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Intragenetic phylogenetics based on mitochondrial DNA variation among fifteen harpactorine assassin bugs with four ecotypes and three morphs (Hemiptera: Reduviidae: Harpactorinae)

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Abstract

Available mitochondrial DNA sequences viz., 16S, Cyt b, Cyt c oxidase subunit – I, and Cyt c subunit-like – I gene of *Rhynocoris* (Kolenati) species were subjected to phylogenetic analysis to understand the intragenetic and intraspecific variations and the role of geographical isolation on speciation; using CLUSTAL W in MEGA version 5.1. This analysis includes fifteen species and four ecotypes of *R. kumarii* Ambrose and Livingstone and three morphs of *R. marginatus* (Fabricius) from four countries viz., Canada, China, Korea, and South Africa. The pairwise genetic distances were calculated and phylograms were constructed using Maximum Likelihood, Maximum Parsimony, and Neighbor-Joining methods. These preliminary analyses not only demarcated the fifteen species of *Rhynocoris*, the four ecotypes of *R. kumarii*, and the three morphs of *R. marginatus*, but also revealed phylogenetic relationships and the role of geographical isolation and polymorphism on speciation.

Keywords: *Rhynocoris*, assassin bugs, biocontrol agents, molecular biosystematics, phylogenetic relationship, speciation, ecotypism, polymorphism, geographical isolation.

Introduction

Assassin bugs have different morphs, biotypes, and ecotypes with various colours and shapes which often mislead a museum entomologist in recognizing the morphs and ecotypes of a particular species.

Hence, classifications of Reduviidae based on morphological characters (Usinger, 1943; Putshkov & Putshkov, 1985; Maldonado, 1990; Schuh & Slater, 1995) may at times become insufficient, and there is an urgent need for a cohesive meaningful classification of Reduviidae based on ecological, morphological, behavioural, cytological, and biochemical data. Moreover, a multidisciplinary biosystematics understanding is imperative to accurately identify reduviids and employ them against a particular insect pest (Ambrose, 1999, Ambrose & Ambrose, 2003, 2009). Although multidisciplinary biosystematics including molecular tools has been attempted on Oriental reduviids (Weirauch, 2008), such an analysis is wanting on non-Oriental reduviids.

This study was undertaken based on available mitochondrial sequences of fifteen species of *Rhynocoris* Kolenati (Table 1), four ecotypes of *R. kumarii* Ambrose and Livingstone, and three morphs of *R. marginatus* (Fabricius). The inclusion of both Indian and non-Indian species of *Rhynocoris* with ecotypes and morphs will further enhance the scope of the work at the intraspecific level and the understanding on the role of geographical isolation in biosystematics.

revealed, the genetic diversity among them suggests ongoing speciation among them. The present findings on the affinity of *Rhynocoris* species do not corroborate with the existing literature on identification of these *Rhynocoris* species based on morphological characters, as Garcia *et al.* (2001) observed in *Triatoma* species.

Conclusion

The results obtained not only have enriched our knowledge on biosystematics but have also supplemented multidisciplinary data. The results further reveals the utility of 16 S, mtCyt b, Cyt C oxidase subunit I, and Cyt c oxidase subunit I-like DNA sequences in phylogenetic analysis. The findings clearly suggest the intraspecific and interspecific phylogenetic affinity and diversity not only in the Indian and non-Indian species of *Rhynocoris* but also among the ecotypes of *R. kumarii* and the morphs of *R. marginatus*. Moreover, the genetic diversity observed among ecotypes and morphs suggesting progression of speciation warrant further studies in this direction that could lead to meaningful revision, regrouping, or replacement of species with new revelations through molecular analysis.

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