

Yaovapa Taprab 2008: Study on the Function of Symbiotic Basidiomycetes of Fungus-Growing Termites of Thailand. Doctor of Philosophy (Bioscience), Major Field: Bioscience, Interdisciplinary Graduate Program. Thesis Advisor: Associate Professor Napavarn Noparatnaraporn, Dr.Eng. 169 pages.

In this study, the experiment was separate into three parts; first, thirty-nine strains of the symbiotic fungi in the nests of fungus-growing termites were cultivated and analyzed phylogenetically based on nuclear ribosomal DNA sequences consisting of internal transcribed spacers, 5.8S rDNA, and partial large subunit (LSU) rDNA. Among these strains, 38 strains were related to *Termitomyces* and the DNA sequences of the ITS1-5.8S rDNA-ITS2 region (530-645 bp) showed more than 72% nucleotide identity to one another and were classified into eight groups. The longer LSU rDNA region (1.2-1.4 kbp) of at least one representative of each of the eight groups was analyzed for their DNA sequences. The phylogenetic analyses of the LSU rDNA indicated that all the eight groups were clustered together with *Termitomyces heimii*, *Termitomyces cylindricus*, *Termitomyces* sp. strain BSI sp1 and *Termitomyces microcarpus*. Second, the phenol-oxidizing enzymes from the fungus combs and *Termitomyces* strains were investigated. The result clearly demonstrated that laccase was the sole detectable phenol-oxidizing enzyme in the fungus combs of *Microtermes* sp., *Odontotermes* sp. and *Macrotermes gilvus*. No peroxidase activity was detected in the fungus combs and low activity was detected in some culture supernatants of *Termitomyces* spp. strains. The laccase cDNA fragments were amplified directly from RNA extracted from fungus combs of five termite species and a fungal isolate using degenerate primers targeting conserved copper binding domains of basidiomycete laccases, resulting in a total of 13 putative laccase cDNA sequences being identified. The full-length sequences of the laccase cDNA and the corresponding gene, *lcc1-2*, were identified from the fungus comb of *Ma. gilvus* and a *Termitomyces* strain isolated from the same fungus comb, respectively. These findings indicate that the symbiotic fungus secretes laccase to the fungus comb. Third, the expressed sequence tag (EST) analysis of a symbiotic fungi and the fungus comb of the *Ma. gilvus* were conducted. A total of 2,613 ESTs were collected and resulted in 1,582 nonredundant tentative consensus sequences. A number of homologous sequences to genes involved in plant cell wall degradation were identified and a majority of them encoded putative pectinolytic enzymes.

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Student's signature

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Thesis advisor's sign

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