



Category: Plant Genomics

Development and validation of molecular markers for sucking pest resistance in Cotton

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Abstract

Cotton (*Gossypium hirsutum* L.) is the world leading natural fiber crop on which the textile industry worldwide is largely based on. Cotton occupies a pivotal position in the Indian economy. Cotton is infested by a large number of insect pests right from the sowing till harvest. Sucking pests cause significant damage to cotton and it is estimated that 22.58 per cent of cotton yield is effected by sucking pests. Among the key pests of cotton the Sap-sucking pests viz., aphid (*Aphis gossypii*), whitefly (*Bemisia tabaci*), Jassids (*Amrasca biguttula*) and thrips (*Thrips tabaci*) cause severe damage and serious threat to the crop at early stage of the crop growth and can also affect the crop stand and yield of cotton. With the onset of monoculture-driven modern agriculture, selective pressure on insects to overcome resistances has dramatically increased. Therefore plant breeders have resorted to high-tech tools to continuously create new insect-resistant crops. An alternative to transgenic approaches is the use of wild relatives of crop plants, searching for desirable traits and then crossing those into the elite cultivars. Such plant breeding has been made substantially easier with the availability of novel sequence-based molecular approaches. Two Recombinant cotton inbred lines (RIL'S) were derived by wide hybridization from wild relatives, which were used to obtain near Iso-genic lines (NIL's) for the sucking pest resistant trait. The objectives of the present study are to develop and validate molecular markers linked to sucking pest resistance by next generation sequencing. A total number of 3450 mapped SSR markers across all 26 chromosomes were used to screen and identify markers linked to the trait of interest. We are also using Next generation sequencing approaches to identify and develop SNP based markers for sucking pest resistance in our cotton lines.

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