Mahogany (*Swietenia macrophylla* King.) as urban tree: tree growth and wood quality variation in a progeny test

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Abstract Mahogany (*Swietenia macrophylla*) is a tree species widely planted not only for timber production but also as a shade tree in urban areas both on the side of the highway (green belt) and other green open areas. The objective of this study was to analyze the genetic variation of growth and wood quality of a mahogany progeny test at the Parung Panjang, Bogor, which will be converted into a seedling seed orchard for high quality seed production. The progeny test was established using a randomized complete block design involving 96 families originating from seven populations (land races) in Java Island, i.e., Cianjur, Sumedang, Tasikmalaya, Magelang, Gundih, Madiun, and Jember. The results showed that the family had a significant effect on all the growth and wood quality parameters. Individual and family heritability for all growth and wood quality traits were categorized into the high, i.e., 0.33 - 0.96 and 0.35 - 0.56, respectively. The selection simulation showed that the selection percentage of 44.68% (45 best families) gave the optimum genetic gain based on growth and wood quality traits.

1. Introduction
Mahogany (*Swietenia macrophylla*) is a neo-tropical wood species that has had important economic value for centuries [1]. In the context of genetic conservation of tropical trees and because of the exploitation for wood trading, mahogany was listed on Appendix II of the Convention on International Trade of Endangered Species (CITES) in 2002 [2]. In Indonesia, mahogany was introduced in 1870 and was cultivated in Java Island since 1897 [3] and became an important tree species for timber production both in small scale and large plantations due to the high quality of wood [4]. Mahogany also has the potential as for medicinal substances [5], controlling surface run off and erosion [6] and has stomata that can adapt to absorb air pollutants [7]. This species is widely planted in urban areas as a shade tree along roads as green belt or other green open areas [7, 8].

One of the negative impacts of the presence of trees in urban areas is the increased danger of trees due to lack of accurate selection of tree species or genotypes or inappropriate tree management [9]. Trees which are cultivated as urban trees must be healthy with a sturdy trunk, strong branches, and balanced crown form so that the trees are not easily broken or fallen. In addition, tree growth must also be
relatively fast so that it can quickly provide optimal shade. Shade trees with fragile stems or branches will certainly be dangerous, so it is necessary to procure plant material that genetically has strong stems and branches, and balanced crown with optimum growth. Some research showed that tree hazard is correlated to tree species, crown form, pests and diseases sensitivity, and tree management practices [10, 11]. In other studies [12], wood specific gravity has a positive linear correlation with the modulus of elasticity and modulus of rupture. Wood strength was positively related to wood density [13] so that the combination assessment between growth, crown structure and wood quality was able to produce superior mahogany for urban shade trees to minimize tree hazards in urban areas.

The tree improvement activity is carried out on progeny test stands in Parung Panjang, Bogor which was established using 96 families from 7 populations in Java Island, and it will be converted into a seedling seed orchard which is expected to be able to produce seeds for both reforestation and urban forest development. The progeny test has high genetic diversity based on the Random Amplified Polymorphic DNA (RAPD) markers [14] and will have implications for the diversity of growth and quality of the wood. Variation in growth and wood quality among family or provenance also was reported on Picea glauca [15], Acacia mangium [16], and Neolamarckia cadamba [17, 18]. This diversity is indispensable in the tree breeding process to select superior genotypes for various reforestation programs.

The purpose of this study was to analyze the genetic variation of growth and wood quality of a mahogany progeny test at the Parung Panjang, Bogor, which would be converted into a seedling seed orchard (SSO) for high quality seed production. This selection will be based on growth, crown form, and wood quality, such as specific gravity, wood density and pilodyn penetration to provide the superior mother trees. Thus, the practice of arboriculture using seeds from the selected mother trees while maintaining wide genetic variation will increase tree growth, increase the resistance of tree stands against pests and diseases [19], and reduce the impact of tree hazards [20].

2. Materials and methods
2.1. Material
The seeds for establishment of the progeny test were collected from 7 populations, i.e., Cianjur, Sumedang, Tasikmalaya (West Java), Magelang, Gundih (Central Java), Jember, and Madiun (East Java) (figure 1). Seed processing and seedling nursery were carried out at the Seed Technology Laboratory and Nagrak Nursery Center, Forest Tree Seed Technology Research and Development Center.
2.2. Experimental design and measurement

The progeny test was established at Parung Panjang Forest Research Station, Bogor, West Java. Geographically, the experiment is located at 106°06' E, 6°20' S and an altitude of 51.71 m asl (figure 1). The type of soil is haplic podzol. The soil nutrient status showed that the total N content ranges from 0.21%-0.29%, P content ranging from 3.0 ppm-5.5 ppm and generally micronutrient content was sufficient except Fe and Br. The acidity of the soil was 5.26 [18, 21].

A progeny test was established using 96 families from seven populations (forest plantation) in Java Island, i.e., Cianjur, Sumedang, Tasikmalaya, Magelang, Gundih, Madiun, and Jember. A completely randomized block design was used to assess the family performance of mahogany using 4 blocks and 5-tree row plots with a spacing of 3 m x 3 m. Planting of seedlings was carried out using basic fertilizer as much as 5 kg of manure compost and 250 g of lime per planting hole. Plant maintenance was done every year with manual weed control and fertilization of 100 g NPK carried out until the 3rd year after out-planting.

The growth measurement (tree height and diameter) was carried out at 10 years and 20 years old. The growth measurement at 10 years old was carried out on tree height and diameter (diameter at breast height, DBH) and has become the basis for individual within family selection, while the measurement of the age of 20 years was the reference for conducting family selection. The measurements at 20 years old were conducted on the tree height, DBH, crown form [16], specific gravity, pilodyn penetration, and wood density. Tree height was measured by numerical scale poles and DBH (1.3 m above ground) using calipers. Crown form was measured by scoring based on field observation on typical trees, i.e., 1) very small and thin crown, 2) small and thin crown, oval form, 3) small crown and divided in two parts with heavy branches, 4) big crown with heavy branches, and 5) big crown with small branches [16]. Pilodyn penetration was measured by Pilodyn® with the specification of the strength 6 J and pin diameter 2.5 cm. The physical properties of specific gravity and wood density were analyzed by small core wood samples (diameter about 5 cm) taken at a height of 1.3 m above ground of standing trees [18].

2.3. Data analysis

The data as the result from measurements of growth traits and physical properties of wood were analyzed using analysis of variance (ANOVA). Before analyzing the variance, the normality of the data was tested.
using the Minitab 16 application based on the Kolmogorov-Smirnov method. If the data did not spread normally, the normality of the data was improved by transforming the data by box-cox method [22].

Analysis of variance was carried out to determine the effect of family and block with the following equation 1 model [23]:

\[ Y_{ij} = m + Fi + Bj + Eij \]  

(1)

Notes: \( Y_{ij} \) = the observation made in the \( i \) family on the \( j \) blocks, \( m \) = the overall mean of the traits, \( Fi \) = the effect of the \( i \) family (\( i = 1, 2, 3, ... \)), \( Bj \) = the effect of the \( j \) block (\( j = 1, 2, 3, 4 \)), \( Eij \) = residual effect (error).

The genetic traits observed were genetic diversity, heritability value, genetic and phenotypic correlations between characters, and genetic gain. Estimating the value of individual heritability has done by comparing the additive genetic variance (\( 4\sigma^2f \)) with the total phenotypic variance. Estimation using the following formula can only be done in a specific environment or location or without comparing with other locations. Heritability value estimation was calculated according to the following formula 1, 2 [24]:

\[ h^2i = \frac{4\sigma^2f}{\sigma^2e + \sigma^2fb} \]  

(2)

\[ h^2f = \frac{\sigma^2f}{\sigma^2e + \sigma^2fb/b + \sigma^2fb/t} \]  

(3)

Notes: \( h^2f \) = family heritability, \( h^2i \) = individual heritability, \( \sigma^2f \) = variance of family, \( \sigma^2fb \) = variance of interaction between family and block, \( \sigma^2e \) = error, \( b \) = number of blocks, \( t \) = number of trees per row plot.

Correlation analysis was conducted to study the closeness of linear relationships between variables or traits. Genetic and phenotypic correlations between characters are calculated using the following formula 4, 5 [24]:

\[ r_{ai} = \frac{cov_{ai}(i)}{(\sigma^2_{ai} * \sigma^2_{ai})^{1/2}} \]  

(4)

\[ r_{pi} = \frac{cov_{pi}(i)}{(\sigma^2_{pi} * \sigma^2_{pi})^{1/2}} \]  

(5)

Notes: \( r_{ai} \) = genetic correlation, \( r_{pi} \) = phenotypic correlation, \( cov_{ai}(i) \) = covariance of additive genetic on the \( i \) trait and the \( j \) trait, \( cov_{pi}(i) \) = covariance of phenotypic on the \( i \) trait and the \( j \) trait, \( \sigma^2_{ai} \) = variance of additive genetic on the \( i \) traits, \( \sigma^2_{pi} \) = variance of additive genetic on the \( j \) traits, \( \sigma^2_{ij} \) = variance of phenotypic on the \( i \) traits, \( \sigma^2_{ij} \) = variance of phenotypic on the \( j \) traits.

Genetic gain (\( G \)) was resulted by the calculation of the magnitude of the population response to selection based on the heritability value and the differential selection. Genetic gain based on selection type was calculated using the following formula 6 [23] and differential selection (\( S \)) could be known according to the following formula 6 [24, 25]:

\[ G = h^2S = h^2I \sigma_{p} ; \ S = Xs - X\mu \]  

(6)

Notes: \( G \) = genetic gain, \( I \) = selection intensity, \( \sigma_{p} \) = standard deviation, \( h^2 \) = heritability, \( S \) = differential selection, \( Xs \) = average of the observed parameter on the population (before selection), \( X\mu \) = average of the observed parameter on the population after thinning selection.

3. Result and discussion
3.1. Growth and wood quality variation
Analysis of variance was carried out to determine the effect of blocks and families on the performance of growth, crown form and physical wood properties. The result revealed a significant effect of family on all traits observed in a progeny trial of mahogany at Parung Panjang, Bogor (table 1).
Table 1. Analysis of variance for tree growth and wood quality of mahogany progeny test at Parung Panjang, Bogor

| Source of variation | H-10 | H-20 | DBH-10 | DBH-20 | CBH-20 | V-20 | CF-20 | SG-20 | PP-20 | WD-20 |
|---------------------|------|------|--------|--------|--------|------|------|-------|-------|-------|
| Block               | 16.524* | 255.029* | 34.395* | 0.003* | 2.882* | 2.512* | 0.936 | 0.075* | 0.003 | 0.002 |
| Family              | 0.330* | 11.336* | 0.605* | 0.000* | 0.201* | 0.395* | 1.084* | 0.015* | 0.005* | 0.003* |

Notes: H-10 = tree height at 10 years old, H-20 = tree height at 20 years old, DBH-10 = diameter at breast height at 10 years, DBH-20 = diameter at breast height at 20 years old, CBH-20 = clear bole height at 20 years old, V-20 = wood volume at 20 years old, CF-20 = crown form at 20 years old, SG-20 = specific gravity at 20 years old, PP-20 = pilodyn penetration at 20 years old, WD = wood density at 20 years old, * = significant at P<0.05

The growth variation of mahogany progeny test in Parung Panjang is quite high, both at 10 years old and at 20 years old (after individual within family selection). This condition indicated that the growth variation occurred at the individual within family and among family’s levels. In general, diameter growth increased after individual within family thinning at 10 years of mahogany stand age from 1.382 cm per year to 1.521 cm per year, while height growth decreased (1.004 m per year to 0.765 m per year). The increase in diameter growth is due to the opening of growing space so that the tree diameter can grow more optimally [26]. However, the growth in height and diameter after thinning was relatively more uniform which can be seen from the coefficients of variance values (table 2).

Table 2. Performance of tree growth and wood quality of mahogany progeny test at Parung Panjang, Bogor

| Parameters                                | Mean  | Minimum | Maximum | Coefficient of variance |
|-------------------------------------------|-------|---------|---------|-------------------------|
| Tree height at 10 years old (m)           | 10.04 | 2.00    | 19.00   | 13.63                   |
| DBH at 10 years old (cm)                  | 13.82 | 2.55    | 32.17   | 17.37                   |
| Tree height at 20 years old (m)           | 17.65 | 8.50    | 27.00   | 7.01                    |
| DBH at 20 years old (cm)                  | 29.03 | 13.69   | 70.06   | 7.31                    |
| Clear bole height at 20 years old (m)     | 5.15  | 1.50    | 14.65   | 25.90                   |
| Volume at 20 years old (m³)               | 0.31  | 0.05    | 1.49    | 42.21                   |
| Crown form at 20 years old               | 3.68  | 1.00    | 5.00    | 11.90                   |
| Specific gravity at 20 years old (        | 0.56  | 0.20    | 1.44    | 9.38                    |
| Pilodyn penetration at 20 years old (mm)  | 16.70 | 12.00   | 21.30   | 4.48                    |
| Wood density at 20 years old (g/cm³)      | 1.02  | 0.37    | 1.59    | 4.97                    |

Notes: DBH = diameter at breast height

Coefficient of variation of the growth and wood properties traits observed in this study ranged from 4.48 to 42.21. The highest value of coefficient of variation was tree volume (42.21), followed by clear bole height (25.9) and DBH at 10 years (17.37). This condition showed that the volume, which is derived from the value of height and diameter, has a large variation. The variation is beneficial for tree improvement programs because phenotypic is an expression of genetics and environment that needs to be known in the implementation of breeding programs [24, 25, 27].

3.2. Genetic parameters
3.2.1. Heritability. The heritability of all parameters measured generally had a relatively high value [28]. Individual heritability values observed at 20 years stand old ranged from 0.47-0.96 with the highest heritability value being the DBH and the lowest was tree height (table 3). The high heritability value was directly proportional to the high genetic diversity based on the analysis using RAPD markers [14]. Although the analysis of variance showed that blocks significantly influence the observed properties
(except crown form and wood density), the proportion of the components of variation of family was larger than components of variation of block. Proportion value between components of variation of blocks and families that have an impact on the value of heritability [24, 28].

Table 3. Heritability of tree growth and wood quality parameters of mahogany progeny trial at Parung Panjang, Bogor

| Parameters                                    | Individual heritability | Family heritability |
|-----------------------------------------------|-------------------------|---------------------|
| Tree height at 10 years old                   | 0.48                    | 0.35                |
| DBH at 10 years old                           | 0.33                    | 0.26                |
| Tree height at 20 years old                   | 0.52                    | 0.37                |
| DBH at 20 years old                           | 0.96                    | 0.56                |
| Clear bole height at 20 years old             | 0.87                    | 0.53                |
| Volume at 20 years old                        | 0.82                    | 0.51                |
| Crown form at 20 years old                    | 0.93                    | 0.55                |
| Specific gravity at 20 years old              | 0.85                    | 0.52                |
| Pilodyn penetration at 20 years old           | 0.91                    | 0.54                |
| Wood density at 20 years old                  | 0.47                    | 0.35                |

Notes: DBH = diameter at breast height

If compared to the heritability value of the progeny test stands at 10 years old with the stand age of 20 years, the heritability value has increased with increasing tree age and after thinning (individual within family selection). This result indicates that the progeny test of mahogany has high enough family variation and the genetic expression on growth increases with age and space to grow up to 20 years. The value of heritability, then, is used to determine the selection strategy [24, 27]. High individual heritability values showed a selection process based on individuals will produce higher genetic gain, and vice versa [30]. Individual selection has been carried out based on evaluations at 10 years stand old leaving one of the best individuals in each family. Thus, the subsequent selection was continued based on family and supported by high family heritability values.

3.2.2. Genetic and phenotypic correlations. Genetic correlation is a tool to streamline the selection process because an increase in one-character improvement will be followed by other characters [24, 31]. DBH had a significant correlation with tree volume ($r^2 = 0.38$), pilodyn penetration ($r^2 = -0.44$), and wood density ($r^2 = -0.45$). In addition, DBH, clear bole height, and volume were negatively correlated with penetration of pilodyn ($r^2 = -0.44$, $r^2 = -0.31$, $r^2 = -0.13$, respectively) which which indicates that increase of DBH, clear bole height and volume will provide a low penetration value [32]. The pilodyn penetration, as a non-destructive method for evaluating the wood hardness as well as the density of outer wood on standing trees, was still being carried out because the application in the field would be faster and easier. However, the applications of pilodyn penetration in several studies still fail in estimation of wood quality [18, 32]. This can be caused by several factors, such as bark thickness, strength of pilodyn pressure used, and needle size [32, 33, 34]. Genetic correlation of volume with specific gravity was positive ($r^2 = 0.34$) so that an increase in volume will be followed by increase in specific gravity. Phenotypically, the DBH also has a significant correlation with tree height ($r^2 = 0.33$) and volume ($r^2 = 0.91$) (table 4).

Table 4. Genetic (upper diagonal) and phenotypic (lower diagonal) correlations for all traits of tree growth and wood quality of mahogany progeny test at 20 years old at Parung Panjang, Bogor

| Parameter     | H   | CBH  | DBH  | V   | SF   | SG   | PP   | WD  |
|---------------|-----|------|------|-----|------|------|------|-----|


The performance of the growth traits (tree height and DBH). The evaluation was carried out at the age of 20 years old of the progeny test to find out the percentage of selection and characters used in the family selection. The percentage of selection needs to know its ability value, also needs to know its genetic gain as a reference in the implementation of family selection. The genetic gain estimation of selection made, or the fewer families left behind will result in higher genetic progress. Several studies have also reported similar results, such as in Nauclea orientalis [35] and Pinus contorta [39]. Percentage of selection affected differential selection which together with heritability values gives magnitude of genetic gain [24, 35]. This is due to the occurrence of a middle value shift due to the selection that has been carried out [40]. Therefore, based on consideration of the selection simulations, further selection (thinning) is carried out with a percent selection of 46.88% or by leaving the 45 best families in each block as the parent tree.

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
| H | - | 0.07 | 0.19 | 0.04 | 0.07 | -0.04 |
| CBH | -0.02 | - | 0.13 | 0.23 | 0.11 | 0.19 |
| DBH | **0.33** | -0.01 | - | **0.38** | -0.15 | 0.26 |
| V | 0.27 | 0.32 | **0.91** | - | 0.02 | **0.34** |
| SF | **0.37** | **0.47** | -0.03 | 0.17 | - | **-0.46** |
| SG | -0.02 | -0.05 | 0.22 | -0.12 | -0.02 | - |
| PP | 0.08 | -0.09 | -0.25 | 0.20 | 0.19 | -0.14 |
| WD | -0.06 | -0.12 | 0.10 | 0.03 | -0.11 | -0.12 |

Notes: see table 5 for the information of parameters, ** = significantly correlated at 99%, * = significantly correlated at 95%

However, the comparison of the beneficial quantities in genetic correlation had a smaller value than the phenotypic correlation. Genetic correlation can be produced due to pleiotropy or linkage, while phenotypic correlation which is a correlation among phenotypic values is a combination of non-additive and environment [34]. A greater phenotypic correlation value compared to genetic correlation made the selection process preferably not based on one character. Based on the results of correlation analysis, DHB can be used as a priority character used in the implementation of the thinning selection.

3.2.3. Genetic gain. High heritability is not sufficient to be able to determine the characters used in the selection process. High heritability values did not indicate a selection response or genetic gain was large, because genetic gain is an outcome of heritability and differential selection. Therefore, even though it has high heritability, the genetic gain obtained may be small if the differential selection is small [24]. Genetic gain showed the level of profit gained in character because of the selection process. High genetic gain coupled with high estimates of heritability give the right direction of action for selection [35, 36].

After the first stage selection was carried out using mass selection (individual within family selection) based on the best performance of the growth traits (tree height and DBH). The evaluation was carried out again at the 20 years old of the progeny test to find out the percentage of selection and characters used in the family selection. The percentage of selection needs to be known after determining the main character that is the basis for selecting an individual or family. Allegations of genetic acquisition provide an illustration of the response that will occur to the next generation of the magnitude of the selection intensity [37]. Efficiency of selection has an important role in the implementation of tree breeding because of the many influences that affect the performance of trees besides genetic factors [15].

The performance of each family being known from the heritability value, also needs to know its genetic gain as a reference in the implementation of family selection. The genetic gain estimation of each family based on measured parameters was conducted to determine the ideal selection intensity [38]. Determination of percentage of selection was based on families which are still experiencing genetic progress by comparing the performance of families to population averages [25]. Percentage of selected families which were not carried out selection thinning was known based on the number of families.

These numbers which were expected to be still experienced genetic gain after selection thinning has been done. Percentage of selection based on growth and quality traits of wood would be simulated as suspected genetic gain. Percentage of selection based on DBH, tree height, clear bole height, volume, crown form, specific gravity, pilodyn penetration, and wood density, respectively 55.21% (53 families), 54.17% (52 families), 47.92% (46 families), 46.88% (45 families), 45.83% (44 families), 39.58% (38 families), and 38.54% (37 families) (table 5).

The simulation results showed the priority or main traits, such as DBH, the smaller the percent of selection made, or the fewer families left behind would result in higher genetic progress. Several studies have also reported similar results, such as in Nauclea orientalis [35] and Pinus contorta [39]. Percentage of selection affected differential selection which together with heritability values gives magnitude of genetic gain [24, 35]. This is due to the occurrence of a middle value shift due to the selection that has been carried out [40]. Therefore, based on consideration of the selection simulations, further selection (thinning) is carried out with a percent selection of 46.88% or by leaving the 45 best families in each block as the parent tree.
of SSO. The selection percentage was chosen because it has the highest genetic gain on the specific gravity and wood density, i.e., 0.0059 (1.054%) and 0.0016 (0.157%), respectively, and the growth (height and DHB) were not significantly different from the percentage of selection with intensity above it (45.83%), so that the family with good growth and optimum wood quality was obtained. The selection process needs to pay attention to the number of families selected because the percentage of selection that is too low causes the effect of inbreeding depression [27, 40]. According to Indonesia National Standard (SNI 8806-2019 Forest tree seed source), the minimum family allowed to be designated as SSO is 25 families so that the mahogany progeny test that has undergone selection (thinning) can be used as SSO.

### 3.2.4. Implication on urban tree development.

Urban trees provide various ecosystem services to urban areas. However, inappropriate tree species or genotype selection and arboriculture practices can increase the negative impacts of urban forests on the people, infrastructure, and environment of the city [9]. The study will select the mahogany superior mother trees in a progeny test at Parung Panjang Forest Research Station based on growth, crown form, and wood quality, such as specific gravity, wood density and pilodyn penetration. The progeny test will be converted to seedling seed orchard to produce high quality seed that will be used on various reforestation, including urban forest development. The use of high-quality seeds from this selection for urban forest development is believed to reduce the risk of tree hazards due to broken branches and fallen trees, thereby increasing safety and comfort in urban areas. In addition, the high genetic diversity of trees planted in urban areas could become significant habitats for biodiversity and genetic conservation [41] and will increase the resistance of the trees to stress, both biotic (pests and diseases) [19] and abiotic stresses [42].

#### Table 5. Total genetic gain for all traits of growth and wood quality of mahogany progeny test at Parung Panjang, Bogor.

| Selected percentage | Genetic gain |
|---------------------|--------------|
|                     | DBH | H | CBH | V | SF | SG | PP | WD |
| Individual selection |     |   |     |   |    |    |    |    |
| - 20% at 10 years old | 1.06 | 0.8525 | - | - | - | - | - | - |
| - Genetic gain (%) | 7.67 | 8.49 | 0.24 | 0.116 | 0.039 | 0.002 | 0.004 | 0.001 | 0.002 |
| Family selection | 1.70 | 8.49 | 0.24 | 0.116 | 0.039 | 0.002 | 0.004 | 0.001 | 0.002 |
| - 55.21% at 20 years old | 5.843 | 1.369 | 2.256 | 12.419 | 0.063 | 0.786 | 0.004 | 0.196 |
| - Genetic gain (%) |     |     |     |     |     |     |     |     |     |
| **Total genetic gain (%)** | **13.513** | **9.860** | **2.256** | **12.419** | **0.063** | **0.786** | **0.004** | **0.196** |
| Individual selection |     |   |     |   |    |    |    |    |
| - 20% at 10 years old | 1.06 | 0.8525 | - | - | - | - | - | - |
| - Genetic gain (%) | 7.67 | 8.49 | 0.24 | 0.116 | 0.039 | 0.002 | 0.004 | 0.001 | 0.002 |
| Family selection | 1.71 | 8.49 | 0.26 | 0.1318 | 0.0396 | 0.0061 | 0.0052 | 0.0005 | 0.0016 |
| - 54.17% at 20 years old | 5.884 | 1.449 | 2.559 | 12.774 | 0.166 | 0.929 | 0.003 | 0.157 |
| - Genetic gain (%) |     |     |     |     |     |     |     |     |     |
| **Total genetic gain (%)** | **13.554** | **9.940** | **2.559** | **12.774** | **0.166** | **0.929** | **0.003** | **0.157** |
| Individual selection |     |   |     |   |    |    |    |    |
| - 20% at 10 years old | 1.06 | 0.8525 | - | - | - | - | - | - |
| - Genetic gain (%) | 7.67 | 8.49 | 0.24 | 0.116 | 0.039 | 0.002 | 0.004 | 0.001 | 0.002 |
| Family selection | 2.02 | 8.49 | 0.30 | 0.1057 | 0.0462 | 0.0015 | 0.0058 | 0.0008 | 0.0016 |
| - 47.92% at 20 years old | 6.963 | 1.673 | 2.052 | 14.903 | 0.041 | 1.036 | 0.005 | 0.157 |
| - Genetic gain (%) |     |     |     |     |     |     |     |     |     |
| **Total genetic gain (%)** | **14.634** | **10.164** | **2.052** | **14.903** | **0.041** | **1.036** | **0.005** | **0.157** |
| Individual selection |     |   |     |   |    |    |    |    |
| - 20% at 10 years old | 1.06 | 0.8525 | - | - | - | - | - | - |
| - Genetic gain (%) | 7.67 | 8.49 | 0.31 | 0.1171 | 0.0474 | 0.0039 | 0.0059 | 0.0011 | 0.0016 |
| Family selection | 2.05 | 8.49 | 0.31 | 0.1171 | 0.0474 | 0.0039 | 0.0059 | 0.0011 | 0.0016 |
| - 46.88% at 20 years old | 7.067 | 1.735 | 2.274 | 15.290 | 0.106 | 1.054 | 0.007 | 0.157 |
| - Genetic gain (%) |     |     |     |     |     |     |     |     |     |
| **Total genetic gain (%)** | **14.737** | **10.226** | **2.274** | **15.290** | **0.106** | **1.054** | **0.007** | **0.157** |

Table 5. Total genetic gain for all traits of growth and wood quality of mahogany progeny test at Parung Panjang, Bogor.
- 45.83% at 20 years old
- Genetic gain (%) 7.078 1.792 10.313 15.516 0.258 0.893 0.001 0.137
Total genetic gain (%) 14.748 10.283 10.313 15.516 0.258 0.893 0.001 0.137

Individual selection 1.06 0.8525 - - - - - -
- 20% at 10 years old
- Genetic gain (%) 7.67 8.49
Family selection 2.35 0.30 0.6907 0.0531 0.0346 0.0052 0.0036 0.0015
- 39.58% at 20 years old
- Genetic gain (%) 8.099 1.676 11.839 17.129 0.940 0.929 0.022 0.147
Total genetic gain (%) 15.769 10.167 11.839 17.129 0.940 0.929 0.022 0.147

Individual selection 1.06 0.8525 - - - - - -
- 20% at 10 years old
- Genetic gain (%) 7.67 8.49
Family selection 2.43 0.30 0.6239 0.0545 0.0272 0.0053 0.0046 0.0014
- 38.54% at 20 years old
- Genetic gain (%) 8.364 1.686 12.115 17.581 0.739 0.946 0.028 0.137
Total genetic gain (%) 16.034 10.177 12.115 17.581 0.739 0.946 0.028 0.137

Notes: H = tree height, CBH = clear bole height, D = diameter, V = volume, CF = crown form, SG = specific gravity, PP = pilodyn penetration, WD = wood density

4. Conclusion
Heritability values are generally categorized as high (individual heritability 0.33-0.96 and family heritability 0.26-0.56) so that it has the possibility of genetic inheritance in the next generation. Genetic and phenotypic correlations performed shows that diameter at breast height has significant correlation with other growth and wood quality parameters. The percentage of selection of 44.68% (45 best families) gives an optimum genetic gain response based on growth and wood quality traits that can be used in the selection process to convert the progeny test to seedling seed orchard. The use of seeds from seedling seed orchards combined with appropriate arboricultural practices will reduce the risk of tree hazards and increase the success of urban forest development that is able to provide safety and comfort for urban residents.

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