Indonesia’s Teak Resources, Breeding and Biotechnology

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Teak Resources
Teak Resources

• Two sources:
  – Commercial plantations ~ >1 million ha
  – community/private plantations

• Intercropping with agriculture plants, particularly in first 2 years

• Old stands in Isl. Java, Muna and Buton (only remnants)
History of teak in Indonesia

• Two school of thoughts:
  – Native (De Veer 1957)

• First introduced to Java in the 7th century, and in Muna Sulawesi in 16th century

• The Dutch found teak in Muna in 1727, but tree ring samples of the oldest teak in Indonesia, which happened to grow in Muna date back to 1565 (J.L. Gaynor 2016. Intertidal History in Islands Southeast Asia).
Teak Plantations

• Management of teak plantations in Java began in 1897, under Dutch colonial authority. Then transferred to Department of Forestry in 1927, and in 1930 to state-owned forestry company (Djatibedrijf).

• In 1940, management of teak forests returned to Department of Forestry until Indonesia’s independence in 1945.

• State forestry company Perhutani was established in 1961 to manage teak plantation in Java.

• Community/private teak plantation established in more recent years.
Community Teak Plantation

- Generally planted as intercropping with maize, peanuts, cassava etc, planted alongside the perimeter of the land, or planted in small block of land.
- In the past, farmers used seeds/seedlings are from unknown sources (unimproved)
Teak Production

• Production from teak plantations in 2016 ~ 500,000 m³; demand for furniture industry ~ 2.5 mill m³. Rotation age is between 40 – 60 years
• Production from community teak unknown
Teak Research

- Perhutani Teak Centre in Cepu Central Java, established in 1997, focus genetic improvement, seed production, tissue culture/clonal propagation
- Faculty of Forestry, University of Gadjah Mada
- CFBTI Yogyakarta, focus genetic improvement, DNA markers (genotyping)
**GENETIC IMPROVEMENT OF TEAK**

- First provenance trial established in 1932, 12 geographical origin: India (Malabar, Central province, Godavari), Indo-China (Hinh, Kay, Kuoai,Kouoc), Indonesia (Muna, Cepu, Pati, Ponorogo, Gundih, Kesamben). Study in 1958 concluded that Malabar, Pati, Cepu and Ponorogo were best suited.


- Subsequently, progeny trials were established in 1987, 1988, 1995 and 1997. Around 125 elite trees selected.

- Clonal trials established in 1999 and 2000, 120 clones tested
Genetic Improvement of Teak

- Seed production from clonal seed orchard ~ 40 ton/year, equivalent to 35,000 ha plantation
- Planting materials from hedge orchard by cutting ~ 24 million plants = 36,000 ha plantation
- Growth of improved clones at age 5 years height - 17.8m, dia. - 18cm. MAI 14m³/ha/yr
How can teak benefits from biotechnology

- Propagation method
- Molecular markers
Molecular markers

Some of the more important applications of genetic markers include:

- Describing mating systems, levels of inbreeding, and temporal and spatial patterns of genetic variation within stands
- Describing geographic patterns of genetic variation
- Inferring taxonomic and phylogenetic relationships among species
- Evaluating the impacts of domestication practices, including forest management and tree improvement, on genetic diversity
- Fingerprinting and germplasm identification in breeding and propagation populations
- Constructing genetic linkage maps and marker assisted breeding
Molecular genetics Study of Teak

- Clone genotyping to ensure clone fidelity. Using SCAR markers, clone banks of some 350 clones had been genotyped.
- Genetic diversity study
- DNA log tracking to check chain of custody (FST/2014/028).
Genetic diversity

- Key to survival and adaptation – conservation of genetic resources
- Potential for utilization – traits improvement
- Extensive variation are found in natural population
- Diversity within population higher than between populations
- Strong geographic origin
- Diversity between natural provenance and landrace
Based on SSR markers, genetic diversity of Indonesian teak was in moderate to high level
UPGMA analysis showed genetic relationship among 22 Indonesian teak populations.

- Genetic relationship
- Muna and others Southeast Celebes populations
- Out-group
- Cepu, other Java populations & NTT

Java populations teak closed to Thailand -> in line with Varhaegen et al. (2010)
Teak stands are found in Muna Isl. and Buton Isl.

In Muna, remnants of old stand can be found in Napabalano nature Reserve, Matakidi and Wakuru.

In Buton, stand designated as Seed Production Area found in Wakonti
Genetic diversity of Indonesian Teak based on SSR markers

<table>
<thead>
<tr>
<th>Population</th>
<th>Island</th>
<th>N</th>
<th>NA ± SE</th>
<th>HO ± SE</th>
<th>uHE ± SE</th>
<th>F ± SE</th>
</tr>
</thead>
<tbody>
<tr>
<td>Kepek</td>
<td>Java</td>
<td>20</td>
<td>4.5 ± 1.5</td>
<td>0.400 ± 0.25</td>
<td>0.445 ± 0.22</td>
<td>0.179 ± 0.16</td>
</tr>
<tr>
<td>Angondara</td>
<td>Southeast Sulawesi</td>
<td>20</td>
<td>3.5 ± 0.5</td>
<td>0.325 ± 0.175</td>
<td>0.566 ± 0.13</td>
<td>0.455 ± 0.20</td>
</tr>
<tr>
<td>Anduna</td>
<td>Southeast Sulawesi</td>
<td>8</td>
<td>2.0 ± 1.0</td>
<td>0.188 ± 0.20</td>
<td>0.288 ± 0.29</td>
<td>0.304 ± 0.29</td>
</tr>
<tr>
<td>Napabalano</td>
<td>Muna</td>
<td>12</td>
<td>2.0 ± 1.0</td>
<td>0.250 ± 0.25</td>
<td>0.313 ± 0.31</td>
<td>0.168 ± 0.31</td>
</tr>
<tr>
<td>Matakidi</td>
<td>Muna</td>
<td>12</td>
<td>3.5 ± 1.5</td>
<td>0.267 ± 0.07</td>
<td>0.495 ± 0.31</td>
<td>0.227 ± 0.34</td>
</tr>
<tr>
<td>Wakuru</td>
<td>Muna</td>
<td>12</td>
<td>2.5 ± 0.5</td>
<td>0.182 ± 0.18</td>
<td>0.415 ± 0.26</td>
<td>0.716 ± 0.28</td>
</tr>
<tr>
<td>Wakonti</td>
<td>Buton</td>
<td>12</td>
<td>3.0 ± 2.0</td>
<td>0.318 ± 0.32</td>
<td>0.374 ± 0.37</td>
<td>0.110 ± 0.37</td>
</tr>
</tbody>
</table>

N: Number of samples, NA: Number of detected alleles, HO: Observed heterozygosity, uHe: unbiased Expected heterozygosity, F: coefficient inbreeding, SE: standard error
Genetic relationship among populations
Teak in Southeast Sulawesi
Distinguish individuals within a population – DNA fingerprinting

Region 1

Population 1

Distinguish individuals from different populations within a region – population genetics

Population 2

Population 3

Region 2

Biogeographic barrier

Distinguish between species – DNA barcoding

Distinguish individuals from different regions - phylogeography
## Possible Applications

<table>
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<tr>
<th>Level of approach</th>
<th>Description</th>
<th>Example of use</th>
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| Population genetics | Study of genetic variation of a species across distance based on evolutionary process | • Source of harvesting, declared country or region  
• Timber harvested from conservation area  
• Timber harvested from natural forest or a plantation |
| DNA fingerprinting  | A way of identifying a specific individual of the same species.              | • Log is traced back to its original stump (is the chain of custody intact)  
• Log laundering (log is swapped with other tree of the same species) |
| DNA barcoding       | A taxonomic method that studies a relatively short portion of DNA to identify it as belonging to a particular species | • Timber is of the declared species (true identity)  
• If it is CITES listed species |
SNP (Single Nucleotide Polymorphism) markers development for population study....
Dunker et al, 2019

- Many molecular markers have been utilized in previous studies on population genetic structure and genetic variation of teak including Amplified Fragment Length Polymorphism (AFLPs), Inter Simple Sequence Repeats (ISSR) microsatellite markers and chloroplast single nucleotide polymorphisms
- 156 SNP markers in teak, *T. grandis* suitable for population genetic studies of the species
- These genetic resources will prove useful for future studies into the population genetics and phylogeography
Thank you