

Identification of Differentially Expressed Novel Genes Against *Fusarium* Wilt in Chickpea Using Dot Blot Technology

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ABSTRACT

Transcriptional remodeling in immune response during vascular wilt, was studied using Dot blot technology i.e., cDNA macro-array using *Ca* EST clones of the subtracted cDNA libraries from susceptible (JG62) and resistant genotypes (WR315). Root tissue sample from WR-315 harvested at different time intervals post *Fusarium* infection was used to evaluate the expression profile during early phase of incompatible interaction. 2112 PCR amplified clones using adapter specific primers were used and blotted onto Gene screen Nylon membrane. Total cDNA probes for differential screening was prepared from the total RNA isolated from the roots of control and pathogen infected plants for both the cultivars. Hybridized blots were scanned using Phosphor imager and 1065 clones showing more than 2.5 fold induction were further analysed. Out of these 1065 clones plasmid preps were made for 783 clones followed by automated DNA sequencing. A cut off score of 100 was put to find the best matches and the top match was used for all the downstream work. Some of the interesting genes fall in the class of regulatory proteins, signaling proteins and defense response proteins are bZIP, bHLH, Zn-finger transcriptional activators, kinases, phosphatases, G-protein coupled receptor, also the downstream proteins such as PR proteins, CHS and CHI.

Key words : Chickpea, Dotblot, EST's, *Fusarium* and Macro-array.