Intrageneric 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 intrageneric 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.
Material and methods

**Taxon sampling.** To understand the intrageneric biosystematics and phylogenetics through molecular markers (viz., 16S, mtCyt b, Cyt c oxidase subunit I gene, and Cyt c oxidase subunit I-like gene), DNA sequences of these species of *Rhynocoris* (Table 1) were subjected to phylogenetic analysis. The sequences of Indian species including ecotypes and morphs obtained from our work are deposited in the National Centre for Biotechnology (NCBI). The sequences of non-Indian species were retrieved from NCBI (Table 2) and all these sequences were taken into consideration.

**Phylogenetic analysis.** The DNA sequences were subjected into pairwise distance analysis and the following phylogenetic trees were constructed: Maximum Parsimony, Maximum Likelihood and Neighbor-Joining with MEGA 5 software (Tamura et al., 2011).

**Pairwise alignment.** Pairwise distances were carried out with gap opening penalty 15 and gap extension penalty 6.66 (Clustal W) (Thompson et al., 1994).

**Maximum Parsimony.** The Maximum Parsimony analyses were analysed with MEGA5 (Tamura et al., 2011). Bootstrap method was used with 100 replications and gap/missing data treatment by complete selection and the search method was Subtree-Pruning-Regrafting (SPR) and substitution based on nucleotide sequences. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (100 replications) was used (Felsenstein, 1985). The Maximum parsimony tree was obtained using the Subtree-Pruning-Regrafting (SPR) algorithm (Nei & Kumar, 2000) with search level 1. The substitution type based nucleotide sequences and the codon positions included were 1st+2nd+3rd+Noncoding and all the positions containing gaps and missing data were eliminated.

**TABLE 1.** Fifteen *Rhynocoris* species, four ecotypes, and three morphs were subjected to phylogenetic analyses.

<table>
<thead>
<tr>
<th>Species</th>
<th>Locality</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>R. altaicus</em> (Kiritshenko)</td>
<td>Xiaowutai Mt., Hebei, China</td>
</tr>
<tr>
<td>△<em>R. fuscipes</em> (Fabricius)</td>
<td>Tamil Nadu, India and Suixi, Zhanjiang, Guangdong, China</td>
</tr>
<tr>
<td><em>R. hoffmanni</em> Hungerford</td>
<td>Nanjian, Dali, Yunnan, China</td>
</tr>
<tr>
<td><em>R. incertus</em> (Distant)</td>
<td>Dongtang, Maolan, Guizhou, China</td>
</tr>
<tr>
<td><em>R. iracundus</em> (Poda)</td>
<td>Tianshan, Xinjiang, China</td>
</tr>
<tr>
<td><em>R. kumarii</em> Ambrose and Livingstone</td>
<td>Tamil Nadu, India</td>
</tr>
<tr>
<td><em>R. longifrons</em> (Stål)</td>
<td>Tamil Nadu, India</td>
</tr>
<tr>
<td><em>R. marginatus</em> (Fabricius)</td>
<td>Tamil Nadu, India</td>
</tr>
<tr>
<td><em>R. marginellus</em> (Fabricius)</td>
<td>Dawei Mt., Pingbian Yunnan, China</td>
</tr>
<tr>
<td><em>R. mendicus</em> (Stål)</td>
<td>Suixi, Zhanjiang, Guangdong, China</td>
</tr>
<tr>
<td><em>R. monticola</em> (Oshanin)</td>
<td>Nileke, Xinjiang, China</td>
</tr>
<tr>
<td><em>R. ornatus</em> (Uhler)</td>
<td>GG, Icheon-si, Korea</td>
</tr>
<tr>
<td><em>R. rubromarginatus</em> (Jakovlev)</td>
<td>Yanqing, Beijing, China</td>
</tr>
<tr>
<td><em>R. segmentarius</em> (Germar)</td>
<td>Limpopo, South Africa</td>
</tr>
<tr>
<td><em>R. ventralis</em> (Say)</td>
<td>British Columbia, Inkaneep, OsoyoosIR1,Canada</td>
</tr>
</tbody>
</table>

Ecotypes of *R. kumarii*

| THE     | Tamil Nadu, India |
| KAZ     |                     |
| MUP     | Tamil Nadu, India  |
| MAR     |                     |

Morphs of *R. marginatus*

| Unknown | Tamil Nadu, India |
| Niger    |                    |
| Nigrosanguineous |                |

Species denoted by * are non-Indian species and △ is Indian as well as non-Indian. The rest of the species are Indian species.
**Maximum Likelihood.** Maximum Likelihood analyses were run in MEGA 5 (Tamura et al., 2011). The evolutionary history was inferred by using the Maximum Likelihood method based on the Tamura-Nei model (Tamura & Nei, 1993). Initial tree for the heuristic search was obtained automatically by applying Neighbor-Joining and BioNJ algorithms to a matrix of pairwise distances estimated using the Maximum Composite Likelihood (MCL) approach and then selecting the topology with superior log likelihood value. The substitution type based nucleotide sequences and the codon positions included were 1st+2nd+3rd+Noncoding and all the positions containing gaps and missing data were eliminated.

**TABLE 2.** Mitochondrial DNA sequences of fifteen *Rhynocoris* species, four ecotypes, and three morphs subjected to phylogenetic analysis.

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<td>HM038434.1</td>
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<tr>
<td></td>
<td><em>R. segmentarius</em> (Germar)</td>
<td>FJ230384.1</td>
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<td>Cytochrome b (cyt b) partial cds;</td>
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<td>EU286540.1</td>
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<td>mitochondrial</td>
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<td></td>
<td><em>R. fuscipes</em></td>
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<td><em>R. hoffmanni</em> Hungerford</td>
<td>EU286542.1</td>
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<td><em>R. iracundus</em> (Poda)</td>
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<td><em>R. incertus</em> (Distant)</td>
<td>EU286548.1</td>
</tr>
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<td></td>
<td><em>R. kumarii</em> Ambrose and Livingstone</td>
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</tr>
<tr>
<td></td>
<td><em>R. longifrons</em> (Stål)</td>
<td>GU225703.1</td>
</tr>
<tr>
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<td><em>R. marginatus</em></td>
<td>GU225700.1</td>
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<td></td>
<td><em>R. marginellus</em> (Fabricius)</td>
<td>EU286544.1</td>
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<td><em>R. monticola</em> (Oshanin)</td>
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<td><em>R. rubromarginatus</em> (Jakovlev)</td>
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<td><em>R. fuscipes</em></td>
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<tr>
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<td>GQ229413.1</td>
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Species denoted by * are non-Indian species. The rest of the species are Indian species.
Neighbor-Joining. Neighbor-Joining analyses were determined with MEGA5 (Tamura et al., 2011). The evolutionary history was inferred using the Neighbor-Joining method (Saitou & Nei, 1987). The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (100 replicates) was used (Felsenstein, 1985). The evolutionary distances were computed using the Tajima-Nei method (Tajima & Nei, 1984). Codon positions included were 1st+2nd+3rd+Noncoding and all positions containing gaps and missing data were eliminated.

Results and discussion

Based on 16S, mtCyt b, Cyt c subunit I gene, and Cyt c subunit like I gene sequences, three phylograms were constructed for each set. The results of Maximum Parsimony, Maximum Likelihood, and Neighbor-Joining trees were analyzed based on the arrangement of each species on the tree.

16S. The Maximum Likelihood tree constructed based on 16S gene (Fig.1) with two parallel clusters; one with the Indian R. marginatus that evolved as a separate lineage, and the second cluster with Indian R. fuscipes and R. segmentarius of South Africa with the branch length of 0.06 and 0.05, respectively exhibits their closeness. It is interesting that the Indian R. fuscipes exhibits closeness to the R. segmentarius of South Africa instead of the R. fuscipes of China. A similar kind of phylogeny is also observed in Neighbor-Joining (Fig.2) tree. The results reveal monophyly (Cui & Huang, 2012) through phylogenetic relationship not only among the native species but also between Indian and non-Indian species. But R. marginatus, instead of clustering with R. fuscipes, diverges in a separate lineage exhibiting phylogenetic disparity. The Indian species R. fuscipes and R. segmentarius of South Africa exhibit affinity despite biogeographical isolation (Mahendran et al., 2006).

![Figure 1](image1.jpg)

**FIGURE 1.** Maximum Likelihood tree based on 16S gene variations showing the relationships of two Indian and one Chinese species of *Rhynocoris*

*Cyt b.* The Maximum Likelihood tree (Fig.3) shows that all the four Indian species are in two clusters. One cluster consists of R. kumarii and R. longifrons whereas another cluster contains R. marginatus and R. fuscipes. But they share a common ancestral node suggesting an affinity between these four sympatric species. Among them, the two morphologically related R. marginatus and R. fuscipes share a common node exhibiting their affinity. Although R. kumarii and R. longifrons are morphologically quite dissimilar, they share a common node which shows their closeness. Baskar (2010) also observed affinity between R. longifrons and R. kumarii and R. marginatus and R. fuscipes. Another cluster consists of eight non-Indian species. These two clusters, one exclusively Indian and another non-Indian, emerge from the same evolutionary rate as a separate lineage that might be due to allopatric speciation with a closer affinity with R. marginellus of China. The line of phylogeny observed for the four Indian species in the Maximum Likelihood tree (Fig.3) is also repeated in Neighbor-Joining and Maximum Parsimony.
trees. However, the phylogenetic hierarchy of non-Indian species observed in the Maximum Likelihood tree differs from that of Neighbor-Joining tree (Fig. 4): *R. iracundus* followed by *R. monticola*, followed by a cluster consisting of *R. marginellus*, *R. mendicus*, *R. altaicus*, *R. rubromarginatus*, and *R. incertus*; and a cluster consisting of *R. hoffmanni* and *R. fuscipes*. A similar trend is observed in Maximum Parsimony tree (Fig. 5): *R. marginellus* and *R. mendicus* cluster followed by *R. iracundus*, *R. incertus*, *R. monticola*, and *R. altaicus*, *R. rubromarginatus* and *R. hoffmanni*. But the affinity between any two species is similar in all three phylograms revealing uniform phylogenetic relationship and suggesting monophyly.

**Figure 2.** Neighbor-Joining tree based on 16S gene variations showing the relationships of two Indian and one Chinese species of *Rhynocoris*

**Figure 3.** Maximum Likelihood tree based on Cyt b variations showing the relationships of four Indian and eight non-Indian species of *Rhynocoris*
FIGURE 4. Neighbor-Joining tree based on Cyt b gene variations showing the relationships of four Indian and eight non-Indian species of *Rhynocoris*

Interestingly, the non-Indian *R. fuscipes*, instead of clustering with Indian *R. fuscipes*, shows its affinity towards other non-Indian species suggesting the role of geographical isolation at the species level. Thus, the intraspecific genetic variations because of geographical locations or as in distantly located ecotypes are revealed (Almeida et al., 2008, and Naranjo et al., 2010).

**Cyt c subunit I.** The Maximum Likelihood, Neighbor-Joining, and Maximum Parsimony trees based on Cyt c gene (Fig. 6,7&8) showed the population of Indian *R. marginatus* formed one cluster and populations of Indian *R. fuscipes*, *R. longifrons*, and *R. kumarii* are together in another cluster with genetic similarity between the Indian *R. kumarii* and *R. longifrons* as observed in the Maximum Likelihood tree for Cyt b gene (Fig.3). But the Indian *R.
fuscipes diverges independently as a separate clade in this cluster. Another phylogenetic lineage shows two non-
Indian species, R. ventralis and R. ornatus, converging together as a cluster, whereas the Indian R. marginatus
stands independently, but shares a common phylogenetic lineage and exhibits its affinity with them. All three
phylograms obtained based on Cyt c gene (Fig. 6,7&8) show a similar phylogenetic relationship and suggest a
monophyly despite geographical isolation. However, Baskar (2010) observed the existence of two main clusters
and a single sub-cluster among the four Indian Rhynocoris species.

**FIGURE 6.** Maximum Likelihood tree based on Cyt c gene variations showing the relationships of four Indian and two non-
Indian species of Rhynocoris

**FIGURE 7.** Neighbor-Joining tree based on Cyt c gene variations showing the relationships of four Indian and two non-Indian
species of Rhynocoris
**Figure 8.** Maximum Parsimony tree based on Cyt c gene variations showing the relationships of four Indian and two non-Indian species of *Rhynocoris*.

**Figure 9.** Maximum Likelihood tree based on Cyt c subunit like I gene variations showing the relationships of four species of *Rhynocoris*, four ecotypes of *R. kumarii* and three morphs of *R. marginatus* of India.

**Cyt c subunit like I.** All the three phylogs (Fig.9,10&11) show two separate lineages of which *R. marginatus*-Niger morph and *R. marginatus*–Nigrosanguineous morph stand independently as a separate cluster. Another line of phylogeny shows two separate clusters of which *R. kumarii* -MAR ecotype and *R. marginatus*-unknown morph share a common cluster. Interestingly, the niger and nigrosanguineous morphs of *R. marginatus* instead of clustering together with the unknown morph of *R. marginatus* (intraspecific affinity) as expected, cluster with *R. kumarii*–Mar ecotype (interspecific affinity). Baskar (2010) and Baskar *et al.* (2012a,b,c) reported genetic diversity among the ecotypes of four Indian *Rhynocoris* species, *R. kumarii, R. marginatus, R. longifrons*, and *R. fuscipes* based on mitochondrial genes and correlated with the ecological diversity of semiarid, scrub jungle, and tropical rainforest habitats. The present results and the findings of Baskar (2010) & Baskar *et al.* (2012a,b,c) suggest the existence of genetic diversity, gene flow with low level of genetic differentiation among the morphs.
and the ecotypes of *Rhynocoris* species as Zaho & Zhu (2011) observed in *Branchiostoma japonicum* Lonnberg. The findings further suggest that the Cyt b fragment is a useful marker to describe the genetic structure of morphs at a particular habitat and ecotypes of closely related habitats (Naranjo, *et al.*, 2010). These observations are contrary to those of Giordana *et al.* (2005) in *Triatoma infestans* (Klug). This contradiction might be the result of the non-dispersal haematophagus feeding behaviour of *Triatoma* in contrast to the dispersal predatory behaviour of *Rhynocoris*.

**FIGURE 10.** Neighbor-Joining tree based on Cyt c subunit like 1 gene variations showing the relationships of four species of *Rhynocoris*, four ecotypes of *R. kumarii* and three morphs of *R. marginatus* of India.

**FIGURE 11.** Maximum Parsimony tree based on Cyt c subunit like 1 gene variations showing the relationships of four species of *Rhynocoris*, four ecotypes of *R. kumarii* and three morphs of *R. marginatus* of India.

The Indian *R. fuscipes*, *R. kumarii* - KAZ ecotype, and *R. kumarii* - THE ecotype lie in the same line of phylogeny as a separate cluster evolved at a uniform rate indicating their similar rate of evolution. But *R. kumarii* - MUP ecotype and *R. longifrons* have evolved at slightly different evolutionary rates, suggesting the intraspecific genetic variations due to ecotypism. Although the interspecific affinity between the morphs and ecotypes has been
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.

Acknowledgments

The authors are grateful to the authorities of St. Xavier’s College (Autonomous), Palayamkottai, Tamil Nadu, India for facilities. We are grateful to the Council of Scientific and Industrial Research (CSIR), Government of India, New Delhi, for financial assistance (Ref. No. 21(0865)/11/EMR-II, 2012-2013 dated 28.12.2011). The authors thank Prof. Carl W. Schaefer, University of Connecticut, USA, who reviewed the manuscript, and Prof. Wanzhi Cai, China Agricultural University, China for his timely support.

References


http://dx.doi.org/10.1603/0022-2585-38.5.675


http://dx.doi.org/10.1590/s0074-02762005000100014


http://dx.doi.org/10.1007/bf02728967


**Acanthaspis pedestris cytochrome oxidase subunit 1-like (COI) gene, partial sequence; mitochondrial**

GenBank: KF443083.1

**FASTA Graphics**

**LOCUS** KF443083 668 bp DNA linear INV 24-AUG-2013

**DEFINITION** Acanthaspis pedestris cytochrome oxidase subunit 1-like (COI) gene, partial sequence; mitochondrial.

**ACCESSION** KF443083

**VERSION** KF443083.1 GI:530891381

**SOURCE** mitochondrion Acanthaspis pedestris

**ORGANISM** Acanthaspis pedestris
Eukaryota; Metazoa; Ecdysozoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Paraneoptera; Hemiptera; Heteroptera; Panheteroptera; Cimicomorpha; Reduviidae; Reduviinae; Acanthaspis.

**REFERENCE** 1 (bases 1 to 668)

**AUTHORS** Ambrose, D.P., Lenin, A.E., Kiruba, A.D. and Manimuthu, M.

**TITLE** Direct Submission

**JOURNAL** Submitted (22-JUL-2013) Entomology Research Unit, St. Xavier's College, Palayamkottai, Tamil Nadu 627002, India

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Acanthaspis quinquespinosa cytochrome oxidase subunit 1-like (COI) gene, partial sequence; mitochondrial

GenBank: KF443082.1

FASTA Graphics

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           Acanthaspis.

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AUTHORS   Ambrose,D.P., Lenin,A.E., Kiruba,A.D. and Manimuthu,M.
TITLE     Direct Submission
JOURNAL   Submitted (22-JUL-2013) Entomology Research Unit, St. Xavier's College, Palayamkottai, Tamil Nadu 627002, India

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Acanthaspis siva cytochrome oxidase subunit I-like gene, partial sequence; mitochondrial
GenBank: KC130938.1

FASTA Graphics

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ACCESSION   KC130938
VERSION     KC130938.1  GI:442569688
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ORGANISM
Eukaryota; Metazoa; Ecdysozoa; Arthropoda; Hexapoda; Insecta;
Pterygota; Neoptera; Heteroptera; Reduviidae;
Acanthaspis.
REFERENCE   1  (bases 1 to 639)
AUTHORS     Ambrose,D.P., Lenin,A.E., Manimuthu,M. and Kiruba,A.D.
TITLE       Phylogeny of species of Reduviinae (Hemiptera: Reduviidae) based
            on mitochondrial DNA sequences
JOURNAL     Unpublished
REFERENCE   2  (bases 1 to 639)
AUTHORS     Ambrose,D.P., Lenin,A.E., Manimuthu,M. and Kiruba,A.D.
TITLE       Direct Submission
JOURNAL     Submitted (05-NOV-2012) Entomology Research Unit, St. Xavier's
            College, Palayamkottai, Tamil Nadu 627002, India

##Assembly-Data-START##
Sequencing Technology :: Sanger dideoxy sequencing
##Assembly-Data-END##

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misc_feature <1..>639
/note="similar to cytochrome oxidase subunit I"

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561 taatattct tataatattct tattacttact atatatattct tattacttact atatatattct tattacttact
601 gcctcctcct cctctctcct cctctctcct cctctctcct cctctctcct cctctctcct cctctctcct
Edocla slateri cytochrome oxidase subunit I-like gene, partial sequence; mitochondrial

GeneBank: KC130939.1

FASTA Graphics
Go to:

LOCUS       KC130939          724 bp    DNA     linear   INV  21-JAN-2013
DEFINITION  Edocla slateri cytochrome oxidase subunit I-like gene, partial sequence; mitochondrial.
ACCESSION   KC130939
VERSION     KC130939.1  GI:442569689
SOURCE      mitochondrion Edocla slateri
ORGANISM    Edocla slateri
            Eukaryota; Metazoa; Ecdysozoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera; Panheteroptera; Cimicomorpha; Reduviidae;
            Reduviinae;
            Edocla.
REFERENCE   1  (bases 1 to 724)  
AUTHORS     Ambrose,D.P., Lenin,A.E., Manimuthu,M. and Kiruba,A.D.
TITLE       Phylogeny of species of Reduviinae (Hemiptera: Reduviidae) based on mitochondrial DNA sequences
JOURNAL     Unpublished
REFERENCE   2  (bases 1 to 724)  
AUTHORS     Ambrose,D.P., Lenin,A.E., Manimuthu,M. and Kiruba,A.D.
TITLE       Direct Submission
JOURNAL     Submitted (05-NOV-2012) Entomology Research Unit, St. Xavier's College, Palayamkottai, Tamil Nadu 627002, India

##Assembly-Data-START##
Sequencing Technology :: Sanger dideoxy sequencing
##Assembly-Data-END##

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Empyrocoris annulata cytochrome oxidase subunit I-like gene, partial sequence; mitochondrial

GenBank: KC130940.1

FASTA Graphics
Go to:

LOCUS        KC130940            641 bp    DNA     linear   INV 21-JAN-2013
DEFINITION   Empyrocoris annulata cytochrome oxidase subunit I-like gene, partial sequence; mitochondrial.
ACCESSION    KC130940
VERSION      KC130940.1  GI:442569690
SOURCE       mitochondrion Empyrocoris annulata
ORGANISM     Empyrocoris annulata
             Eukaryota; Metazoa; Ecdysozoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Heteroptera; Euphlebiomorpha; Heteroptera; Empyrocoris.
REFERENCE    1  (bases 1 to 641)
AUTHORS      Ambrose,D.P., Lenin,A.E., Manimuthu,M. and Kiruba,A.D.
TITLE        Phylogeny of species of Reduviinae (Hemiptera: Reduviidae) based on mitochondrial DNA sequences
JOURNAL      Unpublished
REFERENCE    2  (bases 1 to 641)
AUTHORS      Ambrose,D.P., Lenin,A.E., Manimuthu,M. and Kiruba,A.D.
TITLE        Direct Submission
JOURNAL      Submitted (05-NOV-2012) Entomology Research Unit, St. Xavier's College, Palayamkottai, Tamil Nadu 627002, India

##Assembly-Data-START##
Sequencing Technology :: Sanger dideoxy sequencing
##Assembly-Data-END##

FEATURES             Location/Qualifiers
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/note="similar to cytochrome oxidase subunit I"

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121 acagctctgc ttttattata attttcttca tagttatacc aattataaat gggggatttg
181 gaatttattg atcttctttta atattaggag cttcttgatg atgcttctctc cttcatcttg
241 atataaatgt ttgatattac cttcttcttt aattttatta attttcttgta gtatttgtga
301 aatggagaca ggaactggat gaactgttta tcctccatta tcctctaata ttgctcatgg
361 tggatcatca gtagatttag ctttttttct cttcatcttg cagttttcct cttatatatta
421 ggtgtctatta attttatattat aatatagaa ttataaatat atctttttttgt
481 caattacctt tattttgttg agctgtgaaa ttactgcatt attattactt cttcttttta
541 ctgtattagc aggagctatt accatacttc tctactcag aaacatcagact ctactctatt
601 tgtatctctgc aggacggagg agatctccat ttttccccccc t

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Velitra sinensis cytochrome oxidase subunit 1-like (COI) gene, partial sequence; mitochondrial

GenBank: KF443084.1

FASTA Graphics
Go to:

LOCUS       KF443084            687 bp    DNA     linear   INV  24-AUG-2013
DEFINITION  Velitra sinensis cytochrome oxidase subunit 1-like (COI) gene, partial sequence; mitochondrial.
ACCESSION   KF443084
VERSION     KF443084.1  GI:530891382
SOURCE      mitochondrion Velitra sinensis
ORGANISM    Velitra sinensis
            Eukaryota; Metazoa; Ecdysozoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Heteroptera; Panheteroptera; Cimicomorpha; Reduviidae; Reduviinae; Velitra.
REFERENCE   1  (bases 1 to 687)
AUTHORS      Ambrose,D.P., Lenin,A.E., Kiruba,A.D. and Manimuthu,M.
TITLE       Direct Submission
JOURNAL     Submitted (22-JUL-2013) Entomology Research Unit, St. Xavier's College, Palayamkottai, Tamil Nadu 627002, India

FEATURES             Location/Qualifiers
source 1..687
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121 atagggaggg cagtaatccc tactgtcac acaaatagtg aaattcggtc tggggttatt
181 ccaattgtgc sgattatatg aatgtgtga aataaatgtg aataaatgta ctgtgctaata atgatagga
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541 ttgtaagtttc aatgggatgt tggggttatt cgccttcgg tcaatattat ccgagttttaat
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661 ttatatattt atatagtttt ttataaaa

//
Catamarius brevipennis cytochrome oxidase subunit I-like gene, partial sequence; mitochondrial

GenBank: KF056931.1

References:

1. Ambrose, D.P., Manimuthu, M., Kiruba, A.D. and Lenin, A.E.

JOURNAL: Submitted (17-May-2013) Entomology Research Unit, St. Xavier's College, Palayamkottai, Palayamkottai, Tamil Nadu 627002, India

#Assembly-Data-START#

Sequencing Technology :: Sanger dideoxy sequencing

#Assembly-Data-END#

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121 aataggaggg cagtaattcc tactgatcat acaaatagtg gaattcgttc tggggttatt
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301 ttgcttgata gggggggata aactgttcat ccagttcctg cccctctttc tacaattcta
361 ctgatgaaga acaaggttaa tgatggtgga agtaatcaga atcttatatt atttatctgt
421 gggaatgcca tgtctggggc tccaatcatt aatgggacaa gtcagttccc aaaacctcca
481 attataatag gcataactat aaagaatat aatgatggaat atgggcgcgt tactactaca
541 ttgtaagttt ggtcatctcc aatgaaagat cctggttgtc ctaattcaat tcgaattaat
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Ectomocoris tibialis cytochrome oxidase subunit I-like gene, partial sequence; mitochondrial

GenBank: KF056932.1

FASTA Graphics

LOCUS KF056932 664 bp DNA linear INV 01-JUL-2013
DEFINITION UNVERIFIED: Ectomocoris tibialis cytochrome oxidase subunit I-like gene, partial sequence; mitochondrial.
ACCESSION KF056932
VERSION KF056932.1 GI:514830661
SOURCE mitochondrion Ectomocoris tibialis
ORGANISM Ectomocoris tibialis
  Eukaryota; Metazoa; Ecdysozoa; Arthropoda; Hexapoda; Insecta;
  Pterygota; Neoptera; Heteroptera; Cimicomorpha; Reduviidae;
  Peiratinae; Ectomocoris.
REFERENCE 1 (bases 1 to 664)
AUTHORS Ambrose,D.P., Manimuthu,M., Kiruba,A.D. and Lenin,A.E.
TITLE Direct Submission
JOURNAL Submitted (17-MAY-2013) Entomology Research Unit, St. Xavier's College, Palayamkottai, Palayamkottai, Tamil Nadu 627002, India

FEATURES Location/Qualifiers
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  121 actgcccccag cctctgatct atctactctctt atatgtacat aatgagtccagtatggttcat
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  241 acacataagatt ctcttttactact cccctgtaa taggatatggtg gataaaat
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  661 cggt

//
Ectomocoris cordiger cytochrome oxidase subunit I-like gene, partial sequence; mitochondrial

GenBank: KF056933.1

FASTA Graphics

LOCUS       KF056933       661 bp    DNA     linear   INV 01-JUL-2013
DEFINITION Ectomocoris cordiger cytochrome oxidase subunit I-like gene, partial sequence; mitochondrial.
ACCESSION KF056933
VERSION     KF056933.1  GI:514830662
SOURCE      mitochondrion Ectomocoris cordiger
ORGANISM    Ectomocoris cordiger
            Eukaryota; Metazoa; Ecdysozoa; Arthropoda; Hexapoda; Insecta;
Pterygota; Neoptera; Paraneoptera; Hemiptera; Euhemiptera;
Heteroptera; Panheteroptera; Cimicomorpha; Reduviidae;
Peiratinae; Ectomocoris.
REFERENCE   1  (bases 1 to 661)
AUTHORS     Ambrose,D.P., Manimuthu,M., Kiruba,A.D. and Lenin,A.E.
TITLE       Direct Submission
JOURNAL     Submitted (17-MAY-2013) Entomology Research Unit, St. Xavier's
            College, Palayamkottai, Palayamkottai, Tamil Nadu 627002, India

FEATURES             Location/Qualifiers
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Ectomocoris quadriguttatus cytochrome oxidase subunit I-like gene, partial sequence; mitochondrial

GenBank: KF056934.1

FASTA Graphics

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LOCUS       KF056934             649 bp    DNA     linear   INV 01-JUL-2013
DEFINITION  Ectomocoris quadriguttatus cytochrome oxidase subunit I-like gene, partial sequence; mitochondrial.
ACCESSION   KF056934
VERSION     KF056934.1  GI:514830663
SOURCE      mitochondrion Ectomocoris quadriguttatus
ORGANISM    Ectomocoris quadriguttatus
            Eukaryota; Metazoa; Ecdysozoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Paraneoptera; Hemiptera; Heteroptera; Panheteroptera; Cimicomorpha; Reduviidae; Peiratinae;Ectomocoris.
REFERENCE   1  (bases 1 to 649)
AUTHORS     Ambrose,D.P., Manimuthu,M., Kiruba,A.D. and Lenin,A.E.
TITLE       Direct Submission
JOURNAL     Submitted (17-MAY-2013) Entomology Research Unit, St. Xavier's College, Palayamkottai, Palayamkottai, Tamil Nadu 627002, India

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