

## An old genetic tool in plant biology still has value

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Scientific tools for plant genetics research continuously fade away as newer methods evolve. However, researchers at Mississippi State University have found that one older method, the use of fragmented chloroplast DNA sequences, still stands strong amidst modern technologies.

Chloroplast simple sequence repeats or microsatellites (cpSSRs) are short, repeating fragments of DNA that mark specific locations in a plant's genome. cpSSR markers are used to study plant evolution, such as plant breeding and hybridization in agricultural species and the genetic diversity of <u>plants</u> of conservation concern. They are especially useful for distinguishing plant groups and resolving their evolutionary relationships.

Gregory Wheeler, Associate Professor Lisa Wallace, and colleagues found that plant studies that use cpSSRs are on the rise. The number of plant studies using cpSSRs has doubled in the past ten years. Since 1995, cpSSRs have been used to study wild and cultivated plants from 85 different plant families—the most common being the history of pine trees (Pinaceae family) through the latest ice age.

Many plant research labs are turning to the latest next-generation sequencing methods to collect molecular genetic data because these methods allow for a more complete "fingerprint" of plant DNA. However, as Wallace points out, "There are still a lot of labs that do not have the financial or genomic resources to make next-generation



sequencing methods feasible."

The published review detailing the status of cpSSRs in <u>plant genetics</u> is published in a recent issue of *Applications in Plant Sciences*.

Because cpSSRs remain a popular method, Wheeler and colleagues explored their risks and benefits to uncover the most suitable and informative scientific questions that cpSSRs can answer in future studies.

The most prevalent problem with cpSSRs, which less than 33 percent of studies tested for, is called size homoplasy. Size homoplasy occurs when mutations in the DNA arise independently, causing DNA from different plants to falsely appear similar by evolutionary descent. Size homoplasy can lead scientists to overestimate plant relatedness.

To illustrate the risks of size homoplasy, Wheeler and colleagues pulled from their own data on the plant genus *Acmispon*, a member of the pea family found throughout California, USA. Four of the nine loci tested exhibited size homoplasy within or between species. "I was surprised to find a lack of testing of homoplasy in cpSSR studies given how commonly we detected it in our own data set," comments Wallace.

For future studies, Wallace and colleagues suggest using cpSSRs that were developed for specific plant species. This approach can help avoid problems of size homoplasy and answer questions related to genetic conservation and variability of single species, such as those that are economically and ecologically important.

"There have been major transitions towards NGS techniques in the past decade," says Wallace, "but our paper shows that cpSSRs are still a useful type of marker for many research groups in basic and applied plant sciences." As the number of genetic tools for plant research



expands, Wallace notes that the availability of new study systems will continue to grow, providing new opportunities for the use of cpSSRs in plant biology.

**More information:** Gregory L. Wheeler, Hanna E. Dorman, Alenda Buchanan, Lavanya Challagundla, and Lisa E. Wallace. A review of the prevalence, utility, and caveats of using chloroplast simple sequence repeats for studies of plant biology. *Applications in Plant Sciences* 2(12): 1400059. DOI: 10.3732/apps.1400059

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