

## Utility of sequence-related amplified polymorphism (SRAP) markers

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Today, many ecological and evolutionary studies depend on a wide range of molecular tools to infer phylogenetic relationships, uncover population structure within species, and track quantitative traits. Agricultural studies use these same tools to improve crop yield and increase resistance to pests and disease.

However, many of these methods—such as amplified fragment length polymorphisms (AFLP), inter-simple sequence repeats (ISSR), and random amplified polymorphic DNA (RAPD)—have technical limitations. These include issues of reproducibility, ambiguity in determining homology, and significant demands on both cost and time for researchers.

Sequence-related amplified polymorphism (SRAP) markers show promise as an alternative to traditional markers as they have proved to be highly variable and less technically demanding to obtain and use. This recently developed dominant marker technique produces genome-wide fragments and has been used primarily in studies aimed at crop development. Previous studies have utilized this method to identify pathogen-resistant markers and better understand the genetic basis of fruit and flower form and structure, as well as flowering and fruiting times.

In a new study in a recent issue of *Applications in Plant Sciences*, researchers at Ohio State University have made a case for the use of these markers across a broad range of research fields including plant



systematics, biogeography, conservation, and ecology. "These markers exhibit variation useful for uncovering genetic structure at a variety of taxonomic levels, constructing linkage maps, and have proven valuable for the improvement of agronomic crops," explains Daniel Robarts, lead author of the study.

Robarts and colleagues surveyed hundreds of published peer-reviewed papers and presented a number of case studies to further demonstrate the applicability of these markers in plant biology. "We found SRAP markers to be comparable to AFLP markers in terms of levels of variation, but requiring significantly less technical effort and cost," says Robarts. "Furthermore, these markers provide highly reproducible results and no prior genomic information is necessary, making them ideal for non-model systems."

The study also suggests these markers will be useful when paired with next-generation sequencing technologies. Because SRAP loci are derived from a single forward primer and numerous reverse primers, it would be possible to adapt the technique to enrich genomic libraries for nextgeneration sequencing, providing an efficient protocol for discovery of polymorphisms.

"Although these markers have been primarily used for improvement of crop plants, we are excited about the potential of the SRAP marker technique as a more broadly applicable method in plant sciences. We expect these markers to be especially useful for population-level studies, but our results suggest they will likely provide a useful tool at higher taxonomic levels as well," says Robarts.

**More information:** Daniel W. H. Robarts and Andrea D. Wolfe. 2014. Sequence-related amplified polymorphism (SRAP) markers: A potential resource for studies in plant molecular biology. *Applications in Plant Sciences* 2(7): 1400017. DOI: 10.3732/apps.1400017



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