A new species of agaricomycetes, *Clitopilus lampangensis*, is described based on collections from northern Thailand. This species was distinguished from previously described *Clitopilus* species by its pale yellow to grayish yellow pileus with the presence of wider caulocystidia. Molecular phylogenetic analyses, based on the data of the internal transcribed spacers (ITS) and the large subunit (LSU) of the nuclear ribosomal DNA, and the second largest subunit of RNA polymerase II (*rbp2*) genes, also support the finding that *C. lampangensis* is distinct from other species within the genus *Clitopilus*. A full description, color photographs, illustrations and a phylogenetic tree showing the position of *C. lampangensis* are provided.

**Keywords**
Agaricomycetes, gill mushroom, morphology, phylogeny, tropics

**Introduction**
The genus *Clitopilus* was proposed by Kummer (1987) with *C. prunulus* (Scop.) P. Kummer as the type species. It belongs to the family Entolomataceae of the order Agaricales. This genus is saprotrophic and is widely distributed, especially in northern temperate areas (Singer 1986; Baroni and Watling 1999; Moncalvo et al. 2002; Kirk et al.)
2008; Hartley et al. 2009; Crous et al. 2012; Raj and Manimohan 2018). *Clitopilus* is characterized by basidiocarps that are clitocyboid, omphalinoid or pleurotoid, mostly whitish or occasionally grayish or brownish in color, with pink or pinkish brown spore prints, ellipsoid basidiospores with longitudinal ridges that appear angular in a polar view, and hyphae lack clamp connections (Singer 1986; Noordeloos 1988). There are 30 species of *Clitopilus* worldwide (Kirk et al. 2008), although there are 201 species names recorded in the Index Fungorum (http://www.indexfungorum.org/Names/Names.asp). The taxa list in the Index Fungorum includes synonyms and misidentifications, as well as some species that are not well documented. Formerly, the genus *Clitopilus* included *Rhodocybe* (Moncalvo et al. 2002; Co-David et al. 2009; Vizzini et al. 2011a). However, molecular phylogenetic analyses have provided powerful tools for the identification of *Clitopilus*, leading to the separation of *Clitopilus* from *Rhodocybe* as well as the related genera (*Clitocella* and *Clitopilopsis*) (Cooper 2014; Kluting et al. 2014; Raj and Manimohan 2018).

Only six species, *Clitopilus apalus* (Berk. & Br.) Petch, *C. crispus* Pat. *C. doimaesa-longensis* Jatuwong, Karun. & K.D. Hyde, *C. chalybescens* T.J. Baroni & Desjardin, *C. peri* (Berk. & Br.) Petch and *C. prunulus*, have been reported in Thailand (Baroni et al. 2001; Chandrasrikul et al. 2011; Kluting et al. 2014; Jatuwong et al. 2017). During an investigation of macrofungi in northern Thailand, we found a population of *Clitopilus* which we describe here as a new species based on the morphological and molecular characteristics. To confirm its taxonomic status, the phylogenetic relationship of the new species was determined by the ITS and LSU of the rDNA, and the rbp2 genes.

**Materials and methods**

**Sample collection**

Basidiocarps were collected in Mae Moh District, Lampang Province, northern Thailand in 2018. Basidiocarps were wrapped in aluminum foil and kept in plastic specimen boxes to be transported to the laboratory. Notes on the macromorphological features and photographs were obtained within 24 h of collection. The specimens were dried at 40–45 °C and deposited at the Herbarium of the Sustainable Development of Biological Resources Laboratory, Faculty of Science, Chiang Mai University (SDBRCMU), and BIOTEC Bangkok Herbarium (BBH), Pathumthani, Thailand.

**Morphological studies**

Macromorphological data were recorded from fresh specimens. The recording of color names and codes followed Kornerup and Wanscher (1978). Micromorphological data were recorded from dry specimens rehydrated in 95% ethanol followed by distilled water, 3% KOH or Melzer’s reagent. Anatomical features were based on at least 50
measurements of each structure as seen under a light microscope (Olympus CX51, Japan). For spore statistics, $Q$ is the ratio of spore length divided by spore width and $\bar{Q}$ is the average $Q$ of all specimens $\pm$ standard deviation.

**Molecular phylogenetic studies**

Genomic DNA of dry specimens (1–10 mg) was extracted using a Genomic DNA Extraction Mini-Kit (FAVORGEN, Taiwan). The ITS region of DNA was amplified by polymerase chain reactions (PCR) using ITS4 and ITS5 primers (White et al. 1990), the LSU of rDNA gene were amplified with LROR and LRO5 primers (Vilgalys and Hester 1990), and $rbp2$ gene was amplified with the bRBP2-6F and bRBP2-7.1R primers (Matheny 2005). The amplification program for these three domains was performed in separated PCR reaction and consisted of an initial denaturation at 95 °C for 5 min, followed by 35 cycles of denaturation at 95 °C for 30 s, annealing at 52 °C for 30 s (ITS), 52 °C for 45 s (LSU), and 54 °C for 1 min ($rbp2$), and extension at 72 °C for 1 min on a peqSTAR thermal cycler (PEQLAB Ltd., UK). PCR products were checked on 1 % agarose gels stained with ethidium bromide under UV light. PCR products were purified using a PCR clean up Gel Extraction NucleoSpin Gel and PCR Clean-up Kit (Macherey-Nagel, Germany) following the manufacturer’s protocol. The purified PCR products were directly sequenced. Sequencing reactions were performed and the sequences were automatically determined in the genetic analyzer at 1st Base company (Kembangan, Malaysia) using the PCR primers mentioned above. Sequences were used to query GenBank via BLAST (http://blast.ddbj.nig.ac.jp/top-e.html).

For phylogenetic analyses, the sequences from this study, previous studies and the GenBank database were used and provided in Table 1. The multiple sequence alignment was carried out using MUSCLE (Edgar 2004), and the combined ITS and LSU alignment, and $rbp2$ alignment were deposited in TreeBASE under the study ID 24373 and 24374, respectively. Phylogenetic trees were constructed using maximum likelihood (ML) and Bayesian inference (BI) algorithms, implemented by RAxML v7.0.3 (Stamatakis 2006) and MrBayes v3.2.6 (Ronquist et al. 2012), respectively. *Rhodocybe griseoaurantia* and *R. pallidogrisea* were used as outgroup. The best-fit substitution model for BI and ML analyses were estimated by jModeltest 2.1.10 (Darriba et al. 2012) using Akaike information criterion (AIC). For ML analysis, the bootstrap (BS) replicates were set as 1000 and used to test phylogeny (Felsenstein 1985). Clades with bootstrap values (BS) of $\geq 70\%$ were considered significantly supported (Hillis and Bull 1993). For the BI analysis, the Markov chains were run for one million generations, with six chains and random starting trees. The chains were sampled every 100 generations. Among these, the first 2,000 trees were discarded as burn-in, while the postburn-in trees were used to construct the 50% majority-rule consensus phylogram with calculated Bayesian posterior probabilities. Bayesian posterior probabilities (PP) $\geq 0.95$ were considered significant support (Alfaro et al. 2003).
Table 1. Sequences used for phylogenetic analysis. The newly generated sequences are in bold.

| Taxa                     | Voucher/strain | GenBank accession number | References                        |
|--------------------------|---------------|--------------------------|-----------------------------------|
|                          |               | ITS                      | LSU                               | rpb2                               |                                  |
| Clitopilus albidos       | CAL 1320      | MF926596                 | MF926595                          | MF946579                           | Raj and Manimohan 2018           |
|                          |               |                          |                                   |                                   |                                   |
|                          | CORT:26394WAT| –                        | KR869936                          | KC816906                           | Largent and Bergemann 2016       |
| Clitopilus astroprunulus | MEN2009062    | KC139095                 | –                                 | –                                 | Phillips and Dinis 2012          |
|                          | MEN2009001    | KC139095                 | –                                 | –                                 | Phillips and Dinis 2012          |
| Clitopilus cf. argentinus | MTB480412    | –                        | –                                 | KC816907                           | Kluting et al. 2014              |
| Clitopilus chalybescens  | MFUCC130808   | KP938184                 | –                                 | –                                 | Jatuwong et al. 2017             |
|                          | MFUCC130809   | KP938185                 | –                                 | –                                 | Jatuwong et al. 2017             |
| SDBR-CMUUU70039          |               | MK773645                 | MK764940                          | MK784129                           | This study                       |
| Clitopilus chrischonensis| TOHG 1994     | HM623128                 | HM623131                          | –                                 | Vizzini et al. 2011b             |
| Clitopilus crisipus       | GDM29931      | JQ281489                 | –                                 | –                                 | He et al. 2012                   |
|                          | CORT:9982     | –                        | –                                 | KC816910                           | Kluting et al. 2014              |
|                          | CORT:10027    | –                        | –                                 | KC816911                           | Kluting et al. 2014              |
| Clitopilus cystidiatus    | 26            | –                        | GQ289147                          | GQ289220                           | Co-David et al. 2009             |
| Clitopilus doimaesalongensis|            |                          |                                   |                                   |                                   |
| Clitopilus fusiformis     | SAA51083      | KY385634                 | –                                 | –                                 | Wang et al. 2017                 |
|                          | SAA5189         | KU751777                 | KY385633                          | –                                 | Wang et al. 2017                 |
| Clitopilus giovanellae   | SF14368       | EF413030                 | EF413027                          | –                                 | Moreno et al. 2007               |
| Clitopilus hobsonii      | CBS 270.36    | FJ770395                 | –                                 | –                                 | Hartley et al. 2009              |
|                          | CBS 445.86    | FJ770385                 | –                                 | –                                 | Hartley et al. 2009              |
|                          | DLL9635       | –                        | –                                 | KC816913                           | Kluting et al. 2014              |
|                          | DLL9643       | –                        | –                                 | KC816913                           | Kluting et al. 2014              |
| Clitopilus lampangensis  | SDBR-CMUJK 0147| MK764933                 | MK764935                          | MK784127                           | This study                       |
|                          | SDBR-CMUUNK 0047| MK764934             | MK773856                          | MK784128                           | This study                       |
| Clitopilus kamaka        | KA12-0364     | KR673433                 | –                                 | –                                 | Kim et al. 2015                  |
| Clitopilus orientalis    | CAL 1616      | MG345134                 | MG321558                          | MG321559                           | Raj and Manimohan 2018           |
| Clitopilus passeckerianus| CBS299.35     | MH855682                 | MH867198                          | –                                 | Vu et al. 2019                   |
|                          | P78           | KY962494                 | KY963078                          | –                                 | Unpublished                      |
| Clitopilus pacilloides   | CORT:5809     | –                        | –                                 | KC816919                           | Kluting et al. 2014              |
| Clitopilus peri          | CORT:10033    | –                        | –                                 | KC816920                           | Kluting et al. 2014              |
|                          | CORT:10040    | –                        | –                                 | KC816921                           | Kluting et al. 2014              |
|                          | CORT:10041    | –                        | –                                 | KC816922                           | Kluting et al. 2014              |
| Clitopilus pinicola      | CBS 623.70    | MH859879                 | MH871665                          | –                                 | Vu et al. 2019                   |
| Clitopilus prunulus      | Champ-15      | KX449418                 | –                                 | –                                 | Pérez-Lázaro et al. 2017         |
|                          |               |                          |                                   |                                   | Hartley et al. 2009              |
|                          |               |                          |                                   |                                   | Unpublished                      |
| Clitopilus reticulosporus| DC-2010       | KC865966                 | HM164414                          | HM164416                           | Vu et al. 2019                   |
| Clitopilus scyphoides    | CBS 127.47    | MH856181                 | MH867707                          | –                                 | Vu et al. 2019                   |
|                          | CBS 400.79    | FJ770401                 | –                                 | –                                 | Hartley et al. 2009              |
| Clitopilus subcyphoides  | CAL 1325      | MF927542                 | MF946580                          | MF946581                           | Raj and Manimohan 2018           |
| Clitopilus venosoulicatus| CORT:8111     | –                        | –                                 | KC816930                           | Kluting et al. 2014              |
| Rhodocybe griseoaurantia | CAL 1324      | KX083571                 | KX83574                           | KX083568                           | Unpublished                      |
| Rhodocybe pallidogrisea  | CORT 013944   | NR154437                 | –                                 | KC816968                           | Kluting et al. 2014              |
Results

Phylogenetic analyses

The topology of each single-gene of ITS and LSU, and the combined ITS and LSU phylograms were found to be similar. However, differences were observed in the topology of the rbp2 gene. Therefore, we present only the combined ITS and LSU gene phylogram (Fig. 1), and the single rbp2 gene phylogram (Fig. 2). The combined ITS and LSU sequence dataset consisted of 34 taxa and were comprised of 1774 characters including gaps (ITS: 1–779, LSU: 780–1774). The sequence dataset of rbp2 consisted of 27 taxa and the aligned dataset was comprised of 620 characters that included gaps. The GTR model with gamma rate heterogeneity and invariant sites (GTR+G+I) was the best-fit model used for both ML and BI analyses that were selected by AIC. The average standard deviation of the split frequencies fell to 0.011364 and 0.009837 in the BI analysis of the combined ITS and LSU, and rbp2 sequences, respectively after one million generations. This was observed after the 50% majority consensus phylogram was constructed. The ML analysis of the combined ITS and LSU sequences was based on the parameters estimated under the GTR+I+G model, and the proportion of the invariant sites and the gamma shape parameters were 0.0250 and 0.9320, respectively. Additionally, the tree with log likelihood (-8211.7515) was built after 1000 bootstrapping replications. In the ML analysis of the rbp2 sequence that was based on the GTR+I+G model, the proportion of the invariant sites and the gamma shape parameters were 0.5400 and 1.7960, respectively, while the tree with log likelihood (-3640.1616) was built after 1000 bootstrapping replications.

Both the combined ITS and LSU, and the rbp2 phylograms indicated that the sequences were of a new species, *C. lampangensis*, that had formed a monophyletic clade with high BS (100 %) and PP (1.0) support (Figs 1, 2). A combined ITS and LSU phylogram revealed that the new species was a sister taxon to *C. chalybescens*. In addition, the rbp2 phylogram indicated that the new species was a sister taxon to *C. chalybescens* and *C. peri*.

Taxonomy

*Clitopilus lampangensis* J. Kumla, N. Suwannarach & S. Lumyong, sp. nov.
MycoBank No.: 830890

Fig. 3

**Diagnosis.** Distinguished from other *Clitopilus* species by its pale yellow to grayish yellow pileus with the presence of caulocystidia, and from *C. chalybescens* by its wider caulocystidia, longer basidiospores, and lack of grayish blue color change on the pileus and stipe when bruised.

**Etymology.** ‘lampangensis’, referring to Lampang Province, where the holotype was found.
Figure 1. Phylogram derived from maximum likelihood analysis of the combined ITS and LSU region of nuclear rDNA of 34 sequences. *Rhodocybe griseoaurantia* and *R. pallidogrisea* were used as outgroup. The numbers above branches represent maximum likelihood bootstrap percentages (left) and Bayesian posterior probabilities (right). Only bootstrap values ≥ 50 % are shown, and the scale bar represents ten substitutions per nucleotide position. The fungal species obtained in this study are in bold.
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Figure 2. Phylogram derived from maximum likelihood analysis of rpb2 gene of 27 sequences. Rhodocybe griseoaurantia and R. pallidogrisea were used as outgroup. The numbers above branches represent maximum likelihood bootstrap percentages (left) and Bayesian posterior probabilities (right). Only bootstrap values ≥ 50% are shown, and the scale bar represents ten substitutions per nucleotide position. The fungal species obtained in this study are in bold.

Holotype. THAILAND, Lampang Province, Mae Moh District, (18°24'21"N, 99°42'26"E, elevation 380 m), on ground in a tropical deciduous forest, May, 2018, J. Kumla & N. Suwannarach, SDBR-CMUJK 0147 and BBH 43590 (isotype).

Gene sequence (from holotype). MK764933 (ITS), MK764935 (LSU) and MK784127 (rpb2).
Basidiocarps small, clitocyboid. Pileus 35–50 mm diam., initially convex or somewhat plano-convex with or without a central depression, becoming deeply umbilicate with age; surface pale yellow (4A3) to greyish yellow (4B5), somewhat velutinous, finely pruinose all over; margin incurved to slightly inrolled, entire or slightly wavy. Lamellae subdecurrent to decurrent, white (1A1), crowded, up to 2.5 mm wide, with lamellulae of 1–3 lengths; edge entire or slightly wavy, concolorous with the sides. Stipe 20–25 × 5–8 mm, central, solid; surface white (1A1) to yellowish white (4A2),
A new Clitopilus species from Thailand

finely pruinose all over, densely so towards the apex; base with white cottony mycelium. Odor strong farinaceous. A pale pinkish spore print.

Basidiospores 7.0–9.0 × 3.0–5.0 μm, $Q = 1.40–2.33$, $Q = 1.82 \pm 0.27$, ellipsoid in polar view, amygdaliform to limoniform in side view, with 6–8 prominent longitudinal ridges, colorless, thin-walled. Basidia 17.0–25.0 × 4.0–8.0 μm, clavate, colorless, thin-walled, 2- and 4-spored; sterigmata up to 4 μm long. Lamella-edge fertile. Pleurocystidia and cheilocystidia absent. Lamellar trama subregular; hyphae 2.5–4.0 μm wide, hyaline, thin-walled. Pileus trama compact, hyaline, cylindrical hyphae 5–10 μm wide. Pileipellis a cutis of loosely interwoven hyphae; 3–5 μm wide, hyaline, thin-walled, and terminal cells; subcylindric or narrowly clavate, 4–8 μm wide. Stipitipellis at stipe apex a layer of repent, hyaline, cylindrical hyphae 4–8 μm wide, thin-walled. Caulocystidia 25.5–42.5 × 8.0–15.0 μm, single or clustered, erect or repent, varying in shape from cylindrical to clavate, hyaline, slightly thick-walled. Clamp connections absent in all tissues.

Ecology and distribution. Fruiting solitary or gregarious on soil in a tropical deciduous forest. Known only from northern Thailand

Specimens examined. THAILAND, Lampang Province, Mae Moh District, (18°24’20"N, 99°42’3"E, elevation 375 m), on ground in a tropical deciduous forest, May, 2018, N. Suwannarach & J. Kumla, SDBR-CMUNK 0047, GenBank sequence MK764934 (ITS), MK773856 (LSU) and MK784128 (rbp2).

Discussion

The present study has identified a new species of Clitopilus acquired from northern Thailand based on both morphological characteristics and phylogenetic analyses. Clitopilus lampangensis is characterized by its clitocyboid, pale yellow to grayish yellow basidiocarps, pinkish spore-print, ellipsoid basidiospores with longitudinal ridges and hyphae lacking clamp connections. Thus, these morphological characteristics support its placement into the genus Clitopilus (Singer 1986; Noordeloos 1988). Based on the morphology, the pale yellow to grayish yellow pileus of C. lampangensis distinguishes it from the white and grayish pileus of Clitopilus species, with the exceptions of C. catalonicus, C. djellouliae, C. fasciculatus, C. gallaecicus, C. giovanellae, C. incrustatus, C. luteocinnamomeus and C. prunulus, (Kummer 1871; Singer 1942; Noordeloos 1984; Baroni and Halling 2000; Moreno et al. 2007; Ovrebo and Baroni 2007; Vila et al. 2008; Contu et al. 2011; Desjardins et al. 2015). The characteristics of the basidiocarps and size of the basidia, caulocystidia and basidiospores of C. lampangensis were compared with related Clitopilus species (Table 2). The presence of caulocystidia in C. lampangensis clearly distinguishes it from these related species. Moreover, the pileus of C. lampangensis (35–50 mm in diameter) are larger than C. djellouliae (6–18 mm in diameter; Contu et al. (2011)), C. giovanellae (5–15 mm in diameter; Singer (1942) and Moreno et al. (2007)) and C. catalonicus (up to 15 mm in diameter; Vila et al. (2008)). Prior to this study, C. apalus, C. crispus, C. doimaesalongensis, C. chalybescens, C. peri and C. prunulus had been found in Thailand
### Table 2. Comparison of *Clitopilus lampangensis* with the closely related species.

| Taxa              | Origin                      | Pileus                          | Basidia                                  | Caulocystidia                      | Basidiospores                  |
|-------------------|-----------------------------|--------------------------------|------------------------------------------|------------------------------------|---------------------------------|
| *C. lampangensis*  | Thailand                    | 35–50 mm in diameter, pale yellow to greyish yellow | 17.0–25.0 × 4.0–8.0 μm, 2–4 streigmata | 25.5–42.5 × 8.0–15.0 μm            | Ellipsoid, 7.0–9.0 × 3.0–5.0 μm, 6–8 longitudinal ridges |
| *C. chalybescens*  | Thailand                    | 15–90 mm in diameter, white, yellowish white to greyish blue | 15.0–21.0 × 5.1–8.0 μm, 4 streigmata | 16.0–32.0 × 5.0–7.0 μm             | Ellipsoid, 5.3–7.5 × 3.6–5.0 μm, 8–10 longitudinal ridges |
| *C. peri*         | India, Sri Lanka, Thailand  | 8–22 mm in diameter, white     | 16.0–18.0 × 5.0–7.0 μm, 4 streigmata     | Ellipsoid, 6.7–8.5 × 3.0–4.0 μm, 6–9 longitudinal ridges |
| *C. prunulus*     | Netherlands, Thailand, United State | 25–80 mm in diameter, white, yellowish white to greyish yellow | 25.0–47.0 × 7.0–12.0 μm, 4 streigmata | Absent                          | Ellipsoid, 9.0–14.0 × 4.5–8.0 μm, 6–8 longitudinal ridges |
| *C. fasciculatus* | Netherlands                 | 20–70 mm in diameter, pale brown | Sizes were not reported, 4 streigmata | Absent                          | Ellipsoid, 4.5–6.3 × 3.0–4.0 μm, 3–6 longitudinal ridges |
| *C. gallaecicus*  | Spain                       | 80–90 mm in diameter, creamy, ochre to ochre-brown | 20.0–35.0 × 8.5–10.5 μm, 4 streigmata | Absent                          | Ellipsoid, 8.0–14.5 × 4.5–7.5 μm, 3–6 longitudinal ridges |
| *C. incrutatus*   | Costa Rica, United State    | 80–90 mm in diameter, grayish brown | 16.0–24.0 × 7.0–8.0 μm, 4 streigmata | Absent                          | Ellipsoid, 5.0–6.5 × 3.0–4.0 μm, 3–6 longitudinal ridges |
| *C. djellouliae*  | France                      | 6–18 mm in diameter, light yellowish brown | 22.0–32.0 × 7.5–8.5 μm, 4 streigmata | Absent                          | Ellipsoid, 6.0–9.0 × 4.0–6.0 μm |
| *C. giovanellae*  | Italy, Spain                | 5–15 mm in diameter, grayish to light brown | 14.0–22.0 × 6.5–9.5 μm, 4 streigmata | Absent                          | Ellipsoid, 5.0–8.0 × 3.0–4.0 μm |
| *C. lutocinnamomeus* | Panama                    | 15–45 mm in diameter, light cinnamon-brown | 19.0–27.0 × 6.0–7.0 μm, 4 streigmata | Absent                          | Subglobose to ellipsoid, 4.5–6.0 × 3.5–5.0 μm |
| *C. catalonicus*  | Panama                      | Up to 15 mm in diameter, light yellowish brown | 32.0–40.0 × 6.4–8.0 μm, 4 streigmata | Absent                          | Ellipsoid, 5.3–7.5 × 3.7–4.5 μm |

*This study,* Baroni et al. (2001); Jatuwong et al. (2017); ‘*Pegler* (1986); ‘*Kluting* et al. (2014); ‘Kummer (1871); ‘Desjardin et al. (2015); ‘Noordeloos (1984); ‘Blanco-Dios (2013), Baroni and Halling (2000); ‘Contu et al. (2011); ‘Singer (1942); ‘Moreno et al. (2007); ‘Ovrebo and Baroni (2007) and ‘Vila et al. (2008).

(Baroni et al. 2001; Chandrasrikul et al. 2011; Kluting et al. 2014; Jatuwong et al. 2017). However, *C. apalus*, *C. crispus*, *C. peri* and *C. doimaesalongensis* differ from *C. lampangensis* by their white to chalk-white pileus and a lack of caulocystidia (Pegler 1986; Yang 2000; Jatuwong et al. 2017). The larger basidia and basidiospores, and the absence of caulocystidia in *C. prunulus* clearly differentiate it from *C. lampangensis* (Kummer 1871; Desjardin et al. 2015) (Table 2). Both *C. lampangensis* and *C. chalybescens* have caulocystidia (Baroni et al. 2001; Jatuwong et al. 2017). However, the width of the caulocystidia and the length of the basidiospores of *C. chalybescens* are narrower and shorter than in *C. lampangensis* (Table 2) (Baroni et al. 2001; Jatuwong et al. 2017).

The phylogenetic analyses of the combined ITS and LSU, and *rpb2* sequences confirmed that *C. lampangensis* formed a monophyletic clade which clearly separated it from the other *Clitopilus* species. *Clitopilus lampangensis* forms a sister taxon to *C. chalybescens* and *C. peri*. *Clitopilus peri* differs from *C. lampangensis* by its smaller white basidiocarps (8–22 mm in diameter) and the absence of caulocystidia (Pegler 1986).
Additionally, the different morphological characteristics that exist between *C. lampan-gen sis* and *C. chalybescens* have been mentioned above. Therefore, a combination of the morphological characteristics and the molecular analyses strongly support recognition of a new fungus species. This discovery is considered important in terms of stimulating a deeper investigation of macrofungi in Thailand, and will help researchers to better understand the distribution and ecology of *Clitopilus*.

**Key to *Clitopilus* species known from Thailand**

1. Pileus white to chalk-white colors ................................................................. 2
   – Pileus white or with other colors ................................................................. 5

2. Stipe ≥ 3 mm thick .................................................................................. 3
   – Stipe < 3 mm thick ................................................................................ 3

3. Basidia < 8 μm wide .................................................................................... 4
   – Basidia ≥ 8 μm wide, basidiospores 6.8–9.2 × 4.1–5.5 μm ......................
     ............................................................................................................  C. peri

4. Basidia up to 25 μm, basidiospores 6–8.5 × 4.5–5.5 μm ............................ *C. doimaesalongensis*
   – Basidia up to 30 μm, basidiospores 5.5–9 × 4–6 μm ................................. *C. apalus*

5. Pileus white to pale grayish or yellowish cream colors .............................. 6
   – Pileus pale yellow to greyish yellow colors, caulocystidia present, basidiospores 7.0–9.0 × 3.0–5.0 μm ....................................................... *C. lampangensis*

6. Basidia ≥ 25 μm long, caulocystidia absent, basidiospores 8.0–12.0 × 4.0–6.5 μm ................................................................. *C. prunulus*
   – Basidia < 25 μm long, caulocystidia present, basidiospores 5.3–7.5 × 3.6–5.0 μm ................................................................. *C. chalybescens*

**Acknowledgements**

This work was supported by grants from Chiang Mai University and Center of Excellence on Biodiversity (BDC), Office of Higher Education Commission (BDC-PG3-161005), Thailand. We are grateful to staff of Mae Moh Forestry Industry Organization for their excellent field assistance, and Dr. Eric H.C. McKenzie for English proof reading.

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