P2.09 - Sugarcane mosaic vírus (SCMV)-tolerant maize obtained by RNAi technology

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Today corn is one of the most cultivated cereal in the world (155 million ha). Brazil is the third largest producer, behind only the U.S. and China. Among the great losses faced by agriculture are the pests and diseases in corn such as Mosaic (SCMV) and streak virus (MRFV). The effects caused by mosaic in maize plants are greater if the infection occurs earlier, where experiments can show reduction up to 50%. A search for cultivars more productive, disease resistant and adapted to different conditions can be accelerated with the use of techniques such as gene manipulation and transformation. Thus, the purpose of this research is to test the efficiency to develop a tolerance corn to SCMV by expression the coat protein of this virus with the RNAi technology. From the 250 transgenic events seed were obtained only from 82. Of these, 47 events were germinated, and four seeds per event were tested against the virus. The 15 day-old seedlings were inoculated with the virus (carborudum Bioglobal mesh 600) for 4 consecutive weeks, one injection per week. Of a total of 142 plants that had been tested 26 asymptomatic. It has been also observed a decrease in symptoms in some of the plants tested in the weeks after the first infection. Southern blot, PCR and test with the herbicide were done to confirm the presence of the transgene. The phenotyping of some F3 population has shown that SCMV tolerant maize plants have been obtained by the RNAi technology. These plants have been self pollinated and Southern blot used to identify single copy transgene. The expression of the gene construction and virus quantification have been followed by Real Time PCR.

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P2.10 - Methylation profiling at the maize flowering time locus *Vgt1*

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The *Vegetative to generative transition 1* (*Vgt1*) locus is one of the most commonly identified flowering time QTLs in maize. *Vgt1* was positionally cloned on chrom. bin 8.05 after its Mendelization (Salvi et al., 2007, PNAS, 104: 11376-11381) and shown to correspond to an upstream (70 kb) non-coding regulatory element of *ZmRap2.7*, an Ap2-class transcription factor known to influence flowering time. A transposon (MITE) insertion was identified as a major allelic difference within *Vgt1*. One of the hypotheses is that *Vgt1* might function by modifying *ZmRap2.7* chromatin structure/function through an epigenetic mechanism. Therefore, we decided to investigate the methylation state at multiple regions of ca. 250 bp each, within *Vgt1* and the promoter of *ZmRap2.7*. Following digestion with McrBc, an endonuclease that acts upon methylated DNA, real-time PCR analysis was performed on genomic DNA from near-isogenic maize lines carrying different combinations of late and early alleles at both loci. DNA was extracted from leaves and shoot apexes sampled at several stages of development. Preliminary results showed a reduction in methylation from the first through the fifth leaf stage irrespectively of the genotype at both *Vgt1* and *ZmRap2.7*. Additionally, the C22-4/Gaspé allele/haplotype showed a reduced methylation in comparison to N28. The region closer to the MITE insertion showed a constant and very dense methylation level throughout leaf development and for both alleles. Additional genotypes and stages of development are currently being investigated.