

MEDIA RELEASE

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***Eucalyptus* tapped as the next tree genome to be sequenced, characterised and harnessed for bioenergy, carbon sequestration, and other industrial applications**

OAK RIDGE, TENNESSEE, USA - An ambitious international effort has been launched to decode the genome of *Eucalyptus*, one of the world's most valuable fibre and paper-producing trees—with the goal to maximise its potential in the burgeoning bioenergy market and for capturing excess atmospheric carbon.

The scientific effort to characterise the *Eucalyptus* genome, uniting some two dozen institutions world-wide, is led by Alexander Myburg of the University of Pretoria (South Africa), with co-leaders Dario Grattapaglia, of EMBRAPA and Catholic University of Brasília (Brazil) and Gerald Tuskan of Oak Ridge National Laboratory (United States). The DNA sequence of the 600-million-nucleotide tree genome will be generated under the auspices of the U.S. Department of Energy Joint Genome Institute (DOE-JGI) Community Sequencing Program (CSP) and the information will be made freely available over the worldwide web.

The project will be supported by significant contributions of genomic data and scientific leadership from ArborGen, LLC., a U.S.-based forestry biotechnology company. ArborGen and its New Zealand-based shareholder, Rubicon Limited, will provide access to their private collection of more than 240,000 *Eucalyptus* gene sequences. ArborGen also will work to enable transformation of the model *E. grandis* clone that will be the source of the genomic sequence. Genolyptus, a Brazilian *Eucalyptus* research network directed by project co-leader Grattapaglia, will donate more than 120,000 gene sequences and genetic mapping resources required to assemble and annotate the final genome sequence.

“Sequencing the *Eucalyptus* genome will help us overcome many of the major obstacles toward achieving a sustainable energy future,” said Myburg. “Embedded in this information is the molecular circuit map for superior growth and adaptation in woody plants that can be optimised for biomass production. Its unique evolutionary history, keystone ecological status, and adaptation to marginal

environments make *Eucalyptus* the focus of choice for expanding our knowledge of the evolution and adaptive biology of all perennial plants.”

The genus *Eucalyptus*, comprised of over 700 different species, include some of the fastest growing woody plants in the world and, at approximately 18 million hectares in 90 countries, it is one of the most widely planted genus of plantation forest trees in the world. These trees evolved in the Southern Hemisphere quite separately from Northern Hemisphere tree species. Only the second tree to be sequenced, *Eucalyptus* offers extraordinary opportunities for comparative genomic analysis with *Populus*, the first tree sequenced and published in the journal *Science* by DOE JGI and collaborators in 2006.

“The *Eucalyptus* genome will provide a window into the tree’s metabolic pathways, shedding light on such traits as cold tolerance, osmotic potential, membrane integrity, and other agronomic features,” said co-lead Tuskan. “As the genus is amenable to genetic transformation, it can serve as a validation platform for candidate gene expression studies—helping us to expand *Eucalyptus*’ range and exploit its potential as a bioenergy plantation crop,” said Myburg.

“This monumental project will enable improved breeding strategies for cellulosic ethanol feedstocks and contribute to environmentally sound improvements in productivity for the global forestry industry,” said project collaborator Maud Hinchee, Chief Technical Officer of ArborGen. “This effort will help us advance our goals of producing renewable high-value biomass from a smaller environmental footprint.” Hinchee added that ArborGen brings a wealth of experience with *Eucalyptus* and its enormous potential as a dedicated bioenergy crop, noting that “this fast growing, high yield tree offers a new source of hardwood in the Southern U.S. that can play a key role in national energy security and economic development in the region, in addition to providing numerous environmental benefits.”

Already, a considerable amount of carbon is tied up in *Eucalyptus* biomass. Coupled with the emerging economic incentives for carbon sequestration, *Eucalyptus* is a prime candidate for increased efforts to remove carbon from the atmosphere. “In countries such as Brazil, *Eucalyptus* is used as a source of renewable energy for high quality steel production in a way that reduces the net production of greenhouse gases. *Eucalyptus* is capable of sequestering carbon at rate of 10 tons of carbon/hectare/year and has a positive net carbon balance even when it is used to generate energy from charcoal or for pulp and paper production. Furthermore plantation forestry of *Eucalyptus* plays a crucial role to reduce the pressure on tropical forests and associated biodiversity” said project co-leader Grattapaglia.

“From a phylogenetic standpoint,” said project collaborator **René Vaillancourt, University of Tasmania**, “*Eucalyptus* sits at a pivotal position in the tree of life at the base where the Eurosids split occurred.” This event is estimated to have happened some 100 million year ago, leading to a completely independent evolutionary trajectory from poplar and *Arabidopsis*, the Eurosids that have been sequenced to date. The *Eucalyptus* genome would be the first representative of the Myrtales order of flowering plants contributed to the public databases.

The project will be coordinated and the information disseminated by the *Eucalyptus* Genome Network, EUCAGEN (www.eucagen.org). EUCAGEN was established in 2004 with the aim to promote the generation of public resources for *Eucalyptus* genomic research. More than 130 scientists from 18 countries are currently involved in EUCAGEN. This number is expected to grow as the *Eucalyptus* genome sequence, and the genomic research tools that will result from it, becomes a reality.

EUCAGEN was established following a meeting of international scientists in **Hobart** hosted by the Australian Government's **Cooperative Research Centre** for Sustainable Production Forestry. The network and sequencing effort are actively supported by all leading forest research organisations in Australia. Eminent Australian tree biologists including **Dr Gerd Bossinger** (The University of Melbourne – School of Forest and Ecosystem Science), **Dr Simon Southerton** (Ensis/CSIRO Genetics), **Prof Brad Potts**, **A/Prof René Vaillancourt**, **Dr Dorothy Steane** (The University of Tasmania – School of Plant Science) and **Dr Margaret Byrne** (Department of Environment and Conservation – WA) assisted in the development of the proposal to DOE-JGI.

Professor Brad Potts of the **University of Tasmania** said that the availability of a public domain genome sequence for a eucalypt would mark the beginning of a new era in our understanding of Australia's iconic eucalypts. He said virtually all eucalypts are endemic to Australia and this initiative would have long-term benefits for the conservation and management of Australia's internationally important forest genetic resources.

Dr Gerd Bossinger of the **University of Melbourne** said this initiative would be a major stimulus for research in Australia. He said it would be of enormous value to Australian scientists studying the adaptive response of eucalypts to stresses such as salt, frost and drought tolerance, and help predict the response of Australian forests to climate change.

Dr Simon Southerton, who heads tree molecular breeding research in the Canberra-based **CSIRO** joint venture **ENSIS–Genetics**, said the availability of the genome sequence would accelerate progress in understanding the genetic control of wood properties which determine the profitability of eucalypt plantations in Australia.

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