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MarkerMiner 1.0: An easy-to-use bioinformatics platform for DNA analysis in angiosperms

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Flowering plants, also known as angiosperms, add an allure to the world that is unlike anything else in nature, but more importantly, they sustain us. Most of the fruits, vegetables, grains, beans, nuts, and even herbs and spices that we consume are produced by flowering plants. They all belong to the green plant branch of the tree of life, and a novel DNA analysis software program named MarkerMiner facilitates identification of genes that can be used to elucidate the evolutionary relationships between them.

University of Florida (UF) biologist Srikar Chamala, working with UF Genetic Institute faculty Brad Barbazuk, Pamela Soltis, and Douglas Soltis, along with a team of researchers from the United States, Chile, and Belgium, designed MarkerMiner to facilitate greater progress in angiosperm phylogenetics. There are currently over 300,000 species of angiosperms, within which many finer evolutionary details are unknown. The software will help researchers discover genes useful for inferring evolutionary patterns within plants that appear superficially similar, by aiding close comparisons of their genes.

"MarkerMiner works by filtering through large amounts of assembled transcriptome sequence data [the gene-encoding portion of the genome] to identify single-copy nuclear loci, by making use of conserved low-copy nuclear gene information available from sequenced angiosperm genomes," explains Dr. Chamala, who led the study. "Because gene duplications are very frequent in angiosperms, the putative single-copy status of the genes targeted by MarkerMiner makes them great genetic markers for resolving angiosperm phylogenies."

Despite advances in DNA sequencing technology, analyzing genetic sequence data can be expensive, time-consuming, and a bottleneck for many researchers. MarkerMiner eliminates those constraints by providing an easy-to-use platform, which researchers across the globe with limited bioinformatics training and limited access to high-performance computing resources can leverage to produce phylogenetic markers for any angiosperm group of interest.

A full description of MarkerMiner is available in a recent issue of *Applications in Plant Sciences* (http://www.bioone.org/doi/pdf/10.3732/apps.1400115). The study includes a test in which hundreds of single-copy nuclear loci from four different flowering plant groups were successfully identified. A user manual including source code is publicly available at https://bitbucket.org/srikarchamala/markerminer.

Mohammad Vatanparast, a researcher at the Smithsonian Institution says, "I'm glad that I found MarkerMiner. I'm using it to pull up single-copy orthologous genes from transcriptomes to perform phylogenomic analysis across phaseoloid legumes, a group that contains important species like soybean and common bean. MarkerMiner has great potential to facilitate next-generation sequence research and makes locus selection a lot easier."

Norman A. Douglas, a researcher at Oberlin College, is using MarkerMiner to develop loci for multilocus phylogeography across diverse lineages of gypsum-endemic plants in the Chihuahuan Desert, located in Mexico and the southwestern United States.

"Our first effort took several months of work to identify likely orthologs of single-copy loci in lineages that have few genomic resources, like Nyctaginaceae, Boraginaceae, and some isolated genera in Asteraceae. MarkerMiner simplifies the process greatly, and provides output in several useful formats. I am confident that this pipeline will find wide use in the phylogeography community," says Douglas.

MarkerMiner could soon empower scientists worldwide by making angiosperm research in fields of study such as ecology, evolution, systematics, phylogeography, and population biology more efficient and economical.

Provided by Botanical Society of America

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