

Molecular characterization of brinjal shoot and fruit borer, *Leucinodes orbonalis* (Guenée) (Lepidoptera: Crambidae) based on mitochondrial marker cytochrome oxidase I and their phylogenetic relationship

PR Shashank^{1*}, Rakshit Ojha², T Venkatesan², SK Jalali² & KRM Bhanu²

¹Division of Entomology, Indian Agricultural Research Institute, New Delhi 110 012, India

²National Bureau of Agriculturally Important Insects, P.B. No. 2491, H.A. Farm Post, Hebbal, Bangalore 560 024, Karnataka, India

³Bio-Control Research Laboratories, Pest Control (India) Pvt. Ltd., 36/2, Sriramanahalli, Nr. Rajankunte, Doddballapur Road, Bangalore 561 203, Karnataka, India

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Shoot and fruit borer, *Leucinodes orbonalis* is an important insect pest infesting brinjal or eggplant in India. Molecular characterization of nine different populations belonging to various brinjal growing regions was done using Cytochrome C Oxidase I (COI) gene. Nucleotide analysis of genetic diversity and phylogenetic analysis of the COI indicate that the *L. orbonalis* from different geographical regions are homogenous. The results showed less nucleotide diversity ($\pi = 0.007895$) and overall mean distance (0.008 ± 0.003). Topologies of neighbour-joining (NJ) trees indicate all the populations belong to single major clade. Therefore, it is inferred that there was no significant molecular diversity within *L. orbonalis* of different geographical locations of India with respect to COI.

Keywords: Brinjal, COI, Eggplant, Insect pests, Shoot and fruit borer

Brinjal or Eggplant (*Solanum melongena* L.) is an important solanaceous vegetable, which holds a coveted position among small-scale farmers and low-income consumers of South Asia and this region accounts for nearly 60 and 53% of world's area and production, respectively. Among the biotic stress factors that hamper the production of brinjal, the shoot and fruit borer (*Leucinodes orbonalis* Guenee) is the most serious pest infesting throughout the year at all stages of crop growth, accounting to a loss of around 20.7-60.0% in Tamil Nadu¹ and 70% in Andhra Pradesh^{2,3}. This pest has a countrywide distribution and has become major threat to brinjal cultivation⁴. During early stages of the crop growth, larva bores into the shoots resulting in drooping, withering and drying of the affected shoots. During the reproductive stage, tiny larva bores into the flower buds and fruits. The bored holes are invariably plugged with excreta making the infested fruits unfit for consumption and leading to reduction in their market value. *L. orbonalis* is distributed throughout Africa and Asia^{5,6}.

Mitochondrial genes are commonly chosen for evolutionary studies as they have a number of positive

characteristics such as (i) maternal inheritance with little or no recombination, (ii) general conservation of gene order and composition, (iii) small size compared with the nuclear DNA, and (iv) lack of introns⁷. Mitochondrial DNA have proven to be informative in the study of species diversity and evolutionary processes because it is easy to isolate and contain conserved sequences that make it possible to use universal primers^{8,9}. The DNA sequences are used as genetic 'barcodes' that may potentially be used as a bio-identification system for all animals and has proven to be a useful identification tool for vertebrates such as birds¹⁰, fish¹¹ and hexapod orders such as Lepidoptera¹², Coleoptera¹³, Diptera¹⁴, Hymenoptera¹⁵, Ephemeroptera¹⁶ and Hemiptera¹⁷.

Pheromone trap are being used to trap *L. orbonalis* adults, however from past few years the pheromone trap catches were variable in different regions for the identified pheromone molecule (Bhanu, 2013 Personal communication). This elicited doubt regarding variation in different population of *L. orbonalis*. Therefore, the objective of this study is to determine the extent of genetic variation among populations of *L. orbonalis* from different localities of India by using mitochondrial marker cytochrome C oxidase (COI).

*Correspondence:
E-mail: spathour@gmail.com