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Sequence-related amplified polymorphism molecular markers: A potent tool for plant pathology and plant biotechnology

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Plant biotechnology is known to have immense potential in the area of crop improvement. The target can be achieved by either transgenics or marker-assisted breeding. The latter one does not require biosafety regulations and has become quite popular in the previous decades. There are numerous molecular markers such as random amplified polymorphic DNA (RAPD), inter-simple sequence repeat (ISSR), amplified fragment length polymorphism (AFLP), restriction fragment length polymorphism (RFLP), Single nucleotide polymorphism (SNP), Microsatellites (SSR) etc., being used for improving target traits. SRAP (Sequence-related amplified polymorphism) is a novel and robust PCR based molecular marker technique developed by Li and Quiros (2001). It is based on ORFs (open reading frames) and therefore targets functional genes. It is highly variable and convenient to use marker having inherent biological significance. It offers many advantages over other marker systems as it is simple and reliable, requires a relatively smaller amount of template DNA and has clear high-intensity and co-dominant bands. It is not crop-specific and is highly economical as any of the forward primers can be combined with any of the reverse primers, hence a lot of primer combinations can be made which decreases the total cost. It offers easy isolation of bands for sequencing purpose and is more useful for genetic diversity, hybrid identification, horticultural and agronomic studies. SRAP is also employed for the development of QTL (quantitative trait loci) in advanced hybrids, genetic linkage map construction, sex determination, plant systematics, ecology, conservation, biogeography and fingerprinting studies due to its multi-loci and multi-allelic features. The applications of SRAP markers are now widespread and have been well recognized. SRAP is supposed to emerge as a highly productive marker system in case of crops where genome sequence is not available for marker-assisted breeding and related applications in coming years.

Biography

Bharti Aneja, born on 23rd August 1988 has done Masters and Doctorate in Molecular Biology and Biotechnology from CCS HAU, Hisar, India. Her core area of research in Plant Biotechnology. During Masters, she worked upon "Micronutrient and molecular diversity analysis in mungbean genotypes". The results indicated that SRAP markers were efficient for identification of *Vigna radiata* genotypes and for determination of the genetic relationships among them. Her title of research in Doctorate was "Transcript profiling of stress-inducible MYB transcription factor and related genes in Indian mustard (*Brassica juncea* L. Czern. & Coss.)". She has Post-doctoral research experience of more than four years. As a Research Associate, she worked at ICAR- IIWBR, Karnal for more than two years, where she worked upon metagenomics, precise phenotyping under field and controlled conditions, data collection of different phenotypic traits and their analysis and molecular marker analysis of different wheat varieties.

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