

Sequencing hundreds of chloroplast genomes now possible

January 31 2013

Researchers at the University of Florida and Oberlin College have developed a sequencing method that will allow potentially hundreds of plant chloroplast genomes to be sequenced at once, facilitating studies of molecular biology and evolution in plants.

The chloroplast is the compartment within the plant cell that is responsible for photosynthesis and hence provides all of the sugar that a plant needs to grow and survive. The chloroplast is unusual in containing its own DNA genome, separate from the larger and dominant genome that is located in every cell's nucleus.

Chloroplast [DNA sequences](#) are widely used by plant biologists in genetic engineering and in reconstructing evolutionary relationships among plants. Until recently, though, chloroplast genome sequencing was a costly and time-intensive endeavor, limiting its utility for plant evolutionary and molecular biologists. Instead, most researchers have been limited to sequencing a small portion of the chloroplast genome, which in many cases is insufficient for determining [evolutionary relationships](#), especially in plant groups that are evolutionarily young.

In contrast, complete chloroplast genome sequences harbor enough information to reconstruct both recent and ancient diversifications. New DNA [sequencing technologies](#), termed "next-generation" sequencers, have made it considerably cheaper and easier to sequence complete chloroplast genomes. While current methods using next-generation sequencers allow up to 48 chloroplast genomes to be sequenced at one

time, the new method will allow potentially hundreds of flowering plant chloroplast genomes to be sequenced at once, significantly reducing the per-sample cost of chloroplast genome sequencing.

This new method, reported in the February issue of *Applications in Plant Sciences* (available for free viewing as part of the February Issue in Progress at <http://www.bioone.org/doi/pdf/10.3732/apps.1200497>), relies on efficient separation of chloroplast DNA from other DNA in the cell using short DNA "baits" that were designed from chloroplast genomes that have already been sequenced. These molecular baits effectively concentrate the chloroplast DNA before sequencing (a process termed "targeted enrichment"), dramatically increasing the number of samples that can be sequenced at once.

Greg Stull, a graduate student at the University of Florida and lead author of the study, summarizes the versatility of the new system: "With this method, it should be possible for researchers to cheaply sequence hundreds of chloroplast genomes for any flowering plant group of interest."

The method was specifically designed by the authors of the study such that almost any flowering plant chloroplast genome can be sequenced, regardless of species. Flowering plants represent the largest (~300,000 species) and most ecologically dominant group of land plants, and include all major crop plants.

Provided by American Journal of Botany

Citation: Sequencing hundreds of chloroplast genomes now possible (2013, January 31) retrieved 24 April 2024 from

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