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IUFRO will encapsulate, and distribute in plain language, brief, topical and policy-relevant highlights of those findings, along with information on where/how to access the full documents. The **IUFRO Spotlight** findings will be distributed in a periodic series of emails as well as blog postings.

Eucalyptus genome successfully sequenced

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With a result that offers major potential for the forest industry, an international team of researchers has successfully sequenced and analyzed the genome of *Eucalyptus grandis*.

"Now that we understand which genes determine specific characteristics in these trees, we will be able to breed trees that grow faster, have higher quality wood and use water and land more efficiently," said the lead investigator on the project, Prof. Zander Myburg of the University of Pretoria, South Africa. (See photo.)

"This will also allow us to breed trees better able to cope with future climate change scenarios. In the future, we may even be able to develop and manage eucalyptus plantations as 'bio-factories' to produce specific kinds of sought-after materials and chemicals."

Current uses for *Eucalyptus*, in addition to timber, pulp and paper, include eucalyptus oil used for cleaning and as an industrial solvent, as an antiseptic, for deodorizing, and in cough drops, toothpaste and decongestants. It is also an active ingredient in some commercial mosquito repellents. Increasingly *Eucalyptus* is being looked at for chemical cellulose, used in a wide variety of industrial products from textiles to pharmaceuticals.

Native to Australia, these trees have been introduced worldwide, mainly in tropical and sub-tropical countries – though they can be found along North America's Pacific coast as far north as British Columbia.

Eucalyptus species and hybrids make up the most widely planted hardwood crop globally (over 20 million ha). Eucalypt plantations are grown in over 90 countries as short rotation (6-9 years) wood fibre crops. Their high productivity means there is less reliance and pressure on natural forests, especially in developing countries, where most eucalyptus plantations are grown, Prof. Myburg added.



Photo by Photowise

This is only the second hardwood tree genome (*Populus* was the first) to be sequenced.

Prof. Myburg said being able to compare it to other trees such as *Populus*, willow, spruce and pine will allow us to study the unique biology of these large, long-lived plants that are keystone species for many of the earth's ecosystems.

"Once we are able to boost the growth and wood properties of *Eucalyptus*, the same techniques can be applied to other woody plants with potential as biomass feedstock species for the post-petroleum economy," he said.

What this achievement underlines is "that forest tree research has

entered the post-genomics age," Prof. Myburg added. "We can look toward technology development ... (to come up with) solutions for threats like climate change, pests and diseases, and breed trees with enhanced growth and wood properties for a sustainable forest products industry."

Already many international research teams are using the genome sequence as a reference for gene function studies and as a resource for molecular breeding of eucalyptus trees for enhanced growth, wood formation, disease resistance and abiotic responses to drought, cold and salinity, among other things.

The project was funded by the U.S Department of Energy, Joint Genome Institute (DOE-JGI). An international team of 80 researchers at more than 30 institutions (several of which are IUFRO member organizations) in 18 countries participated in the project. It took them five years to sequence and analyze the 640-million base pair genome.

The findings are available online (www.nature.com) and also in the June 19 edition of the journal *Nature*.

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