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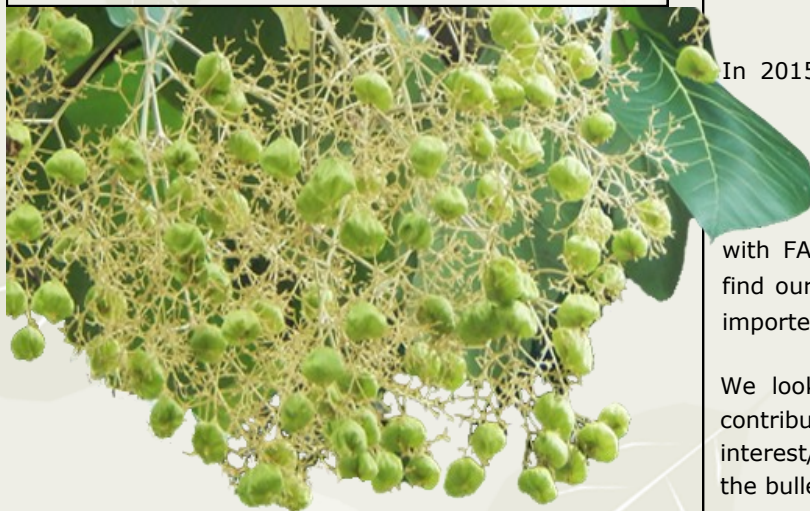
Teaknet Bulletin

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*Wishing a Very
Happy & Prosperous New Year
to all Our Readers*

Editorial

Greetings on the New Year !!

As the Teaknet Bulletin enters the 9th year of publication, we are delighted to present this issue with an interesting contribution on the functional genomics of teak. The research team lead by Prof. Helaine of the University of São Paulo, College of Agriculture, Brazil were able to characterise genes encoding for the specific functions of wood development in teak. This may revolutionize the future tree breeding programmes to improve tree growth and wood quality, especially juvenile wood when aimed at reducing the rotation age of teak. Another report from Australian researchers highlights the improvised sawmilling technology that can assist the local teak communities of Lao PDR and Solomon Islands for improvements in the product quality and better economic returns. A FAO paper on global teak trade in the aftermath of Myanmar log export ban implemented since April 2014 has also been included in the bulletin.

In 2015, TEAKNET was able to make its presence felt once again at global level by organizing the 3rd World Teak Conference in Ecuador. We will also be organizing a Partner Event in the forthcoming Asia Pacific Forestry Week 2016, Philippines during February in association with FAO and IUFRO Teakwood Working Party. You will also find our regular column on the latest prices of plantation teak imported into India.

We look forward for your critical analysis, suggestions and contributions in the form of short articles/news items of interest/research papers of non-technical nature for inclusion in the bulletin.

With warm regards,
P.K. Thulasidas
TEAKNET Coordinator

Functional Genomics of Teak

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Teak is the most valuable commercial timber in the tropics due to its high durability, qualities of color, density and resistance to external environmental factors. Despite its relevance, genetic studies are still limited. For example, gene expression studies of teak genes from different tissues (stem, branch, root, leaf, flower) under treatments and in different environmental conditions are essential to elucidate the molecular biology of teak and provide information for practical purposes.

Advanced methodologies and techniques, including RNA sequencing, quantitative real-time reverse transcription RT-PCR (qRT-PCR) and gene cloning, among many others, are already available. They allow us to study molecular processes of trees and thousands of genes at the same time.

Research on teak biotechnology has traditionally focused on the study of teak population variability and genetic diversity using polymorphic markers in the last 10 years. Several institutions have been involved in those studies in Asia (India, Thailand, Myanmar), Europe (France, Belgium, Germany, Denmark), Africa (Togo, Côte d'Ivoire, Ghana) and in Latin America (Brazil, Costa Rica). The Agriculture College "Luiz de Queiroz" (ESALQ), University of São Paulo (USP) (Brazil) has studied the genetic variability, genomics, transcriptomics, dendrochronology and wood properties of teak, using Brazilian populations (Figure 1).

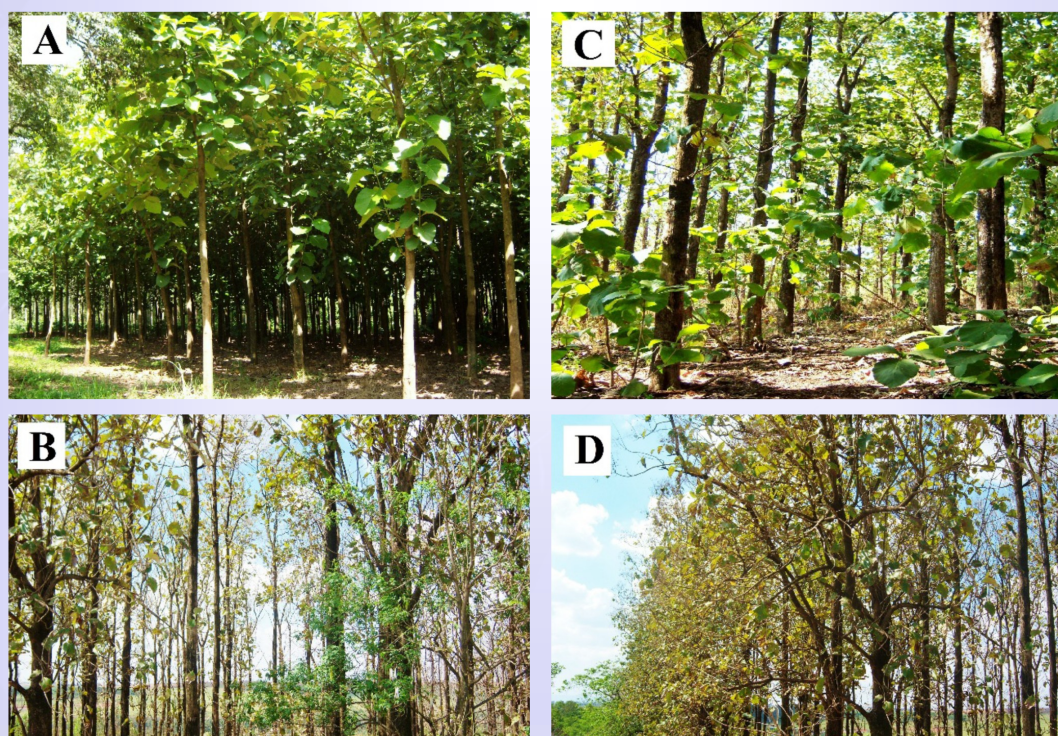


Figure 1. *Experimental field of ESALQ/USP. Piracicaba, São Paulo, Brazil.* Plantations of 14yr old teak (A-B); 62-year-old teak plantations (C-D) used for transcriptomic studies. Rainy season (A, C) ; Dry season (B, D).

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Genetics of secondary xylem, drought tolerance and floral development

Transcriptomes (or functional genomes) lead to identify all the genes in several tissue-specific situations, developmental stages and environmental conditions. The advantage of studying the functional genome of organisms (instead of genomes) is that it makes possible to identify which genes are active, and link to important physiological processes such as drought tolerance, biotic and abiotic stress, biomass, photosynthesis. Moreover, with the study of active genes we can discover new functions in metabolic pathways and hormonal processes. Consequently, these genes can be used for diversity studies, biochemical experiments and tree improvement through marker-assisted selection and genetic transformation. Unlike, complete genomes are generally large, complex, with gene repeats, making it difficult to identify active genes.

In 2015, our laboratory at ESALQ/USP, with the Center for Applied Plant Sciences (CAPS), Ohio State University, obtained 462,260 transcripts in teak for leaves and roots (Figure 2), flowers (Figure 3), seedling, stem and branch secondary xylem (Figure 1 and 4) using the RNA-seq methodology. This database can be considered as the completely functional genome of teak, and may serve as the “teak reference genome” for diverse genetic studies, until the complete teak genome is sequenced. The functional genome is available at the NCBI webpage (<http://www.ncbi.nlm.nih.gov/bioproject/PRJNA287604>).



Figure 2. Two month-old *in vitro* teaks used to sequence roots and leaves by RNA-seq methodology.

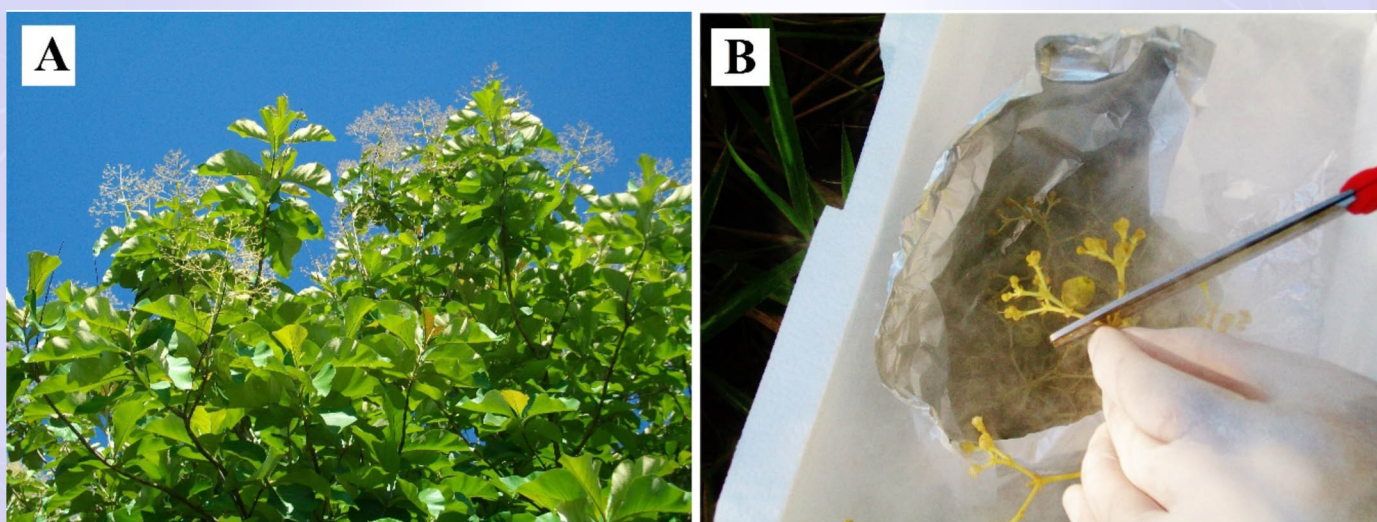


Figure 3.(A) Inflorescences and flowers used for sequencing, coming from 14-year-old teak trees.
(B) Methodology for collection of the plant material, using liquid nitrogen and aluminum foil, before laboratory work.

Read more on page 4



Figure 4. (A) Stem and (B) Branch Secondary xylem of teak used to sequence by RNA-seq methodology.

Moreover, our transcriptomic study found more than 2,000 genes related with specific functions in wood development of teak. Among those genes, members of some families were characterized such as *MYB* transcription factors (called *MYB1-4*), Heat-shock proteins (called *HSP1-4*), carbohydrate and pectin genes, which are directly related with wood processes. Those teak genes are similar to homologous genes of other plants and trees, and showed expression dissimilarity when tree development was studied. For example, Heat-shock proteins seem to aid defending teak against environmental changes, while *MYB* transcription factors are directly influenced by the maturation of teak wood (Galeano *et al.* 2015).

In addition, field collection of sapwood and heartwood allowed us to analyze, for the first time, molecular and biological processes of these tissues (Figure 5). The understanding of how rigidity of teak wood and extractive content are different from most other woods is essential. Also, the quality of the juvenile wood itself is an important target for improvement, and can be assessed at an earlier stage by marker-assisted selection. *MYB1* and *MYB4* genes are only present in mature sapwood, while *MYB2* is only present in juvenile sapwood (Galeano *et al.* 2015). They should be evaluated as molecular markers, to seek trees that keep up fast juvenile growth accelerated for more years, reducing the rotation age and yielding higher percentage of heartwood (Galeano *et al.* 2015).



Figure 5. (A) Teak core sampling of 14- and 62-year-old teak using the Pressler Core Barrel. (B) Manual separation of teak sapwood and heartwood for genetic analysis. (C) Methodology for collection of the plant material, using liquid nitrogen and aluminum foil, before laboratory work.

Furthermore, the teak transcriptome of root showed several genes related to drought tolerance, such as *TPS* (*Trehalose 6-Phosphate Synthase*), *PIP* (*Aquaporin*), *DREB* (*Dehydration Responsive Element Binding Protein*) and *AREB* (*Abscisic Acid Responsive Element Binding Protein*). Certainly, deep genetic research of these genes will be very interesting in the near future.

[Read more on page 5](#)

Additionally, teak productivity and growth are known to decrease after reproductive phase, being affected by the mechanisms of flower development and the long reproductive cycle (Diningrat *et al.* 2015). Indeed, to provide genes related with flower development is essential in order to understand this process at molecular level and try to improve biomass production through regulation of flowering. In 2015, the Institute of Technology, Bandung (Indonesia) and the Pennsylvania State University (United States) (Diningrat *et al.* 2015), obtained the floral transcriptome of teak. This database is composed of 87,365 genes with a further identification of 14 genes (called *TFL1-14*) related with the flower development and regulation of vegetative-reproductive phase transition. For this purpose, they also used the RNA-seq methodology.

The future of teak functional genomics for marker-assisted selection and breeding programs

The understanding of gene function in wood formation, flowering, drought tolerance and other biological processes in teak is essential. Once researchers collect datasets from different tissues and conditions, gene networks can be established to understand the relation between the metabolic pathways.

Further, every study is a challenge due to the huge teak sizes, slow growth and long gestation period, which make breeding programs a long process. Advanced next-generation sequencing is often considered as the best technology nowadays to discover thousands of genes that can be used to improve tropical trees. The fact is that transcriptomics and genomics can be used for breeding programs assisted by molecular markers and in exploiting natural variation in order to achieve improvements in tree growth and wood quality. Currently, Single Nucleotide Polymorphisms (SNPs) aimed at breeding and genomic programs appears as a profitable methodology for selecting trees with better biomass production (as done in trees from the *Pinus*, *Picea*, *Eucalyptus* and *Populus* genera).

Short rotations of around 20 years are known for teak plantations in Brazil and other countries. Growth improvement seems to be essential, and consequently, there is a desire to learn more about molecular processes underlying wood formation. The juvenile wood quality seems to be an interesting feature to get improved. Quality assessment at an early stage (plantlets) by looking for teak with a faster early growth rate will be crucial. This selection will certainly result in a significant reduction of crops rotation with higher percentage of heartwood yield.

The establishment of teak plantations is still encouraged by the high demand and exceptional prices. Unfortunately, there is still a high portion of teak stands raised from seeds of genotypes that have undergone no selection, leading to low-quality wood. The countries that lead the teak market (such as Thailand, Singapore, China and Brazil) have a great concern for the future supply of its products.

To this end, biotechnology and genetics are powerful tools to go straight to the productivity improvement and genotype selection. The genetic database available is useful to develop molecular markers to select teak with specific characteristics and to study its diversity and ecology, aiming to achieve a deeper understanding of the biology of this species. 2015 was the year for functional genomics of teak. Two papers were published, providing priceless information for the academic community and for private or public institutions working with teak. The first article provides 462,260 genes (Galeano *et al.* 2015), and the second one 87,365 genes (Diningrat *et al.* 2015). We encourage laboratories around the world to step up genetics research on teak. Recently, in the World Teak Congress held in Ecuador (2015), the importance of focusing efforts to develop research in the area of teak genetics and genomics, was widely discussed.

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- Galeano, E. Vasconcelos, T.S. Vidal, M. Mejia-Guerra, M.K. Carrer, H. 2015. Large-scale transcriptional profiling of lignified tissues in *Tectona grandis*. *BMC Plant Biology* 15:221.

Asia-Pacific Forestry Week 2016: Partner Event by TEAKNET

22-26 February 2016, Clark Freeport Zone, Pampanga, Philippines

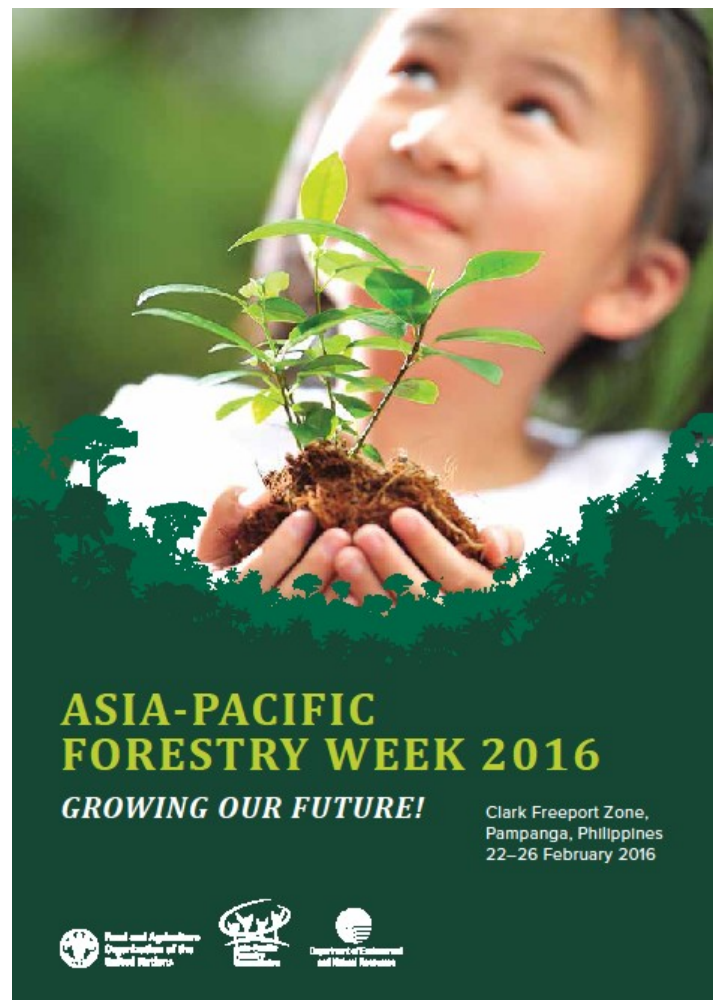
The Food and Agriculture Organization of the United Nations (FAO) and its partners invite people interested in, and committed to, sustainable forest management in Asia and the Pacific to come together for Asia-Pacific Forestry Week 2016 in Clark Freeport Zone, Pampanga, Philippines, 22-26 February 2016. Asia-Pacific Forestry Week (APFW 2016) is expected to be one of the largest and most important forestry gatherings in the region in 2016.

The theme of Asia-Pacific Forestry Week 2016, *Growing Our Future!* is intended to encourage participants to chart new pathways that guide the development of forestry into the future.

A Partner Event- '*Global Significance of Teak- Present and Future*' is proposed to be jointly organised by TEAKNET, FAO and IUFRO Teakwood Working Party (D5.06.02) during the Forestry Week. Interested participants who are attending the Forestry Week are encouraged to join the Partner Event and visit the TEAKNET Exhibition booth in the conference venue.

To know more about Asia Pacific Forestry Week, please visit the webpage

<http://apfw2016.denr.gov.ph>



ASIA-PACIFIC FORESTRY WEEK 2016

GROWING OUR FUTURE!

Clark Freeport Zone,
Pampanga, Philippines
22-26 February 2016



Food and Agriculture
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United Nations



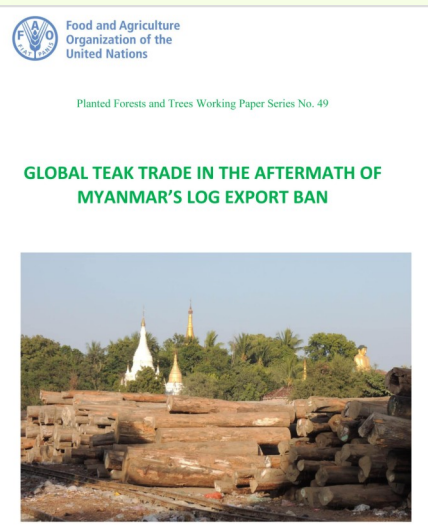
Global Teak Trade in the Aftermath of Myanmar's Log Export Ban

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This report was initially presented as a key-note address in the first session of the Third World Teak Conference, held in Guayaquil, Ecuador, on 11–15 May 2015 (www.worldteakconference.com). Upon the request of many participants, the presentation was elaborated into a detailed market report on the global trade of teak roundwood and sawnwood. The data and information provided are based on national customs data published in the Global Trade Atlas by the Global Trade Information Services (GTIS, www.gtis.com) according to the product identification codes of the Harmonized Commodity Description and Coding System (in brief, the Harmonized System, or HS). The report may give policy and decision makers, investors and managers a better understanding of the important role that teak resources play in the provision of wood products for the national economies of many tropical countries.

As export data from Myanmar are not available, the global teak trade with Myanmar in terms of volume and value has been assessed and evaluated based on official trade statistics of the teak-importing countries.

The paper may be downloaded [here](#)

Australian researchers provide expertise to the Lao PDR and Solomon Islands teak communities

The Forest Products Innovations team based at the Queensland Government's Salisbury Research Facility in Brisbane, Australia have been working with partners in both Lao PDR and the Solomon Islands on a range of teak projects.

In Lao PDR the team has developed log grading rules, installed a spindleless lathe, undertaken recovery studies and sawmill inspections, and held training workshops on drying sawn timber as part of the ACIAR project "*Enhancing key elements of the value chain for plantation grown wood in Lao PDR*". Working with staff from the National University of Laos, the FPI team has produced a best Practice Manual for small log processing with a focus on efficiency and worker safety.

The project will continue until June 2016 with a strong chance of a follow-on research and development project.

Read more on page 8



← Lao sawmillers using the DAF sawing jig to improve sawn accuracy and operator safety during teak sawmilling.

The activities in the Solomon Islands are part of a separate ACIAR project- *"Enhancing economic opportunities offered by community and smallholder forestry in the Solomon Islands"*, which involves training local forestry staff in the use of the DAF tree corer and determination of key wood characteristics from the increment cores using the DAF Wood Value Platform. The Wood Value Platform can be customised to the growers needs with plug-ins available for density, bending stiffness (MOE), shrinkage and for determining wood colour.



Mr. Peter Mailagi uses a color spectrophotometer to measure the colour of a teak sample at Munda Station laboratory.

The DAF tree corer utilises a rechargeable drill and specialised coring bit developed for hard-woods.



Mr. Steve Koloa assists Mr. Peter Mailagi to extract an increment core of a young teak tree in the Solomon Islands.

For details contact

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Prices of Plantation Teak Imported to India

Country of Origin Logs	US\$ per cu.m C&F
Angola	459-574
Belize	350-400
Benin	282-594
Brazil	370-665
Cameroon	405-772
Colombia	426-775
Congo D. R.	451-500
Costa Rica	320-780
Côte d'Ivoire	418-568
El-Salvador	381-732
Ghana	352-874
Guatemala	360-646
Guyana	300-450
Kenya	515-600
Laos	300-605
Liberia	265-460
Malaysia	225-516

Nicaragua	402-505
Panama	368-430
PNG	443-575
Sudan	468-520
Thailand	511-700
Togo	285-590
Trinidad and Tobago	557-680
Uganda	411-510
Sawn wood / Squares	
Benin sawn	530-872
Tanzania sawn	307-613
Uganda sawn	680-900
Brazil squares	370-556
Ecuador squares	318-564
Nigeria squares	286-405

Variations are based on quality, lengths of logs and the average girth.

Courtesy: ITTO TTM Report 19(23): 1-15 December 2015

Editorial Committee

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