

## CHAPTER 5

### GENERAL DISCUSSION AND CONCLUSION

In this study, the powdery mildew fungi in tribe Phyllactinieae were implicated on taxonomy and phylogenetic placement by using morphological characters and rDNA (nuclear ribosomal DNA) sequence analysis. Some powdery mildews have similar morphological characteristics which cause confusing identification of the fungal group. In addition, sufficient information on morphological characteristics of sexual state (teleomorph) is essential to identify powdery mildews at species level. Unfortunately, most powdery mildews do not produce sexual state in tropical or sub-tropical areas. This is a problem for taxonomy of powdery mildew. The molecular technique is a useful tool for precise taxonomy for the identification. The DNA sequences data are used to link anamorph with a holomorph to provide phylogenetic placement for anamorph with unknown teleomorph (Cunnington *et al.*, 2003; Shenoy *et al.*, 2007). Traditionally, taxonomy of powdery mildew fungi based on structure of appendages is valuable information for generic delimitation (Braun, 1987). Bélanger *et al.* (2002) summarized the main taxonomy of powdery mildew as follows: The characteristics of anamorph are useful for the generic taxonomy, whereas the teleomorph provides useful features on the species level.

To surveying and collecting of powdery mildew fungi in Northern part of Thailand, with a primary focus in Chiang Mai Province, the powdery mildews in tribe Phyllactinieae can be found only 30% among all of other tribes. A total of 27 specimens of powdery mildews in tribe Phyllactinieae were identified, of which 13 specimens belonging to *Leveillula* which composed of 5 host families: Euphorbiaceae, Malpighiaceae, Oxalidaceae, Pedaliaceae, Solanaceae and 14 specimens belonging to *Phyllactinia* which composed of 10 host families: Alangiaceae, Boraginaceae,

Caesalpiniaceae, Combretaceae, Euphorbiaceae, Lythraceae, Moraceae, Rosaceae, Urticaceae, Verbenaceae. Within 26 host plant species, 20 species are first recorded in Thailand, in which 4 species of them are first recorded in the world.

In Thailand, powdery mildew fungi in tribe Phyllactinieae were found only 2 genera: *Leveillula* and *Phyllactinia*. *Leveillula* can not be found teleomorphic state and can be pathogenic fungi only on herbaceous plants. *Phyllactinia* is parasitic fungi on tree or wood plants and can found both of anamorphic and teleomorphic state, but not at all species. Furthermore, the symptom of powdery mildew in tribe Phyllactinieae appeared the mycelia on the lower surfaces of leaves (Braun, 1987).

**Genus *Oidiopsis*** is characterized by dimorphic conidia formed singly. The primary conidia are more or less lanceolate, where as the secondary conidia are ellipsoid to cylindrical (Braun, 1987; Bélanger *et al.*, 2002). Eleven host plants species; *Capsicum annuum* var. *grossum*, *Capsicum annuum* var. *minimum*, *Capsicum frutescens*, *Capsicum frutescens* × *C. chinense*, *Capsicum* spp. (darby), *Capsicum* spp. (maxican), *Euphorbia heterophylla*, *Euphorbia pulcherrima*, *Galphimia glauca*, *Oxalis triangularis*, *Sesamum indicum*, *Solanum aculeatissimum* and *Solanum torvum* were found in this study. The perfect state of *Oidiopsis* has never found in Thailand. The molecular analysis was used to aid in the identification for linking anamorphic specimens with their respective teleomorph. The phylogenetic study based on ITS and 28S rDNA indicated that all of 10 data sequences, of which 7 on *Capsicum* spp., 1 on *Euphorbia heterophylla*, 1 on *Solanum aculeatissimum*, and 1 on *S. torvum* are located in a clade of *Leveillula taurica*. The morphological and phylogenetic analyses suggested strongly that the powdery mildew on host plants species are infected by *Leveillula taurica*. Furthermore, phylogenetic study based on ITS region indicated *Oidiopsis* on *Capsicum* spp. formed a clade with *L. taurica* causing powdery mildew on chilli.

**Genus *Ovulariopsis*** *Alangium kurzii*, *Boehmeria siamensis*, *Broussonetia papyrifera*, *Cassia fistula*, *Dalbergia cana*, *Dalbergia lanceolaria*, *Ehretia laevis*, *Euphorbia heterophylla*, *Gmelina arborea*, *Lagerstroma macrocarpa*, *Morus alba*, *Pyrus pyrifolia*, *Senna siamea* and *Terminalia bellirica* were recorded as host plants of genus *Ovulariopsis* in Thailand. The teleomorphic state of *Ovulariopsis* can be found on 7 host plant species in Thailand; *Boehmeria siamensis*, *Cassia fistula*, *Dalbergia cana*, *Dalbergia lanceolaria*, *Gmelina arborea*, *Morus alba* and *Terminalia bellirica*. Genus *Ovulariopsis* characterized by clavate conidia formed singly and having one type. The teleomorph state belongs to the genus *Phyllactinia* characterized by having acicular appendages with bulbous at the base (Braun, 1987). However, dimorphic conidia (primary and secondary conidia) and spirally twisted foot-cells of conidiophores occurred in this study as the unique characteristics of *Ovulariopsis* found on *Lagerstroma macrocarpa*, *Dalbergia lanceolaria* and *Terminalia bellirica*. Furthermore, the anamorphic characteristics of powdery mildew on *Cassia fistula* and *Senna siamea* also appeared the unique characteristics by formed short conidiophores, cylindrical to ellipsoid conidia which are similar to *Erysiphe* emend. (*Pseudoidium*). As the result, molecular phylogenetic analysis were use to solve the confusing characteristics identification. The blast result of these sequences data revealed that powdery mildews on *Cassia fistula*, *Lagerstroma macrocarpa*, *Dalbergia lanceolaria*, *Terminalia bellirica* and *Senna siamea* are identical with *Phyllactinia* that supported by high similarity blast search. The phylogenetic analysis showed the fungal group which having the unique characteristics clustered together at the basal position. And, this fungal group was split from other *Phyllactinia* at early stage of evolution.

Taxonomic studies of powdery mildew fungi in tribe Phyllactinieae using morphological characteristics and phylogenetic approaches demonstrated that host expansion from trees to herb and *Phyllactinia* is paraphyletic group. The molecular phylogenetic analysis based on ITS and 28S rDNA sequences are useful for analyse within Phyllactinieae, but ITS sequences can be used for particular group within *Phyllactinia* in this study. *Phyllactinia* group which having the unique characteristics of anamorph, we did not conduct phylogenetic analysis of ITS sequences because the sequences are too variable and obtain ambiguous alignment. Therefore, molecular analysis based on ITS and 28S rDNA sequences are properly analyses the phylogeny of powdery mildew in tribe Phyllactinieae.