

Early growth evaluation and estimation of heritability in a sengon (*Falcataria moluccana*) progeny testing at Kediri, East Java, Indonesia

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Abstract. Nugroho A, Matra DD, Siregar IZ, Haneda NF, Istikorini Y, Rahmawati R, Amin Y, Siregar UJ. 2021. Early growth evaluation and estimation of heritability in a sengon (*Falcataria moluccana*) progeny testing at Kediri, East Java, Indonesia. *Biodiversitas* 22: 2728-2736. Sengon (*Falcataria moluccana*) is widely cultivated as a monoculture plantation in community forests that still poses a high risk of pest and disease attacks. Although plants naturally show signs of resistance, there is still however a lack of understanding on the influence of relative plant resistance on growth due to environmental and genetic factors. This study was aimed to evaluate the early growth of a sengon progeny testing in Kediri, East Java and to estimate the genetic parameters with respect to its resistance and susceptibility to stem borer and rust disease. Progeny test was designed using randomized complete block design (RCBD) with four blocks as replications. Each block consists of 100 families which was grouped into two categories, 50 families for resistant group and 50 families for susceptible group. Observations were made at the age of 0 and 9 months after planting on 9 individuals per plot in each family. Growth characteristics were measured as germination (%), height (m), and diameter (cm). Results indicated that the sengon growth rate from resistant and susceptible plant groups showed a significant difference. Heritability values are classified as moderate, ranging between 0.107 to 0.133 and 0.102 to 0.150 for height and diameter variables, respectively. These information may be used for gradual selection by considering the appropriate intensity.

Keywords: Genetic parameter, growth, heritability, progeny test, sengon

Abbreviations: FMU: Forest Management Unit; FMR: Forest Management Resort, MAP: Months After Planting

INTRODUCTION

Sengon (*Falcataria moluccana* (Miq.) Barneby & J. Grimes) is a fast-growing species cultivated in plantations in Indonesia (Lelana et al. 2018; Rahayu et al. 2010; Rahmawati et al. 2019; Siregar 2007). Sengon has several notable properties, such as easy to cultivate, economically valuable, and is a type of legume that can fix nitrogen. The ability of legumes to fixate nitrogen has a positive influence on soil fertility Vanlauwe et al. (2019). Hence sengon species are widely used in reforestation and restoration programs (Iskandar and Ellen 2008). In 2019, the selling price of sengon sawn wood in Lampung is Rp 1,200,000 (US\$ 92) per m³ (Utama et al. 2019). Sengon wood can be used for house construction materials (Rahmawati et al. 2019), wooden crates, matches, and raw pulp material (Siregar et al. 2007).

High demand for sengon wood each year led to the expansion of monoculture sengon plantations. The drawback of monoculture is that the plant community will be vulnerable to pest and disease attacks. The most frequent pests and diseases that attack sengon plantations are boktor stem borer (*Xystrocera festiva*) and gall rust

disease (Endang and Haneda 2010; Siregar et al. 2019; Sunandar et al. 2017). Both these pests and disease types may simultaneously attack sengon, which initiate double losses (Darwiati and Anggraeni 2018). Therefore, to satisfy the growing industrial demand for sengon wood, a healthy and productive plantation must be established, particularly the one which has good resistance to pests and diseases. The use of high-quality seeds has been recommended to increase growth rate and resistance to pests and diseases. However, there is still a lack of seed sources established from a genetic trial for resistance to pests and diseases.

In 2020, a progeny trial plot at the Perum Perhutani Kediri Forest Management Unit (FMU) was established using 50 resistant plant families and 50 susceptible plant families to boktor stem borers and gall rust disease. The trial was made to obtain data and information on the growth rate of sengon plants and associated genetic parameters that affect their growth and resistance to pest and disease are lacking. The heritability is estimated based on a population of genetic testing (e.g. breeding population) and be used later for considering a gradual selection and evaluation to produce improved seeds (Zobel and Talbert 1984; Mashudi and Susanto 2016). This study

aims to evaluate the early growth of sengon progeny testing in Kediri, East Java, and to estimate the genetic parameters with respect to its resistance and susceptibility to stem borer and rust disease. Our study is expected to provide information about early evaluation growth of sengon progeny trial for improving *F. moluccana* seeds that are relatively resistant from stem borer and gall rust.

MATERIALS AND METHODS

Seed extraction and preparation

The seeds of *F. moluccana* were collected from Jatirejo Forest Management Resort (FMR), Perum Perhutani, Kediri FMU in January 2018. The seeds were collected from 100 mother trees consisting of 50 boktor and gall rust-resistant plant groups and 50 susceptible plant groups (e.g. 17 boktor prone trees, 17 gall rust-prone trees, and 16 susceptible trees to both). Susceptible trees referred to those trees that were severely attacked by either boktor pest or gall rust, while resistant trees were the trees as control showing no signs of the pest and disease attacks

(Siregar *et al.* 2019). The seeds as control were extracted from adjacent trees and grow on the same plot to minimize environmental influences. The seeds from each family were then immersed in hot water (80 °C) for 5 minutes and then soaked in cold water for 24 hours as priming treatment. After that, the seeds from each family were sown in sowing boxes filled with sand in March 2020. After 14 days, the seedlings with a height of 5 cm, having at least two leaves are transferred to polybags with a media mixture of soil, compost, and husk charcoal (2: 1: 1).

Study area

The sengon progeny trial plot is located in compartment 125D of the Pandantoyo FMR, Perum Perhutani Kediri FMU, East Java (07° 56' 57" S, 112° 11' 42" E) (Figure 1). The plots are stationed at 461 masl with climate type C based on Schmidt and Ferguson, which has an average rainfall of 2.301 mm/year with two peaks of rainy seasons around January and December, and a dry period during July-August (Figure 2), the type of soil at the study site is latosol (Perum Perhutani 2015).

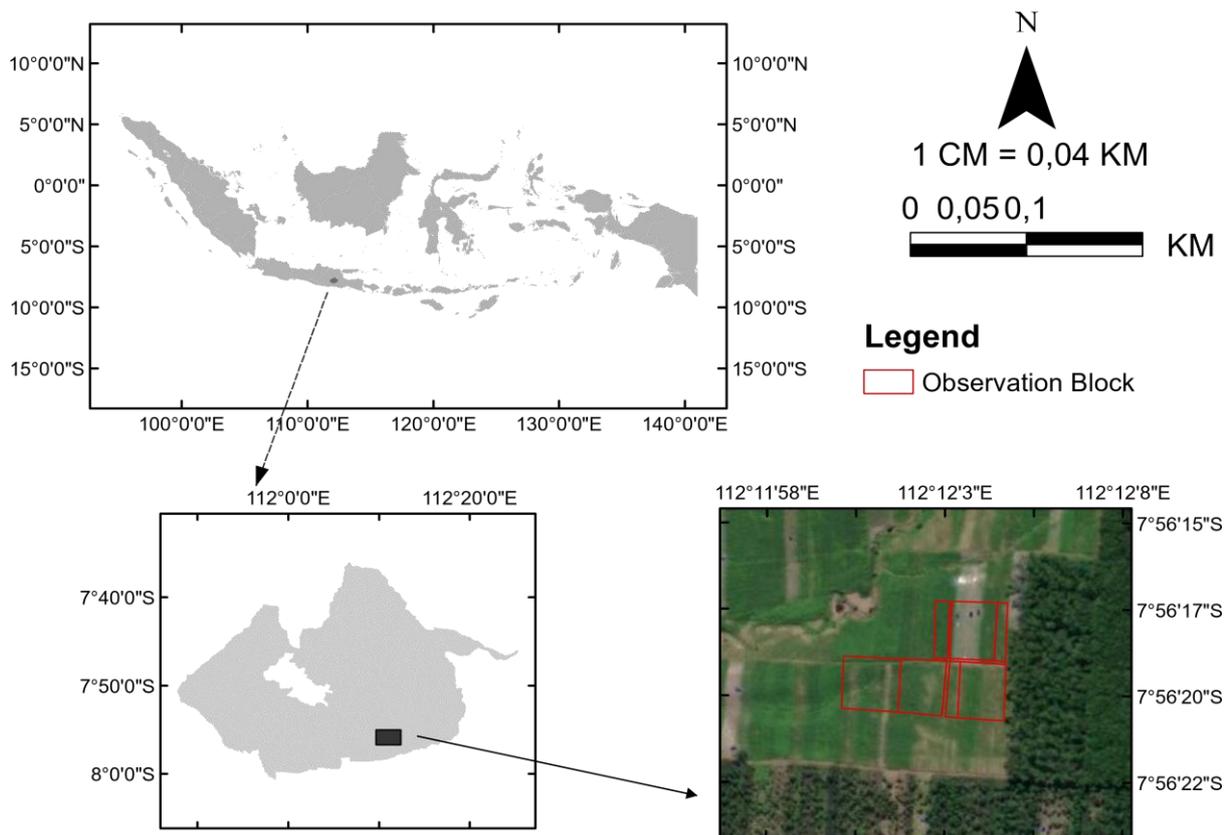


Figure 1. Location of sengon progeny testing plots in Perum Perhutani Kediri FMU, East Java, Indonesia

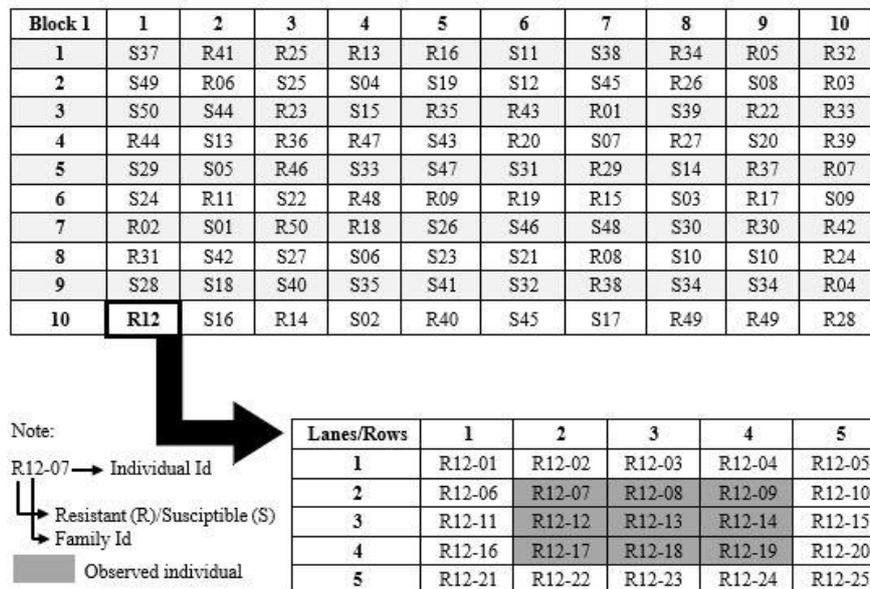


Figure 3. The layout of planting and collecting progeny data in block 1

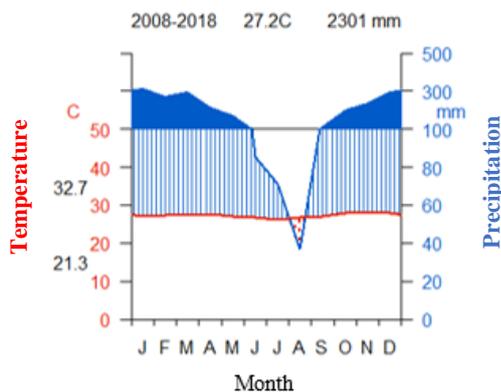


Figure 2. Average monthly temperature and precipitation at Kediri from 2008 to 2018. The relationship of average monthly precipitation (solid and striped blue) to average monthly temperature (red line).

Experimental design

Progeny test was designed using randomized complete block design (RCBD) with four blocks as replications. Each block consists of 100 families which was grouped into two categories, 50 families for resistant group and 50 families for susceptible group. The planting of seedlings used a spacing of 3 m x 2 m with 25 tree square plots. However, observations were only made on inner 9 individual trees (Figure 3). Preparation of the planting area is carried out before planting. Area preparation activities include cleaning the area, making and installing stakes, making planting holes, and adding compost. Cleaning the planting area is carried out to remove shrubs, weeds, and previous plant debris. Furthermore, the soil is hoed so that it is loose and easy to cultivate. The stake is made using bamboo, the length of the stake is 1 meter. The stake is fixed as a sign where the sengon seedlings must be planted,

therefore fixed the stake must be in accordance with the specified spacing. The planting hole is made with a size of 20x20x20 cm right at the stake that has been fixed. For each planting hole, 2 kg of compost is added. The addition of compost is expected to increase the availability of organic matter in the soil.

Character observed

The study began with seed monitoring, the number of germinated seeds was recorded to calculate the germination rate (Sudrajat et al. 2015) of each family with the following formula:

$$PG = \frac{\sum NG I + \sum NG II}{\sum TS} \times 100\%$$

Where: PG = percentage of germination, NG I = Normal number of germinants on the first day of observation, NG II = number of normal germinants on the second day of observation, TS = Total number of seeds sown. Sengon plant growth properties measured in the progeny test plot were the diameter (10 cm from the base of the stem) and plant height. The seedling diameter was measured using a caliper, while the height was measured using a measuring pole from the ground to the top of plants (apical). Diameter and height measurements were carried out in July 2020 and April 2021.

Data analysis

The data obtained were then analyzed to determine the average plant growth, diversity of traits among the families tested, estimated heritability values and genetic correlations between observed traits. Analysis of variance (ANOVA) using Agricole package (R statistics) on each variable was carried out with the following statistical models:

$$Y_{ijkl} = \mu + B_i + R_j + F(R)_{k(j)} + BR_{ij} + BF(R)_{ik(j)} + E_{l(ijk)}$$

where, Y_{ijkl} = observation in the l -th individual of the k -th family of the j -th resistance in the i -block; μ = means; B_i = random effect of block i ($i = 1, 2, 3, 4$); R_j = random effect of resistance j ($j =$ resistance, susceptible); $F(R)_{k(j)}$ = the k -th family random effect ($k = 1, 2, \dots, 100$) on the j th resistance; BR_{ij} = interaction effect between i -th block and j -resistance; $BF(R)_{ik(j)}$ = the interaction between the i -th block and the k -th family in the j -th resistance in the j -block; $E_{l(ijk)}$ = random effect of the l -individual ($l = 1, 2, \dots, 9$) the k -th family on the j -th resistance in the i -block.

Genetic parameters

Heritability is suspected from various component components (Falconer and Mackay 1996). The average heritability of individuals and families for each character is measured using the following formulas:

$$h^2_i = \frac{4\sigma^2_f}{\sigma^2_e + \sigma^2_{fb} + \sigma^2_f}; h^2_f = \frac{\sigma^2_f}{\frac{\sigma^2_e}{bt} + \frac{\sigma^2_{fb}}{t} + \sigma^2_f}$$

Where: h^2_i = individual heritability, h^2_f = family heritability, σ^2_f = family variety, σ^2_{fb} = interaction range between family and block, σ^2_e = residual range, b = number of blocks, t = number of blocks tree per plot.

Phenotypic and genetic correlations of the variance and covariance components are substituted into a standard formula for the moment product correlation coefficient:

$$R_p(xy) = \frac{COVP(xy)}{\sqrt{\sigma^2_p(x) + \sigma^2_p(y)}}; R_g(xy) = \frac{COVf(x,y)}{\sqrt{\sigma^2_f(x) + \sigma^2_f(y)}}$$

Where x = tree height; y = diameter; $\sigma^2(x)$ and $\sigma^2_f(x)$ = variance of phenotypic and genotypic products of x parameters; $\sigma^2_p(y)$ and $\sigma^2_f(y)$ = variance of the phenotypic and genotypic products of the parameter y ; $COVP(xy)$ and $COVf(x,y)$ = the covariance component of the phenotypic and genotypic products of the parameters x and y , respectively, while the covariance component of the properties of x and y is calculated by the formula (O'Neill et al. 2001):

$$COVf(x,y) = 0.5(\sigma^2_{f(x+y)} - \sigma^2_{f(x)} - \sigma^2_{f(y)})$$

Where: $\sigma^2_{f(x)}$ = Components of the various properties of x and y , σ = Variable components of the x family properties, σ = Variable component of the y family.

RESULTS AND DISCUSSION

Growth variation

The critical aspect of the plant breeding program is variations. Variance analysis is carried out to see the information of the variability that occurs among tree growth factors. Variance analysis for height and diameter variables of the sengon plant are shown in Table 1.

In the 0 MAP (months after planting) and 9 MAP sengon progeny test, the family, resistance, and interaction between block and resistance (resistant and susceptible) significantly affected both the height and diameter variables. The value of family and resistance variations indicates that the genetic variation expressed by sengon growth is relatively vast. A vast genetic variation will enable the selection process to produce better genotypes (Jalata et al. 2011). On the other hand, the interaction between block and resistance shows that the growth of sengon is not solely influenced by genetic factors but also by environmental factors.

The initial growth of resistant sengon plants has a higher average value than susceptible sengon plants for each variable (Figure 4). The resistant family group has average germination of 61.16% and 55.24% in the susceptible family group (Figure 4a). The mean plant heights at 0 MAP and 9 MAP for resistant and susceptible groups were 0.64 m, 3.50 m, 0.53 m, and 3.07 m, respectively (Figure 4b). Meanwhile, the average plant diameter was 1.57 cm, 3.24 cm, 1.27 cm, and 2.83 cm, respectively (Figure 4c).

Top ten family

Each family of the two populations group has a different growth rate. The ranking is an essential aspect of plant breeding programs because it shows the performance of each family which can later be used for the selection process. We separated the best families from the resistant and susceptible groups. Table 2 and Table 3 presents the results of the ten best families for the observed variables. The prominent families for the germination rate variable, R33 and S3 families possess the highest average value. In the height variable, the family was consistent into the top ten families at the age of 0 MAP and 9 MAP, namely R4, R12, and S25. On the other hand, R12, R4, R15, S25, and S27 families consistently had the top ten average in respect of diameter.

Table 1. Mean square for growth performance in sengon progeny test

Age	Source of variation	Degree of freedom	Height (m)	Diameter (cm)
0 MAP	Resistance	1	10.029**	8.315**
	Block	3	0.266**	0.035*
	Family(Resistance)	99	0.944**	0.427**
	Block* Resistance	3	0.027*	0.212**
	Block*Family(Resistance)	297	0.017**	0.057**
	Error	3200	0.010	0.006
9 MAP	Resistance	1	39.468**	40.710**
	Block	3	5.821**	9.785**
	Family(Resistance)	99	1.632**	1.926**
	Block* Resistance	3	1.509**	1.030**
	Block*Family(Resistance)	297	1.305 ^{ns}	1.628 ^{ns}
	Error	3200	0.639	0.570

Note: ** = highly significant at $p < 0.01$, * = significant at $p < 0.05$, ns = not significant, MAP = months after planting

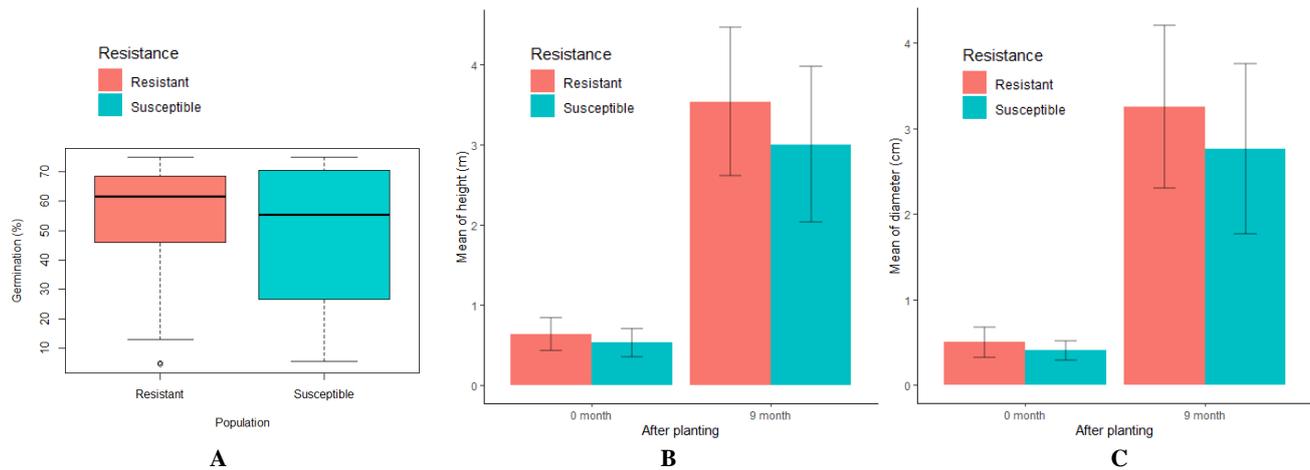


Figure 4. Performance of plant growth in sengon progeny test: A. Germination percentage, B. Height, C. Diameter

Genetic parameters

Estimation of heritability value is required to obtain information on the proportion of genetic factors contribution passed down from the main plant to its progeny. Heritability value is obtained from a comparison between the additive variants and the total phenotypic variants. The approximation of family heritability (h_f) on height and diameter variables is higher than individual heritability (h_i), further illustrated in Table 4. Heritabilities estimation in this study ranged from 0.102 to 0.150. Cotterill and Dean (1990), state that the heritability is considered high should the value is more than 0.3, for moderate heritability is between 0.1 to 0.3, and low heritability is less than 0.1.

Besides heritability value, the selection process in the progeny test is affected by genetic correlations between traits. This value is essential in determining the prediction of the influence and the effectiveness of a trait selection. Table 5 shows that the phenotypic correlation gives a greater value than the genetic correlation between the height and diameter variables of the sengon progeny test.

Discussion

Growth is the process of increasing the size of organic system forms (Azizah et al. 2019). Plant growth is influenced by several aspects such as genetic information, environmental condition, and interactions of internal or external factors. The variables of germination rate, height, and diameter of resistant and susceptible sengon group displayed existing variations among families. The observed differences in growth rate presumably due to differences in the genetic material used. Johnson and Lenhard (2011) stated that plant growth is controlled by genetics, thus differences in genetic formation will affect the appearance

of a particular character. Analysis of genetic diversity using RAPD, SSR, and SNP markers showed grouping between susceptible and resistant sengon plants (Shabrina 2020; Rahmawati 2017; Siregar et al. 2019; Yuskianti and Shiraishi 2017). Shabrina et al. (2019a) supported this result, which found variances in gene expression in prime sengon plants against sengon plants with gall rust through differential expression gene (DEG) analysis. The results of this study indicate that there is an expression of growth inhibitor genes in plants infected by gall rust, such as Retrovirus-related Pol polyprotein from transposon RE2 which plays a role in the synthesis of aspartic protease leads to dwarfing phenomenon in plants (Xia et al. 2004) and Cytokinin dehydrogenase causing cytokinin deficiency in plant tissue (Werner et al. 2003). Whereas in resistant plants group, transcription factor and Ubiquitin carboxyl-terminal hydrolase 13 genes were found which have a role in plant resistance to pathogens (Shabrina et al. 2019b).

Table 2. The ten prominent families based on the variables of germination rate in sengon progeny test

Ranking	Resistant group	Susceptible group
1	R33 (75)	S3 (75)
2	R37 (75)	S5 (75)
3	R22 (73.5)	S8 (75)
4	R13(73)	S15 (75)
5	R8 (72.5)	S16 (75)
6	R4 (72)	S21 (75)
7	R19 (72)	S23 (75)
8	R6 (71.5)	S35 (75)
9	R20 (71.5)	S17 (74)
10	R27 (71.5)	S13 (73)

Table 3. The ten prominent families based on the variables of height and diameter in the sengon progeny test

	Ranking	Resistant group		Susceptible group	
		Height (m)	Diameter (cm)	Height (m)	Diameter (cm)
0 MAP	1	R10 (1.11a)	R9 (0.74a)	S45 (0.93a)	S45 (0.68a)
	2	R9(1.06a)	R8 (0.70b)	S25 (0.78b)	S38 (0.67abc)
	3	R16 (0.97b)	R12 (0.68b)	S35 (0.75cb)	S25 (0.67abc)
	4	R8 (0.97b)	R10 (0.67b)	S26 (0.75cb)	S27 (0.66abcd)
	5	R12 (0.90c)	R6 (0.67c)	S27 (0.75cb)	S26 (0.65abcd)
	6	R11 (0.86cd)	R11 (0.62c)	S44 (0.74cb)	S44 (0.65bcd)
	7	R17 (0.86cd)	R4 (0.61d)	S24 (0.73cd)	S36 (0.65bcd)
	8	R6 (0.83de)	R15 (0.60ed)	S36 (0.72cd)	S35 (0.65bcd)
	9	R23 (0.80fe)	R16 (0.58edf)	S32 (0.72cd)	S32 (0.65bcd)
	10	R4 (0.76fg)	R23 (0.58fg)	S4 (0.69de)	S4 (0.65bcd)
9 MAP	1	R24 (3.34a)	R24 (3.41a)	S23 (3.18a)	S7 (3.26a)
	2	R32 (2.91ab)	R39 (3.31a)	S47 (2.97a)	S5 (3.16ab)
	3	R39 (2.83ab)	R4 (3.22ab)	S7 (2.96b)	S25 (3.13abc)
	4	R4 (2.77b)	R32 (2.83ab)	S28 (2.86b)	S47 (3.12bc)
	5	R30 (2.76b)	R30 (2.82b)	S15 (2.79c)	S15 (3.00bc)
	6	R47 (2.69bc)	R12 (2.75bc)	S5 (2.68cd)	S49 (2.81d)
	7	R15 (2.60c)	R47 (2.75c)	S19 (2.61d)	S13 (2.81de)
	8	R40 (2.49cd)	R15 (2.73de)	S25 (2.56de)	S28 (2.80def)
	9	R36 (2.49cd)	R36 (2.69e)	S50 (2.46de)	S27 (2.63e)
	10	R12 (2.48e)	R49 (2.67f)	S10 (2.39f)	S37 (2.56ef)

Note: The mean value followed by a different superscript on the same columns is significantly different ($P < 0.05$), MAP = months after planting

Table 4. Estimated heritability in sengon progeny test

Age	Individual heritability (h^2_i)		Family heritability (h^2_f)	
	Height	Diameter	Height	Diameter
	0 MAP	0.129	0.137	0.133
9 MAP	0.114	0.102	0.131	0.107

Table 5. Coefficient of genetic correlation (upper diagonal) and phenotypic (lower diagonal) between variables in sengon progeny test

	0 MAP		9 MAP	
	Height	Diameter	Height	Diameter
Height	-	0.311	-	0.130
Diameter	0.506	-	0.693	-

The height and diameter measurement results for both resistant and susceptible sengon groups in this study showed a growth rate in line with age. Hadiyan (2010a) reported that the growth of 4-month-old sengon in Cikampek, West Java, which had the highest average height of 1.98 m and diameter of 0.93 cm. At 12-months-old showed an average height of 2.37 m and a diameter of 4.15 cm (Hadiyan 2010b). Besides being influenced by the genetic material, the variations in the measured variables are influenced by the condition of the research location. Sengon requires a wet climate and loose soil to support its growth (Krisnawati et al. 2011). While differences in the germination rate of each family assumably due to the

diversity in seed quality. According to Yuniarti et al. (2013) and Suharsi et al. (2016), seed quality is influenced by its physical, physiological, and genetic quality. Seed originating from a non-breeding mother tree will produce seeds with low viability. The results of the observation of germination showed that the highest percentage germinated was only 75% (Table 2). The seeds used are seeds that have been stored for 25 months. According to Baskorowati et al. (2017a), a long storage time will reduce the viability of seeds. This happens because during the storage process, the seeds will experience deterioration which causes a decrease in the quality of the seeds.

Seeds family, resistance, and interaction between block and resistance significantly influence both the height and diameter variables. A similar result was found in the 12 months after planting *F. moluccana* (Hardiyanto 2012), 11 months after planting *E. urophylla* (Sumardi et al. 2016), and 12 and 54 months after planting *N. cadamba* (Sudrajat et al. 2016). The value of family variation shows the level of genetic variation of the main tree. Family, resistance, and interaction between block and resistance indicate that the genetic variation expressed by sengon growth is relatively vast. According to Hamrick et al. (1992), species that interbreed with high genetic variation in species and populations in general. Genetic variations are required to improve the adaptability of plants to new environments or pests and diseases (Rahayu et al. 2010).

This study found ten prominent families as shown in Table 3. Family R4 and R12 have been admitted to be the finest family to breed because the two families are always included in the top ten on all variables. Also, R4 and R12 sengon families can be considered to select mother tree candidates. Mahfudz et al. (2010) describe that variations

in the traits of height and diameter growth at the family level are strongly influenced by genetic factors. Thus, traits of plant height and diameter are used as selection criteria for obtaining a productive sengon plant breed that is resistant to pests and diseases. While families with poor growth rates become the plant candidates intended for thinning activities. Thinning will reduce competition between plants and trigger a significant increase in plant growth (Kang et al. 2014; Gradel et al. 2017).

The heritability estimation value in this study was categorized as moderate for height and diameter variables (Table 4). Heritabilities illustrate the proportion of various phenotypic traits associated with genetic effects and are used as a parameter of previous mother tree phenotypes diversity that might be inherited in the next progeny (Edwards 2018). Heritability values ranged from 0 to 1. If the heritability value is close to 1 (one), it means that heritability is high, meaning that genetic factors influence the character's appearance. If the heritability value is close to 0 (null), heritability is low, meaning the character's appearance is influenced by environmental factors (Anna et al. 2020). Family heritability values were found to be greater than individual heritability values (Table 4), indicating that the probability of genetic acquisition would be higher by the selection process between families rather than individual selection. As plants age, their heritability tends to decrease. Rahayu et al. (2020) reported that the individual heritability values for the height of the two months after planting sengon plant were 0.79 and 0.14 in the three months after planting, whereas Setiadi et al. (2014) reported that at eight months after planting sengon plant the heritability was 0.08. Decreasing heritability value during the increasing plant lifetime is due to the phenotype diversity rate of additional diversity (Surlles et al. 1995). Besides being affected by plant maturity, heritability is also influenced by the number of experimental units (individuals per family) and the number of replications/blocks. Greater experimental and test units in the total lead to greater heritability value (Russel and Libby 1986).

The correlation of phenotypes and genotypes between height and diameter characters has positive values. Comparable results were found in 6-months after planting *E. cloeziana* (Li et al. 2016), 12 (Hardiyanto 2012) and 18 months after planting (Baskorowati et al. 2017b) *F. moluccana* and 54 months after planting *N. cadamba* (Chaerani et al. 2019). This reflects a linear relationship, an increase will consecutively follow the plant height variable in diameter value. According to Sudrajat et al. (2015), a greater phenotypic correlation value than genetic correlation explains that breed selection will be more effective with height and diameter traits are combined into account. Plant diameter and height are satisfactory criteria in tree breeding programs (Mulyadiana et al. 2020).

The 0 MAP and 9 MAP sengon growth of resistant and susceptible plant groups demonstrate a significant difference. Heritability values are classified as moderate in the category, with heritability values in height variable ranging between 0.129 to 0.133 (0 MAP) and 0.114 to 0.131 (9 MAP), 0.137 to 0.150 (0 MAP) and 0.102 to 0.107

(9 MAP) in diameter variables. The correlation of phenotypes and genotypes between height and diameter characters has positive values. These information may be used for gradual selection by considering the appropriate intensity. Future research is suggested to repeat the study to progeny test the *F. moluccana* using a similar method at an older age.

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