

Media Release

Chiefs of Staff, News Directors

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Secrets of the eucalypt genetic code unlocked

Scientists have sequenced the genetic code of the eucalypt for the first time, providing fresh insights into the Australian icon that has become the world's favourite hardwood.

The work investigates the formation of the complex oils produced by eucalypts, which can help koala preservation efforts, minimise pest damage to plantations, and could one day lead to eucalypt oils being a base for jet fuel.

Australian researchers from the University of Tasmania, the University of Melbourne, the Victorian Department of Environment and Primary Industries, the Australian National University, Western Australian Department of Parks and Wildlife and the University of the Sunshine Coast collaborated with 30 institutions in nine countries to sequence and analyse the genome of the Flooded Gum (*Eucalyptus grandis*).

"Efforts to sequence the genome of a eucalypt started over a decade ago," explained Dr Dorothy Steane of the University of Tasmania, who was a co-author on the paper which has been published in *Nature*.

"The idea was originally discussed at the inaugural meeting of the International Eucalypt Genome Network, held in Hobart in 2004. Since then, there have been a number of international workshops, meetings and other exchanges that have brought the international eucalypt research community together to discuss, and now create, the resources to unlock the potential of eucalypts as a truly global fuel and fibre source."

Native to Australia, *Eucalyptus* trees have become the world's most widely planted hardwood due to their fast growth, adaptability and complex oils.

"Eucalypts are now the hardwood plantation species of choice in many parts of the world for applications like paper-making and bio-energy. This resource will provide a huge boost for breeding and biotechnological tree improvement programs and has put eucalypts on the same footing as many other important crop species, whose improvement programs have benefited greatly from a sequenced genome," said Dr Antanas Spokevicius of the University of Melbourne.

There are more than 700 species of *Eucalyptus* that grow across a huge range of environments, from the wet tropics, to alpine shrublands to the arid interior.

“The genome sequence of flooded gum provides us with the means to investigate the essential differences between species and to understand how eucalypts have adapted to so many different environments,” said Dr Steane.

Dr Carsten Kulheim from the Australian National University agrees: “The genetic code will help us understand a foundation species of many Australian eco-systems and how these affect other species, from fungi through to koalas.”

The researchers identified 113 genes responsible for synthesising terpenes, the familiar aromatic essential oils of eucalypts. These oils provide chemical defence against pests, as well as providing the oils used in both medicinal cough drops and for industrial processes, and may be extremely important in understanding feeding preferences of animals such as the koala.

The genome sequence consists of 640 million base pairs of DNA, containing more than 36,000 genes – almost twice the number of genes in the human genome. The detailed analysis of the *Eucalyptus* genome revealed an ancient whole-genome duplication event estimated to have occurred about 110 million years ago, almost twice as long ago as the extinction of the dinosaurs.

“Duplication of genes may be one of the reasons that eucalypts have been able to adapt to so many diverse environments across Australia,” said Dr Steane.

The paper is available online:

<http://www.nature.com/nature/journal/vaop/ncurrent/full/nature13308.html>

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