

## **Conspecificity of *Phintella aequipeiformis* Zabka, 1985 and *P. lucai* Zabka, 1985 (Araneae: Salticidae) confirmed by DNA barcoding**

Authors: Hong Luong, Phung Thi, Yamasaki, Takeshi, and Eguchi, Katsuyuki

Source: Revue suisse de Zoologie, 123(2) : 283-290

Published By: Muséum d'histoire naturelle, Genève

URL: <https://doi.org/10.5281/zenodo.155301>

---

The BioOne Digital Library (<https://bioone.org/>) provides worldwide distribution for more than 580 journals and eBooks from BioOne's community of over 150 nonprofit societies, research institutions, and university presses in the biological, ecological, and environmental sciences. The BioOne Digital Library encompasses the flagship aggregation BioOne Complete (<https://bioone.org/subscribe>), the BioOne Complete Archive (<https://bioone.org/archive>), and the BioOne eBooks program offerings ESA eBook Collection (<https://bioone.org/esa-ebooks>) and CSIRO Publishing BioSelect Collection (<https://bioone.org/csiro-ebooks>).

Your use of this PDF, the BioOne Digital Library, and all posted and associated content indicates your acceptance of BioOne's Terms of Use, available at [www.bioone.org/terms-of-use](http://www.bioone.org/terms-of-use).

Usage of BioOne Digital Library content is strictly limited to personal, educational, and non-commercial use. Commercial inquiries or rights and permissions requests should be directed to the individual publisher as copyright holder.

---

BioOne is an innovative nonprofit that sees sustainable scholarly publishing as an inherently collaborative enterprise connecting authors, nonprofit publishers, academic institutions, research libraries, and research funders in the common goal of maximizing access to critical research.

## Conspecificity of *Phintella aequipeiformis* Zabka, 1985 and *P. lucai* Zabka, 1985 (Araneae: Salticidae) confirmed by DNA barcoding

Phung Thi Hong Luong<sup>1,2,\*</sup>, Takeshi Yamasaki<sup>1</sup> & Katsuyuki Eguchi<sup>1</sup>

<sup>1</sup> Systematic Zoology Laboratory, Department of Biological Sciences, Graduate School of Science and Engineering, Tokyo Metropolitan University, 1-1 Minami-Osawa, Hachioji-shi, Tokyo, 192-0397, Japan.

<sup>2</sup> Institute of Ecology and Biological Resources, Vietnam Academy of Science and Technology, 18 Hoang Quoc Viet Road, Cau Giay District, Hanoi, Vietnam.

\* Corresponding author: phungthihongluong@gmail.com

**Abstract:** *Phintella aequipeiformis* Zabka, 1985 was described from a male and *P. lucai* Zabka, 1985 from a female, but the opposite sex of each nominal species remained unknown. Both were collected from the same habitats of the same localities in our field work, and they share some similarities in the body color pattern. Moreover, our results from DNA barcoding show that both are one and the same species. We therefore place *P. lucai* in the synonymy of *P. aequipeiformis*, and provide a redescription of the species on the basis of both sexes.

**Keywords:** Taxonomy - jumping spider - synonyms - Vietnam.

### INTRODUCTION

The genus *Phintella* Strand in Bösenberg and Strand, 1906 (Araneae: Salticidae) is comprised of small and colorful species (Zabka, 2012; Caleb, 2014). A total of 60 species has so far been described, 47 of them from Asia (World Spider Catalog, 2016). Most *Phintella* species, as well as other salticids, show distinct sexual dimorphism in morphology of the first pair of legs and chelicerae and of coloration in the adult instar, and subsequently both sexes are not yet known for nearly half of the nominal species in this genus (World Spider Catalog, 2016). This means that more than a few synonymies are likely hidden in the current classification of the genus *Phintella*.

DNA barcoding has been increasingly introduced into taxonomy and identification of various taxa in recent years (Hebert *et al.*, 2003; Bickford *et al.*, 2006; Fisher & Smith, 2008; Robinson *et al.*, 2009; Pires & Marinoni, 2010). It is especially powerful for revealing male-female complementarity, and subsequently solving synonymies and/or unifying the male-based and female-based classifications (Barrett & Hebert, 2005; Robinson *et al.*, 2009; Ekrem *et al.*, 2010; Tanikawa, 2011; Glowska *et al.*, 2014). Thus, we are in process of revising the classification of Asian species of the genus *Phintella* using DNA barcoding as well as a traditional morphological approach. Our first result is presented here.

*Phintella aequipeiformis* Zabka, 1985 and *P. lucai*

Zabka, 1985 were described from northern Vietnam as different species. The holotype of the former is a male collected from Lao Cai Province, and that of the latter is a female from Yen Bai Province. The two type localities are separated by approximately 80 kilometers. Since their original description, the complementary sex remained unknown for both nominal species. However, conspecificity of *P. aequipeiformis* and *P. lucai* was indicated from the following results of our field work: i) males of *P. aequipeiformis* and females of *P. lucai* were collected from the same habitats of the same localities; ii) there are similarities in the body color pattern. Moreover, our result from DNA barcoding of specimens newly collected from northern and central Vietnam give further evidence for the conspecificity of *P. aequipeiformis* and *P. lucai*. We therefore propose *P. aequipeiformis* as the senior synonym of *P. lucai*, and redescribe *P. aequipeiformis* on the basis of both sexes.

### MATERIALS AND METHODS

**Specimen depositories:** MHNG, Muséum d'histoire naturelle, Geneva, Switzerland; NSMT, National Museum of Nature and Science, Tokyo, Japan; IEBR, Institute of Ecology and Biological Resources, Hanoi, Vietnam; LPC, private collection of corresponding author; HNHM, Hungarian Natural History Museum, Budapest, Hungary.

**Sampling and specimen preparation:** Specimens were collected from northern and central Vietnam (Fig. 1). Each spider was killed using acetyl acid, and, in fresh condition, a series of images of the body in dorsal view was captured at different focal planes by a Canon EOS 60D digital camera with a MPE Canon 65 mm lens. Then a multi-focused montage image was produced using Helicon 6.2.2 Pro from the source images. After the imaging, legs III and IV of the right side of each spider were removed from the body and preserved in 99% ethanol for DNA analysis. The remainder of the body was preserved in 75% ethanol for morphological examination.

**Morphological examination:** Specimens were examined under an Olympus SZX12 microscope. Description of coloration is based on the specimens preserved in ethanol. All measurements are in millimeters (mm).

Abbreviations used in the present paper are as follows: ALE, anterior lateral eye; AME, anterior median eye; PLE, posterior lateral eye; PME, posterior median eye; ERW, width of anterior/median/posterior eye rows between outer margins of eyes in dorsal view; ALE-PME, distance from anterior margin of ALE to posterior margin of PME, with carapace in dorsal view; ALE-PLE, distance from anterior margin of ALE to posterior margin of PLE, with carapace in dorsal view.

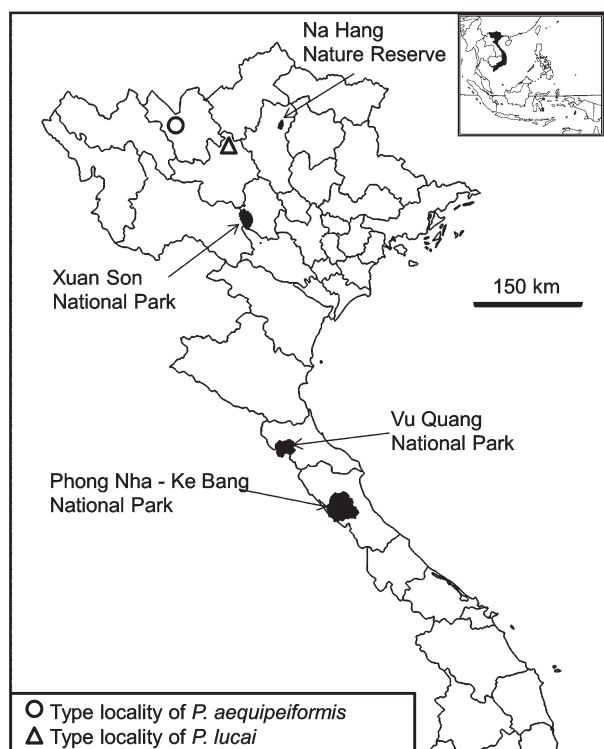


Fig. 1. Map of northern and central Vietnam showing four collection sites and the type localities of *Phintella aequipeiformis* and *P. lucai*.

**Imaging of ethanol-preserved specimens:** Multi-focused montage images of the body and male palp of *Phintella* specimens (Sal-LP-0325, Sal-LP-0329, Sal-LP-0490, Sal-LP-0491, Sal-LP-0586, Sal-LP-0587, Sal-LP-0622) were produced using Helicon 6.2.2 Pro from a series of source images taken by a Canon EOS X5 camera attached to a Nikon SMZ1270 microscope. Female genitalia were detached, and cleared by soaking them in 10% KOH solution at room temperature for about 24 hours. Multi-focused montage images of the genitalia were then produced using Helicon 6.2.2 Pro from a series of source images taken by a Canon EOS X5 camera attached to Nikon Eclipse E600 microscope.

**Morphology-based identification:** *Phintella* specimens were identified by referring to the original descriptions of the species known from Indochina and adjacent areas, and other taxonomic literature (Bösenberg & Strand, 1906; Zabka, 1985; Xie, 1993; Peng *et al.*, 1993; Song *et al.*, 1999; Yin *et al.*, 2012; Prószyński, 2014). Nine males of *P. aequipeiformis* and twelve females of *P. lucai* were found in our collection. These specimens, together with three specimens of *P. versicolor* (Koch, 1846) and two specimens of *P. bifurcilinea* (Bösenberg & Strand, 1906), were used for DNA barcoding.

**DNA barcoding:** Genomic DNA was extracted from leg III or IV of the right side of each spider using the Chelex-TE extraction protocol. Each leg was transferred into a 1.5 mL microcentrifuge tube with 105  $\mu$ L of extraction buffer (a mixture of 100  $\mu$ L of 10% Chelex-TE solution and 5  $\mu$ L Qiagen Proteinase K), incubated at 56°C for about 24 hours, and then heated at 99°C for 10 minutes for inactivating the Qiagen Proteinase K. A standard DNA barcoding region of the COI gene was amplified using the primer set C1-J-1718/C1-N-2776 (Hedin & Maddison, 2001). Each PCR contained 5  $\mu$ L of 2xPCR buffer, 2  $\mu$ L of dNTPs (final 0.4 mM), 0.3  $\mu$ L of 10 pmol/ $\mu$ L forward and reverse primers (final 0.3  $\mu$ M), 0.2  $\mu$ L of 1.0 U/ $\mu$ L DNA polymerase KOD FX Neo (TOYOBO KFX-2015), and 0.5  $\mu$ L of DNA template. The PCR thermal regime consisted of one cycle of 2 min at 94°C; 35 cycles of 10 sec at 98°C, 30 sec at 52°C and 45 sec at 68°C; and a final cycle of 7 min at 68°C. After confirming the PCR amplification on a 2.0% agarose gel, the amplified products were incubated at 37°C for 30 min and at 80°C for 20 min with an Illustra™ ExoStar (GE Healthcare, Buckinghamshire, UK) to remove any excess primers and nucleotides. The cycle sequencing reactions were run with an ABI PRISM BigDye Terminator Cycle Sequencing Kit v.3.1 (Applied Biosystems). The sequencing reaction products were purified, concentrated by ethanol precipitation with sodium acetate, and their nucleotide sequences were determined using an automated sequencer (ABI PRISM 3100, Applied Biosystems). Forward and Reverse strands were assembled after trimming the primer regions and disarrayed parts, and questionable sites were manually

confirmed by referring to the chromatograms of the two strands. This process was done using ChromasPro 1.7.6 (Technelysium Pty Ltd., Australia). In total, 19 sequences of COI from four species of the genus *Phintella*, i.e., seven sequences of *P. aequipeiformis*, seven of *P. lucai*, three of *P. versicolor* and two of *P. bifurcilinea*, were confirmed and submitted to the DDBJ database (accession numbers: LC105655-LC105673) (Table 1).

These sequences, in addition to the homologue sequences of *Phintella piatensis* Barrion & Litsinger, 1995 (Accession No.: AY297396), *Cosmophasis micarioides* (Koch, 1880) (Accession No.: EU815580) and *Telamonia vlijmi* Prószyński, 1984 (Accession No.: KJ598073) provided by other authors (Maddison & Hedin, 2003; Maddison *et al.*, 2008; Kim *et al.*, 2014), were aligned using Muscle (Edgar, 2004) built in MEGA 6.06 (Tamura *et al.*, 2013). Pairwise divergences were calculated using the p-distance (obtained by dividing the number of nucleotide differences by the total number of nucleotides compared) and the Kimura-two-parameter (K2P) distance model (Kimura, 1980). A neighbor-joining tree based on the K2P distance model was created using MEGA 6.06 (Fig. 2).

## RESULTS AND DISCUSSION

### DNA barcoding

The specimens of *Phintella aequipeiformis* and *P. lucai* were recognized as genetically closer to each other than

to specimens of other species (Fig. 2). The pairwise divergence values among 14 individuals (seven males of *P. aequipeiformis* and seven females of *P. lucai*) were 0-0.83% in p-distance and 0-0.84% in K2P. Neither subgroups equivalent to the two nominal species nor any phylogeographic units were recognized within the *P. aequipeiformis* + *P. lucai* group. On the other hand, the pairwise divergence values between the *P. aequipeiformis* + *P. lucai* group and the three congeneric species, i.e., *P. vesicolor*, *P. bifurcilinea* and *P. piatensis*, were 9.35-10.18% in p-distance and 10.15-11.11% in K2P.

Through COI-based DNA barcoding, Blagoev *et al.* (2016) revealed that the mean nearest-neighbor distance based on species was 10 times higher than the mean intraspecific divergence in Canadian spiders (7.85% vs. 0.78%), and 7 times higher in Canadian salticid spiders (7.57% vs. 1.18%). Other studies on various arthropod taxa including spiders (Hebert *et al.*, 2003 for Lepidoptera; Barrett & Hebert, 2005 for spiders; Smith *et al.*, 2005 for Formicidae; Robinson *et al.*, 2009 for spiders; Renaud *et al.*, 2012 for Diptera; Głowska *et al.*, 2014 for syringophilid mites; Doña *et al.*, 2015 for feather mites) suggested that the interspecific divergence values of COI are usually greater than 2-3%, or the intraspecific divergence values of COI are usually less than 2-3%. When applying these thresholds to the present case, the conspecificity of *Phintella aequipeiformis* Zabka, 1985 and *P. lucai* Zabka, 1985 is strongly supported.

### Taxonomic treatment

*Phintella aequipeiformis* and *P. lucai* were described in

Table 1. List of specimens used for DNA barcoding, with DDBJ/GenBank accession numbers.

Species	Sex	Specimen code	Locality	Accession number
<i>Phintella aequipeiformis</i>	Male	Sal-LP-0329	Vietnam, Phu Tho Province, Xuan Son National Park.	LC105658
<i>Phintella aequipeiformis</i>	Female	Sal-LP-0490	Vietnam, Tuyen Quang Province, Na Hang Nature Reserve.	LC105659
<i>Phintella aequipeiformis</i>	Male	Sal-LP-0491	Vietnam, Tuyen Quang Province, Na Hang Nature Reserve.	LC105660
<i>Phintella aequipeiformis</i>	Male	Sal-LP-0531	Vietnam, Tuyen Quang Province, Na Hang Nature Reserve.	LC105661
<i>Phintella aequipeiformis</i>	Male	Sal-LP-0586	Vietnam, Ha Tinh Province, Vu Quang National Park.	LC105662
<i>Phintella aequipeiformis</i>	Male	Sal-LP-0587	Vietnam, Ha Tinh Province, Vu Quang National Park.	LC105663
<i>Phintella aequipeiformis</i>	Female	Sal-LP-0588	Vietnam, Ha Tinh Province, Vu Quang National Park.	LC105664
<i>Phintella aequipeiformis</i>	Female	Sal-LP-0589	Vietnam, Ha Tinh Province, Vu Quang National Park.	LC105665
<i>Phintella aequipeiformis</i>	Male	Sal-LP-0622	Vietnam, Ha Tinh Province, Vu Quang National Park.	LC105666
<i>Phintella aequipeiformis</i>	Female	Sal-LP-0726	Vietnam, Ha Tinh Province, Vu Quang National Park.	LC105669
<i>Phintella aequipeiformis</i>	Female	Sal-LP-0727	Vietnam, Ha Tinh Province, Vu Quang National Park.	LC105670
<i>Phintella aequipeiformis</i>	Female	Sal-LP-0728	Vietnam, Ha Tinh Province, Vu Quang National Park.	LC105671
<i>Phintella aequipeiformis</i>	Female	Sal-LP-0729	Vietnam, Ha Tinh Province, Vu Quang National Park.	LC105672
<i>Phintella aequipeiformis</i>	Male	Sal-LP-0731	Vietnam, Ha Tinh Province, Vu Quang National Park.	LC105673
<i>Phintella bifurcilinea</i>	Male	Sal-LP-0148	Vietnam, Vinh Phuc Province, Me Linh Station.	LC105655
<i>Phintella bifurcilinea</i>	Female	Sal-LP-0681	Vietnam, Vinh Phuc Province, Me Linh Station.	LC105668
<i>Phintella versicolor</i>	Male	Sal-LP-0204	Vietnam, Hai Phong Province, Bach Long Vi island	LC105656
<i>Phintella versicolor</i>	Male	Sal-LP-0271	Vietnam, Lao Cai Province, Sapa Town.	LC105657
<i>Phintella versicolor</i>	Female	Sal-LP-0670	Vietnam, Hanoi city, Ba Vi District.	LC105667



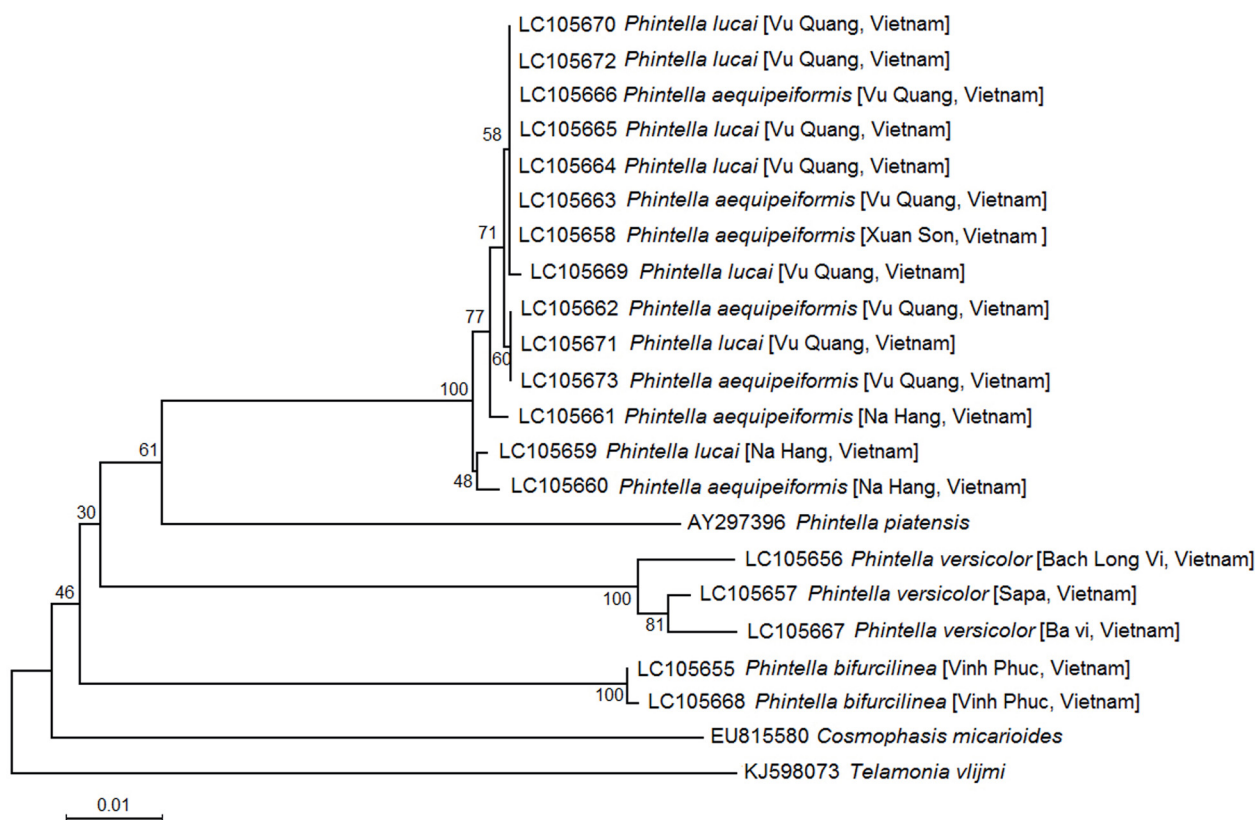


Fig. 2. Neighbor-joining tree generated under the K2P distance model, based on a dataset consisting of 851 bp sequences. Numbers beside nodes refer to bootstrap values (1000 replicates). DDBJ/Genbank accession numbers are placed before species names.

the same publication (Zabka, 1985). We treat *P. lucai* as a junior synonym of *P. aequipeiformis* because *P. aequipeiformis* was redescribed several times (Xie, 1993; Peng *et al.*, 1993; Song *et al.*, 1999; Yin *et al.*, 2012), while *P. lucai* was not. Moreover, it is better to retain *P. aequipeiformis*, which is represented by a male holotype, because males possess more useful characters for identification than females.

### *Phintella aequipeiformis* Zabka, 1985

Figs 3-4

*Phintella aequipeiformis* Zabka, 1985: 427, figs 422-425, 450.  
– Xie, 1993: 358, figs 8-10. – Peng *et al.*, 1993: 151, figs 518-523. – Song *et al.*, 1999: 537, figs 307I, 328A.  
– Yin *et al.*, 2012: 1423, fig. 775a-f. Holotype deposited in HHNM, not examined.

*Phintella lucai* Zabka, 1985: 430, figs 444-446. **Syn. nov.** Holotype deposited in HHNM, not examined.

**Material examined:** Vietnam: MHNG, LC105661, Sal-LP-0531; 1 male; Tuyen Quang Province, Na Hang Nature Reserve; 11.III.2015; leg. Luong & Yamasaki. – MHNG, LC105663, Sal-LP-0587; 1 male; LC105664, Sal-LP-0588; 1 female; LC105672, Sal-LP-0729; 1 female; Ha Tinh Province, Vu Quang National Park; 18.III.2015;

leg. Luong & Yamasaki. – NSMT, LC105662, Sal-LP-0586; 1 male; LC105665, Sal-LP-0589; 1 female; Ha Tinh Province, Vu Quang National Park; 18.III.2015; leg. Luong & Yamasaki. – IEBR-AR-0272; 2 males; IEBR-AR-0331; 1 female; Ha Tinh Province, Vu Quang National Park; 18.III.2015; leg. Luong & Yamasaki. – IEBR-AR-0382; 1 female; Ha Tinh Province, Vu Quang National Park; 23.III.2015; leg. Luong & Yamasaki. – LPC, Sal-LP-0048; 1 female; Quang Binh Province, Phong Nha - Ke Bang National Park; 23.IV.2014; leg. Luong. – LPC, Sal-LP-0325; 1 female; LC105658, Sal-LP-0329; 1 male; Phu Tho Province, Xuan Son National Park; 10.VIII.2014; leg. Luong. – LPC, LC105659, Sal-LP-0490; 1 female; LC105660, Sal-LP-0491; 1 male; Tuyen Quang Province, Na Hang Nature Reserve; 10.III.2015; leg. Luong & Yamasaki. – LPC, Sal-LP-0730; 1 female; Ha Tinh Province, Vu Quang National Park; 18.III.2015; leg. Luong & Yamasaki. – LPC, LC105666, Sal-LP-0622; 1 male; Ha Tinh Province, Vu Quang National Park; 19.III.2015; leg. Luong & Yamasaki. – LPC, LC105669, Sal-LP-0726; 1 female; LC105670, Sal-LP-0727; 1 female; LC105671, Sal-LP-0728; 1 female; Ha Tinh Province, Vu Quang National Park; 23.III.2015; leg. Luong & Yamasaki. – LPC, LC105673, Sal-LP-0731; 1 male; Ha Tinh Province, Vu Quang National Park; 24.III.2015; leg. Luong & Yamasaki.

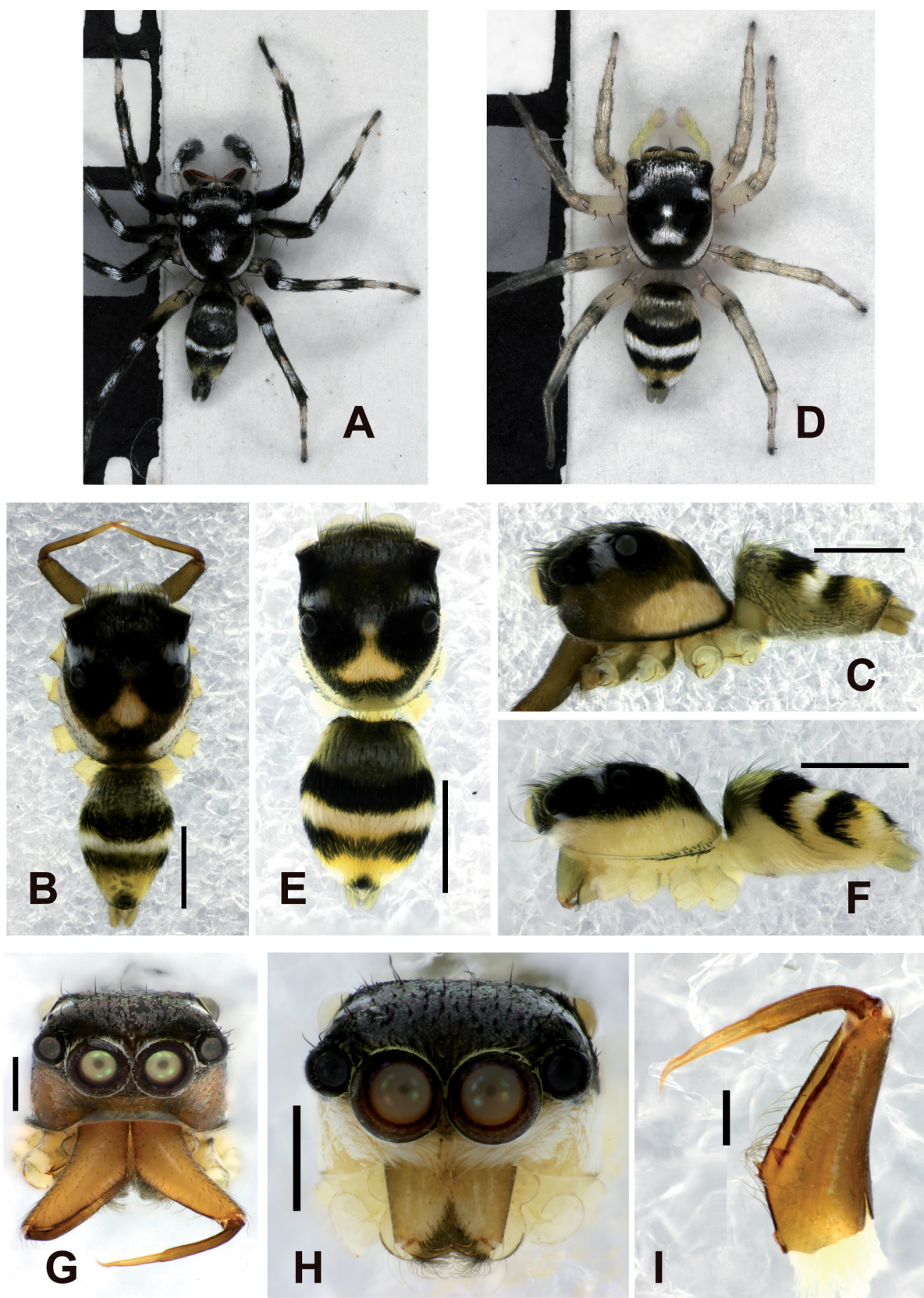


Fig. 3. *Phintella aequipeiformis* specimens from Vietnam; males (A-C, G, I), females (D-F, H). (A-B, D-E) Body, dorsal view. (C, F) Body, lateral view. (G-H) Prosoma, frontal view. (I) Chelicera and fang, ventral view. Scale lines 1 mm (B-C, E-F), 0.5 mm (G-H), 0.2 mm (I). Specimen codes: Sal-LP-0586 (A, I), Sal-LP-0329 (B-C), Sal-LP-0490 (D-F), Sal-LP-0622 (G), Sal-LP-0325 (H).



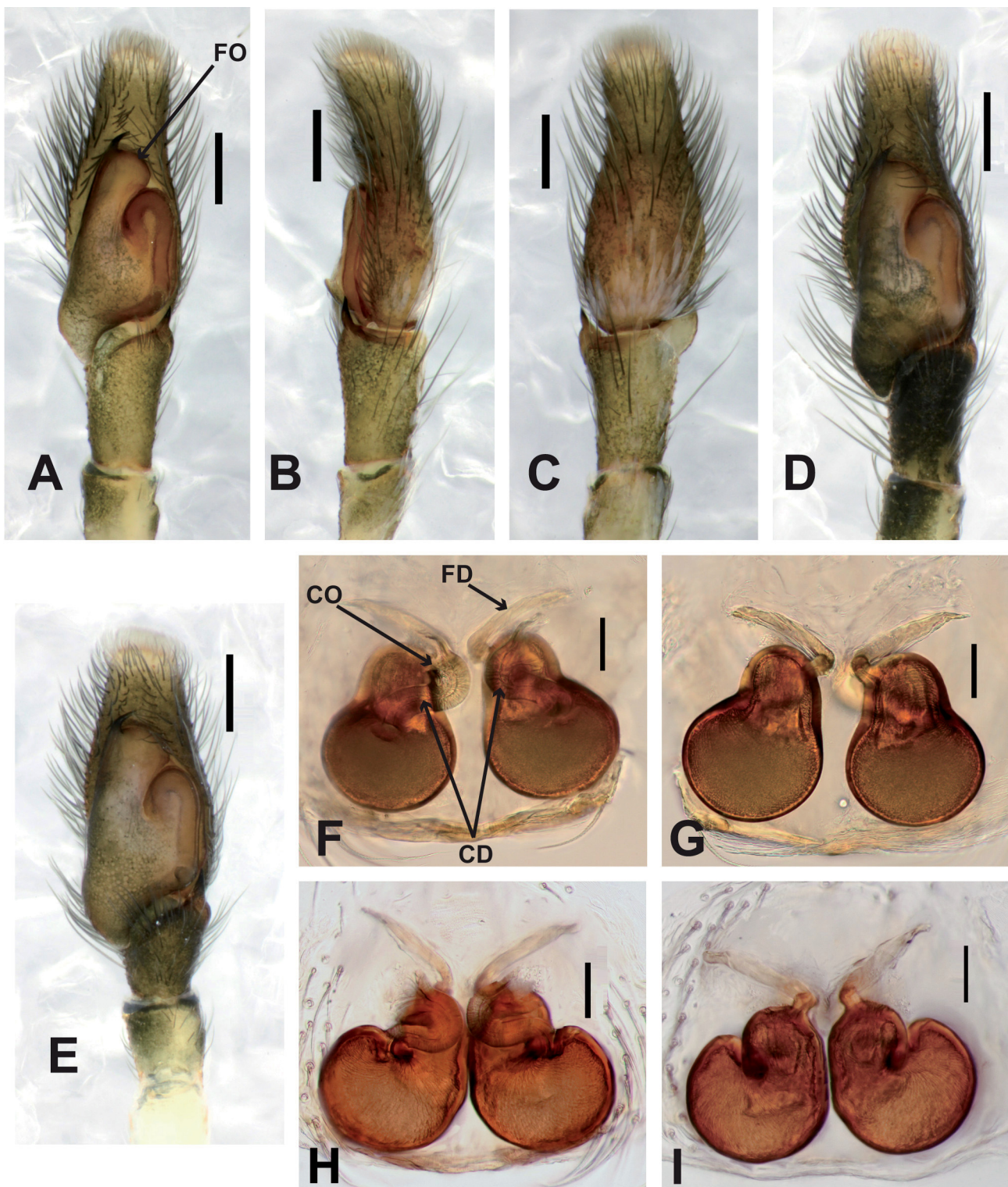


Fig. 4. *Phintella aequipeiformis* specimens from Vietnam; males (A-E), females (F-I). (A, D-E) Palp, ventral view. (B) Palp, retro-lateral view. (C) Palp, dorsal view. (F, H) Epigyne, ventral view. (G, I) Epigyne, dorsal view. Abbreviations: CD, copulatory duct; CO, copulatory opening; FD, fertilization duct; FO, rounded flaky outgrowth. Scale lines 0.2 mm (A-E), 0.05 mm (F-I). Specimen codes: Sal-LP-0329 (A-C), Sal-LP-0491 (D), Sal-LP-0587 (E), Sal-LP-0048 (F-G), Sal-LP-0588 (H-I).

**Diagnosis:** Markings on abdomen of both sexes characteristic, i.e. one white and two black bands of hairs running transversally over dorsum. Embolus short and slightly bent, claw-like; retrolateral corner of anterior part of bulbus rounded, forming a so-called “rounded flaky outgrowth” (Zabka, 1985). Spermathecae large, weakly constricted, and divided into relatively small anterior part and large posterior part.

**Measurements:** *Male* (n=9). Body length 3.32-4.50; carapace length 1.72-2.25; abdomen length 1.53-2.21, width 0.94-1.36; ERW anterior 1.28-1.64; ERW median 1.06-1.41; ERW posterior 1.19-1.54; ALE-PME 0.38-0.55; ALE-PLE 0.79-1.09.

*Female* (n=12). Body length 3.24-4.83; carapace length 1.56-1.97; abdomen length 1.60-2.65, width 1.21-2.00; ERW anterior 1.28-1.51; ERW median 1.08-1.29; ERW posterior 1.24-1.44; ALE-PME 0.42-0.46; ALE-PLE 0.85-0.86.

**Description:** *Male* (Fig. 3A-C, G, I). Carapace mainly black on dorsal surface, yellowish cream tinged with black on lateral surface; AME fringed with whitish gray hairs; dorsum of cephalic part covered with shiny scale-like hairs; area between PME and PLE covered with white scale-like hairs forming white patch; fin-shaped area behind fovea yellowish cream, covered with white scale-like hairs; large yellowish area on lateral surface of thoracic part extending from above coxa II to coxa IV, covered with white scale-like hairs. Clypeus brown to yellowish brown, sparsely covered with whitish transparent scale-like hairs. Chelicera long, pale brown, weakly tinged with brown, with one retrolateral and two prolateral teeth at basal end of fang furrow. Fang long, pale brown. Maxilla and labium pale yellow, weakly tinged with gray or brown. Sternum pale yellow. Abdomen oval, covered with several kinds of scale-like hairs; anterior quarter of dorsum covered with transparent scale-like hairs; middle part of dorsum blackish, with white scale-like hairs forming one white and two black transversal bands, white band running between black bands; posterior part of dorsum yellowish cream, posterior end black, covered with transparent scale-like hairs. Legs with a pattern of black and pale yellow; small patches on dorsum of patellae and tibiae covered with white hairs.

Palp (Fig. 4A-E). Segments with pattern of black and pale yellow; dorsum of patella to cymbium covered with white scale-like hairs. Cymbium slender, tapering with long black hairs. Embolus short and slightly bent, claw-like. Retrolateral corner of anterior part of bulbus rounded, forming so-called “rounded flaky outgrowth” (see Zabka, 1985). Posterior lobe of bulbus well-developed. Sperm duct distally strongly curving behind rounded flaky outgrowth, proximally running along retrolateral margin of bulbus. Retrolateral tibial apophysis short, with relatively thin tip.

*Female* (Fig. 3D-F, H). Carapace almost as in male; its lower lateral surface pale yellow, lighter than that of male, covered with white hairs. Clypeus densely covered with white scale-like hairs. Chelicera, fang, maxilla and labium almost as in male, except for shorter chelicera. Abdomen almost as in male, but more rotund. Legs and palp mostly pale yellow.

Genitalia (Fig. 4F-I). Copulatory openings small, situated near anterior margin of spermathecae. Copulatory ducts narrow, sclerotized, strongly curving. Spermathecae large, weakly constricted, divided into relatively small anterior part and large posterior part; connection points with copulatory ducts located near weak constriction. Fertilization ducts connected to anterior part of spermathecae.

**Distribution:** Vietnam: Lao Cai, Yen Bai, Tuyen Quang, Phu Tho, Ha Tinh, Quang Binh (Zabka, 1985; present study); China: Hunan, Guangxi (Xie, 1993; Peng *et al.*, 1993; Song *et al.*, 1999; Yin *et al.*, 2012).

**Habitat:** This species was found in secondary forests, often on shrubs along forest trails and along forest edges.

**Remarks:** This species shows some variations in the shape of the bulbus and in the length of the palpal tibia (Fig. 4A, D, E), as well as in the shape of the spermathecae (Fig. 4F-I). These varieties occur sympatrically. Our results from DNA barcoding (Fig. 2) strongly suggest that all these varieties belong to a single species.

## ACKNOWLEDGMENTS

This research was sponsored by the Advanced Research Program of the Asian Human Resources Fund of the Tokyo Metropolitan Government, by Sumitomo Foundation Grant for Basic Science Research Projects No. 130648, and by the Japan Society for the Promotion of Science (JSPS) KAKENHI (grant number 24405010, 26304014, 15K07193, 14J04245). We are deeply indebted to Dr Peter J. Schwendinger, Dr Lionel Monod (MHNG) and Dr Dmitri Logunov (Manchester Museum, The University of Manchester, England) for providing valuable comments and suggestions on our manuscript. We would like to thank the Management Board of the Vu Quang National Park, Na Hang Nature Reserve, Xuan Son National Park and Phong Nha - Ke Bang National Park (Vietnam) for help in field work. Thanks to Dr Tran Duc Luong and Mr Le Quang Tuan (Institute of Ecology and Biological Resource, Vietnam) for organizing field trips to Phong Nha - Ke Bang National Park (in April 2014) and Xuan Son National Park (in August 2014). Thanks to Mr Hiroaki Kurushima and Mr Kiyotaka Hori (Tokyo Metropolitan University) for their help with molecular experiments.



## REFERENCES

- Barrión A.T., Litsinger J.A. 1995. Riceland spiders of South and Southeast Asia. *CAB International, Wallingford, UK*, XIX + 700 pp.
- Bickford D., Lohman D.J., Sodhi N.S., Ng P.K., Meier R., Winker K., Ingram K.K., Das I. 2006. Cryptic species as a window on diversity and conservation. *Trends in Ecology & Evolution* 22: 148-155.
- Barrett R.D.H., Hebert P.D.N. 2005. Identifying spiders through DNA barcodes. *Canadian Journal of Zoology* 83: 481-491.
- Blagoev G.A., deWaard J.R., Ratnasingham S., deWaard S.L., Lu L., Robertson J., Telfer A.C., Hebert D.N. 2016. Untangling taxonomy: a DNA barcode reference library for Canadian spiders. *Molecular Ecology Resources* 16: 325-341.
- Bösenberg W., Strand E. 1906. Japanische Spinnen. *Abhandlungen der Senckenbergischen Naturforschenden Gesellschaft* 30: 93-422.
- Caleb J. T. D. 2014. A new species of *Phintella* Strand (Araneae: Salticidae) from India. *Munis Entomology & Zoology* 9: 605-608.
- Doña J., Diaz-Real J., Mironov S., Bazaga P., Serrano D., Jovani R. 2015. DNA barcoding and minibarcoding as a powerful tool for feather mite studies. *Molecular Ecology Resources* 15: 1216-1225.
- Edgar R.C. 2004. MUSCLE: multiple sequence alignment with high accuracy and high throughput. *Nucleic Acids Research* 32: 1792-1797.
- Ekrem T., Stur E., Hebert P.D.N. 2010. Females do count: Documenting Chironomidae (Diptera) species diversity using DNA barcoding. *Organisms Diversity & Evolution* 10: 397-408.
- Fisher B., Smith M. A. 2008. A revision of Malagasy species of *Anochetus* Mayr and *Odontomachus* Latreille (Hymenoptera: Formicidae). *PLoS One* 3: 1-23.
- Głowska E., Dragun-Damian A., Broda L., Dabert J., Dabert M. 2014. DNA barcodes reveal female dimorphism in syringophilid mites (Actinotrichida: Prostigmata: Cheyletoidea): *Stibarokris phoeniconaias* and *Ciconichenophilus phoeniconaias* are conspecific. *Folia Parasitologica* 61: 272-276.
- Hebert P.D.N., Cywinska A., Ball S.L., deWaard J.R. 2003. Biological identifications through DNA barcodes. *Proceedings of the Royal Society of London. Series B: Biological Sciences* 270: 313-321.
- Hedin M.C., Maddison W.P. 2001. A combined molecular approach to phylogeny of the jumping spider subfamily Dendryphantinae (Araneae: Salticidae). *Molecular Phylogenetics and Evolution* 18: 386-403.
- Kim J.Y., Yoon K.B., Park Y.C. 2014. The complete mitochondrial genome of the jumping spider *Telamonia vlijmi* (Araneae: Salticidae). *Mitochondrial DNA* 27: 635-636.
- Kimura M. 1980. A simple method for estimating evolutionary rate of base substitutions through comparative studies of nucleotide sequences. *Journal of Molecular Evolution* 16: 111-120.
- Koch C.L. 1846. Die Arachniden. Getreu nach der Natur abgebildet und beschrieben. Vol. 13. *J.L. Lotzbeck, Nürnberg*, 234 pp.
- Koch L. 1880. Die Arachniden Australiens nach der Natur beschrieben und abgebildet. Vol. 1. *Bauer & Raspe, Nürnberg*, pp. 1157-1212.
- Maddison W.P., Hedin M.C. 2003. Jumping spider phylogeny (Araneae: Salticidae). *Invertebrate Systematics* 17: 529-549.
- Maddison W.P., Bodner M.R., Needham K.M. 2008. Salticid spider phylogeny revisited, with the discovery of a large Australasian clade (Araneae: Salticidae). *Zootaxa* 1893: 49-64.
- Peng X.J., Xie L.P., Xiao X.Q., Yin C.M. 1993. Salticids in China (Arachnida: Araneae). *Hunan Normal University Press*, 270 pp.
- Pires A.C., Marinoni L. 2010. DNA barcoding and traditional taxonomy unified through Integrative Taxonomy: a view that challenges the debate questioning both methodologies. *Biota Neotropica* 10: 339-346.
- Prószyński J. 1984. Remarks on *Viciria* and *Telamonia* (Araneae, Salticidae). *Annales Zoologici (Warszawa)* 37: 417-436.
- Prószyński J. 2014. Monograph of Salticidae (Araneae) of the World 1995-2014. Available at <http://www.peckhamia.com/salticidae/> (accessed 2016).
- Renaud A.K., Savage J., Adamowicz S.J. 2012. DNA barcoding of Northern Nearctic Muscidae (Diptera) reveals high correspondence between morphological and molecular species limits. *BMC Ecology* 12: 24.
- Robinson E. A., Blagoev G. A., Hebert P.D.N., Adamowicz, S.J. 2009. Prospects for using DNA barcoding to identify spiders in species-rich genera. *ZooKeys* 16: 27-46.
- Smith M.A., Fisher B.L., Hebert P.D.N. 2005. DNA barcoding for effective biodiversity assessment of a hyperdiverse arthropod group: the ants of Madagascar. *Philosophical Transactions of the Royal Society B* 360: 1825-1834.
- Song D.X., Zhu M.S., Chen J. 1999. The Spiders of China. *Hebei University of Science and Technology Publishing House, Shijiazhuang*, 640 pp.
- Tamura K., Stecher G., Peterson D., Filipowski A., Kumar S. 2013. MEGA6: Molecular evolutionary genetics analysis version 6.0. *Molecular Biology and Evolution* 30: 2725-2729.
- Tanikawa A. 2011. The first description of a male of *Paraplectana tsushimenis* (Araneae: Araneidae). *Acta Arachnologica* 60(2): 71-73.
- World Spider Catalog. 2016. World Spider Catalog. Natural History Museum Bern. Available at <http://wsc.nmbe.ch>, version 17.0 (accessed 2016).
- Xie L.P. 1993. New records of Salticidae from China (Arachnida: Araneae). *Acta Scientiarum Naturalium Universitatis Normalis Hunanensis* 16: 358-361.
- Yin C.M., Peng X.J., Yan H.M., Bao Y.H., Xu X., Tang G., Zhou Q.S., Liu P. 2012. Fauna Hunan: Araneae in Hunan, China. *Hunan Science and Technology Press, Changsha*, 1590 pp.
- Zabka M. 1985. Systematic and zoogeographic study on the family Salticidae (Araneae) from Vietnam. *Annales Zoologici (Warszawa)* 39: 197-485.
- Zabka M. 2012. *Phlegra* Simon, 1876, *Phintella* Strand 1906 and *Yamangalea* Maddison, 2009 (Arachnida: Araneae: Salticidae) - new species and new generic records for Australia. *Zootaxa* 3176: 61-68.