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# Integrative Taxonomy of a New *Thyropygus* Pocock, 1894 Species from Thailand (Diplopoda: Spirostreptida: Harpagophoridae)

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**ABSTRACT.–** A new juliformian millipede species, *Thyropygus sirindhornae* sp. nov., is described from Chiang Rai Province, Thailand and assigned to the *Thyropygus allevatus* group based on two diagnostic gonopodal characters: (1) the gonopod telopodite with both tibial and femoral spines, and (2) a notably long tibial spine recurved toward the femoral spine. Despite its affiliation with the informal *T. allevatus* group, *T. sirindhornae* sp. nov. cannot be assigned to one of the four informal subgroups of the *T. allevatus* group because it lacks any of the diagnostic characters of these subgroups. Similarly, while the COI DNA barcode data support the distinctiveness of *T. sirindhornae* sp. nov. from other *Thyropygus* species within the *T. allevatus* group (mean interspecific sequence divergence of 0.16 ± 0.02, range: 0.12–0.19), they do not provide information about the sister group relationships or subgroup assignment of the new species. As a result, *T. sirindhornae* sp. nov. is tentatively assigned to the *T. allevatus* group, but is labelled as "incertae sedis" with respect to its sister group relations and subgroup classification. In fact, as the COI phylogeny only included species of the *T. allevatus* group, the assignment of *T. sirindhornae* sp. nov. to this informal species group needs to be confirmed by including representatives of other informal *Thyropygus* species groups.

**KEYWORDS: COI, gonopod, phylogeny**

## INTRODUCTION

The genus *Thyropygus* Pocock, 1894, is one of the most speciose genera of juliformian millipedes in Southeast Asia. To date, 68 species have been described from this region, with 47 of them occurring in Thailand (Pimvichai et al., 2023, 2025). The genus is divided into four informal species groups based on telopodite morphology, the shape of femoral spines, and geographic distribution patterns (Hoffman, 1975): the *T. allevatus* group, the *T. aterrimus* group, the *T. luxuriosus* group, and the *T. erythropleurus* group. The majority of Thai *Thyropygus* species belong to the *T. allevatus* group, which is characterized by two diagnostic characters: (1) the presence of tibial and femoral spines, and (2) a long, recurved tibial spine that extends proximally toward the femoral spine.

Using gonopodal characters and DNA sequence data the *T. allevatus* group is further subdivided into four informal subgroups: (1) the *T. opinatus* subgroup, (2) the *T. induratus* subgroup, (3) the *T. cuisinieri* subgroup, and (4) the *T. allevatus* subgroup (Pimvichai et al., 2009a, 2009b, 2011a, 2011b, 2014, 2016, 2023, 2025). Recent phylogenetic analyses of DNA sequence data have provided robust support for the monophyly of the *T. opinatus* and *T. cuisinieri* subgroups, based on 23 out of 29 and 2 out of 4 species tested respectively. However, the monophyly of the *T. induratus* subgroup is currently no longer supported (9 species tested), although it was previously well-supported in Pimvichai et al. (2014), while the monophyly of the *T. allevatus* subgroup could hitherto not be tested since DNA sequence data are only available for its nominal species. Moreover, the sister-group relationships of *T. allevatus* remain unresolved (Pimvichai et al., 2023, 2025).

Recently, one of us (P. Prasankok) collected three *Thyropygus* specimens in Chiang Rai Province, Thailand, that clearly belonged to the *T. allevatus* group, but whose gonopod morphology neither corresponded to that of any known *Thyropygus* species, nor allowed to assign them to any of the four subgroups within the *T. allevatus* group. Additionally, COI DNA sequence data confirmed that these three specimens were well-differentiated from other species and subgroups in the *T. allevatus* group. Therefore, we here describe these three specimens as a new species, *Thyropygus sirindhornae* sp. nov., within the *T. allevatus* group, but as "incertae sedis" with respect to their eventual subgroup classification.

## MATERIALS AND METHODS

The three living *Thyropygus* specimens were hand-collected. One male was preserved in 70% ethanol for morphological study and two specimens (one ♂ and one ♀) were placed in a freezer at –20 ºC for morphological study and DNA analysis.

This research was conducted respecting the Animal Care and Use regulations (numbers U1-07304-2560 and IACUC-MSU-037/2019) of the National Research Council of Thailand.

### Morphology

Specimens were photographed with a digital camera, and detailed drawings were created with the aid of a stereomicroscope, using the photographs as references. Gonopod morphology is described following the conventions established by Pimvichai et al. (2023). Voucher specimens were deposited in the collections of the Museum of Zoology, Chulalongkorn University, Bangkok, Thailand (CUMZ).

### DNA extraction, amplification and sequencing

Total genomic DNA was extracted from legs of two specimens of *T. sirindhornae* sp. nov. (CUMZ-D00157 and CUMZ-D00157-1) using the NucleoSpin Tissue kit (Macherey-Nagel, Düren, Germany) and following the manufacturer's instructions. PCR amplifications and sequencing of the standard mitochondrial COI DNA barcoding fragment (Hebert et al., 2003) were done as described by Pimvichai et al. (2020). The COI fragment was amplified with the primers LCO-1490 and HCO-2198 (Folmer et al., 1994). The new COI nucleotide sequences have been deposited in GenBank under accession numbers PV612841–PV612842. Sample data and voucher codes are provided in Table 1.

### Alignment and phylogenetic analysis

The COI dataset comprised 63 specimens of 34 nominal *Thyropygus* species and four outgroup species from the harpagophorid subfamily Rhynchoproctinae viz., *Anurostreptus barthelemyae* Demange, 1961, *A. sculptus* Demange, 1961, *Armatostreptus armatus* (Demange, 1983), and *Heptischius lactuca* Pimvichai, Enghoff & Panha, 2010 (Table 1).

The forward and reverse sequences were assembled, and errors or ambiguities were checked, using CodonCode Aligner (ver. 4.0.4, CodonCode Corporation). To confirm sequence identities, all sequences were checked against reference data in GenBank using the Basic Local Alignment Search Tool (BLAST) provided by NCBI. Sequence alignment (660 bp) was conducted using MUSCLE (ver. 3.6, see http://www.drive5.com/muscle; Edgar, 2004). DAMBE (ver. 5.2.65. see http://www.dambe.bio.uottawa.ca/DAMBE/dambe.aspx; Xia, 2018) was used to examine sequences for ambiguous nucleotide sites, saturation, and phylogenetic signal. MEGA11 (ver. 11.0.10, see http://www.megasoftware.net; Tamura et al., 2021) was employed to (1) screen for stop codons, (2) translate nucleotide sequences into amino acids, and (3) compute uncorrected pairwise p-distances among sequences.

Phylogenetic analyses were performed using maximum likelihood (ML) and Bayesian inference (BI). The gamma distribution shape parameter, based on 16 rate categories, was estimated through ML analysis. ML trees were generated using RaxML (ver. 8.2.12, see http://www.phylo.org/index.php/tools/raxmlhpc2_tgb.html; Stamatakis, 2014) on the CIPRES Science Gateway (Miller et al., 2010) under a GTR+G substitution model, with branch support evaluated through 1000 bootstrap replicates. BI trees were constructed with MrBayes (ver. 3.2.7a, see http://www.phylo.org/index.php/tools/mrbayes_xsede.html; Huelsenbeck and Ronquist, 2001), employing substitution models identified via jModelTest (ver. 2.1.10, see https://www.github.com/ddarriba/jmodeltest2/releases; Darriba et al., 2012) using the Akaike Information Criterion (Akaike, 1974). The GTR+I+G substitution model was selected as the best fit.

BI analyses were run for 15 million generations with a heating parameter of 0.01, and trees were sampled every 1000 generations. Convergence was confirmed by ensuring that the standard deviation of split frequencies remained below 0.01. The first 1000 trees were discarded as burn-in, and the consensus tree was generated from the remaining 22502 trees. Node support was assessed using posterior probabilities.

Branches in the ML tree with bootstrap values (BV) ≥ 70% were considered well supported, while those with BV < 70% were regarded as poorly supported (Hillis and Bull, 1993). Similarly, branches in the BI tree with posterior probabilities (PP) ≥ 0.95 were considered well supported, whereas those with PP < 0.95 were regarded as poorly supported (San Mauro and Agorreta, 2010).

## RESULTS

### DNA data and phylogenetic analyses

The uncorrected p-distances between all sequences of *Thyropygus* species for which COI (660 bp) sequences are available ranged from 0.00 to 0.21 (Table A1). The intraspecific sequence divergence in *T. sirindhornae* sp. nov. (2 sequences) was 0.01. The mean interspecific sequence divergence between *T. sirindhornae* sp. nov. and all other *Thyropygu*s species was 0.16 ± 0.02 (range: 0.12–0.19). The mean interspecific sequence divergence within the *T. allevatus* group (all subgroups and *T. sirindhornae* sp. nov included) was 0.14 ± 0.02 (range: 0.02–0.19). The mean interspecific sequence divergences between *T. sirindhornae* sp. nov. and other species of the four subgroups in the *T. allevatus* group were: 0.17 ± 0.00 (range: 0.16–0.17) for the *T. allevatus* subgroup, 0.17 ± 0.01 (range: 0.15–0.19) for the *T. opinatus* subgroup, 0.16 ± 0.01 (range: 0.15–0.17) for the *T. cuisinieri* subgroup, and 0.15 ± 0.01 (range: 0.12–0.17) for the *T. induratus* subgroup. The mean interspecific sequence divergences within subgroups were: 0.12 ± 0.03

**TABLE 1.** Specimens from which the COI gene fragment was used in this study. CUMZ, Museum of Zoology, Chulalongkorn University, Bangkok, Thailand; NHMW, Naturhistorisches Museum, Vienna, Austria. Abbreviations after species names refer to the isolate of each sequence. GenBank accession numbers are indicated for each specimen.

| | **Voucher code** | **Locality** | **COI** |
|---|---|---|---|
| **Family Harpagophoridae** | | | |
| **Subfamily Rhynchoproctinae** | | | |
| *Anurostreptus barthelemyae* Demange, 1961 (Tlb) | CUMZ-D00003 | Thale-Ban N.P., Khuan-Don, Satun, Thailand | KC519469 |
| *A. sculptus* Demange, 1961 (Pl) | CUMZ-D00004 | Phu-Lan-Kha, Nong-Bua- Thale-Ban N.P., Khuan Deang, Chaiyaphum, Thailand | KC519470 |
| *Armatostreptus armatus* (Demange, 1983) (Tpp) | CUMZ-D00006 | Tam Pha-Pong temple, Muang, Chiang Mai, Thailand | KC519472 |
| *Heptischius lactuca* Pimvichai, Enghoff & Panha, 2010 (Us) | CUMZ-D00007 | Mae-Usu, Tha-Song-Yang, Tak, Thailand | KC519473 |
| **Subfamily Harpagophorinae** | | | |
| ***Thyropygus allevatus* group** | | | |
| ***T. allevatus* subgroup:** | | | |
| *T. allevatus* (Karsch, 1881) | | | |
| *T. allevatus* Bb | CUMZ-D00013 | Bang Ban, Ayutthaya, Thailand | KC519479 |
| *T. allevatus* Bk | CUMZ-D00014 | Bang Kruey, Nonthaburi, Thailand | KC519480 |
| ***T. cuisinieri* subgroup** | | | |
| *T. foliaceus* (Demange, 1961) (Kj) | CUMZ-D00050 | Pha Tam, Khong-Chiam, Ubonratchathani, Thailand | KC519514 |
| *T. jarukchusri* Pimvichai, Enghoff and Panha, 2011 (Np) | CUMZ-D00053 | Ban Nong-Pue, Chaturaphakphiman, Roi-Et, Thailand | KC519516 |
| ***T. induratus* subgroup:** | | | |
| *T. induratus* Attems, 1936 | | | |
| *T. induratus* Ldn | CUMZ-D00022 | Kang Lamduan, Nam-Yeun, Ubonratchathani, Thailand | KC519488 |
| *T. induratus* Nru | CUMZ-D00023 | Nang-Rin waterfall, Non-Sa-Ard, Udonthani, Thailand | KC519489 |
| *T. induratus* Ps | CUMZ-D00024 | Phanomsawai, Surin, Thailand | KC519490 |
| *T. induratus* Pw | CUMZ-D00025 | Phu-Wiang, Khon Kaen, Thailand | KC519491 |
| *T. induratus* Ssk | CUMZ-D00026 | Kantararuk, Srisaket, Thailand | KC519492 |
| *T. induratus* Tt | CUMZ-D00027 | Ban Ta Toom, Muang, Maha Sarakham, Thailand | KC519493 |
| *T. laterolobatus* Pimvichai, Enghoff & Panha, 2011 (Ry) | CUMZ-D00048 | Koh Sa-Med, Muang, Ra-Yong, Thailand | KC519512 |
| *T. macrosiamensis* Pimvichai, Enghoff & Panha, 2011 (Kj) | CUMZ-D00049 | Pha Tam, Khong-Chiam, Ubonratchathani, Thailand | KC519513 |
| *T. panhai* Pimvichai, Enghoff & Backeljau, 2023 (PRL) | CUMZ-D00151 | Phu Ruea, Phu Ruea, Loei, Thailand | OP549748 |
| *T. quietus* Attems, 1938 (Cdv) | CUMZ-D00029 | Con Dao N.P., Ba Ria Vung Tau, Vietnam | KC519494 |
| *T. resimus* Attems, 1938 | | | |
| *T. resimus* Kc | CUMZ-D00030 | Kang Ched Khaew, Wat Bod, Phitsanulok, Thailand | KC519495 |
| *T. resimus* Ksp | CUMZ-D00032 | Kang So-Pa, Nakhonthai, Phitsanulok, Thailand | KC519496 |
| *T. resimus* Ntp | CUMZ-D00033 | Poi waterfall, Wang-Thong, Phitsanulok, Thailand | KC519497 |
| *T. resimus* Pk | CUMZ-D00034 | Phu Kum-Khao, Sahussakhan, Kalasin, Thailand | KC519498 |
| *T. resimus* Pnk | CUMZ-D00035 | Phu-No, Ta-Khan-Tho, Kalasin, Thailand | KC519499 |
| *T. resimus* Pp | CUMZ-D00036 | Sae-Ri-Thai cave, Phu-Pan, Sakonnakhon, Thailand | KC519500 |
| *T. resimus* Wnt | CUMZ-D00037 | Wana-Thara resort, Wang-Thong, Phitsanulok, Thailand | KC519501 |
| *T. siamensis* Verhoeff, 1938 (Sa) | CUMZ-D00047 | Chulalongkorn University area, Kang-Khoi, Saraburi, Thailand | KC519511 |
| *T. somsaki* Pimvichai, Enghoff & Backeljau, 2023 (PPLT) | CUMZ-D00152 | Phu Pha Lom, Muang, Loei, Thailand | OP549749 |
| *T. uncinatus* (Demange, 1961) | | | |
| *T. uncinatus* Kdb | CUMZ-D00038 | Khao Kra-Dong, Muang, Buriram, Thailand | KC519502 |
| *T. uncinatus* Pj | CUMZ-D00039 | Parchantakham, Prachinburi, Thailand | KC519503 |
| *T. uncinatus* Pks | CUMZ-D00040 | Phu-Khae, Chalermprakiat, Saraburi, Thailand | KC519504 |
| *T. uncinatus* Pn | CUMZ-D00041 | Rice field, Ban Nong-Pue, Chaturaphakphiman, Roi-Et, Thailand | KC519505 |
| *T. uncinatus* Ps | CUMZ-D00042 | Phanomsawai, Surin, Thailand | KC519506 |
| *T. uncinatus* Rcb | CUMZ-D00043 | Rajabhat Buriram, Buriram, Thailand | KC519507 |
| *T. uncinatus* Sc | CUMZ-D00044 | Koh Si-Chang, Koh Si-Chang, Chonburi, Thailand | KC519508 |
| *T. uncinatus* Sm | CUMZ-D00045 | Srimathani Hotel, Muang, Nakhonratchasima, Thailand | KC519509 |
| *T. uncinatus* Sn | CUMZ-D00046 | Surasammanakhan, Muang, Nakhonratchasima, Thailand | KC519510 |
| ***T. opinatus* subgroup** | | | |
| *T. opinatus* (Karsch, 1881) (Arw) | CUMZ-D00054 | Aerawan waterfall, Srisawad, Kanchanaburi, Thailand | KC519517 |
| *T. inflexus* (Demange, 1989) (Kk) | CUMZ-D00056 | Srinakharin Dam, Srisawad, Kanchanaburi, Thailand | KC519518 |
| *T. bearti* Pimvichai, Enghoff & Panha, 2009 (Ks) | CUMZ-D00057 | Khao Sai, Si Chon, Nakhonsithammarat, Thailand | KC519519 |
| *T. bispinus* Pimvichai, Enghoff & Panha, 2009 (Tm) | CUMZ-D00058 | Thep Muang Thong temple, Lansak, Uthaithani, Thailand | KC519520 |

**TABLE 1.** Continued.

| | Voucher code | Locality | COI |
|---|---|---|---|
| *T. bispinispatula* Pimvichai, Enghoff & Panha, 2009 (Kb) | CUMZ-D00059 | Tam Khao Krieb temple, Lang Suan, Chumporn, Thailand | KC519521 |
| *T. brachyacanthus* Pimvichai, Enghoff & Panha, 2009 (Sk) | CUMZ-D00060 | Sathitkhirirom temple, Khiriratnikhom, Suratthani, Thailand | KC519522 |
| *T. cimi* Pimvichai, Enghoff, Panha & Backeljau, 2016 (Nws1) | CUMZ-D00086 | Namwang Srithammasokarach, Lanska, Nakhonsithammarat, Thailand | KU306519 |
| *T. cristagalli* Pimvichai, Enghoff & Panha, 2009 (Yn) | CUMZ-D00064 | Koh Yao Noi, Koh Yao, Phang-Nga, Thailand | KC519523 |
| *T. culter* Pimvichai, Enghoff, Panha & Backeljau, 2016 (Nr) | CUMZ-D00078 | Rorn waterfall, Khlong Thom, Krabi, Thailand | KC519535 |
| *T. demangei* Pimvichai, Enghoff & Panha, 2009 (Cm) | CUMZ-D00066 | Ban Chang Lang, Hat Chao Mai, Si kao, Trang, Thailand | KC519525 |
| *T. enghoffi* (Demange, 1989) (Kl) | CUMZ-D00067 | Khao Lak Lam Ru, Takuepa, Phang-Nga, Thailand | KC519526 |
| *T. forceps* Pimvichai, Enghoff, Panha & Backeljau, 2016 (Nws2) | CUMZ-D00073 | Namwang Srithammasokarach, Lanska,Nakhonsithammarat, Thailand | KC519531 |
| *T. loxia* Pimvichai, Enghoff & Panha, 2009 (Ty) | CUMZ-D00065 | Tam Yai temple, Tha Cha Na, Suratthani, Thailand | KC519524 |
| *T. mesocristatus* Pimvichai, Enghoff, Panha & Backeljau, 2016 (Pb2) | CUMZ-D00077 | Srikasorn, Rattaphum, Songkhla, Thailand | KC519534 |
| *T. navychula* Pimvichai, Enghoff, Panha & Backeljau, 2016 (KSR) | CUMZ-D00089 | Surin Islands, Khuraburi, Phang-Nga, Thailand | KU306522 |
| *T. peninsularis* Hoffman, 1982 (Wm) | CUMZ-D00011 | Wang-Matcha, Kapoe, Ranong, Thailand | KC519477 |
| *T. planispina* Pimvichai, Enghoff, Panha & Backeljau, 2016 (Tsk2) | CUMZ-D00088 | Tham Sua temple, Muang, Krabi, Thailand | KU306521 |
| *T. quadricuspis* Pimvichai, Enghoff & Panha, 2009 (Hy) | CUMZ-D00069 | Khao Pina temple, Hui Yod, Trang, Thailand | KC519528 |
| *T. richardhoffmani* Pimvichai, Enghoff & Panha, 2009 (TCH) | CUMZ-D00085 | Tham Chang Hai, Hui Yod, Trang, Thailand | KU306518 |
| T. *sutchariti* Pimvichai, Enghoff, Panha and Backeljau, 2016 (KCP) | CUMZ-D00090 | Kaeng Krachan, Kaeng Krachan, Phetchaburi, Thailand | KU306524 |
| *T. undulatus* Pimvichai, Enghoff, Panha & Backeljau, 2016 (Pb2) | CUMZ-D00087 | Khao Pha Nom Bencha, Muang, Krabi, Thailand | KU306520 |
| *T. ursus* Pimvichai, Enghoff, Panha & Backeljau, 2016 (LTK) | NHMW-Inv.7855 | Lanta Islands, Koh Lanta, Krabi, Thailand | KU306523 |
| **Undefined subgroup** | | | |
| *T. sirindhornae* sp. nov. Knn1 | CUMZ-D00157 | Khun Nam Nang Non, Mae Sai, Chiang Rai, Thailand | PV612841 |
| *T. sirindhornae* sp. nov. Knn2 | CUMZ-D00157-1 | Khun Nam Nang Non, Mae Sai, Chiang Rai, Thailand | PV612842 |

(range: 0.02–0.17) for the *T. opinatus* subgroup, 0.12 ± 0.02 (range: 0.07–0.15) for the *T. induratus* subgroup, and 0.11 ± 0.00 for the *T. cuisinieri* subgroup.

The BI and ML COI trees (Fig. 1) placed *T. sirindhornae* sp. nov. with near maximum support among *Thyropygus* species and more precisely within the *T. allevatus* group. Yet, the subgroup assignment and sister group position of the new species were not resolved. Conversely, the sister group relationship between *T. foliaceus* and *T. jarukchusri*, which together form the *T. cuisinieri* subgroup, was maximally supported (BV = 100, PP = 1.00). Also, the monophyly of *T. opinatus* subgroup was well supported (BV = 72, PP = 1.00). There was, however, no support for the monophyly of the *T. induratus* subgroup. Finally, the sister group position of the *T. allevatus* subgroup was unresolved, while its monophyly could not be assessed because it was only represented by its nominal species.

## Taxonomy

### Class Diplopoda de Blainville in Gervais, 1844
### Order Spirostreptida Brandt, 1833
### Suborder Spirostreptidea Brandt, 1833

### Family Harpagophoridae Attems, 1909
### Genus *Thyropygus* Pocock, 1894

## Species description

The new species belongs to the *T. allevatus* group by sharing two diagnostic characters viz. (1) the gonopod telopodite having both tibial and femoral spines, and (2) tibial spine being very long and recurved toward the femoral one (Hoffman, 1975). For a general description of the gonopod morphology of the *T. allevatus* group see Pimvichai et al. (2009a: 21), and for a general description of the external morphology of this group see Pimvichai et al. (2011a: 49).

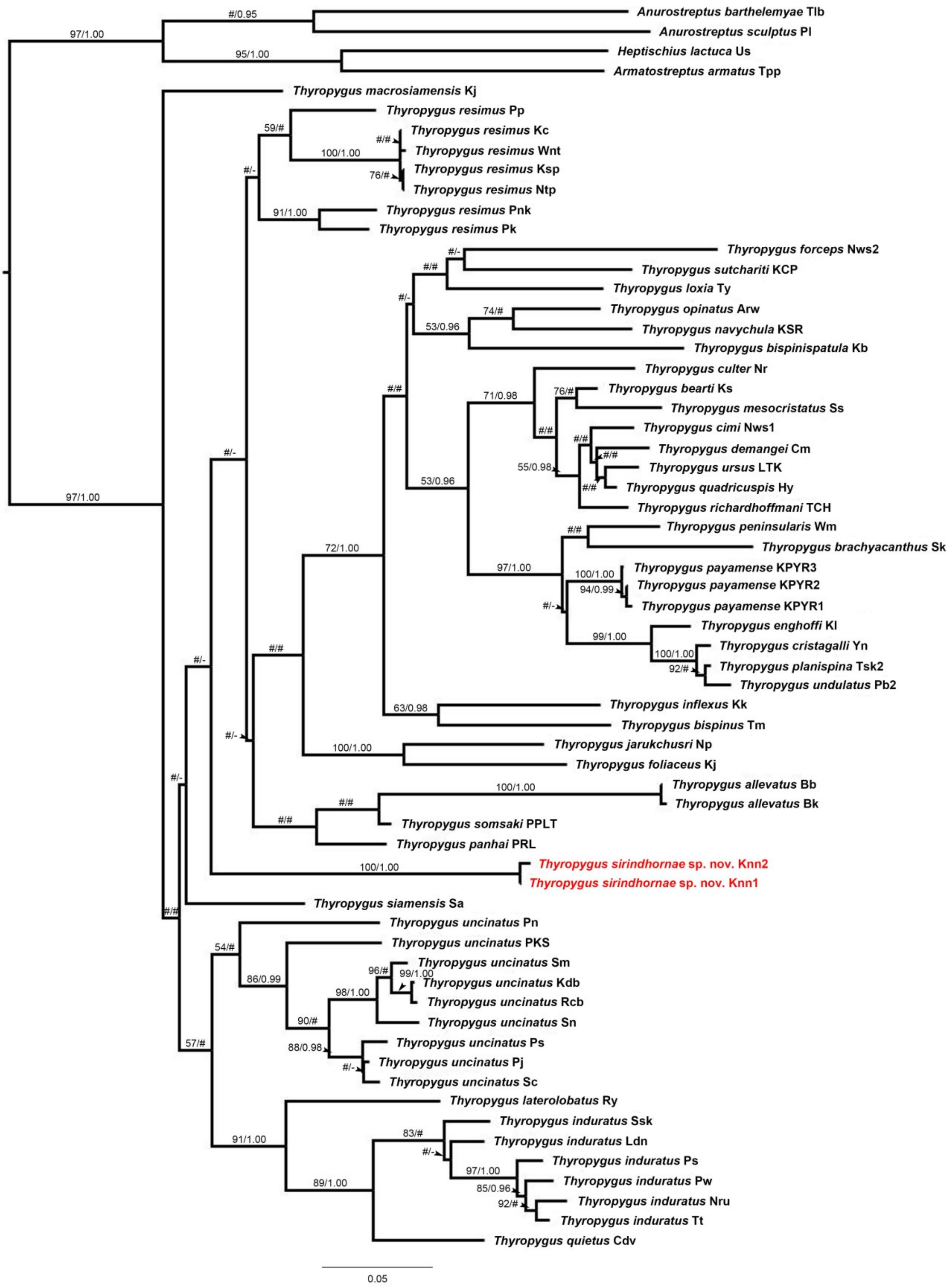

**FIGURE 1.** Phylogenetic relationships of *Thyropygus sirindhornae* sp. nov. within the *T. allevatus* group based on maximum likelihood analysis (ML) and Bayesian inference (BI) of COI sequences (660 bp). Numbers at nodes indicate branch support based on bootstrapping (ML) / posterior probabilities (BI). Scale bar = 0.05 substitutions/site. # indicates branches with < 50% ML bootstrap support and < 0.95 Bayesian posterior probability. - indicates non-supported branches.

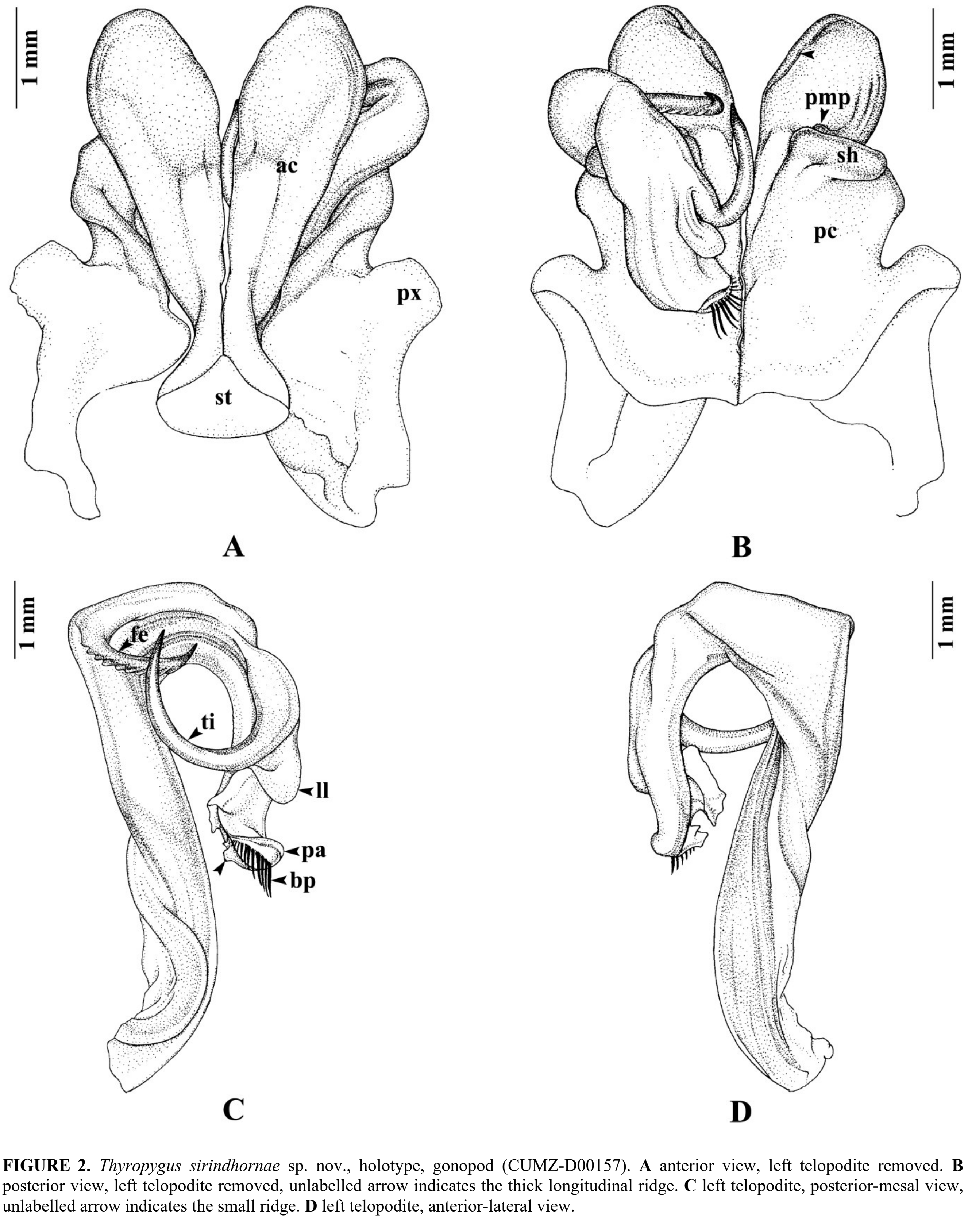

**FIGURE 2.** *Thyropygus sirindhornae* sp. nov., holotype, gonopod (CUMZ-D00157). **A** anterior view, left telopodite removed. **B** posterior view, left telopodite removed, unlabelled arrow indicates the thick longitudinal ridge. **C** left telopodite, posterior-mesal view, unlabelled arrow indicates the small ridge. **D** left telopodite, anterior-lateral view.

**FIGURE 3.** Live *Thyropygus sirindhornae* sp. nov., holotype, (CUMZ-D00157) from Chiang Rai Province, Thailand.

### *Thyropygus sirindhornae* sp. nov.

https://zoobank.org/urn:lsid:zoobank.org:act: 12A1A595-490E-425B-AD89-26CD2054C1E5

(Figs 2–4)

**Material examined.**– Holotype male (CUMZ-D00157), THAILAND, Chiang Rai Province, Mae Sai District, Khun Nam Nang Non, 20°23'01"N 99°52' 54"E, 710 m a.s.l., 14 September 2023, leg. P. Prasankok. Paratypes 1 male (CUMZ-D00157-1), 1 female (CUMZ-D00157-2), same data as holotype.

**Etymology.**– The species is named to honor Her Royal Highness Princess Maha Chakri Sirindhorn on the occasion of her 70th birthday, acknowledging her dedication to promoting biodiversity research and conservation initiatives in Thailand.

**Diagnosis.**– A species of the *T. allevatus* group. Differs from all species of the *T. induratus* subgroup by not having an uncate subterminal lobe (*usl*) on the telopodite. Differs from all species of the *T. opinatus* subgroup by not having an additional projection on the anterior coxal fold (*amp*). Differs from all species of the *T. cuisinieri* subgroup by not having a prominent projecting lobe on the lateral surface of the anterior coxal fold (*apl*) and not having a protruding lobe on the telopodite (*lo*) distal to the femoral spine. Differs from the *T. allevatus* subgroup by not having a flattened process under the palette (*pa*) at the apical part of telopodite. These missing characters are the diagnostic characters of each subgroup. The two unique gonopodal characters of the new species are: (1) mesal margin of anterior coxal fold (*ac*) with a thick longitudinal ridge in posterior view (Fig. 2B, unlabelled arrow), and (2) the palette (*pa*) of telopodite with a small transparent crest (Fig. 2C, unlabelled arrow).

**Description.**– Adult males with 62–63 podous rings, no apodous rings. Length ca. 14–15 cm, width ca. 8.4.–9.7 mm. Adult female with 61 podous rings, no apodous rings. Length ca. 13 cm, width ca. 10.5 mm. Overall color of living animal (Fig. 3) reddish brown, legs yellowish brown; epiproct, paraprocts and hypoproct yellowish brown; metazona dark brown.

**Gonopods** (Fig. 2A–D).– Anterior coxal fold (*ac*) (Fig. 2A) basally narrow, gradually widening towards tip, apically ending in a rounded lobe, mesal margin with a thick longitudinal ridge in posterior view (Fig. 2B, unlabelled arrow). Posterior coxal fold (*pc*) (Fig. 2B) basally with high lateral paracoxites (*px*); mesal process of posterior coxal fold (*pmp*) much lower than *ac*, forming a shelf (*sh*) for accommodation of telopodite. Telopodite (Fig. 2C–D) leaving coxite over shelf of posterior coxal fold; femoral spine (*fe*) extremely long, curving in a horizontal plane, very distinctly crenulated along outer curvature, *in situ* resting against tip of tibial spine; tibial spine (*ti*) very long, slender, curving in an oblique-sagittal plane, *in situ* resting between the two *ac*, its tip close to mesal margin of *ac*; apical part: lamellar lobe (*ll*) small, rounded; palette (*pa*) simple, basally with a small transparent crest (Fig. 2C, unlabelled arrow); distally with ca. ten brownish blepharochaetae (*bp*).

**DNA barcode.**– The GenBank accession number of the COI barcode of the holotype is PV612841 (voucher code CUMZ-D00157) and the COI barcode of the paratype is PV612842 (voucher code CUMZ-D00157-1).

**Habitat.**– Found under leaf litter and crawling around on limestone mountain.

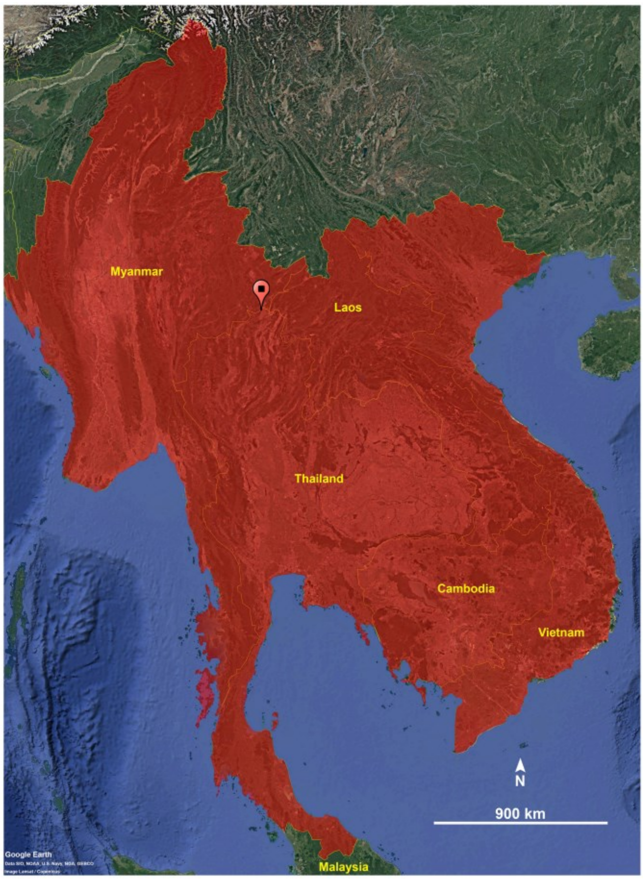

**FIGURE 4.** Distribution of the *Thyropygus allevatus* group (red area) (Pimvichai et al., 2009a, 2009b, 2011a, 2011b, 2014, 2016, 2023, 2025) and location of the type locality of *T. sirindhornae* sp. nov.

**Distribution.**– Known only from the type locality in Chiang Rai Province, Thailand (Fig. 4).

## DISCUSSION

*Thyropygus sirindhornae* sp. nov. unequivocally belongs to the *T. allevatus* group because it shows the two diagnostic characters of this group: (1) the gonopod telopodite bearing both tibial and femoral spines, and (2) the tibial spine being notably long and recurved toward the femoral spine (Hoffman, 1975). However, *T. sirindhornae* sp. nov. does not show any of the diagnostic morphological characters of the four subgroups within the *T. allevatus* group.

DNA barcode data support the distinctiveness of *T. sirindhornae* sp. nov. given its relatively high mean interspecific sequence divergence relative to other *Thyropygus* species (0.16 ± 0.02; range: 0.12–0.19), which exceeds the mean interspecific sequence divergences within the *T. opinatus* subgroup (0.12 ± 0.03, range: 0.02–0.17), the *T. induratus* subgroup (0.12 ± 0.02, range: 0.07–0.15), and the *T. cuisinieri* subgroup (0.11 ± 0.00). Moreover, the phylogenetic analysis of the COI sequences firmly places *T. sirindhornae* sp. nov. within the *T. allevatus* group, but without supporting a sister group relationship. Consequently, neither the morphology, nor the COI sequences of *T. sirindhornae* sp. nov. allow to assign the species to any of the four subgroups of the *T. allevatus* group. Hence, with respect to its sister group relationships and subgroup classification, we consider the new species as "incertae sedis". In fact, even the assignment of *T. sirindhornae* sp. nov. to the *T. allevatus* group needs further confirmation, since our analysis did not include species of other informal *Thyropygus* species groups (Hoffman, 1975), so that the assignment to the *T. allevatus* in the ingroup was not challenged. In this respect, *T. sirindhornae* sp. nov. is even more problematic than *T. panhai* and *T. somsaki* since these two species could be morphologically assigned to the *T. induratus* subgroup, even if their COI sequence data could not confirm this (Pimvichai et al., 2023). Yet, similar to *T. panhai* and *T. somsaki*, the inclusion of *T. sirindhornae* sp. nov. in the COI phylogeny confirmed again the lack of support for the monophyly of the *T. induratus* subgroup, as first reported by Pimvichai et al. (2023), but did not affect the support for the monophyly of the *T. opinatus* and *T. cuisinieri* subgroups. Anyway, in order to better understand the relationships of *T. sirindhornae*, *T. panhai* and *T. somsaki*, it will be necessary, not only to increase the species and DNA marker sampling, but also to make sure that other informal *Thyropygus* groups, and in particular the *T. aterrimus* group from Myanmar and Malaysia, are represented in the analyses.

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## APPENDIX

**TABLE A1.** Estimates of COI sequence divergences within and among *Coxobolellus* species and related taxa expressed as uncorrected p-distances (rounded to two decimals).

| | **Taxa** | **1** | **2** | **3** | **4** | **5** | **6** | **7** | **8** | **9** | **10** | **11** | **12** | **13** | **14** | **15** | **16** | **17** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | *Anurostreptus barthelemyae* Tlb | | | | | | | | | | | | | | | | | |
| 2 | *Anurostreptus sculptus* Pl | 0.15 | | | | | | | | | | | | | | | | |
| 3 | *Armatostreptus armatus* Tpp | 0.18 | 0.17 | | | | | | | | | | | | | | | |
| 4 | *Heptischius lactuca* Us | 0.19 | 0.17 | 0.15 | | | | | | | | | | | | | | |
| 5 | *Thyropygus allevatus* Bb | 0.15 | 0.17 | 0.19 | 0.18 | | | | | | | | | | | | | |
| 6 | *Thyropygus allevatus* Bk | 0.16 | 0.17 | 0.19 | 0.18 | 0.00 | | | | | | | | | | | | |
| 7 | *Thyropygus bearti* Ks | 0.19 | 0.20 | 0.18 | 0.19 | 0.16 | 0.17 | | | | | | | | | | | |
| 8 | *Thyropygus bispinispatula* Kb | 0.19 | 0.19 | 0.20 | 0.19 | 0.15 | 0.15 | 0.13 | | | | | | | | | | |
| 9 | *Thyropygus bispinus* Tm | 0.18 | 0.17 | 0.19 | 0.18 | 0.16 | 0.16 | 0.14 | 0.14 | | | | | | | | | |
| 10 | *Thyropygus cimi* Nws1 | 0.20 | 0.19 | 0.18 | 0.20 | 0.17 | 0.18 | 0.05 | 0.14 | 0.13 | | | | | | | | |
| 11 | *Thyropygus cristagalli* Yn | 0.18 | 0.20 | 0.19 | 0.20 | 0.14 | 0.14 | 0.13 | 0.14 | 0.17 | 0.13 | | | | | | | |
| 12 | *Thyropygus culter* Nr | 0.18 | 0.20 | 0.17 | 0.20 | 0.16 | 0.16 | 0.07 | 0.13 | 0.13 | 0.08 | 0.13 | | | | | | |
| 13 | *Thyropygus demangei* Cm | 0.20 | 0.21 | 0.17 | 0.20 | 0.17 | 0.17 | 0.06 | 0.13 | 0.13 | 0.05 | 0.13 | 0.08 | | | | | |
| 14 | *Thyropygus enghoffi* Kl | 0.17 | 0.18 | 0.17 | 0.17 | 0.13 | 0.13 | 0.11 | 0.13 | 0.14 | 0.12 | 0.05 | 0.12 | 0.13 | | | | |
| 15 | *Thyropygus foliaceus* Kj | 0.20 | 0.18 | 0.20 | 0.20 | 0.15 | 0.15 | 0.14 | 0.15 | 0.15 | 0.14 | 0.17 | 0.15 | 0.14 | 0.15 | | | |
| 16 | *Thyropygus forceps* Nws2 | 0.19 | 0.19 | 0.18 | 0.17 | 0.17 | 0.17 | 0.13 | 0.13 | 0.13 | 0.12 | 0.15 | 0.13 | 0.13 | 0.14 | 0.16 | | |
| 17 | *Thyropygus induratus* Ldn | 0.16 | 0.19 | 0.18 | 0.18 | 0.13 | 0.14 | 0.14 | 0.14 | 0.15 | 0.13 | 0.16 | 0.13 | 0.14 | 0.15 | 0.16 | 0.16 | |
| 18 | *Thyropygus induratus* Nru | 0.17 | 0.20 | 0.18 | 0.19 | 0.14 | 0.15 | 0.15 | 0.15 | 0.16 | 0.14 | 0.18 | 0.13 | 0.14 | 0.16 | 0.17 | 0.16 | 0.06 |
| 19 | *Thyropygus induratus* Ps | 0.17 | 0.20 | 0.19 | 0.17 | 0.14 | 0.14 | 0.14 | 0.14 | 0.16 | 0.14 | 0.17 | 0.13 | 0.14 | 0.15 | 0.17 | 0.16 | 0.06 |
| 20 | *Thyropygus induratus* Pw | 0.17 | 0.20 | 0.18 | 0.18 | 0.14 | 0.14 | 0.15 | 0.15 | 0.16 | 0.14 | 0.18 | 0.14 | 0.15 | 0.15 | 0.17 | 0.16 | 0.06 |
| 21 | *Thyropygus induratus* Ssk | 0.17 | 0.19 | 0.19 | 0.18 | 0.13 | 0.14 | 0.14 | 0.13 | 0.15 | 0.14 | 0.15 | 0.13 | 0.14 | 0.13 | 0.16 | 0.15 | 0.04 |
| 22 | *Thyropygus induratus* Tt | 0.17 | 0.19 | 0.18 | 0.18 | 0.14 | 0.14 | 0.15 | 0.14 | 0.16 | 0.14 | 0.17 | 0.13 | 0.14 | 0.15 | 0.17 | 0.16 | 0.06 |
| 23 | *Thyropygus inflexus* Kk | 0.18 | 0.17 | 0.18 | 0.19 | 0.16 | 0.16 | 0.13 | 0.13 | 0.12 | 0.14 | 0.16 | 0.12 | 0.13 | 0.15 | 0.15 | 0.13 | 0.15 |
| 24 | *Thyropygus jarukchusri* Np | 0.19 | 0.18 | 0.19 | 0.19 | 0.14 | 0.14 | 0.15 | 0.15 | 0.15 | 0.15 | 0.16 | 0.15 | 0.15 | 0.13 | 0.11 | 0.16 | 0.14 |
| 25 | *Thyropygus laterolobatus* Ry | 0.18 | 0.18 | 0.19 | 0.18 | 0.15 | 0.15 | 0.15 | 0.15 | 0.14 | 0.14 | 0.17 | 0.13 | 0.15 | 0.14 | 0.15 | 0.16 | 0.11 |
| 26 | *Thyropygus loxia* Ty | 0.18 | 0.17 | 0.17 | 0.18 | 0.15 | 0.15 | 0.11 | 0.12 | 0.11 | 0.11 | 0.14 | 0.12 | 0.11 | 0.12 | 0.15 | 0.14 | 0.15 |
| 27 | *Thyropygus macrosiamensis* Kj | 0.17 | 0.18 | 0.19 | 0.18 | 0.14 | 0.14 | 0.13 | 0.14 | 0.13 | 0.12 | 0.15 | 0.13 | 0.12 | 0.13 | 0.14 | 0.15 | 0.12 |
| 28 | *Thyropygus mesocristatus* Ss | 0.18 | 0.19 | 0.18 | 0.19 | 0.17 | 0.17 | 0.05 | 0.13 | 0.14 | 0.07 | 0.13 | 0.08 | 0.08 | 0.12 | 0.15 | 0.13 | 0.14 |
| 29 | *Thyropygus navychula* KSR | 0.20 | 0.17 | 0.17 | 0.19 | 0.16 | 0.16 | 0.12 | 0.13 | 0.13 | 0.12 | 0.14 | 0.12 | 0.11 | 0.13 | 0.14 | 0.14 | 0.16 |
| 30 | *Thyropygus opinatus* Arw | 0.18 | 0.18 | 0.17 | 0.18 | 0.15 | 0.15 | 0.11 | 0.12 | 0.14 | 0.12 | 0.12 | 0.12 | 0.12 | 0.11 | 0.15 | 0.13 | 0.14 |
| 31 | *Thyropygus panhai* PRL2 | 0.18 | 0.18 | 0.18 | 0.19 | 0.14 | 0.14 | 0.15 | 0.15 | 0.14 | 0.15 | 0.17 | 0.15 | 0.15 | 0.16 | 0.13 | 0.16 | 0.13 |
| 32 | *Thyropygus brachyacanthus* Sk | 0.20 | 0.19 | 0.19 | 0.20 | 0.17 | 0.17 | 0.12 | 0.14 | 0.16 | 0.13 | 0.10 | 0.12 | 0.13 | 0.10 | 0.17 | 0.16 | 0.16 |
| 33 | *Thyropygus payamense* KPYR1 | 0.19 | 0.19 | 0.18 | 0.19 | 0.15 | 0.15 | 0.10 | 0.15 | 0.13 | 0.10 | 0.09 | 0.12 | 0.11 | 0.08 | 0.16 | 0.14 | 0.15 |
| 34 | *Thyropygus payamense* KPYR2 | 0.19 | 0.19 | 0.18 | 0.19 | 0.15 | 0.15 | 0.10 | 0.15 | 0.13 | 0.11 | 0.09 | 0.12 | 0.11 | 0.08 | 0.16 | 0.14 | 0.15 |
| 35 | *Thyropygus payamense* KPYR3 | 0.18 | 0.19 | 0.18 | 0.19 | 0.14 | 0.15 | 0.10 | 0.15 | 0.13 | 0.10 | 0.09 | 0.12 | 0.11 | 0.08 | 0.16 | 0.14 | 0.14 |
| 36 | *Thyropygus peninsularis* Wm | 0.20 | 0.20 | 0.20 | 0.20 | 0.16 | 0.16 | 0.12 | 0.16 | 0.15 | 0.11 | 0.10 | 0.11 | 0.12 | 0.09 | 0.16 | 0.15 | 0.15 |
| 37 | *Thyropygus planispinus* Tsk2 | 0.18 | 0.19 | 0.19 | 0.19 | 0.14 | 0.15 | 0.13 | 0.14 | 0.16 | 0.13 | 0.02 | 0.13 | 0.13 | 0.05 | 0.17 | 0.16 | 0.16 |
| 38 | *Thyropygus quadricuspis* Hy | 0.20 | 0.19 | 0.18 | 0.19 | 0.17 | 0.17 | 0.05 | 0.13 | 0.13 | 0.03 | 0.13 | 0.07 | 0.03 | 0.12 | 0.14 | 0.12 | 0.14 |
| 39 | *Thyropygus quietus* Cdv | 0.17 | 0.20 | 0.19 | 0.19 | 0.15 | 0.15 | 0.14 | 0.15 | 0.14 | 0.14 | 0.15 | 0.14 | 0.14 | 0.15 | 0.16 | 0.16 | 0.09 |
| 40 | *Thyropygus resimus* Kc | 0.18 | 0.17 | 0.19 | 0.17 | 0.15 | 0.15 | 0.14 | 0.13 | 0.13 | 0.13 | 0.16 | 0.13 | 0.13 | 0.14 | 0.13 | 0.14 | 0.12 |
| 41 | *Thyropygus resimus* Ksp | 0.19 | 0.17 | 0.18 | 0.17 | 0.15 | 0.15 | 0.14 | 0.14 | 0.13 | 0.13 | 0.16 | 0.13 | 0.13 | 0.14 | 0.13 | 0.14 | 0.12 |
| 42 | *Thyropygus resimus* Ntp | 0.19 | 0.17 | 0.18 | 0.17 | 0.15 | 0.15 | 0.14 | 0.14 | 0.13 | 0.13 | 0.16 | 0.13 | 0.13 | 0.14 | 0.13 | 0.14 | 0.12 |
| 43 | *Thyropygus resimus* Pk | 0.18 | 0.17 | 0.18 | 0.18 | 0.14 | 0.14 | 0.14 | 0.14 | 0.12 | 0.14 | 0.16 | 0.14 | 0.13 | 0.14 | 0.14 | 0.15 | 0.12 |
| 44 | *Thyropygus resimus* Pnk | 0.17 | 0.17 | 0.19 | 0.18 | 0.13 | 0.13 | 0.12 | 0.13 | 0.12 | 0.12 | 0.16 | 0.14 | 0.12 | 0.14 | 0.12 | 0.14 | 0.12 |
| 45 | *Thyropygus resimus* Pp | 0.18 | 0.17 | 0.18 | 0.17 | 0.13 | 0.14 | 0.15 | 0.13 | 0.12 | 0.15 | 0.14 | 0.13 | 0.15 | 0.13 | 0.14 | 0.13 | 0.12 |
| 46 | *Thyropygus resimus* Wnt | 0.18 | 0.17 | 0.19 | 0.17 | 0.15 | 0.15 | 0.14 | 0.13 | 0.13 | 0.13 | 0.16 | 0.13 | 0.14 | 0.14 | 0.14 | 0.14 | 0.12 |
| 47 | *Thyropygus richardhoffmani* TCH | 0.20 | 0.19 | 0.18 | 0.19 | 0.16 | 0.16 | 0.05 | 0.14 | 0.13 | 0.05 | 0.14 | 0.08 | 0.05 | 0.12 | 0.14 | 0.13 | 0.14 |
| 48 | *Thyropygus siamensis* Sa | 0.18 | 0.17 | 0.19 | 0.17 | 0.13 | 0.13 | 0.14 | 0.14 | 0.13 | 0.15 | 0.14 | 0.14 | 0.15 | 0.13 | 0.14 | 0.15 | 0.12 |
| 49 | *Thyropygus somsaki* PPLT | 0.17 | 0.17 | 0.19 | 0.18 | 0.11 | 0.11 | 0.16 | 0.14 | 0.13 | 0.16 | 0.17 | 0.16 | 0.16 | 0.15 | 0.14 | 0.16 | 0.13 |
| 50 | *Thyropygus sutchariti* KCP | 0.19 | 0.18 | 0.21 | 0.20 | 0.15 | 0.15 | 0.14 | 0.14 | 0.12 | 0.13 | 0.15 | 0.13 | 0.13 | 0.13 | 0.16 | 0.13 | 0.16 |
| 51 | *Thyropygus uncinatus* Kdb | 0.17 | 0.16 | 0.19 | 0.18 | 0.13 | 0.13 | 0.14 | 0.14 | 0.14 | 0.15 | 0.17 | 0.15 | 0.16 | 0.14 | 0.15 | 0.17 | 0.12 |
| 52 | *Thyropygus uncinatus* Pj | 0.17 | 0.17 | 0.19 | 0.17 | 0.14 | 0.14 | 0.13 | 0.13 | 0.13 | 0.14 | 0.15 | 0.13 | 0.14 | 0.12 | 0.14 | 0.15 | 0.13 |
| 53 | *Thyropygus uncinatus* Pks | 0.17 | 0.18 | 0.18 | 0.18 | 0.14 | 0.15 | 0.14 | 0.15 | 0.15 | 0.14 | 0.16 | 0.14 | 0.14 | 0.14 | 0.15 | 0.15 | 0.14 |
| 54 | *Thyropygus uncinatus* Pn | 0.17 | 0.18 | 0.18 | 0.17 | 0.14 | 0.14 | 0.13 | 0.14 | 0.15 | 0.13 | 0.15 | 0.14 | 0.13 | 0.13 | 0.14 | 0.15 | 0.12 |
| 55 | *Thyropygus uncinatus* Ps | 0.17 | 0.18 | 0.19 | 0.18 | 0.14 | 0.15 | 0.14 | 0.14 | 0.13 | 0.14 | 0.16 | 0.14 | 0.14 | 0.13 | 0.14 | 0.16 | 0.13 |
| 56 | *Thyropygus uncinatus* Rcb | 0.16 | 0.16 | 0.19 | 0.18 | 0.13 | 0.13 | 0.14 | 0.13 | 0.14 | 0.15 | 0.16 | 0.15 | 0.15 | 0.14 | 0.15 | 0.16 | 0.12 |
| 57 | *Thyropygus uncinatus* Sc | 0.17 | 0.17 | 0.20 | 0.17 | 0.14 | 0.14 | 0.14 | 0.14 | 0.13 | 0.14 | 0.15 | 0.13 | 0.14 | 0.12 | 0.14 | 0.15 | 0.13 |
| 58 | *Thyropygus uncinatus* Sm | 0.17 | 0.17 | 0.20 | 0.17 | 0.13 | 0.13 | 0.15 | 0.13 | 0.13 | 0.15 | 0.15 | 0.15 | 0.15 | 0.13 | 0.16 | 0.16 | 0.11 |
| 59 | *Thyropygus uncinatus* Sn | 0.17 | 0.18 | 0.20 | 0.17 | 0.13 | 0.13 | 0.15 | 0.14 | 0.13 | 0.16 | 0.15 | 0.14 | 0.15 | 0.13 | 0.16 | 0.16 | 0.13 |
| 60 | *Thyropygus undulatus* Pb2 | 0.18 | 0.20 | 0.19 | 0.20 | 0.15 | 0.15 | 0.12 | 0.15 | 0.17 | 0.13 | 0.03 | 0.13 | 0.13 | 0.05 | 0.17 | 0.17 | 0.16 |
| 61 | *Thyropygus ursus* LTK | 0.20 | 0.19 | 0.18 | 0.19 | 0.16 | 0.16 | 0.05 | 0.13 | 0.13 | 0.05 | 0.12 | 0.08 | 0.04 | 0.11 | 0.15 | 0.13 | 0.13 |
| 62 | *Thyropygus sirindhornae* sp. nov. Knn2 | 0.21 | 0.19 | 0.20 | 0.20 | 0.17 | 0.17 | 0.17 | 0.17 | 0.15 | 0.17 | 0.18 | 0.17 | 0.17 | 0.17 | 0.17 | 0.17 | 0.15 |
| 63 | *Thyropygus sirindhornae* sp. nov. Knn1 | 0.20 | 0.19 | 0.20 | 0.19 | 0.16 | 0.16 | 0.16 | 0.17 | 0.15 | 0.17 | 0.18 | 0.17 | 0.17 | 0.17 | 0.17 | 0.17 | 0.15 |

## APPENDIX

**TABLE A1.** Continued.

| | **Taxa** | **18** | **19** | **20** | **21** | **22** | **23** | **24** | **25** | **26** | **27** | **28** | **29** | **30** | **31** | **32** | **33** | **34** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | *Anurostreptus barthelemyae* Tlb | | | | | | | | | | | | | | | | | |
| 2 | *Anurostreptus sculptus* Pl | | | | | | | | | | | | | | | | | |
| 3 | *Armatostreptus armatus* Tpp | | | | | | | | | | | | | | | | | |
| 4 | *Heptischius lactuca* Us | | | | | | | | | | | | | | | | | |
| 5 | *Thyropygus allevatus* Bb | | | | | | | | | | | | | | | | | |
| 6 | *Thyropygus allevatus* Bk | | | | | | | | | | | | | | | | | |
| 7 | *Thyropygus bearti* Ks | | | | | | | | | | | | | | | | | |
| 8 | *Thyropygus bispinispatula* Kb | | | | | | | | | | | | | | | | | |
| 9 | *Thyropygus bispinus* Tm | | | | | | | | | | | | | | | | | |
| 10 | *Thyropygus cimi* Nws1 | | | | | | | | | | | | | | | | | |
| 11 | *Thyropygus cristagalli* Yn | | | | | | | | | | | | | | | | | |
| 12 | *Thyropygus culter* Nr | | | | | | | | | | | | | | | | | |
| 13 | *Thyropygus demangei* Cm | | | | | | | | | | | | | | | | | |
| 14 | *Thyropygus enghoffi* Kl | | | | | | | | | | | | | | | | | |
| 15 | *Thyropygus foliaceus* Kj | | | | | | | | | | | | | | | | | |
| 16 | *Thyropygus forceps* Nws2 | | | | | | | | | | | | | | | | | |
| 17 | *Thyropygus induratus* Ldn | | | | | | | | | | | | | | | | | |
| 18 | *Thyropygus induratus* Nru | | | | | | | | | | | | | | | | | |
| 19 | *Thyropygus induratus* Ps | 0.04 | | | | | | | | | | | | | | | | |
| 20 | *Thyropygus induratus* Pw | 0.03 | 0.03 | | | | | | | | | | | | | | | |
| 21 | *Thyropygus induratus* Ssk | 0.07 | 0.06 | 0.07 | | | | | | | | | | | | | | |
| 22 | *Thyropygus induratus* Tt | 0.02 | 0.03 | 0.03 | 0.06 | | | | | | | | | | | | | |
| 23 | *Thyropygus inflexus* Kk | 0.16 | 0.15 | 0.16 | 0.15 | 0.15 | | | | | | | | | | | | |
| 24 | *Thyropygus jarukchusri* Np | 0.14 | 0.14 | 0.14 | 0.13 | 0.13 | 0.16 | | | | | | | | | | | |
| 25 | *Thyropygus laterolobatus* Ry | 0.12 | 0.12 | 0.13 | 0.12 | 0.12 | 0.15 | 0.14 | | | | | | | | | | |
| 26 | *Thyropygus loxia* Ty | 0.15 | 0.15 | 0.16 | 0.15 | 0.15 | 0.13 | 0.14 | 0.14 | | | | | | | | | |
| 27 | *Thyropygus macrosiamensis* Kj | 0.13 | 0.12 | 0.13 | 0.12 | 0.12 | 0.14 | 0.13 | 0.13 | 0.14 | | | | | | | | |
| 28 | *Thyropygus mesocristatus* Ss | 0.15 | 0.14 | 0.15 | 0.14 | 0.15 | 0.13 | 0.16 | 0.16 | 0.13 | 0.15 | | | | | | | |
| 29 | *Thyropygus navychula* KSR | 0.16 | 0.16 | 0.17 | 0.16 | 0.16 | 0.12 | 0.13 | 0.15 | 0.12 | 0.14 | 0.13 | | | | | | |
| 30 | *Thyropygus opinatus* Arw | 0.15 | 0.15 | 0.16 | 0.14 | 0.14 | 0.13 | 0.14 | 0.14 | 0.11 | 0.13 | 0.11 | 0.08 | | | | | |
| 31 | *Thyropygus panhai* PRL2 | 0.14 | 0.14 | 0.14 | 0.14 | 0.14 | 0.15 | 0.13 | 0.13 | 0.14 | 0.12 | 0.16 | 0.13 | 0.15 | | | | |
| 32 | *Thyropygus brachyacanthus* Sk | 0.17 | 0.16 | 0.17 | 0.15 | 0.16 | 0.14 | 0.16 | 0.17 | 0.15 | 0.14 | 0.13 | 0.13 | 0.13 | 0.16 | | | |
| 33 | *Thyropygus payamense* KPYR1 | 0.16 | 0.16 | 0.16 | 0.14 | 0.15 | 0.13 | 0.13 | 0.15 | 0.11 | 0.13 | 0.13 | 0.13 | 0.12 | 0.16 | 0.11 | | |
| 34 | *Thyropygus payamense* KPYR2 | 0.16 | 0.16 | 0.16 | 0.14 | 0.15 | 0.13 | 0.13 | 0.15 | 0.11 | 0.13 | 0.12 | 0.13 | 0.11 | 0.16 | 0.10 | 0.00 | |
| 35 | *Thyropygus payamense* KPYR3 | 0.16 | 0.16 | 0.16 | 0.13 | 0.15 | 0.13 | 0.13 | 0.15 | 0.11 | 0.12 | 0.12 | 0.13 | 0.11 | 0.16 | 0.10 | 0.01 | 0.00 |
| 36 | *Thyropygus peninsularis* Wm | 0.16 | 0.15 | 0.16 | 0.15 | 0.16 | 0.15 | 0.15 | 0.15 | 0.14 | 0.13 | 0.13 | 0.14 | 0.13 | 0.17 | 0.10 | 0.07 | 0.07 |
| 37 | *Thyropygus planispinus* Tsk2 | 0.18 | 0.17 | 0.18 | 0.15 | 0.17 | 0.16 | 0.16 | 0.17 | 0.14 | 0.15 | 0.13 | 0.14 | 0.12 | 0.17 | 0.10 | 0.09 | 0.09 |
| 38 | *Thyropygus quadricuspis* Hy | 0.14 | 0.14 | 0.15 | 0.14 | 0.14 | 0.13 | 0.15 | 0.15 | 0.11 | 0.12 | 0.07 | 0.11 | 0.12 | 0.14 | 0.12 | 0.10 | 0.10 |
| 39 | *Thyropygus quietus* Cdv | 0.09 | 0.09 | 0.10 | 0.09 | 0.09 | 0.16 | 0.15 | 0.11 | 0.14 | 0.12 | 0.16 | 0.16 | 0.15 | 0.15 | 0.15 | 0.13 | 0.14 |
| 40 | *Thyropygus resimus* Kc | 0.12 | 0.12 | 0.13 | 0.12 | 0.12 | 0.13 | 0.12 | 0.11 | 0.12 | 0.13 | 0.14 | 0.12 | 0.13 | 0.10 | 0.16 | 0.15 | 0.14 |
| 41 | *Thyropygus resimus* Ksp | 0.12 | 0.12 | 0.13 | 0.12 | 0.12 | 0.13 | 0.13 | 0.11 | 0.12 | 0.13 | 0.14 | 0.12 | 0.13 | 0.10 | 0.16 | 0.15 | 0.14 |
| 42 | *Thyropygus resimus* Ntp | 0.12 | 0.12 | 0.13 | 0.12 | 0.12 | 0.13 | 0.13 | 0.11 | 0.12 | 0.13 | 0.14 | 0.12 | 0.13 | 0.10 | 0.16 | 0.15 | 0.14 |
| 43 | *Thyropygus resimus* Pk | 0.14 | 0.14 | 0.14 | 0.12 | 0.13 | 0.13 | 0.14 | 0.13 | 0.12 | 0.11 | 0.14 | 0.12 | 0.13 | 0.10 | 0.15 | 0.14 | 0.14 |
| 44 | *Thyropygus resimus* Pnk | 0.14 | 0.14 | 0.13 | 0.12 | 0.13 | 0.12 | 0.13 | 0.13 | 0.12 | 0.10 | 0.13 | 0.13 | 0.13 | 0.10 | 0.15 | 0.14 | 0.14 |
| 45 | *Thyropygus resimus* Pp | 0.14 | 0.13 | 0.14 | 0.12 | 0.14 | 0.14 | 0.13 | 0.12 | 0.13 | 0.11 | 0.15 | 0.12 | 0.12 | 0.10 | 0.14 | 0.15 | 0.14 |
| 46 | *Thyropygus resimus* Wnt | 0.12 | 0.12 | 0.12 | 0.12 | 0.12 | 0.13 | 0.12 | 0.11 | 0.12 | 0.12 | 0.14 | 0.12 | 0.13 | 0.09 | 0.16 | 0.15 | 0.14 |
| 47 | *Thyropygus richardhoffmani* TCH | 0.14 | 0.14 | 0.15 | 0.14 | 0.15 | 0.13 | 0.15 | 0.14 | 0.11 | 0.13 | 0.07 | 0.12 | 0.13 | 0.15 | 0.13 | 0.11 | 0.11 |
| 48 | *Thyropygus siamensis* Sa | 0.13 | 0.13 | 0.13 | 0.13 | 0.13 | 0.15 | 0.13 | 0.12 | 0.15 | 0.10 | 0.15 | 0.14 | 0.14 | 0.11 | 0.15 | 0.15 | 0.14 |
| 49 | *Thyropygus somsaki* PPLT | 0.13 | 0.13 | 0.13 | 0.13 | 0.13 | 0.15 | 0.12 | 0.13 | 0.14 | 0.11 | 0.16 | 0.14 | 0.15 | 0.07 | 0.16 | 0.16 | 0.15 |
| 50 | *Thyropygus sutchariti* KCP | 0.17 | 0.17 | 0.17 | 0.15 | 0.16 | 0.12 | 0.15 | 0.17 | 0.12 | 0.13 | 0.15 | 0.13 | 0.13 | 0.14 | 0.15 | 0.11 | 0.11 |
| 51 | *Thyropygus uncinatus* Kdb | 0.14 | 0.13 | 0.13 | 0.12 | 0.13 | 0.15 | 0.15 | 0.13 | 0.13 | 0.11 | 0.16 | 0.15 | 0.15 | 0.14 | 0.16 | 0.15 | 0.15 |
| 52 | *Thyropygus uncinatus* Pj | 0.13 | 0.13 | 0.13 | 0.13 | 0.13 | 0.13 | 0.15 | 0.12 | 0.13 | 0.11 | 0.15 | 0.15 | 0.13 | 0.14 | 0.15 | 0.15 | 0.15 |
| 53 | *Thyropygus uncinatus* Pks | 0.14 | 0.13 | 0.14 | 0.14 | 0.14 | 0.15 | 0.15 | 0.12 | 0.14 | 0.10 | 0.17 | 0.15 | 0.14 | 0.13 | 0.16 | 0.16 | 0.15 |
| 54 | *Thyropygus uncinatus* Pn | 0.13 | 0.13 | 0.14 | 0.12 | 0.13 | 0.14 | 0.16 | 0.12 | 0.13 | 0.11 | 0.15 | 0.14 | 0.13 | 0.13 | 0.15 | 0.14 | 0.14 |
| 55 | *Thyropygus uncinatus* Ps | 0.14 | 0.13 | 0.14 | 0.13 | 0.14 | 0.14 | 0.15 | 0.13 | 0.13 | 0.11 | 0.16 | 0.15 | 0.13 | 0.14 | 0.16 | 0.15 | 0.15 |
| 56 | *Thyropygus uncinatus* Rcb | 0.13 | 0.13 | 0.13 | 0.12 | 0.13 | 0.15 | 0.15 | 0.13 | 0.13 | 0.11 | 0.16 | 0.15 | 0.15 | 0.14 | 0.16 | 0.15 | 0.15 |
| 57 | *Thyropygus uncinatus* Sc | 0.13 | 0.13 | 0.13 | 0.13 | 0.12 | 0.13 | 0.15 | 0.12 | 0.12 | 0.11 | 0.15 | 0.15 | 0.13 | 0.13 | 0.15 | 0.15 | 0.15 |
| 58 | *Thyropygus uncinatus* Sm | 0.13 | 0.12 | 0.12 | 0.12 | 0.12 | 0.15 | 0.16 | 0.13 | 0.13 | 0.12 | 0.16 | 0.16 | 0.16 | 0.14 | 0.16 | 0.15 | 0.15 |
| 59 | *Thyropygus uncinatus* Sn | 0.14 | 0.13 | 0.13 | 0.13 | 0.13 | 0.15 | 0.15 | 0.12 | 0.14 | 0.12 | 0.17 | 0.15 | 0.16 | 0.14 | 0.16 | 0.15 | 0.15 |
| 60 | *Thyropygus undulatus* Pb2 | 0.17 | 0.17 | 0.17 | 0.15 | 0.17 | 0.16 | 0.16 | 0.17 | 0.14 | 0.15 | 0.13 | 0.15 | 0.12 | 0.17 | 0.11 | 0.10 | 0.10 |
| 61 | *Thyropygus ursus* LTK | 0.14 | 0.13 | 0.15 | 0.14 | 0.14 | 0.12 | 0.15 | 0.15 | 0.11 | 0.12 | 0.07 | 0.11 | 0.12 | 0.15 | 0.11 | 0.10 | 0.10 |
| 62 | *Thyropygus sirindhornae* sp. nov. Knn2 | 0.17 | 0.16 | 0.17 | 0.16 | 0.16 | 0.16 | 0.16 | 0.15 | 0.17 | 0.13 | 0.19 | 0.16 | 0.16 | 0.14 | 0.18 | 0.17 | 0.17 |
| 63 | *Thyropygus sirindhornae* sp. nov. Knn1 | 0.16 | 0.16 | 0.16 | 0.15 | 0.15 | 0.16 | 0.15 | 0.15 | 0.16 | 0.12 | 0.18 | 0.15 | 0.15 | 0.14 | 0.18 | 0.17 | 0.17 |

## APPENDIX

**TABLE A1.** Continued.

| | **Taxa** | **35** | **36** | **37** | **38** | **39** | **40** | **41** | **42** | **43** | **44** | **45** | **46** | **47** | **48** | **49** | **50** | **51** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | *Anurostreptus barthelemyae* Tlb | | | | | | | | | | | | | | | | | |
| 2 | *Anurostreptus sculptus* Pl | | | | | | | | | | | | | | | | | |
| 3 | *Armatostreptus armatus* Tpp | | | | | | | | | | | | | | | | | |
| 4 | *Heptischius lactuca* Us | | | | | | | | | | | | | | | | | |
| 5 | *Thyropygus allevatus* Bb | | | | | | | | | | | | | | | | | |
| 6 | *Thyropygus allevatus* Bk | | | | | | | | | | | | | | | | | |
| 7 | *Thyropygus bearti* Ks | | | | | | | | | | | | | | | | | |
| 8 | *Thyropygus bispinispatula* Kb | | | | | | | | | | | | | | | | | |
| 9 | *Thyropygus bispinus* Tm | | | | | | | | | | | | | | | | | |
| 10 | *Thyropygus cimi* Nws1 | | | | | | | | | | | | | | | | | |
| 11 | *Thyropygus cristagalli* Yn | | | | | | | | | | | | | | | | | |
| 12 | *Thyropygus culter* Nr | | | | | | | | | | | | | | | | | |
| 13 | *Thyropygus demangei* Cm | | | | | | | | | | | | | | | | | |
| 14 | *Thyropygus enghoffi* Kl | | | | | | | | | | | | | | | | | |
| 15 | *Thyropygus foliaceus* Kj | | | | | | | | | | | | | | | | | |
| 16 | *Thyropygus forceps* Nws2 | | | | | | | | | | | | | | | | | |
| 17 | *Thyropygus induratus* Ldn | | | | | | | | | | | | | | | | | |
| 18 | *Thyropygus induratus* Nru | | | | | | | | | | | | | | | | | |
| 19 | *Thyropygus induratus* Ps | | | | | | | | | | | | | | | | | |
| 20 | *Thyropygus induratus* Pw | | | | | | | | | | | | | | | | | |
| 21 | *Thyropygus induratus* Ssk | | | | | | | | | | | | | | | | | |
| 22 | *Thyropygus induratus* Tt | | | | | | | | | | | | | | | | | |
| 23 | *Thyropygus inflexus* Kk | | | | | | | | | | | | | | | | | |
| 24 | *Thyropygus jarukchusri* Np | | | | | | | | | | | | | | | | | |
| 25 | *Thyropygus laterolobatus* Ry | | | | | | | | | | | | | | | | | |
| 26 | *Thyropygus loxia* Ty | | | | | | | | | | | | | | | | | |
| 27 | *Thyropygus macrosiamensis* Kj | | | | | | | | | | | | | | | | | |
| 28 | *Thyropygus mesocristatus* Ss | | | | | | | | | | | | | | | | | |
| 29 | *Thyropygus navychula* KSR | | | | | | | | | | | | | | | | | |
| 30 | *Thyropygus opinatus* Arw | | | | | | | | | | | | | | | | | |
| 31 | *Thyropygus panhai* PRL2 | | | | | | | | | | | | | | | | | |
| 32 | *Thyropygus brachyacanthus* Sk | | | | | | | | | | | | | | | | | |
| 33 | *Thyropygus payamense* KPYR1 | | | | | | | | | | | | | | | | | |
| 34 | *Thyropygus payamense* KPYR2 | | | | | | | | | | | | | | | | | |
| 35 | *Thyropygus payamense* KPYR3 | | | | | | | | | | | | | | | | | |
| 36 | *Thyropygus peninsularis* Wm | 0.07 | | | | | | | | | | | | | | | | |
| 37 | *Thyropygus planispinus* Tsk2 | 0.09 | 0.10 | | | | | | | | | | | | | | | |
| 38 | *Thyropygus quadricuspis* Hy | 0.10 | 0.11 | 0.13 | | | | | | | | | | | | | | |
| 39 | *Thyropygus quietus* Cdv | 0.13 | 0.14 | 0.15 | 0.14 | | | | | | | | | | | | | |
| 40 | *Thyropygus resimus* Kc | 0.14 | 0.14 | 0.16 | 0.13 | 0.12 | | | | | | | | | | | | |
| 41 | *Thyropygus resimus* Ksp | 0.14 | 0.14 | 0.16 | 0.13 | 0.12 | 0.00 | | | | | | | | | | | |
| 42 | *Thyropygus resimus* Ntp | 0.14 | 0.14 | 0.16 | 0.13 | 0.12 | 0.00 | 0.00 | | | | | | | | | | |
| 43 | *Thyropygus resimus* Pk | 0.13 | 0.15 | 0.16 | 0.13 | 0.14 | 0.08 | 0.09 | 0.09 | | | | | | | | | |
| 44 | *Thyropygus resimus* Pnk | 0.13 | 0.15 | 0.15 | 0.12 | 0.14 | 0.10 | 0.10 | 0.10 | 0.05 | | | | | | | | |
| 45 | *Thyropygus resimus* Pp | 0.14 | 0.16 | 0.14 | 0.14 | 0.14 | 0.08 | 0.08 | 0.08 | 0.09 | 0.09 | | | | | | | |
| 46 | *Thyropygus resimus* Wnt | 0.14 | 0.15 | 0.16 | 0.13 | 0.12 | 0.00 | 0.00 | 0.00 | 0.09 | 0.10 | 0.08 | | | | | | |
| 47 | *Thyropygus richardhoffmani* TCH | 0.11 | 0.12 | 0.13 | 0.04 | 0.14 | 0.14 | 0.14 | 0.14 | 0.14 | 0.13 | 0.15 | 0.14 | | | | | |
| 48 | *Thyropygus siamensis* Sa | 0.14 | 0.14 | 0.14 | 0.14 | 0.13 | 0.10 | 0.10 | 0.10 | 0.11 | 0.10 | 0.10 | 0.10 | 0.15 | | | | |
| 49 | *Thyropygus somsaki* PPLT | 0.15 | 0.16 | 0.17 | 0.15 | 0.15 | 0.11 | 0.11 | 0.11 | 0.10 | 0.10 | 0.09 | 0.11 | 0.15 | 0.11 | | | |
| 50 | *Thyropygus sutchariti* KCP | 0.11 | 0.13 | 0.15 | 0.13 | 0.16 | 0.14 | 0.14 | 0.14 | 0.13 | 0.12 | 0.14 | 0.14 | 0.13 | 0.13 | 0.14 | | |
| 51 | *Thyropygus uncinatus* Kdb | 0.15 | 0.14 | 0.16 | 0.15 | 0.12 | 0.12 | 0.12 | 0.12 | 0.12 | 0.12 | 0.11 | 0.12 | 0.15 | 0.11 | 0.12 | 0.15 | |
| 52 | *Thyropygus uncinatus* Pj | 0.15 | 0.14 | 0.15 | 0.14 | 0.11 | 0.11 | 0.11 | 0.11 | 0.12 | 0.12 | 0.11 | 0.11 | 0.14 | 0.10 | 0.13 | 0.15 | 0.05 |
| 53 | *Thyropygus uncinatus* Pks | 0.15 | 0.16 | 0.17 | 0.14 | 0.12 | 0.12 | 0.12 | 0.12 | 0.13 | 0.12 | 0.12 | 0.12 | 0.15 | 0.10 | 0.12 | 0.15 | 0.09 |
| 54 | *Thyropygus uncinatus* Pn | 0.14 | 0.15 | 0.15 | 0.13 | 0.11 | 0.13 | 0.13 | 0.13 | 0.13 | 0.13 | 0.12 | 0.13 | 0.13 | 0.12 | 0.12 | 0.16 | 0.10 |
| 55 | *Thyropygus uncinatus* Ps | 0.15 | 0.15 | 0.16 | 0.14 | 0.11 | 0.12 | 0.12 | 0.12 | 0.12 | 0.12 | 0.12 | 0.12 | 0.14 | 0.10 | 0.13 | 0.15 | 0.06 |
| 56 | *Thyropygus uncinatus* Rcb | 0.15 | 0.14 | 0.16 | 0.15 | 0.11 | 0.12 | 0.13 | 0.13 | 0.12 | 0.13 | 0.11 | 0.12 | 0.15 | 0.11 | 0.12 | 0.15 | 0.00 |
| 57 | *Thyropygus uncinatus* Sc | 0.15 | 0.14 | 0.15 | 0.14 | 0.11 | 0.11 | 0.11 | 0.11 | 0.12 | 0.12 | 0.11 | 0.11 | 0.14 | 0.10 | 0.13 | 0.15 | 0.06 |
| 58 | *Thyropygus uncinatus* Sm | 0.15 | 0.15 | 0.15 | 0.15 | 0.12 | 0.12 | 0.12 | 0.12 | 0.12 | 0.12 | 0.10 | 0.12 | 0.15 | 0.10 | 0.12 | 0.15 | 0.02 |
| 59 | *Thyropygus uncinatus* Sn | 0.14 | 0.14 | 0.14 | 0.15 | 0.11 | 0.12 | 0.12 | 0.12 | 0.12 | 0.13 | 0.11 | 0.12 | 0.15 | 0.10 | 0.13 | 0.16 | 0.04 |
| 60 | *Thyropygus undulatus* Pb2 | 0.09 | 0.10 | 0.02 | 0.12 | 0.15 | 0.17 | 0.17 | 0.17 | 0.16 | 0.15 | 0.15 | 0.17 | 0.13 | 0.14 | 0.17 | 0.16 | 0.16 |
| 61 | *Thyropygus ursus* LTK | 0.10 | 0.11 | 0.12 | 0.02 | 0.14 | 0.14 | 0.14 | 0.14 | 0.13 | 0.13 | 0.14 | 0.14 | 0.05 | 0.15 | 0.16 | 0.14 | 0.15 |
| 62 | *Thyropygus sirindhornae* sp. nov. Knn2 | 0.17 | 0.18 | 0.18 | 0.17 | 0.17 | 0.16 | 0.16 | 0.16 | 0.14 | 0.13 | 0.15 | 0.16 | 0.17 | 0.13 | 0.14 | 0.17 | 0.16 |
| 63 | *Thyropygus sirindhornae* sp. nov. Knn1 | 0.16 | 0.17 | 0.18 | 0.16 | 0.17 | 0.15 | 0.15 | 0.15 | 0.13 | 0.13 | 0.14 | 0.15 | 0.16 | 0.13 | 0.13 | 0.16 | 0.15 |

## APPENDIX

**TABLE A1.** Continued.

| | **Taxa** | **52** | **53** | **54** | **55** | **56** | **57** | **58** | **59** | **60** | **61** | **62** | **63** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | *Anurostreptus barthelemyae* Tlb | | | | | | | | | | | | |
| 2 | *Anurostreptus sculptus* Pl | | | | | | | | | | | | |
| 3 | *Armatostreptus armatus* Tpp | | | | | | | | | | | | |
| 4 | *Heptischius lactuca* Us | | | | | | | | | | | | |
| 5 | *Thyropygus allevatus* Bb | | | | | | | | | | | | |
| 6 | *Thyropygus allevatus* Bk | | | | | | | | | | | | |
| 7 | *Thyropygus bearti* Ks | | | | | | | | | | | | |
| 8 | *Thyropygus bispinispatula* Kb | | | | | | | | | | | | |
| 9 | *Thyropygus bispinus* Tm | | | | | | | | | | | | |
| 10 | *Thyropygus cimi* Nws1 | | | | | | | | | | | | |
| 11 | *Thyropygus cristagalli* Yn | | | | | | | | | | | | |
| 12 | *Thyropygus culter* Nr | | | | | | | | | | | | |
| 13 | *Thyropygus demangei* Cm | | | | | | | | | | | | |
| 14 | *Thyropygus enghoffi* Kl | | | | | | | | | | | | |
| 15 | *Thyropygus foliaceus* Kj | | | | | | | | | | | | |
| 16 | *Thyropygus forceps* Nws2 | | | | | | | | | | | | |
| 17 | *Thyropygus induratus* Ldn | | | | | | | | | | | | |
| 18 | *Thyropygus induratus* Nru | | | | | | | | | | | | |
| 19 | *Thyropygus induratus* Ps | | | | | | | | | | | | |
| 20 | *Thyropygus induratus* Pw | | | | | | | | | | | | |
| 21 | *Thyropygus induratus* Ssk | | | | | | | | | | | | |
| 22 | *Thyropygus induratus* Tt | | | | | | | | | | | | |
| 23 | *Thyropygus inflexus* Kk | | | | | | | | | | | | |
| 24 | *Thyropygus jarukchusri* Np | | | | | | | | | | | | |
| 25 | *Thyropygus laterolobatus* Ry | | | | | | | | | | | | |
| 26 | *Thyropygus loxia* Ty | | | | | | | | | | | | |
| 27 | *Thyropygus macrosiamensis* Kj | | | | | | | | | | | | |
| 28 | *Thyropygus mesocristatus* Ss | | | | | | | | | | | | |
| 29 | *Thyropygus navychula* KSR | | | | | | | | | | | | |
| 30 | *Thyropygus opinatus* Arw | | | | | | | | | | | | |
| 31 | *Thyropygus panhai* PRL2 | | | | | | | | | | | | |
| 32 | *Thyropygus brachyacanthus* Sk | | | | | | | | | | | | |
| 33 | *Thyropygus payamense* KPYR1 | | | | | | | | | | | | |
| 34 | *Thyropygus payamense* KPYR2 | | | | | | | | | | | | |
| 35 | *Thyropygus payamense* KPYR3 | | | | | | | | | | | | |
| 36 | *Thyropygus peninsularis* Wm | | | | | | | | | | | | |
| 37 | *Thyropygus planispinus* Tsk2 | | | | | | | | | | | | |
| 38 | *Thyropygus quadricuspis* Hy | | | | | | | | | | | | |
| 39 | *Thyropygus quietus* Cdv | | | | | | | | | | | | |
| 40 | *Thyropygus resimus* Kc | | | | | | | | | | | | |
| 41 | *Thyropygus resimus* Ksp | | | | | | | | | | | | |
| 42 | *Thyropygus resimus* Ntp | | | | | | | | | | | | |
| 43 | *Thyropygus resimus* Pk | | | | | | | | | | | | |
| 44 | *Thyropygus resimus* Pnk | | | | | | | | | | | | |
| 45 | *Thyropygus resimus* Pp | | | | | | | | | | | | |
| 46 | *Thyropygus resimus* Wnt | | | | | | | | | | | | |
| 47 | *Thyropygus richardhoffmani* TCH | | | | | | | | | | | | |
| 48 | *Thyropygus siamensis* Sa | | | | | | | | | | | | |
| 49 | *Thyropygus somsaki* PPLT | | | | | | | | | | | | |
| 50 | *Thyropygus sutchariti* KCP | | | | | | | | | | | | |
| 51 | *Thyropygus uncinatus* Kdb | | | | | | | | | | | | |
| 52 | *Thyropygus uncinatus* Pj | | | | | | | | | | | | |
| 53 | *Thyropygus uncinatus* Pks | 0.07 | | | | | | | | | | | |
| 54 | *Thyropygus uncinatus* Pn | 0.10 | 0.10 | | | | | | | | | | |
| 55 | *Thyropygus uncinatus* Ps | 0.02 | 0.08 | 0.10 | | | | | | | | | |
| 56 | *Thyropygus uncinatus* Rcb | 0.05 | 0.10 | 0.10 | 0.06 | | | | | | | | |
| 57 | *Thyropygus uncinatus* Sc | 0.01 | 0.07 | 0.10 | 0.02 | 0.06 | | | | | | | |
| 58 | *Thyropygus uncinatus* Sm | 0.06 | 0.09 | 0.11 | 0.06 | 0.02 | 0.06 | | | | | | |
| 59 | *Thyropygus uncinatus* Sn | 0.06 | 0.09 | 0.12 | 0.07 | 0.04 | 0.06 | 0.03 | | | | | |
| 60 | *Thyropygus undulatus* Pb2 | 0.16 | 0.17 | 0.15 | 0.16 | 0.16 | 0.15 | 0.15 | 0.15 | | | | |
| 61 | *Thyropygus ursus* LTK | 0.13 | 0.14 | 0.13 | 0.14 | 0.15 | 0.13 | 0.15 | 0.15 | 0.12 | | | |
| 62 | *Thyropygus sirindhornae* sp. nov. Knn2 | 0.14 | 0.15 | 0.16 | 0.15 | 0.16 | 0.15 | 0.16 | 0.16 | 0.19 | 0.17 | | |
| 63 | *Thyropygus sirindhornae* sp. nov. Knn1 | 0.14 | 0.15 | 0.15 | 0.14 | 0.15 | 0.14 | 0.16 | 0.16 | 0.18 | 0.17 | 0.01 | |