

Species composition and taxonomic structure of Assassin bugs (Heteroptera: Reduviidae) in Southern Uzbekistan, with the first record of *Nagusta goedelii*

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Abstract. Valieva M, Mirzaeva G, Musaev D, Kholmatov B, Akhmedov V, Kimyonazarov S, Hudoyberdieva M, Eshkuvvatov B, Usanov S, Kholmirezayeva A, Kudratov J. 2026. Species composition and taxonomic structure of assassin bugs (Heteroptera: Reduviidae) in Southern Uzbekistan, with the first record of *Nagusta goedelii*. *Biodiversitas* 27 (3): d270331. <https://doi.org/10.13057/biodiv/d270331>. As climate change and urbanization intensify, it is of great importance to determine the systematic structure and diversity of the fauna of natural landscapes that are being degraded. This study presents a comprehensive analysis of the species composition and taxonomic structure of the family Reduviidae (Heteroptera) in Southern Uzbekistan. Based on 162 specimens collected between 2021 and 2024 across four distinct ecological zones (Yakkabog, Sherabad, Nishon, and Termez), a total of 18 species belonging to 12 genera and 5 subfamilies were identified. Sampling was standardized using sweeping, pitfall traps, and light-traps to ensure comparability across different altitudes (800-1300 m asl) and land-use intensities. The subfamily Harpactorinae exhibited the highest diversity (6 species), followed by Reduviinae (5 species) and Stenopodainae (4 species). A major highlight of the study is the first formal record of *Nagusta goedelii* for the fauna of Uzbekistan. The identification of this species was validated through a detailed morphological diagnosis, focusing on key characters such as the prominent post-antennal spines, elongated "neck" structure, and pronotal tubercles, as well as molecular-genetic analysis. Cytochrome Oxidase I (COI) gene sequencing (PX588124.1) and subsequent phylogenetic reconstruction using Maximum Likelihood supported the distinct placement of the Uzbek specimen within the *Nagusta-Serendiba* clade (bootstrap 89-100%). Comparative faunal analysis using Jaccard and Sørensen-Dice coefficients revealed significant regional differentiation. A complete faunal turnover (Cj:0.0) was observed between the mountainous habitats of Yakkabog and the arid lowland zones of Nishon, reflecting the impact of environmental filtering. These findings significantly expand the known distribution of Palearctic reduviids and provide a baseline for future biogeographic and ecological monitoring in Central Asia.

Keywords: COI barcoding, diversity, molecular identification, *Nagusta goedelii*, Reduviidae, species composition

INTRODUCTION

Within the class Insecta, the order Hemiptera: Heteroptera is among the most widespread and ecologically diverse insect groups, currently comprising approximately 45,000 species worldwide (Henry 2017; Hemala et al. 2022). This order occupies a broad range of terrestrial and semi-aquatic habitats and includes taxa with diverse feeding strategies, ecological functions, and adaptive traits that contribute to their success across many biogeographic regions. Among these, the family Reduviidae (assassin bugs) stands out due to its specialized predatory strategies and significance as natural bio-regulators in agroecosystems (Musaev et al. 2023; Medetov et al. 2025). Members of this family are known for their active predation on other arthropods, and their presence often reflects important

ecological interactions within local communities. Despite their cosmopolitan distribution, Reduviidae species exhibit high phenotypic variability and morphophysiological adaptations specific to their biogeographic regions (Cianferoni et al. 2021; Cuesta-Segura 2025; Mamanov et al. 2024). These adaptations may involve differences in morphology, coloration, behavior, and physiological tolerance, which allow species to persist under contrasting environmental conditions.

In Central Asia, the faunal composition of Reduviidae is relatively well-documented in certain areas, with 47 species recorded in Kazakhstan (Esenbekova 2013). In 2003, 13 species were reported in the Khorezm region and the Republic of Karakalpakstan (Khamraev 2003). In Uzbekistan, recent decades have seen fragmented studies focused primarily on the northern and western regions. For

instance, 4 to 24 species have been identified in the Republic of Karakalpakstan and the Southern Aral Sea region (Kulumbetova 1998; Medetov et al. 2025), while 15 species were recorded in the Lower Amudarya (Gandjaeva 2021). To date, a total of 51 Reduviidae species have been documented across various regions of Uzbekistan (Lebedeva et al. 2024; Valiyeva et al. 2025). These records indicate that the family is relatively diverse in the country, but they also show that current knowledge is unevenly distributed across regions and still dependent on scattered surveys conducted in different periods.

The faunal composition of animals has its own characteristics depending on the geographical features of the area in which they are distributed (Cantonati et al. 2020; Narzullayev et al. 2024; Zokirova et al. 2025). In this regard, animals develop structures, behaviors and functional abilities adapted to survive in a changing environment. As a result, species diversity in populations increases or remains stable. According to experts, there is often evidence of phenotypic variability in predatory insects as an adaptation to factors affecting them (Baymuradov et al. 2021; Alimova et al. 2024; Martínez et al. 2025; Naydenov et al. 2025). Such variability is particularly relevant in predatory heteropterans, whose distribution and abundance may respond to habitat conditions, prey availability, temperature, humidity, vegetation structure, and human disturbance. Therefore, regional studies are essential not only for documenting species occurrence, but also for understanding how environmental heterogeneity contributes to the formation of local faunal assemblages.

However, despite this national progress, a knowledge gap remains regarding the Southern Uzbekistan territories. While neighboring regions and northern provinces have updated faunal lists, the species composition, taxonomic diversity, and ecological distribution of assassin bugs in the geographically isolated and climatically distinct zones of Southern Uzbekistan, specifically the Yakkabog, Sherabad, Nishon, and Termez regions, have not been systematically

investigated. Current records lack precise data on how microclimatic parameters and varying levels of anthropogenic impact in these specific areas influence Reduviidae community structures. This absence of detailed regional information limits broader understanding of the distribution patterns of the family in Uzbekistan and reduces the ability to compare southern faunal assemblages with those reported from other parts of the country. For this reason, targeted investigation of these territories is necessary to clarify the current status of Reduviidae diversity and ecological distribution in Southern Uzbekistan. Therefore, this study aims to determine the species composition and taxonomic structure of the Reduviidae family in Southern Uzbekistan, to evaluate the levels of faunal similarity between geographically isolated regions (mountainous vs. desert zones) using standardized biodiversity indices, and to provide the first morphological and molecular-genetic (Cytochrome Oxidase I (COI) gene) characterization of newly recorded taxa for the region.

MATERIALS AND METHODS

Study area and sampling design

Sampling was conducted between 2021 and 2024 across four geographically and climatically distinct regions in Southern Uzbekistan (Figure 1, Table 1). To ensure comparability, sampling effort was standardized across all regions with 20-day interval visits from April to November each year. Yakkabog and Sherabad: Hilly and mid-mountain landscapes (800-1300 m asl). Characterized by moderate humidity, diverse natural vegetation (shrublands and ephemeral grasses), and low-to-moderate land-use intensity. Nishon and Termez: Desert and semi-desert lowlands (up to 900 m asl). Characterized by an arid climate, sparse xerophytic vegetation, and high anthropogenic pressure due to urbanization and intensive irrigated agriculture

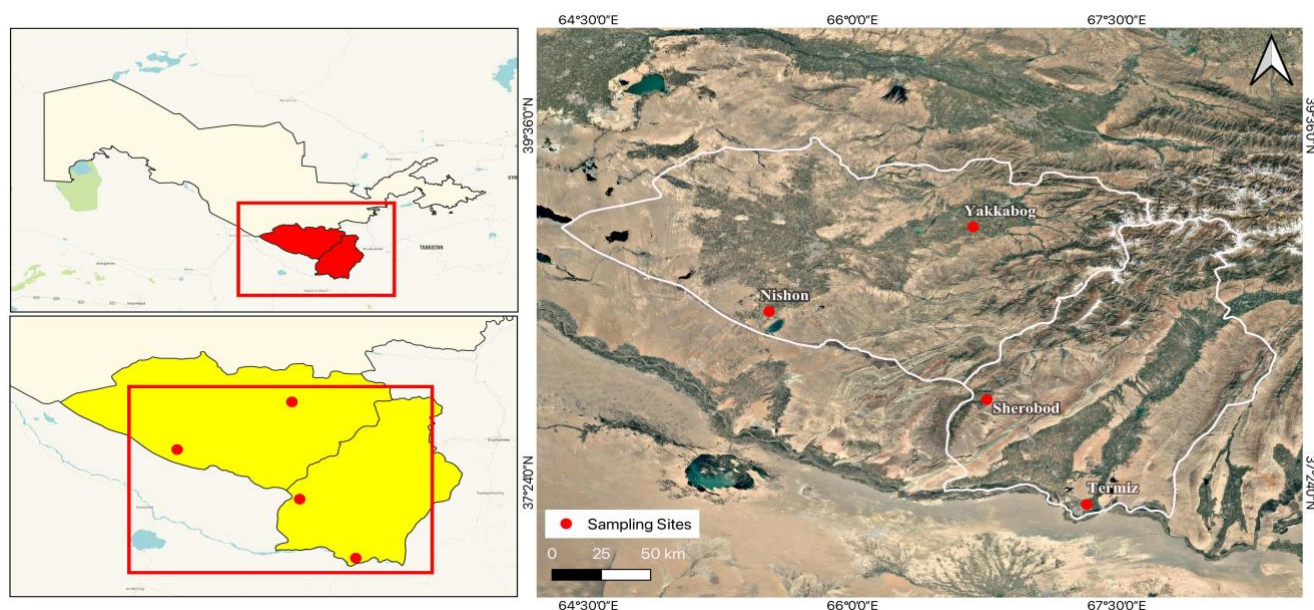


Figure 1. Map of research areas in Southern Uzbekistan

Table 1. Information about samples collected from the regions of southern Uzbekistan in 2021-2024

Station	Altitude (m)	Habitat type	Number of coordinates	Number of samples collected			
				♀	♂	Total	Accession numbers
Yakkabog	800-1300	Hilly/pasture	25	26	37	63	FA_Z_2021_HR_01-63
Nishon	800-1200	Hilly/shrub	6	8	5	13	FA_Z_2021_HR_64-76
Termiz	<900	Desert/agro	13	17	12	29	FA_Z_2021_HR_77-105
Sherobod	<900	Arid/urban	23	22	35	57	FA_Z_2021_HR_106-162
Total			67	73	89	162	

Data collection

A total of 162 specimens were collected using standardized entomological methods applied equally at each station. Hand Collection and Sweeping: Systematic sweeping using a standard entomological net (35-40 cm diameter) was performed in the upper 15-20 cm of the vegetation canopy. Trapping Methods: Pitfall traps (Barber traps) were deployed for ground-dwelling taxa, and Malaise traps (referred to as Melezi in earlier drafts) were used for flying insects. Light Traps: Pelsis UV-A (18W, 368 nm) spectral light traps were used to collect nocturnal species. The traps were operated for 4 hours after sunset during each 20-day expedition. All specimens were preserved in 70% ethanol or pinned as vouchers.

Species identification

Taxonomic identification was performed using morphological keys by Esenbekova (2013), Putshkov and Moulet (2009) and Medetov et al. (2025). For the first national record, *Nagusta goedelii*, identification was confirmed by examining the characteristic post-antennal spines and pronotal structures. All vouchers, including the sequenced specimen, are deposited in the Institute of Zoology of the Academy of Sciences of the Republic of Uzbekistan (Tashkent) and are available for re-examination.

Molecular analysis

Molecular analysis was performed according to the method of Habeeb et al. (2011). An adult bug was placed in a centrifuge tube containing 300 µL of homogenization buffer and 75 µL of lysis buffer, and ground using a thin glass rod. The whole content was incubated at 65°C for 30 min (under a controlled environment). To this, 17 µL of 8M potassium acetate was added. The tubes were incubated in ice for 30min overnight. The incubated samples were centrifuged at 15,000 rpm for 15 min at 4°C. The aqueous phase was transferred to a new tube, and 400 µL of absolute ethanol was added (to precipitate the Nucleic Acid content from the aqueous phase). Precipitated Nucleic Acid is pelleted out by centrifuging at 12,000 rpm for 15 min at 4°C. Pellet was retained. Air-dried pellet was dissolved in 20 µL of T.E buffer and stored at 20°C for further use. The DNA concentration and purity were assessed using a spectrophotometer. DNA purity was determined by calculating the absorbance ratio A260/280.

Amplification and sequencing of COI gene region: Mitochondrial DNA (mtCOI) fragments were amplified using primers-forward primer LEP-F 5'-ATTCAACCAATCATAAAGATAT-3' and reverse primer

LEP-R 5-TAAACTTCTGGATGTCCAAAAA-3 (Hebert 2004). For the Polymerase Chain Reaction (PCR), the following components were used: distilled water (7.1 µL), 10x PCR buffer (1 µL), dNTP (0.2 µL), each primer (0.25 µL), Taq polymerase (0.2 µL), making a total volume of 10 µL. Amplification was carried out in a thermocycler for 35 cycles. PCR was performed according to the following scheme: i) stage denaturation of DNA at 95°C for 2 min, ii) stage denaturation of DNA at 93°C for 20 sec, iii) stage annealing of primers at 52°C for 45 sec, iv) stage elongation at 72°C for 2 min, v) stage chain elongation at 72°C for 10 min. The process from the second to the fourth stage was repeated in cycles up to 35 times. The reaction was performed using a PCR instrument. PCR products were analyzed by gel electrophoresis on a 1% agarose gel, at 50V for 30 mins, and the DNA fragments in the gel were visualized using a UV trans-illuminator. The purified PCR product was sequenced with the help of a sequence scanner v1 from ABI.

Phylogenetic analysis

The COI sequence obtained after sequencing was translated and its family was assessed with the help of InterProScan database. Similar sequences to ours are downloaded from the National Center for Biotechnology Information (NCBI) database after performing a search for similar sequences using the Blast tool. The DNA sequences were edited, and consensus sequences were calculated using the Mega X software. The isolates obtained and additional sequences from the GenBank database were aligned using default settings in the MAFFT v.7 online tool and Clustal Omega 1.2.2 software, then edited in Genius Prime software. The nucleotide sequences belonging to the ITS region were used to construct a maximum likelihood (ML) phylogenetic tree using IQ-TREE version 1.6.12 with ultrafast bootstrap analysis based on 1000 replicates. The analyses were performed on the CIPRES Science Gateway V 3.3. The mitochondrial COI gene sequence of *Rocconota annulicornis* MW984327 was used as an outgroup to facilitate the generation of consensus trees. The resulting phylogenetic tree was analyzed and edited using iTOL v6.6 software.

Data analysis

The Chekanovsky-Sørensen coefficient was calculated using the following formula (Uralov et al. 2025):

$$S = \frac{2a}{2a + b + c}$$

Where, a: the number of species common to both areas, b and c: the number of species in each area.

The Jaccard coefficient was calculated using the following formula (Akramov et al. 2025; Narzullayev and Subbotin 2025):

$$S_j = \frac{j}{(a + b - j)}$$

Where, j: the number of species common to both areas, a and b: the number of species in each area.

The similarity dendrogram according to the Jaccard and Chekanovsky-Sørensen coefficients was constructed using the PAST 4.0.7z program (Ergasheva et al. 2024; Kudratov et al. 2024; Rayimova et al. 2024).

RESULTS AND DISCUSSION

Species composition of Assassin bugs in Southern Uzbekistan

A total of 162 specimens of assassin bugs were collected and identified, representing 18 species across 12 genera and 5 subfamilies (Table 2). The subfamily Harpactorinae showed the highest species richness (6 species), followed by Reduviinae (5 species) and Stenopodainae (4 species). At the generic level, *Reduvius* and *Rhynocoris* were the most diverse, each represented by 3 species. The distribution

of species among genera is shown in Figure 4. The highest species richness was recorded in Yakkabog and Sherabad (8 species each), while Nishon exhibited the lowest diversity with only 3 recorded species. *Peirates hybridus* was the most frequently encountered taxon, occurring in three out of the four study regions (Table 2).

The highest diversity of assassin bugs was observed in the Yakkabag and Sherabad regions, with 8 species each. Only 3 species of reduvid ants were recorded in the Nishan area. Among the identified reduvid assassin bugs, *P. hybridus* was found in three of the studied regions, while *Reduvius elegans*, *Stirogaster fausti*, *Rhynocoris iracundus*, *Rhynocoris monticola*, and *Ectomocoris ululans* were recorded in two regions each. The remaining 12 species were observed in only one region. Among the identified species, one species, *Nagusta goedelii*, was recorded for the first time for the regions of Uzbekistan (Table 2, Figure 2). Ishikawa et al. (2007) reported that the species composition of the Reduviidae family varies even in relatively close areas in their studies on the islands of Java and Bali (Ishikawa et al. 2007). According to experts, the diversity of species in the Reduviidae family is likely due to morphological changes that allow them to hide from predators or to avoid being detected by food sources (Masonick et al. 2025).

Table 2. Species composition and distribution of Reduviidae across four study regions

Subfamily	Genus/species	Yakkabog	Nishon	Termiz	Sherobod
Reduviinae	Genus <i>Reduvius</i>				
	<i>Reduvius elegans</i> (Jakovlev, 1885)	-	+	+	-
	<i>Reduvius pallipes</i> Klug, 1830	-	-	-	+
	<i>Reduvius testaceus</i> (Herrich-Schaeffer, 1845)	-	-	-	+
	Genus <i>Holotrichius</i>	+	-	-	-
	<i>Holotrichius apterus</i> (Jakovlev, 1879)				
Stenopodainae	Genus <i>Pasira</i>				
	<i>Pasira basiptera</i> Stål, 1859	+	-	-	-
	Genus <i>Oncocephalus</i>				
	<i>Oncocephalus termezanus</i> (Kiritshenko, 1914)	-	-	+	-
	<i>Oncocephalus plumicornis</i> (Germar, 1822)	-	-	+	-
	Genus <i>Stirogaster</i>				
Harpactorinae	<i>Stirogaster fausti</i> (Jakovlev, 1874)	+	-	+	-
	Genus <i>Pygolampis</i>				
	<i>Pygolampis bidentata</i> (Goeze, 1778)	+	-	-	-
	Genus <i>Rhynocoris</i>				
	<i>Rhynocoris iracundus</i> (Poda, 1761)	+	-	-	+
	<i>Rhynocoris monticola</i> (Oshanin, 1870)	+	-	-	+
Peiratinae	<i>Rhynocoris abramovii</i> (Oshanin, 1871)	-	+	-	-
	Genus <i>Coranus</i>				
	<i>Coranus (Coranus) aegyptius</i> (Fabricius, 1775)	-	-	-	+
	<i>Coranus griseus</i> (Rossi, 1790)	-	-	-	+
	Genus <i>Nagusta</i>				
	<i>Nagusta goedelii</i> (Kolenati, 1857)**	+	-	-	-
Phymatinae	Genus <i>Ectomocoris</i>				
	<i>Ectomocoris ululans</i> (Rossi, 1807)	+	-	+	-
	Genus <i>Peirates</i>				
Phymatinae	<i>Peirates hybridus</i> (Scopoli, 1763)	-	+	+	+
	Genus <i>Phymata</i>				
Total	<i>Phymata crassipes</i> (Fabricius, 1775)	-	-	-	+
		8	3	6	8

Note: +: recorded, -: not recorded. **: First record from Uzbekistan

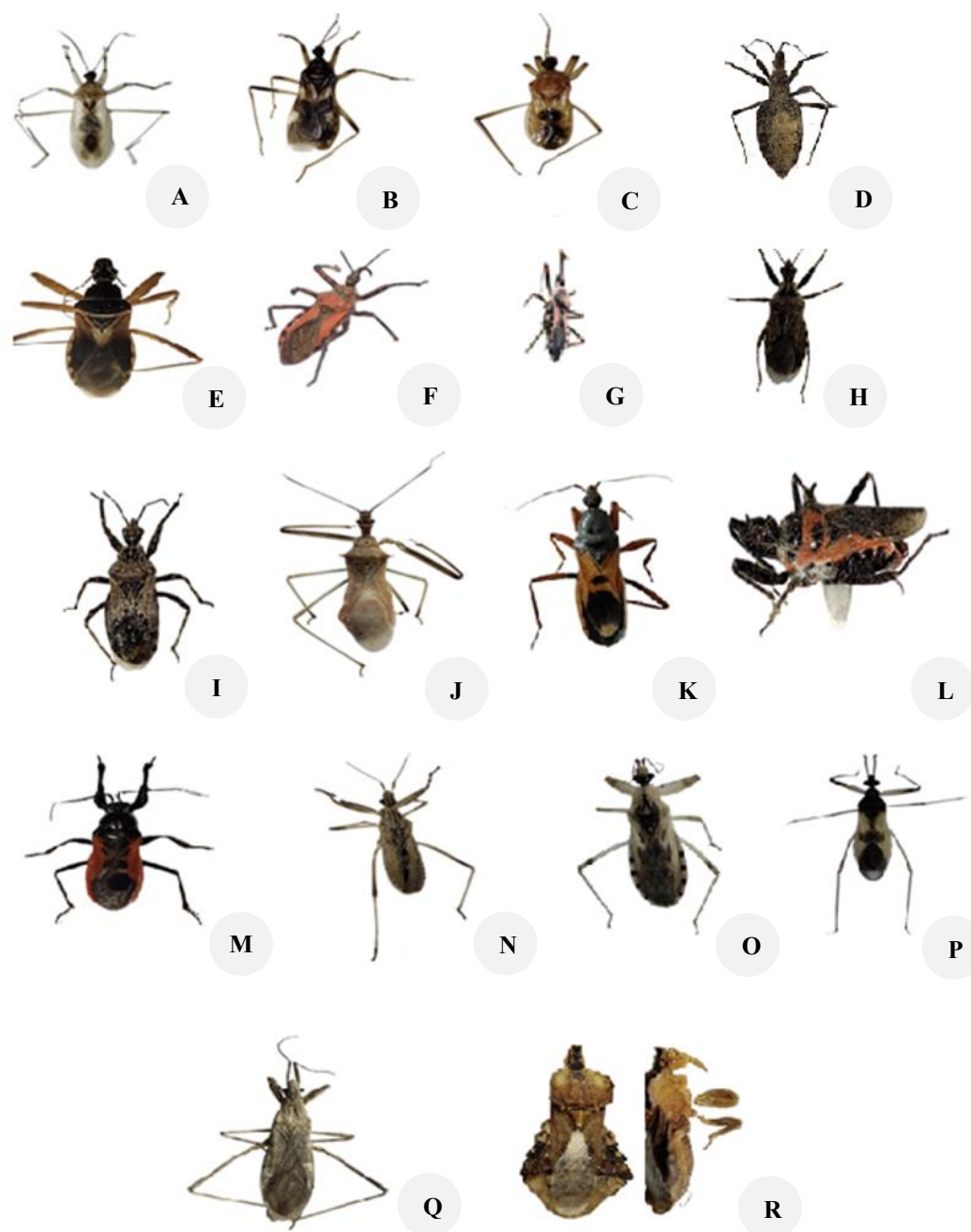


Figure 2. The species of Assassin bugs (Heteroptera: Reduviidae) of Southern Uzbekistan (photos by the authors): A. *Reduvius elegans*, B. *Reduvius pallipes*, C. *Reduvius testaceus*, D. *Holotrichius apterus*, E. *Pasira basiptera*, F. *Oncocephalus termezanus*, G. *Oncocephalus plumicornis*, H. *Stirogaster fausti*, I. *Pygolampis bidentata*, J. *Rhynocoris iracundus*, K. *Rhynocoris monticola*, L. *Rhynocoris abramovii*, M. *Coranus aegyptius*, N. *Coranus griseus*, O. *Nagusta goedelii*, P. *Ectomocoris ululans*, Q. *Peirates hybridus*, R. *Phymata crassipes*

Analysis of taxon composition of Assassin bugs in Southern Uzbekistan

According to the distribution indicators of the subfamilies of the Reduviidae family in the studied areas of southern Uzbekistan, the subfamilies with the largest number of genera in the region are Reduviinae, Stenopodainae and Harpactorinae. 75.0% of the genera in the studied area (9 genera) belong to these subfamilies (Figure 3A). It was also noted that the subfamilies Harpactorinae (6 species),

Reduviinae (5 species) and Stenopodainae (4 species) are dominant with a relatively large number of species (Figure 3B).

According to the distribution of identified Reduviidae species across genera, representatives of the genera *Reduvius* and *Rhynocoris* (3 species each), *Oncocephalus* and *Coranus* (2 species each) are most common in Southern Uzbekistan. It was also found that 8 genera of reduviids have one species each (Figure 4).

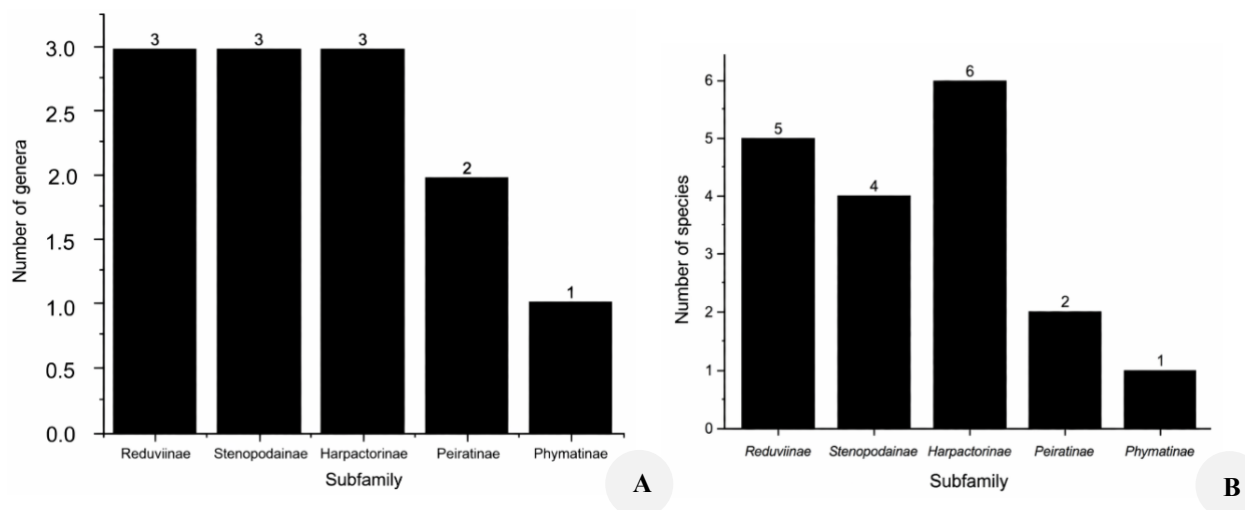


Figure 3. Division of genera (A) and species (B) into subfamilies of Assassin bugs in Southern Uzbekistan

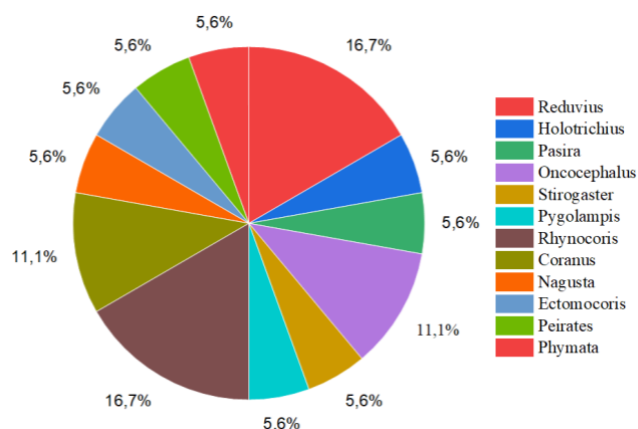


Figure 4. Division of species into genera of Assassin bugs in Southern Uzbekistan

Similarity of species composition of Assassin bugs in Southern Uzbekistan

Study regions were subjected to comparative analysis and similarity between regions was assessed using Jaccard and Chekanovsky-Sørensen coefficients (Table 3). Similarity indices (Table 3) indicate a partial faunal overlap between Nishon and Termez (C_j : 0.29). This similarity likely reflects broadly comparable environmental conditions, as both regions are characterized by arid lowland landscapes and high temperatures. In contrast, the zero similarity between Yakkabog and Nishon (C_j : 0.0) highlights a complete faunal turnover, driven by the significant altitudinal gradient and differences in vegetation structure. It should be noted that the lower specimen counts in Nishon (n : 13) compared to Yakkabog (n : 63) may limit the precision of richness comparisons, a factor common in rapid biodiversity assessments.

The results of the similarity analysis were depicted in dendrograms using the hierarchical clustering method (UPGMA: average linkage method). According to the dendrogram analysis, the Nishan and Termez regions are combined into one cluster, Yakkabag and Sherabad into independent clusters, and finally these two main clusters are combined (Figure 5).

In general, such a mosaic nature of the species composition of reduviids in the studied areas is explained by the geographical isolation of the territories, differences in microclimate, the structure of the vegetation cover and the varying degree of anthropogenic impact (Diaz et al. 2025). As a result, each region has formed its own specific insect complex, which indicates the need to develop nature protection measures taking into account the preservation of biodiversity and regional faunal characteristics (Pazilov et al. 2026).

First records of *Nagusta goedelii* from Uzbekistan

The study recorded *Nagusta goedelii* for the first time in Uzbekistan (PX588124.1). We found populations of *N. goedelii* in one location in Qashqadaryo egion, Yakkabog' District, Qatag'on Village (38°56'12"N 66°44'12"E), 621 m asl, apricot tree, 02.07.2024, 1 ♂, observed by Valieva M, Mirzaeva G and Grebennikov det. K.

The morphological characters, molecular genetics and phylogenetic characteristics of this species were determined and described. *N. goedelii* develops through incomplete metamorphosis: egg → nymph → imago. The insects lay their eggs on leaves (Figure 6).

The body is slender and slightly hairy, brown in color. The head is elongated, more than twice as long as it is wide. There are two horn-like spines behind the place where the whiskers are attached. The pronotum is hexagonal in shape, with two impassable conical protrusions on it.

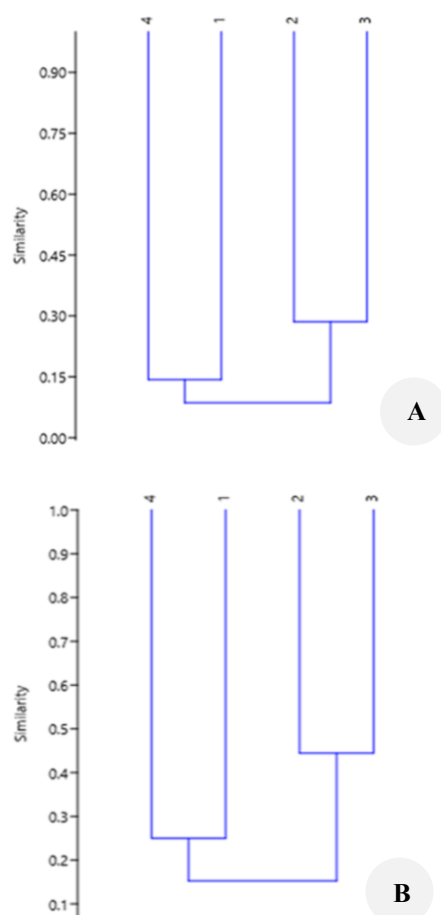


Figure 5. Similarity dendrogram of the Assassin bugs in Southern Uzbekistan based on: A. Jaccard coefficients, and B. Chekanovsky-Sørensen coefficients. 1: Yakkabog, 2: Nishon, 3: Termiz, 4: Sherobod

Table 3. Similarity coefficients of Assassin bugs in Southern Uzbekistan (Jaccard/Chekanovsky-Sørensen)

Research areas	Yakkabog	Nishon	Termiz	Sherobod
Yakkabog	1	0.0	0.29	0.25
Nishon	0.0	1	0.44	0.18
Termiz	0.17	0.29	1	0.14
Sherobod	0.14	0.10	0.08	1

They shed their exoskeleton several times until reaching the nymph stage, then transition to the imago stage (Putshkov 1987). The species *N. goedelii* is distinguished by its sharp spines behind the antennae, as well as its long neck, long antennae, and front legs (Figure 7). The adult predatory bug is usually active and hunts prey. Based on its feeding specialization, *N. goedelii* is zoophagous and overwinters as an imago. According to its habitat, it is a dendrobiont—it can be found in forests, agricultural fields, and on fruit trees (Putshkov and Moulet 2009; van der Heyden 2023).

According to the results of a phylogenetic analysis based on the nucleotide sequences of the mtDNA COI (Cytochrome Oxidase I) gene of the species *N. goedelii* belonging to the genus *Nagusta*, the evolutionary relationships of the sample taken for the study were determined, and the phylogenetic tree topology was divided into several clear clusters (clades) (Figure 8).

The reliability of the nodes in the phylogenetic tree was assessed using the bootstrap reselection method, and bootstrap values ranged from 58% to 100%. The specimen *Rocconota annulicornis* MW984327 was used as an outgroup in the phylogenetic analysis. This taxon occupied a separate branch in the phylogenetic tree, clearly separated from all other taxa, and was supported by a high bootstrap value ($\approx 100\%$). This confirms the reliability of the overall topology of the tree and the monophyletic nature of the internal clades. The first major clade identified in the phylogenetic tree included species belonging to the genera *Serendiba* and *Nagusta* and was characterized by moderate to high bootstrap values (approximately 79-90%). This clade included *Serendiba hymenoptera* KJ629613, *Sycanus bifidus* OR734026, *Sycanus bicolor* KJ629620, *Nagusta tuberosa* MW982783, and the study specimen *Nagusta goedelii* Uzb PX588124.1. In particular, the fact that *Nagusta goedelii* Uzb PX588124.1 is located on the same branch as *N. tuberosa* and is supported by high bootstrap values ($\approx 89-100\%$) of this branch reliably confirms the genetic closeness of this specimen to the species *N. goedelii* and its taxonomic status.

The second clade, consisting of species belonging to the genus *Zelus*, was distinguished with a high level of confidence (bootstrap $\approx 90-100\%$). This clade included *Zelus tetracanthus* HQ106458 and *Zelus luridus* MN621024, which were found to have a close phylogenetic relationship. These species formed a monophyletic group and showed a separate evolutionary direction. The third clade contained two isolates of the species *Isyndus planicollis*—*Isyndus planicollis* KJ629611 and *Isyndus planicollis* KJ629610. This pair was supported by the maximum bootstrap value (100%), indicating a very high level of genetic similarity between isolates within the same species. The fourth largest clade included species belonging to the genus *Epidaus* and was characterized by high bootstrap values ($\approx 79-100\%$). This clade included isolates *Epidaus bachmaensis* PQ142834 and PQ142835, *Epidaus xuliangae* KJ630228, and *Epidaus nigricornis* KJ630096 and KJ630092. The species *Epidaus bachmaensis* and *Epidaus nigricornis* formed separate subclades, each of which was supported by high bootstrap values ($\approx 90-100\%$), indicating that they were clearly genetically differentiated. The results of the phylogenetic analysis showed that the COI marker has a high informative value in determining interspecific and intraspecific genetic relationships. In particular, the close phylogenetic relationship of the *Nagusta goedelii* Uzb PX588124.1 specimen with the species *N. tuberosa*, confirmed by high bootstrap values, allowed us to clearly determine the taxonomic position of the research object.

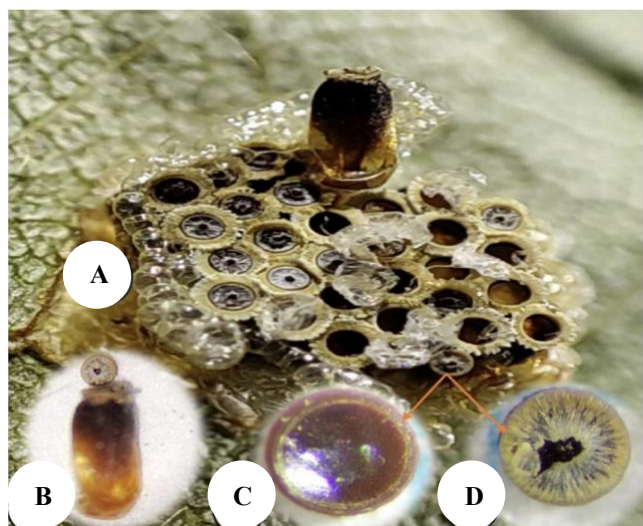


Figure 6. Eggs of *Nagusta goedelii*. A: appearance of the egg cluster (ootheca), B: egg after the larva has emerged (the egg lid remaining attached together with the exuvia), C-D: internal and external views of the egg lid

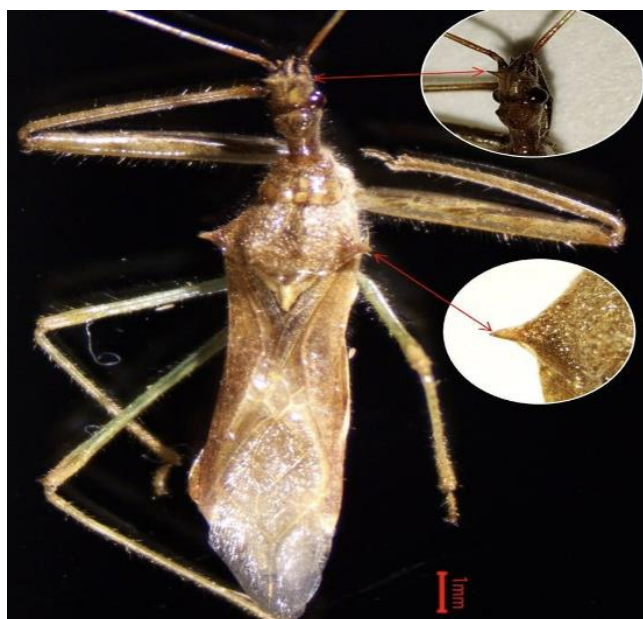


Figure 7. Adult *Nagusta goedelii* (Yakkabog)

Maximum-likelihood (ML) genetic distance analysis based on the nucleotide sequences of the mtDNA COI (Cytochrome Oxidase I) gene of the species *N. goedelii* belonging to the *Nagusta* genus, allowed us to determine

the degree of evolutionary closeness and differentiation between the taxa involved in the study (Figure 9).

Bioinformatic analysis based on the COI gene confirmed that the *Nagusta goedelii*_Uzb specimen was clearly differentiated as an independent taxon, consistent with the results of the phylogenetic tree. The smallest genetic distance for the *Nagusta goedelii*_Uzb study specimen was recorded with *S. hymenoptera* KJ629613 and *N. tuberosa* MW982783, indicating a relatively close evolutionary relationship between the taxa. The results obtained indicate genetic stability within the species and high accuracy of the COI marker at the species level.

Nagusta is a genus of the subfamily Harpactorinae, and currently includes 37 formal species (Putshkov and Moulet 2009), although the number of species and taxonomic limits of the genus in tropical regions needs clarification (Sankararaman et al. 2022). Four species are reliably recorded from the Palearctic region, 3 of them are not reliably recorded out of North Africa and the Arabian Peninsula, and one reaches the territory of Iran.

Nagusta goedelii is the only member of the genus out of the tropics and southern subtropics. Its current known distribution includes Austria, Bosnia and Herzegovina, Bulgaria, Croatia, Slovakia, Slovenia, Greece, Hungary, Macedonia, Moldova, Montenegro, Romania, southern Russia, Serbia, the European part of Turkey, and Ukraine. Outside Europe, the species is recorded in Armenia, Azerbaijan, Cyprus, Georgia, Iraq, Iran, Israel, Syria, Turkmenistan, and the Asian part of Turkey (Putshkov and Moulet 2009; Hemala et al. 2022). By the early 21st century, the known range of *N. goedelii* extended northwest to Austria and the Czech Republic, south to Israel, and east to southern Turkmenistan (Putshkov and Moulet 2010). Since then, the species has expanded significantly across Europe (Hemala et al. 2022; Cuesta-Segura 2025). Records now reach as far north as the Baltic region, northern Germany, and the Netherlands; westward to northern Spain; and southwest to Sardinia and Rome (Cianferoni et al. 2021). However, data on the species' distribution and range dynamics in the eastern part of its range, outside the Mediterranean zone, remain scarce. The reasons for this rapid dispersal of the species remain controversial and unclear. It is clear, however, that the new data on the distribution of *N. goedelii* in Central and Western Europe cannot be explained by the insufficient study of the fauna of these regions. The authors suggest that the main factor driving the species' range expansion is climate change, leading to an increase in its potential range. This study documents new records of the species in Uzbekistan and analyzes potential range shifts across Central Asia under varying climatic conditions over different time periods. The authors assess these findings to determine whether the species should be considered native or alien to the country.

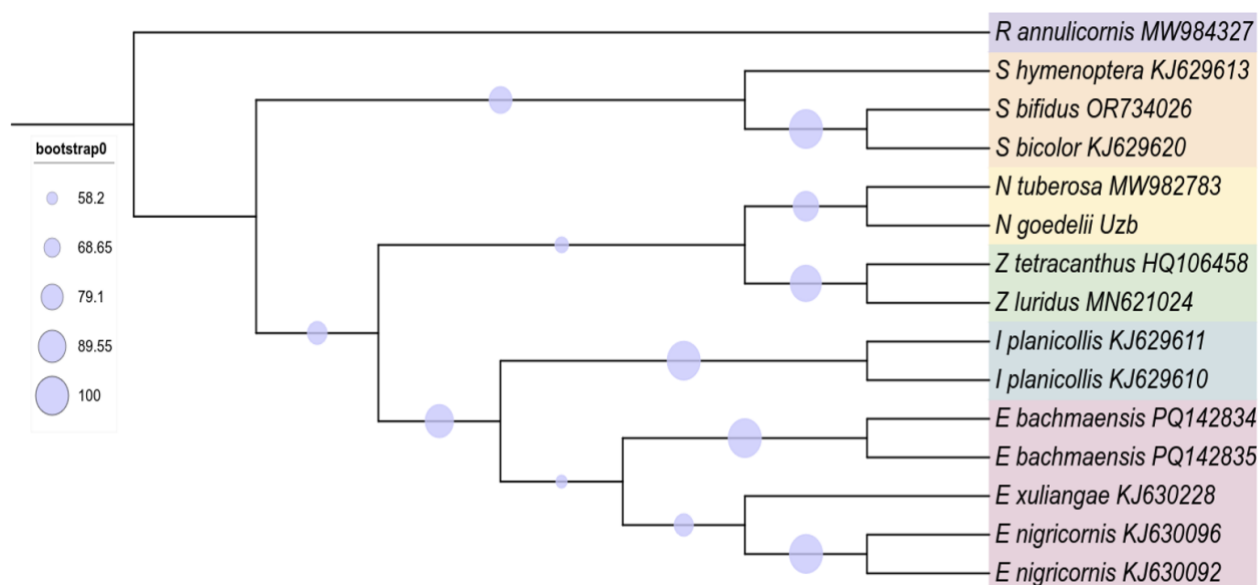


Figure 8. Phylogenetic analysis based on nucleotide sequences of the COI gene of the *Nagusta goedelii*_Uzb PX588124.1

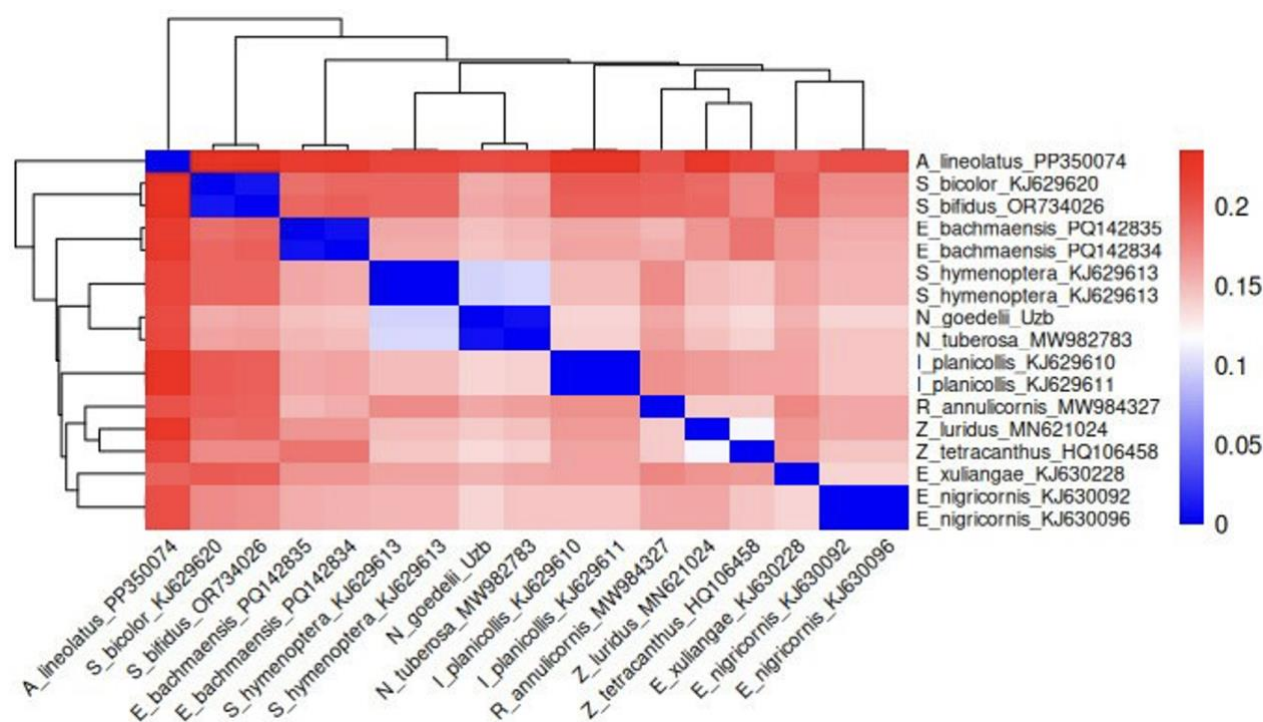


Figure 9. Analysis of genetic distance between *Nagusta goedelii* PX588124.1 and other species

In conclusion, this study provides a comprehensive update on the Reduviidae fauna of Southern Uzbekistan, documenting 18 species across 12 genera. *N. goedelii* is formally recorded for the first time in Uzbekistan, supported by both morphological diagnosis and COI gene sequencing. A clear faunal differentiation was identified between mountainous and desert regions. The highest species richness was observed in the mid-mountain habitats of Yakkabog and Sherabad (8 species each), while the arid zones of Nishon showed significantly lower diversity (3

species). The integration of molecular barcoding with classical morphology reinforces the taxonomic stability of the identified taxa and provides a reference for future entomological surveys in the region. The recorded species, particularly the dominant Harpactorinae, function as key predatory components in their respective ecosystems. These results emphasize the need for continued biodiversity assessments in Southern Uzbekistan's transition zones to better understand the regional distribution of predatory Heteroptera.

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