

Leaves, trunk and roots: Geneticists reveal how a tree knows to grow

April 29 2010, by Stu Hutson

(PhysOrg.com) -- Countless words have been put to paper over the years in attempts to describe the beauty of a tree -- including carefully crafted passages by the world's most gifted writers. But those writings pale in comparison to the intricacy of a tree's own genetic script.

A team at the University of Florida's Institute of Food and Agricultural Sciences, led by geneticist Matias Kirst, has completed a first study of how the byzantine interplay of elements within a tree's [genetic code](#) spell out different structures, such as leaves, trunk and roots.

All cells in a tree have the same [genetic information](#), whether it's in a leaf or a root. However, how that genetic information is translated into the various tree structures is based on a complex set of interactions, said Kirst, a researcher with the UF Genetics Institute.

In the English language, a silent "e" on the end of a word can affect how the vowels in the middle of the word are pronounced. Even a word's placement in a sentence can change its meaning.

Similarly, the expression of genes spelled out in one section of DNA is often regulated by a gene or multiple genes somewhere else in the genetic code. In turn, those genes moderate the activities of others — forming networks of intertwined genetic activity.

In a paper that will be published in the May 4 issue of the journal [Proceedings of the National Academy of Sciences](#), the team reports the

first mapping of these networks of interactions as they affect different parts of two types of cottonwood trees.

While similar genetic network mapping has been done of [human cells](#), this represents the first time that this level of understanding has been reached in the plant world.

“These are relationships we could never begin to understand without advanced computer modeling techniques that are only now possible,” said Arthur Berg, who contributed genetic statistical analysis to the study while at UF, and is now a professor of biostatistics at Penn State College of Medicine in Hershey.

The analysis also revealed that certain gene networks are active only within specific parts of the tree. Meanwhile, other gene networks were active throughout the tree.

Knowing which genes are expressed only in some parts of the tree and which are expressed throughout the tree is key to researchers and breeders attempting to develop trees and other plants best suited for biofuel, pulp, paper and timber production, Kirst said.

One of the common problems encountered by plant breeders is that breeding for one trait can have negative outcomes in other parts of the plant. For example, a florist breeding for larger flowers may find that the flowers have less scent. This is because the genes responsible for one trait, such as flower size, may have other responsibilities within the plant.

By recognizing such genes, researchers can find solutions, such as specifically targeting secondary [genes](#) active only in the desired part of the plant.

The work will help develop trees that are specifically suited to being used as feedstock for cellulosic ethanol, an environmentally friendly and

renewable substitute for gasoline.

However, it is likely that many other plants will have similar [gene networks](#) to those discovered in the cottonwood [trees](#) — potentially leading to more sophisticated ways of improving food crops.

Provided by University of Florida

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