

Genetic mapping of sugarcane aphid resistance in sorghum line SC112-14

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Abstract Text:

Sugarcane aphid [*Melanaphis sacchari* (Zehntner)] is a destructive pest of sorghum [*Sorghum bicolor* (L.) Moench] worldwide. Since 2013, sugarcane aphids (SCA) began to infect grain sorghum in south Texas, spread across North America and has become a significant pest in all sorghum growing areas of the continent. The economic impact on the sorghum industry have led to multiple research efforts directed at identifying different resistance sources and the most adequate strategy to control the pest. Today, a limited number of resistance sources have been identified in sorghum germplasm adapted to temperate regions. In this study, a recombinant inbred line (RILs) population derived from crossing the sugarcane aphid (SCA) resistant line SC112-14 with the susceptible line PI609251 were evaluated for their SCA resistance response in Georgia during two consecutive years. The resistance response was determined based on the aphid population size (APS) and plant damage (APD). Each RIL plot was rated twice each year before flowering, approximately two weeks apart, to generate two APS (APS_1 and APS_2) and APD (APD_1 and APD_2) scores. Segregation for SCA resistance was observed for the first APS and both APD scores, and the broad-sense heritability estimate ranged from 0.71 to 0.76, respectively. A genome scan using a high-density linkage map of 3,838 SNPs detected an 81 kb genomic region in chromosome 6 with 2.5 cM of length (Figure 1). This locus explained 50 - 55% of the phenotypic variation and includes seven genes including two (Sobic06G.015200 and Sobic06G.015250) that have protein kinase and leucine rich repeats domains, both features are common among *R*-genes. Comparative mapping analysis found that the resistance source in SC112-14 is new and is located 8 and 10 cM downstream of the Henong 16 (*RMES-1*) and Tx2783 resistance loci, respectively (Figure 2). Previous studies found that the SC112-14 anthracnose resistance response was controlled by a locus in chromosome 5, therefore, this line is becoming an important germplasm that can be immediately used in breeding programs for the development of new sorghum hybrids and varieties with resistant to anthracnose and sugarcane aphid.

Figure 1. Genome scan for sugarcane aphid (SCA) resistance response in recombinant inbred lines derived from the cross of SC112-14 and PI609251 evaluated in Tifton, Georgia, U.S. in 2018 and 2019. Inclusive composite interval mapping (ICIM) using the logarithm value of the first SCA population size and two scores of plant damage. The first and second score were taken two weeks apart.

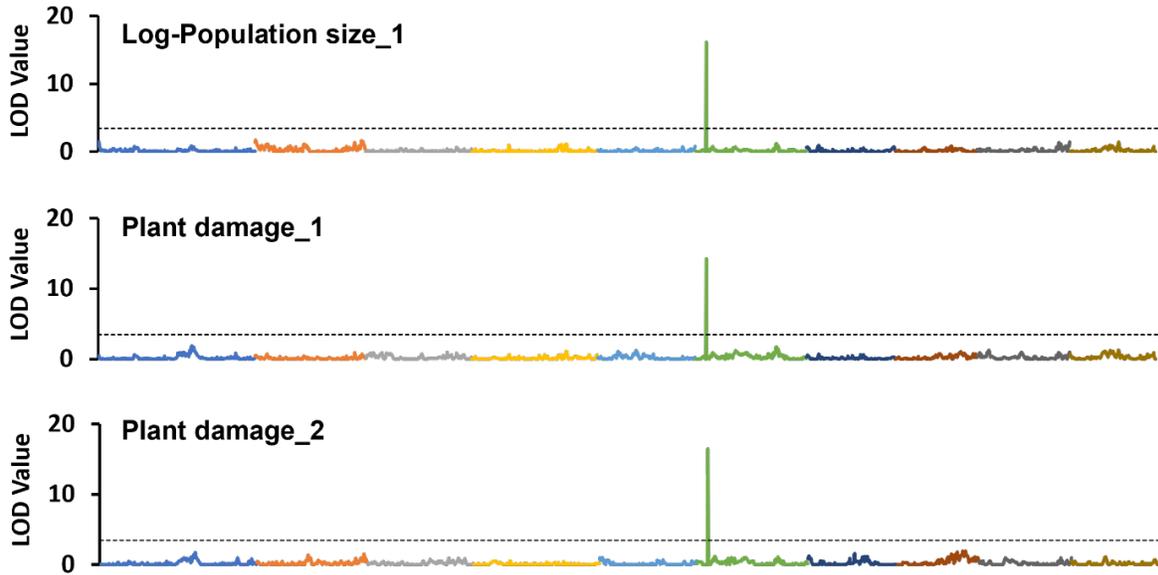
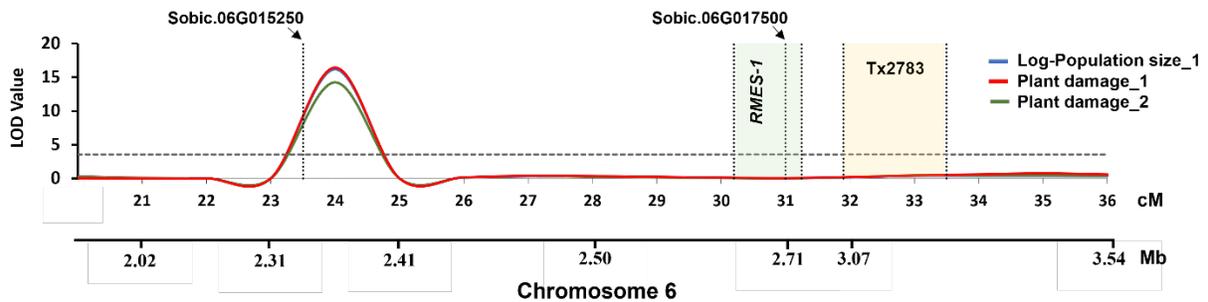


Figure 2 Genomic regions associated with the sugarcane aphid (SCA) resistance response in sorghum line SC112-14. Candidate genes and genomic regions associated with the SCA resistance response observed in sorghum line Henong 16 (*RMES-1*; Wang et al. 2013), 407B (Zhang et al. 2020) and Tx2783 (Wang et al. 2021) are delimited within the associated region.



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