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Genotyping of Tomato Cultivars and Hybrids using ddRAD

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Abstract

Tomato (*Solanum lycopersicum*) is a major crop plant and a model system for fruit development. *Solanum* is one of the largest angiosperm genera and includes annual and perennial plants from diverse habitats. ddRAD-seq is one of the most cost-effective methods in next generation sequencing (NGS) for generating robust genotyping data which permits high throughput simultaneous discovery and genotyping of sequence polymorphism either with or without an existing reference genome. Advantage of ddRAD technique was investigated by performing data analysis of sequence obtained through low pass whole genome sequencing and ddRAD protocol. Here we present a high-quality reduced represented genome sequence of domesticated tomato with the aim of understanding genetic variations in cultivated tomato; single nucleotide polymorphism (SNP) markers covering the whole genome of eight cultivars and four F_1 hybrids were developed through G*enotyping-By-Sequencing*. We have sequenced twelve tomato varieties using Illumina HiSeq 4000, next generation sequencing platform. The raw data was subjected to preprocessing and aligned with *reference tomato genome downloaded from ensembl release 36.* The SNPs/INDELs were identified for each of the tomato varieties. A total of 30746 SNPs and 913 INDELs were identified. We investigated for homozygous polymorphic markers between PKM-1 and Arka Abha and found 745 markers which can be used as markers for fingerprinting. The homozygous polymorphic markers will be utilized for genetic mapping and trait association in a mapping population.

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