



Molecular diversity of *Sesamia inferens* (Walker, 1856) (Lepidoptera: Noctuidae) from India

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Abstract

Pink stem borer, *Sesamia inferens* (Walker, 1856) (Lepidoptera: Noctuidae) is reported to infest many graminaceous crops and cause significant losses. *S. inferens* cause damage by killing the central shoot and producing a characteristic symptom called “dead heart”. Since graminaceous crops are an important source of food for humans and their livestock, impetus should be given on designing efficient management strategies against pink stem borer. The study of genetic variability of pest populations enables to interpret the ecological investigations correctly and also helps to comprehend the dissimilar response of pest to management tactics. The present study was undertaken to evaluate the diversity in *S. inferens* populations using mitochondrial cytochrome oxidase subunit I sequences from India, Pakistan, China and Indonesia. Analysis revealed a very low nucleotide diversity in Indian populations ($\pi=0.00981$), as compared to a high nucleotide diversity in the sequences outside India ($\pi=0.4989$). The phylogenetic analysis also did not show any clustering among populations within India and Pakistan. However, the nearest neighbour for the Indian and Pakistan population is a sequence from Indonesia followed by China indicating possible ancestral background. This is the maiden attempt to assess the molecular diversity of Indian populations in comparison to populations from other Asian countries.

Keywords Stem borer · mtCOI · Homogeneity · Genetic diversity · India

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