

# **Microarray Expression Profiling of Wilt Responsive Genes In Chickpea (*Cicer arietinum*)**

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## **ABSTRACT**

Microarray is a technology to measure and analyze the expression of thousands of genes expressed at any given time. DNA microarray technology, especially the use of Gene Chip microarrays, has become a standard tool for parallel gene expression analysis. DNA microarray uses between hundreds and hundreds of thousands of DNA probes arrayed on a solid surface to interrogate the abundance and/or binding ability of DNA or RNA target molecules. In the present study non redundant unigene set comprising 384 clones (192 Clones from Incompatible library (WR315), 192 clones from compatible library (Jg62) and 72 control clones were selected for the microarray and microarray hybridization was carried out using probes prepared from resistant and susceptible plants after *Fusarium* infection at 0hr and 48hr in chickpea. Microarray analysis showed differences in the pattern of expression between compatible and incompatible interaction. Micro array hybridization on the array set using two different time points showed global differences in pattern of expression between compatible and incompatible interaction and the expression ratios were similar to earlier hybridization experiments for majority of genes under study. For majority of the genes similar expression ratios were obtained using macro array and microarray.

*Key words: Chickpea, Expressed sequence tag (EST), Fusarium wilt, Genomics and Microarray.*