

DNA Barcoding for Valuable Tree Species in Indonesia

Ulfah Juniarti Siregar

Professor in Forest Biotechnology
Department of Silviculture,
Faculty of Forestry and Environment, IPB University

Introduction: Illegal Timber

Violations in the Timber Trade

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Monitoring reveals Indonesia's 'legal timber' scheme riddled with violations

HANS NICHOLAS JONG
ASIA

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WRI (2026)



Document falsification



Misdeclaration of timber origin and/or species



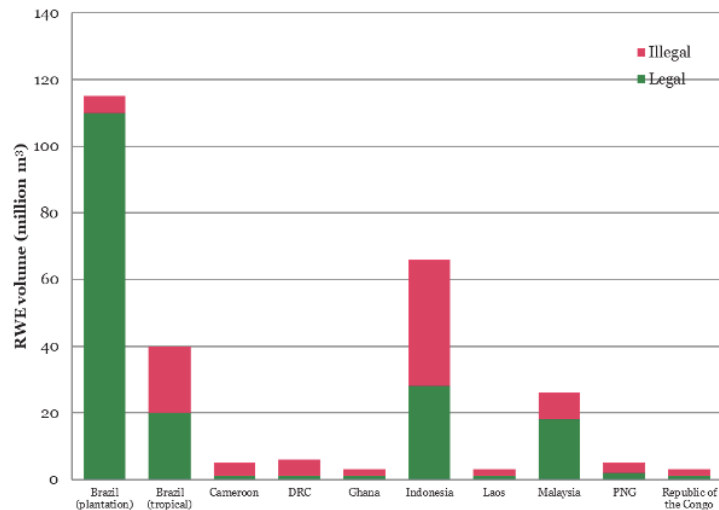
Customs fraud



Logging outside concession boundaries

Status of Illegal Timber

The State of Illegal Logging Enforcement in Indonesia



In 2013, Indonesia was among the world's three largest producers of illegal timber, with approximately 50% of its timber production estimated to originate from illegal sources



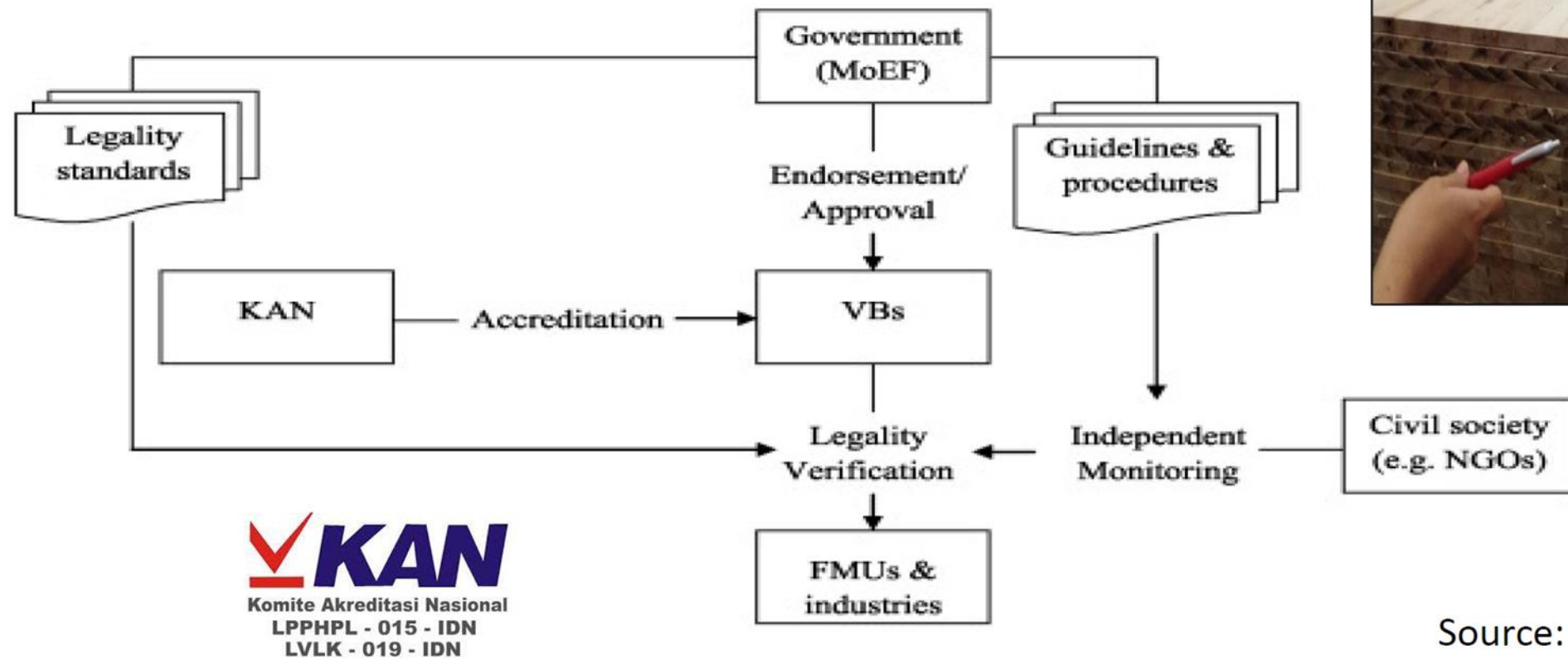
Most illegal timber trade cases are prosecuted under the Forestry Law (Law No. 41/1999) and the Law on the Prevention and Eradication of Forest Destruction (Law No. 18/2013)

Indonesia is the only country authorized to issue FLEGT licenses and has implemented the Timber Legality Assurance System (SVLK) through mandatory certification



Timber Legality System in Indonesia

Timber Legality System - SVLK



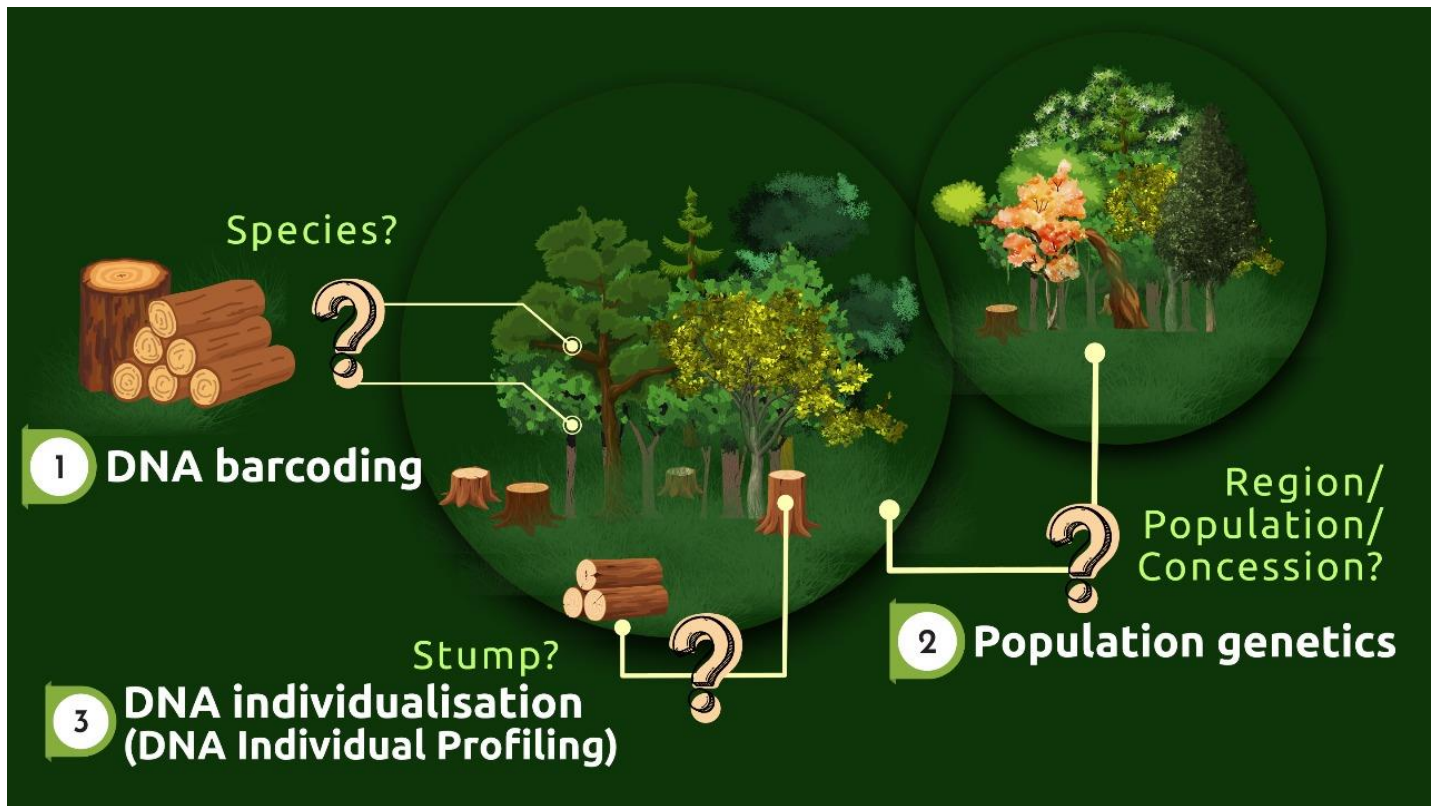
Source: Maryudi (2016)

Molecular Wood Identification :

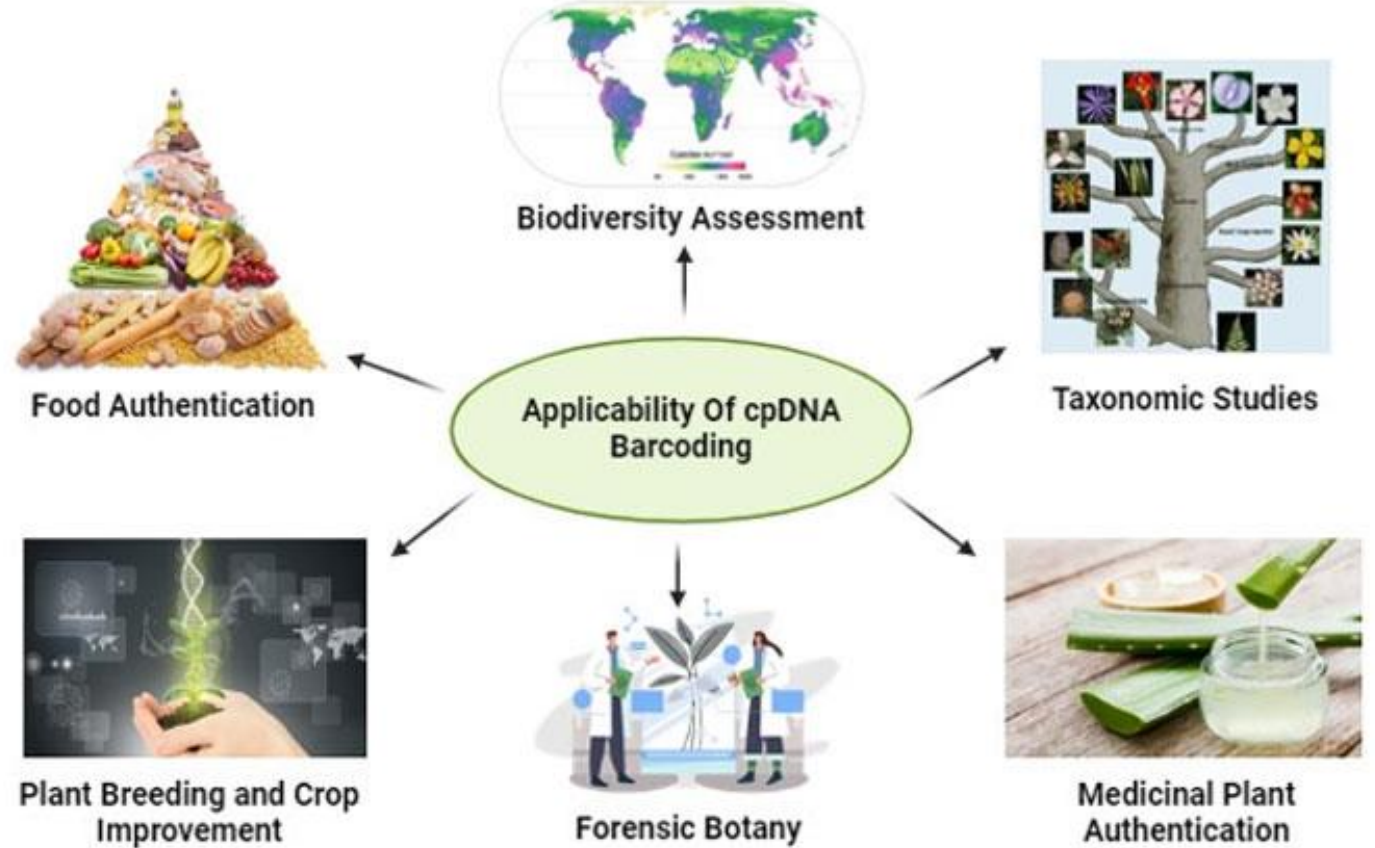
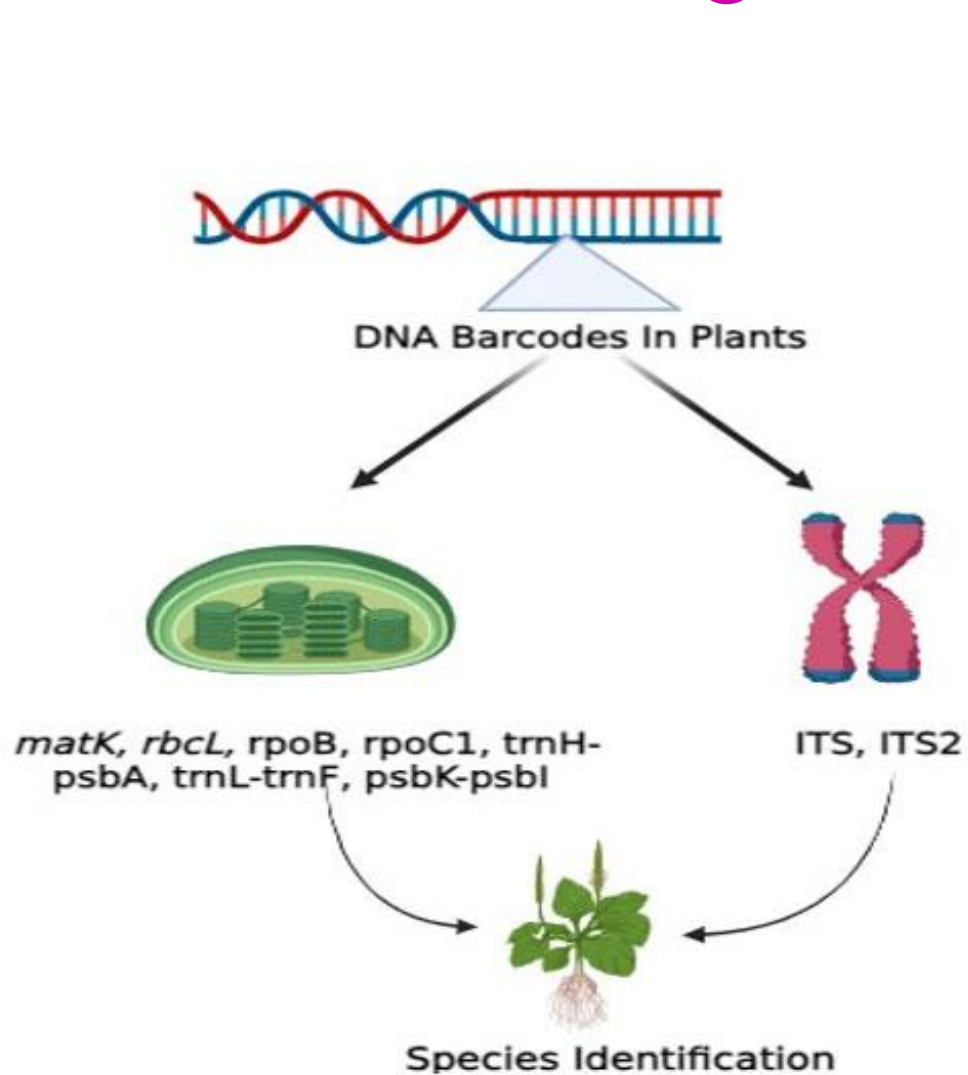
- Conventional DNA markers
- DNA Barcoding
- SNP: abundant and more specific markers

Wood Identification Technologies Supports Law Enforcement

- Provides scientific evidence as recognized under Supreme Court Regulation (PerMA) No. 1/2023 on Guidelines for Adjudicating Environmental Cases
- Supports investigations that are subject to a 90-day time limit under Article 39 of the Forest Destruction Prevention and Eradication Law (P3H Law)
- Enables prosecutors to pursue additional or cumulative criminal sanctions
- Forestry non-tax state revenues (PNBP), particularly PSDH and Reforestation Funds (DR), are assessed based on timber origin (island) and species.



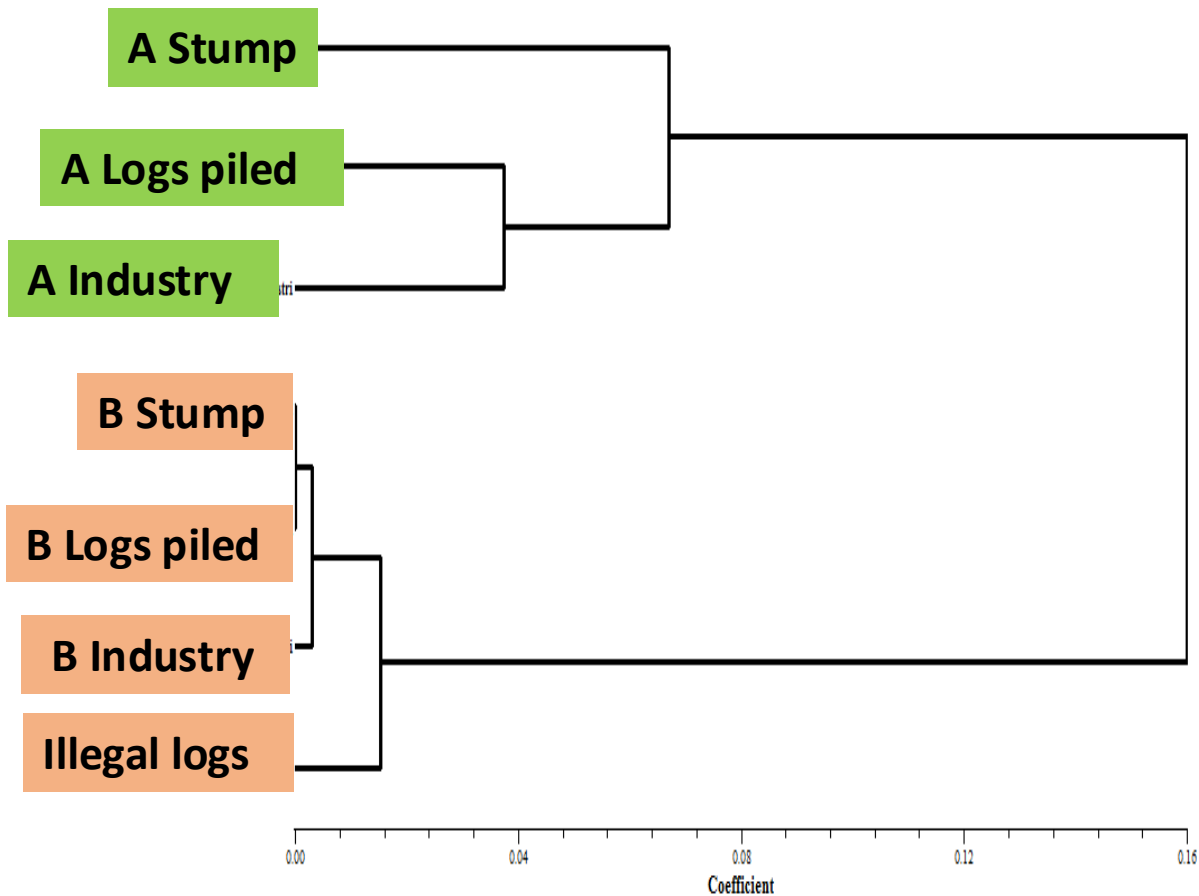
DNA Barcoding



Behura et al. 2024

CASE STUDY: Concession Companies in Kalimantan

Dipterocarp: Assessed using Microsatellite markers

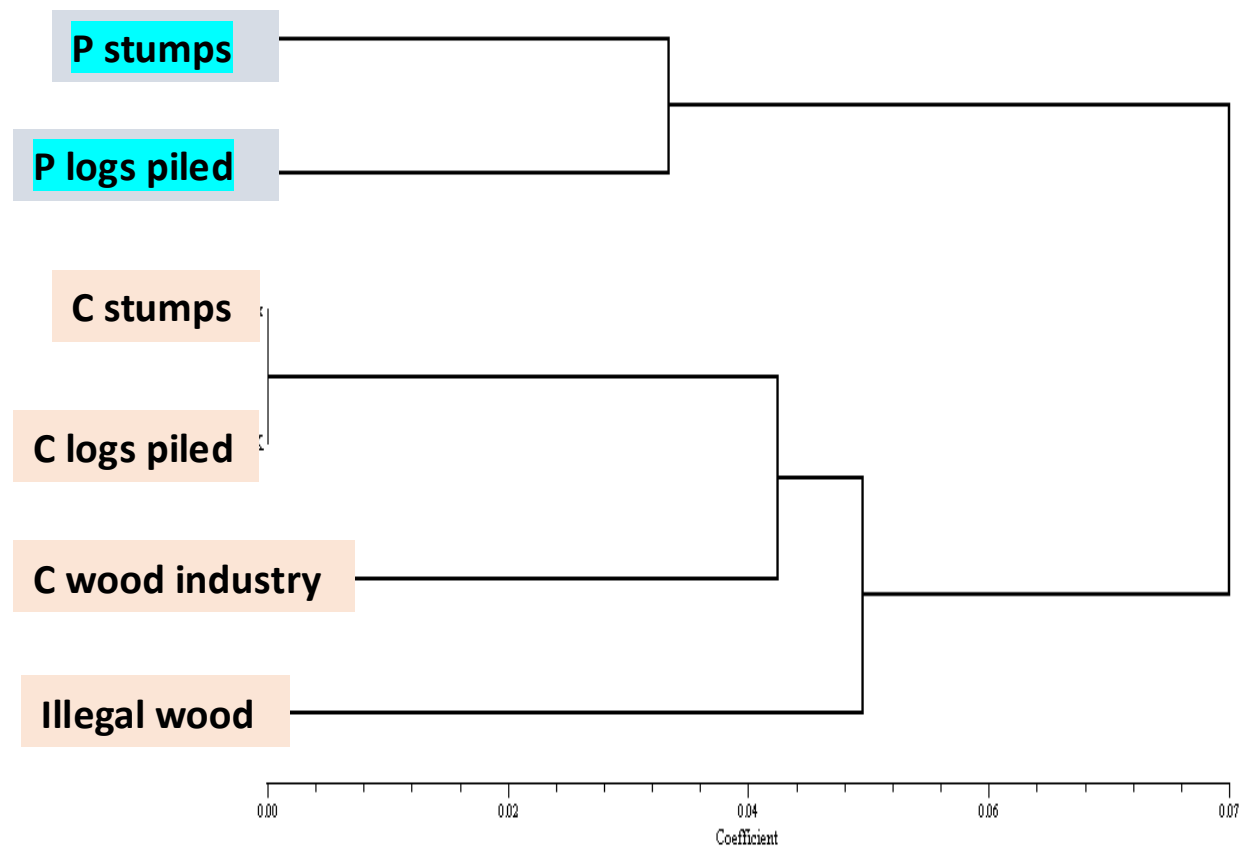


No	Location	Sample No.				Total
		Stump	Logs piled	Wood Industry	Illegal Wood	
1	Company A	20	20	20	40	160
2	Company B	20	20	20	(Jakarta – different island)	

Yunanto 2010

CASE STUDY: TEAK Plantation

Teak: Assessed using RAPD



No	Location	Age	Sample No.				Elevation (asl)
			Stump	Piled logs	Illegal	Industry	
1	FMU C	(30-40 yr)	11	11	7	12	69 m
2	FMU P	(50-60 yr)	20	20	-	-	96 m

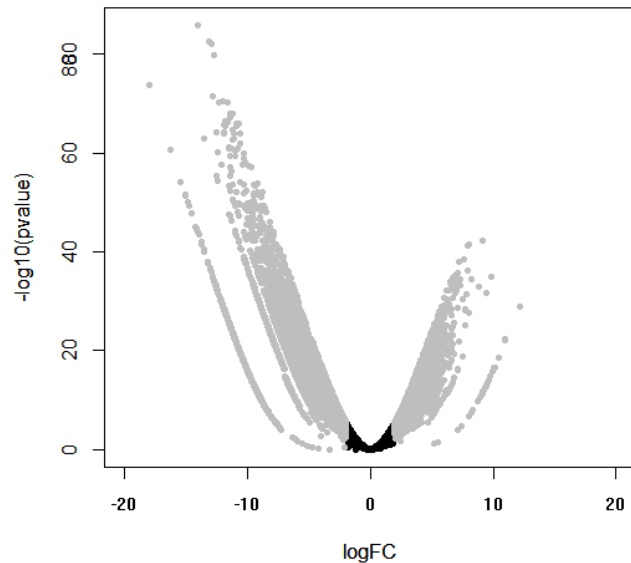
Siregar et al. 2008)

Fingerprinting and Profiling: Most advance techniques

- **Rely on high-throughput technology powered by next-generation sequencing platforms**
- **Bypass traditional gel-based limitations to provide dense, genome-wide single nucleotide polymorphism (SNP) profiles**
- **There are several types:**
 - **High-Throughput Sequencing & Reduced Representation:**
 1. **Genotyping-by-Sequencing (GBS)**
 2. **Restriction site-Associated DNA sequencing (RAD-seq)**
 - **High-Precision SNP Genotyping:**
 1. **KASP (Kompetitive Allele Specific PCR)**
 2. **DNA microarrays (SNP Chips)**
 - **Functional and Targeted Fingerprinting:**
 1. **Start Codon Targeted (SCoT) Polymorphism**
 2. **Targeted Region Amplified Polymorphism (TRAP)**

Development of *SNP* markers: for tree resistance

Analysis of *transcriptomics*:
Resistant and susceptible trees have different set of expressed genes (both up-regulated and down-regulated) related to resistance to pest and disease



No	Sequence ID	logFC	Gene name
	Up-regulated		
1	FalSK.97594.1.T.79583.c4.g2.i2	12.17	Transcription factor CPC
2	FalSK.82701.1.T.79466.c1.g1.i4	10.96	Serine carboxypeptidase-like 18
3	FalSK.95586.66090.T.88690.c1.g1.i13	10.40	Serine carboxypeptidase-like 18
4	FalSK.95586.109491.T.81468.c3.g4.i2	10.10	Universal stress protein A-like protein
5	FalSK.61811.0.T.83289.c6.g2.i1	10.07	Cytochrome P450 78A5
6	FalSK.95586.84704.T.84126.c0.g1.i4	9.86	Ubiquitin carboxyl-terminal hydrolase 13
7	FalSK.95586.114481.T.84961.c0.g3.i6	9.78	NAD(P)H-dependent 6-deoxychalcone synthase
8	FalSK.95586.114551.T.84150.c0.g3.i2	9.78	UPF0057 membrane protein At2g24040
9	FalSK.110044.1.T.78909.c1.g1.i2	9.62	Retrovirus-related Pol polyprotein from transposon RE1
10	FalSK.110044.0.T.78909.c1.g1.i1	9.54	Retrovirus-related Pol polyprotein from transposon RE1
	Down-regulated		
1	FalSK.95586.47482.T.84387.c9.g3.i1	-16.27	Fasciclin-like arabinogalactan protein 12
2	FalSK.95586.51624.T.88608.c2.g2.i11	-15.41	ATP synthase protein MI25
3	FalSK.95586.43003.C22450	-14.55	Cytochrome c oxidase subunit 1 (Fragment)
4	FalSK.95586.51538.T.89133.c2.g2.i2	-14.21	Cytochrome c oxidase subunit 1
5	FalSK.95586.73299.C24188	-14.19	RNA-directed DNA polymerase homolog
6	FalSK.95586.35682.T.89651.c2.g1.i5	-14.12	NADH-ubiquinone oxidoreductase chain 5
7	FalSK.95586.60006.T.89651.c2.g1.i8	-14.04	NADH-ubiquinone oxidoreductase chain 5
8	FalSK.95586.39961.T.80573.c3.g1.i8	-13.97	COBRA-like protein 4
9	FalSK.95586.49425.T.89133.c2.g1.i6	-13.53	Cytochrome c oxidase subunit 1
10	FalSK.95586.58752.T.88479.c6.g3.i6	-13.03	Photosystem II CP47 reaction center protein

Alleles related to resistance

Parameter (%)	WRKY 40			IAA 1			IAA 2		
	AA	AT	TT	CC	CA	AA	CC	CA	AA
Disease incidence	100	100	-	100	100	100	100	100	100
Severity	52.66	88.61	-	74.87	53.33	54.45	69.52	47.22	55.96
Mortality	31.40	47.22	-	41.88	25.92	33.33	42.06	27.78	29.29
	A $\leftarrow$ T			C $\rightarrow$ A			C $\rightarrow$ A		

Comparison of Fast-growing (FT) vs. Conventional Teak (CT)



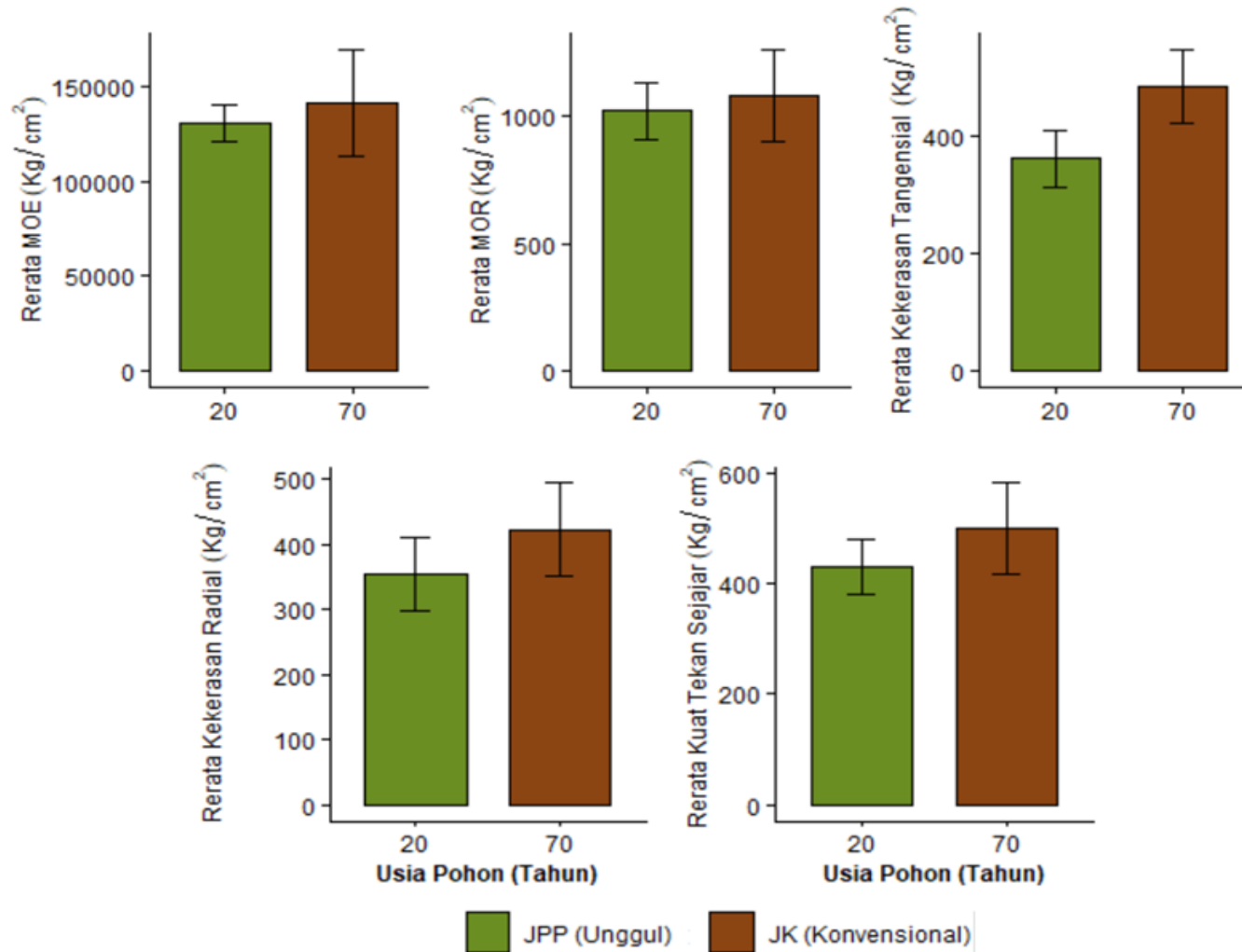
38 cm (FT 20 yrs)



38 cm (CT 70 yrs)



22 cm (CT 20 yrs)



- Differences in several wood properties between FT 20 yrs and CT 70 yrs were not significant
- Clonal forestry in teak plantation made it possible and easier to fingerprint the clones

Lessons Learned:

- Molecular genetic markers showed consistency in timber forest products throughout timber chain of custody
- Success of DNA isolation from wood is a precondition for feasible application of technologies
- Requirements for full application of molecular markers and fingerprinting in forensic genetics in forestry depend on:
 - establishment of complete data base on genetic variations of important timber species
 - cheap and easy methods for DNA analysis



DATA NOTE

De novo transcriptome for sengon (*Falcataria*) displaying resistance against boktor stem borers (

Ulfah J. Siregar^{1,2*}, Aditya Nugroho³, Hasyati Shal Deden D. Matra⁴

Received: 13 July 2021 | Revised: 14 October 2021 | Accepted: 25 November 2021
DOI: 10.1111/cobi.13873

CONTRIBUTED PAPERS

Tropical and subtropical Asia's valued tree species under threat

Hannes Gaisberger^{1,2} | Tobias Fremout^{3,4} | Chris J. Kettle^{1,5} | Barbara Vinceti¹ | Della Kemalasari⁶ | Tania Kanchanarak^{6,7} | Evert Thomas⁴ | Josep M. Serra-Diaz⁸ | Jens-Christian Svenning⁹ | Ewan Sill¹⁰ | Wishes Bhattacharya¹¹ | Kandasamy Balasubramanian¹² | Gudrun Alisc
Volume 22, Number 5, May 2021
Pages: 2728-2736

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Article

De novo transcriptome datasets of *Shorea* *langeran* leaves and basal stem in



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E-ISSN: 2085-4722
DOI: 10.13057/biodiv/d220534

Policy and Economics
Issue 7, April 2007, Pages 822-829



Trypsin inhibitor activities as defense mechanism of sengon (*Falcataria moluccana*) against nest attack

BIODIVERSITAS
Volume 20, Number 9, September 2019
Pages: 2698-2706

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Fingerprinting sengon (*Falcataria moluccana*) accessions resistant to boktor pest and gall rust disease using microsatellite markers

ULFAH J. SIREGAR^{1,2*}, DEWI RAHMAWATI², APRILIYA DAMAYANTI¹

¹Department of Silviculture, Faculty of Forestry, Institut Pertanian Bogor. Jl. Ulin, Kampus IPB Dramaga, Bogor 16680, West Java, Indonesia.
Tel/fax.: +62-812-1062154, *email: ujsiregar@gmail.com.

²Southeast Asian Regional Centre for Tropical Biology (SEAMEO BIOTROP). Jl. Raya Tajur Km 6, Bogor 16134, West Java, Indonesia

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of heritability in a sengon Kediri, East Java, Indonesia

SIREGAR³, NOOR F. HANEDA³, YUNIK IN⁴, ULFAH J. SIREGAR^{3,*}
onment, Institut Pertanian Bogor. Jl. Ulin Lingkar Akademik,
*email: aditya_gembilnugroho@apps.ipb.ac.id
Jl. Kamfer, Dramaga, Bogor 16680, West Java, Indonesia
r. Jl. Ulin Lingkar Akademik, Dramaga, Bogor 16680, West
ulfahjs@apps.ipb.ac.id
ol Pos 6, Cepu, Blora 58302, Central Java, Indonesia

s of sengon (*Paraserianthes*) in a community forest plantation, and its genetic diversity in East Java, Indonesia

.Y. Massijaya^a✉, N. Ishibashi^c✉, K. Ando^c✉

BMC Research Notes



Commentary

Extraction, Amplification and Characterization of Wood DNA from Dipterocarpaceae

YANTI RACHMAYANTI, LUDGER LEINEMANN, OLIVER GAILING and REINER FINKELDEY*

Institute of Forest Genetics and Forest Tree Breeding, Georg-August-Universität Göttingen, Büsgenweg 2, 37077 Göttingen, Germany

Abstract. A successful DNA extraction from wood yielding appropriate DNA quality for PCR amplification allows molecular genetic investigations of wood tissue. Genotypes, the origin of sampled material, and species can be identified based on an investigation of wood if suitable information on genetic variation patterns within and among species is available. Potential applications are in forensics and in the control of the timber and wood

its in Southeast Asia and Japan based on analysis of 16S rRNA

Charles², Bibian Diway², John Sabang², amiya⁴, Shawn Lum⁵, Ulfah J. Siregar⁶, hiko T. Miyashita^{1*}

DATA NOTE

De novo assembly of transcriptome dataset from leaves of *Dryobalanops aromatica* (Syn. *Dryobalanops sumatrensis*) seedlings grown in two contrasting potting media

Iskandar Zulkarnaen Siregar^{1*}, Fifi Gus Dwiyantri¹, Ulfah Juniarti Siregar¹ and Deden Derajat Matra²

Open Access



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**Iskandar Z. Siregar
Deden D. Matra (Alm.)
Noor F. Haneda
Hasyiyati Shabrina
Arie Aqmarina
Desman Napitupulu
Auraga Dewantoro
M. Iqbal Maulana
Tedi Yunanto
Rahma Zafirah**

**Dewi Rahmawati
Apriliya Damayanti
Aditya Nugroho
Hamzah Saidina
Buma Larosa
Januard K. Sihombing
Ayu Indah Lestari
Puti A. Saimima
Yauvina
Irma. M. Situmorang**

**Nofri Yanti
Siti Azizah Yahya
Fitria Zahra Oktavia
M. Majidu
Revi Juniar S.
Esti Nurianti
Fitri Indriani
Fifi Gus Dwiyantri
Rahadian Pratama
Others**



IPB University
— Bogor Indonesia —

Kampus
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Thank You

