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Genetic variation of seven years old *Araucaria cunninghamii* progeny test in Bondowoso East Java

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Abstract. *Araucaria cunninghamii* is conifer trees with great commercial value for tropical and sub-tropical region. The genetic variation in growth i.e: height, diameter, volume was examined on 7 years old of *A. cunninghamii* progeny test at the area of Forest for Special Purpose (KHDTK) in Bondowoso, East Java. The progeny trial included 80 families from six provenances, with four replications and four trees in each row plots. The analysis showed that there were great variations of genetic growth within provenances and between provenances. It was discovered that *A. cunninghamii* from Fak-fak Papua had the best height growth (mean height= 10.65 m with volume mean annual increments =8.39 m3 ha-1 year-1), while A. cunninghamii from Serui Papua had the best diameter growth (mean diameter =15.84 cm).The individual heritability for height and diameter were classified as moderate (h^2i = 0.16; 0.30). The genetic correlation between the height and diameter was quite strong (r_g = 0.79). As a result of the findings, the future genetic program strategy in the research will focus on increasing genetic biodiversity for the species in order to increase Mean Annual Increment (MAI) for supplying Indonesia's wood demand.. The genetic diversity will be achieved through some steps in the strategy i.e: best genetic growth selection within provenances; combining of genetic of the best growth between provenances; and establishment of the progeny trial for next generations.

1. Introduction

Araucaria cunninghamii Aiton ex D. Don (*Araucariaceae*) is conifer trees with high value of timber; the products generally used for plywood, pulp, paper, carpentry and also produce sap [1] . It grows naturally in the tropical forests of Papua, Papua New Guninea and Queensland, it becomes a potential income for local people [2]. Several demonstration plots have been established in various countries such as Congo, Uganda, China, Vietnam, Thailand and Hawaii, and it showed great potential for plantations, while new large-scale development was carried out in Australia around 44,000 ha and around 3,500 ha in Papua New Guinea [3] .

The development program of Araucaria plantations on a large scale with high productivity requires superior seed to improve the growth despite the fact that the silviculture implementation should also be undertaken. [4] mentioned that the used of superior seeds should have accountable genetic traits produced through a series of breeding programs. One of the breeding programs to produce genetic improved seed through selection activities of the best individual trees is designed in a progeny trial. In Indonesia, the breeding and genetic conservation program of *A. cunninghamii* was initiated through two stages of development of progeny trials in Bondowoso. First progeny trial was established in December 2002 and the second establishment were undertaken in January 2008 [2]. There was no recent information regarding the genetic parameters of those progeny trials. Therefore, this study was aimed to determine the growth performance and genetic parameters of 7-year-old of *A. cunninghamii* progeny test in Bondowoso, East Java.

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2. Materials and Method

This study was conducted on seven years old progeny trial of *A. cunninghamii* located in the forest area of special purpose (KHDTK) at Bondowoso, East Java Indonesia as part of The Centre for Biotechnology and Tree Improvement Research. The progeny test was arranged in a randomized complete block design, comprises of 80 families, four tree line plot and four blocks as replication. The 64 open pollinated families were originated from six different seed sources presented in Table 1. Assessment of the traits was conducted on all individual trees in this plot. Height, diameter at breast height (DBH) and the volume were the three quantitative traits included in the assessment. *Height (Ht)* referred to the total tree height, measured to the nearest 0.1 m. Diameter was defined as the stem diameter taken at 1.3 m from ground level.

Table 1. Seed sources information of progeny test of *A. cunninghamii* in Bondowoso, East Java [2]

No	Provenances	Number of families	Suburb	Lat. (^{0}S)	Long.(^{0}W)	Alt (m asl)
1	Serui	(11)	Kanobon	02 º - 34 '	135 º - 11 '	800
2	Wamena	(28)	Napua	04 º - 21 '	135 º - 11 '	1600
3	Manokwari	(12)	Kebar	02 º - 59 '	139 º - 09 '	1200
4	Jayapura	(6)	Cyklop	04 º - 25 '	140 º - 38 '	1600
5	Fak-fak	(7)	Fak-fak	02 º - 34 '	132 º - 31 '	900
	INDONESIA	***64***				
6	Queensland	(16)	Yarraman	26 º - 52 '	152 º - 25 '	1000
	AUSTRALIA	***16***				
	TOTAL	***80***				

2.1. *Statistical analysis*

The individual trait data were analyzed using the ANOVA procedure in Genstat Version 5.3.2 to check for homogeneity of variances. Analyses on the data were based on the following linear model that has been described before to a randomized block design with a nested pattern as follows [5] :

$$Y_{ijkl} = \mu + B_i + P_j + F(P)_k + BF(P)_{ik} + E_{ijkl}$$

where :

μ = the overall mean
B_i = the effect of the i^{th} replicate
P_j = the effect of the j^{th} provenances
$F(P)_k$ = the effect of the k^{th}family nested in the j^{th} provenances
$BF(P)_{ik}$ = the interaction effect of i^{th}replicate and k^{th}family nested in the j^{th} provenances
E_{ijk} = the residual error with a mean of zero
Y_{ijk} = the plot means of the k^{th}family, j^{th}provenances, i^{th}replicate

Duncan Multiple Range Test (DMRT) was undertaken to determine the differences in the effect of each treatment when the results of the analysis of variance show significant differences.

2.2. Genetic parameters

The mean family variance components were used to estimate mean covering individual tree heritability (denoted as h^2_i) separately for each trait as presented below [6, 7, 5]. Meanwhile, the progeny was assumed to be half sibs and additive genetic variance ($\sigma^2 A$) was estimated as $1/3(\sigma^2_f)$ genetic variance among families within provenances.

$$h^2_i = \frac{3\,\sigma^2_f}{\sigma^2_f + \sigma^2 b_f + \sigma^2_e}$$

where :

h^2_i = individual tree heritability
s^2_f = variance between families-within-provenances groups
s^2_{bf} = variance between families and replications
s^2_e = variance error
n = the mean of number of trees each plot
b = the mean of number of replications

Genetic correlations (denoted r_g) were calculated according methodologies described by [8] based on the following formula:

$$r_g = \frac{Cov_f(X,Y)}{[\sigma_f^2(x) \,.\, \sigma_f^2(y)]^{1/2}}$$

where :

$Cov_f(X,Y)$= covariance of the two traits at the family level
σ_f^2 (x) = family- level variance components of trait (x)
σ_f^2 (y) = family- level variance components of trait (y)
r_g = genetic correlations

The volume of trees was calculated using formula:

$$V = ¼\,\pi \times (D)^2 \times T \times f$$

where :

V = volume of tree (m^3)
D = stem diameter (cm)
T = height (m)
f = shape figures = 0.486 [9].

3. Result and Discussion

3.1. Growth parameters

Analysis of variance was performed to test the different of families and provenances in height, diameter and stem volume of the progeny test (Table 2). It showed that the height, diameter and volume were significantly different between the replications, families, provenances also the interactions between replications and provenances.

Table 2. The analysis of variance of height, diameter and volume 7 years old progeny test of *A. cunninghamii* in Bondowoso, East Java

Sources	DF	Mean Square		
		Height	Diameter	Volume
Block	3	73.32**	43.15**	0.019**
Provenances	5	7.90*	86.22**	0.009**
Family (Provenances)	74	9.01**	15.83**	0.004**
Block*Family (Provenances)	234	6.84**	6.18**	0.002**
Error	622	2.62	5.26	0.001

The significant difference between provenances of *A. cunninghamii* in terms of height and diameter was estimated due to the seed origin diversity impact. The DNA analysis of *A. cunninghamii* revealed the diversity of this species by RAPD (0.295); showing the genetic diversity still exists within population and large enough to support breeding activities. While the average genetic distance between populations is 0.194. It means that more than 85% of genetic diversity is distributed within the population, while the rest is located between populations [10]. This diversity indicated the potential genetic enhancement through selection activities can be done in this species. High levels of diversity were also found in younger *A. cunninghamii* progeny test ages 1 year, 2 years and 5 years old for the characters of tree height and stem diameter [11, 2] .

Meanwhile, in other conifer types, it was reported [12] that there was a high diversity in height and stem diameter among families in the 10-year-old *Pinus sylvestris* L progeny test in Sweden. High diversity in height and stem diameter among families also reported in the 15-year-old of *Pinus banksiana* Lamb progeny test [13] . The variation of growth i.e height and diameter were also reported several progeny test of *Agathis loranthifolia; Pinus sylvestris; Pinus strobus* L [14, 12].

In this study, the average of height and diameter growth of the *A. cunninghamii* is better than conifer species elsewhere. This is presumably due to the environmental conditions of the site are more in accordance with the location from which seeds were collected, thus the *A. cunninghamii* more easily adapt to local environmental conditions [15] . Several studies reported that, the average growth in height and diameter was only 15.92 m; 17. 43 cm in the 15 years old progeny test of *A. cunnighamii* [16], and in the 6 years old the average height and diameter was 6.37 m; 7.79 cm [17].

In general, the volume increment of each provenance of *A. cunninghamii* in this study showed good growth. The largest volume exhibited by *A. cunninghamii* from Fak-Fak (0.103 m3), whereas the smallest increment was originated from Queensland (0.079 m3). The difference in growth performance generally not only caused by differences in genetic material (type), but also caused by the differences in environmental factors, such as soil type and fertility, intensity of maintenance and climate factors, especially rainfall. On the other hand, Queensland's provenance originating from outside Indonesia that exhibited the lowest volume. Other studies on 21 years old *Araucaria angustifolia* progeny test was reported the lower average of volume (0.010 m3) and 6 years old progeny test of *A. cunninghamii* (0.011 m3) [18, 17]; and 15 years old of other conifer species (*Pinus caribaea var. Bahamensis*) is 0.0207 [19].

3.2. Genetic parameters

Predicted individual tree heritabilities and genetic correlation between growth in progeny test of *A. cunninghamii* at Sumberwringin test in Bondowoso, East Java are given in Table 3.

Table 3. Predicted individual tree heritabilities and genetic correlation between growth in progeny test of *A.cunninghamii* at Sumberwringin trial in Bondowoso , East Java

Traits	Individual tree heritability	Genetic correlation between height and diameter at 130 cm
Height	0.16	0.79
Diameter at 130 cm	0.30	

Genetic correlation between height and diameter in the progeny test were strongly associated, it appears that selection for diameter is likely to affect the height favorably. Individual heritability was considered moderate for growth (height and diameter) studied from the seven years measurement of progeny test of *A. cunninghamii* at Sumberwringin Bondowoso, East Java. The predicted individual heritability will be applied for selection trees in the progeny test to improve growth to obtain the best of genetic gain. The best genetic gains of growth can be used to improve Mean Annual Increment (MAI) of *A. cunninghamii.* Moderate heritability estimates on individual tree for height (r_g=0.28) also was found by [20] in the trial of 7-years old black pine in Vlachokerasia. The tree selection of black pine was able to improve the genetic gain to 24% for volume.

The significant difference between provenances of 7 years old progeny test of *A. cunninghamii* in Bondowoso, East Java indicates that the importance of choosing the right seed source. The variation in height and diameter growth between families is very significant. The best character and volume growth performance was were observed in families from Fak-Fak, Serui and Queensland, while the best diameter characters were observed in families from Serui, Fak-Fak, Wamena and Jayapura. The genetic variation among the families tested in this progeny test is high, allowing for a wide range of selection options in order to achieve optimum genetic enhancement. Estimated heritability of hight and diameter were consiered moderate to high, indicates that both traits measured are strongly controlled by genetic factors. The height and diameter are positively correlated, so the improvement of one trait will positively improve the other trait.

In order to determine the breeding strategy for *A. cunninghamii,* periodic evaluation needs to be done to obtain the information of the growth rate and the value of genetic parameters after the age of 7 years up to end of the cycle.

4. Conclusion

The significant difference between provenances of seven years old progeny test of *A. cunninghamii* in Bondowoso, East Java indicates that the importance of choosing the right seed source. The variation in height and diameter growth between families is very significant. The best character and volume growth performance were found in families from Fak-Fak, Serui and Queensland, while the best diameter characters were observed in families from Serui, Fak-Fak, Wamena and Jayapura. Genetic variation among families tested in this progeny test is high providing broad opportunities for selection in obtaining maximum genetic enhancement. Estimated heritability of height and diameter were moderate to high, indicates that both traits measured are strongly controlled by genetic factors. The height and diameter are positively correlated, so the improvement of one trait will positively improve the other trait.

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