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prepared by

Eleanor Dormontt and Andrew Lowe

*co-authors/
contributors/
collaborators*

Rainbo Belton, Maxwell Burdick, Kor-jent van Dijk, Bianca Dunker, Soo Lim Goh, Martin Golman, Mehm Ko Ko Gyi, Duncan Jardine, Dona Kireta, Avalyn Lim, Arif Malik, I.L.G. Nurtjahjaningsih, Richard Pakau, Dan Raymond, Anto Rimbawantu, Jomaine Tang, Darren Thomas, Wilson Tubulae, Hugo Volkaert, Vongvilai Vongkamsao, Thwe Thwe Win

approved by

Nora Devoe

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2 Executive summary

Teak is one of the most commercially important timbers in the world. Its timber is valued for its durability and water resistance, and is used for boat building, exterior construction, veneer, carving, turnings, and for furniture manufacture.

Australia is committed to working in partnerships with producer countries to reduce the trade in illegal timber into Australia for the economic benefit of producer countries and to improve environmental outcomes globally. One of the primary ways that illegal timber enters the market is through mixing into legitimate supply chains and associated document fraud. DNA markers are being used successfully for other timber species to distinguish between species, between populations and even between individuals of timber species. The cost of this technology is dropping dramatically and is already cost effective when used in conjunction with document verification audits. DNA technology is suitable for developing checks of existing chain-of-custody compliance claims, and has been developed in this project to validate the legality claims of teak from project partner SE Asian countries.

Specific objectives:

1. To develop and apply DNA chain of custody verification tests to teak sourced from community forests in Laos, Solomon Islands, PNG and Indonesia
2. To develop and apply DNA chain of custody verification tests to teak sourced from natural forests in Laos, Myanmar and Thailand
3. To enhance knowledge and capacity and develop a regional approach to DNA verification for teak

A global map of teak genetic variation - Across the entire project, more than 1,600 teak tree samples were collected across the natural and planted range of teak in SE Asia and the Pacific Islands.

Genetic analysis of 600 of these samples has produced an initial global map of teak genetic variation. It is clear from this map that the major geographic regions/countries where teak grows can be distinguished genetically (i.e. India, Myanmar, Thailand, Laos and Indonesia). In general, results indicate that the genetic clusters which dominate each country are qualitatively different, and are likely to facilitate good provenance determination for unknown samples. This work is being prepared for scientific publication.

At a country level:

Indonesia - A single genetic cluster dominated teak plantations from Java. Teak from Sulawesi and surrounding islands was quite different to Java, and suggests that these populations are not merely translocations from Javan plantations but from a separate, potentially indigenous, source.

A DNA chain of custody approach was used to trace teak timber along a supply chain within the Perhutani Forest Management Unit at Cepu. These results suggest that paperwork does not always accurately reflect timber origins to exact tree, but that broader genetic provenance testing approaches indicate legitimate timber origins from the expected plantation location.

Myanmar - Analysis of population structure reveals at least five genetic clusters across Myanmar, separating the country into northern, eastern, central, western and southern genetic groups. Assessing the five most likely population assignments, and allowing a 100 km tolerance, 99% of reference samples could be accurately assigned back to their origin, and will be valuable to verify geographic origin claims for this country.

Project partners Double Helix Tracking Technologies utilised the Myanmar teak genetic database to assess claims of timber origin on behalf of their customers. In each case, DNA was extracted from the unknown wood (taken from logs at the sawmill) and assigned

back to probable origin based on the genetic reference database. Results were provided in the form of maps, indicating likely provenance. Where assigned area overlapped with the claimed concession, the claim was considered verified. In all cases claims were verified, and this information has been used to support teak exports to Europe.

Solomon Islands and PNG - Despite best efforts, we were unable to obtain samples in time to analyse DNA before the end of the project – but are available for future work.

Application to control trade of illegal logged products - With the development of genetic reference data, claims of origin of harvest stated on government documents can be scientifically validated all along the Chain of Custody from natural forest. Specification, packing and measurement Lists delivered with logs to sawmills, and removal passes showing transport of logs all indicate origin of harvest. DNA verification can also be applied to exclude high risk areas, such as conflict zones and border areas associated with illegal logging and cross border smuggling. DNA testing combined with localised Area Risk Assessments allow for discrimination between negligible and high risk areas.

DNA testing can also be used to support a simplified system to verify claim of smallholder or plantation forest origin. It would contribute to building assurance around a simplified, low cost certification or third-party verification programme designed to support smallholders' sale of timber into higher value markets. The approach has been trialled and shown to work for large-scale industrial state-owned plantations in Indonesia (Perum Perhutani). Two methods were trialled: The first was to use a chain of custody test to check that logs at different point in the supply chain came from the same tree. This proved 90% accurate with current operating standards. The second tested whether logs matched the genetic profile of their source plantation. This method proved 100% accurate and is recommended for application to plantation systems, both large scale and small holder.

From the work of this project we can conclude that genetic identification of teak is a promising prospect for augmenting existing paper-based processes for timber certification, and can be applied to both natural forest and plantation situations to verify legality of origins and support market access and trust in high value international timber markets.

Two workshops (Solomon Islands Development Trust in Honiara on 28th June 2017; Provincial Agriculture & Forestry Office (PAFO) Luang Prabang, Laos on 25th-26th September 2018) were held as part of this project, and training in field and laboratory procedures was provided to project partners from Indonesia, Laos, PNG, Solomon Islands and Myanmar.

3 Background

Teak is one of the most commercially important timbers in the world. Its timber is highly valued for its durability and water resistance, and is used for boat building, exterior construction, veneer, carving, turnings, and for furniture manufacture. The ACIAR forestry program has invested significantly in the development of teak based agroforestry systems and associated value-added processing systems in Laos, Indonesia, Papua New Guinea and Solomon Islands.

Australia is committed to working in partnerships with producer countries to reduce the trade in illegal timber into Australia for the economic benefit of producer countries and to improve environmental outcomes globally. One of the primary ways that illegal timber enters the market is through mixing into legitimate supply chains and associated document fraud. This results in illegal timber in the supply chain with false claims of legal origin. Removing the doubt about the origin of timber supplies creates certainty for industry and consumers, opens markets for timber and increases taxation revenue for governments in developing countries (Nellemann 2012). It also provides a mechanism for community forestry suppliers to demonstrate sustainability to the global market.

Australia introduced illegal logging regulation on 30 November 2014, which requires importers of timber products to ensure they are sourced from legal timber harvesting operations. To support this new regulation, Australia wants to encourage and support increased legal trade between Indonesia and Australia. An improved system of chain-of-custody verification is required to sustain forest resources and enable access to the increasing number of high-value markets sensitive to legality issues, including the EU, US, Australia and others.

DNA markers are being used successfully for other timber species to distinguish between species, between populations and between individuals of timber species (Dormontt et al 2015). The cost of this technology is dropping dramatically and is already cost effective when used in conjunction with document verification audits (Lowe et al 2016). DNA technology is suitable for developing checks of existing chain-of-custody compliance claims, and has already been proven to be effective for other species in other countries (e.g. merbau in Indonesia, and oak products from China; Lowe et al 2010).

In the Solomon Islands, Indonesia and PNG, teak is grown in plantations by government or private companies or smallholder farmers. In Laos, teak is sourced from both natural and planted forests, with at least 15,000 hectares of smallholder teak plantations now established in the Luang Prabang region. Smallholder teak growers have difficulty in meeting international requirements related to legality verification and/or forest certification. Cost effective mechanisms to support farmers to supply timber into external markets and thereby improve livelihoods need to be explored. Being able to verify the supply chain of timber to point of export is a key way of supporting small holder producers gain access to international markets. The previous ACIAR projects have trialled DNA verification systems to work alongside certification systems in Indonesia (SVLK) and Myanmar (MTA).

In Myanmar and Thailand much of the teak is sourced from managed natural forests. Whilst the forest concession from which particular teak logs originate from are stamped, over harvesting and mixing of lots are common practices. A draft genographic map for the natural teak forests in Myanmar teak was generated as part of the previous ACIAR project and has been expanded to include Thailand and Laos under this project, to allow source verification via DNA of teak harvested from natural forests in the region.

The ACIAR Forestry Program aims to contribute to poverty alleviation and natural resource conservation and rehabilitation through scientific support for the establishment, management and sustainable utilisation of forests, providing optimum social, economic and environmental benefits to partner countries and Australia. This project contributes to the sustainable management of forests, and efficient and sustainable forest industries.

4 Objectives

The project aimed to facilitate the development of DNA-based verification systems for teak timber that are applicable to countries in the Asia-Pacific region. It extends the application of DNA markers to verify legal sourcing for teak from Indonesia and Myanmar to Laos and Thailand, with further opportunities in Solomon Islands, PNG. This expansion covers planted and naturally occurring teak across the main producing countries of SE Asia and the Pacific.

Specific objectives:

1. To develop and apply DNA chain of custody verification tests to teak sourced from community forests in Laos, Solomon Islands, PNG and Indonesia
2. To develop and apply DNA chain of custody verification tests to teak sourced from natural forests in Laos, Myanmar and Thailand
3. To enhance knowledge and capacity and develop a regional approach to DNA verification for teak

5 Methodology

1. Partner liaison
 - a. Professional networks of project partners utilised to identify and engage with suitable partners in in Lao PDR, Myanmar, Thailand, Solomon Islands and PNG.
 - b. Email and telephone negotiations undertaken to secure contracts and required authorisations for collection and export of teak samples.
 - c. Training on collection methodologies provided in person in Lao PDR and through documentation and phone consultation for Solomon Islands and PNG.
 - d. Training in genetic techniques was provided to partners from Indonesia and Myanmar.
2. Workshops
 - a. Regional workshop on DNA timber verification held in the Solomon Islands, organised by partners Double Helix in collaboration with in-country consultant Dr Richard Pauku from Maraghoto Consultancy.
 - b. Final workshop in Lao PDR organised by partners Double Helix in collaboration with in-country coordinator Mr Vongvilai Vongkamsao from the National Agriculture and Forestry Research Institute (NAFRI).
3. DNA extraction and analysis
 - a. Samples were sent for analysis to the Advanced DNA Identification and Forensic Facility at the University of Adelaide either as pre-extracted DNA (from Myanmar, and Thailand) or as preserved leaf and cambium material (from Lao PDR and PNG)
 - b. DNA was extracted using the Qiagen Plant Mini Kit on the Qiacube extraction robot including extraction blank controls
 - c. Samples were genotypes using the Agena MassArray iPlex Gold system using a final set of 142 single nucleotide polymorphism (SNP) markers developed and optimised through two previous SRAs (FST/2014/028 and FST/2015/007).
 - d. Genetic data was analysed using the programs GenAlEx (Peakall & Smouse 2006), Structure (Pritchard et al 2000) and GeneClass2 (Piry et al 2004).

6 Achievements against activities and outputs/milestones

Objective 1: To develop and apply DNA chain of custody verification tests to teak sourced from community forests in Solomon Islands, PNG and Indonesia

no.	activity	outputs/ milestones	completion date	comments
1.1	Identify and engage with suitable smallholders and wood manufacturing SMEs in Solomon Islands, PNG and Indonesia	Agreements with suitable smallholders and wood manufacturing SMEs to partner on the project	Small-holder samples from Indonesia were negotiated with FORDIA during 2018	Suitable smallholders were not identified from Solomon Islands or PNG
1.2	Physical samples of teak wood from standing trees, felled logs and processed products	Physical samples of teak wood from standing trees, felled logs and processed products	Indonesian samples received 02/05/2018; PNG samples received 26/11/2018; Solomon Island samples still to be received	Samples provided from Indonesia were community forests, naturalised stands and plantation material from Java In consultation with partners in PNG and Solomon Islands, it was agreed that samples were to be obtained from specific landraces as opposed to paired samples across supply chains, in order to enable genetic characterisation of stocks and identification of potential original provenances for future genetic improvement options. Unfortunately samples were not provided in time for genetic analysis from PNG, and are still in transit from Solomon Islands.
1.3	Statistical analysis of probable supply chain integrity	Statistical analysis of probable supply chain integrity	Indonesia 24/09/2018; PNG and Solomon Islands result pending;	

Objective 2: To develop and apply DNA chain of custody verification tests to teak sourced from natural forests in Laos, Myanmar and Thailand

no.	activity	outputs/ milestones	completion date	comments
2.1	Identify and engage with managers of suitable natural forest concessions and wood manufacturing SMEs in Laos, Myanmar and Thailand.	Agreements with managers of suitable natural forest concessions and wood manufacturing SMEs to partner on the project	During 2018	Managers of suitable natural forest concessions and wood manufacturing SMEs were identified and involved in the project from Laos, Myanmar and Thailand.
2.2	Collect paired field samples from natural forests and along various points in the supply chains	Genographic map of natural teak populations in the region	24/09/2018	Complete genographic map will be published in journal article, expected publication date early 2020. Paper describing the single nucleotide polymorphism markers and variation published 2019 – (Dunker et al)

2.3	Test the likelihood of mixing and claim falsification along these supply chains using DNA markers	Statistical analysis of probable supply chain integrity	2019	See results and discussion
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Objective 3: To enhance knowledge and capacity and develop a regional approach to DNA verification for teak

no.	activity	outputs/ milestones	completion date	comments
3.1	Hold regional workshop on DNA timber verification in the Solomon Islands	Report on the discussions and outcomes of the workshop. Collaborative in-principle agreements with appropriate stakeholders for future research and implementation project(s)	28/06/2017	Report attached (Appendix 1)
3.2	Hold regional workshop on DNA timber verification in Laos/Thailand	Report on the discussions and outcomes of the workshop. Collaborative in-principal agreements with appropriate stakeholders for future research and implementation project(s)	26/09/2018	Report attached (Appendix 2)
3.3	Present the results of activities associated with objectives 1, 2 and 3	Project report	09/07/2019	See results and discussion
3.4	Assess the prospects for utilising this technology to enhance access to international timber markets	Documented plan for future project requirements Report on cost effectiveness and applicability	30/04/2018	See results and discussion

7 Key results and discussion

The current project is the third SRA supported by ACIAR focussing on teak genetic identification with the current project team. Whilst previous project reports have been produced, the current report seeks to integrate the results from all three SRAs to give a complete picture of the teak work to-date. Therefore, the following results and discussion summarises the outcomes from FST/2014/028, FST/2015/007 and FST/2016/025.

A graphic illustration of the project activities can be found at Appendix 3.

7.1.1 Marker development and sample collection

Development of genetic markers for the identification of teak

Throughout the course of the research activities, a final set of 156 single nucleotide polymorphisms (SNPs) were developed for genetic analysis in teak. These markers were discovered using a ddRAD approach and final set of 132 were optimised for use on the MassArray genotyping platform. Details of the development of these markers and their variability in Myanmar populations are described in Dunker et al (2019, Appendix 4).

Sample Collections

Across the entire project, more than 1,600 samples from across the natural and planted range of teak in SE Asia and the Pacific Islands were collected. This set includes 1000 samples have been acquired for analysis (see table 1) but were outside the scope of the current project so could not be genotyped in the current funding round. These samples remain available for analysis in future project rounds.

Table 7.1 Teak individuals collected for the project. Figures in brackets indicate where samples have been received but not analysed.

Country	partner	origin	populations	individuals
Myanmar	ECCDI	natural	14	153
Myanmar	Uni Tokyo (Thwe Thwe Win)	natural	21	123 (+710)
Laos	NAFRI	natural	5	50
Thailand	Kasetsart University	natural	various	49
Indonesia	FOERDIA	Sulawesi, natural?	5	103
India	FOERDIA	Provenance trial (Indonesia)	4	6
Myanmar	Uni Tokyo (Thwe Thwe Win)	plantation	various	(279)
Indonesia	FOERDIA	plantation	11	121
Costa Rica, China, Indonesia,	Uni Tokyo (Thwe Thwe Win)	plantation	3	(51)
Solomon Islands	SIDI	plantation	TBC	
PNG	Forestry Dept	plantation	NA	29

Out of these samples, 600 have been genotyped using the available SNP markers.

7.1.2 Results contributing to objective 1: Develop and apply DNA chain of custody verification tests to teak sourced from community forests in Solomon Islands, PNG and Indonesia

Teak in Indonesia

Examination of teak wood sources in Indonesia was in two parts,

1. Chain of custody within the Perhutani Forest Management Unit in Cepu

Thirty three cambium and seven solid wood samples collected from Perum Pehrutani (Figure 1) were successfully genotyped. Of these, 22 were from logs in the mill and 18 from the remaining stumps in the ground (according to the paperwork accompanying the logs in the mill).



Figure 1. Sampling at Perhutani Forest Management Unit in Cepu

General view of the log yard

Marking of the log consists of tree number, cutting number, length of the log, volume and forest district.



The stump

General view of trees ready for harvest – the trees had been girdled one year earlier to allow the wood to air drying thus minimizing damage when felled



Border mark



Samples taken from stump

In the comparison of the samples of different tissue types taken from the same tree at the same time (e.g. cambium and wood taken from logs in the mill, or cambium and wood taken from stumps in the forest), all expected matches were obtained.

Twenty comparisons were made between materials collected at different points in the supply chain (log in the mill vs. stump in the forest). Eighteen of the 20 comparisons produced the expected matches between samples. Two comparisons indicated that samples from these different points in the supply chain did not match (only ~60% of loci in these comparisons were the same vs ~99% in other comparisons).

These results strongly indicate that in two cases the tested samples did not originate from the same tree (10% incorrect tree assignment). However, when these samples were compared to the broader global teak database, 100% of log samples were consistent with the correct plantation origin.

These results suggest that paperwork does not always accurately reflect timber origins to exact tree, but that broader genetic provenance testing approaches indicate legitimate timber origins from the expected plantation location.

2. Provenancing of teak from plantations and naturalised forests in Indonesia

224 samples collected from across plantations in Java and from naturalised and plantation forest in Sulawesi and surrounding small islands (Buton, Muna) were genotyped using the developed markers (Figure 2). Results indicated that a single genetic cluster dominated teak plantations in Java. Teak from Sulawesi and the surrounding islands was quite different to that which occurs in Java and therefore could be used to differentiate teak from Javan vs Sulawesian origin.

The result is also interesting in that it helps to resolve long standing questions on the origin of teak in the islands off Sulawesi and indicates that they are not, as has been suggested, merely translocations from Javan plantations, but is from a separate, potentially indigenous, origin.

These results are being prepared for a publication on teak genetic variation in Indonesia

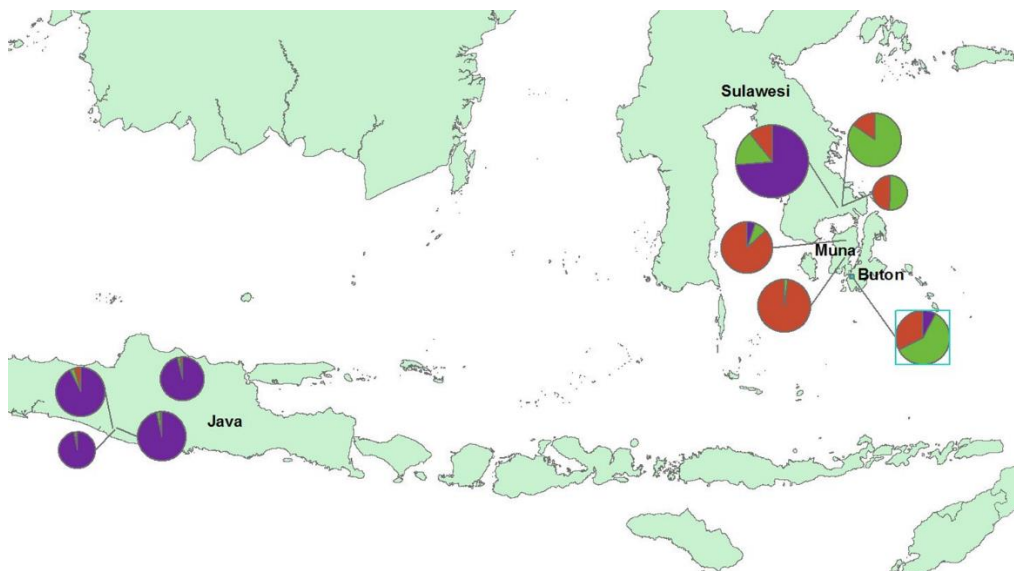


Figure 2. Preliminary Indonesian teak map (n=224) showing genetic clusters

Teak in Solomon Islands and PNG

Despite best efforts to organise samples from Solomon Islands and PNG, we were unable to obtain samples in time to analyse the DNA before the end of the project. PNG samples have since been received and are being analysed. Solomon Island samples have been collected but are still in transit to Adelaide. We continue to chase these samples in the hope that they can be obtained and analysed. Results from the PNG analysis could not be included in this report, due to time constraints, but will be provided to ACIAR when available.

7.1.3 Results contributing to objective 2: develop and apply DNA chain of custody verification tests to teak sourced from natural forests in Laos, Myanmar and Thailand

Natural teak variation in Lao PDR and Thailand

Samples from three natural forests locations in Lao PDR (n=26) and 10 natural forest locations in Thailand (n= 49) were well differentiated indicating good capacity for utilisation of the developed DNA markers for origin verification in these countries (Figures 3 and 4). These results will be explored in the global teak map publication currently in preparation.

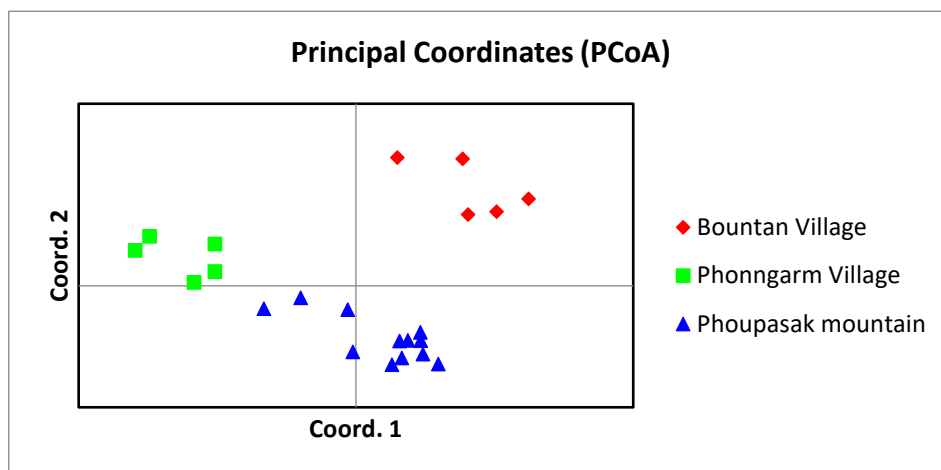


Figure 3. PCoA of genetic distance for natural teak populations in Lao PDR

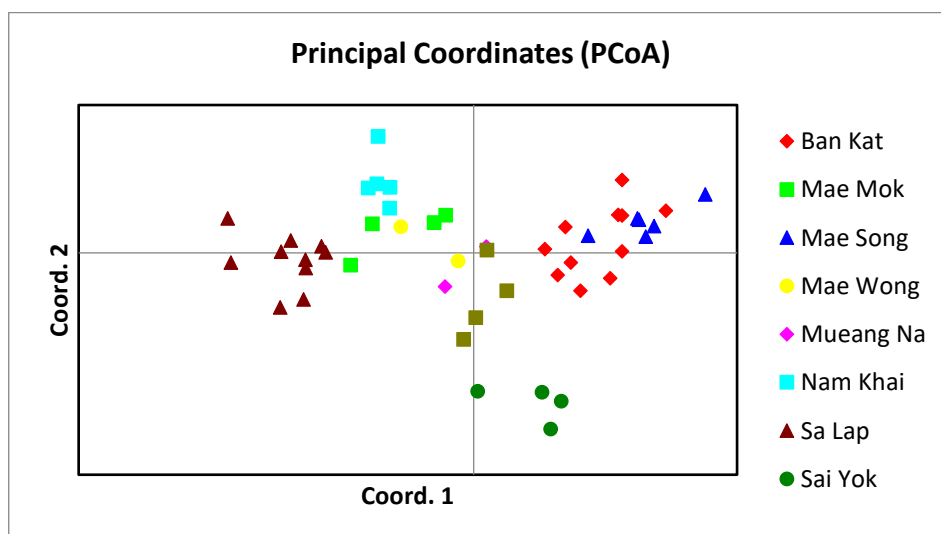


Figure 4. PCoA of genetic distance for natural teak populations in Thailand

Natural teak variation in Myanmar

Across three ACIAR projects (including work previously undertaken in SRAs FST/2014/028 and FST/2015/007), the reference data for Myanmar has been built to a point where we now have genetic profiles for 263 different individuals from 34 different natural forest sites in Myanmar. In some cases, nearby sites were amalgamated where sample sizes were less than five individuals and genetic signatures were similar to give 25 populations for assignment purposes. Analysis of population structure revealed 5 genetic clusters across Myanmar, separating the country into northern, eastern, central, western and southern genetic groups (Figure 4).

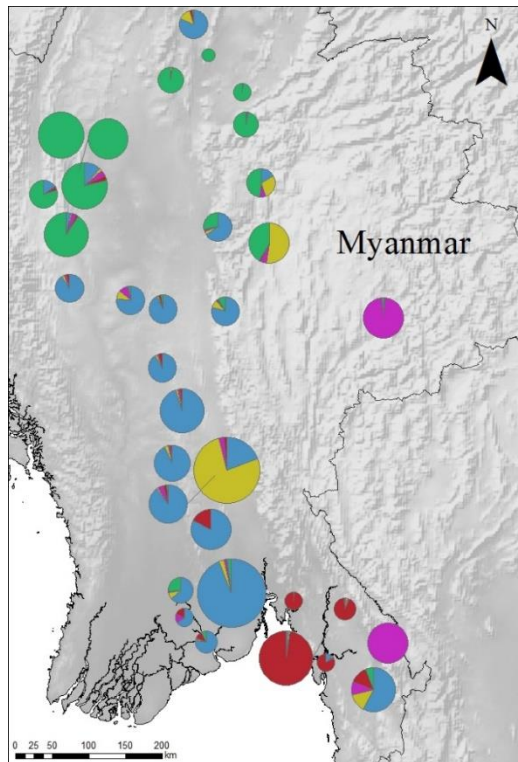


Figure 4. Myanmar teak map (n=263) showing genetic clusters

The genetic structure revealed supported previous work done by Dr Thwe Thwe Win using microsatellites (Win et al 2015), however this work builds on those results by revealing additional genetic structuring in areas previously unsampled, such as the mid-east and very south east parts of the country (Figure 4). Further, these markers are suitable for analysis from DNA derived from wood, which typically is not the case for microsatellite data.

Assignment capacity of the reference data was assessed using the software GeneClass2 with default settings. Assessing the five most likely population assignments provided by GeneClass2, and allowing a 100 km tolerance, 99% of reference samples could be accurately assigned back to their origin, and will be valuable to verify geographic origin claims for this country.

These data are currently being prepared for publication.

Chain of custody verification

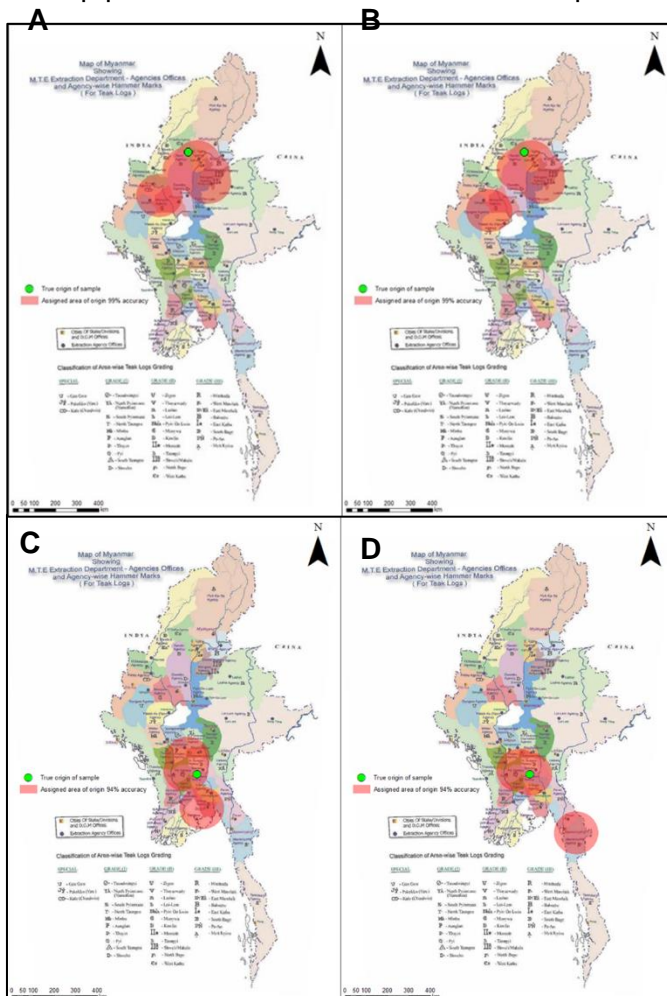
To ensure the exclusion of erroneous data, an 85% loci pass rate was applied to all samples. Any genotypes with 15% missing data, or more, were excluded from further analysis. Under these conditions, genotypes from 19 pairs of technical replicates could be compared to calculate the error rate. The average rate of errors per locus was 0.18% (less than 1%, which is very low for this type of analysis).

For one tree where leaf, cambium from the standing tree, cambium from the felled tree and solid timber were all extracted and genotyped, all samples produced the same genotype. At one locus the timber sample produced an allele call that was inconsistent with the other tissue types. However this was within the expected margin of error. These results are consistent with those found in Indonesia, where the genotypes from solid timber and cambium were compared from five logs from Perum Perhutani plantation, again the genotypes were consistent at ~99% of loci, within the expected range for matched samples.

These results demonstrate that DNA can be extracted from different parts of the tree and return identical genotypes as expected. On this basis, tissue from the same tree can be accurately matched at different points in the supply chain, and conversely, where DNA tests indicate a non-match, this is a reliable indicator that the wood does not come from the expected tree.

Industry Testing

Project partners Double Helix Tracking Technologies have utilised the Myanmar teak genetic database to assess claims of timber origin on behalf of their customers. In each case, DNA was extracted from the unknown wood (taken from logs at the sawmill) and assigned back to probable origin based on the genetic reference database. Results were provided in the form of maps, indicating the likely provenance. Where this assigned area overlapped with the claimed concession, the claim was considered verified. In all cases the claims were verified (Figure 5), and this information has been used to support teak exports to Europe and there has been interest from competent authorities for these tests to help provide additional assurance of compliance with EUTR.



7.1.4 Results contributing to objective 3: enhance knowledge and capacity and develop a regional approach to DNA verification for teak

Regional Teak Map

Genetic analysis of all teak timbers included in the study has facilitated the development of an initial regional map of teak genetic variation (Figure 6).

In general, results indicate that the genetic clusters which dominate each country are qualitatively different, and are thus likely to facilitate good provenance determination for unknown samples. It is clear from this map that the major geographic regions/countries where teak grows can be distinguished genetically (i.e. India, Myanmar, Thailand, Laos and Indonesia).

Full exploration of these patterns will be available in a forthcoming publication, expected end 2019.

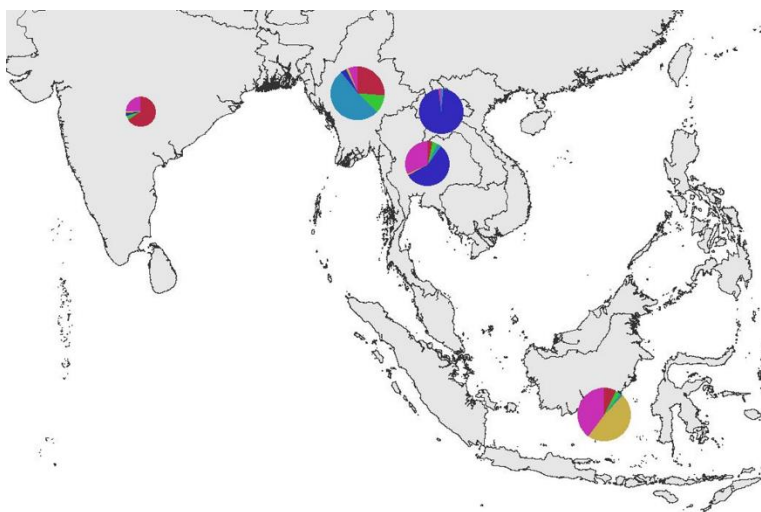


Figure 6. Preliminary global teak map by country (n=605) showing genetic clusters

However, from the work of this project we can conclude that genetic identification of teak is a promising prospect for augmenting existing paper-based processes for timber certification and can potentially be utilised in both natural forest and plantation situations to verify legality of origins and support market access and trust in high value international timber markets. Two scenarios of application – natural forest and smallholder/plantation forest – are outlined below.

Prospects for utilising this technology to enhance access to international timber markets

Application One – harvest from natural forest – test case Myanmar

The situation

There now exists the opportunity to integrate DNA testing with timber legality and sustainability certification schemes being developed in Myanmar.

The market drivers behind this development are:

- the controversial nature of Myanmar teak in consumer markets, due to widely publicised cases of illegal logging and conflict;
- active enforcement of the EU Timber Regulation and Australian Illegal Logging Prohibition Regulation by those country's authorities, with regards to Myanmar teak consignments;

- the encouraging response from the Myanmar government to implement changes to improve forest governance;
- the development and implementation of a Myanmar Timber Legality Assurance System (MTLAS), and other initiatives aimed at preparing Myanmar for negotiations with the European Union relating to a future EU Forest Law Enforcement Governance and Trade (FLEGT) Voluntary Partnership Agreement.

Problem

Despite significant progress in Myanmar over the last three years in the adoption of third party verification systems, the development of the Myanmar Timber Legality Assurance System, and engagement by the Programme for the Endorsement of Forest Certification (PEFC), there remains significant challenges for importers of Myanmar teak to prove adequate Due Diligence to mitigate risk of illegal timber in their consignments.

The underlying problem is that documentation issued by the Myanmar government as proof of legal harvest, transport, trade and production is considered not reliable. In other words, the existing document-based systems utilised in Myanmar to prove legality along the supply chain, whilst extremely detailed and comprehensive, lack credibility amongst the enforcement authorities of export markets.

Furthermore, a number of additional rules implemented by the government since 2016 to control illegal timber smuggling include:

- Logs sold in local currency (Myanmar kyats / MMK) are intended exclusively to supply the domestic timber market.
- Products manufactured from timber from forest conversion, as well as confiscated illegal timber, cannot be exported.
- Products manufactured from timber harvested in “conflict areas” under a Modified Procedure harvest practices prior to 2015 have now been discontinued. Risk of this type of controversial timber is higher in identified conflict areas.
- Timber harvest in the Bago Yoma area is under a 10-year moratorium since May 2016, in order to allow this area to recover from high deforestation.

Any timber harvested illegally in these areas will have to pass through government chain of custody systems in order to access export markets, through substitution of legal with illegal timber parcels.

These problems are likely to persist, even as third party verification or certification systems are developed, since these too will rely in great part on the verification of government issued documentation.

Solution

With the development of genetic reference data, claims of origin of harvest stated on government documents can be scientifically validated all along the Chain of Custody.


For example, certified letters issued by Myanmar Timber Enterprise (Figure 6). Specification, packing and measurement Lists delivered with logs to sawmills, and removal passes showing transport of logs all indicate origin of harvest.

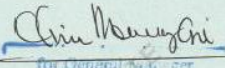
DNA verification can also be applied to exclude high risk areas, such as conflict zones and border areas associated with illegal logging and cross border smuggling. DNA testing combined with localised Area Risk Assessments that are being conducted as part of Myanmar’s timber certification programme allow for discrimination between negligible and high risk areas.

THE REPUBLIC OF THE UNION OF MYANMAR
MINISTRY OF NATURAL RESOURCES AND ENVIRONMENTAL CONSERVATION
MYANMA TIMBER ENTERPRISE
EXTRACTION DEPARTMENT

CERTIFIED LETTER Issue No. **59/2018-2019**

This is to certify that the following information on logs sold with Delivery Order/Invoice No. 1998/2017-2018 (L), Lot No. DG (TWT) - 124, Specification No. TRLU - 1150/2017-2018 and Quantity of 41 logs and 36.062 tons extracted and transported in accordance with rules and regulations prescribed by Extraction Department and relevant organizations:

(1) Extraction Agency/Range	-	Homalin Extraction Agency, Homalin Range (5).
(2) Administrative District/Township	-	Hkamti District, Homalin Township.
(3) Reserved/Unclass Forest & Compartment No.	-	Nan Htein Kwinn Extension Reserved Forest, Compartment No(17,18), Nan Htein Kwinn Reserved Forest, Compartment No (79, 80, 81)
(4) Extraction year	-	2015-2016
(5) Species	-	Teak
(6) Entry permission by Forest Department	-	Mawlaik/ Hkamti District Forest Department, 27-10-2015 Dtd, Letter No - 3170-71/ Tha (Ka)1
(7) Revenue Mark	-	
(8) Agency Classification Hammer Mark	-	H
(9) Production Depot	-	Dagon (South) Depot


 for General Manager
 (Khin Maung Kyi)
 Deputy General Manager

Date : 4th May 2018

Figure 6. Example Certified Letter issued by Myanmar Timber Enterprise (with location data highlighted).

Recommendations

Whilst the resolution of the genetic reference database can be improved through additional sampling and genotyping of each timber extraction agency, its current resolution is still useful enough to either support or reject a regional claim of origin. DNA traceability works on top of existing document controls, verifying the accuracy of documents and records required under a simple but otherwise vulnerable control system, thereby supporting systems in development in Myanmar.

Now that the initial investment in DNA reference data for the species has been made, the cost of rolling out the traceability system to other areas where the species is harvested is marginal (at about US\$25 000 per harvest zone). Ongoing running costs (of sampling and testing) would be incorporated into fees charged by Certification Bodies.

Export markets gain access to a wider range of controlled timber sources, and responsible exporters gain better access to overseas markets based on sustainable and controlled volumes of product.

Application Two – smallholder and industrial teak plantations – test cases in Indonesia and Laos

Situation

The plantation teak market is dominated by industrial scale plantations in Indonesia. Market access for these sources is easier due to the size of companies involved, and their ability to invest in long-term plans to achieve certification of plantations over a large area.

Conversely, smallholder plantation operators across S. E. Asia and the Pacific face widely documented challenges to achieving certification and associated high value market access (Flanagan et al, 2018). Current certification systems are far too complex and expensive for small holders, even if they form a cooperative.

Without some form of third party certification, access to lucrative international markets is limited for smallholders but would be one of the best ways to ensure improved regional benefit and direct farm level income generation.

Solution

DNA testing could be used to support a simplified system to verify claim of smallholder forest origin. It would contribute to building assurance around a simplified, lower cost certification or third party verification programme designed to support smallholders' sale of timber into higher value markets.

The approach has been trialled and shown to work for large-scale industrial state-owned plantations in Indonesia (Perum Perhutani). Two methods were trialled: The first was to use a chain of custody test to check that logs at different point in the supply chain came from the same tree. This proved 90% accurate with current operating standards.

The second was to test whether logs matched the genetic profile of their source plantation. This method proved 100% accurate and is recommended for application to plantation systems, both large scale and small holder.

Recommendations

- Develop plantation specific genetic profiles that will support claims of origin by smallholder plantation owners.
- Work with country experts in the development of certification systems for smallholders, integrating
- DNA testing as a low cost Chain of Custody solution.
- Apply periodic testing of timber from plantation sources. Attention derived from the application of DNA testing will help in the promotion of smallholder verification systems to international markets.
- International promotion, focusing on the story and benefits of supporting smallholder teak production will help gain new markets for verified smallholder timber sources. A provenance brand could also be developed to support such promotional efforts.

Workshops

A total of four workshops were held across the three projects:

1. 'Application of genetic information for the verification of teak' held at the FORDA meeting rooms at Jogjakarta on 5th May 2015. Report available Appendix 5.
2. 'Securing the supply chain for Teak in Myanmar using DNA' was held in Yangon on the 25th of February 2016. Report available Appendix 6.
3. 'Developing DNA-based chain of custody systems for legally-sourced teak' held at the Solomon Islands Development Trust in Honiara on 28th June 2017. Report available Appendix 1.
4. 'Developing DNA-based chain of custody systems for legally-sourced teak - Closing Workshop' held at Provincial Agriculture & Forestry Office (PAFO) Luang Prabang on 25th-26th September 2018. Report available Appendix 2.

Training

- Sampling – Three field teams from ECCDI in Myanmar were trained on sample collection methodologies through the provision of a remote training program by Double Helix Tracking Technologies, 1st-4th February 2016 (Appendix 7); The field team from Lao PDR was training in person, by Double Helix Tracking Technologies, 5th-6th June 2017 (Appendix 8). Field sample training was provided to PNG and Solomon Island partners by video link.
- DNA analysis – Dr Thwe Thwe Win from the University of Forestry and Environmental Science in Myanmar, visited the laboratories of the Advanced DNA, Identification and Forensic Facility at the University of Adelaide between 11th and 21st September 2018. During her visit, Dr Win worked alongside ADIFF researchers to learn new techniques in DNA extraction and amplification from teak timbers. Dr Win contributed to the publication of the genetic markers (Dunker et al 2019, Appendix 4) and broader analysis of the genetic structure of teak in Myanmar for a publication in preparation. Dr Win presented her research to the University of Adelaide and travelled to the final workshop to present alongside the project partners in Lao PDR (Appendix 2). The visit has increased Dr Win's skills and cemented the collaborative relationship between the University of Adelaide and the University of Forestry and Environmental Science in Myanmar. Training was provided to Indonesian partner scientists during a sampling trip.

8 Impacts

8.1 Scientific impacts – now and in 5 years

The project has developed genetic resources for teak that can be applied to timber material to determine individual tree level identity as well as regional identity. Detailed genetic maps have been developed that will be published shortly, along with the existing publication (appendix 4) detailing the genetic marker development, this can be used by researchers, governments and industry to verify the origin of teak. Future work will build upon this research to expand the genetic characterisation of teak across the world.

8.2 Capacity impacts – now and in 5 years

The project has developed the capacity to undertake DNA tests to verify the origins of teak. This capacity has been demonstrated in industry through the verification of origin of claims in Myanmar, and the verification of plantation origin in Java. Training on sampling has been provided to technicians from Laos PDR, Myanmar, Solomon Islands and PNG, and on genetic techniques to researchers from Myanmar and Indonesia in these techniques. Currently this work can be undertaken in Australia to support claims of origin in teak. In five years we anticipate that capacity will have grown in producer countries to complete these tests independently to support local teak industries.

8.3 Community impacts – now and in 5 years

8.3.1 Economic impacts

Reducing illegal logging in developing countries returns revenue back to communities and governments through taxation systems, rather than this revenue being lost through illegal networks. The DNA tests developed in this project, if implemented as part of a legality system, can allow this economic benefit to be returned to producer communities and local governments.

8.3.2 Social impacts

Reducing illegal logging in developing countries can help support small-holder and forest dwelling communities, through economic returns, and promote self-govern sustainable forest production practises. The DNA tests developed in this project, if implemented as part of a legality system, can allow this social benefit to be returned to producer communities and local regions.

8.3.3 Environmental impacts

Being able to police timber supplies and reduce the level of illegal logging in timber supply areas has the capacity to support the sustainably management and conservation of natural forest blocks. The DNA tests developed in this project, if implemented as part of a legality system, can allow this environmental benefit to be returned to producer communities and local regions.

8.4 Communication and dissemination activities

Alongside the workshops undertaken as part of the project as a whole (appendices 1, 2, 5 and 6). One scientific paper has been published (appendix 4) and three more are in preparation (see appendix 3 for outputs). The following conferences and meetings have been attended in which this project was presented:

1. APEC – Illegal Logging forum (February 2019, Santiago, Chile), Attended by Prof Andrew Lowe
2. IAWA-IUFRO symposium 2019 (May 20-22 2019, Beijing, China), attended by Dr Eleanor Dormontt
3. GTTN Regional Workshop 2019 (May 23 2019, Beijing, China), attended by Dr Eleanor Dormontt and Mr Daren Thomas
4. Interpol SE Asian Regional workshop (June 2019, Singapore), attended by Ms Jomaine Tang

9 Conclusions and recommendations

9.1 Conclusions

From the work of this project we can conclude genetic identification of teak is a promising prospect for augmenting existing paper-based processes for timber certification and can potentially be utilised in both natural forest and plantation situations to verify origins and support market access.

9.2 Recommendations

Immediate and demonstrated application of the developed teak genetic resources to verify forest of origin in Myanmar, Laos and Thailand, as well as verification back to an established genetic profile of specific plantations in Laos and Indonesia.

DNA should be implemented to augment existing paper-based processes for timber certification and can potentially be utilised in both natural forest and plantation situations to verify legality of origins and support market access and trust in high value international timber markets.

Further work to develop the global teak map and associated capabilities is required and falls under three themes:

1. Develop capacity within teak producer nations to apply the genetic tests to independently support their teak export industries
 - a. Optimise DNA test for low-tech labs
 - b. Increase technical capacity through improvements in access to equipment
 - c. Increase technical capacity through training and development opportunities in Australia and in producer country laboratories
2. Work with governments to expand the reference data for natural teak populations
 - a. Genotype samples already acquired (n=710 from Myanmar)
 - b. Greater coverage in Myanmar, Lao PDR and Thailand (leverage existing networks built throughout project)
 - c. Extend coverage to include natural populations in India (formalise partnership with Kerala Forest Research Institute)
3. Working with government and industry to develop genetic profiles for plantations
 - a. Genotype samples already acquired (n=330 from Myanmar, PNG, Solomon Islands, Costa Rica, China, Indonesia)
 - b. Build networks and raise awareness of the potential for genetic verification in other teak growing regions e.g. tropical Africa and South America

10References

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10.2 List of publications produced by project

- Published:** Dunker, B., Dormontt, E.E., Dixon, R.R., Jardine, D.I., Kireta, D., Nurtjahjaningsih, I.L.G., Win, T.T., Rimbawanto, A. and Lowe, A.J., (2019). A set of 156 SNP markers for teak (*Tectona grandis* Linn. f.). *Conservation Genetics Resources*, 1-3.
- In preparation:** Dormontt, E.E., Dunker, B., Dixon, R.R., Jardine, D.I., Kireta, D., Nurtjahjaningsih, I.L.G., Win, T.T., Rimbawanto, A. and Lowe, A.J. (in prep) Establishment of a global teak reference database for teak (*Tectona grandis* Linn. f.) for timber verification.
- Win, T.T. Dormontt, E.E., Dunker, B., Dixon, R.R., Jardine, D.I., Kireta, D., Nurtjahjaningsih, I.L.G., , Rimbawanto, A. and Lowe, A.J. (in prep) Genographic map of Myanmar teak (*Tectona grandis* Linn. f.) for timber verification.
- Rimbawanto, A., Dormontt, E.E., Dunker, B., Dixon, R.R., Jardine, D.I., Kireta, D., Nurtjahjaningsih, I.L.G., Win, T.T., and Lowe, A.J. (in prep) Teak in Indonesia: chain of custody in plantations and the origins of naturalised island populations.

11 Appendixes

11.1 Appendix 1:

Report Solomon Islands Workshop 2017

11.2 Appendix 2:

Report Lao PDR Closing Workshop 2018

11.3 Appendix 3:

Diagram of activities for FST/2014/028, FST/2015/007 and FST/2016/025

11.4 Appendix 4:

Publication: Dunker, B., Dormontt, E.E., Dixon, R.R., Jardine, D.I., Kireta, D., Nurtjahjaningsih, I.L.G., Win, T.T., Rimbawanto, A. and Lowe, A.J. (2019). A set of 156 SNP markers for teak (*Tectona grandis* Linn. f.). *Conservation Genetics Resources*, 1-3.

11.5 Appendix 5:

Report Jogja Workshop 2015

11.6 Appendix 6:

Report Myanmar Workshop 2016

11.7 Appendix 7:

Report Myanmar Training 2016

11.8 Appendix 8:

Report Lao PDR Training 2016