

Growth Characteristics of 100 Open-pollinated Families in an Early-age Test of *Agathis loranthifolia* in West Java, Indonesia

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Abstract : Early results from a field trial of *Agathis loranthifolia* are reported from a progeny test of 100 open-pollinated families in west Java, Indonesia. The average of height and diameter at root collar (DRC) was 40.18 cm and 0.52 cm at age 15 months. Family survival rate ranged from 86.5% at age 10 months to 81.7% at age 15 months. Family means of 10 best and 10 poorest families for each trait indicated that there was a large difference of growth performances among individual families. For height and DRC growth, the poorest groups had averages of 33.98 cm and 0.43 mm while the averages of the best groups were 47.35 cm and 0.62 mm at age 15 months as a difference of 39.36% and 43.65%, respectively. Differences between the best group and the test population mean, which is the selection differential, were implying that genetic gain from selection for the improvement of height and DRC growth would be achieved. The family variances of DRC and height were relatively small compared to replicate and residual variances. Family heritabilities for both studied traits were fluctuated, and the genetic coefficients of variation for DRC and height at age of 15 months were 7.19% and 5.22%, respectively.

Key words : genetic component, heritability, correlation, breeding strategy, selection

Introduction

Agathis loranthifolia is native to Papua New Guinea, New Britain, Central Malesia (Maluku, Celebes and Philippines), Kalimantan and Sumatra. It can grow up to 65 m tall with a diameter of up to 200 cm. The seedling needs shade and growth is slow during the first year. Later, when released from competition from weeds, growth is rapid. It is cultivated as a plantation tree and used in enrichment planting and reforestation in various areas within the natural range, especially in Irian Jaya. It has also been planted intensively in Java, outside the natural range because the species is important from the ecological, silvicultural, industrial, genetic and landscape points of view in Indonesia (Hardiyanto and Na'iem, 2001; Nurhasybi and Sudrajat, 2002).

A. loranthifolia is wind pollinated, and female and male cones are on different branches on the same tree. In plantations in Java, cone production begins when the tree is about 15 years old, and viable seeds are usually

produced after the age of 25 years. Trees produce flowers and fruits throughout the year, but the best fruiting season is from August to October. The seed has no dormancy and does not need pretreatment before sowing. Germination percentage of 90-100% is reached within 10 days. Vegetative propagation is done by stem cutting from seedlings aged 7 months (30 cm tall) dipped in IBA 10 ppm. Roots will emerge 6-8 weeks after the stem cutting has been placed in the rooting bed (Nurhasybi and Sudrajat, 2002).

Indonesia has over 120 million hectares of natural forests among 195 million hectares total land area. These represent a tenth of the World's remaining tropical rainforests and they are also vital to Indonesia's economic development, meeting most of the domestic demand for wood. Owing to factors such as logging, conversion of forest land to other uses, fire and shifting cultivation, Indonesia's forests are being degraded and deforested at an unprecedented rate (Hardiyanto and Na'iem, 2001).

Plantation forests in Indonesia are found mainly on Java, and cover an area of about two million hectares. They consist of teak (*Tectona grandis*), Merkus pine (*Pinus merkusii*), mahogany (*Swietenia macrophylla*),

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rosewood (*Dalbergia latifolia*), agathis (*Agathis loranthifolia*), cajuput (*Melaleuca cajuputi*) and other species. By 2000, about 2.5 million hectares of plantations had been established on outer islands, particularly Sumatra and Kalimantan (Ministry of Forestry, 2000; Kartodihardjo and Supriono, 2000).

A tree improvement program has not yet initiated with *A. loranthifolia* in Indonesia. So, the Korea Forest Research Institute has been supporting Indonesian tree breeding cooperating with the Ministry of Forestry, Indonesia and the Korea International Cooperation Agency since 2005. The cooperation has selected 100 plus trees of *A. loranthifolia* throughout whole Java Island in Indonesia and established the progeny test of open pollinated families in Jasinga, west Java. Improvement of growth traits is the main objective of the program (RSSNC, 2007).

The objectives of this study are (i) to survey the survival of 100 selected plus trees of *A. loranthifolia* in Java, (ii) to estimate genetic parameters of growth traits of the open pollinated progenies, and (iii) to identify superior families of the *A. loranthifolia* for reforestation in west Java. We also discussed genetic constitutes in relation to the genetic improvement of *A. loranthifolia* in Java, Indonesia.

Materials and Methods

1. Progeny trial and data assessment

Open pollinated seeds were collected from the selected 100 plus trees of *A. loranthifolia* growing in several artificial populations that reached at rotation age (over 40 years) from west Java. Growth, tree form, stem straightness, disease/insect resistance, seed availability were all taken into account in the parental selection. To reduce the likelihood of relatedness, the trees were separated by a minimum of 100 meters.

Seeds were collected from the selected plus trees and extracted by the seed research team of the Bogor Agricultural University (IPB). Then, seeds were sown in polyethylene pots (22 cm×18 cm) filled with vermiculate, perlite and peatmoss (1:1:1 in volume). After sowing, the seeded pots were placed in nursery beds where they were arranged in a randomized complete block design. Seedlings were grown for two months (December 2006 to January 2007) in local nurseries at Gunung Walat nursery near planting site in the west Java.

Outplanting started at early February 2007 and seedlings were transplanted within a week. Weeding was carried out four times during the first year and three times during the second year. On the nursery and planting site, families were arranged in randomized complete blocks, with eight replicates of 4-trees in line per plot in the field (lat. 6° 30' S, long. 106° 33' E, elev. 820 m). The

spacing was 2.5 m×2.5 m in the field whereas seeding containers were side by side in the nursery.

We measured growth traits (seedling height and diameter at root collar) at different ages of 0, 10 and 15 months. Here, age 0 means the measurement just before the outplanting (i.e., assessment in the nursery stage).

2. Statistical analyses

Individual tree data for seedling height and diameter at root collar were checked for normality using the SAS Univariate procedure (SAS Institute Inc., 2002). Plot means (i.e., the average of all trees from a given family within a replication) improved the normality of data for both traits at the different ages, as mentioned Jansson and Danell (1993). Therefore, plot means were employed for both traits at the different ages in subsequent analyses, in order to improve the normality and on the basis that this decision does not affect the precision with which any parental breeding value is predicted (White and Hodge, 1989).

Separate analyses of variance were fitted for each growth trait at different ages for examination the differences among families, using the MIXED procedure in SAS program according to the following linear mixed model:

$$y_{ij} = \mu + B_i + F_j + e_{ij} \quad (1)$$

where y_{ij} is the plot means of the dependent variable of the i^{th} replicate of the j^{th} family, μ is the overall mean, B_i is the random effect of the i^{th} replicate, F_j is the fixed effect of the j^{th} family and e_{ij} is the random residual error term.

Variance components for individual traits, were estimated with the linear mixed Model (1), but considering family as random effect rather than a fixed effect. Heritability of family (h_f^2 , (2)) was estimated as follows,

$$h_f^2 = \frac{\sigma_f^2}{\sigma_f^2 + \sigma_h^2 + \sigma_e^2} \quad (2)$$

where σ_f^2 , σ_b^2 and σ_e^2 are the family genetic variance, replicate variance component and residual variance, respectively. To compare the absolute level of family genetic variance across the traits, the genetic coefficients of variation (GCV) was calculated with the formula (3) as follows,

$$h_f^2 = \frac{\sigma_f^2}{\sigma_f^2 + \sigma_b^2 + \sigma_e^2} \quad (3)$$

where σ_f^2 , σ_b^2 is the family genetic variance and \bar{x} is the population mean.

The family genetic correlations (r_f) among pairs of traits at the age of 0, 10 and 15 months were estimated using a bivariate model that was extended from the

univariate linear mixed model (1) also considering family as random effect. Given that, some family genetic correlations were difficult to estimate due to estimations were out of the parameter space, genetic correlations were also calculated with the predicted family breeding values using Pearson's correlation by the CORR procedure in SAS program. In order to determine to what extent the variation in one trait is associated with that in others, phenotypic correlations among pairs of traits at the age of 0, 10 and 15 months were also obtained with the CORR procedure in SAS.

All analyses were performed by means of Restricted Maximum Likelihood (REML) (Patterson and Thompson, 1971), using Average Information algorithm implemented with ASREML (Gilmour *et al.*, 2006). One important limitation of the REML (co)variance estimates is that their distribution is unknown. Only approximate measure of precision of the estimates based on asymptotic theory can be calculated. Standard errors of the heritability and family genetic correlation were computed approximately with the "delta method" based on Taylor expansion (Lynch and Walsh, 1998) using an ASREML post-processing program (Gilmour *et al.*, 2006).

Expected genetic gain (G) was calculated by Falconer's (1981) formula (4) as follows,

$$\Delta G = ih_f^2 \sigma_p \quad (4)$$

where i is the intensity of selection taken from Becker (1984), and σ_p is the family phenotypic standard deviation of each trait.

Results and Discussion

Based on individual assessment, data of overall survival rate, means value, standard deviation and range for diameter at root collar (DRC) and height growth (HT) at the 0, 10 and 15 months are shown in Table 1. Survival

Table 1. Number of tree with records (n), survival, overall means (Mean), standard deviation (SD) and range for diameter at root collar (DRC) and height growth (HT) under different ages in the progeny trial of *A. loranthifolia* in west Java, Indonesia (based on individual assessment data).

Trait	Age	n	Survival (%)	Mean (cm)	SD	Range (cm)
DRC	0	3,200	100	0.27	0.124	0.1 - 0.7
	10	2,769	86.5	0.47	0.136	0.1 - 1.2
	15	2,613	81.7	0.52	0.235	0.1 - 1.6
HT	0	3,200	100	23.8	8.603	10.0 - 77.0
	10	2,769	86.5	36.4	12.101	10.0 - 100.0
	15	2,613	81.7	40.2	18.635	10.0 - 110.0

rate increased 13.5% at age 10 months and 18.5% at age 15 months, respectively. Also a large difference of survival rate among families was found and the range of average survival rate was from 62.5% to 96.9% at age 15 months. The grand mean of height at age 15 months was 40.18 cm and that of diameter at root collar was 0.518 cm. The standard deviation for both traits increased with the ages from 0, 10 and 15 months.

1. Family effect and variation of family means

Highly significant ($p < 0.001$) differences of both growth traits at ages of 0, 10 and 15 months, among the 100 families were found from the analysis of variance using the family linear mixed Model (1) (data not shown). Figure 1 shows a large phenotypic variation of diameter at root collar and height growth among the 100 open-pollinated families of *A. loranthifolia* at age 15 months.

Table 2 shows family means of 10 best and 10 poorest families for each trait, indicating the magnitude of family variation. Large variation among family means was found. For height growth and root collar diameter, the

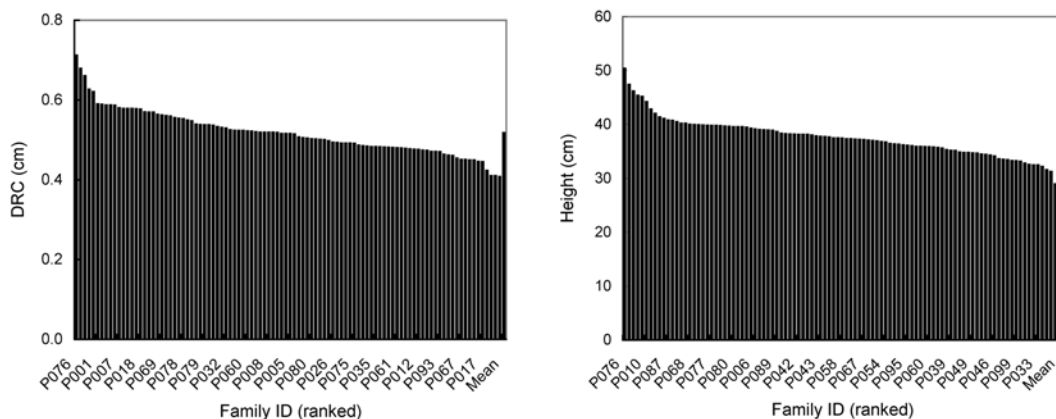
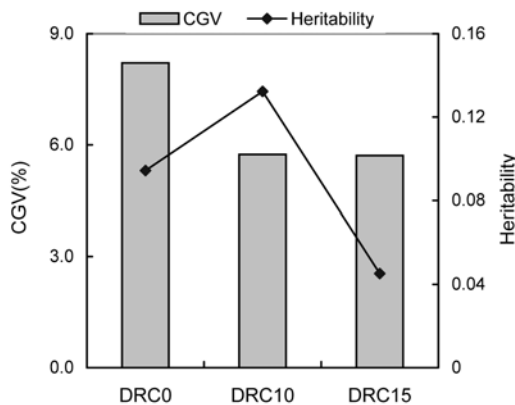


Figure 1. Averages of the diameter at root collar (DRC) and height of the 100 open-pollinated families of *A. loranthifolia* at age 15 months.

Table 2. Ranking of the 10 best and the 10 poorest families of *A. loranthifolia* based on the height and DRC performances at age of 0, 10 and 15 months.

Family rank ^a	Age 0		Age 10		Age 15	
	Height	DRC	Height	DRC	Height	DRC
1	31.31	0.365	45.64	0.604	52.54	0.712
2	29.97	0.347	44.92	0.565	51.05	0.679
3	29.29	0.344	44.80	0.564	48.71	0.661
4	28.63	0.340	43.07	0.544	48.50	0.627
5	28.28	0.340	42.97	0.544	48.50	0.620
6	28.22	0.337	42.68	0.534	46.87	0.590
7	28.16	0.334	42.19	0.530	45.50	0.589
8	28.09	0.332	42.03	0.519	44.70	0.587
9	28.00	0.328	41.88	0.519	43.58	0.587
10	27.75	0.322	41.79	0.517	43.58	0.587
X1	28.77	0.339	43.20	0.544	47.35	0.624
91	20.00	0.233	31.50	0.432	35.76	0.451
92	19.93	0.232	31.30	0.421	35.64	0.450
93	19.78	0.230	31.25	0.421	35.44	0.450
94	19.66	0.228	31.07	0.419	35.05	0.449
95	19.56	0.227	30.58	0.417	34.08	0.446
96	19.50	0.225	30.21	0.417	33.58	0.445
97	19.28	0.225	29.89	0.416	33.29	0.423
98	19.13	0.217	29.86	0.414	33.16	0.410
99	19.06	0.213	29.85	0.404	33.16	0.410
100	18.78	0.210	28.89	0.400	30.63	0.408
X2	19.47	0.224	30.44	0.416	33.98	0.434
X	23.83	0.275	36.36	0.473	40.16	0.518
D1(%)	47.78	51.16	41.91	30.67	39.36	43.65
D2(%)	20.73	23.42	18.81	14.99	17.92	20.56

^aThe best and the poorest families were not the same for traits and ages. D1 is the differences (%) between mean of the best (X1) and the poorest (X2) group of the 10 families, and D2 is the differences (%) between mean of the best group (X1) and the test mean (X)



poorest groups had averages (X2) of 33.98 cm and 0.43 mm, respectively while the averages of the best groups (X1) were 47.35 cm and 0.62 mm at age 15 months, respectively; a difference (D1) of 39.36% and 43.65%.

Differences (D2) between the best group (X1) and the test mean (X), which is the selection differential, were smaller but still significant (Table 2). As expected, differences among individual families were much greater. For example, at 15 months of age, the worst family was 30.63 cm tall and 0.41 cm DRC, while the best family measured 52.5 cm tall and 0.71 cm DRC, i.e. a difference of 171.6% and 174.4 %, respectively.

2. Genetic variation among families

The family genetic variances of DRC and height were relatively small compared to replicate and residual variances across ages (Table 3). Family heritabilities for both studied traits were not stable by ages (Figure 2). Although, the average heritability estimates for DRC and height across ages were 0.040 and 0.077, respectively. The ability of traits to respond to the selection can be compared by the genetic coefficients of variation (GCV) that measures levels of genetic variation while accounting for scale and size effect. The GCV was 7.19% and 5.22% at age 15 months for DRC and height, respectively (Figure 2). Thus, it has been demonstrated that *A. loranthifolia* half-sib families possess considerable genetic variation in the DRC and height traits, suggesting that selection for improvement would be promising.

3. Correlations in time and among traits

Positive and highly significant ($p < 0.0001$) phenotypic correlations were found between DRC and height growth for all ages (Table 4). They ranged from 0.684 for HT10/DRC10 to 0.214 for HT0/DRC15. As expected, phenotypic correlation between traits at the same age was higher than that at across ages.

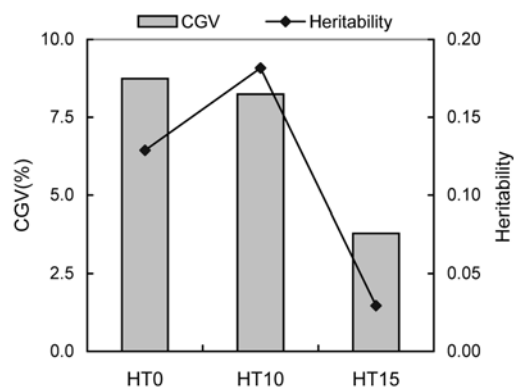


Figure 2. Coefficients of genetic variation (CGV) and family heritabilities (h^2) for 100 open-pollinated *A. loranthifolia* families at different ages. The traits of diameter at root collar (DRC) and height growth (HT) are followed by a number which represents the age of measurement in months.

Table 3. Family genetic variance (σ_f^2), replicate variance (σ_b^2) and residual variance (σ_e^2) with their approximate standard errors in parenthesis for 100 open-pollinated *A. loranthifolia* families.

Trait	Age	σ_f^2	σ_b^2	σ_e^2
DRC	0	0.0005 (0.0002)	0.0039 (0.0021)	0.0049 (0.0003)
	10	0.0007 (0.0002)	0.0051 (0.0028)	0.0048 (0.0003)
	15	0.0014 (0.0006)	0.0212 (0.0123)	0.0177 (0.0010)
HT	0	4.3392 (1.1540)	13.0171 (7.1148)	29.3419 (1.5767)
	10	8.9798 (2.0316)	39.9477 (21.5695)	40.4666 (2.1981)
	15	4.3954 (2.2415)	43.6341 (25.6194)	73.1689 (4.2966)

Table 4. Phenotypic (upper diagonal, probability values) and genetic (lower diagonal, approximate standard errors) correlation coefficients between traits and among ages for the 100 open-pollinated progenies of *A. loranthifolia*.

Trait	Age	DRC			HT		
		0	10	15	0	10	15
DRC	0	-	0.404 <.0001	0.274 <.0001	0.672 <.0001	0.352 <.0001	0.417 <.0001
	10	0.805 (0.1478)	-	0.501 <.0001	0.395 <.0001	0.684 <.0001	0.654 <.0001
	15	0.803 (0.2554)	0.972* (0.0)	-	0.214 <.0001	0.330 <.0001	0.653 <.0001
HT	0	1.000 (0.0044)	0.749 (0.1372)	0.673 (0.2393)	-	0.524 <.0001	0.492 <.0001
	10	0.969* (0.0)	0.908 (0.0603)	0.960 (0.2097)	0.988* (0.0)	-	0.647 <.0001
	15	0.947* (0.0)	0.983* (0.0)	0.989* (0.0)	0.994 (0.2003)	0.985* (0.0)	-

*Standard errors equal to zero indicates that the parameter is forced to keep in the theoretical parameter space.

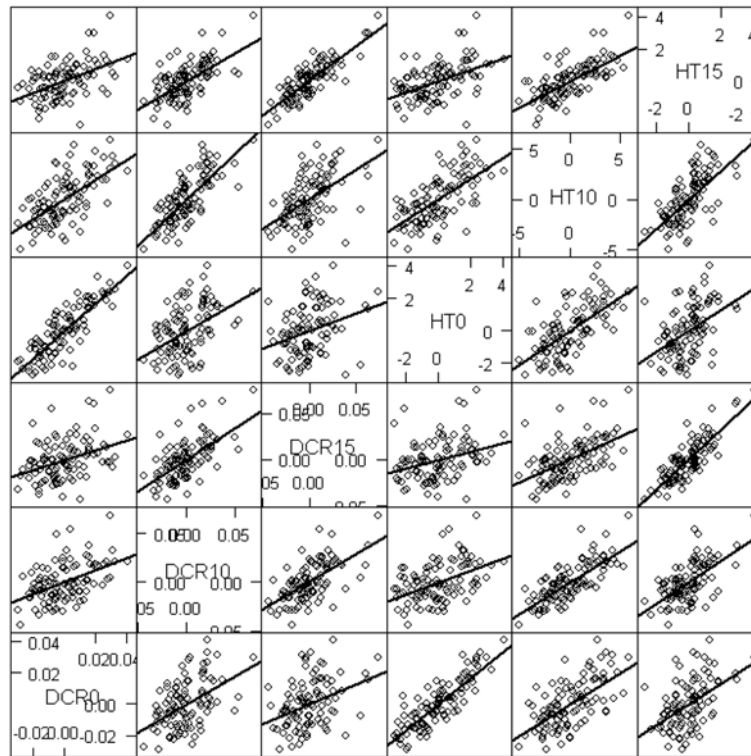
Estimates of family genetic correlation between DRC and height at age of 0, 10 and 15 months obtained via the Average Information algorithm were high (Table 4), implying that selection for any one of these traits would result in a highly correlated response to selection in the others. However, estimates genetic correlations between DRC15/DRC10, HT10/DRC0, HT10/HT0, HT15/DRC0, HT15/DRC10, HT15/DRC15 and HT15/HT10 were difficult to estimate due to estimations were out of the parameter space (i.e. indicating convergence problems). A drawback of the second differentials Average Information algorithm is that it can result in parameter estimates out of the parameter space when no constraints to be positive definite are imposed on the (co)variance matrix. Attempts to keep the family correlations in the theoretical parameter space (i.e., $r_f \leq 1$) and using a hybrid scheme (i.e., combined the Expectation-Maximization and Average Information algorithm), yielded genetic correlations very close to 1. These family correlations are indicated in Table 4 as parameters having standard errors equal to zero. Figure 3 shows a scatter plot matrix with linear regression of the predicted family breeding values for DRC and height growth among ages, by means of the univariate Model (1) and using family

as random effect. The linear regressions did not support the high values (close to 1) of the family genetic correlation out of the parameter space (i.e. those indicated in Table 4 with standard errors equal to zero).

4. Genetic gain

High genetic gain was expected when selecting best 10, 20, 30 and 40 families out of 100 tested at age 15 months, especially for height (Table 5). Heritability for DRC was higher than that for height, but the phenotypic standard variation of DRC was smaller than that of height. The expected genetic gain for height growth was, therefore, higher than that for DRC (Table 5), implying that it would be efficient to select families showing superior height growth in order to expect higher genetic gain.

Selection is based on the principle that the average genetic value of selected families would be better than the average of families in the base population (Zobel and Talbert, 1984). The improvement that could be made from selection is a function of the heritability and the variation of the traits. In the present study, the family heritability was low, but the total amount of variation for the traits was large enough to influence the selection dif-



Scatter Plot Matrix

Figure 3. Scatter plot matrix and linear regression of family breeding values for diameter at root collar (DCR) and height growth (HT) at age of 0, 10 and 15 months. Lines provided an indication of correlation between traits and among ages. The traits of diameter at root collar (DRC) and height growth (HT) are followed by a number which represents the age of measurement in months.

Table 5. Estimates of family heritability (h_f^2) and expected genetic gain (G) when selecting best 10, 20, 30 and 40 families out of 100 tested at age 15 months for diameter at root collar (DRC) and height growth (HT).

Traits	h_f^2	ΔG (%) when selecting best families			
		10	20	30	40
DRC	0.034	0.333	0.266	0.220	0.183
HT	0.036	22.33	17.81	14.74	12.29

ferential.

This study reports the early evaluation of the DRC and height traits of *A. loranthifolia* in west Java, Indonesia. Based on the progeny performances, it would be expected that the progenies from the selected families could be not much better than the mean of the selected families. However, there would be the greatest opportunity to improve the genetic gain by increasing selection differential.

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