

Molecular Diversity of Cotton Bollworm (*Helicoverpa armigera* Hübner) Using Rapd Markers

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Abstract: The bollworm, *Helicoverpa armigera* Hübner (Lepidoptera : Noctuidae) is a polyphagous pest of worldwide occurrence inflicting annual crop damage in India US dollar 1 billion. In India this insect occurs as a major pest in many economically important crops, including cotton, pigeonpea, chickpea, tomato, okra and blackgram. Understanding the genetic variation among the *H. armigera* populations occurring on cotton plants has become essential to understand the variation in their susceptibility to different insecticides, including *Bacillus thuringiensis*. In this preliminary study diversity among 5 cotton bollworm, *Helicoverpa armigera* (Hübner) populations from different geographic regions of North Karnataka, Indian state was done using RAPD markers. Nineteen selected RAPD markers generated a total of 58 PCR amplicons, of which 26 were polymorphic across all 5 populations. An average of 6.44 amplicons per primer was noted. All populations could be differentiated from one another using specific primers; specific band(s) could be potentially used to differentiate individual populations. Genetic relationships between the populations were evaluated by generating a similarity matrix using NTYSS PC2 package and a phenetic dendrogram was generated by UPGMA method. Principal component analysis separated the 5 populations into different groups based on band sharing data. Populations showed varied degrees of genetic similarity within a range of 0.84 to 0.00. Also, the populations appeared to be more dispersed on the principal component plot indicating a wide genetic base. On a larger scale, genetic differences among populations appear to result from low dispersal rates between populations. The level of genetic variation detected between the *H. armigera* populations with RAPD-PCR analysis suggests that it is an efficient marker technology for delineating genetic relationships amongst populations and estimating genetic diversity, thereby gaining insight into genetic structure of populations and its further use in formulation of appropriate area wide management strategies for this pest.

Key words: *Helicoverpa armigera* • RAPD markers • Cotton bollworm • Karnataka

INTRODUCTION

Assessing the nature of molecular diversity, extent and spread is essential for understanding the behaviour, response to selection pressure, structure and dynamics of different insect populations and their management. Availability of reliable polymorphic markers often restricts the exact estimation of molecular diversity between individuals or different populations. Elucidation of molecular diversity in geographical populations can be an important aspect to study the pest populations and their management [1, 2, 3]. Within an ecosystem, the extent of molecular diversity between geographical populations

depends on many factors including gene flow between populations, host range and time since separation [3]. Molecular differences within and between geographic populations of an ecosystem are likely to be defined by the population fluxing patterns as influenced by various ecological factors in the immediate past and the historical pressures on the genome [4, 5].

PCR-RAPD approach has been handy and convenient technique for studies of molecular diversity and genome mapping [6] when compared to RFLP markers. Being simple and non radioactive, the technique is quite sensitive and used to detect molecular diversity in many organisms [7, 8].