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## Survey of parental polymorphism in tomato (*Solanum lycopersicum*) cultivars with the aid of Simple Sequence Repeat (SSR) markers

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**T**omato (*Solanum lycopersicum* L., 2n=24) is one of the major perennial crops and an excellent model plant for genomic research of the family Solanaceae. The trend towards reduction of genetic diversity among modern tomato cultivars, as elucidated by the previous studies, has implications on the future programmes of management and use of tomato genetic resources. The present study involves genotyping of early blight (IIHR 2101, IIHR 2843), heat (IIHR 2202, IIHR 2843), drought (IIHR 2190, IIHR 2843) and some other parental lines involved in fruit quality related traits (IIHR 249, IIHR 2866, Arka Vikas) of tomato. A survey conducted between these parental lines harbouring a set of 308 SSRs (attached with M13 sequence) revealed 56.7%, 40.7%, 32.5%, 46.1% polymorphism for early blight, heat, drought and other fruit quality trait related parental lines of tomato respectively. These 179 polymorphic markers were identified through M13-tailed PCR principle; thereby identifying the alleles through Genetic Analyzer by using Peak Scanner v1.0 Software. Construction of a Linkage Map could be ensued procuring the generated genotyping data which could further avail QTL analysis and identification of markers linked to traits.

### Biography

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