SNP Discovery and Application in Genetic Studies of the Tasar Silkworm (Antheraea Mylitta)

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Abstract:

Tasar Silkworm, Antheraea mylitta is an economically important wild silkmoth species distributed across India. A number of morphologically and ethologically well-defined ecotypes are known for this species that differ in their primary food plant specificity. Most of these ecotypes do not interbreed in nature, but are able to produce offspring under captive conditions. In the present investigation the SNP discovery by alignment of sequences obtained from direct sequencing of genomic PCR products using WILDSILKBASE has identified potential EST-SSR marker to recognise single nucleotide polymorphism by comparing various tasar ecoraces, which was hitherto not reported so far. Single nucleotide polymorphism (SNP) analysis have been developed to distinguish the genetic diversity among silkworm species. A recent report has brought to light that lipo proteins are found to be synthesized in fat body and secreted to haemolymph, from which they are utilised during adult development, transported to yolk granules in adult female and yolk proteins of silkworm egg., B. mori (Pietrzyk et al., 2013). Since the 30-kDa family of lipoprotein from insect haemolymph has been the focus of a number of studies in the recent past, the present work has been focused on PCR-EST phylogenetic analysis of 5 ecoraces in Tasar silkworm, which has so far not been reported.

Keywords:

Tasar silkworm, Antheraea mylitta, Single nucleotide polymorphism, ecotypes.