TREND OF WITHIN FAMILY-PLOT SELECTION PRACTISED IN THREE SEEDLING SEED ORCHARDS OF *EUCALYPTUS PELLITA* IN INDONESIA

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LEKSONO, B. & KURINOBU, S. 2005. Trend of within family–plot selection practised in three seedling seed orchards of *Eucalyptus pellita* in Indonesia. A trend of within family–plot selection was examined by applying a retrospective selection index to the result of the selection in three seedling seed orchards of *Eucalyptus pellita* in South Sumatra, Indonesia. The orchards were established in randomised complete block designs with five-tree row plot. Within family–plot selections were conducted twice with selection intensities of around 40% at the first selection (36 months after planting) and 50% at the second selection (58 months). The results were analysed with the retrospective selection index using data on height, diameter and stem form measured before each selection. In terms of standardized index weight, diameter was found to be the highest priority trait throughout the two stages of selection in all the orchards. Height was considered as a second priority trait at the first within family–plot selection, whereas relative priority of stem form was increased at the second selection. Expected gains from within family–plot selection were positive for all of the traits in both selection stages and mean cumulative gains were 2.7% for height, 3.9% for diameter and 1.7% for stem form.

Key words: Genetic gain – retrospective selection index – standardized index weight

LEKSONO, B. & KURINOBU, S. 2005. Trend pemilihan dalam famili–plot yang diamalkan oleh tiga kebun biji benih (anak benih) *Eucalyptus pellita* di Indonesia. Trend pemilihan dalam famili–plot dikaji menggunakan indeks pemilihan tinjau balik ke atas hasil pemilihan di tiga kebun biji benih (anak benih) *Eucalyptus pellita* di Sumatra Selatan, Indonesia. Kebun berasaskan reka bentuk blok lengkap rawak dengan plot mengandungi barisan-barisan lima pokok. Pemilihan dalam famili–plot dijalankan dua kali dengan kadar pemilihan sekitar 40% pada pemilihan pertama (36 bulan selepas penanaman) dan 50% pada pemilihan kedua (58 bulan). Keputusan dianalisis menggunakan indeks pemilihan tinjau balik ke atas data ketinggian, diameter dan bentuk batang yang diperoleh sebelum pemilihan. Diameter merupakan sifat paling utama pada dua peringkat pemilihan di semua kebun. Ketinggian dianggap sebagai sifat kedua utama pada peringkat pemilihan pertama manakala keutamaan bentuk

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batang bertambah pada peringkat pemilihan kedua. Perolehan jangkaan daripada pemilihan dalam famili–plot adalah positif bagi semua sifat pada kedua-dua peringkat pemilihan. Purata perolehan terkumpul untuk ketinggian, diameter dan bentuk batang masing-masing 2.7%, 3.9% dan 1.7%.

Introduction

Genetic improvement programmes for *Eucalyptus pellita,* currently recognised as a promising eucalypt for industrial planting in the lowland tropics (Eldridge *et al.* 1993), are being conducted to increase its productivity (Hashimoto *et al.* 1996, Harwood *et al.* 1997). In the recurrent selection applied to *E. pellita,* selection and mating are done in seedling seed orchards. However, genetic gains resulted from selection in the orchard are not always accurately predictable in the case of multi-trait improvement. This is because with within family–plot selection the priority of target traits is largely dependent on breeders' preference or intuition.

One of the practical ways to reduce the uncertainty of the prediction may be the application of a retrospective selection index (Yamada 1977). With this method, weighting coefficients for index selection for the trait of concern are derived from the results of actual selection. Then these weights can be used to predict genetic gain from the selection. Kurinobu *et al.* (1996) applied this method to the preliminary results of within family–plot selection in seedling seed orchards of *Acacia mangium, E. pellita* and *E. urophylla.* In the case of *Eucalyptus* first time, they reported that almost equal weight was allocated to both growth and stem form. However, the trend of selection throughout the whole process of within family–plot selection has not been analysed yet.

In this study, a retrospective selection index was applied to the two stages of within family–plot selection in three seedling seed orchards of *E. pellita* established in South Sumatra, Indonesia. The trend of selection across the two stages of within family–plot selection was examined using the derived weighting coefficients of the selection index.

Materials and methods

The three seedling seed orchards of *E. pellita* (referred to as Ep002, Ep003 and Ep004) were established in January 1995 in South Sumatra (latitude 4° S, longitude 104° E, altitude 80 m asl). The soil type of the site was acrisol, previously occupied by *Imperata cylindrica.* The annual rainfall was 2781 mm, with a pronounced dry season from May till September. In the three seedling seed orchards, individual-tree lots of CSIRO seed collection from Papua New Guinea were planted separately; 48 open pollinated families from South Kiriwo, 39 families from North Kiriwo and 34 families from Serisa Village were tested in EP002, Ep003 and Ep004 respectively. The design of the orchards was a randomised complete block, which was initially laid out as 12 replications of five-tree-row plot with 4 × 1.5 m spacing.

Within family–plot selection was made by three steps of thinning: the poorer two trees out of the five per plot were culled in the first step at 24 months after planting, then the poorest one out of the remaining three was removed in the second step at 36 months, and the best one per plot was retained in the final step at 58 months. Local tree breeders and company staff practised these steps of selection. The first measurement was done prior to the first culling (age 24 months) and the second measurement was done before the third culling (age 58 months). The retained trees after the completion of within family–plot selection were taken measurement in each orchard. Measured traits were height, diameter at breast height (dbh) and stem form. Stem form was measured subjectively by scoring 1 to 3 (1: very crooked, 2: slightly crooked and 3: straight). For the convenience of data analysis, the within family–plot selection was considered as two stages; the first and the second steps of culling were aggregated as the first selection stage and the third step was regarded as the second selection stage. Thus the approximate selection intensities were 40% for the first selection and 50% for the second selection.

Analysis of variance and covariance were made using individual-tree data (Y_{ijk}) in the respective orchards with the following linear model:

$$Y_{ijk} = \mu + R_i + F_j + RF_{ij} + \varepsilon_{ijk} \quad \ldots\ldots\ldots\ldots \; (1)$$

where Y_{ijk} is the k-th individual tree data of the j-th family in the i-th replication and μ, R_i, F_j, RF_{ij} and ε_{ijk} are the overall mean, the i-th replication effect, the j-th family effect, the plot (interaction) effect of the j-th family in the i-th replication, and the within family-plot error with Y_{ijk} respectively.

The variance and covariance components for family, plot and within family–plot were estimated by equating mean squares or mean cross-products to their expectations (Harvey 1979). Individual-tree heritabilities (h^2) for the three traits were calculated using the following formula (Williams & Matheson 1994):

$$h^2 = 2.5\,\sigma_f^2 / [\sigma_f^2 + \sigma_p^2 + \sigma_w^2] \quad \ldots\ldots\ldots\ldots \; (2)$$

where σ_f^2, σ_p^2, σ_w^2 are estimates of variance components for family, plot and within family–plot variance respectively. Phenotypic correlations ($r_{p\,i,j}$), which was equivalent to the within family–plot correlation in this study and genetic correlation ($r_{g\,i,j}$) among the three traits were calculated as follows (Falconer 1981):

$$r_{p\,i,j} = \mathrm{cov}_{w\,(i,j)} / [\sigma_{wi}^2 \,.\, \sigma_{wj}^2]^{1/2} \quad \ldots\ldots\ldots\ldots \; (3)$$

$$r_{g\,i,j} = \mathrm{cov}_{f\,(i,j)} / [\sigma_{fi}^2 \,.\, \sigma_{fj}^2]^{1/2} \quad \ldots\ldots\ldots\ldots \; (4)$$

where $\mathrm{cov}_{w\,(i,j)}$ and $\mathrm{cov}_{f\,(i,j)}$ are the within family–plot and among-family covariance components between the i-th and the j-th traits respectively. σ_{wi}^2 and σ_{wj}^2 are the within family–plot variance components between the i-th and the j-th traits respectively. σ_{fi}^2 and σ_{fj}^2 are the among-family variance component between the i-th and the j-th trait respectively.

The selection differential for each trait ($\Delta\, p_w$) was calculated as differences between the mean of selected trees and the population mean before selection. Then the coefficients of weight for the retrospective index (b_w) were calculated as follows (Yamada 1977):

$$b_w = P_w^{-1} \;.\; \Delta p_w \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots \; (5)$$

where P_w^{-1} is the inverse of the phenotypic variance–covariance matrix, the elements of the matrix being within family–plot variances and covariances in this study. Genetic gain by within family–plot selection ($\Delta\, g_w$) was predicted using the following formula (Yamada 1977):

$$\Delta g_w = G_w \, . \, b_w \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (6)$$

where G_w is the genetic variance–covariance matrix, elements of which were assumed equal to three-quarters of the genetic variances and covariances, which in turn were assumed to be equal to 2.5 times of family variance and covariance components in this study. To evaluate efficiency of the index obtained by equation (5), biserial correlation (r_b) was calculated by using the following formula (Yamada 1977):

$$r_b = (I_s - I) \,/\, (I_q - I) \ldots\ldots\ldots\ldots\ldots\ldots\ldots (7)$$

where I is an average index value of the whole population. I_s and I_q are average index values for the actually selected population and for the population selected according to the indices respectively. This correlation was calculated using data only from the plots where both the culled trees and the selected ones retained before selection in order to avoid over-estimation.

Results and discussion

Genetic parameters

Growth of trees in three seedling seed orchards was considered to be fairly good, ranging from 8 to 10 m in height at 24 months, and about 20 m at 58 months, although the growth in Ep002 was slightly slower than those in other orchards (Table 1). Average scores for stem form in the three orchards were all the same (about 2.3). This indicates that most of the trees have straight stems.

Family variation was significant for all traits except stem form in Ep002. Estimates of heritability seemed to be different between orchards, between age of

Table 1 Heritability and variances for the measured traits before within family–plot selection at 24 and 58 months in three provenance seedling seed orchards

Parameter	First assessment (age 24 months)				Second assessment (age 58 months)			
and trait	Mean	Heritability	Family variance	W. plot variance	Mean	Heritability	Family variance	W. plot variance
Ep002								
Height (m)	8.04	0.098	0.1652 **	2.6411	19.20	0.196	0.4793 **	3.6579
Dbh (cm)	7.42	0.158	0.3129 **	4.1117	14.72	0.164	0.4756 **	4.8768
Stem form (1–3)	2.29	0.011	0.0029 ^{ns}	0.6821	2.28	0.015	0.0019 ^{ns}	0.2984
Ep003								
Height (m)	9.81	0.208	0.3299 **	2.9613	19.73	0.294	0.8111 **	4.5407
Dbh (cm)	8.01	0.196	0.4502 **	5.0084	15.71	0.191	0.6051 **	6.1332
Stem form (1–3)	2.25	0.061	0.0122 **	0.5067	2.32	0.121	0.0164 **	0.2818
Ep004								
Height (m)	9.57	0.084	0.1269 **	2.9966	20.27	0.144	0.3719 **	4.2560
Dbh (cm)	8.33	0.082	0.1895 **	5.3387	15.96	0.128	0.3887 **	6.2469
Stem form (1–3)	2.35	0.023	0.0043 *	0.4910	2.17	0.111	0.0146 *	0.3134

** = Significant at the 1% level, * = significant at the 5% level, ns = not significant at the 5% level
Ep002, Ep003 and Ep004 number of families 48, 39 and 34 respectively.

Table 2 Correlations among traits used for the retrospective selection index

Trait	First within family–plot selection			Second within family–plot selection		
	Height	Dbh	Stem form	Height	Dbh	Stem form
Ep002						
Height	–	0.871	0.259	–	0.615	0.195
Dbh	0.996	–	0.335	0.942	–	0.191
Stem form	1.053	0.889	–	-0.156	0.503	–
Ep003						
Height	–	0.862	0.574	–	0.709	0.197
Dbh	0.939	–	0.588	0.938	–	0.222
Stem form	0.791	0.809	–	0.402	0.246	–
Ep004						
Height	–	0.811	0.473	–	0.637	0.119
Dbh	0.910	–	0.444	0.556	–	0.136
Stem form	0.662	0.568	–	0.273	0.285	–

Correlations above diagonals are within family–plot phenotypic correlations and below diagonals are estimated genetic correlations.

measurement and between traits. Estimated heritabilities were higher at the second measurement except for dbh in Ep003 and stem form in Ep004. Those for growth were highest in Ep003, followed by Ep002 and Ep004 at both ages of measurement. For stem form, estimated heritability was lowest in Ep002, while in other orchards, heritabilities were significant, ranging from weak to moderate.

The size of within family–plot variance of stem form was the smallest among the traits and it decreased with age, whereas those of height and dbh increased, clearly due to scale effects (Table 1). Phenotypic correlations among the traits were all positive in the three orchards (Table 2). However, correlations at the second selection (age 58 months) were weaker than those at the first selection (age 24 months). Correlations between height and dbh were high at the first selection, but decreased to around 0.65 at the second selection. This decreasing trend was also observed in correlations with stem form. In the case of genetic correlation, a trend of change in the correlation was not obvious. However, the relationship between growth and stem form seemed to get weaker at the second selection.

Retrospective selection index

Selection differentials on the three traits were all positive at each stage of selection in the three orchards (Table 3). Among the three traits, selection differentials for dbh were greatest in all the orchards. Likewise, the coefficient of weight for dbh was greatest at the first selection, except in Ep003. On the other hand, the coefficient for stem form was greatest in spite of its smaller selection differentials at the second selection. This is probably due to the nature of formula 5, where the coefficient of weight tends to be greater when the within family–plot variance is small with no strong correlations between other traits.

Table 3 Result from the application of retrospective selection indices to the two stages of within family-plot selection.

Trait	First within family-plot selection					Second within family-plot selction				
	Selection differential	Rate (%)	Coefficient of weight	Gain	Gain (%)	Selection differential	Rate (%)	Coefficient of weight	Gain	Gain (%)
Ep002		r_b=0.677		(725/956)			r_b=0.704		(258/330)	
Height	0.725	9.01	0.078	0.133	1.66	0.463	2.41	0.017	0.174	0.90
Dbh	0.973	13.11	0.167	0.182	2.46	0.766	5.20	0.139	0.191	1.30
Stem form	0.194	8.45	0.106	0.016	0.71	0.096	4.22	0.204	0.006	0.26
Ep003		r_b=0.842		(622/777)			r_b=0.799		(280/351)	
Height	1.071	10.92	0.128	0.282	2.88	0.505	2.56	0.002	0.226	1.14
Dbh	1.447	18.07	0.170	0.334	4.17	0.803	5.11	0.119	0.197	1.25
Stem form	0.342	15.18	0.182	0.047	2.09	0.101	4.37	0.235	0.017	0.74
Ep004		r_b=0.883		(582/693)			r_b=0.823		(272/324)	
Height	1.024	10.70	0.053	0.106	1.11	0.527	2.60	0.012	0.096	0.47
Dbh	1.552	18.63	0.232	0.137	1.64	0.924	5.79	0.133	0.151	0.94
Stem form	0.293	12.50	0.196	0.014	0.58	0.116	5.36	0.285	0.018	0.83

Gain were predicted by equation 5. r_b is the biserial correlation coefficient calculated with formula 7. Numbers in parentheses are number of trees correctly predicted wih the retrospective selection index and that of trees used for prediction respectively. Two out of the five trees and one out of the two trees per lot were selected at the first selection and the second selection.

Biserial correlations in Ep003 and Ep004 were equal or greater than 0.8, while those in Ep002 were slightly lower (about 0.7) at both stages of selection (Table 3). The rate of trees correctly predicted with the retrospective selection index gave similar results, all exceeding 0.75. This indicates that the indices derived from the results of selections in the three orchards can be regarded as sufficiently accurate to describe the trend of within family–plot selection actually practised in the orchards.

Since the coefficients of weight were scale-dependent, they were adjusted by multiplying with phenotypic standard deviation of the respective trait: square root of within family–plot variance in this study (Figure 1). With this standardization, the coefficients can be regarded as weights actually allocated per unit of standard deviation and thus they are comparable between traits. As in the preceding analysis, the standardized coefficient for dbh was the largest. Hence, it was regarded as the highest priority trait in both stages of selection.

The coefficients of weight for the growth traits were decreased in size at the second selection. This reduction was partly due to the fact that the second selection was less intensive than the first selection; selection rate in the second selection was 0.5, and 0.4 at the first selection. In contrast, the coefficients for stem form were almost equal or even increased in the second selection. This indicated that the relative priority of stem form was increased in the second selection.

The trend of within family–plot selection found in this study seemed in accordance with the actual conditions of trees in the seedling seed orchard of *E. pellita*. The difference in growth had the first priority at both stages of within family–plot selection because the growth represented by tree size was the most noticeable

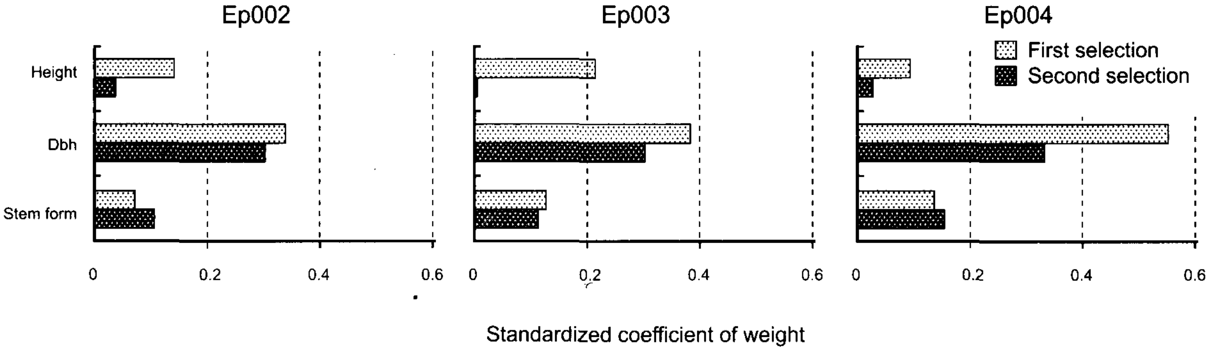

Figure 1 Standardized ceofficients of weight for the three traits based on the result of within family–plot selection in the three seedling seed orchards

criterion for those making the within family–plot selection. On the other hand, stem form, which might have been mostly concealed by foliage at the first selection, had become more obvious and thus the relative priority was increased at the second selection.

Genetic gains predicted by formula 6 using the coefficient of weight were positive on all traits at both stages of selection in the three orchards. Among the three traits, relative gains in dbh, which received the highest selection intensity, were the greatest ranging from 1.6 to 4.2% at the first selection then reduced to around 1.0% at the second selection. Predicted gains for height were greater than those of stem form not only at the first selection but also at the second selection, except in Ep004. This is probably due to the higher heritabilities of height as well as its stronger genetic correlations with dbh as compared with those of stem form.

Averages of the cumulative gains across the two stages of within family–plot selection in the three orchards were 2.7, 3.9 and 1.7% for height, dbh and stem form respectively. Although a simple summation of relative gains at different ages of selection may lead to an over-estimation, it is evident that the within family–plot selection practised in the seedling seed orchards was in favour of improving growth. In the case of *E. pellita,* this result is desirable because a slower growth compared with *Acacias* (Harwood *et al.* 1997), currently considered as a major drawback with this species for large-scale plantation establishment, would be improved with this within family–plot selection.

Conclusions

The highest priority trait throughout the two stages of within family–plot selection in the three orchards was dbh. Height growth was considered as a second priority trait at the first selection, whereas its priority was diminished and replaced with stem form at the second selection. Expected gains by within family–plot selection were positive on all traits at each stage of selection and they were in the order of dbh, height and stem form.

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