ASSESSMENT OF *IN SILICO* BAC-BASED SSR MARKER DEVELOPMENT FOR TOMATO (*SOLANUM LYCOPERSICUM.*L)

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Abstract

Tomato landraces which is less sensitive to environmental stresses and grown mainly under rain fed conditions are still grown in small farms due to quality and special demand of some consumers. These landraces are valuable sources of genetic characteristic, which is of plant breeder's interest to include in breeding programs for crop improvement. Since 1983, seed samples of tomato landraces were collected from local farmers throughout the country and conserved in the gene bank of the National Center of the Agricultural Research and Extension (NCARE).

Molecular markers are very important tool for plant breeding, diversity studies, recombination rates, QTL analysis, fine mapping and MAS. Expanding the available arsenal of DNA molecular markers is needed for tomato as many predicted gene sequences have no known phenotypes, on the other hand, several genomic areas yielded ESTs without any predicted or putative genes.

The international tomato sequencing project is continuously depositing both genomic and EST sequences at the SGN site hosted by University of Cornell, NY, USA. The deposited data were used to pull out a representative chromosomes sequences as BAC clones. They range from 90-138 kb in size.

Development of SSR markers from map-referenced BAC clones was a very effective means of targeting markers to marker scarce positions in the genome. Flanking DNA sequences were then analyzed for the presence of suitable forward and reverse PCR primers to assay the SSR loci. Several computational tools are currently available for the identification of SSRs within sequence data as well as for the design of PCR primers suitable for the amplification of specific loci.

The usefulness of SSR markers was investigated by assessing genetic similarity (GS) among the tomato landraces and commercial cultivar for diversity analysis. A total of

12 loci (27 alleles) were scored. All these loci (100%) were polymorphic. The calculated PIC values for the incorporated new SSR markers ranged from 0.62 to 0.97 (mean 0.89). The SSRs type (CT) 26 (AT) 27 and (TTC) 6(TTA) 4 had the highest PIC value (0.97), while the (CAA) 5(A) 8 the lowest PIC value (0.62).
According to tomato EST analysis, some of our SSR markers developed such as mono, and di -nucleotides are related to some genes such as T(16) SSR repeat is related to hydroxyproline- rich glycoprotein , which is a family protein from *Arabidopsis thaliana*. On the other hand, some of the tri-nucleotide SSR repeats are coding for proteins such as AAC(4) A(11) repeat which is putative homologus protein to A7Q2S4 from *Vitis vinifera*.