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A New Record of *Pheidole hainanensis* Chen, Ye, Lu, & Zhou, 2011 (Hymenoptera: Formicidae) from Vietnam

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Abstract. *Pheidole hainanensis* Chen, Ye, Lu, & Zhou, 2011 is previously known only from Hainan Province, China. In the present paper, this species is newly recorded from the Chu Yang Sin National Park, Dak Lak Province, Vietnam. A partial sequence (Folmer region) of mitochondrial COI gene is also provided for DNA barcoding in the future studies.

Key words: Myrmicinae, ant, Indo-Chinese Peninsula, DNA barcoding

Introdution

The genus *Pheidole* Westwood, 1839 is one of the most abundant and species-rich genera of ants in the world, and contains more than a thousand valid species (Wilson, 2003; Bolton, 2017). The worker caste of *Pheidole* ants is typically subdivided into two morphologically distinct subcastes: the major worker (major) and minor worker (minor).

Pheidole hainanensis Chen, Ye, Lu, & Zhou, 2011 was originally described from Hainan Province, China, and has never been recorded outside Hainan Island. In the course of our recent field survey in an evergreen forest in Central Highlands of Vietnam (Chu Yang Sin National Park, Dak Lak Province: Fig. 1), a colony fragment of *P. hainanensis* was collected. In the present paper, *P. hainanensis* is newly recorded from Vietnam, highlighting its distribution in the Indo-Chinese Peninsula. Additionally, a partial sequence (Folmer region) of mitochondrial COI gene is also provided for DNA barcoding in the future studies.

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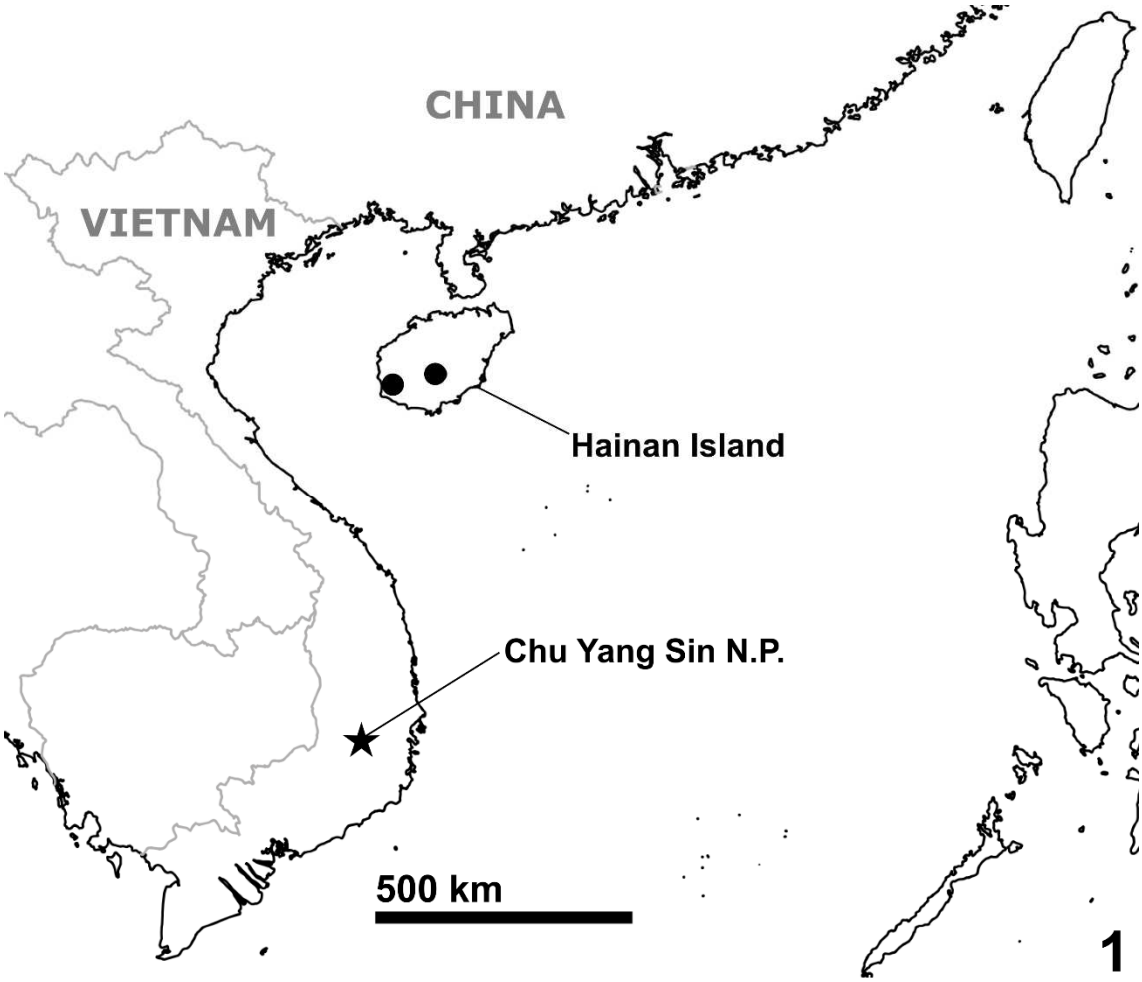


Figure 1. Distribution map of *Pheidole hainanensis*. The new record is shown by a black star.

Material and methods

The materials examined in this paper will be deposited in the following collections: the Institute of Ecology and Biological Resources, Vietnam (IEBR); Systematic Zoology Laboratory, Tokyo Metropolitan University, Tokyo, Japan (TMUZ: curated by the first author). Multi-focused images were produced by Helicon Focus Pro 6.7.1 (Helicon Soft Ltd.) from a series of source images taken using a Lumix DMC GX8 digital camera attached to a Nikon AZ100 stereomicroscope. The color balance and contrast were adjusted using GIMP 2.8 (available at http://www.gimp.org).

Measurements and indices were taken as follows: head length (HL: maximal head length between transverse lines spanning the anteriormost points of clypeus and posteriormost points of head); head width (HW: maximal head width excluding eyes); scape length (SL: length of antennal scape excluding the basal condylar bulb); pronotal width (PW: maximal width of pronotum in dorsal view); mesosomal length (ML: diagonal length of mesosoma in lateral view, from the base of anterior slope of pronotum to the posterobasal angle of metapleuron); petiolar length (PtL, from the anterodorsalmost point of petiolar peduncle to the posterodorsal corner of petiole in lateral view); petiolar width (PtW, maximal width of petiolar node in dorsal view); postpetiolar length (PPtL, maximal length of postpetiole in lateral view, excluding helcium); postpetiolar width (PPtW, maximal width of postpetiole in dorsal view); cephalic index (CI = HW/HL × 100); scape index (SI = SL/HW × 100); petiolar index 1 (PtI1 = PtL/PPtL × 100); petiolar index 2 (PtI2 = PtW/PPtW × 100).

A minor was used for DNA extraction by Chelex-TE method (details see Satria et al., 2015). Then, a 658 bp region (Folmer region) of the mitochondrial cytochrome c oxidase subunit I (COI) gene was amplified using the primers LCO-EG and HCO-EG (Eguchi et al., 2016). PCR amplifications, cycle sequencing reactions, sequencing using ABI PRISM 3130xl (Applied Biosystems) and sequence assembly using ChromasPro 1.7.6 (Technelysium Pty Ltd.) were conducted by following Rijal et al. (2015). The determined sequence (590 bp) was submitted to International Nucleotide Sequence Database (INSD: http://www.insdc.org) via DNA Data Bank of Japan (DDBJ): accession number LC341396.

Results

***Pheidole hainanensis* Chen, Ye, Lu, & Zhou, 2011**

(Figs. 2–10)

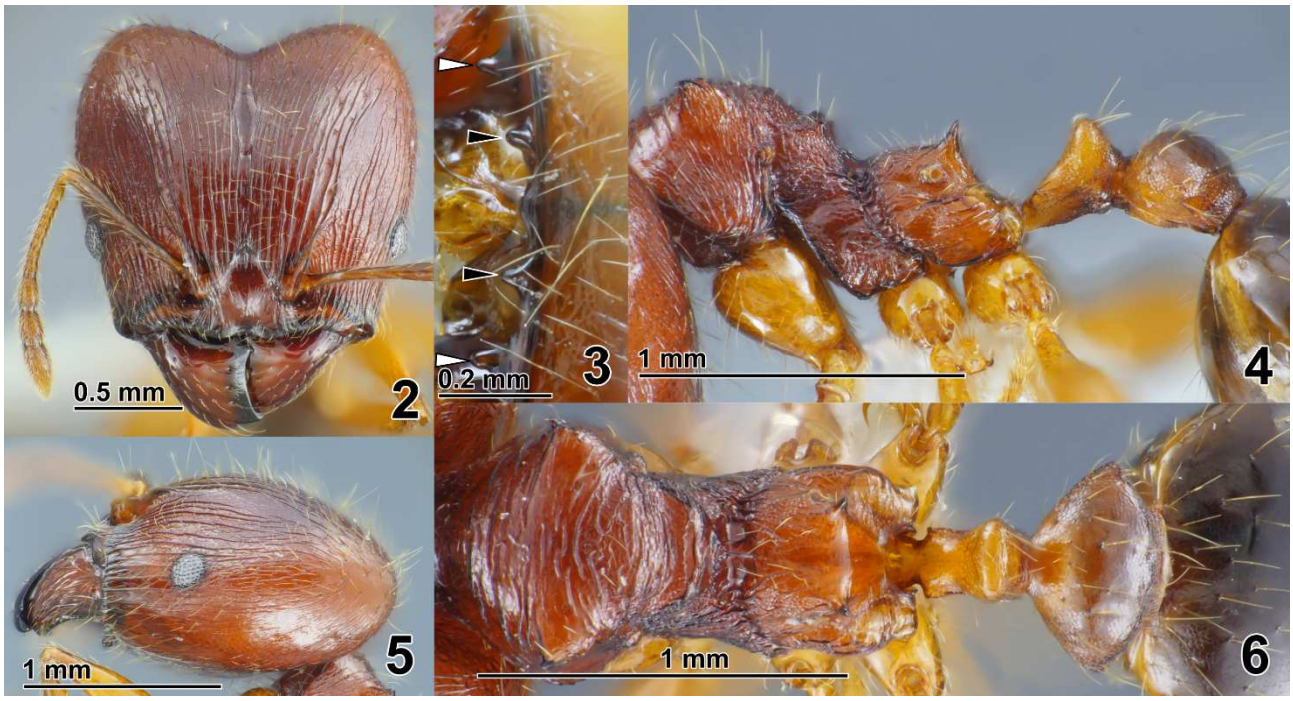
Material examined. 3 majors, 3 minors, colony ID: AKY08iii16-06, N 12°25'35-42", E 108°19'16-29", ca. 850m alt., Chu Yang Sin National Park, Dak Lak Province, Vietnam, 8. III. 2016, A. Yamada leg. (2 majors, 2 minors in IEBR; 1major, 1minor in TMUZ).

Material used for DNA barcoding. 1 minor, colony ID: AKY08iii16-06, individual ID: AIK20160418-12 (TMUZ). The 590 bp of barcode sequence is available at INSD (accession number: LC341396).

Measurements and indices. MAJOR. HL: 1.43–1.52 mm; HW: 1.46–1.54 mm; SL: 0.74–0.79 mm; PW: 0.66–0.67 mm; ML: 1.19–1.25 mm; PtL: 0.31–0.36 mm; PtW: 0.20–0.22 mm; PPtL: 0.28–0.33 mm; PPtW: 0.49–0.57 mm; CI: 101–103; SI: 51–54; PtI1: 103–120; PtI2: 39–43 (n = 3). MINOR. HL: 0.65–0.67 mm; HW: 0.62 mm; SL: 0.70–0.71 mm; PW: 0.40–0.41 mm; ML: 0.86–0.87 mm; PtL: 0.22–0.23 mm; PtW: 0.11 mm; PPtL: 0.24–0.27 mm; PPtW: 0.25–0.27 mm; CI: 93–95; SI: 112–114; PtI1: 80–94; PtI2: 41–44 (n = 3).

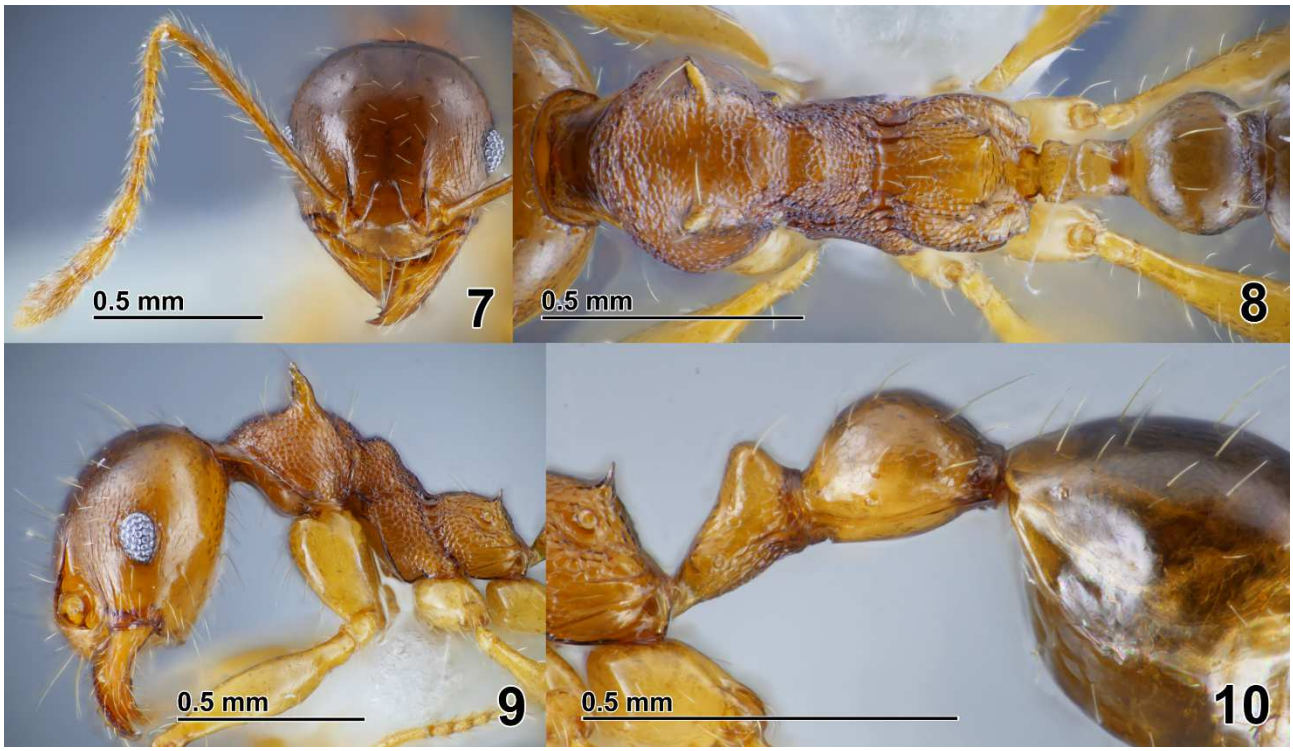
Diagnosis of the worker. *Pheidole hainanensis* can be distinguished from other Asian congeners by the combination of the following characters of the major and minor.

In the major, head in full-face view longitudinally rugose (Fig. 2), without deep impression on the vertex in lateral view (Fig. 5); hypostoma with inconspicuous median and conspicuous submedian processes (black arrows in Fig. 3) in addition to conspicuous lateral processes (white arrows in Fig. 3); pronotum with a pair of robust triangular angles (Figs. 4, 6); posterior slope of promesonotal dome in lateral view with a conspicuous prominence (Fig. 4); petiole in lateral view almost as long as or a little longer than postpetiole (PtI1: 103–120); petiolar node in dorsal view about 0.4 times as broad as postpetiole (PtI2: 39–43); first gastral tergite smooth and shiny (Fig. 6).



Figures 2–6. Major worker (colony ID: AKY08iii16-06) of *Pheidole hainanensis*. (2) Head in full-face view. (3) Hypostoma in ventral view; black and white arrows inidicate submedian processes and lateral processes respectively. (4) Mesosoma and waist in lateral view. (5) Head in lateral view. (6) Mesosoma and waist in dorsal view.

In the minor, the vertex of head smooth and shiny (Fig. 7); median clypeal carina absent; preoccipital carina conspicuous dorsally and laterally (Fig. 8); pronotum with a pair of short and robust spines (ca. 0.12 mm); posterior slope of promesonotal dome in lateral view with a conspicuous prominence (Fig. 9); mesosoma entirely punctate; propodeal spines very small (Fig. 10); petiole in lateral view a little shorter than postpetiole (PtI1: 80–94); petiolar node in dorsal view about 0.4 times as broad as postpetiole (PtI2: 41–44).



Figures 7–10. Minor worker (AKY08iii16-06) of *Pheidole hainanensis*. (7) Head in full-face view. (8) Mesosoma and waist in dorsal view. (9) Head and mesosoma in lateral view. (10) Waist and gaster in lateral view.

Remarks. In the genus *Pheidole*, the spinescent morphology of pronotum is seen in restricted species (Sarnat et al., 2017). Among other congeners in the Indo-Chinese Peninsula, only one species, *P. leloi* Eguchi & Bui, 2016, is known to exhibit the spinescence. However, *P. hainanensis* is easily distinguished from the *P. leloi* by the smooth vertex of head and a pair of shorter pronotal spines in the minor, and absence of distinct pronotal spines in the major (both the major and minor of *P. leloi* have a pair of elongate and pointed pronotal spines).

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越南新紀錄種海南大頭家蟻之記述 (膜翅目：蟻科)

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摘要: 海南大頭家蟻 *Pheidole hainanensis* Chen, Ye, Lu, & Zhou, 2011 早前僅知分布於中國海南省，本文新紀錄海南大頭家蟻於越南多樂省朱楊申國家公園，同時提供粒線體細胞色素 c 氧化酶 I (COI) 的部分序列 (福爾梅區域 Folmer region) 作為未來 DNA 條碼研究之所需。

關鍵詞: 家蟻亞科、螞蟻、中南半島、DNA 條碼