The growth and genetic potentials of gempol (Nauclea orientalis L.) as shading trees in urban landscapes

F Riany1, I Z Siregar2 and D J Sudrajat3
1Department of Silviculture, Faculty of Forestry, Bogor Agricultural University, Bogor 16680, West Java, Indonesia
2Department of Silviculture, Faculty of Forestry, Bogor Agricultural University, Bogor 16680, West Java, Indonesia
3Research and Development Centre of Forest Trees Propagation Technology, Bogor 16001, West Java, Indonesia

E-mail: izonsiregar@gmail.com

Abstract. Gempol (Nauclea orientalis L.) is a fast-growing species with a wide crown and large diameter. This native species has the ability to replenish soil fertility and to control erosion and may be integrated in urban landscapes for genetic conservation purposes. However, the ecological function of the species as well as the genetic potentials of this species have not been investigated. This study aimed to assess the growth performance and to evaluate the genetic potentials of gempol by utilizing the progeny test stand that was established in 2011 using a Randomized Complete Block Design (RCBD). The area was divided into 10 blocks in which each block was represented by 49 families planted using 4-tree-plot replication. The observation showed that as much as 67% of the trees had a straight stem form with the average score of 4.38. The diameter ranged between 9.17 – 14.23 cm, with a total height that ranged 5.90 – 8.60 m and a crown diameter with a range of 2.06 – 3.32 m. Depending on the traits, the heritability varied between low to high. Clear bole height performed the highest heritability with a value of 0.60 (family) and 0.52 (individual). A Crown diameter indicated a moderate positive correlation with a diameter degree of 0.328 and denoted a strong positive correlation with a total height degree of 0.798.

1. Introduction
The increasing awareness of a sustainable forest management and a green economy has raised the commitment of various parties to establish a sustainability realization. Green economy, which elaborates the development of national strategies for sustainable development incorporating measures for integrating environment and development [1], will provide great opportunity for forest plantation of Indonesia to increase its wood production as much as 64,068 million cubic meters of wood by 2030. In order to realize it immediately, the development and improvement program toward fast-growing species is applied widely, where one of the species included was gempol (Nauclea orientalis L.) from Rubiaceae family. This species is distributed in Australia, Indonesia and Thailand. In Australia, the bark of the species can be used for medicine, the fruits and the leaves are all edible and usually being consumed by Australians and Indonesians. In Indonesia, this species can be found naturally in Sumatera, Java, Sulawesi and Papua [2, 3]. This species has a promising prospect in producing timbers and products for pulp and paper industries. Moreover, this species is prospective for urban landscape
development, especially in terms of phytoremediation and for a land rehabilitation program, especially at the river areas [4, 2]. The species is the best alternative for the reclamation program because gempol has a phytoremediation function and plays an important role as pioneer species. Some studies indicated that gempol can still be grown effectively in the area that is polluted by heavy metals. The previous study evidenced that gempol can associate with Arbuscular Mycorrhiza Fungi (AMF) to accumulate and absorb metals that are contained in the soil, such as Fe, Mn, Zn, Cu, Pb and Cd. The study also pointed that the species had a high adaptability level toward wetland, construction and mining areas [5].

The Forestry sector has been evolved to a new era where genetically superior plants are being developed sustainably through tree improvement program. The aim of the tree improvement program nowadays is to provide superior plant material in order to establish superior stands with high quality performance, either for conservation or development programs. However, the improvement and evaluation program toward less common species, such as gempol (N. orientalis) unfortunately has not been performed so far, considering that gempol has a lot of promising prospects that need to be explored, especially for forest restoration, plantation and rehabilitation programs [6].

The demand for genetically improved seed has been increasing to support high productivity plantation stands but insufficient seed supply of gempol is often seen as a major bottleneck for the development of planting programs. Seed orchard establishment might be one of the alternatives to increase the genetic quality in gempol improvement program. Seed orchard establishment using plant material from a well-improved seed produced a well-established population with better growth and better stem form compared to a population which was grown by trees from seed production area (APB) [7]. However, the gempol plantation forest has not been established well enough in many areas in Indonesia and even if it has been established, its number has been growing from seeds with low genetic quality. Should it keep happening, it would lead to a decrease of genetic quality in future generations of this species and also a decrease in productivity [4]. To meet the high demand for improved seed and to improve the productivity of the species, Balai Penelitian Teknologi Perbanyakan Tanaman Hutan (BPTPTH)/Research and Development Center of Forest Trees Propagation Technology Bogor initiated a tree improvement program for gempol (Nauclea orientalis L.) by establishing progeny stands in 2012.

Although N. orientalis has a promising prospect in land recoveries and timber productions, there is a lack of improved seed and reliable genetic information to support successful plantation programs in Indonesia. Genetic information is required in forming the efficient operation of breeding programs through which the quality and productivity of the stands can be improved. Should the plantation take place in the urban areas, the stands are expected to not only improve the ecosystem function of the area but also to conserve and maintain the genetic diversity of the species. The aim of this study was to assess the growth performance and to predict genetic variation and parameters from 49 families of gempol at the age of 5 years in Parung Panjang Research Forest, Bogor. This study also proposed a development program towards less common species through genetic conservation and tree improvement programs.

2. Methodology

The research was carried out in Parung Panjang Research Forest which is under the authorization of Research and Development Center of Forest Trees Propagation Technology Bogor. Geographically, the area is located in 06°20’ LS (south latitude), 106°06’ BT (east longitude) at the altitude of 52 meters above sea level. Average annual rainfall reaches 2,440 mm/year with an average temperature of 28°C [8]. The observation was carried out by measuring the dimensions of stand trees using measuring tape, clinometer and haga hypsometer. The material used for this research was the progeny trial stands of gempol at the age of 5 years which was established using Randomized Complete Block Design (RCBD) with 10 blocks. Each block was represented by 49 trees coming from half-sib families in which every family was represented by 4 trees in one row plot (4-tree-plot). The population went
through 2 stages of selection since the age of 3 years (2014-2015) and the previous selection in 2016 had left 1 tree in every 4-tree-plot which meant that at the end of the third stage of selection, every 49 trees were represented by 1 tree in a row. The families came from 2 types of populations, specifically 23 families from Banten and 26 families Majalengka, West Java.

2.1. Procedures
Primary data were observed by the stands of measurements, which included:

2.1.1. Total height and clear bole height. Total height and clear bole height were measured using haga hypsometer. The measurement was performed by aiming the device from the base to the peak of the trees at 20 meters distance. For clear bole height, the measurement was performed by aiming the device from the base to the lowest base of permanent branch.

2.1.2. Diameter. Diameter was measured using measuring tape at height of 1.30 meters above the ground or at the breast height.

2.1.3. Crown diameter. Crown diameter was measured through the length of the crown in 4 (four) directions, i.e. in azimuth 0°, 90°, 180° and 270°. The results were then averaged.

2.1.4. Stem form. Stem form was evaluated using scoring system which consisted of 1 – 5 score range, as indicated by figure 1.

![Figure 1. Sketch of stem scoring, from left to right, the form was scored 5, 4, 3, 2 and 1[9].](image)

2.2. Data analysis
The measurement data were analyzed using analysis of variance (ANOVA) to see the growth variation. This trial was designed using one-way Randomized Complete Block Design (RCBD) and was formulated in equation 1 [8]:

\[ Y_{ijk} = m + F_i + B_j + Fbij + E_{ijk} \]  

Information:
- \(Y_{ijk}\) = \(k^{th}\) observation \((k = 1, 2, 3,..)\) at \(i^{th}\) family \((i = 1, 2, 3,..)\) in \(j^{th}\) block \((j = 1, 2, 3,..)\)
- \(m\) = Mean value
- \(F_i\) = Effect of \(i^{th}\) family \((i = 1, 2, 3,..)\)
- \(B_j\) = Effect of \(j^{th}\) block \((j = 1, 2, 3,..)\)
- \(Fbij\) = Effect of interaction between the \(i^{th}\) family and the \(j^{th}\) block
- \(E_{ijk}\) = Error
Individual and family heritability was quantified using equation (2) and (3) [10]:

\[ h^2_i = \frac{4\sigma^2_f}{\sigma^2_e + \sigma^2_{fb} + \sigma^2_f} \]  

\[ h^2_f = \frac{\sigma^2_f}{\frac{\sigma^2_e}{b} + \frac{\sigma^2_{fb}}{t} + \sigma^2_f} \]  

Information:

- \( h^2_i \) = Individual heritability
- \( h^2_f \) = Family heritability
- \( \sigma^2_f \) = Family variances
- \( \sigma^2_{fb} \) = Variances of interaction between family and block
- \( \sigma^2_e \) = Error variances
- \( b \) = Number of blocks

Genetic gain was quantified to predict the response of the population towards selection and it was predicted using following formula in table 1 [11]:

**Table 1.** Total genetic gain which was resulted from different types of selection methods.

| Selection Method   | Genetic Gain                                                                 |
|--------------------|------------------------------------------------------------------------------|
| Within-family Election | \( G = i_3 \sigma_p h^2_i \left(1 - r\right) \left\{\frac{(n-1)/n(1-t)}{1}\right\}^{1/2} \) |
| Family Election     | \( G = i_2 \sigma_p h^2_f \left(1 + (n-1)r\right)/\left(n(1 + (n - 1)/t)\right)^{1/2} \)  |

Information:

- \( i_3 \) = Percentage of individual within-family selection
- \( i_2 \) = Percentage of family selection
- \( \sigma_p \) = Variation on a trait
- \( h^2_i \) = Individual heritability
- \( h^2_f \) = Family heritability
- \( t \) = Interclass correlations (0.25 \( h^2 \))
- \( n \) = Average number of trees per family

3. Results and discussion

3.1. Physical performance

Gempol (N. orientalis) is a native species that is distributed from Australia, Indonesia until Thailand and can be found in various types of vegetation, but it reaches its best performances in rain-forest ecosystem. In the plantations, N. orientalis can be associated with Eucalyptus camaldulensis, Melaleuca argentea, Castanospermum austral, Beilschmiedia obtusifolia and Syzygium tierneyanum. Instead of only reaching its best performance in rain forest ecosystem, this species is also adaptive to a wide range of ecosystems, such as dry lands, wet lands and river side ecosystem, as long as the altitude is no more than 500 meters above the sea level. This species can be the best choice for replantation program in the river side area since this species also reaches its best performance when planted in alluvial soils which usually are found at the side of the river areas [2, 3].
Gempol is also categorized as Multi-Purposes Tree Species (MPTS) because the body parts of the trees can be used for ecological, social and economic purposes. For ecological purposes, the species can provide a great width of crown diameter for a shading tree. This character of gempol makes gempol as a suitable species for urban development where the crown can provide shade areas in cities. Moreover, gempol is functioned as pioneer species in degraded land, such as in post-mining areas. Gempol can replenish the soil by shedding the leaves. Gempol has great width of crown to conserve the soil from rapid fall down of rain. The activity of its root also conserves the water availability in the area that makes the succession process goes well without much disruption such as erosion and the run-off area. The species is also known to be a key species in community forests and be associated with agroforestry crops [3]. In Parung Panjang, this species provides social function for local people because the forest floor under gempol stands is used for agroforestry practices and gempol provides a great ecological support for the crops. Through these practices, both local people and the stakeholders feel the benefit from the trees. As an economic function, gempol serves as a great material for timber productions and paper industries. In Indonesia, the quality of gempol woods are included in Quality Category Class II and Durability Category Class IV which means that the woods perform a great strength toward mechanical action but exhibit a poor durability toward pests and diseases after being cut down from the living trees [12]. Gempol possesses a great length of fiber to produce a high quality paper in pulp and paper industries with the length of 1.600 mm. The full stand and the leaves of gempol can be seen at figure 2.

![Figure 2. The performance of a) gempol tree (N. orientalis) at the age of 5 years, b) cross section of gempol leaves. Source: personal documentation.](image-url)

3.2. Growth variation and stands condition in progeny test stands of Nauclea orientalis L.

Figure 3 portrays that all of the observed traits, such as total height, clear bole height, diameter and crown diameter indicating that there was a variance on growth among the families. The variance shown in the figure was a positive signal to continue tree improvement programs for selection and genetic evaluation since larger variation would provide larger potential for responding selection [13]. Phenotypic traits such as individual healthiness, stem straightness, branch architecture, tree height and diameter are measurable traits that can be used for trees selection. The population that displays the
straight stem is a good prefix in the tree improvement program to continue the program to genetic evaluation and selection. This study enlisted that 67% of the trees performed a straight stem with the average score of 4.38. A study related to stem straightness indicated that stem straightness could be used as a milestone for stands evaluation since large positive correlation among them has been illustrated [9].

![Histogram of D](image)

**Figure 3.** Histogram in *N. orientalis* stands for a) diameter, b) total height, c) clear bole height and d) crown diameter.

The trees grew with a diameter of 9.17 – 14.23 cm and a total height up to 5.90 – 8.60 m with a total age of 5 years old. Clear bole height ranged between 2.34 – 4.15 m and crown diameter ranged between 2.06 – 3.32 m. Different family occupied different rankings on each traits measured. Overall, the observation proved that promising families were from Banten. Various families occupied different ranking on each parameters. Family number 27 from Banten had the highest diameter, family number 47 from Majalengka had the highest height, family number 13 from Banten had the highest clear bole height and family number 15 from Banten had the longest crown diameter. Therefore, overall, the observation indicated that promising families came from Banten. The results of ANOVA are shown in table 2 and table 3.

At the age of 5 years old, ANOVA pointed that the family did not show significant effect on all traits meanwhile the block contributed significant effects. This meant that the variation was mostly environmental. The lack of genetic diversity in the population demonstrated that the population might have small potential for responding selection (genetic gain). The previous research that was conducted in provenance stands of sengon Solomon described that the family variance was not significantly different on height and diameter growth and furthermore led to homogeneity in growth at the age of 6 months and 18 months [14]. The research suggested that low genetic diversity or genetic basis of the constituent attributed to the uniformity in growth.
Table 2. Analysis of variance of the observed traits on progeny stands of *Nauclea orientalis* at the age of 3 and 4 years.

| Traits/Age      | Source of Variance | Degree of Freedom | Sum of Squares | Mean Square | F Value | Pr > F |
|-----------------|---------------------|-------------------|---------------|-------------|---------|--------|
| Diameter/3 Years Old | Block              | 9                 | 11296741.46   | 1255193.50  | 125.61* | <.0001 |
|                  | Family              | 48                | 1619435.82    | 33738.25    | 3.38*   | <.0001 |
|                  | Family * Block      | 421               | 16947832.94   | 40256.14    | 4.03*   | <.0001 |
|                  | Error               | 1245              | 12440919.00   | 9992.71     |         |        |
| Diameter/4 Years Old | Block              | 9                 | 2129.620305   | 236.624478  | 59.99*  | <.0001 |
|                  | Family              | 48                | 635.327000    | 13.235979   | 3.36*   | <.0001 |
|                  | Family * Block      | 412               | 4599.647614   | 11.164193   | 2.83*   | <.0001 |
|                  | Error               | 349               | 1376.682617   | 3.944649    |         |        |
| Total Height/3 Years Old | Block              | 9                 | 11296741.46   | 1255193.50  | 125.61* | <.0001 |
|                  | Family              | 48                | 1619435.82    | 33738.25    | 3.38*   | <.0001 |
|                  | Family * Block      | 421               | 16947832.94   | 40256.14    | 4.03*   | <.0001 |
|                  | Error               | 1245              | 12440919.00   | 9992.71     |         |        |
| Total Height/4 Years Old | Block              | 9                 | 872.050825    | 96.894536   | 94.37*  | <.0001 |
|                  | Family              | 48                | 205.579789    | 4.282912    | 4.17*   | <.0001 |
|                  | Family * Block      | 412               | 1349.069694   | 3.274441    | 3.19*   | <.0001 |
|                  | Error               | 349               | 358.340833    | 1.026765    |         |        |

*a*Source: [15, 16]; Calculation was done in 2015 and 2016; *significantly different at 5%.

Table 3. Analysis of variance of the observed traits on progeny stands of *Nauclea orientalis* at the age of 5 years.

| Traits/Age      | Source of Variance | Degree of Freedom | Sum of Squares | Mean Square | F Value | Pr > F |
|-----------------|---------------------|-------------------|---------------|-------------|---------|--------|
| Diameter/5 Years Old | Block              | 9                 | 1224.313482   | 136.034831  | 18.92*  | <.0001 |
|                  | Family              | 48                | 429.688981    | 8.951854    | 1.24    | 0.1358 |
|                  | Family * Block      | -                 | -             | -           | -       |        |
|                  | Error               | 408               | 2934.144478   | 7.191531    |         |        |
| Total Height/5 Years Old | Block              | 9                 | 1071.327901   | 119.036433  | 64.35*  | <.0001 |
|                  | Family              | 48                | 107.211532    | 2.233574    | 1.21    | 0.1710 |
|                  | Family * Block      | -                 | -             | -           | -       |        |
|                  | Error               | 408               | 754.773362    | 1.849935    |         |        |
| Clear Bole Height/5 Years Old | Block              | 9                 | 523.7644071   | 58.1960452  | 52.27*  | <.0001 |
|                  | Family              | 48                | 61.0977838    | 1.2728705   | 1.14    | 0.2459 |
|                  | Family * Block      | -                 | -             | -           | -       |        |
|                  | Error               | 408               | 455.340764    | 1.113303    |         |        |
| Crown Diameter/5 Years Old | Block              | 9                 | 35.20611268   | 3.91179030  | 9.54*   | <.0001 |
|                  | Family              | 48                | 33.4683322    | 0.69725694  | 1.70    | 0.0036 |
|                  | Family * Block      | -                 | -             | -           | -       |        |
|                  | Error               | 408               | 167.3314101   | 0.4101260   |         |        |

*b*The calculation was conducted in April 2017; *significantly different at 5%; the dash sign (-) displays that the calculation was not performed in this section.

However, before the study was conducted, the stands had undergone the individual selection within the plot and individual selection within the family at the age of 3 and 4 years, thus in 2017, the selection retained one tree in every 4-trees-plot and the interaction between family and block could not
be measured. The previous individual within-family selection was undertaken based on the total height and diameter on trees with the performance below the average so that in recent days, the stands are composed by trees with performance above the average which means that the genetic materials that compose the stands had reached the fixation of well-improved genes. Furthermore, the genes fixation made the stands to be more homogenous. In the other hand, there was also a possibility of the homogeneity of the traits to happen because of the plants originated from only 2 (two) locations which could only provide a limited diversity. The selection in the early ages would provide a large change in gene frequency. In addition, selection in the early ages would accelerate the occurrence of certain alleles in order for the end of the selection where the stands composed and structured by fixed genes and may be led to genetic homogeneity [17]. This research also followed the same patterns with the previous literature. Based on table 2 and table 3, the family was significantly different from the total height and diameter during the measurement of 3 and 4 years old stands meanwhile later on, after simultaneous selection, the family did not show significant differences on the total height and diameter.

3.3. Correlation between the observed traits and the crown diameter
As mentioned in the tree improvement program, the coefficient of correlation expresses the relation between one trait and another. Coefficiency of correlation also expresses the degree of change of certain traits as a response to improvements toward another trait [8, 18]. The correlation between the observed traits with the quality of wood of *Nauclea orientalis* L. is displayed in table 4.

|                       | Diameter | Total Height | Clear Bole Height | Bole Height | Crown Diameter |
|-----------------------|----------|--------------|-------------------|-------------|----------------|
| Diameter              | 0.755**  |              |                   |             |                |
| Total Height          |          | 0.434**      |                   | 0.002       |                |
| Clear Bole Height     | 0.434**  | 0.674**      |                   | 0.198**     |                |
| Crown Diameter        | 0.437**  | 0.198**      | 0.002             |             |                |

**significantly correlated at the rate of 99%; *correlated at the rate of 95%**

The results illustrated that all the correlations except between the clear bole height and the crown diameter were highly significant. These results indicated that the diameter growth would likely affect the increase of the crown diameter in growth, as well as the total and clear bole height. This demonstrated that the improvement toward the diameter and the total height would increase the crown diameter. Therefore, favorable improvements should be based on both the diameter and the total height. The diameter and the total height evidenced a positive correlation with the crown diameter most of the time and the relation between these traits could be used for dimension modelling [19].

3.4. Individual and family heritability
The heritability of progeny stands of *Nauclea orientalis* L. was quantified frequently annually since the age of 1 year. Individual and family heritability of *Nauclea orientalis* L. at the age of 5 years is illustrated in table 5 below.

Based on the heritability grouping, individual heritability of the total height and diameter of *Nauclea orientalis* L. at the age of 5 years were considered low, with the value of 0.18 and 0.20, respectively. The individual heritability of the crown diameter was moderate, with a value of 0.27. This result indicated the same trend for family heritability where heritability of the total height and diameter was considered low and the family heritability of the crown diameter was considered...
moderate. Meanwhile, the clear bole height performed the highest individual and family heritability with a value of 0.60 and 0.52, respectively.

| Phenotype          | Family Heritability | Individual Heritability |
|--------------------|---------------------|-------------------------|
| Total height       | 0.18 (low)          | 0.08 (low)              |
| Clear Bole height  | 0.60 (high)         | 0.52 (high)             |
| Diameter           | 0.20 (low)          | 0.10 (low)              |
| Crown diameter     | 0.42 (moderate)     | 0.27 (moderate)         |

The classification was adapted from [20]: low heritability (h² < 0.2), moderate heritability (0.2 < h² < 0.5), high heritability (h² > 0.5).

Overall, it can be concluded that the total phenotypic variance in the total height and diameter consisted of larger proportions of environment variance at both individual and family levels. Meanwhile, clear bole height showed the highest heritability which means that this trait was more influenced by genetic variance than by environmental variance. Since the age of 1 year, the heritability of progeny stands had experienced changes until the age of 5 years. The changing on heritability over the years for total height and diameter traits is shown in figure 4.

The ANOVA and heritability quantification displayed that the variance within the population in gempol progeny stands almost entirely consisted of environment variance instead of family variance. The result was probably affected by differences in the site quality where the stands were grown. Local people living around the forest cultivated agricultural crops on the forest floor by using agroforestry system. The cultivated plants were varied among the sites. Agroforestry practices and the heterogeneity of cultivated plants might have affected the differences among sites, which also contributed to environmental variance.

In progeny trials and in the tree improvement program, variance among sites should be reduced in such a way so that the genetic variance can be calculated. Previous study regarding the reduction of total variation investigated that decent replications in an experimental design would reduce environmental variance to certain effects and would increase the heritability throughout the growth period. His research explained that the heritability of a 1-year-old *Hevea brasiliensis* increased from 0.50 to 0.67 at the age of 3 years for diameter traits since the progeny stand had been established in 3 locations, in which every location was divided into 10 replications [22].

The low heritability for primary traits (diameter and the total height) in present study indicated that best families may not be precisely identified in this age. Selection of the best families may have to wait in certain amount of time in order to gain the genetic performance in the population. Higher heritability ensures greater response in breeding program, allowing recombination of the best individuals in a shorter period of time [23].
Figure 4. Fluctuating changes in family and individual heritability for a) diameter and b) the total height at various ages.

In this case, the selection between the families could be done in progeny stands of *Nauclea orientalis* L. in Parung Panjang since the stands have passed the individual selection at the age of 3 years and 4 years. Selection between families was the last stage of selection of *Nauclea orientalis* L. stands, where the aim of this selection was to retain individuals from the best families to be the maternal stands for future improvement. Thus, at the end of the selection, one tree from the best families was maintained on each plot as the maternal stands [10].

3.5. *Selection and genetic gain*

Genetic gain of a generation is a factor of interaction between heritability and selection intensity (table 1). The expected genetic gain of progeny stands of *Nauclea orientalis* L. in Parung Panjang is presented at table 6.
The table illustrates that the lower the number of families retained in a population, the higher the genetic differences of the population and the bigger in genetic gain of the generation. Selection simulation was conducted with 10% intensity (retaining 44 best families), 20% intensity (retaining 40 best families), 30% intensity (retaining 34 best families) and 40% intensity (retaining 30 best families). The selection towards the total height by leaving 44 best families (10% intensity) provided a genetic gain of 0.017 and contributed to 1.18% of height increment. Meanwhile, if the selection was carried out by leaving 34 best families (40% intensity) the genetic gain of 0.060 would provide 4.01% increment to total height. The same result applied to other traits as well.

**Table 6.** Expected genetic gain total for the observed traits at various selection intensities on the progeny trial stands of *N. orientalis* L.

| Selection Intensity | Selection Strategy | Total Height | Diameter | Clear Bole Height | Crown Diameter |
|---------------------|--------------------|--------------|----------|-------------------|----------------|
| 75%                 | Within-family selection\(^a\) | 0.019        | 0.932    | -                 | -              |
| 10%                 | Family selection\(^b\)            | 0.122        | 0.336    | 0.157             | 0.373          |
| Genetic gain total  |                    | 0.141        | 1.268    | 0.157             | 0.373          |
|                     |                    | (1.18%)      | (1.47%)  | (2.20%)           | (1.75%)        |
| 75%                 | Within-family Election | 0.019        | 0.932    | -                 | -              |
| 20%                 | Family selection    | 0.244        | 0.672    | 0.314             | 0.075          |
| Genetic gain total  |                    | 0.263        | 1.604    | 0.314             | 0.075          |
|                     |                    | (1.98%)      | (2.55%)  | (3.51%)           | (3.09%)        |
| 75%                 | Within-family selection | 0.019        | 0.932    | -                 | -              |
| 30%                 | Family selection    | 0.366        | 1.009    | 0.472             | 0.112          |
| Genetic gain total  |                    | 0.385        | 1.940    | 0.472             | 0.112          |
|                     |                    | (3.24%)      | (4.21%)  | (5.13%)           | (4.92%)        |
| 75%                 | Within-family selection | 0.019        | 0.932    | -                 | -              |
| 40%                 | Family selection    | 0.488        | 1.345    | 0.629             | 0.149          |
| Genetic gain total  |                    | 0.507        | 2.277    | 0.629             | 0.149          |
|                     |                    | (4.01%)      | (5.20%)  | (6.20%)           | (5.93%)        |

Source: the observation was done at the age of 3 years; observation was done in April 2017; dash sign (-) shows that the observation was not done, the percentage (%) was measured based on the average changes of the character before and after selection; selection intensity (%) was determined based on the percentage of trees that were thinned/cut down in a plot (within-family selection) and in a block (family selection).

Genetic gain of *Nauclea orientalis* L. population expressed the response of population toward selection and the result showed that selection would increase the genetic performance on the observed traits. Selection that left 30 best families in each block performed the highest genetic gain. Should selection be performed in certain population, the selected population is expected to provide favorable gain on genetic variance and is expected to gain productivity [17]. The calculation of genetic gain on progeny trial stands portrayed that selection would increase the genetic performance on the observed
traits at certain rates. Since in Indonesia, a seed orchard must contain at least 25 mother trees in order to be productive, selection intensity is limited to 40% where a selection will maintain 30 mother trees in each block. The family selection that provided a favorable increase in the population was the selection with a 40% intensity (retaining 30 best families on each block).

Both within-family selection (with the intensity of 75%) and family selection as a result in a significant increase in genetic gain. The total genetic gain at various intensities was expected to generate a better gempol population in the next generation after the execution of family selection. This study was conducted to determine the most favorable intensity to produce the stands in which generated primary traits (diameter, total height and crown diameter) much faster and greater. Based on that consideration, the selection shall be better if performed with 40% intensity which would maintain 30 best families on each block as the next maternal stands. The selection increased total height and diameter significantly as much as 0.507 and 2.277 in total, respectively. Moreover, the selection increased the increment of total height and diameter as much as 5.20% and 4.01%, respectively, compared to the stands before family selection. In addition, selection with 40% intensity gained the genetic performance of the crown diameter as much as 0.149 which contributed to 5.93% increment compared to the stands before family selection.

Genetic gain is strongly affected by genetic variation and heritability. The increase in genetic gain may be achieved through the increase in selection differential, additive genetic variation and the decrease in environmental variations. The populations with a high heritability ($h^2 = 1$) and a high differential value ($D_s = 3.48$) generated the greatest genetic gain. In addition, the lower the number of maternal trees maintained in a population, the greater the possibility to increase genetic gain through selection [21].

4. Conclusions

The observation indicated that as much as 67% of the trees providing a straight stem form with the average score of 4.38. ANOVA indicated that families did not have significant effect on the observed traits. Depending on the traits, the heritability varied between low to high. Crown diameter as the indicator for shading trees in urban landscapes demonstrated moderate heritability with a value of 0.27 (individual heritability) and 0.42 (family heritability). Meanwhile clear bole height illustrated the highest heritability with the value of 0.52 (individual heritability) and 0.60 (family heritability).

The selection intended to produce stands with the wide crown, improvement toward diameter and the total height might be effective since there was a strong positive correlation between the crown diameter and the diameter and total height. The selection could be performed by leaving 30 of the best families in each block (40% selection intensity) in order to gain the favorable genetic material.

References
[1] UN Department of Economic and Social Affairs, Division for Sustainable Development 2012 A Guidebook to the Green Economy (New York: UNDESA)
[2] Orwa C Mutua A Kindt R Jamnadass R and Simonis A 2009 Agroforestry Database: a Tree Reference and Selection Guide Version 4.0 (Kenya: World Agroforestry Centre)
[3] Muslich M Wardani M Kalima T Ruliati S Damayanti R Hadjib N Pari G Suprapti S Iskandar M I Abdurachman Basri E Heriansyah I Tata H L 2013 Atlas Kayu Indonesia Jilid IV [Indonesia Wood Atlas Volume IV] 2013 ed Krisdianto Barly Abdurrohim S Mandang S S (Bogor: Pusat Penelitian dan Pengembangan Keteknikan Kehutanan dan Pengolahan Hasil Hutan (PUSTEKOLAH)) (In Indonesian)
[4] Putri K P Yulianti and Danu 2016 Keragaman pertumbuhan bibit gempol (Nauclea orientalis L.) dari beberapa pohon induk [Seedling growth variation of gempol (Nauclea orientalis L.) from several mother trees] J Hutan Tropis 4 (1) 8–13 (In Indonesian)
[5] Tuheteru F D Kusmana C Mansur I Iskandar and Tuheteru E J 2016 Potential of Ionkid (Nauclea orientalis L.) for phytoremediation of acid mined drainage at PT. Bukit Asam
Tbk. (Persero), Indonesia Research Journal of Botany 11 (1–3) 9–17
[6] Alberta Forest Service 1998 Tree Improvement: Applied Research and Technology Transfer ed Puri S (New Hampshire: Science Publishers Inc)
[7] Leksmono B Nirsatmanto A Setyo R and Sofyan A 2007 Uji perolehan genetik kebun benih semai generasi pertama (F-1) jenis Acacia mangium di tiga lokasi [Genetic gains trial of first-generation seedling seed orchards of Acacia mangium established in three locations] J Penelitian Hutan Tanaman 4 (1) 1–67
[8] Williams E R Matheson A C and Harwood C E 2002 Experimental Design and Analysis for Tree Improvement Second Edition (Collingwood: CSIRO Publishing)
[9] Harijoko Sumarjo Budiman I Suherman E and Tocin 2006 Manual Seleksi Pohon Plus [Manual for plus trees selection] (Sumedang: Balai Perbenihan Tanaman Hutan Jawa dan Madura) (In Indonesian)
[10] Sutrisno L 2007 Pendugaan nilai heritabilitas pada tegakan uji keturunan Acacia mangium Willd generasi kedua di Parungpanjang [Skripsi] [Heritability quantification on progeny trial stands of second generation Acacia mangium in Parungpanjang] [Undergraduate thesis]. (Bogor: Faculty of Forestry, Bogor Agricultural University) (In Indonesian)
[11] Iriantono D Sudrajat D J and Ismawati I 2000 Mutu fisik, fisiologi dan keragaman genetik benih Acacia mangium Willd. Asal kebun benih Parungpanjang, Bogor [Physical, physiological qualities and genetics variation of Acacia mangium Willd. seeds originally from Parungpanjang seed orchard, Bogor] J Teknologi Perbenihan 7 (2) 42–53 (In Indonesian)
[12] Tuweteru F D Kusmana C Mansur I and Iskandar 2014 Karakteristik buah dan mutu morfofisiologis benih lonkida (Nauclea orientalis L.) dari habitat alami di Sulawesi Tenggara [Fruit and morpho-physiology seed characteristics of lonkida (Nauclea orientalis L.) from natural habitats in South East Sulawesi] J Pemuliaan Tanaman Hutan 8 (3) 152–170 (In Indonesian)
[13] White T L Adams W T and Neale D 2007 Forest Genetics (Oxfordshire: CAB International)
[14] Setiadi D Baskorowati L and Susanto M 2014 Pertumbuhan sengon Solomon dan responnya terhadap penyakit karat tumor di Bondowoso, Jawa Timur [Growth of sengon Solomon and its response to gall rusts diseases in Bondowoso, East Java] J Pemuliaan Tanaman Hutan 8 (2) 121–136 (In Indonesian)
[15] Danu Sudrajat D J Yulianti B and Pujiastuti E 2015 Laporan Kegiatan Balai Penelitian dan Pengembangan Teknologi Perbenihan Tanaman Hutan [Seed source development in Parung Panjang. Research and Development Centre of Forest Trees Propagation Technology Activity Report] (Bogor: BPTPTH Bogor) (In Indonesian)
[16] Danu Sudrajat D J Yulianti B and Pujiastuti E 2016 Laporan Kegiatan Balai Penelitian dan Pengembangan Teknologi Perbenihan Tanaman Hutan [Seed source development in Parung Panjang. Research and Development Centre of Forest Trees Propagation Technology Activity Report] (Bogor: BPTPTH Bogor) (In Indonesian)
[17] Syukur M Sujiprihati S and Yuniarti R 2015 Teknik Pemuliaan Tanaman [Tree improvement techniques] (Jakarta: Penebar Swadaya) (In Indonesian)
[18] Hartl D L and Clark A G 2007 Principles of Population Genetics Fourth Edition (Sunderland: Sinauer Associates, Inc.)
[19] Harjana A K 2013 Model hubungan tinggi dan diameter tajuk dengan diameter setinggi dada pada tegakan tengkawang tungkul putih (Shorea macrophylla (de Vriese) P.S. Ashton) dan tungkul merah (Shorea stenoptera Burck.) di Semboja, Kabupaten Sanggau [Correlation model between height and crown diameter with diameter at breast height on tengkawang tungkul putih (Shorea macrophylla (de Vriese) P.S. Ashton) and tungkul merah (Shorea stenoptera Burck.) stand in Semboja, Sanggau Regency] Jurnal Penelitian Dipterokarpa 7 (1) 7–18 (In Indonesian)
[20] Susiana E 2006 Pendugaan nilai heritabilitas, variabilitas dan evaluasi kemajuan genetik beberapa karakter agronomi genotipe cabai (Capsicum annuum L.) F4 [Skripsi] [Estimation of heritability, variability and evaluation of genetic gain of several agronomy characteristics of chili (Capsicum annuum L.) genotype F4: Undergraduate thesis]. (Bogor: Faculty of Forestry, Bogor Agricultural University) (In Indonesian)

[21] Wright J W 1962 Genetics of Forest Tree Improvement (Michigan: Food and Agriculture Organization of the United States)

[22] Goncalves P D S Aguiar A T D E da Costa T D B Goncalves E C P Scaloppi Junior E J and Branco R B F 2009 Genetic variation and realized genetic gain from rubber tree improvement. Sci. Agric 1 (66) 44–51

[23] Dlamini L N Pipatwattanakul D and Maelim S 2017 Growth variation and heritability in a second-generation Eucalyptus urophylla progeny test at Lad Krating Plantation, Chachoengsao Province, Thailand. Journal of Agricultur and Natural Resources 51 (2) 63–136