Gene-based Molecular Markers Technique in Discriminating Brassica Cultivars

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Abstract—*Molecular markers are useful tool not only for mapping genes, but also useful in studying diversity and fingerprinting of individuals of plant species. The next generation sequencing (NGS) technology, with its high-throughput potential has enabled to design molecular markers based on transcriptome sequence data. In the past, SSR markers were usually designed from sequence information of inter-genic regions of genome. On the other hand, the gene-based SSR (Simple sequence repeats) markers, generated from gene-rich regions, have advantage over traditional SSR makers. Any inherent variation in such gene-based SSR markers among the individuals, in addition to providing information about structural polymorphism can also be explored for functional polymorphism, if any. The availability of large number of such gene-based SSR markers in public domain allowed us to explore for the markers that can be applied towards large number of cultivated brassicas. In the present study, we identified a set of over fifty g-SSR (genic-Simple sequence repeat) markers that worked not only with Brassica juncea (Indian mustard) but also with Brassica nigra, Brassica carinata, Eruca sativa, Brassica rapa and Crambe sps. Applications of such markers in high-throughput based fragment analyzer have great promises in discriminating brassica germplasm and thus enable us to digitize variety/ accessions.*