Expressed Sequence Tags Identification for Fusarium Wilt Resistance in Chick Pea (*Cicer arietinum*)

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ABSTRACT

Expressed sequence tags(EST)s have wide spread use viz., as a molecular marker and base material for gene expression studies. For the present analysis two subtracted libraries one from the resistant chickpea cultivar (WR315) and the other from the susceptible chickpea cultivar (JG62) to the *Fusarium* wilt pathogen were being used. Genes with altered expression upon pathogen infection were enriched by the subtraction procedure and were cloned in pGEMT Easy vector. Subtracted libraries after the insert screening were stored as glycerol stocks in 96 well microtitre plates and further analyzed by sequencing the inserts using automatic sequencing machine. The sequences were processed further to remove vector sequences like blast search against the existing databases available at the NCBI site. A cut off score of 100 was put to find the best matches and the top match was used for all the down stream work. Initially all the sequences were analysed using Blast-X Programme followed by Blast-N and TBlast-x. Sequences showing no significant match after the Blast search were further analysed using Stand alone Blast to remove redundant clones. Some of the interesting genes fall in the class of regulatory proteins, signaling proteins and defense response proteins as for example, bZIP, bHLH, Zn-finger transcriptional activators, kinases, phospahatases, G-protein coupled receptor and this study paved way to identify EST's upon Fusarium infection in Chickpea.

Key words: Chickpea, EST, Fusarium wilt.