CHAPTER 6

GENERAL DISCUSSION AND CONCLUSION

Previous studies on fungi from *Pandanus* have focused mainly on the taxonomy of saprobes. In addition, *Dracaena* has been little studied for fungi. This study was initiated in order to obtain the diversity of saprobic and pathogenic fungi developing on *Dracaena lourieri* and three *Pandanus* species. The effects of tissue types, seasons, sites and stage of decay on fungal occurrence on *Pandanus* species were examined. The disease lesions on *Dracaena* and *Pandanus* and some interested saprobes taxa were described and illustrated. The family Magnaporthaceae with a new species, *Ophioceras chiangdaoensis* sp. nov. and related genera were implicated on taxonomy and phylogenetic placement by using morphological characters and rDNA sequence analyses.

6.1 Biodiversity of pathogenic and saprobic fungi on *Dracaena* and *Pandanus*

Numerous studies have reported that occurrence of pathogenic and saprobic fungi on plants are widespread and vary throughout a broad range of host orders, families and genera worldwide. Diversity surveys of saprobes on temperate terrestrial monocotyledons have been carried out such as on culms of the cocksfoot (Webster, 1956, 1957), on couch grass (Hudson and Websters, 1958), on leaves of pea (Dickinson, 1967). However, extensive studies of fungal diversity have recently been investigated e.g. on banana, bamboo, grasses and palms from tropical rainforests in Thailand and other countries (Fröhlich and Hyde 1999, 2000; Taylor *et al.*, 2000; Hyde *et al.*, 2001; Photita *et al.*, 2001, 2003a; Wong and Hyde, 2001; Yanna *et al.*, 2001b, 2002; Bussaban *et al.*, 2004) as well as those on species of *Pandanus* (Whitton, 1999; Dulymamode *et al.*, 2001a; McKenzie *et al.*, 2002). The high diversity of saprobes with various new fungal taxa on Pandanaceae from tropical countries has been reported by Whitton, (1999), Dulymamode *et al.*, (2001a) and McKenzie *et al.*,

(2002). In the present study, the pathogenic and saprobic fungi communities occurring on *Dracaena loureiri* and *Pandanus* species from Thailand are diverse, and several new fungi were found. The results indicated that both *Dracaena* and *Pandanus* plants particularly wild plants supported a large numbers of fungal communities that concluded with more undescribed fungi.

It is generally thought that saprobes are less likely to be restricted in their host than pathogens (Dulymamode *et al.*, 2001a). However, in the present study, low numbers of fungi were found common among *Dracaena lourieri* and *Pandanus* spp. from different sites. In addition, fungal communities occurring on plants from different sites were less similar than those from the same site. This indicates that fungal communities also vary between sites. Tissue effects on fungal communities were found on decaying leaves, leaf sheaths, proproots and seeds of *Pandanus* species. The recurrence of certain fungi on various tissue types may be due to differences in nutritional requirements, or the ability of the fungi to utilize different substrates (Adaskaveg *et al.*, 1991; Ingold and Hudson, 1993). Yanna *et al.* (2001a, b) has also found the recurrence of fungi on certain tissue types on palms. There were no seasonal patterns of fungal occurrence on the *Pandanus penetrans* collected in this study. This may have been due to the small seasonal differences in the study area which has a tropical climate. No seasonal differences were observed between the saprobic fungi collected from palms in a tropical forest in Hong Kong (Yanna *et al.*, 2001a, b). The effect of seasonality may be more acute in temperate region where greater fluctuation in temperature, humidity and rainfall usually occur. Further studies are however, required to elucidate the effects of seasonality. Fungal communities occurred on *P. penetrans* leaves during the pioneer, mature and later stages of decay were distinct, and completely decay within 18 months. In succession, fungal composition pattern are affected by changing of substrata composition and competitive ability of the fungi (Frankland, 1992; Promputtha *et al.*, 2002; Yanna *et al.*, 2002). The enzymatic activities of these fungi also warrants further investigation in order to understand whether their abundance on specific tissue types is due to differing enzymatic capabilities (Yanna *et al.*, 2001a, b).

6.2 The relationships between pathogenic and saprobic fungi on *Dracaena* and *Pandanus*

In the current study, I collected and identified saprobic and pathogenic fungi on selected *Dracaena* and *Pandanus* species. Fungal communities occurring on both plant genera are primarily saprobes rather than parasites. Some pathogenic fungi that identified in this study have also been encountered as saprobes including species of *Acremonium*, *Aspergillus*, *Cladosporium*, *Colletotrichum*, *Curvularia*, *Fusarium*, *Guignardia*, *Myrothecium*, *Nigrospora*, *Oxydothis*, *Penicillium*, *Phomopsis* and *Sporidesmium*. The relationships between saprobic and pathogenic fungi were observed by testing the pathogenicity of these fungi. *Colletotrichum gloeosporioides*, *Curvularia lunata*, *Fusarium oxysporum*, *Guignardia* sp. and *Phomopsis* sp. caused disease symptoms on *Dracaena* or *Pandanus* leaves in the experimental system. Some pathogens have a latent phase within the host tissue and some saprobes can also be facultative parasites (Photita *et al.*, 2003a). It has also been observed that certain endophytes become pathogenic when the host plant is stressed (Millör, 1980; Andrews *et al.*, 1985). It is therefore quite feasible that saprobes, endophytes and pathogens of the same plants may be the same strain/species. Unfortunately, only a few endophytic fungi have been isolated from *Dracaena* and *Pandanus* in this study. More collections of endophytes are warranted to elucidate the relationship between all these fungi. Further studies are also needed to identify the sterile isolates to establish if they are the same species as the saprobes.

6.3 Molecular and morphological characters of fungi in family Magnaporthaceae

Molecular tools especially DNA sequencing, are now increasingly being used for the identification of fungi (Chen *et al.*, 1999; Berbee, 2001; Rossman *et al.*, 2001a, b; Wanderlei-Silva *et al.*, 2003; Jeewon *et al.*, 2004; Cai *et al.*, 2006; Kodseub *et al.*, 2006). A range of analysis methods are in use and the method adopted in this study appears to be sufficient evidence to establish a new order to accommodate the Magnaporthaceae (chapter 6), and phylogenetic affinities of the family is close to the order Diaporthales and Ophiostomatales. Base preliminary on morphological characters it can be seen that the selected taxa of the Magnaporthaceae in this study

(*Buergenerula, Gaeumannomyces, Mycoleptodiscus*, *Ophioceras*, *Pseudohalonectria* and *Pyricularia*) centred around *Magnaporthe* differ from those of Diaporthales and Ophiostomatales. In the Magnaporthaceae a stromata is lacking, black ascomata are immersed, often with long hairy necks and paraphyses are thin-walled tapering. Asci are often cylindrical, persistent, fairly thick-walled and have a massive J+ apical ring (except *M. salvinii*, J-), and ascospores are septate, and often filiform (Cannon, 1994; Kirk *et al.*, 2001). The Diaporthales and Ophiostomatales have also been recognized as a distinct order within the perithecial ascomycetes by using molecular analyses (Chen *et al.*, 1999; Zhang and Blackwell, 2001; Castlebury *et al.*, 2002). Thus, the morphological characteristic used to define the Diaporthales and Ophiostomatales are considered reliable indicators of the orders. The Diaporthales is characterized by ascomata that are usually aggregated into a pseudostromata, with long-necks, asci which are thick-walled with J- apical ring, and ascospores vary, and the anamorph is coelomycetous (Kirk *et al.*, 2001). In the Ophiostomatales stromata are absent, ascomata are hyaline or black, thin-walled, usually with long-necks and ostiolar setae, while asci are small and evanescent, ascospores are usually small, and the anamorph is hyphomycetous (Kirk *et al.*, 2001).

Molecular techniques have a great use to assist in 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 Magnaporthaceae such as species of *Buergenerula*, *Gaeumannomyces*, *Magnaporthe*, *Mycoleptodiscus*, *Ophioceras*, *Pseudohalonectria* and *Pyricularia*.

6.4 Future work

Knowledge of fungi on *Dracaena* and *Pandanus* is still incomplete. Future research should concentrate on:

1. Biodiversity, geographic distribution and tissues specific information for fungi on species of *Dracaena* and *Pandanus* is incomplete. There are also large geographic distribution gaps where fungi on *Dracaena* and *Pandanus* have not been

studied. Further collections of these both genera are needed to examine the fungi from different parts of Thailand and other tropical countries.

2. Information of fungal communities occurring in different stages of decay on different tissue types of *Dracaena* and *Pandanus* species are also needed for better estimations of global diversity.

3. The endophytic fungi on *Dracaena* and *Pandanus* are unknown. Further experiments need to be set up to investigate biodiversity and life strategies of endophytic, pathogenic and saprobic fungi.

4. The studies of benefit agents or novel compounds (e.g. antifungal agent, enzymes) from fungi on Dracaena and Pandanus have not been carried out. For example, the bio-control of plant diseases should be examined by using endophytes as biological control agents. The organic fertilizer may rapidly decay by using saprobes as activator agents.