

EST, COSII, and Arbitrary Markers Give Similar Estimates of Nucleotide Diversity in Cultivated Tomato (*S. lycopersicum*)

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Because cultivated tomato (*Solanum lycopersicum*) is low in genetic diversity, public, verified single nucleotide polymorphisms (SNP) markers within the species are in demand. To promote marker development we resequenced fragments of 51 genes in a diverse set of 31 tomato lines. Three classes of markers were sampled: i) 26 expressed-sequence tag (EST), ii) 14 Conserved Ortholog Set II (COSII) or unigene, and iii) 11 published genes, 10 of which are related to fruit quality. The latter two types contained mostly noncoding DNA. Totals of 156 SNPs and 35 indels were found in 24 kb. The distributions of nucleotide diversity estimates among marker types were not significantly different from each other. These data demonstrate that public EST databases and noncoding regions are a valuable source of unbiased SNP markers in tomato.