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DETERMINATION AND DISTRIBUTION OF CRY1-TYPE GENES IN *Bacillus thuringiensis* ISOLATED FROM NORTH INDIA

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Abstract

Bacillus thuringiensis (*Bt*) is a spore-forming bacterium which produces insecticidal crystal protein in the sporulation phase. Polymerase chain reaction (PCR)-based identification of *Bacillus thuringiensis* toxin genes has become a routine step in most *B. thuringiensis* isolation and characterization initiatives. In the present study, eighteen native *Bt* isolates from diverse habitats of North India were taken for the presence of *cryI* type genes. The distribution of *cryI* gene families in native *Bt* isolates was examined by PCR amplification of genes with three sets of corresponding PCR primers. In native *Bt* isolates many variant bands were also observed in addition to expected bands on PCR amplification. Different sets of primers for the same gene give different results due to different sites of primer binding. Maximum number of isolates showed expected bands when primers designed by Ceron were used compared to other primers. However, with other primers, the numbers of variant bands was larger. The isolates, SK-13, 63 and 105 showed the maximum number of *cryI*-type genes, followed by SK-20, 28, 48, 88, 94, 301, 304 and 307, whereas SK-3 showed the presence of only 3 *cryI*-type genes. RFLP analysis of 1.6 kb fragment indicated the presence of variant bands from the reference strains. Several promising isolates with predicted toxicity towards lepidoptera have been observed in this study.

Key words: *Bt* isolates, *cry* gene, molecular characterization, PCR analysis

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