

**Research Article****Characterization of Fusarium Wilt Tolerance in Cotton****Rani D Nimbalkar<sup>1</sup>, Vivek P Chimote<sup>2\*</sup>, Subhash S Mehetre<sup>3</sup> and Bhausaheb D Pawar<sup>2,4</sup>**

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**Abstract**

The Fusarium wilt is the most limiting factor in the production of Asiatic *Gossypium arboreum* cotton and resistance breeding remains only viable strategy. A single dominant gene controlling wilt susceptibility was observed in segregants of AKA-7 (moderately tolerant) × Dh-2 (susceptible) cross during inheritance studies. On Resistance Gene Analogue (RGA) analysis, NLRR-inv1/2 277bp marker amplified only in tolerant parent and bulk. Further, this marker amplified in wilt tolerant F<sub>2</sub> individuals; while it was absent in susceptible F<sub>2</sub> progenies. It also got amplified in another tolerant genotype PA141. On sequence homology search for the sequence of this 277 bp marker yields highly similar hit sequences of large insert *Gossypium* BAC clones with the marker region flanked by retro transposes and caffeic acid methyl transferase gene involved in lignin precursor biosynthesis. Identified NLRR-inv1/2 277bp RGA marker is a likely candidate for molecular tagging of wilt tolerance in Asiatic cotton.

**Key words:** *Fusarium oxysporum*, *Gossypium arboreum*, inheritance, molecular tagging, wilt

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