



## Characterization of SNPs in strawberry cultivars in China

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**ABSTRACT.** Single nucleotide polymorphisms (SNPs) occur at high frequencies in both plant and animal genomes and can provide broad genome coverage and reliable estimates of genetic relationships. The availability of expressed sequence tag (EST) data has made it feasible to discover SNPs. DNA analysis is crucial in genetic studies not only for strawberry breeding programs but also for characterization of hybrids and species. We cloned 96 EST sequences, and 116 SNPs were discovered by comparing 16 strawberry cultivars grown in the region of Nanjing, China. Sequence alignment of 6 group sequences derived from 16 sample cultivars yielded 116 SNPs, within a total genomic sequence length of 1755 bp. The SNPs were discovered with a mean frequency of one SNP per 15 bp. These SNPs were comprised of 57% transitions, 32.7% transversions, 8.6% InDels, and 1.7% others, based on which a phylogenetic tree was constructed. Among the 116 SNPs, 75% were located within the open reading frame (ORF), while 25% were located outside the ORF. All 16 cultivars scattered well in the

dendrogram derived from the SNP data, demonstrating that SNPs can be a powerful tool for cultivar identification and genetic diversity analysis in strawberries.

**Key words:** SNPs; Strawberry; EST; Genetic diversity