VIP GENES IDENTIFICATION IN ISOLATES OF *Bacillus thurigiensis*

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The pest control in agricultural production is a widely discussed issue, and the biological control is an effective alternative that minimizes the use of chemical insecticides. For crops such as maize, cotton, soybean and potato, biological control can be accomplished through the use of insecticides based on *Bacillus thuringiensis*. *B. thuringiensis* is a natural soil bacteria and it is present in diverse environments, Gram-positive, aerobics, entomopathogenic, and it is used in biological pest control. It is characterized by the production of toxic proteins to insects, either in the vegetative phase or sporulation, and the most important are: Cry, Cyt and Vip. The goal of this work was the identification of vip (Vegetative Insecticidal Protein) classes and subclasses, through polimerase chain reaction (PCR), in potentially toxic to lepidopteran larvae isolates of *B. thuringiensis*. The study featured a panel of seventeen strains previously known, of samples originating from Amazon region and belonging to the "bank of Bt" of 'Laboratório de Controle Biológico' at Embrapa Maize and Sorghum. Strains were grown in Luria-Bertani culture at 30ºC for 72h, and after this period was performed a genomic DNA extraction. PCR amplification was done for all DNA samples, for a positive control and for a blank control, using Taq DNA Polymerase kit with primers for the characterization of genes: *vip3Aa1*, *vip3Aa2*, *vip3Ah1*, *vip2*, *vip3*, *vip3Ab2*, *vip3Af1*, *vip3Ae* and *vip3Ba1*. The PCR product was applied in a 2.0% agarose gel, and the presence or absence of genes was evaluated based on the size of amplified fragment. Different pair of primers were used to verify the vip genes amplifications under study. Of the 17 strains analyzed, only one amplified all nine subclasses of vip genes tested. The others strains showed amplification products belonging to one or more subclass of vip genes, as follow – two strains: a gene amplified; two strains: two genes amplified; six strains: three genes amplified; three strains: four genes amplified; three strains: five genes amplified. The gene *vip3Aa2* was the most present (94.1%) in the study, whereas *vip3Ah1*, *vip3Ae1* and *vip3Ba1* genes were found less frequently (5.9%). Our results suggest that the polymerase chain reaction technique allowed identifying different classes and subclasses of *B. thuringiensis* vip genes, as well as showing the genetic variability of this class of genes in isolates of this pathogen.

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