Jurnal Riset Biologi dan Aplikasinya, Volume 7, Issue 1, March 2025

Jurnal Riset Biologi dan Aplikasinya
https://journal.unesa.ac.id/index.php/risetbiologi

Genetic Variation of F2 Progeny Test *Acacia auriculiformis* A. Cunn. Ex Benth. at KHDTK Blok Playen, Gunungkidul

Prasojo Katon Dewanto[1], Supriyadi[1], Malihatun Nufus[1*], Dwi Siwi Yuliastuti[2]
[1]Study Program of Forest Management, Faculty of Agriculture, Universitas Sebelas Maret (UNS)
Surakarta, Indonesia, 57126
[2]Center for Standard Testing of Forestry Instruments (BBPSIK), Purwobinangun, Pakem, Sleman, Yogyakarta, Indonesia, 55582
* Corresponding author, e-mail: malihatunufus@staff.uns.ac.id

Article History

Received	:	18 February 2025
Revised	:	20 March 2025
Accepted	:	27 March 2025
Published	:	31 March 2025

Keywords

Forest improvement; genetic gain; heritability; tree breeding

ABSTRACT

Acacia auriculiformis is one of a priority species for forestry in Indonesia. This species has great potential. Breeding of the *A. auriculiformis* species in KHDTK Blok Playen, Gunungkidul, has reached the second-generation breeding cycle. Further evaluation of the *A. auriculiformis* progeny test planting in KHDTK Block Playen is needed to develop a certified and more optimal seedling seed orchard. This study aimed to evaluate the growth of 9-year-old *A. auriculiformis* progeny test in KHDTK Blok Playen, Gunungkidul. Data collection of tree growth included total height, diameter, branch-free stem height, and stem straightness. Measurements were conducted using the census method on 30 families with four tree plots in 12 blocks of F2 *A. auriculiformis* progeny test at the KHDTK Blok Playen. The results of the analysis of variance show that the family source of variation significantly affected the four growth characteristics observed. These results indicate that genetic factors greatly influence the diversity or variation in the measured characters. Strong phenotypic correlation was found between height with diameter character (0,569) and the branch-free stem height with a stem-straightness (0,633). In general, the family and individual heritability values in this study were classified as high. The genetic gain from individual selection (within plot selection) at 25% intensity showed moderate to very high values, ranging from 3.123%-16.494% for the four observed characteristics.

How to cite: Dewanto, P. K., Supriyadi, Nufus. M., & Yuliastuti, D. S. (2025). Genetic Variation of F2 Progeny Test *Acacia Auriculiformis* A. Cunn. Ex Benth. at KHDTK Blok Playen Gunungkidul. *Jurnal Riset Biologi dan Aplikasinya*, 7(1):99-109. DOI: 10.26740/jrba. V7n1.p.99-109.

INTRODUCTION

One of the requirements for the successful development of plantation forests in the future is the provision of high-quality seeds, which are superior in genetic quality and adaptability to the environment in which they grow. Such seeds will improve tree quality, wood production, and resistance to pests and diseases while also shortening the growth cycle (Leksono, 2016). In other words, high-quality seeds are an effective input for plantation forest development.

The government has regulated efforts to provide superior quality seeds through the Minister of Forestry Regulation P.1/Menhut-II/2009, concerning the Implementation of Forest Plant Seeds by developing genetic resources to protect, maintain, and ensure the availability of genetic material. The development of these genetic resources is carried out through 3 stages: determining priority species, observing genetic variation, and conserving genetic resources. The determination of priority species has been regulated in the Decree of the Director General of Watershed Management and Social Forestry (BPDASPS) SK.62/V-SET/2014 on Priority Forest Tree Species in the Context of Genetic Resources Development and Development of Superior Seed Sources. The priority species included in the decree are Acacia species in the Sumatra bioregion group and the Maluku Papua bioregion. One of the species is *Acacia auriculiformis*, a species of acacia originating from wet tropical forests in the north of the Australian continent, Papua New Guinea, and the Maluku islands of Indonesia (Kariming & Zulkifly, 2023).

In the Development of Watershed Management and Social Forestry (BPDASPS) Decree No. 62 of 2014, *Acacia* sp. is the priority species of forest trees that are used as materials for woodworking, tools, and plywood, as well as raw materials for pulp and paper, fiberboard, and particle board, and for renewable energy production. Specifically, *A. auriculiformis* is also one of the fast-growing species that is very suitable for land rehabilitation because of its roots' ability to form symbiotic relationships with N-fixing bacteria. Its wood is ideal for firewood, charcoal, and light building construction (Sunarti et al, 2013). In addition, *A. auriculiformis* can also be used as a raw material for particle boards, a source of tannin as a tanning agent, a raw material for adhesives, and its polyphenol content can be used as an inhibitor of the corrosion rate of its bark (Mutiar et al., 2020). Given the numerous applications of *Acacia* species, a breeding program is needed to increase productivity and improve the desired growth characteristics, both in terms of wood quality and incremental growth.

The tree breeding program is one of the steps in plantation forest development to achieve optimal conditions by using genetic principles to improve plant traits (Handayani et al., 2018). One of the activities carried out in the tree breeding program is the testing of a tree stand. The test treatment in silviculture plantations helps assess and evaluate the quality and performance of trees, with one method being progeny testing. The progeny test is intended to estimate the breeding value of parent trees by comparing the performance of their offspring. In addition, the assessment of parent trees become more accurate because the number of offspring from each parent is evaluated under environmental conditions that are more controlled than the environmental conditions in which the parents are located (Hardiyanto, 2010).

Special Purpose Forest Area (KHDTK) Blok Playen, Gunungkidul is a location to develop seed sources from introduced trees with good quality. One of the species developed in KHDTK Blok Playen is *A. auriculiformis.* Breeding of *Acacia* species, especially *Acacia auriculiformis* in KHDTK Blok Playen, Gunungkidul has been carried out up to the second generation breeding cycle using introduced species from Papua New Guinea and Queensland, Australia. The growth of this progeny test was evaluated previously when the trees were 18 months old after planting, with measurements taken for height, diameter at breast height (DBH), and stem shape. The results showed high genetic diversity in all observed traits. The individual heritability value ranged from 0.140 to 0.309, while the family heritability ranged from 0.763 to 0.840 (Handayani et al., 2018). After this study, no further evaluation have been performed on the plants at productive age. In this study, the evaluation was conducted at the age of 9 years because *A. auriculiformis* starts to produce seeds at 4-5 years of age. In addition, at 10-12 years old, *A. auriculiformis* reaches its full productive capacity, yielding a high volume of growth increment (Schmerbeck, 2014). Therefore, further evaluation of the *A. auriculiformis* progeny test plantation at KHDTK Playen is needed to develop a certified and more optimized seedling nursery. This study aimed to evaluate the growth of 9-year-old *A. auriculiformis* progeny test in KHDTK Blok Playen, Gunungkidul.

MATERIALS AND METHODS

Study Area

The research was conducted on *A. auriculiformis* progeny test plantation stands constructed with a randomized complete block design (RCBD), comprising 30 families, 12 blocks, and 4 trees per plot (total 1440 trees), with a spacing of 3 x 1.5 meters in Special Purpose Forest Area (KHDTK) Blok Playen, Banyusuco Village, Playen District, Gunungkidul Regency, Yogyakarta Special Region Province. Data collection on tree growth, including total height, branch-free stem height (TBBC), stem diameter, and stem straightness, were carried out from July to August 2024.

Data Collection

Field data collection in this study included quantitative and qualitative characteristics. Quantitative traits measured for tree were total tree height, diameter, and branch-free stem height (TBBC). Qualitative trait of the trees measured was stem straightness scoring. Measurements were done using the census method on 1440 trees in 12 blocks of the F2 progeny test of *A. auriculiformis* in KHDTK Blok Playen (Figure 1).

Data Analysis

Analysis of Variance

The data collected from measurements and observations in the field were then statistically analyzed using analysis of variance. Data analysis was performed using R-Studio software.

Phenotypic Correlation Between Characters

Phenotypic correlations between characters can be estimated using the standard formula for Pearson's moment product correlation coefficient. Correlations were analyzed using R-Studio Software. Before the correlation analysis, the data was tested for normality and met the normality assumption. The strength of the correlation coefficient between characters was classified as very weak (0.00 - 0.19), weak correlation (0.20 - 0.39), moderate correlation (0.40 - 0.55), strong correlation (0.56 - 0.75), and very strong correlation (0.76 - 1.00).

Heritability

Heritability values were calculated to determine the growth of height, TBBC, diameter, and stem straightness influenced by environmental factors, genetics, and their interaction. According to Zobel and Talbert (1984), the calculation of heritability in a narrow sense (narrow-sense heritability), the ratio of the total additive genetic variance to the phenotypic variance was used, as follows:

$$h^2i = \frac{4\sigma_f^2}{\sigma_f^2+\sigma_{fb}^2+\sigma_e^2}$$

$$h^2f = \frac{\sigma_f^2}{\sigma_f^2+\frac{\sigma_{fb}^2}{b}+\frac{\sigma_e^2}{nb}}$$

$$h^2w = \frac{3\sigma_f^2}{\sigma_e^2}$$

Note:

h^2i = Individual heritability
h^2f = Family heritability
h^2w = Heritability within families
σ_f^2 = Variance of families
σ_{fb}^2 = Variance of families and block interactions
σ_e^2 = Variance of error
n = Number of trees per plot
b = Number of blocks

Genetic Advance and Genetic Gain

The estimation of genetic progress and genetic gain values in the progeny test was used to express the response to selection. The genetic advance and genetic gain values in this study were estimated with selection ratios of 75%, 50% and 25%, leaving 3, 2, and 1 tree from 4 tree plots, respectively. Within-plot selection was used to retain the best performing individuals in each plot. Genetic gain in response to selection was estimated using Falconer's (1981) formula:

$$R = I \times h^2w \times \sigma_w$$

$$R\,(\%) = \frac{R}{\bar{x}} \times 100\%$$

Where:

R = genetic advance
R (%) = genetic gain
h^2w = heritability within families
I = Intensity of selection 75% (I=0,1763 (Becker, 1992)
Intensity of selection 50% (I=0,5207 (Becker, 1992)).
Intensity of selection 25% (I=1,0558 (Becker, 1992)).
σ_w = phenotypic standard deviation
$\bar{x}$ = average character value

RESULTS AND DISCUSSION

Genetic Variation of Growth

The growth of tree stands in the *A. auriculiformis* progeny test showed diversity, both in the growth of progeny that showed a positive trend (superior) and another that showed a negative trend (poor). The average growth of each progeny family tested is presented in Table 1. The different growth expression of each plant is caused by genetic factors and its adaptability to the environment. An environment that is suitable for the characteristics of a plant species will produce more optimal plant growth. In accordance with the statement of Prehaten et al. (2018), the performance of a plant species, whether good or poor, is influenced not only by internal factors, such as the genetic properties and physiological properties of trees, but also by external . factors, including soil and climate conditions.

The growth of the 9-year-old *A. auriculiformis* progeny test in KHDTK Blok Playen was analyzed using analysis of variance (ANOVA). The result shows the presence of growth variation, with significant or insignificant sources of variation observed in the blocks and families for each character measured, including growth in height, diameter, branch-free stem height, and stem straightness. The

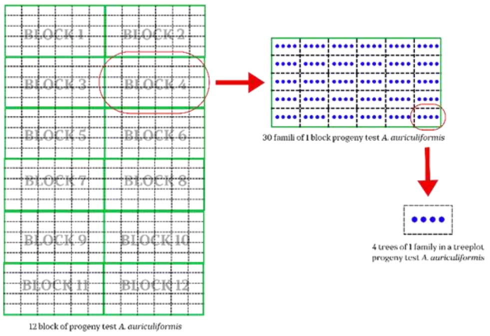

Figure 1. Details design of progeny test *A. auriculiformis* in KHDTK Blok Playen

Table 1. The average of each character of *A. auriculiformis* trees stand in KHDTK Blok Playen

Family	Average			
	Height (m)	Diameter (cm)	TBBC (m)	SS (score)
2	15.53	10.15	4.43	69.77
3	16.55	13.43	4.79	67.91
4	17.30	13.77	5.23	69.13
7	15.93	11.39	5.19	71.00
9	16.40	12.47	3.97	68.84
10	16.30	12.66	6.49	77.67
11	17.07	13.07	5.35	75.71
12	17.01	13.61	5.56	74.67
13	16.58	14.13	4.53	73.33
14	16.69	12.73	4.77	74.63
15	16.54	12.98	6.29	77.14
16	17.26	13.43	5.65	75.24
18	16.69	13.42	4.66	68.70
19	13.96	10.09	4.82	69.73
20	15.15	12.30	3.48	61.05
23	15.91	11.10	4.03	67.14
24	16.35	12.00	3.89	70.24
25	16.69	13.64	6.62	79.09
26	15.63	11.55	4.77	63.50
27	15.75	12.17	6.21	72.82
28	16.01	11.90	3.34	57.56
29	16.26	12.99	6.06	78.05
31	16.25	14.02	3.74	65.65
32	16.21	12.07	5.16	69.55
33	15.88	9.75	5.13	80.00
35	14.82	10.61	4.81	73.66
36	15.46	12.02	3.54	64.19
37	17.19	12.73	5.74	77.33
38	15.95	11.41	4.17	67.39
39	16.68	13.07	5.53	77.27

Note: TBBC = Branch-free stem height, SS = Stem straightness

variance analysis in this study was used to determine other genetic parameters in tree breeding programs. The results of the variance analysis of *A. auriculiformis* plants are presented in Table 2. Based on Table 2, the results of the analysis of variance for the block source of variation (environment) demonstrate a significant influence on the growth characters of height, diameter, and stem straightness. These results indicate that diversity or variation in these three characters is strongly influenced by environmental factors that control genes. Quantitative traits (height, diameter, or angle that forms the straightness of the stem) are phenotypic characters that emerge from a complex growth process controlled by several additive and non-additive genes (Larasati et al., 2024). In the growth of *A. auriculiformis*, there is a block (environmental) influence on the growth characteristics of plant height and diameter, according to Toaha & Beddu (2024), because additive genes ppredominantly influence growth characteristics,such as height and diameter, which are more susceptible to environmental control . In addition, the block effect on diameter growth in this study was also influenced by the planting distance of *A. auriculiformis* (1.5 m x 3 m), which was inconsistent because the number of individuals in each block was different due to the number of dead and non-growing stands that minimized competition for growing space between *A. auriculiformis* plants.

According to Maulidan et al. (2021), the growth of tree diameter is influenced by the environment, such as the density (spacing) and the intensity of light, with the lower the density (wide spacing), the greater the diameter of tree. The effect of blocks on stem straightness is also related to the impact of blocks on stem height and diameter growth. This is because the growth of tree trunks, such as height and diameter is not optimal within each block, resulting in a variety of stem straightness outputs from each block. In contrast to the character of branch-free stem height, which shows no significant difference. The character of branch-free stem height in the *A. auriculiformis* progeny test in this study was not affected by environmental factors.

The results of the analysis of variance for the effect of family on the characters of height, diameter, branch-free stem height, and stem straightness showed significant differences in each family on the four tree growth characters. In addition to environmental factors in the form of blocks, the family also plays a role in the performance of *A. auriculiformis* for all observed characters. These results indicate that genetic factors strongly influence the diversity or variation in the measured characters. The real influence of family on all observed growth characters is related to the ability to inherit genetic traits from the parent tree. In the growth characteristics of height, diameter, and stem straightness, the significant effect was found in the block and family factors. Similar results were reported by Islam et al. (2022), who discovered that the source of variation of family and block significantly affected the height and diameter of 3-year-old tembesu (*Fagraea fragrans* Roxb.) progeny test plants in Banyuasin Regency. In contrast, the character of branch-free stem height only has a significant effect on the family factor. This indicates that genetic factors can significantly affect all observed growth characters, while environmental factors do not affect the character of branch-free stem height. Thus, the fact that only the family factor affects the character demonstrates the high genetic influence on the branch-free stem height character. This is an essential factor in breeding programs. The significant effect of a given family treatment on the progeny test indicates that the progeny test is suitable for selection purposes (Sebbenn et al., 2003).

The results of variance analysis for the effect of the interaction source of diversity of family and block showed the same results as the effect of the block source of diversity. According to Dewi (2016), the significance of a plant diversity source for a given trait/character indicates that any appearance or phenotype will be influenced by genetic and environmental factors (family or block), where a plant grows and develops. In this study, the characters of height, diameter, and stem straightness exhibited very significant results from the interaction effect of family and block. This indicates that the growth of the characters of height, diameter, and straightness of the stem is influenced by the interaction between genetic and environmental factors, while the character branch-free stem height is only influenced by genetic factors.

Phenotypic Correlation Between Characters

According to Hardiyanto (2010), phenotypic correlation refers to the relationship between the measured values of two traits in a population. This value expresses the degree of closeness of the two phenotypic characters observed in response to environmental influences. The phenotypic correlation between characters of *A. auriculiformis* is presented in Table 3.

Based on Table 3, the phenotypic correlation analysis between characters shows that the height and diameter characters have a positive correlation classified as strong (0.569). This strong correlation is attributed to the fact that larger or thicker diameters have more vascular tissue for water and nutrient transport, which is vital for growth and reproduction, including height growth (Kurniasari & Sulistyono, 2023). The correlation value shown demonstrates the improvement of diameter characters in *A. auriculiformis* trees, which will be followed by an improvement in height characters and vice versa. According to Mashudi and Baskorowati (2015), the height and diameter characteristics of forestry plants generally have a high correlation value. A strong correlation between height and diameter characters was also reported in other studies on *A. auriculiformis* and other forestry plants. As in the results of research by Herdyantara (1992), the progeny test of the 1-month-old and 6 months old *A. auriculiformis* in Wanagama I had a phenotypic correlation between height and diameter of 0.972 at 1-month-old and 0.990 at 6 months old . In Mahat's research (1999), the 4-years-old *A. auriculiformis* provenance test in Serdang Malaysia had a phenotypic correlation of 0.88 between height and diameter . Furthermore, Setiadi and Fauzi (2015) reported that a combination of provenance and descent tests of *Araucaria cunninghamii* in Bondowoso correlated with height and diameter of 0.62 at the 5-years-old and 0.82 at the 10-years-old.

Correlation test results also showed that a strong positive relationship was also found in the character of branch-free stem height with stem straightness of 0.633 (Table 3). Meanwhile, the correlation test results between the character of branch-free stem height and diameter showed a very weak correlation (0.094), because the high or low branch-free stem height does not affect the growth of tree diameter, and vice versa. These results indicate that the improvement of branch-free stem height traits will be followed by a strong improvement in stem straightness traits by 63.3%, but only a very weak improvement in diameter growth (9.4%). According to Mashudi and Baskorowati (2015), a high positive correlation value is a good indicator that can facilitate selection implementation.

The favorable characters to be used as priority characters for selection candidates in this study are the diameter character, followed strongly by the height character, and then the branch-free stem, with the stem straightness character also strongly influenced. Thus, the four characters can be improved together. This is in line with the opinion of Erwi et al. (2015), a positive relationship between one character and another character demonstrates that both characters can be improved together, as long as improving one character will improve the other character, and there is no negative correlation between them. If the correlation remains consistent until the age of selection, selection can be carried out effectively and efficiently by focusing on just one of the character (Mashudi and Baskorowati 2015).

Heritability

Heritability describes the condition of strong or weak genetic factors in controlling a character (Haryjanto and Prastyono 2014). There are three heritability values estimated in this study, including individual heritability, family heritability, and within-family heritability. The individual and family heritability values of the 9-year-old *A. auriculiformis* progeny test at KHDTK Blok Playen are presented in Table 4. Based on Table 4, the heritability value of the 9-year-old *A. auriculiformis* progeny test indicate that the individual character height of 0.189 and diameter of 0.169 fall into the medium category, while the heritability value for branch-free stem height (0.325) and stem straightness (0.33) are classified as high. According to Jameela and Soegianto (2014), high heritability values indicate the diversity of these characters is more highly influenced by genetic factors than by environmental factors. Similar results were reported by Erwin et al. (2015), who found that the high heritability value in agarwood plants (*Aquilaria malaccensis* Lamk) indicated a greater role of genetic factors. The differences of the heritability values between these characters suggest that the characters of branch-free stem height and stem straightness have a greater chance of inheriting traits than those of height and diameter when selected at the individual level. The lower values of individual heritability for height and diameter characters indicate that the environment (block) has a greater influence on the growth of these plant characters. According to Azizah (2016), factors that affect the high and low value of heritability estimates include not only genetic factors but also environmental factors, such as disease and pest infestations.

The family heritability values from the four characters are classified as high. The high value of family heritability in these four characters indicates that genetic factors dominate plant growth more than environmental factors, which makes it favorable for conducting family selection in the progeny test. According to Suwandana (2019), the effectiveness of selection is more efficient when the heritability value of a character is high, because genetic factors are more influential than environmental factors. The heritability value of the family for height (0.619) is smaller than that for diameter (0.631). The heritability value of the branch-free stem height family is 0.804, which is greater than that of stem straightness (0.769). The high heritability value of the family in the four characters is in accordance with the statement of Zobel and Talbert (1984), who noted that the estimation of the heritability value of the family is based on the average value of the number of individuals. Therefore, the influence of the block as an environmental factor can be minimized, especially as the number of tree plots increases,

The heritability values found in this study were generally higher at the family level than at the individual level. Similar findings showing that family heritability tends to be higher than individual heritability, were also reported by Halawane (2015) in his study on the progeny test of 1.5-years-old Nyatoh (*Palaquium obtusifolium*), and by Rinaldi (2018) in the progeny test of 10-months-old red Jabon (*Neolamarckia macrophylla* (Roxb.) Bosser). The heritability values for height, diameter, and stem straightness have increased compared to Handayani et al. (2018) research, which evaluated trees at 18 months. The individual heritability values obtained for height, diameter, and stem shape ranged from 0.140 to 0.309.

Table 2. Results of variance analysis of *A. auriculiformis* progeny test in KHDTK Blok Playen

Character	Variety source	Degree of freedom	F probability
Height	Blok	11	0.000***
	Famili	29	0.000***
	Blok×Famili	308	0.000***
	Error	886	
Diameter	Blok	11	0.000***
	Famili	29	0.000***
	Blok×Famili	308	0.001**
	Error	886	
Branch-free stem height	Blok	11	0.347 ns
	Famili	29	0.000***
	Blok×Famili	308	0.307 ns
	Error	886	
Stem straightness	Blok	11	0.000***
	Famili	29	0.000***
	Blok×Famili	308	0.000***
	Error	886	

Note: × = interaction, *** = very significant influence at the 99.9% confidence level, ** = very significant influence at the 99% confidence level, * = very significant influence at the 95% confidence level, ns = no significant effect at the 95% confidence level

Table 3. Phenotypic Correlation Between Characters

Character	Height	Diameter	TBBC	SS
Height	-	-	-	-
Diameter	0.569 (strong)	-	-	-
TBBC	0.237 (weak)	0.094 (very weak)	-	-
SS	0.304 (weak)	0.254 (weak)	0.633 (strong)	-

Note: TBBC = Branch-free stem height, SS = Stem straightness.

Table 4. Individual and family heritability of 9-year-old *A. auriculiformis* progeny test in KHDTK Blok Playen

Heritability	**Height**	**Diameter**	**TBBC**	**SS**
Individual (h^2i)	0.189 (Medium)	0.169 (Medium)	0.325 (High)	0.33 (High)
Famili (h^2f)	0.619 (High)	0.631 (High)	0.804 (High)	0.769 (High)
Within famili (h^2w)	0.176	0.144	0.269	0.299

Table 5. Estimation of genetic advance and genetic gain of 9-year-old *A. auriculiformis* progeny test in KHDTK Blok Playen at 25%, 50%, and 75% selection intensity

Character	Selection intensity	Genetic advance	Genetic gain (%)	Category
Height	25%	0.507	3.123	Medium
	50%	0.25	1.540	Low
	75%	0.084	0.517	Low
Diameter	25%	0.652	5.235	Medium
	50%	0.321	2.577	Low
	75%	0.108	0.86	Low
Branch-free stem height	25%	0.813	16.494	Very high
	50%	0.401	8.135	High
	75%	0.135	2.738	Low
Stem straightness	25%	5.181	7.291	High
	50%	2.555	3.595	Medium
	75%	0.865	1.217	Low

decreased, the heritability value of the family for height, diameter at breast height (dbh), and stem shape ranged from 0.763 to 0.840. This progeny test experienced changes in heritability values, which can be interpreted as follows: for the same character in different age ranges, the influence of environmental in the form of blocks decreased for individual stands, while genetic factors increased. Meanwhile, the influence of blocks on stands per family increased and genetic factors decreased. The trend of heritability that fluctuates over time indicates that the genetic factors of growth performance are not fixed. According to Susanto and Mashudi (2018), changes in heritability at each age can be influenced by the presence of epistasis alleles and the interaction of genes with the environment, which can cause complex changes in heritability values.

Genetic Advance and Genetic Gain

Genetic advance measures the magnitude of population change after the genetic selection process (Karyawati et al. 2019). Estimation of genetic advance and genetic gain of 9-year-old *A. auriculiformis* progeny test with several percentage levels are presented in Table 5.

The selection intensity was carried out at 3 levels: 25% (leaving 1 individual in each tree plot), 50% (leaving 2 individuals in each tree plot), and 75% (leaving 3 individuals in each tree plot). The genetic advance in Table 9 shows that the values vary at the three levels of selection intensity. The four characters calculated showed increased genetic progress as the percentage of the selected/abandoned population decreased (Table 5). This can be interpreted that the fewer the populations selected, the higher the value of genetic advance obtained, and the greater the genetic gain. Apart from the intensity of selection applied, the genetic gain is also closely related to heritability values (Islam et al., 2022). Given the relatively higher family heritability values (Table 4), family selection will produce higher genetic gain compared to individual selection within plots. However, family selection will reduce the number of families (clones) and the existing genetic diversity. A limited number of clones can lead to very low genetic diversity (Pelawi, 2020). Overtime, populations with low genetic diversity are at risk of decreased adaptability to abiotic environmental changes, such as climate change (Axelson et al., 2020; Flanagan et al., 2018; Buckley et al., 2019), as well as biotic environments, such as pest resistance (Zas et al., 2017).

The highest genetic gain was obtained from 25% selection intensity for all growth characters. At 25% selection intensity, the genetic gains were 16.494% for branch-free stem height (very high), 7.291% for stem straightness (high), 5.235% for diameter (medium), and 3.123% for height (medium) (Table 5). These results align with the heritability values within the family found in this study (Table 4). The heritability values for the branchless stem's height and the stem's straightness were higher than those of diameter and height. These results are also consistent with the order of the genetic advance values for each observed character. The results demonstrate that the value of genetic advance will have implications for the genetic gain, which shows a consistent trend: an increase in genetic progress followed by an increase in genetic gain. The relationship between the tendency of genetic progress value and genetic gain is in accordance with the findings of Hamdi et al. (2003), who stated that an increase in the value of genetic gain in one selection cycle can be indicated by the value of genetic progress. The genetic gain for given character is also determined by the intensity of selection used and its heritability value. The high value of heritability obtained will indicate the possibility of greater genetic gain. In addition, the increasing intensity of the selection applied will reduce the value of genetic gain obtained (Adinugraha et al. 2013).

Selection

Selection is carried out at the individual level to maintain the number of families and individuals. Low selection intensity can potentially cause inbreeding depression effects (Syukur et al. 2012). Therefore, careful consideration is needed in determining the selection strategy. Based on the genetic gain, the 25% selection scheme with the highest genetic progress of all characters is considered optimal for obtaining high genetic gain by maintaining 1 of 4 trees in each tree plot. With individual selection at 25% intensity, the evaluation of the *A. auriculiformis* progeny test will result in a genetic gain of 3.123% for the height, 5.235% for diameter, 16.494% for the branch-free stem height, and 7.291% for the stem straightness (Table 4).

CONCLUSION

The genetic variation in all growth traits of the 9-year-old *A. auriculiformis* progeny test in KHDTK Blok Playen showed that the characters,such as height, diameter, branch-free stem height, and stem straightness were influenced by genetic factors. The phenotypic correlation between the traits revealed a positive relationship across all characteristics. A strong positive relationship was found between height and diameter (0.569), followed by branch-free stem height and stem straightness (0.633), indicating that improvements in one of these characters will be followed strongly by the others. In general, the family and individual heritability values in this study were classified as high, suggesting significant potential for improving the quality of the progeny test plants. To evaluate the growth of progeny test plants and increase the productivity and quality of *A.auriculiformis* as an optimization of seed sources through Seed Orchard (KBS), an individual selection scheme with a 25% selection intensity is thought to be optimal for achieving genetic advance and high genetic gain.

ACKNOWLEDGMENTS

The author would like to thank the Head of the Center for Forestry Instrument Standards Testing (BBPSIK) Yogyakarta and the KHDTK Blok Playen management team, Mr. Sunaryanto (staff), for the permits that have been granted.

REFERENCES

Adinugraha. H. A., Pudjiono, S., & Mahfudz. (2013). The variation in growth and genetic parameters of 5-year-old teak progeny test in Gunung Kidul, Yogyakarta. *Jurnal Pemuliaan Tanaman Hutan*. 7(3):167-168. https://doi.org/10.20886/jpth.2013.7.3.167-178. [Indonesian]

Axelsson, E. P., Grady, K. C., Lardizabal, M. L., Nair, I. B., Rinus, D., & Ilstedt, U. (2020). A pre-adaptive approach for tropical forest restoration during climate change using naturally occurring genetic variation in response to water limitation. *Restoration Ecology*, *28*(1), 156-165. https://doi.org/10.1111/rec.13030

Becker, W. A. (1992). Manual Quantitative Genetics (Fifth). Pullman, Enterprises. https://www.cabidigitallibrary.org/doi/full/10.5555/19870101387

Buckley, J., Widmer, A., Mescher, M. C., & De Moraes, C. M. (2019). Variation in growth and defence traits among plant populations at different elevations: Implications for adaptation to climate change. *Journal of Ecology*, 107(5), 2478-2492. https://doi.org/10.1111/1365-2745.13171

Dewi, E. S. (2016) *Pemuliaan Tanaman*. Unimal Press. (In Press). http://repository.unimal.ac.id/id/eprint/2063

Erwi, L., Muin, A., Burhanuddin. (2015). Heritability test of agarwood (*Aquilaria malaccensis* Lamk) at four years old in the demonstration plot of the Forestry Service of Ketapang Regency. *Jurnal Hutan Lestari*. 3(2):300-312. https://doi.org/10.26418/jhl.v3i2.10652. [Indonesian]

Falconer, D. S. (1981). *Introduction to quantitative genetics*. Longman Group Ltd. UK. https://www.cabidigitallibrary.org/doi/full/10.5555/19810162173

Flanagan, S. P., Forester, B. R., Latch, E. K., Aitken, S. N., & Hoban, S. (2018). Guidelines for planning genomic assessment and monitoring of locally adaptive variation to inform species conservation. *Evolutionary applications*, 11(7), 1035-1052. https://doi.org/10.1111/eva.12569

Halawane, J., Kinho, J., & Irawan, A. (2015). Genetic variation of plant growth on progeny test of nyatoh (*Palaquium obtusifolium*) age 1.5 year in Batuangus forest research station, North Sulawesi. In *Prosiding Seminar Nasional Masyarakat Biodiversitas Indonesia*. 1(4): 819-823. https://doi.org/10.13057/psnmbi/m010426

Hamdi A, El-Ghareib AA, Shafey SA, Ibrahim MAM. (2003). Genetic variability, heritability, and expected genetik advance for earliness and seed yield from selection in lentil. *Egypt J Agr Res*. 81:125-137. https://dx.doi.org/10.21608/ejar.2003.276089

Handayani, B. R., Kartikaningtyas, D., Setyaji, T., Sunarti, S., & Nirsatmanto, A. (2018). Genetic diversity of introduced species *Acacia auriculiformis* observed in second generation progeny trial in Gunungkidul, Yogyakarta. *Prosiding Seminar Nasional Masyarakat Biodiversitas Indonesia*. 4(1): 47-51. https://doi.org/10.13057/psnmbi/m040107

Haryjanto L, Prastyono. (2014). Estimation of genetic parameters of nyawai seedlings (*Ficus variegata* Blume) from Lombok Island. *Jurnal Penelitian Kehutanan Wallacea*. 3(1):37-45. https://doi.org/10.18330/jwallacea.2014.vol3iss1pp37-45. [Indonesian]

Hardiyanto EB. 2010. *Pemuliaan Pohon Lanjut*. Universitas Gadjah Mada, Yogyakarta. Conchbooks.

Herdyantara, A. B. (1992). Korelasi Genetik Antara Tinggi Dan Diameter Batang Pada Uji Keturunan *Acacia auriculiformis* A. Cunn, Umur 6 Bulan Di Wanagama I. Thesis. https://etd.repository.ugm.ac.id/penelitian/detail/171192

Setiadi, D., & Fauzi, M. A. (2015). Genetic parameters in the provenan test and progeny test combinations of *Araucaria cunninghamii* from Manokwari (Papua) in Bondowoso, East Java. *Jurnal Penelitian Kehutanan Wallacea*, 4(2), 129-136. https://doi.org/10.18330/jwallacea.2015.vol4iss2pp129-136. [Indonesian]

Islam, S., Aluyah, C., Sosilawati, E., Muslimin, I., & Sofyan, A. (2022). Evaluation of the growth of a 3-year-old progeny test of tembesu (*Fagraea fragrans* Roxb) at KHDTK Kemampo, Banyuasin Regency. *ULIN: Jurnal Hutan Tropis*, 6(1), 80-90. http://dx.doi.org/10.32522/ujht.v6i1.6963. [Indonesian]

Jameela H. dan Soegianto A. 2014. Genetic Diversity and Heritability of Yield Component Traits in the F2 Population of Green Bean (*Phaseolus vulgaris* L.) Resulting from the Cross between Introduction and Local Varieties. *Jurnal Produksi Tanaman*, 2 (4), 324 – 329. https://protan.studentjournal.ub.ac.id/index.php/protan/article/view/113. [Indonesian]

Kariming, M., & Zulkifly, R. (2023). Morphological Characteristics and Biomass Potential of *Acacia* (*Acacia Auriculiformis*) in Hasanuddin University. http://repository.unhas.ac.id:443/id/eprint/29464

Karyawati AS, Sari GN, Waluyo B. (2019). Genetic variability, heritability, and genetic progress of several quantitative traits in F3 soybean lines resulting from crosses. *AGRO*, 6(2):134–143. https://doi.org/10.15575/5174. [Indonesian]

Kurniasari, R., & Sulistyono, E. (2023). Growth and Production of Numbu Variety Sorghum (*Sorghum bicolor* (L.) Moench) with Different Organic Fertilization Treatments. *Buletin Agrohorti, 11*(1), 69-78. https://doi.org/10.29244/agrob.v11i1.46616. [Indonesian]

Larasati, W., Kusumarini, N., Farhatul Wahida, B., Nurul Zulkarnaen, R., & Rifqi Hariri, M. (2024). Investigating the Taxonomic Value of Leaf Architecture in *Ixora* and *Psychotria* (Rubiaceae) Found in the Bogor Botanic Gardens' Living Collections. *Jurnal Riset Biologi Dan Aplikasinya*, *6*(1), 12–19. https://doi.org/10.26740/jrba.v6n1.p12-19

Leksono, B. (2016). Repeated Selection in Tropical Forest Plant Species for the Independence of Superior Seeds. *Bogor: Badan Penelitian, Pengembangan dan Inovasi*. KLHK. [Indonesian]

Mahat, M. N. (1999). Genetic variation of growth and selected wood properties of four-year-old Acacia auriculiformis Provenances of Serdang, Malaysia. *Bangalore: Institute of Wood Science and Technology*. http://psasir.upm.edu.my/id/eprint/9985/1/FH_1999_9_A.pdf

Maulidan, A., Arifin, Y. F., & Pujawati, E. D. (2021). Study of Plant Growth in Post-Mining Areas of the Highlands in South Kalimantan. *Jurnal Sylva Scienteae*, *4*(2), 206-217. https://doi.org/10.20527/jss.v4i2.3330. [Indonesian]

Mashudi, Baskorowati L. 2015Estimation of genetic parameters in a 2-year-old progeny test of Alstonia scholaris in Gunung Kidul, Yogyakarta. *Jurnal Pemuliaan Tanaman Hutan*, 10(2):1–11. https://doi.org/10.20886/jpth.2015.9.1.1-11. [Indonesian]

Mutiar, S., Kasim, A., & Asben, A. (2020). Bark Characteristics of *Acacia auriculiformis* A. Cunn. ex Benth. and Acacia mangium Willd. From Industrial Plantation Forest. *Jurnal Penelitian Kehutanan Wallacea.* 9(1), 43-49. https://doi.org/10.18330/jwallacea.2020.vol9iss1pp43-49

Pelawi, D. F. B., Indrioko, S., Hidayati¹, F., & Wibowo, A. (2020). Evaluation of the 20-Year-Old Clonal Test of Teak (*Tectona grandis* Lf) at KPH Cepu Perum Perhutani. *Jurnal Pemuliaan Tanaman Hutan*, 14(1), 29-41. https://doi.org/10.20886/jpth.2020.14.1.33-41. [Indonesian]

Prehaten, D., Indrioko, S., Hardiwinoto, S., Na'iem, M., & Supriyo, H. (2018). The Influence of Several Chemical and Physical Soil Characteristics on the Growth of 30 Families in a 10-Year-Old Teak (*Tectona grandis*) Progeny Test. *Jurnal Ilmu Kehutanan*, *12*(1), 52-60. https://doi.org/10.22146/jik.34109. [Indonesian]

Rinaldi, S. P. (2018). Effect of gamma irradiated seeds of Jabon Merah (*Neolamarckia macrophylla* (Wall.) Bosser) to genetic diversity. *IOP Conference Series Earth and Environmental Science*, 1115(1):012027. https://doi.org/10.1088/1755-1315/1115/1/012027

Schmerbeck, J., & Naudiyal, N. (2014). Acacia auriculiformis. *Enzyklopädie der Holzgewächse: Handbuch und Atlas der Dendrologie*, 1-12. https://doi.org/10.1002/9783527678518.ehg2014002

Sebbenn AM, Pontinha AAS, Giannotti, Kageyama PY. 2003. Genetic variation in provenance-progeny test of *Araucaria angustifolia* (Bert.) O. Ktzr. In Sao Paulo, Brazil. *Silvae Genetica*, 52:5-6. https://www.cabidigitallibrary.org/doi/full/10.5555/20043108623

Sunarti, S., Na'iem, M., Hardiyanto, E. B., & Indrioko, S. (2013). Breeding strategy of Acacia Hybrid (*Acacia mangium× A. auriculiformis*) to increase forest plantation productivity in Indonesia. *Jurnal Manajemen Hutan Tropika*, 19(2), 128-137. https://doi.org/10.7226/jtfm.19.2.128

Susanto, M., & Mashudi, M. (2018). Genetic Growth Trends Among Populations of *Hibiscus macrophyllus* Roxb. Ex Hornem in Java. *Bioeksperimen: Jurnal Penelitian Biologi*, 4(1), 20-28. https://doi.org/10.23917/bioeksperimen.v4i1.5926. [Indonesian]

Syukur, M., Sujiprihati, S., & Yuniarti, R. 2012. *Teknik Pemuliaan Tanaman*. Depok: Penebar Swadaya. Conchbooks.

Toaha, A. Q., & Beddu, M. A. (2024). Adaptability and Survival Rate of 4-Year-Old Sandalwood Plants in Parangloe District, Gowa Regency. *Jurnal Kehutanan dan Lingkungan*, 1(1),50-58. https://ecoforest.fapertauim.ac.id/index.php/ecoforest/article/view/26

Zas, R., Björklund, N., Sampedro, L., Hellqvist, C., Karlsson, B., Jansson, S., & Nordlander, G. (2017). Genetic variation in resistance of Norway spruce seedlings to damage by the pine weevil *Hylobius abietis*. *Tree Genetics & Genomes*, 13, 1-12. https://doi.org/10.1007/s11295-017-1193-1

Zobel, B. 1. a., & Talbert, J. a. (1984). *Applied forest tree improvement*. New York, New York, United States John Wiley and Sons. Conchbooks.