

**Marker identification and QTL mapping for fusarium wilt disease  
resistance in banana (*Musa* sp.)**

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**ABSTRACT**

Fusarium wilt of banana (FWB), a soil-borne disease caused by *Fusarium oxysporum* f. sp. *cubense* (FOC), leads to vascular browning, leaf yellowing, and eventual plant death, and is a major threat to the global production of banana. Since currently no effective chemical treatment is able to control this disease, breeding for resistant cultivars offers the most economic and efficient means. However, conventional techniques have been limited in FOC resistance breeding due to sterility, long generation period, and polyploidy nature of bananas. Biotechnological advances through molecular marker-assisted selection (MAS) breeding provide another strategy for the introgression of resistant genes. On-field and greenhouse phenotyping indicated segregation for resistance in populations resulting from crossing susceptible cultivars with wild resistant genotype *Musa acuminata* ssp. *malaccensis*. The segregation ratio of susceptible to resistant progenies (3:1) revealed that FOC resistance is controlled by a single recessive gene. Genotyping by DArTseq generated 2802 SNP markers from mapping populations and 11 linkage groups were constructed. Data analysis revealed that FOC resistance is controlled by a locus near the distal end of chromosome 10. These findings provide breeders with a platform for developing new FOC-resistant cultivars via MAS.

**Keywords:** Banana, Fusarium wilt of banana, *Fusarium oxysporum* resistance, linkage map, markers

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