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COMPARATIVE STUDIES ON 12S AND 16S MITOCHONDRIAL rDNA SEQUENCES IN PENTATOMOMORPHAN BUGS (HEMIPTERA: HETEROPTERA: PENTATOMOMORPHA)

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ABSTRACT: Nucleotide sequences of the mitochondrial 12S and 16S ribosomal RNA gene fragments (12S rDNA and 16S rDNA) of twenty species of Pentatomomorpha and a single out-group species (i.e. Triatoma dimidiata, representing the infraorder Cimicomorpha) have been determined. Their nucleotide composition, substitution patterns and nucleotide divergence were investigated. To evaluate the usefulness of the 12S rDNA and 16S rDNA sequences for phylogenetic inference, the obtained data sets were analyzed using different methods (MP, ME, NJ, Bayesian estimation). The average A + T contents in studied species were as high as in other previously investigated Heteroptera (above 75%), except for the Aradidae where the A + T content for 12S and 16S rDNA fragments were below 70%. The A/G and T/C transition biases found in both rDNA fragments agreed with the observations suggesting that the transitional substitutions occur more readily than transversional substitutions; however, the observed A/T transversion frequency in the 16S rDNA of Pentatomomorpha was distinctly lower (18.78%) than that found in cimicomorphan Anthocoridae (54.52%). Undirectional nucleotide pair frequencies, in 12S rDNA and 16S rDNA fragments increase linearly with an increase in taxonomic level indicating that the rate of nucleotide substitutions is constant along studied taxonomic levels. Results of our studies suggested that the nucleotide sequences of 12S and 16S rDNA fragments can be regarded as a good marker for resolving the phylogeny of closely related genera. Moreover, it was found that the Bayesian inference analysis of the combined 12S/16S rDNA dataset appears to be the most appropriate method for phylogenetic reconstructions in Pentatomomorpha when the mitochondrial ribosomal RNA genes are used.

KEY WORDS: Hemiptera, Heteroptera, Pentatomomorpha, mitochondrial DNA, nucleotide sequences, nucleotide substitutions, nucleotide divergence, molecular phylogeny, 12S rDNA, 16S rDNA, Bayesian estimation.

Introduction

Insect mitochondrial genome consists of 13 protein-coding genes (PCGs), 22 transfer RNA genes and two ribosomal RNA genes (i.e., 12S rDNA and 16S rDNA); it contains also a major non-coding region called the control region or A+T-rich region (Simon et al. 1994, Boore 1999, Wolstenholme 1992, Li et al. 2009).

In recent years, different regions of the mtDNA (including the 12S rDNA and 16S rDNA subunits) have been regarded as good molecular markers for phylogenetic inference (for a review, see, e.g., Simon et al. 2006, Vogler and Monaghan 2007, Bybee et al. 2010).

The 12S rDNA, was initially regarded to be highly conserved and has mostly been applied to understand the genetic diversity and phylogeny at higher taxonomic levels, such as in phyla, classis and orders, whereas the 16S rDNA was very often used in studies at the familial and generic level (for a review, see, e.g., Simon et al. 1994, Gerber et al. 2001). However, in insects, these gene fragments have been proved informative also in species-level studies (e.g., Kambhampati 1995, Shawn 1996, Dopman et al. 2002, Saux et al. 2003, Yoshizawa and Johnson 2003, Cook et al. 2004, Nagaraja et al. 2004, Mahendran et al. 2006, Liu et al. 2008), or even in intraspecific investigations (Johnson et al. 2004).

However, in Heteroptera, those two fragments of mtDNA have only been sporadically used in phylogeographic and phylogenomic studies, i.e., 16S in Triatominae of Reduviidae (Hypša et al. 2002, Silva de Paula et al. 2007) and in Pentatomoidea (Li et al. 2006, Grazia et al. 2008), and 12S only in Triatominae of Reduviidae (Hypša et al. 2002).

Many studies have suggested that nucleotide composition and substitution biases in mitochondrial DNA may affect the final results of phylogenomic analyses (e.g., Simon et al. 1994, 2006, Lockhart et al. 1994, Dowton and Austin 1995, 1997, Mindell and Thacker 1996). Therefore, it appears important to define the suitability of the nucleotide sequences for the phylogeny of certain insect taxa.

Such comparative studies on the characterization of the mitochondrial rDNA sequences have almost been neglected in Heteroptera. The nucleotide composition, substitution patterns and nucleotide divergence of the 16S rDNA sequences were determined only in eight species of the family Anthocoridae (Muraji et al. 2000). In a single paper (Hua et al. 2008) the complete (or nearly complete) mt-genomes of fifteen heteropteran species were analyzed with respect to their genome organization and gene rearrangement, but with no special attention to both ribosomal RNA genes.

Since no other heteropteran mitochondrial rDNA sequences have been characterized yet, we decided to investigate the mitochondrial 12S and 16S rDNA sequences of the heteropteran infraorder Pentatomomorpha, and provide the analyses of

their nucleotide composition, nucleotide divergence and base substitutions, as well as to evaluate their phylogenetic utility.

Material and methods

The species used in this study are listed in Table 1. In total, 20 species representing 14 families and five superfamilies of the infraorder Pentatomomorpha, and a single outgroup species (i.e. *Triatoma dimidiata*, representing the infraorder Cimicomorpha) were analyzed.

Table 1. Details of specimens of Pentatomoidea used in comparative and phylogenetic analyses

	species	GenBank (NCBI) accesion numbers				
	PENTATOMOMORPHA	128	16S	Complete mt-genome		
	ARADOIDEA					
	ARADIDAE					
1.	Neuroctenus parus Hsiao	-	-	NC_012459.1		
	COREOIDEA					
	ALYDIDAE					
2.	Riptortus pedestris (Fabricius)	-	-	EU427344.1		
	COREIDAE					
3.	Hydaropsis longirostris (Hsiao)	-	-	EU427337.1		
	RHOPALIDAE					
3.	Rhopalus latus (Jakovlev)	-	-	EU427333.1		
4	Stiatonlaumus subviridis Usino			[as Aeschyntelus notatus Hsiao]		
4.		-	-	NC_012000.1		
	REDVTIDAE					
5	BERTIIDAE			EU/27246 1		
5.		-	-	EU427540.1		
6	Geocoris pallidinamis (A. Costa)			NC 012424 1		
0.	LVGAFIDAE	-	-	NC_012424.1		
7	Luganus aquestris (Linnanus)	1023/067	1023/072			
7.	MALCIDAE	JQ254707	JQ234772	-		
8	Malcus inconspicuous Štys			FU/27330 1		
о.		-	-	L0427559.1		
	CYDNIDAE					
0	CIDNIDAE Schirus luctuosus Mulsont at Pay	10234068	1023/073			
9.	Sentrus tuctuosus Mutsant et Rey	JQ254908	JQ234973	-		
10	. Macroscytus gibbulus (Ellenrieder)	-	-	NC_012457.1 [as <i>Macroscytus subaeneus</i> (Dallas)]		

PLATASPIDAE

11. Coptosoma bifarium Montandon	-	-	NC_012449.1
12. Megacopta cribraria (Fabricius)	-	-	NC_015342.1
SCUTELLERIDAE			
13. Eurygaster testudinaria (Geoffroy)	JQ234969	JQ234974	-
PENTATOMIDAE			
14. Antheminia lunulata (Goeze)	JQ234970	JQ234975	-
15. Carpocoris purpureipennis (De Geer)	JQ234971	JQ234976	-
16. Halyomorpha halys (Stål)	-	-	NC_013272.1
17. Nezara viridula (Linnaeus)	-	-	NC_011755.1
PYRRHOCOROIDEA			
LARGIDAE			
18. Physopelta gutta (Burmeister)	-	-	EU427343.1
PYRRHOCORIDAE			
19. Dysdercus cingulatus (Fabricius)	-	-	EU427335.1
CIMICOMORPHA			
REDUVIOIDEA			
REDUVIIDAE			
20. Triatoma dimidiata (Latreille)	-	-	NC_002609.1

The partial mtDNA sequences (12S and 16S rDNA) of four pentatomoid and one lygaeoid species were analyzed (see Table 2); their nucleotide sequence data were submitted to GenBank (the accession numbers are listed in Table 1 and Table 2). All other sequences used in our study were obtained directly from GenBank (Table 1). For a question of proper identification of *Macroscytus subaeneus*, the only named species of the family Cydnidae placed into GenBank database (see Lis J.A. and Lis B.2011).

Specimens of all studied species were collected directly in pure ethanol (for collecting data, see Table 2). DNA extraction, purification and amplification were performed at the Centre for Biodiversity Studies (Department of Biosystematics, Opole University, Poland) using techniques described by Lis J.A. et al. (2011). All primer sequences used for their PCR amplification are also listed in Lis J.A. et al. (2011). The remains of the studied specimens were inserted in tubes with 96% ethanol and lodged in a deep freezer (for the Opole University sample numbers, see Table 2). Sequencing was conducted at the Health Care Centre GENOMED (Warsaw, Poland).

Sequence alignments were made with Clustal X (using default parameters) in MEGA 4.0.2 software (Tamura et al. 2007, Kumar et al. 2008). The obtained sequences were used in BLAST searches, which showed their high similarities to sequences of other pentatomomorphan species (this procedure ensured our results were not contaminants).

Table 2. Details of specimens of Lygaeoidea and Pentatomoidea used for comparative and phylogenetic analyses (stored at the Center for Biodiversity Studies, Department of Biosystematics, Opole University, Poland)

	Superfamily/ family/ species	subunit	Locality data	GenBank (NCBI) accesion numbers	Opole University sample number
LY	GAEOIDEA				
LY	GAEIDAE				
1.	Lygaeus equestris (Linnaeus)	12S	Štramberk, NE Moravia,	JQ234967	ES2
		16S	Czech Republic, 2010	JQ234972	
PEN	JTATOMOIDEA				
CYI	DNIDAE				
2.	Sehirus luctuosus Mulsant et Rey	12S	Suchy Bór n. Opole,	JQ234968	3P1
		16S	Lower Silesia, Poland, 2009	JQ234973	
SCU	JTELLERIDAE				
3.	Eurygaster testudinaria (Geoffroy)	12S	Łagów, Wielkopolsko-	JQ234969	86ET
		16S	Kujawska Lowland, Poland, 2009	JQ234974	
PEN	JTATOMIDAE				
4.	Antheminia lunulata (Goeze)	12S	Szaniec n. Busko Zdrój,	JQ234970	125C
		16S	Małopolska Upland, Poland, 2010	JQ234975	
5.	Carpocoris purpureipennis (De Geer)	12S	Suchy Bór n. Opole,	JQ234971	122CP
	-	16S	Lower Silesia,	JQ234976	
			Poland, 2007		

The nucleotide composition, substitution patterns and nucleotide divergence were calculated in MEGA 4.0.2 (Tamura et al. 2007, Kumar et al. 2008). The pattern of nucleotide substitutions was estimated using Maximum Composite Likelihood (Tamura et al. 2004). All positions containing gaps and missing data were eliminated from the datasets (Complete-deletion option). The overall transition/transversion bias (*R*) was calculated for each data set, where $R = [A*G*k_1 + T*C*k_2]/[(A+G)*(T+C)]$ (Tamura et al. 2004).

Phylogenetic analyses using maximum parsimony (MP), minimum evolution (ME) and neighbor-joining (NJ) approaches were performed using MEGA 4.0.2 software (Tamura et al. 2007, Kumar et al. 2008).

It was recently suggested (e.g., Li et al. 2006, Hahn 2007, Ronquist and Deans 2010, Rasmussen and Kellis 2011) these methods frequently make reconstruction errors and can be not sufficiently accurate for systematic use. Therefore, in order to avoid the possible effect of gene duplication and loss events on our inferences, the phylogenetic trees of Pentatomomorpha were also calculated using the Bayesian estimation. Bayesian inferences (BI) trees (inferred from separate and combined data set) were obtained with MrBayes v. 3.2 (Ronquist et al. 2011) using the Markov Chain Monte Carlo technique (MCMC).

We chose the evolutionary model GTR + I + Γ (nst=6), and each run lasted for 1,000,000 generations with a sampling frequency every 100th generation, giving 10,000

samples. MCMC sampling was used with a Metropolis coupling set to use four Markov chains (three heated and one cold chain) with a starting temperature of 0.1 (default in MrBayes v.3.2). Burning percentage was set to default, discarding the first 25% of the samples from the cold chain. After 1,000,000 generations, the standard deviations of split frequencies were <0.005 for 12S, 16S and combined 12S/16S analyses.

All trees for MP, ME and NJ were edited using MEGA 4.0.2 (op. cit.); all BI trees were edited using FigTree 1.3.1 (Rambaut 2009).

Results and discussion

Nucleotide alignment. We obtained 376-base pair long sequences for the 3' end of the 12S rDNA (Fig. 1) and 428-base pair long sequences for the 3' end of the 16S rDNA (Fig. 2).

In the 12S rDNA sequences – 122 conserved sites, 242 variable sites, 173 parsimonyinformative sites and 64 singleton sites were detected, while in 16S rDNA sequences – 161 conserved sites, 262 variable sites, 209 parsimony-informative sites and 53 singleton sites were detected. Our results suggest that in Pentatomomorpha the 16S rDNA sequences are a little more conserved than the 12S rDNA sequences (38.6% for conserved sites in the 16S sequences; 33.8% for conserved sites in the 12S sequences). These results are contrary to those regarding the 12s rDNA sequences highly conserved in insects, and useful for understanding the genetic diversity and phylogeny only at higher taxonomic levels. Additionally, when the variable sites of the 16S rDNA sequences of our twenty species of Pentatomomorpha are compared to those of eight species of the family Anthocoridae representing Cimicomorpha (Muraji et al. 2000), it can be supposed that the 16S rDNA sequences are more conserved in Cimicomorpha than they are in Pentatomomorpha (variable sites: 44.0% in Anthocoridae, 60.3% in studied Pentatomomorpha).

Nucleotide composition. The average A + T contents in studied species of Pentatomomorpha were 76.1% and 75.1%, for the 12S rDNA and16S rDNA, respectively (Table 3 and 4). The similar high A + T content in the 16S rDNA was observed also in other Heteroptera (Muraji et al. 2000; Hua et al. 2008; Lee et al. 2009; Li, Liu et al. 2011; Li, Gao et al. 2011). Only in *Neuroctenus parus* (Aradidae) the A + T content was distinctly lower than in other pentatomomorphan bugs (68.2% for12S rDNA, 69.4% for 16S rDNA). Such low A + T content was noticed in Aradidae also by Hua et al (2008). The fact of low A + T content may validate the isolated position of the family Aradidae within this infraorder (this family is sometimes regarded as not belonging to Pentatomomorpha, but constituting a separate infraorder within the suborder Heteroptera (see Sweet 2006).

Taxon	Nu	Nucleotide frequencies (in %)				
	Т	С	А	G	(bp)	
Neuroctenus parus (Aradidae)	27.8	20.7	40.4	11.1	324	
Riptortus pedestris (Alydidae)	30.9	16.4	44.8	7.9	330	
Hydaropsis longirostris (Coreidae)	30.3	16.1	45.5	8.2	330	
Rhopalus latus (Rhopalidae)	33.5	13.6	45.1	7.7	337	
Stictopleurus subviridis (Rhopalidae)	31.1	14.8	44.9	9.2	325	
Yemmalysus parallelus (Berytidae)	32.8	13.6	45.5	8.1	332	
Geocoris pallidipennis (Geocoridae)	32.3	15.9	43.7	8.1	334	
Lygaeus equestris (Lygaeidae)	31.8	14.7	45.3	8.3	327	
Malcus inconspicuus (Malcidae)	32.7	14.5	43.6	9.1	330	
Sehirus luctuosus (Cydnidae)	32.6	16.3	42.4	8.6	337	
Macroscytus gibbulus (Cydnidae)	32.1	14.6	44.1	9.2	349	
Coptosoma bifarium (Plataspidae)	33.5	15.7	41.5	9.2	337	
Megacopta cribraria (Plataspidae)	29.9	17.2	44.1	8.8	331	
Eurygaster testudinaria (Scutelleridae)	31.7	15.0	44.3	9.1	341	
Antheminia lunulata (Pentatomidae)	33.3	14.6	44.3	7.7	336	
Carpocoris purpureipennis (Pentatomidae)	33.1	13.9	44.4	8.6	338	
Halyomoropha halys (Pentatomidae)	32.6	14.2	45.1	8.1	344	
Nezara viridula (Pentatomidae)	32.9	14.2	45.1	7.8	346	
Physopelta gutta (Largidae)	29.3	16.7	45.1	9.0	335	
Dysdercus cingulatus (Pyrrhocoridae)	34.0	13.1	44.5	8.4	335	
Average for Pentatomomorpha	31.9	15.3	44.2	8.6	334.9	
<i>Triatoma dimidiata</i> (Reduviidae) [Cimicomorpha]	31.5	20.1	38.3	10.2	324	
Average for Heteroptera	31.9	15.5	43.9	8.7	334.4	

Table 3. Nucleotide content of the 12S rDNA sequences of 21 species used in this study

Taxon	Nu	Total			
1 22011	Т	С	А	G	(bp)
Neuroctenus parus (Aradidae)	27.4	19.7	42.0	10.9	402
Riptortus pedestris (Alydidae)	33.9	14.1	41.8	10.1	404
Hydaropsis longirostris (Coreidae)	32.4	16.2	42.4	9.0	401
Rhopalus latus (Rhopalidae)	33.4	16.0	41.0	9.6	407
Stictopleurus subviridis (Rhopalidae)	32.3	15.1	43.4	9.2	403
Yemmalysus parallelus (Berytidae)	35.4	12.7	41.6	10.2	401
Geocoris pallidipennis (Geocoridae)	34.5	14.5	41.8	9.3	400
Lygaeus equestris (Lygaeidae)	33.6	13.5	44.9	8.0	399
Malcus inconspicuus (Malcidae)	31.8	14.3	44.5	9.5	400
Sehirus luctuosus (Cydnidae)	35.8	13.9	42.3	8.0	411
Macroscytus gibbulus (Cydnidae)	32.0	16.1	42.7	9.3	410
Coptosoma bifarium (Plataspidae)	31.0	17.4	39.7	11.9	403
Megacopta cribraria (Plataspidae)	28.0	16.6	44.3	11.1	404
Eurygaster testudinaria (Scutelleridae)	32.2	16.7	42.3	8.8	407
Antheminia lunulata (Pentatomidae)	31.0	16.7	43.3	8.9	406
Carpocoris purpureipennis (Pentatomidae)	31.7	17.1	41.7	9.5	398
Halyomoropha halys (Pentatomidae)	33.9	15.5	41.8	8.8	407
Nezara viridula (Pentatomidae)	32.8	14.8	43.7	8.6	405
Physopelta gutta (Largidae)	32.0	15.8	43.3	9.0	400
Dysdercus cingulatus (Pyrrhocoridae)	36.4	13.9	42.3	7.4	404
Average for Pentatomomorpha	32.6	15.5	42.5	9.4	403.6
<i>Triatoma dimidiata</i> (Reduviidae) [Cimicomorpha]	29.8	17.8	43.0	9.5	400
Average for Heteroptera	32.4	15.6	42.6	9.4	403.4

Table 4. Nucleotide content of the 16S rDNA sequences of 21 species used in this study

Nucleotide substitutions (Table 5 and 6). There were a total of 285 positions in the final 12S rDNA dataset, and 342 positions in the final 16S rDNA dataset. The nucleotide frequencies are 0.438 (A), 0.309 (T/U), 0.159 (C), and 0.094 (G) in the 12S rDNA sequences, and 0.396 (A), 0.324 (T/U), 0.173 (C), and 0.106 (G) in the 16S rDNA sequences. The transition/transversion rate ratios are $k_1 = 1.965$ (purines) and $k_2 = 2.278$ (pyrimidines) for 12S rDNA, and $k_1 = 1.6$ (purines) and $k_2 = 2.077$ (pyrimidines) for 16S

rDNA. The overall transition/transversion bias (R) is similar for both studied gene fragments, i.e., 0.485 for 12S rDNA and 0.494 for 16S rDNA. Strong A/G and T/C transition biases were found in both rDNA fragments (25.4% and 25.96%, respectively, in 12S rDNA; 20.96% and 26.91%, respectively, in 16S rDNA) what agrees with observations suggesting that the transitional substitutions occur more readily than transversional substitutions (Brown et al. 1979; Kondo et al. 1993). However, our results relating to the frequency of nucleotide substitutions in 16S rDNA fragments among species of Pentatomomorpha stay in contradiction with the frequency among eight species of Anthocoridae – see, Table 6 in the present study, and the Table 3 in Muraji et al. (2000). Moreover, a very high A/T transversion frequency (54.52%) and a zero G/C transversion frequency in the sequences of 16S rDNA among species of Anthocoridae (Muraji et al. 2000) were not observed among species studied by us (transversion frequency 18.78%, 7.28%, respectively). This may suggest diverse transitional and transversional biases in the mitochondrial rDNA sequences in different infraorders of Heteroptera.

Table 5. Frequency of nucleotide substitutions in the 12S rDNA sequences among studied species of Pentatomomorpha. Each entry shows the probability of substitution from one base (row) to another base (column) instantaneously. Rates of different transitional substitutions are shown in bold and those of transversional substitutions are shown in italics

	Α	Т	С	G
А	-	7.52	3.87	4.49
Т	10.64	-	8.82	2.29
С	10.64	17.14	-	2.29
G	20.91	7.52	3.87	-

Table 6. Frequency of nucleotide substitutions in the 16S rDNA sequences among studied species of Pentatomomorpha. Each entry shows the probability of substitution from one base (row) to another base (column) instantaneously. Rates of different transitional substitutions are in bold and those of transversional substitutions are in italics

	Α	Т	С	G
А	-	8.45	4.51	4.43
Т	10.33	-	9.37	2.77
С	10.33	17.54	-	2.77
G	16.53	8.45	4.51	-

Nucleotide divergence. The pairwise comparisons were made between sequences on three different taxonomic levels (Table 7), i.e., between pairs of genera representing the same family, between families (pairs of genera representing different families within the

same superfamily), and between superfamilies (pairs of genera representing different superfamilies within the same suborder). Our studies showed that undirectional nucleotide pair frequencies, in 12S rDNA and 16S rDNA fragments, increased linearly with an increase in taxonomic level (from genera to superfamilies). These results stay in accordance with results of study on the 16S rDNA in Anthocoridae (Muraji et al. 2000), where also no plateau has been observed in the frequency of base substitutions within the studied taxa.

Pairwise comparisons between:	12S	rDNA	16S rDNA		
	mean	minmax	mean	minmax.	
Genera	1/1 8	96209	15.0	11 / 10 0	
(within the same family)	14.0	9.0-20.9	15.9	11.4-19.9	
Families	18 /	10.0-24.7	19.8	14 7-24 4	
(within the same superfamily)	10.4	10.0-24.7	17.0	14.7-24.4	
Superfamilies	26.3	18 3-31 8	25.4	19.0-28.3	
(within the same infraorder)	20.5	10.5 51.0	23.4	17.0 20.5	

Table 7. Percentage of nucleotide substitutions in the 12S rDNA and 16S rDNA fragments among studied species of Pentatomomorpha

Phylogenetic inference. In our studies, we found that the 12S and 16S rDNA sequences of pentatomomorphan bugs contained nucleotide composition and substitution biases, which may restrict their phylogenetic utility. To assess the usefulness of these rDNA fragments for phylogenetic inference, the obtained data sets (Figs 1 & 2) were analyzed using several widely accepted methods, i.e., maximum parsimony (MP), minimum evolution (ME) and neighbor-joining (NJ) analyses (Figs 3-4). Moreover, in order to avoid the possible effect of gene duplication and loss events on our inferences, the phylogenetic trees of Pentatomomorpha were also calculated using the Bayesian estimation (Fig. 5). In general, the nucleotide sequences of 12S and 16S rDNA fragments seem to be a good marker to resolve the phylogeny of pentatomomorphan taxa, e.g., even closely related genera (Figs 3-5), what was also confirmed for the 16S rDNA in Anthocoridae (Muraji et al. 2000). The taxa in various families and superfamilies always formed distinct clades regardless the estimation method (Figs 3-5). As the most important, only the topology of the phylogenetic tree obtained from the Bayesian inference analysis of the combined 12S and 16S rDNA dataset agreed completely with conventional classification (Table 1); the topologies of other trees only partially correspond to it. Moreover, our results are very similar to the results of the studies on complete mitochondrial genomes in Pentatomomorpha (Hua et al. 2008).

Conclusions

This was the first study to examine the nucleotide composition, substitution patterns, nucleotide divergence of the 12S and the 16S mitochondrial rDNA fragments, and their usefulness for phylogenetic inference in pentatomomorphan bugs. Our results suggest that in Pentatomomorpha:

(1) the 16S rDNA sequences are more conserved than the 12S rDNA sequences;

- (2) the average A + T contents in studied species are as high as in other previously investigated Heteroptera (above 75%), except for the Aradidae where the A + T content for 12S and 16S rDNA fragments are below 70%;
- (3) the A/G and T/C transition biases found in both rDNA fragments agree with the observations suggesting that the transitional substitutions occur more readily than transversional substitutions;
- (4) the A/T transversion frequency in the 16S rDNA is distinctly lower (18.78%) than that found in the cimicomorphan Anthocoridae (54.52%);
- (5) the undirectional nucleotide pair frequencies, in 12S rDNA and 16S rDNA fragments increase linearly with an increase in taxonomic level;
- (6) the nucleotide sequences of 12S and 16S rDNA fragments can be regarded as a good marker to resolve the phylogeny of closely related genera;
- (7) the Bayesian inference analysis of the combined 12S/16S rDNA dataset appears to be the most appropriate method for phylogenetic reconstructions when the mitochondrial ribosomal RNA genes are used.

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Figures

Fig. 1. Nucleotide sequences of 12S rDNA in species used in the study. Nucleotide identical to the reference, Neuroctenus parus, are indicated by a dot. Dashes indicate deletions

Nouroctopus parus (Aradidae)	GATAGTARCC	ATTACTTCCA	AATCOTOTTT	AATGGCCCCC	TTCCAA-	GGACC	[60]
Bintortus nedestris (Aludidae)	A AC AT	C T	T	AATAT.	AATT	CAA.ATAT	1 601
#Hydaropsis longirostris (Coreidae)	AC A AA		CA	C. TTAAATT	AAATTC-	CAAAT.AA	(601
#Phonalus latus (Phonalidae)	AT A TTA	T	Δ	C. TAAATTT	AAATCCA	AATAAAT.TA	1 601
Stictopleurus subviridis (Rhonalidae)	т д дд			ATAAGTA	TTACAT	A	601
#Yemmalysus parallelus (Berytidae)	A.A.AAAG	тт.	т	.C-AATTTT.	A TTC	AAA AT	601
(Geocoris nallidinannis (Geocoridae)	A AATCAA	C	AC.	C ATATTAT	A A.C	ATA TA	1 601
#Lygaeus equestris (Lygaeidae)	A A AA	T		C-CATTTATG	ATA	TA-TAA	r 601
#Malcus inconspicuus (Malcidae)		TT.		C. AA. TAAT	AATAC	CTATT	[60]
#Sebirus luctuosus (Cydnidae)	T A TAA			C AAT	TT.TT	TACAGTT	[60]
#Macroscytus gibbulus (Cydnidae)	T TA GTA			C. AAGTA	AAA.TT	CACTACTT	601
#Coptosoma bifarium (Plataspidae)	TATAA	A.T	A	C.ATTA	ATT.T	AAAAT.T	[60]
#Megacopta cribraria (Plataspidae)	T A AT		A	CTTA	ATA	TACATAT.T-	[601
#Eurygaster testudinaria (Scutelleridae)	CATTT	A		C A. GAATA	ATACAATT	TATTACCT.T	[60]
#Antheminia lunulata (Pentatomidae)	TAC.T	AATT.		T.AT-AATA	AATA	TAAATAT	[60]
#Carpocoris purpureipennis (Pentatomidae)	TA TA.	AATT.		C. AT-AGTG	AATA	CATCTAT	[60]
#Halvomoropha halvs (Pentatomidae)	TTTT.	AATT.		AA-ATTA	AT.CA	TAAAT-T	[60]
<pre>#Nezara viridula (Pentatomidae)</pre>	T	AT.		C AA-AGTA	AAT A	TACTTAT	[60]
#Physopelta gutta (Largidae)		TG.T	AC	CATATATA	A.TC	ATAA.TA	[60]
#Dysdercus cingulatus (Pyrrhocoridae)	CTAA	TTT.	T	ATAAAAT	ATT	TAAT.AG	[60]
#Triatoma dimidiata (Reduviidae)	TAGAA	GCT		C.AATATT	.TCAT	T	[60]
#Neuroctenus parus (Aradidae)	AACCCAATTA	TACAAA	AACTGTAA	CCCATCATCA	CCTTCTGCAC	TG-CTGCACC	[120]
#Riptortus pedestris (Alvdidae)		TTCA	TT	TCA.	TACT.T	AA	[120]
#Hydaropsis longirostris (Coreidae)		T AA	TT	TTCA.	ATAAT.T	AT	[120]
#Rhopalus latus (Rhopalidae)	A.	T CA	TT	TCA.	TAAT.T	AT	[120]
#Stictopleurus_subviridis_(Rhopalidae)	AT.C.CA.	TA-	-TT.A	AT.	TAAT.T	A	[120]
#Yemmalysus_parallelus_(Berytidae)	TTTTTG.	TCT	TT	A.AA.	.TTAAT.T	AA	[120]
#Geocoris pallidipennis (Geocoridae)	T.G.A.	TCA	TTA	TTCA.	C.T.AT	AA	[120]
#Lygaeus_equestris_(Lygaeidae)	.TTT.C.A.T	TCA	TAA	T TTCA.	AAAAT.T		[120]
#Malcus_inconspicuus_(Malcidae)	TTA.	T.C.AA	TT	TTCA.	TAAA.T	A	[120]
#Sehirus luctuosus (Cydnidae)	ATTC. AAG	.TATA	-CC.A	TCAT	C.TAA	A	[120]
#Macroscytus gibbulus (Cydnidae)		.TA.AC	TT	TTCA.	C.TA.T	A	[120]
#Coptosoma bifarium (Plataspidae)	AT.CA.	.TTTAT	-TT.A	TGA.	C.TAAT.T	AG	[120]
#Megacopta cribraria (Plataspidae)	.GAT.CA.	.TACA	-T.A	TCT.	CCTACT.T	A	[120]
#Eurygaster testudinaria (Scutelleridae)	A.	.TATA.G	-T.A	TCAT	TAAT.T	AA-T	[120]
#Antheminia lunulata (Pentatomidae)		.TA.ATA-	TT	TTCT.	C.TCAT.A	A	[120]
#Carpocoris purpureipennis (Pentatomidae)	TTA.	ATATA-	TT	TTCA.	CAA.T	A	[120]
#Halyomoropha halys (Pentatomidae)	A.	. AATA A-	TTA	TTCA.	T.C.T.AT	AAG	[120]
#Nezara viridula (Pentatomidae)	A.	.AATAAA	TT	TTCA.	A.C.T.AT.T	AA	[120]
#Physopelta gutta (Largidae)	T.TCA.	GTA.TAA	CT	TCA.	TAAT.T	A	[120]
<pre>#Dysdercus_cingulatus_(Pyrrhocoridae)</pre>	A.	TCA	TTA	TTCA.	TAAT.T	AA	[120]
#Triatoma_dimidiata (Reduviidae)	T.TTAA.	T.CA	TT	TC.TC-T	TTACT	A	[120]
#Neuroctenus_parus_(Aradidae)	TTGACCTARA	ATATTACA	74	-AAATGAATT	AAGAAAATAA	CCCTA	[180]
#Neuroctenus_parus_(Aradidae) #Riptortus_podostris_(Alydidae)	TTGACCTAAA G.C	ATATTACA TAATT.	7A	-AAATGAATT TTA.TAA	AAGAAAATAA	CCCTA	[180] [180]
#Keuroctenus_parus_(Aradidae) #Riptortus_pedestvis_(Alydidae) #Mydaropsisi_dongivostvis_(Coreidae)	TTGACCTAAA G.C G.C	ATATTACA TAATT. TCATT.	7A A A	-AAATGAATT TTA.TAA T.GA.TAA	ААДАААТАА T CT	CCCTA	[185] [185] [185]
MNeuroctenus_parus_(Aradidae; #Riptortus_pedestris_(Alydidae) #Mydaropsis_longirostris_(Corecidae) #Rhopalus_latus_(Rhopalidae)	TTGACCTAAA G.C G.C G.C	ATATTACA TAATT. TCATT. TAATT.	7A A A	-AAATGAATT TTA.TAA T.GA.TAA TTA.T.A	AAGAAAATAA T CT	CT T T	[180] [180] [180] [180]
Mauroctenus_parus_(Aradidas;) REiptortus_podostrīs_(Alydidas) Bydaropis_longirostris_(Coreidas) REhopalus_lātus_[Neopelidas) Bšīctopievus_subvirtūs_(Neopelidas)	TTGACCTAAA G.C G.C G.C	ATATTACA TAATT. TCATT. TAATT. TAATTC	ТА А А	-XAATGAATT TTA.TAA T.GA.TAA TTA.T.A -TAA.T.	AAGAAAATAA T CT TC	CCCTA	[180] (180] [180] [180] [180]
Neuroctenus_parus_(Aradidae; Nhiptortus_pedestrig_(Alydidae) Nydarophis_longirostris_(Coreidae) Rhopalus_lotus_(Notaridae) Batictoplaurus_subvirinis_(Rhopalidae) Yermalyaus_prialblus_(Berytidae)	TTGACCTAAA G.C G.C G.C C	ATATTACA TAATT. TCATT. TAATT. TAATTC A.T-T-	7A A A	-ARATGART TTA.TAR T.G.A.TAR TTA.T.R -TA.T. TT.T.A	AAGAAAATAA T CT TC T	CCCTA T T AATTAA	[180] (180] [180] [180] [180] [180]
Neuroctenus_parus_(Aradidae; Rhitortus_pedestris_(Alydidae) Rhydarophis_longiroskris_(Coreidae) Rtictoplurus_Ubvitidis_(Rhongilidae) Vfermsiyaus_peiallelus_(Nerytidae) Vfermsiyaus_peiallelus_(Nerytidae)	TTGACCTAAA G.C G.C C C C	ATATTACA TAATT. TAATT. TAATT. TAATTC TA. CT-	7A A A	-AAATGAATT TTA.TAA T.GA.TAA TTA.T.A -TAA.T TT.T.A AT.T.A	AAGAAAATAA T CT TC TS TGATT	CCCTA T T AATTAA AATTT	[185] (185] (185] (180] (180] (180] (180]
Neuroctenus parus (Aredidae; Rhibortus pedestris (Alydidae) Rhydacopis longirostris (Coreidae) Rhopaus (Rhopaidae) Ratictoplauva_s(Rhopaidae) Recorris_Rallelus (Rherviake) Recorris_Rallidae(Rherviake) Ruyaaus_qeustris (Lygaeidae)	TTGACCTAAA G.C G.C G.C G.C G.C 	ATATTACA TAATT. TCATT. TAATTC AA.T-T- TA.C-T- AACT.	7A A A A A	-AAATGAATT TTA.TAA T.GA.TAA TTA.T.A -TAA.T TT.T.A AT.T.A A.T.A	AAGAAAATAA T CT TC T T	СССТА т т т Алттал Алттал	[185] (185] (185] (180] (180] (180] (180] (180]
Reurottenus_parus_(Aradidae; RAjptortus_pedestris_(Alydidae) Rydaropsis_longirottris_(Coreidae) Rhopa.ug_iatz_(Movpaildae) Rhopa.ug_iatz_(Movpaildae) Verma.yuus_parallelus_(Rerytidae) Recorsis_pallidipenni_(Recorridae) Rhygaus_equestris_(Lydaeidae) Masicus incomprisus_(Relidae)	TTGACCTAAA G.C G.C C C 	ATATTACA TAATT. TAATT. TAATT. TAATTC A.TT- TA.CT. AACT. TA.TT.	7A A A A A	-ARATGARTT TTA.TAR T.GA.TAR TTA.T.A -TA.T. T.T.T.A AT.T.A T T	AAGAAAATAA CT TC T TC TGATT TCC	CCCTA T T AATTAA AATTAA	(185) (183) (183) (180) (180) (180) (180) (180) (180)
Reuroctonus_paruus_(Aradidae; #Liptottus_pedegtris_(Al-Miles) #Liptottus_pedegtris_(Al-Miles) #Ropolus_latus_(Reopalidae) #Ropolus_latus_(Reopalidae) #Terma.yuus_parallelus_(Berytidae) #Terma.yuus_parallelus_(Berytidae) #Naitus_incompicus_(Malidae) #Nairus_incompicus_(Malidae)	TTGACCTAAA G.C G.C C.C T.G.C T.G.C T.G.C G.C	ATATTACA TAATT. TCATT. TAATT. TAATTC AA.T-T- TA.CT- TA.T-T. TAATT.	7A A A A A	-ARATGART TTA.TAR T.G.A.TAR TTA.T.A -TAA.T. TT.T.A A.T.A AA TAA.TA. TAA.TA.	AAGAAAATAA 	CCCTA T T AATTAA AATTT 	(182) (183) (183) (180) (180) (180) (180) (180) (180) (180)
Neuroctenus_parus_(Aradidae; Rhiptortus_pedestris_(Alydidae) Hyydaropsis_longirostris_(Coreidae) Hydarogsis_longirostris_(Coreidae) Hotparus_schriftis_(Neurolidae) Hotparus_schriftis_(Neurolidae) Hygarus_quuettis_(Hydreidae) Henirostrus_longirous_(Mairidae) Henirostrus_longirost. Marransytus_iHobuls_(Cydniae)	TTGACCTAAA G.C G.C 	ATATTACA TAATT. TAATT. TAATT. TAATTC ATT- TA.CT- TA.TT. TCATTT TCATTT	7A A A	- AAATGAATT T A. TAA T A. TAA T A. T. A T A. T T. T. A A T T T T	AAGAAAATAA T CT TC TG.ATT TCC T 	CCCTA T T ANTTAAAATTT 	[182] (182] (182] (180] (180] (180] (180] (180] (180] (180] (180]
Reuroctenus_parus_(Aradidae; Haptortus_podestris_(Alydidae) Haptortus_podestris_(Alydidae) Happoli_latus_(Nepsiliae) Hattorpievos_potritis_(Repsiliae) Verma;yuu_parallelus_(Mertidae) Habtors_potritis_(Neddad) Habtors_potritis_(Neddad) Habtorsytus_gibbulus_(Sydhidae) Hamars,Lucatus_(Sydhidae) Hamars,Lucatus_(Sydhidae)	TTGACCTAAA 	ATATTACA TAATT. CATT. TAATT. TAATTC A.T-T- TA.T-T- TA.T-T. TA.T-T. AT-TT AT-TT A.CT-TT A.CT-TT	7A A A A A A	-AAATGAACT TTA.TAA T.G. A.TAA TTA.T.A TTA.T.A ATA.T. T.T.T.A ATAA.TA TTAA.TA TTAA.TA TTAA.TAA TTA.TAA	AAGAAAATAA T CT TC TGATI TCC GT. GT.	CCCTA T T AATTAA AATTT AAATT TCTT	(180) (180) (180) (180) (180) (180) (180) (180) (180) (180) (180) (180)
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Neuroctenus_parus_(Aradidae; #Aptortus_pedestris_(Alydidae) #Aydaropuis_longirostris_(Coreidae) #Attoropiworg_obvirtis_(Drobalidae) Wrema:yuu_parallelus_(Bertvidae) Hocorsi_pallidjenni_(Gocorridae) Hocorsi_pallidjenni_(Gocorridae) Hocorsi_pallidjenni_(Gocorridae) Hocorsi_pallidjenni_(Gocorridae) Hocorsi_pallidjenni_(Gocorridae) Hocorsi_sibulis_(Cydidae) Hocorsi_sibulis_(Cydidae) Hocorsi_sibulis_(Cydidae) Hocorsi_sibulis_(Cydidae) Hocorsi_sibulis_(Cydidae) Hocorsi_sibulis_(Cydidae) Hocorsi_sibulis_(Cydidae)	TTGACCTARA G.C 	ATATTACA TAATT. TAATT. TAATT. TAATTC A.TT. AACT. TCATTT ATTT AACTT AACTT AACTT AACTT AACTT AACTT AACTT	ТА А А А А А А С С С	-ARATGARTT TTA.TAR T.G.A.TAR TTA.T.R TT.A.T. A.T.R TT.A.T. A.T.R T.AR T.A	ANGAAAATAA T TT T T T T 	CCCTA T T T AATTAA AATTT AAATT TCTT T	(185) (185) (186) (180) (180) (180) (180) (180) (180) (180) (180) (180) (180) (180) (180) (180)
Reuroctonus_perus_(Aradidae; #Liptottus_pedeguts_(Altore) #Liptottus_pedeguts_(Altore) #Ropolus_latus_(Encridae) #Ropolus_latus_(Encridae) #rema.yuus_petallelus_(Berytidae) #rema.yuus_petallelus_(Berytidae) #Naitus_latus_(Berytidae) #Naitus_Lotonus_(Edudae) #Naitus_Lotonus_(Edudae) #Mercmaytms_gibellus_(Cydidae) #Mercmaytms_gibellus_(Cydidae) #Mercmaytms_gibellus_(Cydidae) #Mercmaytms_gibellus_(Cydidae) #Mercmaytms_gibellus_(Cydidae) #Mercmaytms_gibellus_(Cydidae) #Naitus_Lotonus_(Berytma) #Mercmaytms_gibellus_(Cydidae) #Naitus_Cydidae) #Naitus_Cydidae)	TTGACCTARA 	ATATTACA TAATT. TAATT. TAATTC TAATTC TAAT-TC TATT. TATT. 	TA A A AC C C C C C C C C C C C C C C C C C C	-ARATGARCT TTA.TAR T.G.A.TAR TTA.T.N TTA.T.N TT.A ATA.T. ATA.T. ATAA.TA. ATAA.TA ATAA.TA ACA.GA ACA.GA ACA.GA.T.C TTBA.TCG	AAGAAAATAA T TT TC T TC C C CC CC CC CC	CCCTA T T AATTA AATTT TT TCT1T TCT1T TT	(185) (183) (186) (186) (180) (180) (180) (180) (180) (180) (180) (180) (180) (180) (180) (180) (180) (180) (180) (180)
Neuroctenus_paruu_(Aradidae; #Aptortus_pedestris_(Coreidae) #Mydaropsis_longicostris_(Coreidae) #Mydaropsis_longicostris_(Coreidae) #Stictopleuroj Juvicitis_(Nebpalidae) Wermaryuus_petallelus_(Merytidae) Hogoszis_gequatris_(Lyqueidae) Halcus incomprous_(Melidae) Halcus incomprous_(Melidae) Halcus incomprous_(Melidae) Halcus incomprous_(Melidae) Halcus incomprous_(Melidae) Halcus incomprous_(Melidae) Halcus incomprous_(Melidae) Halcus incomprous_(Melidae) Halcus incomprous_(Melidae) Handonnia lonclata_(Pentatomidae) Handonnia lonclata_(Pentatomidae)	TTGACCTAAA G.C G.C G.C G.C G.C G.C G.C G.C G.C G.C G.T G.C	ATATTACA TAATT. TAATT. TAATT. AATT. AACT.	ТА А А А А А А С С С С	-ARATGARCT TTA.TAR TTA.TAR TTA.T.R -TAR.T AT AA.T. TT.T.A. TT.AR.T. AA.TAR TTAR.TAR TTAR.TAR ACA.GA. AC.GA.TCA TTAR.TCA TTAR.TCA	ANGAAAATAA T TT T T 	CCCTA T T AATTAA AATTAA AATTT AAATTT TCT1T TCT1T C ATTT TT	(180) (180)
Reuroctenus_porus_(Aradidae; Alptortus_podogtris_(Al)didae) Alptortus_podogtris_(Al)didae) Alptortus_podogtris_(Al)didae) Alptortus_latus_(Berytidae) Merconzipallidpenni_(Cocorridae) Merconz_podus_(Berytidae) Merconzytus_pitaleus_(Mercidae) Merconzytus_gibbclus_(Cydnidae) Merconzytus_gibbclus_(Cydnidae) Merconzytus_gibbclus_(Cydnidae) Merconzytus_gibbclus_(Cydnidae) Merconzytus_gibbclus_(Cydnidae) Merconzytus_gibbclus_(Cydnidae) Merconzytus_gibbclus_(Cydnidae) Merconzytus_gibbclus_(Cydnidae) Merconzytus_gibbclus_(Cydnidae) Karypostar_cesculinaria_(Scutelletidae) Karpenois purpuripenia_(Peniatacnidae) Merconzelatus_diae) Merconzelatus_(Cydnidae) Merconzelatus_Cydnidae	TTGACCTAAA 	ATATTACA TAATT. TCATT. TAATTC 	TA A A A A A A A C C	- XAATGAACT TT A. TAA TT A. TAA TT A. T. A TT A. T. A TT. T. A T. T. T. T. T. T. T. A T. T. AA. TAA TT AA. TAA A CA. GA. A CA. GA. A CA. GA. TT AA. TCA TT AA. TCA TT AA. TCA TT AA. TCA	AAGAAAATAA T TC T T 	СССТА Т Р Р Р Р Р Р	(185) (185) (186) (186) (186) (186) (186) (186) (186) (186) (186) (186) (186) (186) (186) (186) (186) (187)
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Reuroctonus_psrug_[Aradidae; #Liptottus_pdotgtris_(Al_Mice) #Liptottus_pdotgtris_(Al_Mice) #Ropolus_latzs_(Rhopalidae) #Ropolus_latzs_(Rhopalidae) #Terms_ywa_pstallelus_(Berytidae) #Terms_ywa_pstallelus_(Berytidae) #Nairus_latonus_(Edhudae) #Nairus_latonus_(Edhudae) #Nairus_latonus_(Edhudae) #Nairus_latonus_(Edhudae) #Nairus_latonus_(Edhudae) #Nairus_latonus_(Edhudae) #Nairus_latonus_(Edhudae) #Nairus_latonus_(Edhudae) #Nairus_latonus_(Edhudae) #Nairus_latonus_(Edhudae) #Nairus_latonus_(Edhudae) #Nairus_latonus_(Edhudae) #Nairus_latonus_(Edhudae) #Nairus_tus_eta_tus_tus_tus_tus_tus_tus_tus_tus_tus_tus	TTGACCTAAA 6.C 	ATATTACA TAATT. TAATT. TAATTC A.T-TC A.T-TC A.C-T' A.C-T' A.C-T' A.C-T' A.CTT A.C-T' A.C.C' A.C-T' A.C-T' A.C-T' A.C-T' A.C-T' A.C-T' A.C-T' A.C-T' A.C-T' A.C-T'	TA A A A A C C C C C C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C A C C C C C C C C C C C C C C <t< td=""><td>-ARATGARCT TTA.TAR T.GA.TAR TTA.TA. A.TA.T. A.TA.T. A.TA.T. AT.T.A. AT.T.A. AT.T.A. AT.T.A. AT.T.A. ATA.TAR TCB.TAR ACRASTO TTA.T.TA TTA.T.TA A.TA.T.A. A.TA.T.A. A.TA.T.A. A.TA.T.A. A.TA.T.A.</td><td>AAGAAAATAA CT TC TGATT TCC C C C CC CT TC TC TC TC CC CT T</td><td>CCCTA T P RATTAA. AATT T AATT TCT AAATT TCT AAATT TCT AAATT AATT AATT</td><td>[185] (185] (185] (180] (180) (180) (180) (180) (180) (180) (180) (180) (180) (180) (180) (180) (180) (180) (180) (180) (180) (180) (180)</td></t<>	-ARATGARCT TTA.TAR T.GA.TAR TTA.TA. A.TA.T. A.TA.T. A.TA.T. AT.T.A. AT.T.A. AT.T.A. AT.T.A. AT.T.A. ATA.TAR TCB.TAR ACRASTO TTA.T.TA TTA.T.TA A.TA.T.A. A.TA.T.A. A.TA.T.A. A.TA.T.A. A.TA.T.A.	AAGAAAATAA CT TC TGATT TCC C C C CC CT TC TC TC TC CC CT T	CCCTA T P RATTAA. AATT T AATT TCT AAATT TCT AAATT TCT AAATT AATT AATT	[185] (185] (185] (180] (180) (180) (180) (180) (180) (180) (180) (180) (180) (180) (180) (180) (180) (180) (180) (180) (180) (180) (180)
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Reuroctonus_psrug_[Aradidae; #Liptottus_pdotgstr5; (A.1416a) #Liptottus_pdotgstr5; (A.1416a) #Ropolus_latzs_(Ropalidae) #Ropolus_latzs_(Ropalidae) #rems_ysus_pstallelus_(Berytidae) #rems_ysus_pstallelus_(Berytidae) Mairos inconspicus_(Ralidae) #Rairos (Lotonus_(Cydnudae) #Rescong.crg10ks[Ls](Solidae) #Rescong.crg10ks[Ls](Solidae) #Rescong.crg10ks[Ls](Solidae) #Rescong.crg10ks[Ls](Solidae) #Rescong.crg10ks[Ls](Solidae) #Rescong.crg10ks[Ls](Solidae) #Rescong.crg10ks[Ls](Solidae) #Rescong.crg10ks[Ls](Solidae) #Rescong.crg10ks[Ls](Solidae) #Rescong.crg10ks[Ls](Solidae) #Rescong.crg10ks[Ls](Solidae) #Rescong.crg10ks[Ls](Fertatomidae) #Rescong.crg10ks[Ls](Solidae) #Riymorgons_bilys_(Cyrifosolidae) #risions_crus_fsdotf](Solidae) #Riymorgons_psrug_(Aradidae) #Riymorgons_psrug_(Aradidae) #Riymorgons_psrug_(Aradidae) #Riymorgons_psrug_(Aradidae) #Riymorgons_psrug_(Aradidae) #Riymorgons_psrug_(Aradidae)	TTGACCTAAA 	ATATTACA TAATT. TCAT-T. TAATT. TAATT. TAATTC TAAT. TAAT. TAAT. TAAT. 	TA TA A A A A A A A A C C C C A C A C A C A A A	-ARATGARCY -ARATGARCY T A. TAA T A. TAA T A. TAA T A. T A. T A. T A. T A. T A. T A	AAGAAAATAA CT TC T TC 	СССТА Т Т ААТТАА ААТТАА 	[183] [183] [183] [180] [180] [180] [180] [180] [180] [180] [180] [180] [180] [180] [180] [180] [180] [180] [180] [180] [180] [240] [240]
<pre>Neuroctenus_parus_(Aradidae; Atytortus_pedestris_(Alydidae) Mydaroppis_[ungirostris_(Coreidae) Mydaroppis_[ungirostris_(Coreidae) Mydaroppis_ungirostris_(Coreidae) Mecorcis_pallidepnis_(Cocorridae) Hoecorcis_pallidepnis_(Cocorridae) Hoecorcis_pallidepnis_(Cocorridae) Heinirs,Locorris_(Cydindae) Hestronytus_gibbulks_(Cydindae) Hestronytus_gibbulks_(Cydindae) Hestronytus_Gibbulks_(Cydindae) Hestronytus_Cibration(FileCoreidae) Hestronytus_Cibration(FileCoreidae) Hestronytus_Cibration(FileCoreidae) Hestronytus_Cibration(FileCoreidae) Hestronytus_Cibration(FileCoreidae) Hestronytus_Cibration(FileCoreidae) Hestronytus_Cibration(FileCoreidae) Hystortus_pedestris_(Kydidae) Hystortus_pedestris_(Kydidae) Hystoroppis_ion(FileCoreidae) Hystoroppis_Congriss_Coreidae) Hysto</pre>	TTGACCTARA G.C.	ATATTA CA TAT CA TAAT CI TAAT CI TAAT CI TAAT CI TAAT CI TAA CI TA CI TA CI AA. C- CT AA CI AA CI CI CA. CI CG. C. CG. C.	ТА А А А А А С С С А С А А С А А А А	- AATGARCY - AATGARCY T A. TAA T A. TAA T A. TAA T A. TAA T AA. T. T AA. T. T	ABGAAAATAA CT TC T.TC T.T.T.T T.T.T.T.T	СССТА Т Т ААТТТАА ААТТТАА 	[185] (185] (185] (186] (180) (240)
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Reuroctenus_parus_(Aradidae; Riptortus_podestris_(Alydidae) Riptortus_podestris_(Alydidae) Riptortus_podestris_(Ripalidae) Rictorpleuro_potvricis_(Ripalidae) Resorcis_palidipensi (Recorridae) Resorcis_palidipensi (Recorridae) Resorcis_palidis_[Reduvidae) Resorcis_parus_(Aladidae) Resorcis_parus_(Aladidae) Resorcis_parus_(Aladidae) Resorcis_palidis_[Reduvidae) Resorcis_parus_(Aladidae) Resorcis_parus_(Aladidae) Resorcis_parus_(Aladidae) Resorcis_parus_(Aladidae) Resorcis_parus_(Aladidae) Resorcis_parus_(Aladidae) Resorcis_parus_(Aladidae) Resorcis_parus_(Aladidae) Resorcis_parus_(Aladidae) Resorcis_parus_(Aladidae) Resorcis_parus_(Aladidae) Resorcis_parus_(Aladidae) Resorcis_parus_(Aladidae) Resorcis_parus_Resorcis_(Respalidae) Resorcis_parus_Resorcis_(Resorcis) Resorcis_parus_Resorcis_(Respalidae) Resorcis_parus_Resorcis_(Respalidae) Resorcis_parus_Resorci	TTGACCTAAA G.C. G.C. G.C. G.C. G.C. T.G.C. T.G.C. G.C.	ATATTA CA TAAT CI TAAT CI TA	ТА ТА А. А. А. А. А. А. А. А. С. С. С. А. С. А.	- ARATGAATT - T. A. TAA T. G. A. TAA T. G. A. TAA - T. A. TA - T. A. TAA - T. A. TAAA - T. A.	AAGAAAATAA C	CCCTA T T. ANTRA ANTRA T T	[183] (183] (183] (180) (180) (240)
Response paragramma (Aradidae) Alphottus podogtris (Alydidae) Alphottus podogtris (Alydidae) Hoppolus latzs (Hoppildae) Stittoplavous jubvicis (Hoppildae) Stittoplavous jubvicis (Hoppildae) Haicus incompicus (Malidae) Haicus incompicus (Malidae) Haranowyta (Hollardae) Haranowyta (Hollardae) Hysopolla (Hollardae) Hysopolla (Hollardae) Hysopolla (Hollardae) Hysopolla (Hollardae) Hysopolla (Hollardae) Hysopolla (Hollardae) Hysopolla (Hollardae) Hysopolla (Hollardae) Hiltoplava (Hollava) Hiltoplava (Hollava) Hiltoplava (Hollava) Hiltoplava (Hollava) Hiltoplava (Hollava) Hiltoplava (Hollava) Hiltoplava (Hollava) Hiltoplava (Hollava) Hiltoplava (Hollava) Hiltoplava (Hollav	TTGACCTAAA G.C. G.C. G.C. G.C. G.C. T.G.C. T.G.C. T.G.C. G.C.	ATATTA CA TAATT. TAATT. TAATT. TAATT. TAAT. 	TA TA A A A A C A C C C A C C A C A C A C A C A C A C A C A C A C A C A A A A A A A	-ANATGART T A. TAA T A. TAA T A. TAA T A. TA T A. T. A T A. TAA T	AAGAAAAAAAA T C T T T T T TG TG TG TG TG TG TG TG T	CCCTA T AATTAA AATTAA AATT TAAAT7 TAAAT7 TAAAT7 TAAAT7 AATT AATT AATT AATT AATT AATT C C.C.C.C.C.C.C.C.C.C.C.C.C.C.C.	[183] [183] [180]
Restrictions perus [Aredides] Historius Politics [Alixidae] Historius Politics [Alixidae] Hopolus [atts [Nepslide] Hopolus [atts [Nepslide] Hopolus [atts [Nepslide] Hopolus [atts [Nepslide] Hostorius [Alixide] Hostorius [Alixide] H	TTGACCTAAA G.C. G.C. G.C. G.C. G.C. G.C. G.C. G	ATATTA CA TATT C. TAT C. 	ТА ТА А	-ARATGAAT -ARATGAAT T A. TAA T A. TAA T A. TAA T A. T. A T A. T. A	AλGAAAATAA C	СССТРА Т,Т,	(180) (180)
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Response parus (Aradidas) Aradiana (Aradidas) Aradidas) Aradidas Aradidas) Aradidas	TTGACCTARA G.C. G.C. G.C. G.C. G.C. T.G.C. T.G.C. T.G.C. G.C.	ATATTACA TAATT-A. TAATT-G. TAATT-G. TAATTG TAATTG TAATTG TAATT-TT 	TA TA A A A A A A C C C A C A C A C A C A A A A A A A A A A A A	- ARATGAACT TT A TAA T G	AAGGAAAATAA T C T C T <td< td=""><td>СССТА Т. Т. АЛТТАА. АЛТТАА. АЛТТАА. АЛТТ</td><td>[180] (180]</td></td<>	СССТА Т. Т. АЛТТАА. АЛТТАА. АЛТТАА. АЛТТ	[180] (180]
Reurotionis_porus_(Aradidae; Riptottus_podestris_(Alydidae) Riptottus_podestris_(Alydidae) Riptottus_podestris_(Rippalidae) Rictorpierus_potvricis_(Rippalidae) Resorat_politidenni (Rosoridae) Meinos incompicus_(Malidae) Meinos incompicus_(Malidae) Meinosytus_sibelus_(Sydidae) Meinosytus_sibelus_(Sydidae) Mernosytus_sibelus_(Sydidae) Mernosytus_icsuburita_(Scitelletidae) Rosponoi bays_(Pottonidae) Rosponoi bays_(Pottonidae) Ristorus_potest_ Ristorus_potest_(Ristoridae) Pristama_cionidis_(Ristoridae) Pristama_cionidist_(Ristoridae) Ristorus_podestris_(Nigdidae) Historus_podestris_(Nigdidae) Historus_podestris_(Nigdidae) Historus_podestris_(Ristoridae) Ristorus_podestris_(Ristoridae) Ristorus_podestris_(Ristoridae) Ristorus_incompicus_(Malidae) Ristorus_incompicus_incompicu	TTGACCTARA G.C. G.C. G.C. G.C. G.C. G.C. G.C. G.C	ATATTA CA 	TA TA A A A A A A A C C C C C A C C A C A C A C A C A C A	- ARATGAACT TT A. TAA TG A. TAA TG A. TAA TG A. TAA TT TA. T A	ANGGARAATAA T C T C T C T T C TG TG TG TC C TG T C T	СССТА Т. Т. Т. Т. 	[183] (183] (180]
Response paragraphic (Alydiae) Alydotta podogtris (Alydiae) Alydotta podogtris (Alydiae) Hoppicus latz, (Hoppilde) Stittplaug_abvicis(hoppilde) Haranyua patallela, (Bertidae) Haranyua patallela, (Bertidae) Haranyua (Malidae) Haranyua (Mal	TTGACCTAAA G.C. G.C. G.C. G.C. G.C. G.C. G.C. G	ATATTA CA 	TA A. A. A. A. A. A. A. COUNDACA C. A.	-ARATGAATT T A. TAA T A. TAA T A. TAA T A. TAA T A. TAA T A. TAA T A A T A A T A. TAA A A. TAA T A A. A. TAA T A. A. TAA T A A. A. TAAA T A. A. TAAA T A. A. TAAA T A	ANGAAAATAA C T C T T T C T T T T G T G T G T G T G T G T G G T T T <tr td=""> T <tr td=""> <</tr></tr>	СССТА Т. ААТТАА ААТТАА ААТТАА ААТТ АААТТ АААТТ АААТ	[180] (180]
Restrictions perus [Aredides] Restrictions [Restrict [Alpidiae] Restricting [Restrict [Alpidiae] Restrictions [Restrict [Respective] Restrictions [Source [Respective] Restrictions [Source [Restricted] Restrictions [Source [Restricted] Restrictions [Source [Restricted] Rescore [Constant] [Restricted] Rescore [Restricted] Rescore [Restricted] Rescore [Restricted] Rescore [Restricted] Rescore [Restricted] Rescore [Restricted] Rescore [Restricted] Rescore [Restricted] Restric	TTGACCTARA G.C. G.C. G.C. G.C. G.C. G.C. G.C. G.C	ATATTACA TAAT-0. TAAT-0. TAAT-0. TAA1. TAA1. TAA1. TAA1. TAA1. TAA1. TAA1. AAAAAA	TA TA A A A A A A A A A A A C A C A C A	- ANATGAACT TT A. TAA TG A. TAA TG A. TAA TG A. TAA TT TA. T A	ARGAAAATAA C	СССТА Т АЛТТАА ААТТАА ААТТТ ААТТТ АААТТ АААТТ АААТТ ААТТ АААТ АААТ	(183) (183) (180)
Response of the second	TTGACCTAAA G.C. G.C. G.C. T.G.C. T.G.C. G.C. G.C.	ATATTACA 	TA A A A A A A C C C C A C A C A C A C A	- ARATGART T A. TAA T	ANGAAAATAA T C	СССТА Т. Т. Т. 	(185) (185) (186)
Reuroctons perus Aradidas; Andreas and a second and a second and a second and a second a sec	TTGACCTAAA G.C. G.C. G.C. G.C. G.C. G.C. G.C. G	ATATTA CA CAAT ACAT CAAT ACAT 	TA A	- ANATGAACT TT A. TAA TT A. TAA TT A. T. A TT	ANGANATAN C T C T T T C T T C T T T C T C T C T C T C T T	CCCTA 	(185) (183) (180)
Response post (Algorithm (Algorithm) Response (Algorithm) Respon	TTGACCTARA G.C. G.C. G.C. G.C. G.C. G.C. G.C. G.C	ATATTACA TAAT-CI TAAT-CI TAA.C-TC AAT-T-TC AAT-T-TC AAT-T-TC AAT-T-TC AAT-TC 	TA TA A A A A A A A A C C C C A C C C A C A C A C A C A	- ARATGART T A TAA T A TAA T	ANGGAABATAA T C	СССТА Т. Т. Т. 	(185) (185) (186)
Response paragraphic (Aradidae) Alphottus podogtris (Alydidae) Alphottus podogtris (Alydidae) Hoppolus latzs (Hoppildae) Stittoplanus jubvicis (Hoppildae) Haransyna pitallelus (Bertidae) Haransyna (Malidae) Haransyna (Malidae) Haransyna (Halidae) Haransyna (Halidae) Hysgopila (Halidae) Hysgopila (Halidae) Hysgopila (Halidae) Hysgopila (Halidae) Hitoppila (Halidae) Hitop	TTGACCTAAA G.C. G.C. G.C. G.C. G.C. G.C. G.C. G	ATATTACA 	TA A A A A A A A A A A C C C C A C C C C C C A C A	- ARATGARTT TT A. JRA TT A. JRA TT A. T. A. TT A. T. A. TT A. T. A. TT A. T. A. TT T T	ABGAAATAA CT TC. TT TC. TT TC. T.C. T.C. T.C. T.C. T.C. T.C. T.C. T.C. T.T.T. T.T. T.T.T. T.T. T.T.T. T.T. T.T.T.T. T.T. T.	СССТА Т ААТТАА ААТТАА ААТТАА ААТТ ААТТ ААТТ ААТТ ААТТ ААТТ ААТТ ААТТ С. ААТТ ААТТ С. С. 	1.88.) 1.18.) 1.18.) 1.18.) 1.18.) 1.18.0 1.24.0 1.
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#Neuroctenus_parus_(Aradidae)
#Riptortus_pedestris_(Alydidae) #Hydaropsis longirostris (Coreidae) #Rhopalus_latus_(Rhopalidae) #Stictopleurus subviridis (Rhopalidae) #Yemmalysus_parallelus_(Berytidae) #Geocoris pallidipennis (Geocoridae) Geocoria_salldipennis_(Geocoridae) Evyaeua equestis_(Lyaeudae) Headinas (Cydnidae) Macrosofus gibbula_(Cydnidae) Macrosofus gibbula_(Cydnidae) Hoogacofa_cribaria_(Dataspidae) Mogacofa_cribaria_(Pentatonidae) Eurygastef_cetudinaria_(Seutelleridae) Matheminia_lumulata_(Pentatonidae) #Antheminia__Untilst__(Fentatomidae)
#Carpocoris_purpurseipennis_(Pentatomidae)
#Ralyomoropha_halys_(Pentatomidae)
#Nezara_viridula_(Pentatomidae)
#Physopelta_gutta_(Largidae)
#Dysdercus_cingulatus_(Pyrrhocoridae) #Triatoma dimidiata (Reduviidae)

#Neuroctenus parus (Aradidae) #Riptortus_pedestris_(Alydidae) #Hydaropsis_longirostris_(Coreidae) Htydropais_iongirostris_(corsidae) (
Htydropais_itus_(htydraidae)
Stciroplawrus_subviridis_(htydraidae)
Stciroplawrus_subviridis_(htydraidae)
Stciroplawrus_subviridis_(htydraidae)
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Stars_iongirus_Maicidae)
Stars_iongirus_Maicidae)
Stars_iongirus_Maicidae)
Mtegracota_cribraria_(Plataspidae)
Stars_iongirus_Stars_(Subviridiae)
Starsia_cribraria_(Plataspidae)
Starsia_cribraria_cribraria_(Plataspidae)
Starsia_cribraria_ #Halyomoropha_halys_(Pentatomidae) #Halyomoropha_halys_(Pentatomidae)
#Nezara_viridula_(Pentatomidae)
#Physopelta_gutta_(Largidae)
#Dysdercus_cingulatus_(Pyrhocoridae)
#Triatoma_dimidiata_(Reduviidae)

#Neuroctenus parus (Aradidae)	AF
<pre>#Riptortus_pedestris_(Alydidae)</pre>	
#Hydaropsis_longirostris_(Coreidae)	
<pre>#Rhopalus latus (Rhopalidae)</pre>	
#Stictopleurus subviridis (Rhopalidae)	
#Yemmalysus parallelus (Berytidae)	
#Geocoris pallidipennis (Geocoridae)	
<pre>#Lygaeus equestris (Lygaeidae)</pre>	
#Malcus inconspicuus (Malcidae)	
<pre>#Sehirus_luctuosus_(Cydnidae)</pre>	
#Macroscytus_gibbulus_(Cydnidae)	
#Coptosoma_bifarium_(Plataspidae)	
#Megacopta cribraria (Plataspidae)	
#Eurygaster_testudinaria (Scutelleridae)	
#Antheminia_lunulata_(Pentatomidae)	
<pre>#Carpocoris_purpureipennis_(Pentatomidae)</pre>	
#Halyomoropha_halys_(Pentatomidae)	
<pre>#Nezara_viridula_(Pentatomidae)</pre>	
<pre>#Physopelta_gutta_(Largidae)</pre>	
#Dysdercus_cingulatus_(Pyrrhocoridae)	
<pre>#Triatoma dimidiata (Reduviidae)</pre>	

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	.AAAT	CC	AG	A.A		T	[300]
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	.AAGAT	GC	AG	A.A	c		[300]
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	.AAAT		A.T	A.A	–		[300]
	.AAAT		AG	A.A	–	C	[300]
	.AAAT		TGA	A.A.A		GC	[300]
	.AAAT	T	AG	A.A.A.			[300]
	TAAT	T	AGG	A.A.C	C	T	[300]
	TAAT		AG	A.A	–	T	[300]
	TAAT		A.G	A.T	AT	T	[300]
	TAAAT	c	AGG	A.T	AT	T	[300]
	TAAT	C	AGG	ATA		T	[300]
	TAAT	c	AG	A.A.T		C	[300]
e)	TAAT		AG	A.A.T	A	TC	[300]
	.AAT	T	AG	A.A.T	C	T	[300]
	TAAT	c	AG	A.A.T	A	T	[300]
	. AAT AT	T	AG	A.A	–	A	[300]
	. AA AT	G	AG	A.ATA		A	[300]
	TAAC	c	AGGGA	ACA	C		[300]
	TCTTTTAATT	TAAAGATC	-TACTATTAA	TCTTAAAGGT	AAAAAT	AACAACTAC-	[360]
	A	A	TAT	.ACTGC	${\mathbb T}AA\text{-}\dots {\mathbb T}$.	TTTG-	[360]
	C	CA	та	.A.AGC	TTACT.	T TT G-	[360]
		A	та	.ATGA	$T AT \dots T$.	T.A.TTAT	[360]
	A	.TAA	TA	.ACG.T.	TT.	TTC.A-	[360]
		.TAA	TAT	AC.CGA	AA.TT	G.TC.A-	[360]
	CT	AA	та	CCGAC.	TTT.TTT.	T.ATG-	[360]
	CT	C.AGAA-A	та	AA. TGA	AACTT - A	T TC . A-	13601

CCTCGTGGCA TATCAATTAA GAAACAGGTT CCTCTGATAG GATTAAA-TT ACCGCCAAAT [300]

3601 3601 .TA....T.....G..A.-A TA..C......AA..T..-- ---ATTT..G T...TC.T-[360] 13601 [360] 13601 13601 [360] 13601 [360] 13601 13601

[376]

Fig. 2. Nucleotide sequences of 16S rDNA in species used in the study. Nucleotide identical to the reference, *Neuroctenus parus*, are indicated by a dot. Dashes indicate deletions

Neuroctenus parus (Aradidae) #Riptortus_pedestris_(Alydidae)
#Hvdaropsis longirostris (Coreidae) #Rhopalus_latus_(Rhopalidae) #Stictopleurus subviridis (Rhopalidae) #Yemmalysus_parallelus_(Berytidae) #Geocoris pallidipennis (Geocoridae) #Lygaeus_equestris_(Lygaeidae) #Malcus inconspicuus (Malcidae) #Sehirus_luctuosus_(Cydnidae) #Macroscytus_gibbulus_(Cydnidae) #Coptosoma bifarium (Plataspidae) #Megacopta_cribraria_(Plataspidae)
#Euryqaster testudinaria (Scutelleridae) #Halyomorpha_halys_(Pentatomidae) #Nezara viridula (Pentatomidae) #Physopelta_gutta_(Largidae) #Dysdercus cingulatus (Pyrrhocoridae) #Triatoma_dimidiata_(Reduviidae)

#Neuroctenus parus (Aradidae) #Riptortus_pedestris_(Alydidae)
#Hydaropsis longirostris (Coreidae) #Rhopalus_latus_(Rhopalidae)
#Stictopleurus_subviridis_(Rhopalidae) #Yemmalysus_parallelus_(Berytidae)
#Geocoris_pallidipennis_(Geocoridae) #Lygaeus_equestris_(Lygaeidae) #Malcus_inconspicuus_(Malcidae) #Sehirus_luctuosus_(Cydnidae) #Macroscytus gibbulus (Cydnidae) #Coptosoma_bifarium_(Plataspidae) #Megacopta cribraria (Plataspidae) #Eurygaster_testudinaria_(Scutelleridae) #Antheminia lunulata (Pentatomidae) #Carpocoris_purpureipennis_(Pentatomidae) #Halyomorpha halys (Pentatomidae) #Nezara_viridula_(Pentatomidae)
#Physopelta_gutta_(Largidae) #Dysdercus_cingulatus_(Pyrrhocoridae)
#Triatoma_dimidiata_(Reduviidae)

#Neuroctenus_parus_(Aradidae) #Riptortus_pedestris_(Alydidae) #Hydaropsis_longirostris_(Coreidae) #Rhopalus_latus_(Rhopalidae) #Stictopleurus subviridis (Rhopalidae) #Yemmalysus parallelus (Berytidae) #Geocoris pallidipennis (Geocoridae) #Lygaeus_equestris_(Lygaeidae) #Malcus inconspicuus (Malcidae) #Sehirus_luctuosus_(Cydnidae) #Macroscytus_gibbulus_(Cydnidae) #Coptosoma_bifarium_(Plataspidae) #Megacopta_cribraria_(Plataspidae)
#Eurygaster_testudinaria_(Scutelleridae) #Antheminia_lunulata_(Pentatomidae) #Carpocoris_purpureipennis_(Pentatomidae #Halyomorpha_halys_(Pentatomidae) #Nezara_viridula_(Pentatomidae) #Physopelta_gutta_(Largidae) #Dysdercus cingulatus (Pyrrhocoridae) #Triatoma_dimidiata_(Reduviidae)

#Neuroctenus_parus_(Aradidae) #Riptortus pedestris (Alydidae) #Hydaropsis longirostris (Coreidae) #Rhopalus_latus_(Rhopalidae)
#Stictopleurus subviridis (Rhopalidae) #Yemmalysus_parallelus_(Berytidae)
#Geocoris_pallidipennis_(Geocoridae) #Lygaeus_equestris_(Lygaeidae) #Malcus inconspicuus (Malcidae) #Sehirus_luctuosus_(Cydnidae) #Macroscytus gibbulus (Cydnidae) #Coptosoma_bifarium_(Plataspidae) #Megacopta_cribraria_(Plataspidae)
#Eurygaster testudinaria (Scutelleridae) #Antheminia lunulata (Pentatomidae) #Carpocoris_purpureipennis_(Pentatomidae) #Halyomorpha_halys_(Pentatomidae)
#Nezara_viridula_(Pentatomidae) #Physopelta_gutta_(Largidae)
#Dysdercus_cingulatus_(Pyrrhocoridae) #Triatoma_dimidiata_(Reduviidae)

CTCGTCCCTA AGGTAATTAT ATCTTATTAT CC--GCAATC ACGGGATCAA AA--ATACAC 601 601 601 601 60] 601 1 601 601 601 601 601 601 601 601 601 601 601 601 G.TA.....C.TAT.A. .A-TA...A TAT......T 1 601 TRATTRATGA A-AATAAATA AAAGTAAGTT AATAAAATTA CTCCATCACC CCAACGAAAA

[120]

TA--ATCAAT TA-ATATAAC CCAAACAAAT ATAAAGAATA ATAAAAATAG ATTAA-----[180] .T-AT.T.TA ..A...A ..T AGTT.A.T.A C.T..T.T.T. ATT..TATA .A...A----[180] 11801 [180] .--A..T.TA A.T.AC...T TTT.--TC.A .--.TC..A. TA.CT..ATA .A..TA-AAT [180] . -AT.TTTA GTT.A-...- AT...T...A -.TG.T..A. ..T..TTA. .A.T.A----..-ATCTTT. ..C..C...- AA.C.A...- -.T..TTT. GATGT.A.A GA.T.A----[180] 180 .T-A..TT.A ATT.A.A.C- ATTT.A...- -....AT--. .AT.....A ...A..A----..-A...C.A ATT.A..T.- ATGT.ATT.A -....T.A.T.A.A ...T.A----11801 180 11801 [180] (180) ----.TT. A.C....T AA.T.A.T.A .CC..TT.....T...CCA CAA.TA-A--.C--..A.A A.C.AT..T AATT.A.T.C CA..T.-- --..TTATA CA..TGAA-[180] [180] .T--..A.T. A.-.CT..TT ATCT.ATC.C TA...T...- -...G....A CA...-AAA-[180] .----. A.A.ATA..T AT.T.ATT.A CC..TA.... T...T.T.T TAAT.AAAA----.A.GA ..C..A.TA AT...A.T.A CC.T.-..- -...T...A .ACTTATAA-[180] 1180 11801 [180]

--TARAATTC TATAGGGTCT TCTCGTCCCA CAT-CCARAT GTTAGCCTTT GAACTAACAA --....TTG ..A-AA.... T.....TG...A. [240] [240] [240] [240] 12401 [240] [240] [240] --....T. TGG-AA.T.. C.A...T... T....C.A.T [240] [240] [240] 12401 [240] [240] [240] [240] [240] [240] [2401

#Neuroctenus_parus_(Aradidae) #Riptortus_pedestris_(Alydidae) #Hydaropsis longirostris (Coreid. #Rhopalus_latus_(Rhopalidae)
#Stictopleurus subviridis (Rhopa. #Yemmalysus_parallelus_(Berytida #Geocoris pallidipennis (Geocori #Lygaeus_equestris_(Lygaeidae) #Malcus inconspicuus (Malcidae) #Sehirus_luctuosus_(Cydnidae) #Macroscytus gibbulus (Cydnidae) #Coptosoma bifarium (Plataspidae #Megacopta_cribraria_(Plataspida #Eurygaster testudinaria (Scutel #Antheminia lunulata (Pentatomid #Carpocoris purpureipennis (Pent #Halyomorpha_halys_(Pentatomidae #Nezara viridula (Pentatomidae) #Physopelta_gutta_(Largidae)
#Dysdercus cingulatus (Pyrrhocor #Triatoma_dimidiata_(Reduviidae)

#Neuroctenus parus (Aradidae) #Riptortus_pedestris_(Alydidae)
#Hydaropsis longirostris (Coreidae) #Rhopalus latus (Rhopalidae) #Stictopleurus_subviridis_(Rhopalidae) #Yemmalysus_parallelus_(Berytidae) #Geocoris_pallidipennis_(Geocoridae) #Lygaeus_equestris_(Lygaeidae)
#Malcus inconspicuus (Malcidae) #Sehirus_luctuosus_(Cydnidae) #Macroscytus gibbulus (Cydnidae #Coptosoma bifarium (Plataspidae) #Megacopta_cribraria_(Plataspidae) #Eurygaster testudinaria (Scutelleridae) #Antheminia lunulata (Pentatomidae) #Carpocoris_purpureipennis_(Pentatomidae) #Halyomorpha_halys_(Pentatomidae) #Nezara_viridula_(Pentatomidae) #Physopelta_gutta_(Largidae)
#Dysdercus_cingulatus_(Pyrrhocoridae) #Triatoma_dimidiata_(Reduviidae)

#Neuroctenus parus (Aradidae) #Riptortus pedestris (Alydidae) #Hydaropsis_longirostris (Coreidae) #Rhopalus_latus_(Rhopalidae) #Stictopleurus_subviridis_(Rhopalidae) #Yemmalysus parallelus (Berytidae) #Geocoris_pallidipennis_(Geocoridae) #Lygaeus_equestris_(Lygaeidae)
#Malcus_inconspicuus (Malcidae) #Sehirus_luctuosus_(Cydnidae) #Macroscytus gibbulus (Cydnidae) #Coptosoma_bifarium_(Plataspidae)
#Megacopta_cribraria_(Plataspidae) #Eurygaster_testudinaria_(Scutelleridae) #Antheminia lunulata (Pentatomidae) #Carpocoris_purpureipennis_(Pentatom #Halyomorpha halys (Pentatomidae) #Nezara viridula (Pentatomidae) \$Physopelta_gutta_(Largidae)
\$Dysdercus cinqulatus (Pyrrhocoridae) #Triatoma_dimidiata_(Reduviidae)

#Neuroctenus_parus_(Aradidae) TGTTTTTG [428] #Riptortus_pedestris (Alydidae) [428] #Hydaropsis_longirostris_(Coreidae) #Rhopalus_latus_(Rhopalidae) #Stictopleurus subviridis (Rhopalidae) #Yemmalysus_parallelus_(Berytidae)[428] #Geocoris_pallidipennis_(Geocoridae)[428] #Lygaeus_equestris_(Lygaeidae)
#Malcus_inconspicuus_(Malcidae)[428] #Sehirus_luctuosus_(Cydnidae) [428] #Macroscytus gibbulus (Cydnidae) [428] #Coptosoma_bifarium_(Plataspidae) #Halyomorpha_halys_(Pentatomidae) #Nezara_viridula_(Pentatomidae) #Physopelta_gutta_(Largidae) [428] #Dysdercus cingulatus (Pyrrhocoridae) #Triatoma_dimidiata_(Reduviidae)

	GTTAAATTCA	CACAATA	TAATTAAGAA	AGAAAGCCCC	TCGTCCAACC	ATTCATACAA	[300]
	A	тА-А.Т.Т	AAA		G		[300]
ae)	A.C	TT-A-A-T.T	AA	CT.AT	A . T	T.T.	[300]
	A.C	TT-A-A.T.T	AAA	TC.AT		т	[300]
lidae)	A	ТА-А.Т.Т	AAA	TT.ATT		T.C.	[300]
e)	A.A	тАт.т	AA	T.T.TAT.			[300]
dae)	AA.	AC-TTA.T.T	A	TT.ATT	c		[300]
	A	AATT.T	A	TTATTTT			[300]
	A.A	тА	A	T.TAT.TT		тт	[300]
	A	A.TAAAT	AA	TT.ATATT	AT.G	c.	[300]
	AT	ATTCT.G	GCA	TT.AAGTT	A A		[300]
1	AG	TTAACT	A	TTTTT.			[300]
e)	A	TTAATT	A.G.A	TCGAAT	.TAA		[300]
leridae)	A	ACGATT	ATG.A	CCCA.ATT	.TA	C	[300]
ae)	A	ATTA	AT A		A		[300]
atomidae)	A	ACCA.T	ATG.A	TTCT			[300]
}	A	ATAATT	AT A	T.TTT		GT.C.	[300]
	AT	ATTT-T	AT A				[300]
	GT.	AT-TAA.T.T	A	TCTA	A	C	[300]
idae)	A	AT-TTA.T.T	A	TTTA.TT.			[300]
	AT	TA-A.T	A.C.A	CT.ATAT.		тт.с.	[300]

GCCTCCAATT AAAAGACAAT TGATTATGCT ACCTTTGCAC AGTCAGTATA CTGCGGCCAT [360] 13601 13601 13601 1360 13601 [360] 13601 1360 1360 13601 1360 1360 1360 13601 1360 [360] 1360

TTAATTA--- CCAATCATAG GGCAGGTCAG ATCTAAAATA AA----TAAT CAATAGAACA [420] .A.----A TA.....T.ACT.. .C.....T .TT---A... .T....G... [420]A.--T TA.....T. A.....C..A .C..G...........A..-...C..G... 1420 [420] [420] A. A. --- A AT.T. T. A. CT. ... CT. T. .T-----T.A AG... [420] Fig. 3. Phylogenetic trees for 12S rDNA sequences of 21 species used in this study generated by: A – neighbor-joining (NJ) analysis; B – minimum evolution (ME) analysis; C-E – maximum parsimony (MP) analysis (C-D – two most parsimonious trees, E – consensus tree). The percentage of replicate trees (A-D) and parsimonious trees (E) in which the associated taxa clustered together are shown next to the branches



Fig. 4. Phylogenetic trees for 16S rDNA sequences of 21 species used in this study generated by: A - neighbor-joining (NJ) analysis; B - minimum evolution (ME) analysis; C - maximum parsimony (MP) analysis. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (500 replicates) are shown next to the branches





Fig. 5. Phylogenetic trees obtained from the Bayesian inference analyses of the 12S rDNA sequences (A), 16S rDNA sequences (B), and combined 12S/16S rDNA dataset (C) of 21 species used in this study. The Bayesian posterior probabilities are indicated at each node

