kg p⁻¹ yr⁻¹

BNo = total bunch number in no.p⁻¹ yr⁻¹

HINC = average annual height increment in dm p⁻¹ yr⁻¹

KF = kernel to fruit ratio (%)

MF = mesocarp to fruit ratio (%)

^b mass selection

^c correlated response

^d For multiple traits Δg for each component trait is expressed as percentage over its corresponding value for mass selection

^e Δg expressed as percentage of trial mean

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