

## **Mapping of Genomic Region linked to Fusarium wilt Resistance in AP-42 inbred line of Castor (*Ricinus communis* L.)**

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### **ABSTRACT**

The study was aimed at mapping the genomic region linked to Fusarium wilt resistance in a castor inbred line AP-42. A set of 95 F<sub>2</sub> plants derived from the cross between AP-42 and a susceptible line JI-35 was raised in wilt sick plot during *khariif* 2019 and their reactions to *Fusarium oxysporum* f.sp. *ricini* infection were scored. All the plants were genotyped using 110 SNP markers. Using the SNP genotypic data, a genetic linkage map of 1296.4 cM was constructed with an average marker distance of 11.8 cM. The length of individual linkage group ranged from 77.0 cM (LG-10) to 182.1 cM (LG 1). QTL analysis was performed following composite interval mapping approach. A major QTL linked to Fusarium wilt resistance was mapped on to the chromosome-6 flanked by the SNP markers Rc 43141-440 and Rc 29609-144169. The QTL identified in this study is novel comparing the other mapped QTLs. As the wilt resistance in AP-42 inherits as dominance, it is a highly desirable source for developing resistant parental lines and hybrids in castor. Markers linked to wilt resistance in AP-42 will assist in faster and efficient deployment of resistance genes into elite genetic background.

**Key Words:** *Castor, Fusarium wilt, Linkage map, QTL and SNP markers*