

1927 Quantitative trait loci controlling resistance to *Thielaviopsis basicola* in diploid cotton

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Black root rot (BRR), incited by the soil born pathogen *Thielaviopsis basicola* is an interesting host-pathogen system to study evolutionary differences leading to R-gene formation and divergence in cotton (*Gossypium* spp). Tetralopid cotton (*G. hirsutum* and *G. barbadense*) are highly susceptible; however, resistant types have been identified in A-genome diploid cotton (*G. herbaceum* var. "A20"). Genetic mapping was used to determine the chromosomal locations of quantitative trait loci (QTLs) that confer resistance to the BRR pathogen. A population of F2 individuals (*G. herbaceum* X *G. arboreum*) and F3 progeny families was examined using 159 simple sequence repeats (SSR). A genetic component that controls resistant and susceptible reactions resulting from *T. basicola* infestations could be explained by two QTLs. The QTLs on Chromosomes 1 (*Rtbq1*) and 10 (*Rtbq10*) each explained 15.1 and 11.9% of the total phenotypic variation, respectively. A focus to determine the underlining DNA sequence of these R-genes is a key step toward studying their evolution in *Gossypium*. Research activities to clone each gene and transfer resistance into Upland cotton are ongoing.