

**P-61 (186)****DATA MINING APPROACH IN FENUGREEK (*TRIGONELLAFOENUM- GRACEUM L.*) TO IDENTIFY EST-SSR MARKERS RELATED TO MAJOR GENES INVOLVED IN SALINITY TOLERANCE**

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Fenugreek (*Trigonellafoenum- graceum L.*) is a leafy vegetables belongs to the family Fabaceae which is important for its numerous medicinal properties and effects in the treatment of several diseases. Fenugreek has relatively high resistance to salinity and drought stress. The study of genetic variation leads to the production of reliable markers for the selection of varieties with better characteristics in terms of the production of secondary metabolites and varieties which are resistant to drought and salinity stress. SSR markers which derived from ESTs are more useful than genomic markers because they are the representative of the transcript and thus, directly related to the functional genes. EST-SSR markers can be used as a potential marker for the analysis of genetic variation, MAS, etc. The aim of this study was the EST-SSR mining of genes involved in resistance to salinity in Fenugreek with the focus on *APX*, *CAT*, *ATPase*, *GSHS* and *GR* genes. For this purpose, we used RNA-seq data which were available in the NCBI database and 5 EST database were examined. In general, 10 EST-SSR markers were identified in these genes. Among them, 2 EST-SSRs with repeat length 3 and tandem size 9bp were related to *APX*, 2 EST-SSRs with repeat length 3 and 1 and tandem size 9 and 10bp, respectively were related to *GSHS*, 2 EST-SSRs with repeat length 3 and tandem size 9bp were related to *GR*, 1 EST-SSR with repeat length 3 and tandem size 9bp was related to *CAT* and 1 EST-SSR with repeat length 3 and tandem size 9bp was related to *ATPase*. These predicted markers can be used for the identification of different species of *Trigonella*, genetic diversity analysis, and genetic study in fenugreek. It is also provides a valuable source for genetic analysis of other plants of Fabaceae family

**Keywords:** Ascorbate-glutathione pathway, bioinformatics analysis, salinity stress tolerance