IDENTIFICATION OF MOLECULAR MARKERS ASSOCIATED WITH A GENE SUSCEPTIBLE TO THE HERBICIDE ENVOKE® IN COTTON

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Abstract

The herbicide Envoke® (active ingredient trifloxysulfuron sodium) has been used widely to control weeds such as morningglory species (*Ipomoea* spp.) in cotton fields. Although most cotton (*Gossypium hirsutum* L.) varieties are tolerant to this herbicide, cotton variety Paymaster HS26 was found to be susceptible. A delay in maturity and yield loss occurred when HS26 plants were treated with the herbicide Envoke®. In order to understand the genetic control of this susceptibility, we made a cross between HS26 and Stoneville 474. Four hundred fifty F2 progeny were planted at the Plant Science Research Center, Mississippi State, MS in 2011. Plants were sprayed with 4.25g (0.15 oz.) active ingredients/acre about 30 days post planting. Herbicide damage on F2 plants was scored at 7 days and 12 days post treatment, respectively. Our results clearly showed that the susceptibility to the herbicide Envoke® in HS26 was controlled by one single recessive gene designated *als*. Using bulked segregant analysis strategy, 2132 SSR markers were screened between the two DNA bulks along with the two parental varieties. Polymorphic markers were analyzed in the 450 F2 progeny. The gene *als* is located on chromosome 20, and three SSR markers were identified as closely linked to *als*. Developing closer SSR and SNP markers is in progress, and will be presented.