



Resistance Gene Analogs and STS Markers Colocalized with a Major QTL conferring resistance to SCMV in Tropical Maize

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The common mosaic caused by Sugarcane Mosaic Virus (SCMV) is the most important virus disease affecting maize crops in Brazil. The development of resistant cultivars is the most effective way to control this disease. Despite its economic importance, there are few studies about resistance gene analogs (RGA) and QTL mapping conferring resistance to common mosaic in tropical maize. A major QTL associated with SCMV resistance has been mapped on chromosome 3, but the molecular mechanisms controlling this disease are still unclear. The aim of this study was to identify molecular markers and candidate genes colocalized with a major QTL for SCMV resistance in tropical maize lines. Initially, RGAs were identified in the QTL region on chromosome 3 using bioinformatics tools. A total of 10 candidate genes were selected as targets for primers design and DNA sequencing to identify polymorphisms among maize lines L18 and L520 resistant, and L19 susceptible to SCMV. Subsequently, restriction sites were identified in polymorphic positions and two molecular markers based on CAPS were developed for the RGAs. Also, six STS markers previously used for QTL fine mapping were tested and two of them were polymorphic between L18 and L19. Moreover, the expression pattern of four candidate genes was evaluated by qPCR using L18 and L19 leaves, at zero and nine days after rubbing the inoculum or just buffer. One candidate gene was highly expressed in resistant line in all conditions in comparison to the susceptible line, suggesting a putative association with SCMV resistance. Financial Support: Embrapa, Fapemig.