IDENTIFICATION OF QTLS IN COTTON CONFERRING RESISTANCE TO THE BACTERIAL BLIGHT PATHOGEN

R.J. Wright, P.M. Thaxton,
A.H. Paterson, and K.M. El-Zik
Department of Soil and Crop Sciences
Texas Agricultural Experiment Station
Texas A& M University
College Station, TX

Abstract

Bacterial blight of cotton (*Gossypium hirsutum* L) , incited by the pathogen *Xanthomonas campestris* pv. *malvacearum* (Smith) Dye (*Xcm*), is a disease that can cause substantial yield loss and reduced fiber quality. In the U.S., yield losses due to *Xcm* average 1.5% of the annual cotton crop. Yield losses in Asian and African countries can exceed 50%. The characterization,at the molecular level, of plant genes that confer resistance to pathogenic organisms is a giant step toward improving the effectiveness of breeding crops with durable resistance. This study was conducted to map genes in cotton that confer resistance to races of the bacterial blight pathogen. Mapping populations consisted of five parental cotton (*G. hirsutum*) lines representing different genetic backgrounds and gene combinations. Four parents are isogenic lines for *Xcm* resistance genes (Empire B_2, B_3, B_2b_6 , and B_4) and a genotype (S295) containing the B_{12} resistance gene. These five populations segregating for resistance to *Xcm* were developed from crosses between the *G. hirsutum* parents and Pima S7, a *G. barbadense* parent, to ensure genetic polymorphism across the genome. To substantiate the association between marker data and conferred resistance to the pathogen, four *Xcm* races (1,4,7, and 18) were used to evaluate individual plants in the segregating F_2 populations. To date, three QTLs have been identified of which all map to D-subgenome chromosomes. Several markers linked to the B_{12} gene have been identified in the S295 mapping population. The region containing the B_{12} locus has been defined to an interval of approximately 14 cM. The B_2 gene was identified in both the Empire B_2 and Empire B_2b_6 populations. Additional markers which map within this region are currently being used in both populations. These markers will enable the fine mapping of the B_2 locus within this region. Two markers linked to the putative b_6 locus were found in the Empire B_2b_6 population. Both markers identifying the b_6 gene in this population, also identify the B_{12} in the S295 population. The alignment of conserved markers indicates that both genes map in the same region of the genome. The B_{12} and b_6 genes may be alleles at the same locus or independent loci linked within this region. Additional markers that could more closely define this relationship are currently being studied. Continuing mapping experiments are currently being conducted on these and the Empire B_3 and Empire B_4 populations.

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