Genetic variation of *Gmelina arborea* Roxb in Trenggalek, East Java

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**Abstract.** White teak (*Gmelina arborea* Roxb) is an introduced species of the verbenaceae. This study observed genetic variation of *G. arborea* in Trenggalek, East Java. Incomplete Block Design was used for this trial comprising four replications, five populations, 50 families, and three tree plots with planting space of 3 x 2 m. Significant differences between seed origins for height and survival rate were exhibited in this study; however, no significant differences between populations for diameter traits at 1st year old. Meanwhile, significant differences between populations for height, survival rate existed at second years old. The mean survival rate at first and second years old were 98.44% and 95.95%, height were 1.23 m and 2.86 m, and stem diameter was 2.18 cm and 3.66 cm. Moderate heritability's showed for height and diameter were \((h^2_i = 0.29; h^2_f = 0.30), (h^2_i = 0.24; h^2_f = 0.38), (h^2_i = 0.19; h^2_f = 0.30), (h^2_i = 0.18; h^2_f = 0.28)\). Genetic correlation for height and diameter were \(r_g = 0.75\), and \(r_g = 0.89\). Genetic variation growth of *G. arborea* progeny test can be used as basic information of the plus trees selection with good performance. Therefore, the open pollination between remaining plus tress will produce a good quality of seed, which will increase the volume of timber harvested.

1. **Introduction**

The use of quality seeds from seed orchards will determine the success of the plantation forest program. Since the use of seeds from unknown seed sources or provenances is the main factor causing the unsuccessfulness plantation. Therefore, several targets such as high stand productivity (increment), good wood quality, sustainable production forest sustainability could not be managed [1].

White teak (*Gmelina arborea*) is generally planted by farmers in community forests to fulfill timber needs. This species belongs to the Verbenaceae family with a medium durable class, and it has moisture content ranges from 12-15%. The wood is easy to work with and is resistant to weather. Therefore, it is often used as building construction material, pulp, paper and other wood crafts [2, 3]. Other widely studied uses are its potential as a medicinal plant, i.e., from the roots, leaves, fruit and stem bark [4, 5, 6]. Therefore, *G. arborea* has a good prospect to be developed both in plantations and as a rehabilitation/enrichment plant as an alternative to address the increasing wood demand. This species grows naturally in Cambodia, China (Yunnan and Kwangsi Chuang Provinces), India, Laos, Myanmar, Nepal, Pakistan, Sri Lanka, Thailand, and Vietnam [7, 8]. This species grows rapidly and only takes ten years to be harvested, which usually reaches 50 cm in diameter and a total height of 30 m. Moreover, it has beautiful wood colors and architecture similar to teak. The rapid growth and the pattern of wood architectures attract farmers and industries to develop and establish the plantation using good quality seeds.
There was no seed orchard or seed source of *G. arborea* stand in Java, even though the demand for high-quality seeds from this species is high. In order to provide a good seed of *G. arborea*, the Center for Forest Biotechnology in Tree Improvement (CFBTI) collaborated with East Java Forest Service to establish the progeny test for identifying the seed origin of *G. arborea* with best productivity and adaptation for commercial use [9]. The progeny test then will be converted as a seed orchard after thinning several trees with bad performances. Therefore, this study will determine the seed origin of *G. arborea* based on several characters, i.e., growth (height and diameter) and survival rate, by estimating the heritability value and genetic correlations.

2. Materials and Methods

2.1. Research materials and location

The seed origin of *G. arborea* Roxb was provided from 5 provinces (Table 1). Those were established plantation for progeny test in 2016 at Trenggalek Regency, East Java Province, at an altitude of 750 m above sea level with 0-30% land slope, having an annual average rainfall of 5083 mm year\(^{-1}\). This area has climate type C with a rainy season starting in November and ending in March, while the soil type includes Litosol [10].

| No | Seed Origin (Province) | Altitude (m asl) | Latitude-South | Longitude-East | Soil Type |
|----|------------------------|------------------|----------------|---------------|-----------|
| 1  | Bantul (Yogyakarta)    | 146              | 07°56’13”      | 110°27’34”    | Regosol    |
| 2  | Bogor (West Java)      | 252              | 07°59’80”      | 113°49’17”    | Latosol    |
| 3  | Ketapang (Lampung)     | 159              | 05°44’64”      | 105°44’35”    | Aluvial    |
| 4  | Bondowoso (East Java)  | 800              | 08°32’32”      | 116°14’10”    | Andosol    |
| 5  | Lombok (West Nusa Tenggara) | 310          | 06°20’49”      | 106°06’33”    | Latosol    |

Source: [11]

2.2. Trial design

Incomplete block design (IBD) was used and comprised of 5 seed origins as treatments, four replications, 50 families, and three tree plots with a spacing of 3x2 m.

2.3. Data collections

The collected data in this study were total height, diameter and survival rate. The height was measured from the base of the stem to the tip using a measuring pole. The diameter was measured at the stem at breast height (1.30 m) above the ground using a caliper. At the same time, the survival rate was calculated by comparing the number of living plants divided by the number of plants at the establishment x 100%.

2.4. Data Analysis

The mean of each measured parameter from each plot was measured separately. These data were used as an input to analyze the diversity of parameters between seed origin. Duncan's Multiple Range Test (DMRT) was undertaken if a significant difference was found in this source of variation [12]. Data were analyzed using analysis of variance to determine the variations between seed origin and between families. The model of analysis of variance used as follow:

\[
Y_{ijk} = \mu + B_i + P_j + F(P)k + BF(P)_{ik} + E_{ijkl}
\]

Remarks:

\[Y_{ijk} = \text{individual observations of the } k\text{-th tree from the } j\text{-family in the } i\text{-block}
\]

\[\mu = \text{general mean value}
\]

\[B_i = \text{block effect}
\]

\[P_j = \text{effect of seed origin to } j
\]

\[F(P)_{k} = \text{effect of } k \text{- family in } j \text{- field race}
\]
BF_{ij} = the effect of the interaction of the i-th block on the k-th family in the seed origin j
E_{ijk} = random error

To determine the effect of genetic factors on the phenotype, the estimated heritability values were calculated according to [13] as follows:

\[
h_{ij}^2 = \frac{\hat{\sigma}_{f}^2}{\hat{\sigma}_{f}^2 + (\hat{\sigma}_{bf}^2) / b + (\hat{\sigma}_{e}^2) / nb}
\]

\[
h_{ii}^2 = \frac{3 \hat{\sigma}_{f}^2}{\hat{\sigma}_{f}^2 + \hat{\sigma}_{bf}^2 + \hat{\sigma}_{e}^2}
\]

Remarks:
- \( h_{ij}^2 \) = family heritability value
- \( h_{ii}^2 \) = individual heritability value
- \( \hat{\sigma}_{f}^2 \) = component variant family
- \( \hat{\sigma}_{bf}^2 \) = component of the interaction variant between blocks and families
- \( \hat{\sigma}_{e}^2 \) = component of the variant error
- \( n \) = harmonic average number of trees per plot
- \( b \) = harmonic mean of the number of blocks

The component variants of the family (\( \hat{\sigma}_{f}^2 \)) are assumed to be 1/3 of the additive genetic variants (\( \hat{\sigma}_{A}^2 \)) because the seeds were collected from open-pollinated plus, where some of the seeds probably are the result of inbreeding with relatives [14]. The value of genetic correlation (\( r_g \)) on several traits was calculated according to the following equation [15]:

\[
r_g = \frac{\hat{\sigma}_{f(xy)}}{\sqrt{\hat{\sigma}_{f(x)} \cdot \hat{\sigma}_{f(y)}}}
\]

Meanwhile, to calculate the covariance component for these two properties (x and y), using the following formula:

\[
\hat{\sigma}_{f(xy)} = 0.5 (\hat{\sigma}_{f(x+y)} - \hat{\sigma}_{f(x)} \cdot \hat{\sigma}_{f(y)})
\]

Remarks:
- \( r_g \) = genetic correlation
- \( \sigma_{f(x+y)} \) = covariance component for the x and y properties
- \( \sigma_{f(x)}^2 \) = additive variance component for x and y properties
- \( \sigma_{f(x)}^2 \) = additive variance component for property x
- \( \sigma_{f(y)}^2 \) = additive variance component for property y

3. Results and Discussion
3.1. Adaptability
The adaptation of plants to their environment is necessary for survival, which is reflected by the high ability to survive and reproduce in a particular environment. Therefore, the survival rate is also important information in progeny tests [16]. This study revealed that one year old of G. arborea has an average survival rate of 98.44%; and only slightly decreased when it reached two years old, i.e., 96.01% (Table 2). The best survival rate at 1 year age is G. arborea from Ketapang, followed by Bantul, Bogor and Bondowoso. At two years old, the seed origin of Ketapang remains to have a relatively higher survival rate, followed by Bondowoso, Bantul, Lombok and the lowest one from Bogor. Generally, G. arborea has a high survival rate, as reported by [17] on the provenance test of G. arborea in India at two years old from 12 provenances tested with a mean survival rate of 92%. Also reported by farmers in Sumbawa (NTB/West Nusa Tenggara) and Timor (NTT/East Nusa Tenggara) [18] showed a high survival
percentage (100% and 99%) of 21 months old of *G. arborea* planted as agroforestry. This indicates that this species has no serious problem with the various types of area development.

Table 2. DMRT test for survival rate, total height and diameter.

| Seed origin          | Survival (%) | Height (m) | Diameter (cm) | Survival (%) | Height (m) | Diameter (cm) |
|----------------------|--------------|------------|---------------|--------------|------------|---------------|
|                      | 1st year     | 2nd year   | 1st year      | 2nd year     | 1st year   | 2nd year      |
| Bantul (Yogyakarta)  | 98.74 b      | 96.01 bc   | 1.27 a        | 3.03 a       | 2.20 a     | 4.08 a        |
| Bogor (West Java)    | 98.55 c      | 93.76 d    | 1.24 ab       | 2.94 ab      | 2.22 a     | 3.83 ab       |
| Ketapang (Lampung)   | 99.34 a      | 98.28 a    | 1.28 a        | 2.95 ab      | 2.28 a     | 3.73 ab       |
| Bondowoso (East Java)| 98.49 d      | 96.58 b    | 1.15 b        | 2.61 c       | 2.04 a     | 3.14 c        |
| Lombok (West Nusa Tenggara) | 97.10 e | 95.12 c    | 1.20 ab       | 2.78 bc      | 2.15 a     | 3.53 bc       |
| Means                | 98.44        | 95.95      | 1.23          | 2.86         | 2.18       | 3.66          |

Remarks: the average value associated with the same letter, not significantly different on a 95% confidence level.

The analysis of variance showed that seed origin was significantly different in terms of survival rate at first and 2nd-year-old (Table 2). The variation of survival rate between provenance (seed origin) was also reported by [19] at one year old of the provenance trial in Matalam (South Philippines). The differences in adaptation patterns between the 1st and second years in this study indicated that seed origins show different adaptation traits. The seed origin is a population that has adapted to a specific environment in which it is planted. This seed origin is formed from planting in a new environment; therefore, natural selection will work and produce individuals with good adaptability. [20] argued that variations in a trait in a tree species can occur between geographic areas.

A ranking was made by summarizing all average parameters to determine the best seed origin. The best seed origin has the smallest total rank, and the worst seed origin has the largest total rank (Table 3).

Table 3. Ranks of all parameters for each seed origin of 1 and 2 years old white teak.

| Seed origin          | Survival | 1 year old | Diameter | Total | Survival | 2 years old | Diameter | Total |
|----------------------|----------|------------|----------|-------|----------|-------------|----------|-------|
|                      | 1 year    | Height     | Diameter |       | 2 years  | Height      | Diameter |       |
| Bantul (Yogyakarta)  | 2         | 2          | 3        | 7     | 1        | 1           | 5        |
| Bogor (West Java)    | 3         | 3          | 5        | 8     | 3        | 2           | 10       |
| Ketapang (Lampung)   | 1         | 1          | 1        | 3     | 1        | 2           | 3        |
| Bondowoso (East Java)| 4         | 5          | 14       | 18    | 5        | 5           | 12       |
| Lombok (West N T)    | 5         | 4          | 4        | 13    | 4        | 4           | 12       |

3.2. Variation of growth
The mean height and diameter of *G. arborea* varied between seed origin and also between years of observation. For example, at the 1-year-old, *G. arborea* from Ketapang exhibited the highest growth, either diameter or total height. Meanwhile, at two years old, the origin from Bantul showed the best growth compared to others.

The Anova revealed that 1-year old *G. arborea* varied significantly between seed origin in terms of survival rate and height (Table 4). However, at two years old, all characters measured showed significantly varies between seed origin. Thus, the variation of growth and survival rates were commonly found in the young age plantations such as *G. arborea*, which is generally influenced by environmental conditions such as sunlight intensity, average annual rainfall and physical and chemical fertility conditions of the soil [18, 19].
Table 4. Analysis of variance for survival rate, total height, and diameter of 1- and 2-years old.

| Source of variation | Degrees of freedom | Survival | Middle Square | Height | Diameter |
|---------------------|--------------------|----------|---------------|--------|----------|
| **1-year-old**      |                    |          |               |        |          |
| Replication         | 3                  | 817.37** | 13786.63**    | 12.54**|          |
| Seed Origin         | 4                  | 128.01** | 2263.92*      | 0.71ns |          |
| Family (Seed origin)| 45                 | 7339.51**| 2119.36**     | 1.79** |          |
| Rep*Fam (Seed origin)| 145             | 21021.37**| 3245.17**     | 1.96** |          |
| Error               | 349                | 0.0019   | 1197.802      | 0.605  |          |
| **2-years-old**     |                    |          |               |        |          |
| Replication         | 3                  | 2566.93**| 196810.21**   | 77.23**|          |
| Seed origins        | 4                  | 1280.81**| 20030.93**    | 8.56** |          |
| Family (Seed origin)| 45                 | 711.51** | 17803.46**    | 7.17** |          |
| Rep*Fam (Seed origin)| 145             | 501.97** | 16356.54**    | 6.74** |          |
| Error               | 349                | 8.49     | 4211.01       | 1.722  |          |

Remarks: ** = significant different at 0.01; *= significant different at 0.05; ns = not significant different

The analysis of variance at 1 and 2 years old showed that the growth and survival rate of *G. arborea* differ significantly between replications, between families, and between the interaction of replication and family. However, the diameter between seed origin does not vary significantly at the 1-year-old, assuming that the genetic matters did not express yet at this young age. This finding revealed that blocking as replication has a significant effect on the differences of all characters measured. This is probably caused by the differences of site characters between blocks, such as the slope, humidity, and exposure to sunlight. Therefore, variation of all characters is also found between families, which is mainly due to the blocking effect. Thus, seed origin differences influence the growth and survival of *Gmelina arborea*, due to the variation of environmental conditions of its original population. Therefore, environmental factors in the long term will affect the genetic performance of growth and survival rate.

Variation of growth (height and diameter) between replications and between families are common in progeny test, for instance, in progeny test of 24 months of teak [21], at *Araucaria cunninghamii* which showed the growth variation at 18 months old and five years old [22, 23], at *Falcataria moluccana* [24] also at *Ficus variegata* [25]. Therefore, the variation between families at a progeny test will be benefi a breeding program since the data can be used for family selection. Therefore, the family performing bad growth can be culled off and remaining with good growth.

3.3. Genetic parameters

The estimated heritability values and genetic correlations of height and diameter of *G. arborea* progeny test are presented in Table 5.

Table 5. The estimated value of individual heritability, family, and genetic correlation of *G. Arborea*.

| Year | Character | Height | Diameter | Genetic correlation (r<sub>g</sub>) |
|------|-----------|--------|----------|------------------------------------|
|      |           | h<sub>i</sub> | h<sub>f</sub> | h<sub>i</sub> | h<sub>f</sub> | h<sub>i</sub> | h<sub>f</sub> |              |
| 1    | 0.29      | 0.30   | 0.24     | 0.38     | 0.75     |              |
| 2    | 0.19      | 0.30   | 0.18     | 0.28     | 0.89     |              |

Estimated heritability is a parameter for describing the strength and weakness of a character under the control of genetic factors to determine and select the tree breeding programs [20]. Table 5 shows the estimated heritability values of individuals (h<sup>2</sup><sub>i</sub>) and families (h<sup>2</sup><sub>f</sub>) at 1<sup>st</sup> and 2<sup>nd</sup> years old for height (h<sup>2</sup><sub>i</sub> = 0.29-0.19, h<sup>2</sup><sub>f</sub> = 0.30-0.30) and diameter (h<sup>2</sup><sub>i</sub> = 0.24-0.18, h<sup>2</sup><sub>f</sub> = 0.38-0.28). The heritability value was classified as moderate in this study [26].
The estimated heritability of individuals and families for the diameter and height of G. arborea at 1 and 2 years was categorized as medium heritability. Individual heritability for both height and diameter decreased in the second year compared to the first year. The decrease in heritability can be thought that the genetic performance has not shown any stability. Therefore the genetic gain of growth of this progeny test cannot be predicted at two years old. The progeny test at one year old showed high genetic diversity; however, the genetic diversity of growth showed a decrease at two years old. This result affects individual selection activities (forward selection). Therefore the selection to select the best individual cannot be carried out. Similar family heritability for tree height at one year and two years old shows that the family's performance (mother tree) on tree height was stable. This result can be used as fundamental information that tree selection (Backward Selection) based on the best family can be made.

The genetic correlation was calculated to determine the genetic relationship between height and diameter traits in the progeny test of G. arborea. The genetic correlation values between height and diameter traits at first and second years old were classified as strong positive correlation ($r_1 = 0.75$ and $r_2 = 0.89$). This strong correlation is very important for undertaking the selection due to selection of one trait (diameter) will also improve the height.

4. Conclusion
The estimated heritability of G. arborea exists in this progeny test. The mean survival rate first and 2nd-year-old was 98.44% and 95.95%; the mean height was 1.23 m and 1.28 m, respectively, with the G. arborea from the Ketapang (Lampung) performed the best at both characters. Meanwhile, the average diameter of G. arborea was 2.18 cm and 3.66 cm, with (Ketapang) Lampung seed origin showed the best diameter in the 1st year and Bantul (Yogyakarta) in the 2nd year. The estimated individual ($h^2_i$) and family ($h^2_f$) heritability values of fir1st and 2nd-year-old were moderate values. The genetic correlation between stem diameter and height showed high and positive, confirming that this progeny test had a strong and positive genetic correlation. It is very beneficial in growth selection programs. Tree selection in the progeny test can be made using only one trait, using only the diameter or height parameter. Selection of trees by using the diameter means will also choose the best tree height.

References
[1] Fathoni T T, Wardhana A and Leksono B 2012 Kebijakan Badan Litbang Kehutanan Dalam Pembangunan Sumber Benih dan Status Pemuliaan Tanaman Hutan Saat Ini Prosiding Seminar Pembangunan Sumber Benih. Peran Sumber Benih Ungguh Dalam Mendukung Keberhasilan Penanaman Satu Milyar Pohon BBPBPTH Yogyakarta 30 Juni 2011
[2] Gonzalez G, Moya R, Mong F, Cordoba R and Coto J C 2004 Evaluating the strength of finger jointed lumber of Gmelina arborea in Costa Rica New For. 28 219-323
[3] Vallejos J, Moya R and Serrano R 2015 Effects of thinning on diameter, heartwood, density and drying defects of Gmelina arborea Maderas Cienc. y Tecnol. 17 365-72
[4] Patil S M, Kadam V J and Ghosh R 2009 Invitro Antioxidant Activity of Methanolic Extract of Stem Bark of Gmelina arborea Roxb. (Verbenaceae) Int. J. PharmTech Res. 1 1480-4
[5] Pathala D, Harini A and Hegde P 2015 A Review on Gambhari (Gmelina arborea Roxb.) J. Pharmacogn. Phytochem. 4 127-32
[6] Kulkarni Y A and Veeranjaneyulu A 2013 Effects of Gmelina arborea extract on experimentally induced diabetes Asian Pac. J. Trop. Med. 602-8
[7] Dvorak W S 2004 K A P P in the N 2004 World view of Gmelina arborea: opportunities and challenge New For. 28 111-126
[8] Tenorio C, Moya R, Valverde J C and Arias-Aguilar D 2019 Biomass production and characteristics of short rotation plantations of clones of Gmelina arborea in three spacings Silvae Genet. 68 92-100
[9] Finkeldy R 2005 Pengantar Genetika Hutan Tropis Terjemahan Edje Djamhuri, Iskandar Z S, Ulfah J S, and Arti W Kertadikara Fakultas Kehutanan IPB
[10] Kabupaten Trenggalek Dalam Angka 2017 Badan Pusat Statistik Kabupaten Trenggalek, Provinsi Jawa Timur

[11] Setiadi D 2016 Keragaman Pertumbuhan Semai Gmelina arborea Roxb Dari Beberapa Sumber Asal Benih Di Indonesia Proceeding Seminar Nasional Biodiversitas VI, Surabaya 3 September 2016. Departemen Biologi Fakultas Sain dan Teknologi Universitas Airlangga Surabaya

[12] Steel R G D and Torrie J 1980 Principles and Procedures of Statistic. Mc Graw-Hill, Inc

[13] White T L, Adams, W T and Neale D 2007 Forest Genetic CABI Publishing, UK

[14] Hardiyanto E B 2011 Diklat Mata Kuliah Pemuliaan Pohon Lanjut (Tidak dipublikasikan) Pogram Pasca Sarjana Fakultas Kehutanan Universitas Gadjah Mada, Yogyakarta

[15] Williams E R, Matheson A C and Harwood C 2002 Experimental Design and Analysis for Use in Tree Improvement Second edition CSIRO Publishing

[16] Finkeldey R and Hattemer H 2007 Tropical Forest Genetics Springer - Verlag Berlin Heidelberg

[17] Lauridsen E B and Kjaer E D 2002 Provenance research in Gmelina arborea Linn., Roxb.A summary of results from three decades of research and a discussion of how to use them The International Forestry Review 4(1) 20-29

[18] James M R, Mulawarman and Purnomosidi D 2004 Gmelina arborea available species for smallholder tree farming in Indonesia. New For. 28 207-15

[19] Corpuz O S and Carandang W M 2012 Effect of root growth potential, planting distance and provenance on the growth and survival of Gmelina arborea Roxb Asia Life Sci. 21 231-48

[20] Zobel B J and Talbert J 1984 Applied Forest Tree Improvement John Wiley and Sons New York

[21] Kumar A 2007 Growth performance and variability in different clones of Gmelina arborea (RoxB.) Silvae Genet. 56 32-6

[22] Setiadi D 2010 Keragaman Genetik Uji Provenans dan Uji Keturunan Araucaria cunninghamii Pada Umur 18 Bulan di Bondowoso, Jawa Timur J. Pemuliaan Tanam. Hutan 4(1) 1-8

[23] Setiadi D dan M S 2012 Variasi Genetik Pada Kombinasi Uji Provenans dan Uji Keturunan Araucaria cunninghamii di Bondowoso Jawa Timur J. Pemuliaan Tanam. Hutan 6(3) 157-66

[24] Hadiyan Y 2010 Pertumbuhan dan Parameter Genetik Uji Keturunan Sengon (Falcataria moluccana) di Cikampek Jawa Barat J. Pemuliaan Tanam. Hutan 4(2) 101-108

[25] Haryjanto L, Prastyono and V Y 2014 Variasi Pertumbuhan dan Parameter Genetik pada Tiga Plot Uji Keturunan Nyawai (Ficus variegata Blume) di Bantul J. Pemuliaan Tanam. Hutan 8(3) 137-51

[26] Cotteril P P and Dean C A 1990 Successful Tree Breeding With Index Selection CSIRO, Melbourne

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Authors' contribution
All authors contributed equally to this work as the main contributor.