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# Tree's leaves genetically different from its roots

Cottonwood trees show genetic differences across individuals as well as within populations.

Ed Yong

10 August 2012

Black cottonwood trees (*Populus trichocarpa*) can clone themselves to produce offspring that are connected to their parents by the same root system. Now, after the first genome-wide analysis of a tree, it turns out that the connected clones have many genetic differences, even between tissues from the top and bottom of a single tree.

“The variation within a tree is as great as the variation across unrelated trees,” says Ken Paige, an evolutionary biologist at the University of Illinois at Urbana-Champaign, who led the team that made the discovery.

“This could change the classic paradigm that evolution only happens in a population rather than at an individual level,” says Brett Olds, a biologist in Paige’s laboratory, who presented the research at the 2012 Ecological Society of America Annual Meeting in Portland, Oregon.

Such somatic mutations — those that occur in cells other than sperm or eggs — are familiar to horticulturalists, who have long bred new plant varieties by grafting mutant branches onto ‘normal’ stocks. But until now, no one has catalogued the total number of somatic mutations in an individual plant. “Most of the research hasn’t been genome-wide. It’s usually a certain region or certain genes,” says Olds. “This is the first one across entire genomes.”

The black cottonwood is ideal for such a study. It lives for up to 200 years and grows to 30–50 metres tall, so its tissues are separated by long distances and long spans of growth — and it forms connected clones. In 2006, it became the first tree to have its full genome sequenced<sup>1</sup>.



Black cottonwood trees show a surprising amount of genetic diversity.

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## Parent clones

Olds collected samples from 11 parent-clone sets of black cottonwood parents and their connected offspring. For each one, he sequenced the full genomes of tissues from the highest buds, the lowest branches and the roots. “Five years ago, this kind of project would have been prohibitively expensive,” says Ari Novy, a plant biologist at the US Botanic Garden in Washington DC, who was not involved in the study. “Olds has made great use of next-generation sequencing technology.”

When Olds compared these sequences to the reference cottonwood genome, he found 188,406 mutations that were unique to just one tissue sample, differing even from other parts of the same tree. Of these, 8,629 mutations fell within protein-encoding DNA sequences and 5,529 resulted in amino-acid changes in the encoded proteins.

“When people study plants, they’ll often take a cutting from a leaf and assume that it is representative of the plant’s genome,” says Olds. “That may not be the case. You may need to take multiple tissues.”

Other surprises emerged when Olds used the tissue-specific amino-acid changes to build a family tree of the different cottonwood tissues. In one tree, the top buds of the parent and offspring were genetically closer to each other than to their respective roots or lower branches. In another tree, the top bud was closer to the reference cottonwood genome than to any of the other tissues from the same individual.

The tissue-specific mutations affected mainly genes involved in cell death, immune responses, metabolism, DNA binding and cell communication. Olds think that this may be because many of the mutations are harmful, and the tree reacts by destroying the mutated tissues or altering its metabolic pathways and the way it controls its genes, which leads to further mutations.

The findings have parallels to cancer studies. Earlier this year, scientists showed<sup>2</sup> that separate parts of the same tumour can evolve independently and build up distinct genetic mutations, meaning that single biopsies give only a narrow view of the tumour’s diversity<sup>3</sup>.

*Nature* doi:10.1038/nature.2012.11156

## References

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**Nature** ISSN 0028-0836 EISSN 1476-4687

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