

Virus Family: *Geminiviridae*

Category: Genetic Diversity/Evolution

Title: The perspective for the use of genetically modified common beans in Brazil based on genetic diversity of *Bean golden mosaic virus*

Authors: T. A. L. SILVA, R. S. FONTENELE, J. C. FARIA, F. J. L. ARAGÃO, AND S. G. RIBEIRO

Address: Embrapa Recursos Genéticos e Biotecnologia, Parque Estação Biológica – Brasília, DF, Brazil

Abstract: Bean golden mosaic is the most important viral disease affecting common beans (*Phaseolus vulgaris*) in Brazil. It is caused by *Bean golden mosaic virus* (BGMV) and is prevalent in all bean producing areas. Aiming to control the disease, a transgenic bean elite line was developed with an intron-hairpin construction to silence the AC1 viral gene. This line shows high resistance to BGMV with the capacity to contain the replication of the virus both in the green house and in the field. The silencing through small interfering RNAs (siRNA) is sequence specific and a high identity to the transgene is required to assure resistance since gene silencing can be inefficient when the identity is lower than 90%. To guarantee the broad use of transgenic cultivars in the different regions of the country, we have analyzed the sequence of begomoviruses isolated from bean samples from several states. A total of 85 bean samples were collected. Total DNA from dried leaves was extracted with Extract-N-Amp™ Plant PCR Kit followed by RCA reaction using *Phi-29* polymerase. PCR reaction with primers BGMV-HPXHO and PAR1c484 amplified a ~1.3Kb fragment encompassing part of the AC1 gene, the entire common region and part of the coat protein gene. Sequences obtained from 25 isolates were analyzed and compared with corresponding sequences from BGMV-[BR:GO 87-1] (M88686). The identity was between 85,2% and 97,4% indicating that most likely only BGMV is infecting common beans in the field. Although some isolates have sequence identities lower than 90% over the entire PCR fragment, the portion corresponding to that used in the RNAi construction is highly identical (between 90,5 and 98,8%). These results will warrant the large scale use of transgenic cultivars resistant to BGMV based on RNAi over the Brazilian territory.

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