

The shortest DNA sequences reveal insights into the world's tallest trees

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Coast redwoods are famous for being the tallest trees in the world, but their height is not the only thing that sets them apart. Unlike most conifer trees, coast redwoods can reproduce by sprouting from cut stumps, fallen logs, and roots. Researchers from the University of California, Berkeley, are uncovering important information about patterns of coast redwood clones with a new DNA analysis method that could help forest management and preservation efforts.

The new method, described in a recent issue of *Applications of Plant Sciences*, will enable scientists to identify clonal lineages and study how clonal diversity varies throughout the geographic range of this species. Coast redwoods are among the oldest living trees on earth and, although they once occupied much of the northern hemisphere, today's native coast [redwood forests](#) can only be found in a 450-mile strip of land along the coast of northern California to southern Oregon.

To date, very little research has been done to elucidate the clonal patterns of coast redwood. This is partly due to another aspect that sets redwoods apart from other woody plants—they are hexaploid, meaning that there are six copies of each homologous chromosome in the genome, instead of two.

"Genetic analyses of polyploid organisms are difficult due to higher numbers of alleles," explains Lakshmi Narayan, the graduate student who led the UC Berkeley study. "In addition to their hexaploid condition, another challenge in determining the genotypic identity of

clonal plants is the possibility of somatic mutation, where a mutation occurs that changes the genotype of an individual in a clonal lineage. These mutations have the potential to confound genotyping studies seeking to identify the origin of shoots."

Narayan designed the new protocol to overcome challenges associated with mutations and with the high genetic copy number in redwood DNA. Narayan and her colleagues tested the clonal identification protocol by collecting DNA samples from 770 redwoods and successfully identified 449 distinct clones.

A key aspect of the new method is the use of short repeating DNA sequences from different coast redwood tissue types. The short DNA sequences, known as microsatellites, are present in all living organisms and widely used to distinguish individuals from one another. The researchers analyzed microsatellite data from coast redwood cambium, leaf, and sprout tissue.

"One novel aspect of our protocol was the use of different tissue types to verify consistent identification of alleles between samples," explains Narayan. "Requiring that alleles amplified in multiple tissue types from the same individual before scoring them made our protocol more conservative. This potentially reduced potential for misidentification. The other novel aspect of our work was the extensive use of data simulation to test the resolution of our genetic markers and scoring protocol."

Because they are a fast-growing tree species, young redwoods are commercially valued for timber production while ancient redwoods remain protected. Genetic data produced from the new protocol could help guide sustainable forest management of commercial young-growth forests and also improve efforts to preserve ancient redwood populations.

Says Narayan, "We hope the methods presented in this paper will be applicable to other species, in addition to being useful for genotyping [coast redwoods](#). Our future research will employ this methodology to study the variation in levels of clonal diversity throughout the species' range, and look at how clonal reproduction may affect the physical structure of redwood forests."

More information: Lakshmi Narayan, Richard S. Dodd, and Kevin L. O'Hara. 2015. A genotyping protocol for multiple tissue types from the polyploid tree species *Sequoia sempervirens* (Cupressaceae). *Applications in Plant Sciences* 3(3): 1400110. [DOI: 10.3732/apps.1400110](#)

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