

## **Molecular Marker Development in Post-genomic Era: Leveraging Multiple Resources for Marker Development in Cotton and Other Crops**

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While the importance of molecular marker technology was realized more than two decades ago, high-throughput marker development came into vogue only after the availability of hundreds of thousands of sequences in public databases. Many examples now exist where markers are being used routinely in breeding programs for marker-assisted selection (MAS) of traits of interest or marker assisted recovery of genome of interest. Genetic analysis with thousands to tens of thousands of markers is now possible due to the availability of high to ultra high-throughput genotyping platforms and marker systems such as SSRs and SNPs. The most important pre-requisite to accomplish MAS or marker-assisted genome recovery is the availability of markers. While it is obvious that markers, once developed, are extremely useful tools, their development especially with conventional molecular approaches is laborious, expensive and time consuming. Development of highly efficient enrichment methods, for example, for SSR marker development offers an economical route for marker development. Even better, mining of ever increasing public sequence repertoire using computational tools offers an attractive and promising alternative to molecular methods for rapid development of markers. We have developed an improved molecular method in our lab, created enriched SSR marker libraries and generated hundreds of SSR markers in cotton. In order to rapidly mine thousands of ESTs and genomic sequences in cotton and other crops, we have developed a high-throughput tool and identified thousands of SSR-containing sequences for marker development. Moreover, to improve the utility of a given SSR marker, we have also used the flanking sequences of mapped SSR markers to develop SNP markers. We have used available genomic sequences to develop SSR and SNP markers for enriching the genomic regions of interest. The wealth of genomic sequence information available in the current post-genomic era permits the use of a combination of these and other potential approaches for rapid development of thousands of markers towards enrichment of genetic maps. In this poster, we present results obtained from several of such approaches for the rapid and high-throughput development of SSR and SNP markers in cotton and other crops.