



Phylogenomic placement and revision of *Iranattus* Prószyński, 1992 jumping spiders (Salticidae, Plexippini, Plexippina)

Kiran Marathe^{1,2*}, Rishikesh Tripathi^{3*}, Ambalaparambil V. Sudhikumar³, Wayne P. Maddison^{4*}

- 1 Department of Zoology, University of British Columbia, 6270 University Boulevard, Vancouver, British Columbia, V6T 1Z4, Canada
- 2 National Centre for Biological Sciences, Tata Institute of Fundamental Research, GKVK Campus, Bengaluru, 560065, India
- 3 Centre for Animal Taxonomy and Ecology, Department of Zoology, Christ College, Irinjalakuda, Kerala, 680 125, India
- 4 Departments of Zoology and Botany and Beaty Biodiversity Museum, University of British Columbia, 6270 University Boulevard, Vancouver, British Columbia, V6T 1Z4, Canada

https://zoobank.org/4488FFD3-5621-439E-9253-058E974EB0B3

Corresponding author: Kiran Marathe (marathe12@gmail.com)

Academic editor: Danilo Harms ◆ Received 1 March 2024 ◆ Accepted 18 April 2024 ◆ Published 14 May 2024

Abstract

The jumping spider genus *Iranattus* Prószyński, 1992, distributed from Africa to southwestern Asia, has been placed within the Harmochirina because of their male palp structures and elongated third legs. Here, we present phylogenomic evidence that it belongs instead to the subtribe Plexippina, further supported by the presence of two coupling pockets in the female epigyne. In this study, we redescribe *I. principalis* (Wesołowska, 2000) and *I. rectangularis* Prószyński, 1992. Additionally, the female of *I. rectangularis*, the type species of the genus, is described for the first time, and we report its range extension east to India.

Key Words

Afrotropics, Araneae, biodiversity research, classification, deserts, Harmochirina, Indomalaya, phylogenomics, systematics, taxonomy, xeric scrublands

Introduction

When Prószyński (1992) originally described the jumping spider genus *Iranattus* Prószyński, 1992, based on a single male specimen from Iran, he characterized it by features such as a simple tegulum (bulbus) and embolus, unusual cymbial apophysis, and an extraordinarily long pair of legs (which his text erroneously states are the fourth pair, but which in fact are the third, as in his figures 35–36). These traits led Maddison (2015) to place it within the Harmochirina, some of which have very long third legs (e.g., *Neaetha* Simon, 1885), and some of which (e.g., *Pellenes limbatus* Kulczyński, 1895) have an apophysis on the male cymbium very similar to that of *Iranattus*. A relationship with

Harmochirines was suggested by Wesołowska (2000), who, when describing *Monomotapa* Wesołowska, 2000 (later synonymized with *Iranattus*; Prószyński 2017), commented on its similarity in body and leg lengths with the harmochirines *Neaetha* Simon, 1885, and *Pellolessertia* Strand, 1929.

Subsequent studies and new material now give the opportunity to reconsider the phylogenetic placement of *Iranattus*, currently composed of two species (World Spider Catalog 2024). Females were unknown until Wesołowska and Russell-Smith's (2022) recent redescription of the African *I. principalis* (Wesołowska, 2000), known from Côte d'Ivoire, Nigeria, and Zimbabwe (Wesołowska 2000; Wesołowska and Russell-Smith 2011, 2022). We have recently collected *I. rectangularis* Prószyński, 1992,

These authors are with equal authorship.

in India, allowing us to not only characterize it through living photographs and natural history information but also to describe its female for the first time and to gather genetic data. We set out to clarify its placement phylogenomically using ultraconserved element (UCE) data and with information on female genitalic morphology. Additionally, we provide a comprehensive generic diagnosis and redescribe both species.

Materials and methods

Materials examined

The specimens of *I. rectangularis* were recently collected from the Desert National Park, Rajasthan, India. They are currently housed in the collection of the Centre for Animal Taxonomy and Ecology (CATE), Christ College, Kerala, with plans for eventual transfer to the Research Collections at the National Centre for Biological Sciences (NCBS), Bengaluru, Karnataka, India (http://collections.ncbs.res.in), for permanent deposition. NRC-AA-#### represent NCBS voucher codes of *I. rectangularis* used for taxonomic work, where #### represents a four-digit number.

The *I. principalis* specimens used in this study were in vials in a large jar of poorly labeled salticid specimens in the Natural History Museum, London (NHMUK). All the vials in the jar contained, typically, African salticids. Their labels bore only codes of the form "PNB ###", where ### is a two- or three-digit number. We interpret these to likely be Lamotte's collection from Parc Nacional Banco (hence, "PNB"), Côte d'Ivoire, from which Wanless (1985) cites similar code labels under *Sonoita lightfooti* Peckham & Peckham, 1903, e.g., PNB 179, PNB 146. Some specimens are identified by voucher codes of the form DDKM21.###, where ### is a three-digit number.

Morphology

We examined and photographed ethanol-preserved specimens using an Olympus OM-D E-M10 II camera mounted on an Olympus SZX12 or a Leica DMC4500 camera attached to a Leica M205 C stereoscope. We used a drawing tube attached to a Nikon ME600L compound microscope to prepare illustrations of *I. principalis*. We used clove oil for clear viewing of epigyne after digesting the internal epigynal soft tissues with pancreatin. We stacked photographs using Helicon Focus 7.6.6 Pro. We prepared the drawings of *I. rectangularis* specimens by digitally tracing the photographs.

Descriptions of color patterns are based on ethanol-preserved specimens. Carapace length is measured from the base of the anterior median eyes to the posterior margin of the carapace medially, while abdomen length is measured from the anterior to the end of the anal tubercle. All measurements are in millimeters. Leg measurements are represented as follows: total length (femur, patella,

tibia, metatarsus, and tarsus). Abbreviations used here are as follows: **CO**, copulatory opening; **ECP**, epigynal coupling pocket; **PME**, posterior median eye; **PLE**, posterior lateral eye; **RTA**, retrolateral tibial apophysis.

Taxon sampling for phylogenomic analysis

To test the phylogenetic placement of *Iranattus*, molecular data was gathered for *I. rectangularis* and added to Marathe et al.'s (2024) UCE phylogenomic dataset, which included 15 plexippines, two harmochirines, and one salticine. Because *Iranattus*'s former placement in the Harmochirina was based in part on some *Pellenes* having a similar cymbial apophysis, one such *Pellenes* (*Pellenes limbatus*) was added to the dataset to give the harmochirines the best chance to capture *Iranattus* in the phylogenetic analysis. An extra outgroup taxon, *Chrysilla volupe* (Karsch, 1879), was also added. The total set of 21 species used in the phylogenomic analysis, with their taxonomic authority indicated, is listed in Table 1.

Ultraconserved element (UCE) data

Molecular data was gathered for UCE loci using target enrichment sequencing methods (Faircloth 2017), using the RTA_v2 probeset (Zhang et al. 2023), and following the protocols of Marathe et al. (2024).

Raw demultiplexed reads were processed with PHY-LUCE v. 1.6 (Faircloth 2016), quality control and adapter removal were performed with Illumiprocessor wrapper (Faircloth 2013), and assemblies were created with SPAdes v. 3.14.1 (Nurk et al. 2013) using options at default settings. The UCE loci were recovered using RTA_v2 probeset (Zhang et al. 2023). The recovered loci were aligned with MAFFT using L-INS-i option (Katoh and Standley 2013). The aligned UCE loci were then trimmed with Gblocks (Castresana 2000; Talavera and Castresana 2007) using -b1 0.5, -b2 0.7, -b3 8, -b4 8, -b5 0.4 settings and re-aligned with MAFFT using L-INS-i option within Mesquite v. 3.81 (Maddison and Maddison 2023b). As in the analysis of Maddison et al. (2020), suspected paralogous loci were deleted based on branch lengths in RAxML (Stamatakis 2014) inferred gene trees. Loci represented in fewer than 10 taxa total were deleted.

Phylogenetic analysis

Maximum-likelihood phylogenetic and bootstrap analyses were performed with IQ-TREE v. 2.2.0 (Nguyen et al. 2015) using the Zephyr v. 3.31 package (Maddison and Maddison 2023a) in Mesquite v. 3.81 (Maddison and Maddison 2023b) on the concatenated, unpartitioned UCE dataset with 20 taxa. For the phylogenetic tree inference, the option -m TEST (standard model selection followed by tree inference, edge-linked partition model,

Table 1. Specimens used in phylogenomic analysis.

Species	Voucher	Sex	Locality	Lat, long
Anarrhotus fossulatus Simon, 1902	AS19.1319	8	Singapore	1.379, 103.816
Artabrus erythrocephalus (C.L. Koch, 1846)	AS19.2205	8	Singapore	1.355-7, 103.774-5
Baryphas ahenus Simon, 1902	d536	8	South Africa	-25.95, 30.56
Bianor maculatus (Keyserling, 1883)	NZ19.9864	3	New Zealand	-42.1691, 172.8090
Carrhotus sp.	AS19.4650	8	India	12.2145, 75.653-4
Chrysilla volupe (Karsch, 1879)	AS19.6089	8	India	12.223, 76.627
Epeus sp.	DDKM21.055	8	Singapore	1.355, 103.78
Evacin bulbosa (Żabka, 1985)	AS19.2123	8	Singapore	1.406, 103.971
Evarcha falcata (Clerck, 1757)	RU18-5264	8	Russia	53.721, 77.726
Ghatippus paschima Marathe & Maddison, 2024	IBC-BP833	8	India	12.220-1, 75.657-8
Habronattus hirsutus (Peckham & Peckham, 1888)	IDWM.21018	8	Canada	48.827, -123.265
Hyllus keratodes (van Hasselt, 1882)	DDKM21.028	8	Malaysia	3.325, 101.753
Hyllus semicupreus (Simon, 1885)	AS19.4415	8	India	12.2156, 75.6606
Iranattus rectangularis Prószyński, 1992	DDKM21.091	juv.	India	26.28, 70.40
Pancorius dentichelis (Simon, 1899)	SWK12-0042	8	Malaysia	1.605-6, 110.185-7
Pancorius petoti Prószyński & Deeleman-Reinhold, 2013	SWK12-0195	8	Malaysia	1.603-4, 110.185
Pellenes limbatus Kulczyński, 1895	RU18-5679	8	Russia	50.0501, 89.3878
Plexippus paykulli (Audouin, 1826)	AS19.7337	8	India	12.825-6, 78.252-3
Ptocasius weyersi Simon, 1885	DDKM21.069	8	Singapore	1.36, 103.78
Telamonia festiva Thorell, 1887	DDKM21.048	8	China	21.8105, 107.2925
Thyene imperialis (Rossi, 1846)	AS19.6443	8	India	12.216, 76.625

no partition-specific rates) was used with 10 search replicates. For the bootstrap analysis, a single IQ-TREE search was used for each of the 1000 search replicates.

Data availability

The raw sequence reads obtained from UCE capture are stored within the Sequence Read Archive (BioProject: https://www.ncbi.nlm.nih.gov/bioproject/1101580), and their accession numbers are listed in Table 1. The UCE loci matrices from SPAdes assemblies, pre-Gblocks, and the concatenated matrices used for phylogenetic and bootstrap analysis, along with trees, are available on the Dryad data repository (https://doi.org/10.5061/dryad.ht76hdrpz).

Results

Phylogenetic results

Table 2 lists the sequence data recovered from the 21 taxa. 3398 UCE loci were initially recovered. Of these, 3140 remained after removing those represented in fewer than 10 taxa, and 3104 remained after removing those suspected to include paralogies on branch lengths. These were concatenated into the final matrix, whose aligned length is 2779616 base pairs, in which each taxon had on average ~2.2 million base pairs of sequence data (min. 985191, max. 2462121).

The phylogenetic results are shown in Fig. 1. The reciprocal monophyly of the subtribes Plexippina and Harmochirina

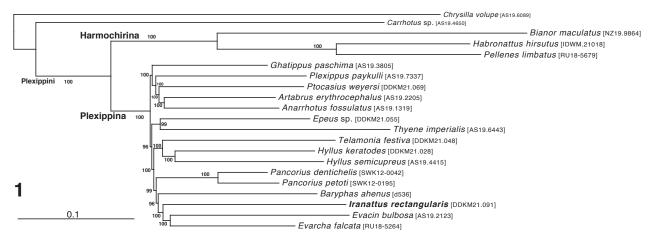


Figure 1. The IQ-TREE-based maximum-likelihood tree, represented here, is the best of 10 replicates, inferred from a concatenated dataset of 3104 UCE loci. The numbers at the nodes are the percentage recovery of the clade based on 500 bootstrap replicates. *Iranattus rectangularis* is recovered distantly from the subtribe Harmochirina and placed as the sister lineage to *Evarcha sensu lato* within the subtribe Plexippina.

Table 2. Specifics of molecular data used for this phylogenomic analysis. Molecular data was generated based on the RTA_v2 probeset. "SRA" is the Sequence Read Archive accession number available through NCBI; "Reads pass QC" is the number of reads after the removal of adapter contamination and low-quality bases using Illumiprocessor; "Total UCE loci" is the total number of UCE loci recovered with RTA_v2 probeset; "After paralogy filter" is the number of UCE loci after deletion of suspected paralogous loci based on branch length ratios; "In at least 10 taxa" is the number of UCE loci in at least 10 or more taxa after branch length criteria; "Filtered UCE sequence length" is the concatenated sequence length of filtered UCE loci; "Total loci" is the number of UCE loci represented among all taxa.

Species	Voucher	SRA	Reads pass QC	Total UCE loci	In at least 10 taxa	After paralogy filter	Filtered UCE sequence length
Anarrhotus fossulatus	AS19.1319	SRR27728361	15542927	2525	2444	2414	2100562
Artabrus erythrocephalus	AS19.2205	SRR27728359	14903498	2837	2792	2759	2333639
Baryphas ahenus	d536	SRR27728358	2653688	2256	2243	2217	985191
Bianor maculatus	NZ19.9864	SRR27728369	7914005	2962	2853	2820	2422490
Carrhotus sp.	AS19.4650	SRR27728370	5272657	2920	2838	2806	2324883
Chrysilla volupe	AS19.6089	SRR28802507	4968344	2877	2782	2752	2313910
Epeus sp.	DDKM21.055	SRR27728357	13896435	2897	2834	2802	2452270
Evacin bulbosa	AS19.2123	SRR27728356	10851810	2766	2684	2653	2157554
Evarcha falcata	RU18-5264	SRR27728355	11538276	2762	2714	2683	2215341
Ghatippus paschima	IBC-BP833	SRR27728354	7881860	2893	2836	2804	2430054
Habronattus hirsutus	IDWM.21018	SRR27728360	6581974	2821	2732	2702	2218729
Hyllus keratodes	DDKM21.028	SRR27728353	11349372	2926	2843	2811	2415960
Hyllus semicupreus	AS19.4415	SRR27728368	9874003	2942	2874	2839	2422661
Iranattus rectangularis	DDKM21.091	SRR28802508	14825117	2926	2849	2818	2008593
Pancorius dentichelis	SWK12-0042	SRR27728367	6025337	3092	3022	2988	2316987
Pancorius petoti	SWK12-0195	SRR27728366	5116119	2980	2908	2875	2304191
Pellenes limbatus	RU18-5679	SRR28802506	4288156	2661	2603	2576	1977916
Plexippus paykulli	AS19.7337	SRR27728365	7445183	2931	2852	2817	2186676
Ptocasius weyersi	DDKM21.069	SRR27728364	9926900	2880	2821	2790	2326688
Telamonia festiva	DDKM21.048	SRR27728363	7908436	2950	2889	2855	2462121
Thyene imperialis	AS19.6443	SRR27728362	7797854	2893	2818	2789	2421843
			Average:	2843	2773	2741	2228488
			Minimum:	2256	2243	2217	985191
			Maximum:	3092	3022	2988	2462121
			Total loci:	3398	3140	3104	2779616

is consistent with previous molecular phylogenetic studies with both Sanger sequencing and UCEs (Maddison and Hedin 2003; Maddison et al. 2008; Bodner and Maddison 2012; Marathe et al. 2024). The phylogenetic structure within Plexippina is largely consistent with Marathe et al. (2024) and has generally high bootstrap values.

Iranattus is nestled well within Plexippina, placed as a sister lineage to Evarcha Simon, 1902 sensu lato (see Fig. 1). The harmochirine included in the analysis with a similar cymbial apophysis, Pellenes limbatus, is placed as expected within the harmochirines. Thus, the similarities between Iranattus and harmochirines noted by Wesołowska (2000) and Maddison (2015) are convergences.

The placement of *Iranattus* in the Plexippina is also supported by the form of the epigyne. Wesołowska and Russell-Smith (2022) report a pair of coupling pockets in *I. principalis*, one on either side of a central atrium housing the copulatory openings, the same as we have found in *I. rectangularis* (Figs 22, 28). This arrangement is discordant with that of harmochirines, which have a single epigynal coupling pocket placed centrally, anterior to the margin, flanked by copulatory openings on either side. Two pockets are typical, however, for members of

the Plexippina (e.g., Evarcha, Baryphas Simon, 1902; Pancorius Simon, 1902; Telamonia Thorell, 1887; Vicirionessa Wesołowska & Russell-Smith, 2022).

We therefore recognize *Iranattus* as a member of the subtribe Plexippina.

Taxonomic results

Family Salticidae Blackwall, 1841 Tribe Plexippini Simon, 1901 Subtribe Plexippina Simon, 1901

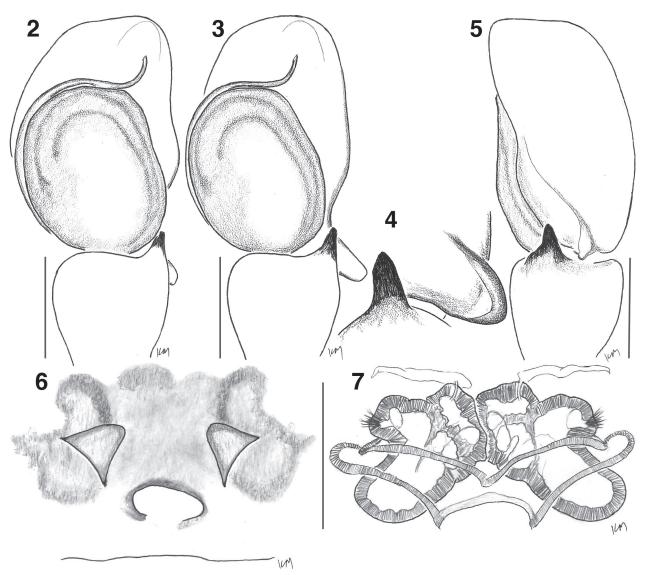
Iranattus Prószyński, 1992

Figs 2-41

Iranattus Prószyński, 1992: 97-98, f. 35-40.

Monomotapa Wesołowska, 2000: 159, f. 42–46 (synonymized by Prószyński, 2017: 36.).

Type species. *Iranattus rectangularis* Prószyński, 1992. Species included. *Iranattus principalis* (Wesołowska, 2000); *Iranattus rectangularis* Prószyński, 1992.



Figures 2–7. *Iranattus principalis* genitalia drawings. **2.** Male left palp, ventral view (DDKM21.089); **3.** Ditto, oblique view (DDKM21.089); **4.** Ditto, oblique view, closeup of the cymbial apophysis (DDKM21.089); **5.** Ditto, retrolateral view (DDKM21.089); **6.** Epigyne, ventral view (DDKM21.090); **7.** Vulva, dorsal view (DDKM21.089). Scale bars: 0.2 mm.

Diagnosis. The remarkably long third legs of Iranattus (Figs 15, 18, 30, 32) and scoop-shaped cymbial apophysis (Fig. 4) differentiate it from all other plexippines. The very robust carapace, bulging outward at the PLE and bearing the PLEs on tubercles, is unusual but shared also with Afrobeata Caporiacco, 1941, and Vailimia Kammerer, 2006. Vailimia especially might be confused with Iranattus, as they share erect hairs on the carapace (see Figs 34, 38, 41) and a compact crouch stance, but, besides the cymbial apophysis and long third legs, Iranattus also has a shorter embolus lacking membrane (membrane-accompanied long embolus in Vailimia), a short RTA (long and curved in Vailimia), and two distinct deep conical ECPs (absent in Vailimia). From Afrobeata, Iranattus differs in having longer third legs, a cymbial apophysis (lacking in Afrobeata), a shorter embolus (longer in Afrobeata), a simple short RTA (bifurcated in Afrobeata), shorter copulatory ducts (long in Afrobeata), and deep conical ECPs (shallow in Afrobeata). Some other plexippines have cymbial apophyses (Plexippoides Prószyński, 1984; Epeus Peckham & Peckham, 1886; and *Erasinus* Simon, 1899), but their apophyses are different in shape—in *Iranattus*, a long, broad blade with a rounded tip, concave in front so as to form a scoop; in *Plexippoides*, sharply pointed, for example.

Iranattus principalis (Wesołowska, 2000)

Figs 2-19

Monomotapa principalis Wesołowska, 2000: 160, 42-46.

Monomotapa principalis Wesołowska & Russell-Smith, 2011: 581, 96–98, 229–230.

Iranattus principalis Prószyński, 2017: 36, 14K, 17F (transferred from Monomotapa).

Iranattus principalis Wesołowska & Russell-Smith, 2022: 47, 29A–D, 30A–D.

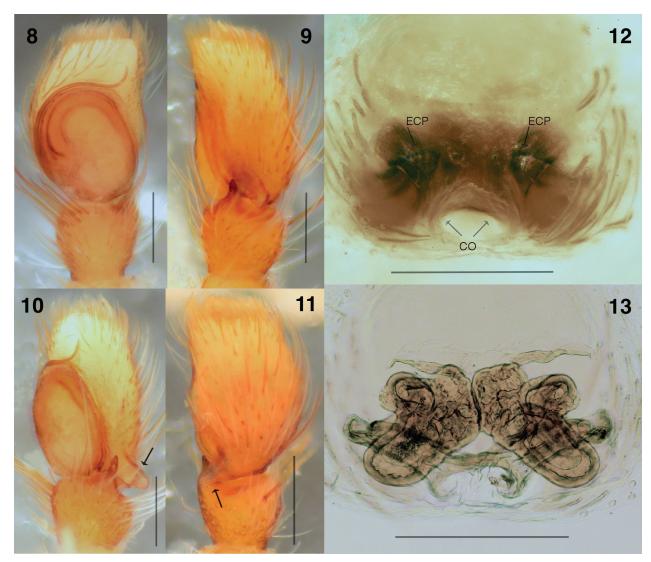
Materials examined. In NHMUK, lacking complete labels. These are likely from Parc Nacional Banco, Côte d'Ivoire (see "Materials examined" for explanation).

Diagnosis. Larger than *I. rectangularis*, with an almost ovoid tegulum with a less prominent shoulder, RTA slightly bent near the tip (Figs 10, 11), and a multi-chambered spermatheca sandwiched between copulatory ducts dorsally and the epigynal plate ventrally.

Description. ♂ (DDKM21.089). Measurements: Carapace 2.2 long, 2.1 wide. Abdomen length 1.7; width 1.4. Leg measurements: I–11.2 (3.4, 2.2, 2.4, 1.8, 1.3); II–10 (2.8, 2, 2.4, 1.5, 1.2); III–16.6 (6.3, 2.9, 3.2, 2.5, 1.7); IV–10.1 (3.7, 1.6, 1.7, 1.8, 1.3). Leg formula III-IV-II-I. *Carapace* wider than abdomen. Ocular area shaped like an isosceles trapezoid, narrow at the anterior eye row and wide at the PLEs. PLEs on tubercles. Thoracic area slopes acutely downward behind ocular area. Ocular area anteriorly golden yellow, and remaining carapace dark brown. Lateral sides posteriorly and back sparsely covered with pale

hairs. *Clypeus* narrow, yellowish-brown sparsely covered with hairs. *Chelicerae* vertical, narrow, yellowish brown. *Palp* (Figs 2–5, 8–11): Embolus medium-long, starting at 7 o'clock. RTA stout, short with blunt tip. Cymbium extends retrolaterally to form scoop-shaped apophysis. Tegulum prolaterally rounder; retrolaterally slightly angular at distal and proximal edges. *Legs*: III femur distinctly long. Femur golden yellow, distal segments yellowish-brown. *Abdomen* narrow, ovoid. Golden yellow with less prominent transverse pale bands. Spinnerets yellowish.

♀ (DDKM21.090). Measurements: Carapace 5.1 long, 5.1 wide. Abdomen length 6.4; width 4.8. Leg measurements: I–11.7 (3.8, 1.8, 2.7, 2.1, 1.3); II–11.6 (3.3, 2.8, 2.4, 1.8, 1.3); III–19.7 (6.9, 3.3, 4.7, 3.1, 1.8); IV–11.4 (2.9, 2.1, 2.3, 2.6, 1.5). Leg formula III-I-II-IV. *Carapace* shape similar to male, width about same as abdomen. Brown, sparsely covered with pale hairs. *Clypeus* similar to male. *Chelicerae* similar to male. *Legs* similar to male. *Abdomen* ovoid, bulky, yellowish, covered with brown hairs, and more posteriorly.



Figures 8–13. *Iranattus principalis* genitalia photographs. **8.** Male left palp, ventral view (DDKM21.089); **9** Ditto, retrolateral view (DDKM21.089); **10.** Ditto, oblique view (DDKM21.089); **11.** Ditto, retrolateral view (DDKM21.089); **12.** Epigyne, ventral view (DDKM21.090); **13.** Vulva, dorsal view (DDKM21.089). **ECP**, epigynal coupling pocket. **CO**, copulatory opening. Scale bars: 0.2 mm. Arrows in Figs **10** and **11** point to the scoop-shaped retrolateral cymbial apophysis.

Spinnerets yellowish. *Epigyne* (Figs 6, 7, 12, 13): Medially located copulatory opening flanked by conical-shaped ECP.

Natural history. Wesołowska and Russell-Smith (2022) report *Iranattus principalis* as collected from the branches of savannah shrubs. G. Azarkina (pers. comm.) has seen material of this species from canopy fogging in tropical savannas in Cameroon (2♀ 8.40°N, 12.80°E) and Côte d'Ivoire (1♀ 8.40°N, 12.80°E; 2♂ 2♀ 8°44′N, 3°49′W) in the Musée royal de l'Afrique centrale, collected from the trees *Cola laurifolia*, *Combretum fragrans*, *Anogeissus leiocarpus*, and *Crossopteryx febrifuga*.

Distribution. Côte d'Ivoire, Nigeria, Zimbabwe, and Cameroon.

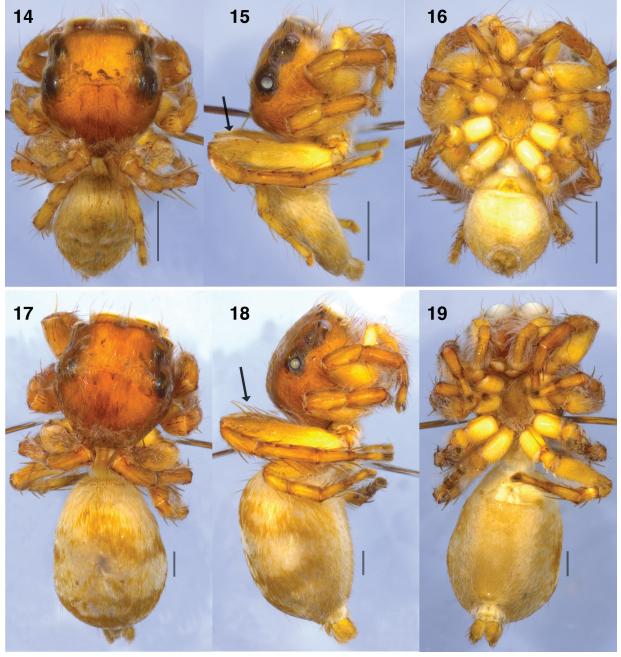
Iranattus rectangularis Prószyński, 1992

Figs 20-41

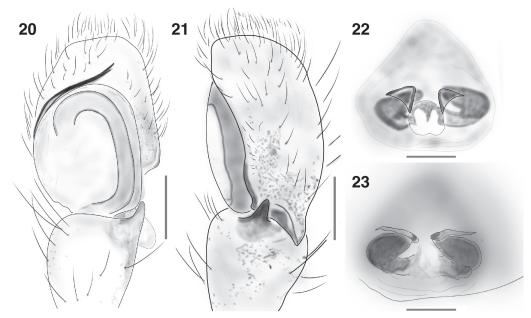
Iranattus rectangularis Prószyński, 1992a: 97, f. 35-40.

Materials examined. 1 ♂, 1♀, & 4 juveniles. From INDIA: RAJASTHAN: Jaisalmer: Thar Desert: Desert National Park, Myajlar area, 26.28°N, 70.40°E, 275 m elev., 20 Aug 2022, leg. R. Tripathi.

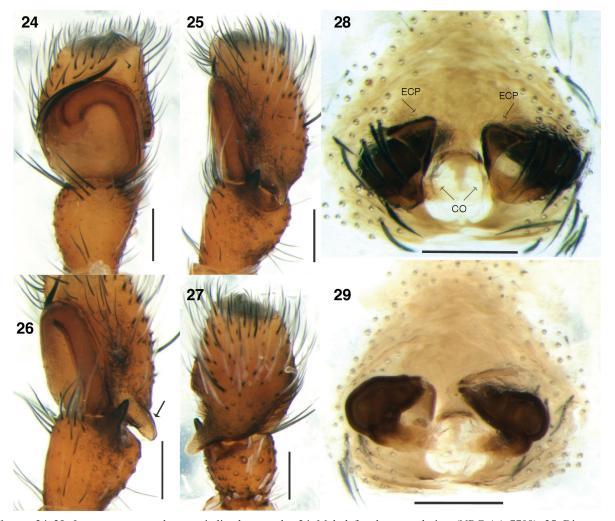
Diagnosis. Smaller than *I. principalis*, with a bright orange face and erect hairs on the carapace, an angular tegulum with a prominent shoulder, a simple RTA, and a simple spermatheca with copulatory ducts ventrally.



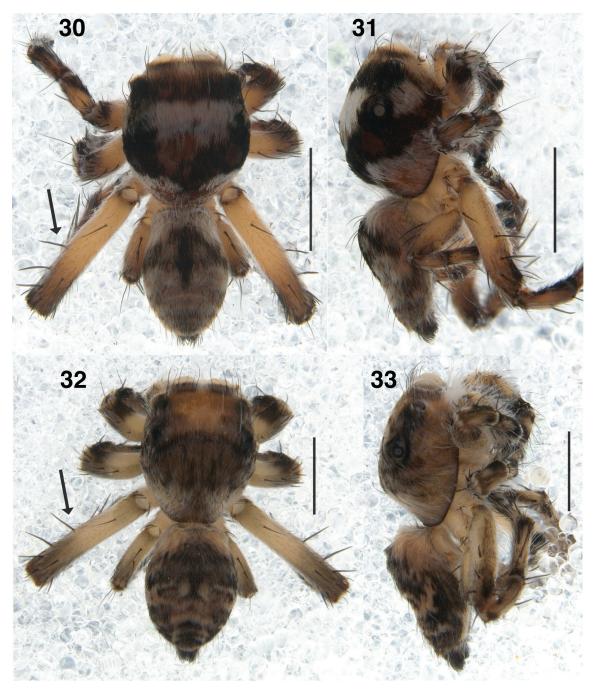
Figures 14–19. *Iranattus principalis* habitus. **14.** Male, dorsal view (DDKM21.089); **15.** Ditto, lateral view (DDKM21.089); **16.** Ditto, ventral view (DDKM21.089); **17.** Female, dorsal view (DDKM21.090); **18.** Ditto, lateral view (DDKM21.090); **19.** Ditto, ventral view (DDKM21.090). Scale bars: 1 mm. Arrows in Figs **15** and **18** point to the long third legs.



Figures 20–23. *Iranattus rectangularis* genitalia drawings. **20.** Male left palp, oblique view (NRC-AA-7708); **21.** Ditto, retrolateral view (NRC-AA-7708); **22.** Epigyne, ventral view (NRC-AA-7709); **23.** Vulva, dorsal view (NRC-AA-7709). Scale bars: 0.1 mm.



Figures 24–29. *Iranattus rectangularis* genitalia photographs. **24.** Male left palp, ventral view (NRC-AA-7708); **25.** Ditto, retrolateral view (NRC-AA-7708); **26.** Ditto, oblique view (arrow points to the scoop-shaped retrolateral cymbial apophysis); **27.** Ditto, dorsal view (NRC-AA-7708); **28.** Epigyne, ventral view (NRC-AA-7709); **29.** Vulva, dorsal view (NRC-AA-7709). **ECP**, epigynal coupling pocket. **CO**, copulatory opening. Scale bars: 0.1 mm.



Figures 30–33. *Iranattus rectangularis* habitus. **30.** Male, dorsal view (NRC-AA-7708); **31.** Ditto, lateral view (NRC-AA-7708); **32.** Female, dorsal view (NRC-AA-7709); **33.** Ditto, lateral (NRC-AA-7709). Scale bars: 1 mm. Arrows in Figs **30** and **32** point to the elongated third legs.

Description. ♂ (NRC-AA-7708). Measurements: Carapace 1.46 long, 1.26 wide. Abdomen length 1.32, width 0.86. Leg measurements: Leg I 2.04 [0.69, 0.33, 0.48, 0.32, 0.22], leg II 1.88 [0.67, 0.33, 0.44, 0.28, 0.16], leg III 3.56 [1.52, 0.55, 0.72, 0.43, 0.34], leg IV 1.94 [0.70, 0.31, 0.34, 0.38, 0.24. Leg formula: III–IV–II. *Carapace* wider than abdomen. Ocular area shaped like an isosceles trapezoid, narrow at the anterior eye row and wide at the PLEs. PLEs on tubercles. Thoracic area slopes acutely downward behind ocular area. Ocular area from base of front eyes to PMEs orange, covered with black hairs, posterior with pale hairs. Pale erect hairs on ocular area. Pale

hair patch beneath PMEs. Black hair band starts anteriorly, encircles carapace at ocular area edge. White band along lateral edge, narrow front, broadens posteriorly and behind. *Clypeus* narrow. Orange, covered with pale hairs, more densely near integument edge. *Chelicerae* vertical, narrow, yellowish brown. *Palp* (Figs 20, 21, 24–27): Embolus medium-long, starting at 9 o'clock, somewhat thick. RTA stout, short with blunt tip. Cymbium extends retrolaterally to form scoop-shaped apophysis. Tegulum prolaterally rounder; retrolaterally angular at distal and proximal edges. *Legs*: III femur distinctly long relative to others. Femur yellowish, distal segments yellowish



Figures 34-41. Iranattus rectangularis habitus. 34-38. Male; 39-41. Female.

covered with black hair. *Abdomen* narrow, ovoid. Brown with gray hair overlay. Spinnerets brown.

♀ (NRC-AA-7709). Measurements: Carapace 1.91 long, 1.56 wide. Abdomen length 1.83, width 1.27. Leg measurements: Leg I 2.67 [0.95, 0.53, 0.56, 0.36, 0.27], leg II 2.41 [0.85, 0.47, 0.50, 0.32, 0.27], leg III 4.30 [1.78, 0.70, 0.92, 0.50, 0.40], leg IV 2.44 [0.87, 0.40, 0.42, 0.44, 0.31]. Leg formula III–IV–II. *Carapace* shape similar to male. Ocular area orange anteriorly, white hairs sparsely posteriorly. Pale erect hairs on ocular area. Thoracic slope covered with black hairs. Lateral sides covered with pale hairs, almost merging behind. *Clypeus* similar as in male. *Chelicerae* similar to male. *Legs* similar to male.

Abdomen shape comparable to male, but with a 'kite'-shaped black color pattern between posterior edge and median. **Epigyne** (Figs 22, 23, 28–29): Medially located copulatory opening flanked by conical-shaped ECP.

Natural history. *Iranattus rectangularis* was collected from the branches of non-native *Vachellia tortilis* alongside artificial water canals in the Desert National Park, a xeric and desert ecosystem located in Rajasthan, India (Figs 42, 43). The mosaic of orange, black, and grey body coloration helps them blend in with the branches, making them inconspicuous, except that in the field, the orangish faces of males (Fig. 34) sometimes stood out.

Distribution. Iran, India (Rajasthan).



Figures 42, 43. *Iranattus rectangularis* habitat. **42.** *Vachellia tortilis* woodland; **43.** Aerial views of the landscape of the Desert National Park, Rajasthan, India.

Discussion. *Iranattus rectangularis* is reported for the first time east of Iran, in western India. This seemingly 'disjunct' distributional pattern is quite possibly due to a lack of collecting between the sites and mirrors that of *Stenaelurillus marusiki* Logunov, 2001 (Salticidae: Aelurillina), where the type locality of *S. marusiki* is Iran. However, it has been reported much farther southeast in Maharashtra, India (Marathe et al. 2022). With the transfer of *Iranattus* to Plexippina, the subtribe now contains 35 genera, and the number of plexippines in India stands at 47 species and 18 genera.

Acknowledgements

Collection of I. rectangularis was facilitated by the Bustard Recovery Programme of the Wildlife Institute of India (WII), funded by the National Compensatory Afforestation Fund Management and Planning Authority, Government of India, and supplemented by an additional grant from the Rajasthan State Pollution Control Board. RT and AVS thank Rev. Fr. Jolly Andrews, CMI of Christ College (Irinjalakuda), for facilities and NCBS research collections. RT acknowledges the support of Dr. Sutirtha Dutta, Dr. Manju Siliwal, and Mr. Ashish Kumar Jangid from WII, as well as the Rajasthan State Forest Department, for the collecting permit. Special thanks to Sohan Lal Genwa and Amrat Genwa for their assistance during field activities. RT thanks Anshuman Pati and Jason D. Gerard for habitat photographs. RT acknowledges CSIR-UGC for fellowship. KM thanks Dr. Krushnamegh Kunte, NCBS, for providing the lab space and supplies. KM and WPM thank Carol Ritland and Allyson Miscampbell of the Genetic Data Centre at the University of British Columbia for assistance with lab facilities. We thank J. Beccaloni (NHMUK) for the loan of *I. principalis* specimens. We thank Galina Azarkina for providing information on additional material of *I. principalis* she examined. We thank Dmitry Logunov, Galina Azarkina, and Tamás Szűts for their time reviewing the manuscript and providing valuable comments. Funding to WPM was provided by an NSERC Canada Discovery Grant.

References

Bodner MR, Maddison WP (2012) The biogeography and age of salticid spider radiations (Araneae: Salticidae). Molecular Phylogenetics and Evolution 65(1): 213–240. https://doi.org/10.1016/j. ympev.2012.06.005

Castresana J (2000) Selection of conserved blocks from multiple alignments for their use in phylogenetic analysis. Molecular Biology and Evolution 17(4): 540–552. https://doi.org/10.1093/oxfordjournals.molbev.a026334

Faircloth BC (2013) illumiprocessor: a trimmomatic wrapper for parallel adapter and quality trimming. https://doi.org/10.6079/J9ILL

Faircloth BC (2016) PHYLUCE is a software package for the analysis of conserved genomic loci. Bioinformatics (Oxford, England) 32(5): 786–788. https://doi.org/10.1093/bioinformatics/btv646

Faircloth BC (2017) Identifying conserved genomic elements and designing universal bait sets to enrich them. Methods in Ecology and Evolution 8(9): 1103–1112. https://doi.org/10.1111/2041-210X.12754

Katoh K, Standley DM (2013) MAFFT Multiple Sequence Alignment Software Version 7: Improvements in Performance and Usability. Molecular Biology and Evolution 30(4): 772–780. https://doi. org/10.1093/molbev/mst010

Maddison WP (2015) A phylogenetic classification of jumping spiders (Araneae: Salticidae). The Journal of Arachnology 43(3): 231. https://doi.org/10.1636/arac-43-03-231-292

Maddison WP, Hedin MC (2003) Jumping spider phylogeny (Araneae : Salticidae). Invertebrate Systematics 17(4): 529. https://doi.org/10.1071/IS02044

Maddison DR, Maddison WP (2023a) Zephyr: a Mesquite package for interacting with external phylogeny inference programs. http://zephyr.mesquiteproject.org

Maddison WP, Maddison DR (2023b) Mesquite: a modular system for evolutionary analysis. http://www.mesquiteproject.org/ [August 18, 2023]

Maddison WP, Bodner MR, Needham KM (2008) Salticid spider phylogeny revisited, with the discovery of a large Australasian clade (Araneae: Salticidae). Zootaxa 1893(1): 49. https://doi.org/10.11646/zootaxa.1893.1.3

Maddison WP, Beattie I, Marathe K, Ng PYC, Kanesharatnam N, Benjamin SP, Kunte K (2020) A phylogenetic and taxonomic review of baviine jumping spiders (Araneae, Salticidae, Baviini). ZooKeys 1004: 27–97. https://doi.org/10.3897/zookeys.1004.57526

Marathe K, Sanap R, Joglekar A, Caleb JTD, Maddison WP (2022)
Three new and notes on two other jumping spider species of the genus *Stenaelurillus* Simon, 1886 (Salticidae: Aelurillina) from the Deccan Plateau, India. Zootaxa 5125(1): 1–19. https://doi.org/10.11646/zootaxa.5125.1.1

Marathe K, Maddison WP, Kunte K (2024) *Ghatippus paschima*, a new species and genus of plexippine jumping spider from the Western Ghats of India (Salticidae, Plexippini, Plexippina). ZooKeys 1191: 89–103. https://doi.org/10.3897/zookeys.1191.114117

- Nguyen L-T, Schmidt HA, Von Haeseler A, Minh BQ (2015) IQ-TREE: A fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. Molecular Biology and Evolution 32(1): 268–274. https://doi.org/10.1093/molbev/msu300
- Nurk S, Bankevich A, Antipov D, Gurevich A, Korobeynikov A, Lapidus A, Prjibelsky A, Pyshkin A, Sirotkin A, Sirotkin Y, Stepanauskas R, McLean J, Lasken R, Clingenpeel SR, Woyke T, Tesler G, Alekseyev MA, Pevzner PA (2013) Assembling Genomes and Mini-metagenomes from Highly Chimeric Reads. In: Deng M, Jiang R, Sun F, Zhang X (Eds) Research in Computational Molecular Biology. Lecture Notes in Computer Science. Springer Berlin Heidelberg, Berlin, Heidelberg, 158–170. https://doi.org/10.1007/978-3-642-37195-0 13
- Prószyński J (1992) Salticidae (Araneae) of the Old World and Pacific Islands in several US collections. Annales Zoologici, Warszawa 44: 87–163.
- Prószyński J (2017) Pragmatic classification of the world's Salticidae (Araneae). Ecologica Montenegrina 12: 1–133. https://doi.org/10.37828/em.2017.12.1
- Stamatakis A (2014) RAxML version 8: A tool for phylogenetic analysis and post-analysis of large phylogenies. Bioinformatics (Oxford, England) 30(9): 1312–1313. https://doi.org/10.1093/bioinformatics/btu033

- Talavera G, Castresana J (2007) Improvement of Phylogenies after Removing Divergent and Ambiguously Aligned Blocks from Protein Sequence Alignments. Kjer K, Page R, Sullivan J (Eds) Systematic Biology 56: 564–577. https://doi.org/10.1080/10635150701472164
- Wanless FR (1985) A revision of the spider genera *Holcolaetis* and *Sonoita* (Araneae: Salticidae). Bulletin of the British Museum (Natural History). Bulletin of the British Museum, Natural History. Zoology 48: 249–278. https://doi.org/10.5962/bhl.part.23463
- Wesołowska W (2000) New and little known species of jumping spiders from Zimbabwe (Araneae: Salticidae). Arnoldia Zimbabwe 10: 145–174.
- Wesołowska W, Russell-Smith A (2011) Jumping Spiders (Araneae: Salticidae) from Southern Nigeria. Annales Zoologici 61(3): 553–619. https://doi.org/10.3161/000345411X603409
- Wesołowska W, Russell-Smith A (2022) Jumping spiders from Ivory Coast collected by J.-C. Ledoux (Araneae, Salticidae). European Journal of Taxonomy 841(1): 1–143. https://doi.org/10.5852/ejt.2022.841.1943
- World Spider Catalog (2024) World Spider Catalog. https://wsc.nmbe.ch/ [August 18, 2023]
- Zhang J, Li Z, Lai J, Zhang Z, Zhang F (2023) A novel probe set for the phylogenomics and evolution of RTA spiders. Cladistics 39(2): 116–128. https://doi.org/10.1111/cla.12523

ZOBODAT - www.zobodat.at

Zoologisch-Botanische Datenbank/Zoological-Botanical Database

Digitale Literatur/Digital Literature

Zeitschrift/Journal: Zoosystematics and Evolution

Jahr/Year: 2024

Band/Volume: 100

Autor(en)/Author(s): Marathe Kiran, Tripathi Rishikesh, Sudhikumar Ambalaparambil Vasu, Maddison Wayne P.

Artikel/Article: Phylogenomic placement and revision of Iranattus PrószyÅ, ski, 1992 jumping spiders (Salticidae, Plexippini, Plexippina) 531-542