

Thesis Title	Identification of Ectomycorrhizal Fungi of <i>Dipterocarpaceae</i> in Dry Dipterocarp Forests Based on Sequences of Internal Transcribed Spacer (ITS) and Mitochondrial Large Subunit Ribosomal DNA
Thesis Credits	12
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Abstract

The family *Dipterocarpaceae* forms a dominant family in tropical forests. Since the structures of the plants are uniform and their wood is hard, many species have been exploited in general construction. In the last few decades, dipterocarp forests had been overlogged and degraded, thus planting dipterocarps has gained much attention. Dipterocarps are unusual among tropical trees in being associated with ectomycorrhizal fungi. Ectomycorrhizal fungi are the mutually beneficial symbioses of fungi and fine roots, and are responsible for the uptake of nutrients that support the tree growth. The potential use of ectomycorrhiza in reforestation depends upon the knowledge of biological diversity and symbiotic range between these two organisms. Therefore, the species of ectomycorrhizal fungi in the forest have essentially been identified. Prior to development of molecular techniques, the study of symbiotic relationship between these two organisms was difficult because of no simple way to identify each species. Molecular methods have facilitated this study. In this work, indigenous symbiotic fungi in ectomycorrhizae in dry dipterocarp forests were identified by amplification of internal transcribed spacer (ITS) consisting of ITS1, 5.8SrDNA, and ITS2 and a portion of mitochondrial large subunit of ribosomal DNA (mt LrDNA) using PCR technique. The sequences of the PCR products were evaluated to identify the genera of ectomycorrhizae. Thirty eight samples of ectomycorrhizal roots were collected from three dipterocarp forests in the north and north-east of

Thailand, *i.e.*, Queen Sirikit Botanic Garden in Chiangmai province, Sarawin Natural Park in Maehongson province, Sakaerat Environmental Research Center, and Takrut Rang mountain in Nakornratchasima province. Phylogenetic analyses and comparison of the DNA sequences from ectomycorrhizae and mushrooms (both in collections and available databases) were performed to identify mycorrhizal fungi. The results revealed that the most abundant of fungi were in group Thelephoroid (*Thelephora* spp. and *Tomentella* spp.) and Family *Russulaceae* (*Russula* spp., *Lactarius* spp., and *Gymnomyces* sp.). Some species of these fungi showed broad host range and distributed in all three dry dipterocarp forests. Only few species of Family *Cortinariaceae* (Cortinaroid and *Inocybe* spp.) and Family *Sclerodermataceae* (*Scleroderma* sp. and *Pisolithus* spp.) were also found in some ectomycorrhizal roots.

Keywords : Ectomycorrhizal fungi / *Dipterocarpaceae* / Dry dipterocarp forests / Internal transcribed spacer / Mitochondrial large subunit ribosomal DNA