

**QTL ANALYSIS OF BACTERIAL BLIGHT
RESISTANCE GENES IN COTTON
USING RFLP MARKERS
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Recent advancements of molecular techniques have allowed for the development of a saturated genetic map of a plant genome. In cotton, a detailed restriction fragment length polymorphism (RFLP) map containing 705 RFLP loci is now available for genomic studies. Bacterial blight of cotton incited by the pathogen *Xanthomonas campestris* pv. *malvacearum* (*Xcm*) is a disease that can cause substantial yield losses, and occurs in most cotton producing countries of the world. Molecular mapping studies were conducted on two populations segregating for *Xcm* resistance. This enabled the location of Quantitative Trait Loci (QTL) which accounted for variation in resistance to *Xcm*. Both populations were inoculated with races 1 and 18 of *Xcm* separately, and disease reactions graded. Populations were composed of F₂ individuals derived from interspecific crosses between *Gossypium hirsutum* and *G. barbadense* cultivars (Tamcot SP 37 x Pima S6; Tamcot CD3H x Pima S6). Selective genotyping, a strategy for reducing the cost and work load of molecular mapping experiments was employed for this QTL study. Molecular markers spanning the genome at about 20 cM intervals were used to detect QTL's. Two QTL's were identified in the Tamcot SP 37 x Pima S6 population, with both mapping to A subgenome chromosomes. One QTL segregating in the Tamcot CD3H x Pima S6 population was identified. The genomic origin of this QTL is not yet known. All three QTL's map to different regions of the genome. Continuing mapping experiments are currently being conducted on these and other populations to determine gene action, gene effect and to establish which resistance (*B*) genes are identified by these QTL's. Fine mapping of resistance genes will provide cotton breeders with the tool to use marker assisted selection in the deployment of gene combinations that will ultimately result in higher levels of resistance, and are more durable to changes in the virulence of the pathogen.