CHAPTER 8

GENERAL DISCUSSION

The forests of northern Thailand are tropical rain forests, and this is where the sources for newly discovered species are mainly situated (Desjardin *et al.*, 2004). Unfortunately there have been limited field studies to document the diversity of macro-fungi from the region. This study was initiated in order to obtain the diversity of boletes (*Basidiomycota*, *Boletales*) in the major national parks of upper northern Thailand. The effects of sites and host trees were also examined. Some interested boletes species were described and illustrated. The new taxa and some interested species genera were implicated on taxonomy and phylogenetic placement using morphological characters and rDNA sequence analyses.

8.1 Diversity of boletes represent in upper northern National Park of Thailand

Numerous studies have reported that distribution of macro-fungi is widespread. The basidiomycetes (also boletes) of temperate Europe and North America have been studied intensively for nearly 200 years, and accordingly, are relatively well documented (Desjardin, *et al.*, 2004). The high diversity of boletes with various new taxa from tropical forests has been reported in several countries such as China (Zang *et al.*, 2001; Wang *et al.*, 2003), Japan (Hongo and Izawa, 1998; Komiyama and Yamada, 2000; Takahashi 2003), Malaysia (Corner, 1972) as well as Thailand

(Chantorn *et al.*, 2007; Seehanan *et al.*, 2007; Seehanan and Petcharat, 2008; Chandrasrikul *et al.*, 2008). In the present study, the boletes species from rainforests in upper northern Thailand are diverse, and several new fungi were found. The results indicated that national parks particularly forests covered with *Fagaceae* supported a large numbers of boletes species that concluded with more undescribed fungi.

8.2 Molecular and morphological characters of boletes species from Thailand

Molecular tools especially DNA sequencing, are now increasingly being used for the identification of fungi (also boletes). Recent phylogenetic studied based on large taxon sampling and multiple gene loci consistently has been resolved a large clade that contain *Agaricales*, *Atheliales* and *Boletales* (Binder *et al.*, 2006; Binder and Hibbett, 2002; Larsson *et al.*, 2004; Matheny *et al.*, 2006). A range of analysis methods are in use and the method adopted in this study appears to provide sufficient evidence to establish a new species of the *Phlebopus* (Chapter 6).

Molecular techniques have a great use to assist the identification of taxa in genera and species complexes and define boundaries and relationships of taxa. In the present study, such techniques proved identification and determined the phylogenetic relationship within member of *Boletineae* and *Sclerodermatineae* (*Boletales*) such as species of *Boletus*, *Heimioporus*, *Rubinoboletus*, and *Tylopilus*.

8.3 Usefulness of this study

According to tree species in the genera *Pinus*, *Quercus*, *Lithocarpus*, *Castanopsis*, *Dipterocarpus*, *Shorea*, *Hoppea* and other dipterocarps are dependent upon mycorrhizal fungi for their survival, knowledge of the mushrooms associated

with them as boletes will give us a better understanding of the ecology of these important timber trees. A long surveyed, the vegetation in national parks in upper northern Thailand constitutes of mid- and high-elevation rainforests and are dominated by ectomycorrhizal trees belonging to the *Dipterocarpaceae*, *Fagaceae* and *Pinaceae*.

Understanding the host preference of boletes species in northern Thailand aided local people in locating new source of edible species of this mushroom and thereby benefit the local economy. Many species are edible in northern Thailand as well as in other parts of Thailand.

Species documented from the study region compared with those from other areas of the world to gain a better understanding of biogeography patterns and address questions concerning species dispersal. In chapter 5-7 gave detail of species move with their plant associates.

Phylogenetic studied of boletes are currently available only for a limited number of species from temperate regions of Australia, Europe North America and South America. A few of phylogenetic analyses contain DNA sequence of Asian species. Phylogenetic studies of Asian boletes species give us a better understanding of the evolution of the boletes on a worldwide scale, and aid in the biogeographically analyses indicated above.