# CHAPTER 5

## SUBORDER BOLETINEAE

*Boletineae* is a large group of boletes previously contain 2 families of *Boletaceae* and *Strobilomycetaceae*. Member of this suborder are well-known and well-described in the temperate region, newer research has shown significant diversity in tropical and southern hemisphere regions as well. E. J. H. Corner found evidence of at least 60 species on the island of Singapore alone. In 1972 he described 140 species from the Malay Peninsula and Borneo and estimated there were an equal number again to be found.

Family *Boletaceae* is a family of boletes, which nearly as widely distributed as agarics (gill mushroom), this include the Cep or King Bolete (*Boletus edulis*). Even after recent changes in taxonomy that have moved many members out of the *Boletaceae*, it remains a large family with many genera. Currently, 28 genera are recognized in this family included: *Afroboletus*, *Aureoboletus*, *Austroboletus*, *Boletellus*, *Boletochaete*, *Boletus* (included *Heimioporus*), *Bothia*, *Buchwaldoboletus*, *Chalciporus*, *Chamonixia*, *Fistulinella*, *Gastroboletus*, *Gastroleccinum*, *Gastrotylopilus*, *Leccinum*, *Paxillogaster*, *Phylloboletellus*, *Phylloporus*, *Pulverboletus*, *Royoungia*, *Setogyroporus*, *Singeromyces*, *Sinoboletus*, *Tubosaeta*, *Tylopilus*, *Veloporphyrellus*, *Xanthoconium*, and *Xerocomus*. The genus *Porphyrellus* and *Strobilomyces* which have been placed in family *Strobilomycetaceae* are also included in this family (Halling, 2008).

Many other genera formerly part of this family have been moved into other, smaller families as work with molecular phylogeny shows that they are more distantly related, even if physically similar. Representative of this adjustment is the move of the slimy-capped genus *Suillus* to *Suillaceae*.

The genus belongs to suborder/family identified in Chapter 6-7 are organized in alphabetical order. For each genus the name of the type is given and the genus is introduced, and then information on the species with photographic plates is provided. Notes are provided on the taxonomy and distinctive features of each species with reference to published literature. Phylogenetic trees are constructed and discussed in some species if their sequences are available.

## DESCRIPTION, PHOTOGRAPHIC FIGURES OF BOLETES IN SUBORDER BOLETINEAE

***Boletus*** Dill. ex Fr. (including *Xerocomus*) **(Boletaceae: Boletineae)**

**Type species:** *Boletus edulis* Bull.

**References:** Corner, (1972); Halling, (2008).

**Pileus** dry to subviscid, glabrous to tomentose to fibrillose, microscopically a trichodermium or ixotrichodermium. **Context** white to yellow, staining blue or not changing. **Hymenophore** adnexed to adnate to subdecurrent, white to yellow to greenish yellow, staining blue to blue-green or not changing with pores concolorous or sometimes red to brownish red. **Stipe** dry, rarely viscid, glabrous to subpruinose to reticulate or sometimes alveolate, with basal mycelium variously colored. Spore deposit olive brown. Spores smooth, fusoid. **Hymenial cystidia** present. **Clamp connections** absent.

The genus is distribution in temperate and tropical. It is generally reported as ectomycorrhizae associated with *Pinaceae*, *Fagaceae*, *Betulaceae*, *Dipterocarpacae*, *Myrtaceae*, *Casuarinaceae, Caesalpinoid* Legumes. This genus remains as the basic genus after all others have been separated based on idiosyncratic features. It may not be homogeneous or monophyletic.

***Boletus borneensis*** Corner (Figures. 5.1)

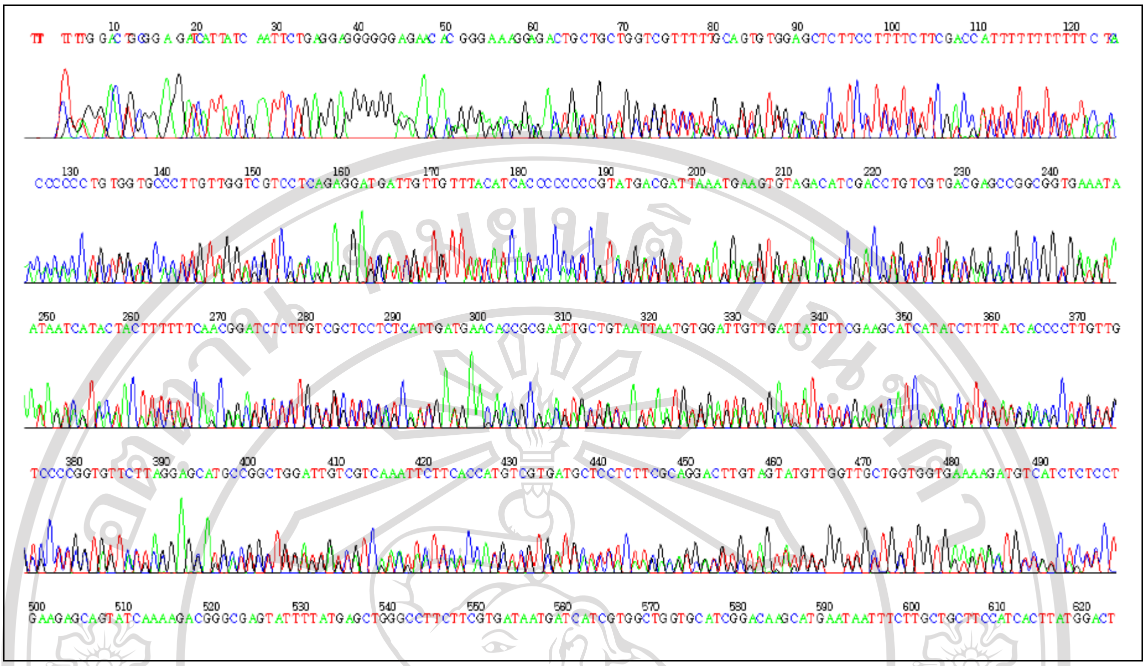
**Pileus** 80 mm diam., convex, dry, minutely subtomentose, not cracked, brown, negative in KOH, **context** white to pale yellow, bruising,turned brown in KOH. **Tubes** adnate, 10 mm long, yellow, **pores** circular or nearly so, concolored with tubes, small, 2/mm and turned blue in KOH. **Stipe** 130 mm long, 28 mm wide at apex, 30 mm at middle, 45 mm at base, brown; **context** white to pale yellow, bruising red green. **Basal mycelium** pale yellow. **Spore print** not obtained. **Basidiospores** 12-15.2 × 5.2-6 µm, smooth, boletoid, pale vinaceous chocolate. **Edibility** edible. **Sequence** of ITS region has been done but unsuccessful when do blast search in NCBI webpage.

***Habitat*****:** On the ground in mountain forest.
***Known distribution*****:** Borneo, Kinabalu.

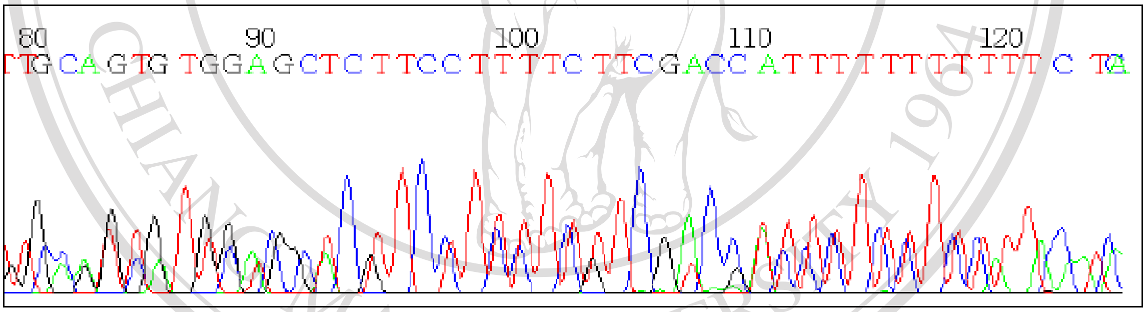
***Specimens examined:*** THAILAND: Chiang Mai Province, Muang Chiang Mai, Suthep Pui National Park, in rainforest Huay Kok Ma, 16 June 2005, *S. Thongklam* CMU-*SL019*.

**Figure 5.1** ***Boletus borneensis*****. a-c.** Basidiocarp. **d-f.** Basidiospores. Scale bar: a-c. = 20 mm; d-f. = 10 µm.

***Notes*****:** The general morphology both macroscopic and microscopic of the current samples collected from Doi Suthep Pui National Park best fit *B. borneensis* as reported by Corner 1972. Unfortuned the ITS sequence of this sample is not good to use for construct phylogenetic tree because no significant similarity sequence found when do blast search. That error result possibly due to the interfear bases line that can see in the whole sequence as shown in figure 5.2.



a.



b.

ITS sequence of Boletus borneensis CMU-SL019

TTTTTTTGGACTGCGGAGATCATTATCAATTCTGAGGAGGGGGGAGAACACGGGAAAGGAGACTGCTGCTGGTCGTTTTTGCAGTGTGGAGCTCTTCCTTTT
CTTCGACCATTTTTTTTTTTCTCACCCCCCTGTGGTGCCCTTGTTGGTCGTCCTCAGAGGATGATTGTTGTTTACATCACCCCCCCCGTATGACGATTAAATGA
AGTGTAGACATCGACCTGTCGTGACGAGCCGGCGGTGAAATAATAATCATACTACTTTTTTCAACGGATCTCTTGTCGCTCCTCTCATTGATGAACACCGCG
AATTGCTGTAATTAATGTGGATTGTTGATTATCTTCGAAGCATCATATCTTTTATCACCCCTTGTTGTCCCCGGTGTTCTTAGGAGCATGCCGGCTGGATTGT
CGTCAAATTCTTCACCATGTCGTGATGCTCCTCTTCGCAGGACTTGTAGTATGTTGGTTGCTGGTGGTGAAAAGATGTCATCTCTCCTGAAGAGCAGTATCA
AAAGACGGGCGAGTATTTTATGAGCTGGGCCTTCTTCGTGATAATGATCATCGTGGCTGGTGCATCGGACAAGCATGAATAATTTCTTGCTGCTTCCATCAC
TTATGGACTTGTTGTCCACTCGCTTTTTCTACTACTAGGTCGTGATGATGATGAACATTGTTGCGAAGATCATGATTGTTGTGCTTCTTAACTTGTTCTCCTCT
CATGTAGGACTACCCCCTGATCTTCTTCATATCATCAATCGGAGGAAGA

c.

**Figures 5.2 ITS sequence of *Boletus borneensis* CMU-SL019. a.** A graph of ITS sequence. **b.** Example of the problem part that found in the sequence. **c.** ITS sequence.

**_Boletellus_ Murrill** **(Boletaceae: Boletineae)**

**Type species:** *Boletellus ananas* (M.A. Curtis) Murrill

**References:** Corner, 1972; Komiyama and Yamada, 2000; Sanmee, 2004; Chandrasrikul *et al*., 2008; Halling 2008.

**Pileus** typically dry, rarely subviscid, scaly or tomentose, microscopically a trichodermium, sometimes with appendiculate remnants at margin; **context** white or yellow, often changing to blue. **Hymenophore** tubulose, adnexed, white at first, soon yellow, often staining blue. **Stipe** central, usually pruinose, rarely with an apical reticulum, dry, sometimes staining blue; **basal mycelium** white, very rarely yellow. **Basidiospore** olive brown in deposit, longitudinally ridged/winged or slightly veined, inamyloid or rarely dextrinoid. **Hymenial cystidia** usually present. **Clamp connections** usually absent, rarely present (one sp., *B. fibuliger*). KOH and $NH_4OH$ reactions negative (more species need testing).

Distribution worldwide but apparently not in Southern South America. The genus is ectomycorrhizae associated with *Caesalpiniaceae*, *Casuarinaceae*, *Dipterocarpaceae*, *Fagaceae*, *Myrtaceae* and *Pinaceae*.

***Boletellus emodensis*** (Berk) Singer (Figures 5.3)

*Basionyms*: *Boletus emodensis* Berk

**Pileus** 40-80 mm diam., convex then plane, pinkish red (10A3-10B6), dry, tomentose then cracking into large and small floccose scales, sometime recurved, exposing yellow flesh underneath, with red star-like rays hanging along the margin,

**context** pale yellow, brusing blue in KOH. **Tubes** 1-2 mm wide, angular, yellow then brownish olive (4D6-4E8), brusing blue in KOH. **Stipe** 55 mm long, 6 mm wide at apex and middle, 10 mm at base, cylindrical, not turn blue in KOH, **context** fibrous, solid, not turn blue in KOH. **Basal mycelium** white. **Basidiospores** 20.7-22.2 × 6.4-8.6) µm, elongate, somewhat ellipsoid or cylindrical, longitudinally strait, olivaceous brown. **Edibility** edible.

***Habitat*:** Gregarious on ground in the forest cover with *Caesalpiniaceae*, *Casuarinaceae*, *Dipterocarpaceae*, *Fagaceae*, *Myrtaceae* and *Pinaceae*.

***Known distribution*:** Malaysia, Singapore, Viet Nam, .

***Specimens examined:*** THAILAND: Chiang Mai Province, Muang Chiang Mai, Suthep Pui National Park, in rainforest Sanggasabhasri Lane to Huai Kok Ma, 22 May 2005, *S. Thongklam* CMU-*ST014*; Chiang Mai Province, Jom Thong, Inthanon National Park, in rainforest Mae Ya Waterfall, 20 November 2005, *S. Thongklam*, CMU *SL057*; Phayao Province, Muang Phayao, Doi Luang National Park, at Jum Pa Thong Waterfall forest, 22 May 2005, *S. Thongklam* CMU-*SL075*.

***Notes*:** *Boletellus emodensis* is distinguished by the pinkish red pileus with scales on pileus surface, the fibrillose stipe and the longitudinally striate spores. It differs from *B. ananus* in the pileus cortext which is pale yellow instead of whitish. The general characteristic of the current specimens are similar to the description B. emodensis given by Corner (1972) and Sanmee (2004).

**Figures 5.3** ***Boletellus emodensis***. a-d, f. Basidiocarp**.** e. Basidiospore. Scale bar: a-d, f = 1 cm, e = 10 µm.

## ***Heimioporus*** *E. Horak* (*=Heimiella*) **(Boletaceae: Boletineae)**

**Type species:** *Heimioporus retisporus* (Pat. & C.P. Baker) E. Horak

**References:** Corner, (1972); Horak, (2004); Chandrasrikul *et al*., (2008); Halling, (2008).

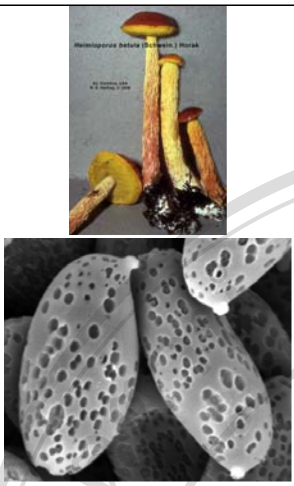
**Pileus** dry, subtomentose, microscopically a palisadic trichodermium. **Context** white to yellow, not staining. Hymenophore adnexed, yellow, sometimes staining blue. Stipe dry, pruinose to reticulate, with white basal mycelium. **Basidiospores** olive brown, alveolate-reticulate to reticulate or with pit-like perforations, elongate-ellipsoid to short ellipsoid, lacking a suprahilar place. **Hymenial cystidia** present. **Clamp connections** absent.

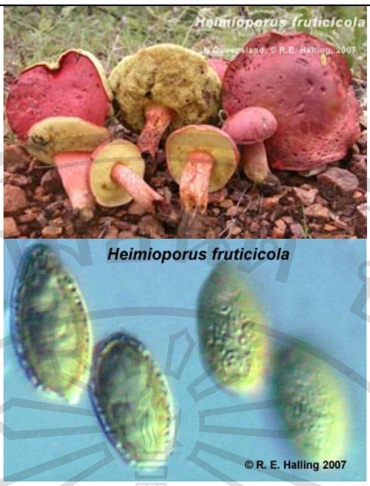
The genus is generally found in eastern Asia, south east Asia, Australia, Mexico, Belize, and Costa Rica. And it is ectomycorrhizae associated with *Fagaceae*, *Dipterocarpaceae*, *Myrtaceae*, *Casuarinaceae*.

Approximatly 14 records of *Boletellus* and *Heimiella* species have been revised and replaced the names as *Heimeiporus* by Horak (2004) (Table 5.1, Figure 5.4).

**Table 5.1** The current names of *Heimioporus* species (Horak, 2004; Halling, 2008).

| **Current names (*Heimioporus*)** | **Original names** |
|---|---|
| *Heimioporus alveolatus* (R. Heim & Perr.-Bertr.) E. Horak | *Heimiella alveolata* R. Heim & Perr.-Bertr. |
| *H. anguiformis* (R. Heim), E. Horak | *H. anguiformis* R. Heim |
| *H. betula* (Schwein.) E. Horak | *H. betula* Schwein. |
| *H. fruticicola* (Berk.) E. Horak | *H. fruticicola* Berk. |
| *H. ivoryi* (Singer) E. Horak | *H. ivoryi* Singer |
| *H. japonicus* (Hongo) E. Horak | *H. japonica* Hongo |
| *H. kinabaluensis* (Corner) E. Horak | *H. kinabaluensis* Corner |
| *H. mandarinus* (Cesati) E. Horak | *H. mandarina* Cesati |
| *H. nigricans* (M. Zang) E. Horak | *H. nigricans* M. Zang |
| *H. punctisporus* (Corner) E. Horak | *H. punctispora* Corner |
| *H. retisporus* (Pat. & C.P. Baker) (Boedijn) E. Horak | *H. retispora* (Pat. & C.P. Baker ) Boedijn |
| *H. rubropunctus* (Hongo) E. Horak | *H. rubropunct* Hongo |
| *H. subretisporus* (Corner) E. Horak | *H. subretispora* Corner |
| *H. xerampelinus* (M. Zang & W.-k. Zheng) E. Horak | *Boletellus xerampelinus* M. Zang & W.-k. Zheng |


*H. betula*
(Halling, 2008)



*H. fruticicola*
(Halling, 2008)


*H. ivoryi*
(Halling, 2008)


*H. japonicus*
(Halling, 2008)

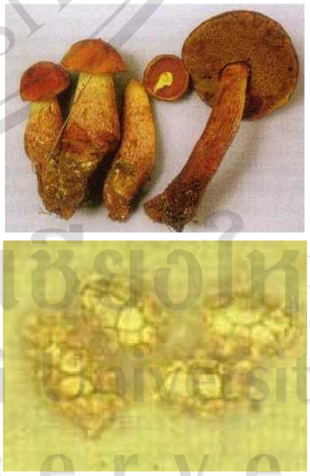

*H. kinabaluensis*
(Corner, 1972).

*H. mandarinus*
(Halling, 2008)

*H. rubropunctus*
(Halling, 2008)


*H. retisporus*
(Chandrasrikul *et al*., 2008)


*H. retisporus*
(Corner, 1972).


*H. subretisporus*
(Chiu - see in Corner, 1972).

**Figures 5.4** Basidiocarps and basidiospores of *Heimioporus* spp. for comparison with the collection in this study.

***Heimioporus retisporus*** (Pat. & C.P. Baker) E. Horak (Figure 5.5)

**Synonymy:** *Boletus retisporus* Pat. & C.F. Baker
*Heimiella retispora* (Pat. & C.F. Baker) Boedijn
*Strobilomyces retisporus* (Pat. & C.F. Baker) X.L. Mao

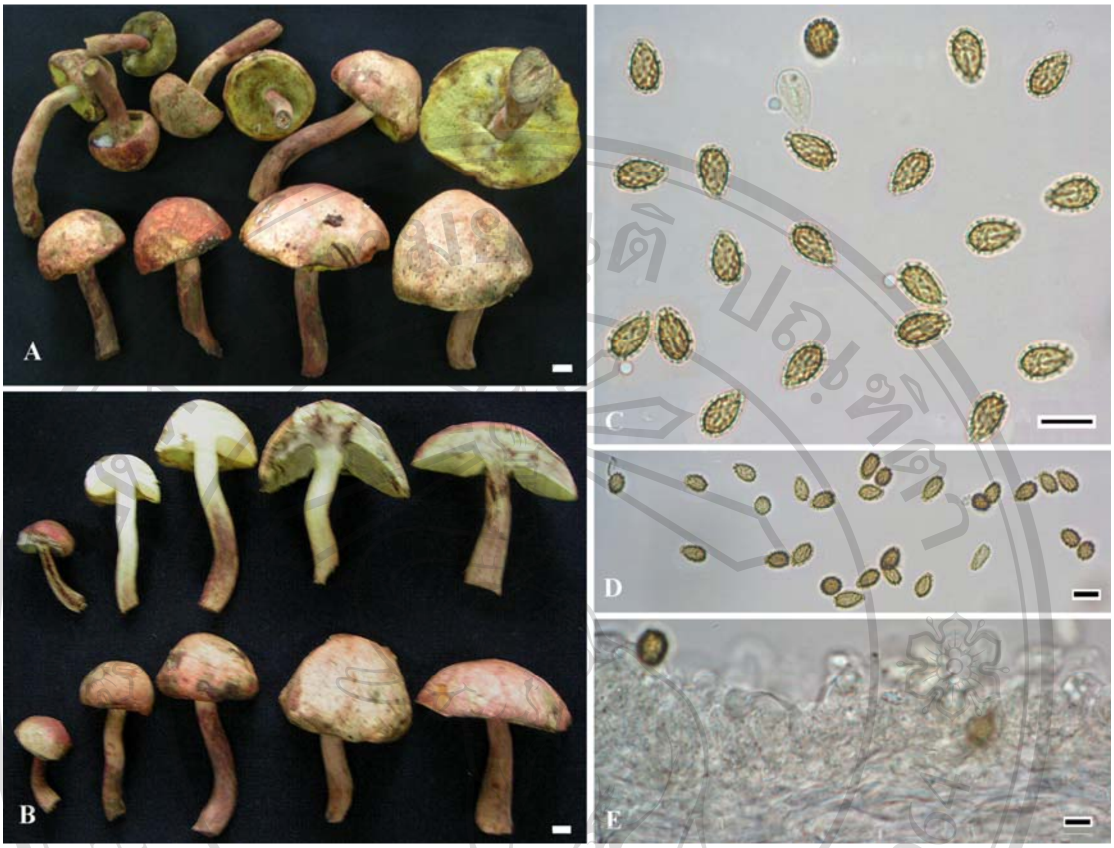
**Pileus** 27-85 mm diam., convex then plane, eventually with upturn margin, dry, subtomentose, dark crimson discoloring yellowish pink with crimson blotches, finally entirely clear yellow or with a pinkish tinge in the centre, sometime wholly pinklish or pale brownish drab, not bruising blue; **tubes** yellow green, 6-15 mm, sinuate, ventricose or nearly free; **pores** compound, angular, at first crimson becoming paler and finally yellow green, 0.7-1 mm. **Stipe** cylindric to subclavate, 33-87 mm long, 6-11 mm thick at the apex, 7-16 mm at the base; **context** more or less ribbed with faint elongate meshes, becoming finely scurfy-villous, crimson becoming pale with age, the apex clear yellow and rather coarsely reticulate. **Spore print** olive brown. **Basidiospores** 21.6-23.2 × 13.2-15.3 µm, **basidiospore-body** 17.9-18.5 × 10.5-11.1 µm, ellipsoid, reticulated in the hyaline exospore with regular brown meshes, deep olive brown in mass.

**Sequences** 958 bp of 28S rDNA and 453 bp of ITS region were sequenced from the *H. retisporus* CMU-SL073 in this study (Figures 5.6).

***Habitat*****:** On the ground in the forest, generally gregarious, common in the lowlands and mountains to 1300 m amsl. Often attached to decaying wood.

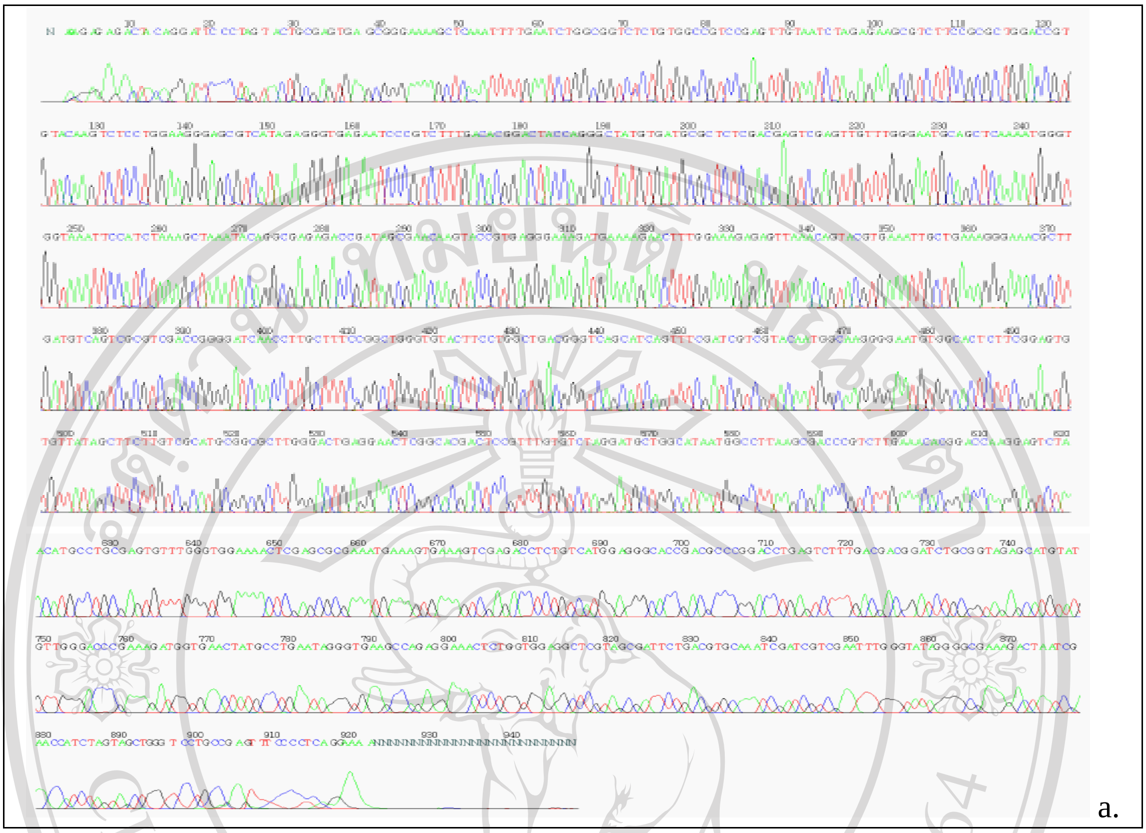
***Known distribution*****:** China, south east Asia.

***Specimens examined:*** THAILAND: Chiang Rai Province, Khun Chae National Park, in rainforest, 2 August 2006, *S. Thongklam* CMU-*SL073*.



**Figures. 5.5.** ***Heimioporus retisporus***. **a-b.** Basidiocarps. **c-d.** Basidiospores. **e.** Basidia. Scale bar: a-b. = 10 mm, c. = 20 µm, d-e. = 10 µm.

***Notes***: *Heimiopora retisporus* is the commonest species of *Heimioporus* in south east Asia. This collection of *H. retisporus* agrees with those of *Heimiella retispora* described by Boedijn (1960) (see in Corner 1972) and Corner (1972). This taxon has somewhat bigger basidiospores (17.9-18.5 × 10.5-11.1 µm vs. 9-11 × 8-10 µm) than those specimen described by Corner (1972). The 28S rDNA sequence (958 bp) of this collection is identities to those of *Heimiella retispora* AF050650 97% (851/877) with Gaps = 5/877. In the phylogenetic tree is also shown both sequences are clade together (Figure 4.8) which confirmed the identification of genus level. Unfortuned the ITS sequence of this genus has only one sequence of *Heimiella japonica* to compare (Figure 5.7). Unfortuned the ITS sequence obtained in this study is quite short to represent the taxa that have no record in GenBank.



***Heimioporus retisporus*_CMU-SL073_28S rDNA_958 bp** b.

**TTACCCGCTTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAACTACAGGATTCCCCTAGTAACTGCGAGTGAAGCGGGAAAAGCTCAAATTTTGAATCT
GGCGGTCTCTGTGGCCGTCCGAGTTGTAATCTAGAGAAGCGTCTTCCGCGCTGGACCGTGTACAAGTCTCCTGGAAGGGAGCGTCATAGAGGGTGAGAATC
CCGTCTTTGACACGGACTACCAGGGCTATGTGATGCGCTCTCGACGAGTCGAGTTGTTTGGGAATGCAGCTCAAAATGGGTGGTAAATTCCATCTAAAGCTA
AATACAGGCGAGAGACCGATAGCGAACAAGTACCGTGAGGGAAAGATGAAAAGAACTTTGGAAAGAGAGTTAAACAGTACGTGAAATTGCTGAAAGGGAA
ACGCTTGATGTCAGTCGCGTCGACCGGGGATCAACCTTGCTTTCCGGCTGGGTGTACTTCCTGGCTGACGGGTCAGCATCAGTTTCGATCGTCGTACAATG
GCAAGGGGAATGTGGCACTCTTCGGAGTGTGTTATAGCTTCTTGTCGCATGCGGCGCTTGGGACTGAGGAACTCGGCACGACTCCGTTTGTGTCTAGGATG
CTGGCATAATGGCCTTAAGCGACCCGTCTTGAAACACGGACCAAGGAGTCTAACATGCCTGCGAGTGTTTGGGTGGAAAACTCGAGCGCGAAATGAAAGTG
AAAGTCGAGACCTCTGTCATGGAGGGCACCGACGCCCGGACCTGAGTCTTTGACGACGGATCTGCGGTAGAGCATGTATGTTGGGACCCGAAAGATGGTG
AACTATGCCTGAATAGGGTGAAGCCAGAGGAAACTCTGGTGGAGGCTCGTAGCGATTCTGACGTGCAAATCGATCGTCGAATTTGGGTATAGGGGCGAAA
GACTAATCGAACCATCTAGTAGCTGGTTCCTGCCGAAGTTTCCCTCAGGA**

***Heimioporus retisporus*_CMU-SL073_ITS_453 bp** c.

**GGGACTGCGGAAGGACATTATCGAACACTTGTAAAGGGGAGATCAGATCGGCGGATTCCACTCGGAACTGTTGCTGGCGGACATACGTCTGCATGTGCAC
GTTCTGGCGTCCGCTTTTCCGGTCGACCTTTTGCAATCTTCATTTACACCTGTGCACCTATTGTAGGTCTTCGCAAGAGGATCTATGTCTTTCATAACACTATT
TTGTATGGCCATAGAATGTATCGATCGTCTGTGATGGACGAGAGAAAAAATATATTACAACTTTCAGCAACGGATCTCTCGGTTCTCGCATCGATGAAGAAC
GCAGCGAATTGCGATAAGTAATGTGAATTGCAGATTTTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCTCCTTGGTATTCCGAGGAGCATGCCTGTT
TGAGTGACATTCAATTCTCAACCATGTCTNCCTTGATCATTCTGG**

**Figures 5.6** 28S rDNA and ITS sequences of *Heimioporus retisporus* CMU-SL073. a. A graph of 28S rDNA sequence. b. 28S rDNA sequence. c. ITS sequence.

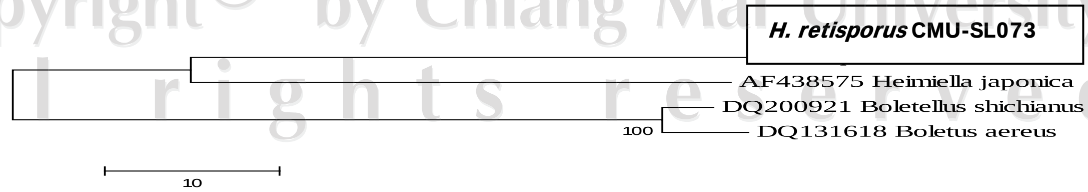


**Figure 5.7** Phylogeny tree base on maximum parsimony (MP) analyses of ITS sequences. The number under the branches indicate MP bootstrap support proportion from 1000 replications.

***Tylopilus*** P. Karst **(Boletaceae: Boletineae)**

**Type species:** *Tylopilus felleus* (Bull.) P. Karst.

**References:** Corner, (1972); Chandrasrikul *et al*., (2008); Halling (2008).

**Pileus** dry, glabrous to subtomentose, microscopically a trichodermium or subhymeniform. Context white, unchanging or staining pale brown, red then black, or rarely blue. **Hymenophore** adnexed, white then pinkish flesh colored to purplish brown to rusty brown, staining brown. **Stipe** dry, pruinose to glabrous to reticulate, to finely scabrous. **Spore** deposit pinkish flesh colored to purplish brown, to rusty brown. Spores smooth, fusoid. **Hymenial cystidia** present, usually as pseudocystidia. **Clamp connections** absent.

This genus is distribution worldwide. It is generally reported as ectomycorrhizae associated with *Betulaceae*, *Casuarinaceae*, *Fagaceae*, *Pinaceae*, and *Myrtaceae*.

***Tylopilus virens*** (Chiu) Hongo (Figures 5.8)

*Basionym: Boletus virens* Chiu

**Pileus** 38-63 mm diam., dry, convex, decurved margin, slightly wrinkle, minute velvety, olive brown (4D6-4E8), negative in KOH, **context** thick sponge. **Tubes** adnexed, 4 mm long, yellowish white (4A2), **pores** circular or nearly so, concolored with tubes, small, 2/mm and negative in KOH. **Stipe** 55-60 mm long, 8 mm wide at apex, 10 mm at middle, 15 mm at base, grayish yellow to orange yellow (4B6-4B8) and negative in KOH. **Context** thick sponge, orange yellow (4B7-4A8). *Basal* *mycelium* grayish yellow (4B5). **Spore print** not obtained. **Basidiospores** 10-14 × 4-6 µm, ellipsoid, smooth, thin wall. **Edibility** edible.

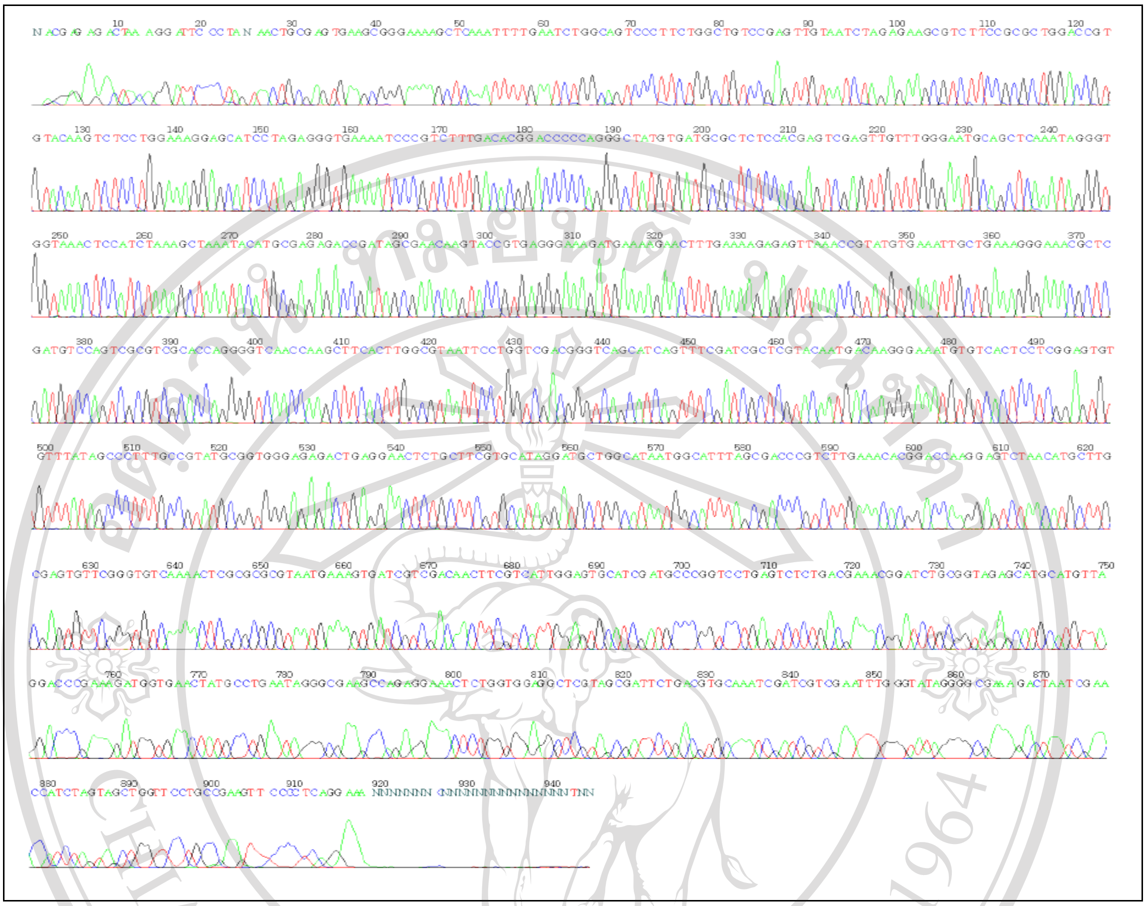
***Sequences*:** 916 bp of 28S rDNA and 926 bp of ITS region were sequenced from the *T. virens* CMU-SL053 in this study (Figure 5.9-5.10). A phylogenetic relationship within the *Boletales* species tree of this specimen based on 28S rDNA sequence is given in Figure 4.8. Figure 5.11 show a phylogenetic tree of *Tylopilus* species base on maximum parsimony (MP) analyses of 28S rDNA sequences and ITS sequences.

***Habitat*:** On the ground in oak-forest, frequent.

***Known distribution*:** Africa, Australia, Borneo, China, Japan, New Zealand, Thailand.

***Specimens examined:*** THAILAND: Chiang Mai Province, Muang Chiang Mai, Suthep Pui National Park, in rainforest Huay Kok Ma, 3 November 2005, *S. Thongklam* CMU-*SL053*.

**Figures 5.8** ***Tylopilus virens*. a-c.** Basidiocarp. **d.** Hymenopore and basidiospores. Scale bar: a-c. = 10mm; d. = 10 µm.



a.

***Tylopilus virens***_CMU-SL053_28S rDNA_916 bp

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GCGTCTTCCGCGCTGGACCGTGTACAAGTCTCCTGGAAAGGAGCATCCTAGAGGGTGAAAATCCCGTCTTTGACACGGACCCCCAGGGCTATGTGATGCGC
TCTCCACGAGTCGAGTTGTTTGGGAATGCAGCTCAAATAGGGTGGTAAACTCCATCTAAAGCTAAATACATGCGAGAGACCGATAGCGAACAAGTACCGTG
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CAAGCTTCACTTGGCGTAATTCCTGGTCGACGGGTCAGCATCAGTTTCGATCGCTCGTACAATGACAAGGGAAATGTGTCACTCCTCGGAGTGTGTTTATAG
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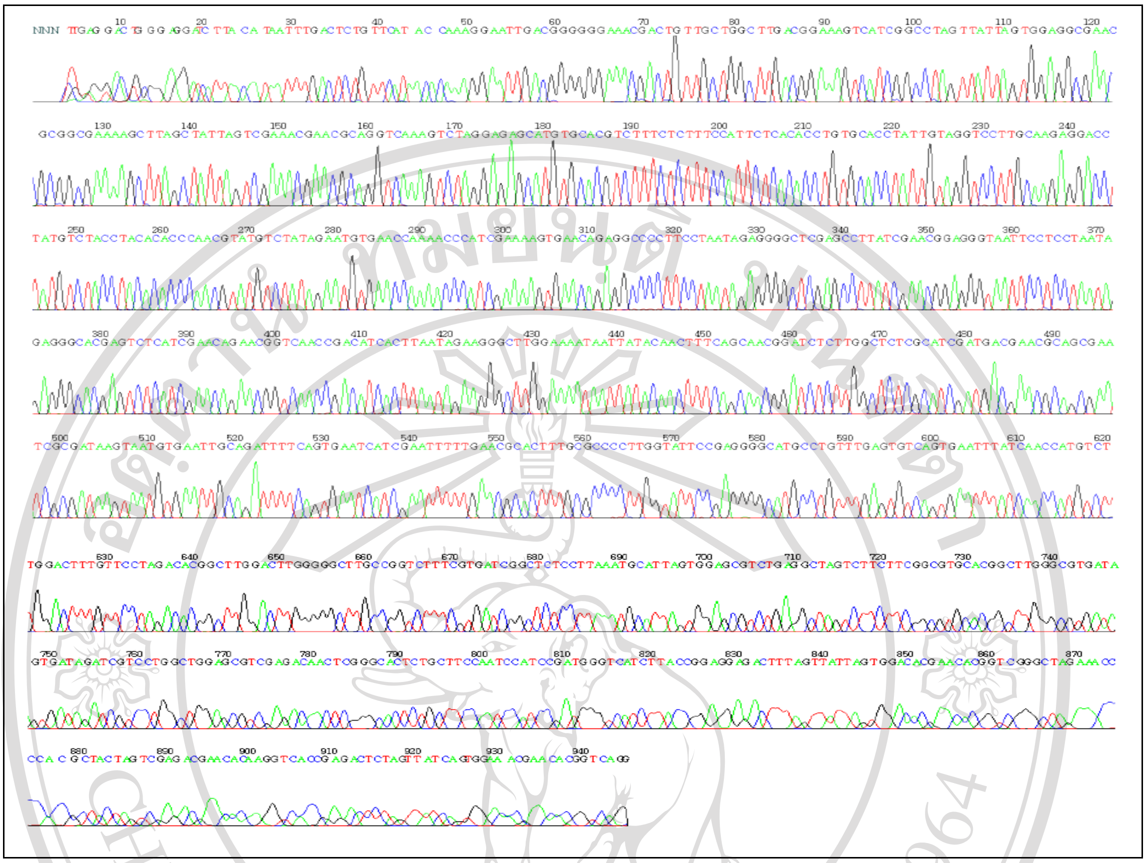
AGTCTAACATGCTTGCGAGTGTTCGGGTGTCAAAACTCGCGCGCGTAATGAAAGTGATCGTCGACAACTTCGTCATTGGAGTGCATCGATGCCCGGTCCTG
AGTCTCTGACGAAACGGATCTGCGGTAGAGCATGCATGTTAGGACCCGAAAGATGGTGAACTATGCCTGAATAGGGCGAAGCCAGAGGAAACTCTGGTGG
AGGCTCGTAGCGATTCTGACGTGCAAATCGATCGTCGAATTTGGGTATAGGGGCGAAAGACTAATCGAACCATCTAGTAGCTGGTTCCTGCCGAAGTTTCC
CTCAGGA
```

b.

**Figs 5.9** **28S rDNA sequence of *Tyropilus virens* CMU-SL053.** a. A graph of 28S rDNA sequence. b. 28S rDNA sequence.



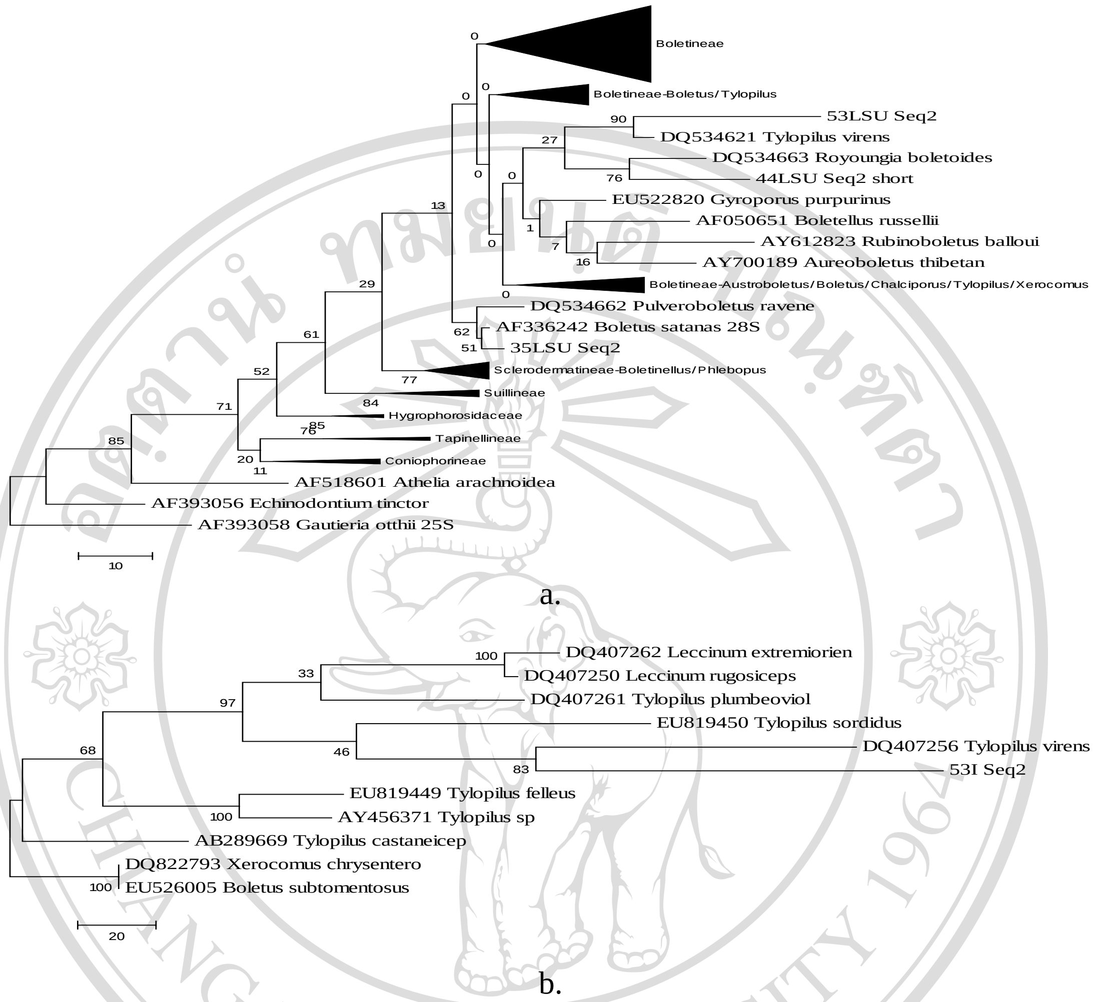
a.

*Tylopilus virens*_CMU-SL053_ITS_926 bp

**TGGGACTGCGGAGGATCATTAACAATAATTTGACTCTGTTCATAACACAAAGGAATTGACGGGGGGAAACGACTGTTGCTGGCTTGACGGAAAGTCATCGG
CCTAGTTATTAGTGGAGGCGAACGCGGCGAAAAGCTTAGCTATTAGTCGAAACGAACGCAGGTCAAAGTCTAGGAGAGCATGTGCACGTCTTTCTCTTTCC
ATTCTCACACCTGTGCACCTATTGTAGGTCCTTGCAAGAGGACCTATGTCTACCTACACACCCAACGTATGTCTATAGAATGTGAACCAAAACCCATCGAAAA
GTGAACAGAGGCCCCTTCCTAATAGAGGGGCTCGAGCCTTATCGAACGGAGGGTAATTCCTCCTAATAGAGGGCACGAGTCTCATCGAACAGAACGGTCAA
CCGACATCACTTAATAGAAGGGCTTGGAAAATAATTATACAACTTTCAGCAACGGATCTCTTGGCTCTCGCATCGATGACGAACGCAGCGAATCGCGATAAG
TAATGTGAATTGCAGATTTTCAGTGAATCATCGAATTTTTGAACGCACTTTGCGCCCCTTGGTATTCCGAGGGGCATGCCTGTTTGAGTGTCAGTGAATTTAT
CAACCATGTCTTGGACTTTGTTCCTAGACACGGCTTGGACTTGGGGGCTTGCCGGTCTTTCGTGATCGGCTCTCCTTAAATGCATTAGTGGAGCGTCTGAGG
CTAGTCTTCTTCGGCGTGCACGGCTTGGGCGTGATAGTGATAGATCGTCCTGGCTGGAGCGTCGAGACAACTCGGGCACTCTGCTTCCAATCCATCCGATG
GGTCATCTTACCGGAGGAGACTTTAGTTATTAGTGGACACGAACACGGTCGGGCTAGAAACCCCACCGCTACTAGTCGAGACGAACACAGTCACGAGACTC
TAGTATCAGTG**

b.

**Figures 5.10 ITS sequences of *Tyropilus virens* CMU-SL053.** a. A graph of ITS sequence. b. An ITS sequence.



**Figures 5.11** Phylogeny tree of *Tylopilus* species based on maximum parsimony (MP) analyses. a. 28S rDNA sequences. b. ITS sequences. The number above the branches indicate MP bootstrap support proportion from 1000 replications.

***Notes*****:** *Tylopilus virens* is distinguished by the olive colors over the pileus surface that become brown with time. This record collected from Doi Suthep Pui National Park at Sangasabhasri Lane to Huai Kok Ma similar to those described by Corner (1972) and also its habitat under *Pinus densiflora* with *Castanopsis cuspidate* var *sieboldii* (Japan); these conifers also occur in our collection site of Suthep Pui National Park but different species e.g. *P. kesiya, C. acuminatissima* and *C. argyrophylla*. Identification of this specimen has confirmed by the molecular analyses of 28S rDNA and ITS sequences with strongly support (Figures 5.11). The sequence of 28S rDNA and ITS region are very similar to those of *T. virens* DQ534621 and *T. virens* DQ407256 respectively.