

Full Length cDNA Library Construction Towards Identification Of Fusarium Wilt Resistance Genes In Chickpea (*Cicer arietinum*)

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ABSTRACT

Chickpea wilt caused by *Fusarium oxysporum* f. sp. *ciceris* is one of the major yield limiting factors in chickpea. The disease causes 10–90% yield loss annually in chickpea. Eight physiological races of the pathogen (0, 1A, 1B/C, 2, 3, 4, 5 and 6) are reported so far whereas additional races are suspected from India. Mapping of wilt resistance genes in chickpea is difficult because of minimal polymorphism; however, it has been facilitated to great extent by the development of sequence tagged microsatellite site (STMS) markers and EST's that have revealed significant interspecific and intraspecific polymorphism. Markers linked to six genes governing resistance to six races (0, 1A, 2, 3, 4 and 5) of the pathogen have been identified and their position on chickpea linkage maps were elucidated. These genes lie in two separate clusters on two different chickpea linkage groups. While the gene for resistance to race 0 was situated on LG 5 and those governing resistance to races 1A, 2, 3, 4 and 5 spanned a region of 8.2 cM on LG 2. Cloning of wilt resistance genes is desirable to study their evolution, mechanisms of resistance and their exploitation in wilt resistance breeding and wilt management. So for the present study full length cDNA library was constructed from wilt resistance cultivar of Chickpea i.e., WR315 against most virulent race of Fusarium i.e., Race1, and subsequently paved way to clone few of the wilt resistance genes such as PR proteins, MAP kinases and Transcription factors.

Keywords: *cDNA library, Chickpea, and Fusarium*