

Studies on Phylogeny of *Helicoverpa armigera* Populations from North Western Himalaya Region with Help of Cytochromeoxidase I Sequence

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Abstract : The similar morphology associated with high genetic variability poses problems in phylogenetic studies of *Helicoverpa armigera* (Hubner). To identify genetic variation of North Western Himalayan population's, partial (Mid to terminal region) cytochrome c oxidase subunit I (COX-1) gene was amplified and sequenced for three populations collected from Pantnagar, Almora, and Chinyalisaur. The alignment of sequences with other two populations, Nagpur representing central India population and Anhui, China representing complete COX-1 sequence revealed unanimity in middle region with eleven single nucleotide polymorphisms (SNPs) in Nagpur populations. However, the consensus is missing when approaching towards terminal region, which is associated with 15 each SNPs and pair base substitutions in Chinyalisaur populations. In minimum evolution tree, all the five populations were majorly separated into two clades, one comprising of only Nagpur population and the other with rest. Amongst, North Western populations, Chinyalisaur one is promising by forming a separate clade. The pairwise genetic distance ranges from 0.025 to 0.192 with the maximum between *H. armigera* populations of Nagpur and Chinyalisaur. This genetic isolation of populations can be attributed to a key role of topological barriers of weather and mountain ranges and temporal barriers due to cropping patterns.

Keywords : cytochrome c oxidase subunit I, northwestern Himalayan population, *Helicoverpa armigera* (Noctuidae: Lepidoptera), phylogenetic relationship, genetic variation

Conference Title : ICAE 2017 : International Conference on Advances in Entomology

Conference Location : Vienna, Austria

Conference Dates : June 21-22, 2017