

Dissertation Title Phytopathogenic and Post-harvest Fungi on Selected Economically Fruits in Northern Thailand

Author Alireza Armand

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Advisor Assistant Professor Kitiphong Khongphinitbunjong, Ph. D.

Co-Advisor Adjunct Professor Kevin David Hyde, Ph. D.
Mahamarakkalage Mary Ruvishika Shehali Jayawardena, Ph. D.

ABSTRACT

Thailand is a leading global producer of tropical fruit crops, renowned for its diverse and high-quality produce, including mangoes, durians, rambutans, longans, and pineapples. These fruit crops are integral to the country's economy, contributing significantly to export revenues and local livelihoods. Cultivation of fruit crops supports the agricultural sector, employing millions of farmers and fostering rural development. Beyond economic value, these fruits hold cultural and nutritional significance, forming a vital component of traditional diets and health practices.

Despite Thailand's favourable climate and fertile soils, fungal diseases pose a serious threat to fruit production, both pre- and post-harvest. Pre-harvest infections by pathogenic fungi, associated with symptoms such as anthracnose, fruit rot, and leaf blight, often manifest or worsen during post-harvest handling, storage, and transportation, leading to significant losses in fruit quality and marketability. Isolation and identification of these fungi are essential to understand their diversity, pathogenicity, and infection mechanisms. Accurate identification using morphological and molecular techniques enables the development of targeted management strategies, including resistant cultivars, biological control agents, and integrated disease management practices. Post-harvest disease management, focusing on early detection, fungicidal treatments, and optimized storage conditions, is equally critical to ensuring fruit quality and extending shelf life.

The comprehensive survey of fungal pathogens associated with diverse tropical fruit crops in northern Thailand aimed to expand the understanding of fungal diversity, host-pathogen relationships, taxonomic novelties and new host or geographical records of pathogenic species and their potential impacts on the crops. Fresh samples of main tropical crops and economically important plants exhibiting specific symptoms were collected across local markets and orchards from multiple locations, including Chiang Mai, Chiang Rai, Lamphun, and Phayao Provinces, followed by the application of a polyphasic identification approach that combined morphological assessments with multi-locus phylogenetic analysis. Furthermore, pathogenicity assays were conducted on selected crops, including avocado, mango, and pineapple.

This study identified numerous fungal species associated with a range of symptoms, including leaf blight, dieback, fruit rot, and anthracnose, affecting key economic crops such as mango, avocado, durian, pineapple, longan, rambutan, langsat, guava, mangosteen, lychee, and papaya. Additionally, various fungal species were found to be associated with symptoms such as leaf blight, leaf spots, and dieback on ornamental plants. Herbarium specimens of the fungi described in the thesis were deposited in the Mae Fah Luang University (MFLU) Fungarium, Chiang Rai, Thailand. Living cultures were deposited in the Culture Collection of Mae Fah Luang University (MFLUCC). The obtained DNA sequences were verified, submitted to GenBank, and made available for public reference.

Pathogenicity assessment revealed that most of the strains isolated from mango (91.6%) were pathogenic to mango fruits and leaves, although their levels of virulence varied significantly. The pathogenic genera tested against mango included *Botryosphaeria*, *Colletotrichum*, *Diaporthe*, *Neofusicoccum*, *Neopestalotiopsis*, *Neoscytalidium*, *Pestalotiopsis*, *Pseudopallidocercospora*, and *Zasmidium*. Pathogenicity tests conducted on *Colletotrichum endophyticum*, *C. fructicola*, *C. siamense*, and *C. henanense* isolated from avocado indicated that these species were pathogenic to avocado fruits and leaves, exhibiting varying degrees of aggressiveness. Furthermore, pathogenicity tests on pineapple leaves demonstrated that *Colletotrichum fructicola* strains were pathogenic to the leaves. The study identified the main post-

harvest fungal species associated with mango and avocado, and assessed their virulence.

A total of 260 potentially pathogenic isolates were obtained, all belonging to ascomycetes. This study identified 20 genera, including *Albonectria*, *Bisifusarium*, *Botryosphaeria*, *Cercospora*, *Colletotrichum*, *Diaporthe*, *Fusarium*, *Lasiodiplodia*, *Lasmenia*, *Neocosmospora*, *Neofusicoccum*, *Neopestalotiopsis*, *Neoscytalidium*, *Paramyrothecium*, *Pestalotiopsis*, *Phyllosticta*, *Pseudocercospora*, *Pseudopallidocercospora* gen. nov., *Pseudoplagiostoma*, and *Zasmidium*. The 260 isolates were classified into 82 taxa, 10 families (*Apharknessiaceae*, *Botryosphaeriaceae*, *Diaporthaceae*, *Glomerellaceae*, *Mycosphaerellaceae*, *Nectriaceae*, *Phyllostictaceae*, *Pseudoplagiostomataceae*, *Sporocadaceae*, *Stachybotryaceae*), and six orders (*Amphisphaeriales*, *Botryosphaeriales*, *Diaporthales*, *Glomerellales*, *Hypocreales*, *Mycosphaerellales*) in *Dothideomycetes* and *Sordariomycetes*, comprising 22 new species and 60 previously known species. This research also revealed 19 new geographical records and 80 new host records, the majority associated with main crops.

The newly described species are *Albonectria durionigenum*, *A. lansii*, *Bisifusarium mangiferae*, *B. thailandica*, *Cercospora alocasiicola*, *Colletotrichum durionigenum*, *C. thasutense*, *Diaporthe capsicicola*, *D. durionis*, *D. lansii*, *D. perseae-americanae*, *D. tamarindi*, *N. iridicola*, *N. iridis*, *N. litchii*, *N. litchiicola*, *N. mangiferae*, *N. mangifericola*, *N. mangiferigena*, *Paramyrothecium amorphophalli*, *Pseudopallidocercospora mangiferae*, and *Zasmidium mangiferae*. Additionally, *Pseudopallidocercospora* was illustrated as a new genus, associated with leaf spots of *Mangifera indica*. All these species were illustrated and described with confirmed morphology and molecular phylogeny.

The morpho-molecular data revealed the occurrence of 16 *Colletotrichum* species viz. *C. asianum*, *C. brevisporum*, *C. durionigenum*, *C. endophyticum*, *C. fructicola*, *C. gigasporum*, *C. gloeosporioides*, *C. guajavae*, *C. henanense*, *C. musae*, *C. musicola*, *C. plurivorum*, *C. siamense*, *C. thasutense*, and *C. tropicicola*, *C. truncatum* in northern Thailand. The species were associated with anthracnose, leaf blight, leaf spots, and fruit rot. This study provides an update information of occurrence

and distribution of main *Colletotrichum* species associated with important crops in Thailand. Moreover, *Colletotrichum* was identified as the most frequent genus representing 91 (35%) strains, and *Colletotrichum siamense* was the dominant species showing a wide host range, isolated from more than 15 plant genera. This study revealed Twenty-eight new host records of *Colletotrichum* species viz. *C. endophyticum* (from *Psidium guajava* and *Theobroma cacao*), *C. fructicola* (*Sapodilla sapote*, *Bauhinia* sp., *Ficus religiosa*, and *Piper nigrum*), *C. gigasporum* (from *Durio zibethinus*), *C. guajavae* (from *Mangifera indica*), *C. henanense* (from *Persea americana*), *C. musicola* (from *Lagerstroemia* sp.), *C. siamense* (from *Asplenium nidus*, *Dendrobium* sp., *Durio zibethinus*, *Dracaena fragrans*, *Morinda citrifolia*, *Polyscias balfouriana*, *Diospyros virginiana*, *Solanum lycopersicum*, *Sphagneticola trilobata*, *Hibiscus rosa-sinensis*, *Dimocarpus longan*, *Chamaedorea seifrizii*, *Syzygium jambos*, *Vanilla planifolia*, and *Lansium domesticum*), *C. thasutense* (from *Theobroma cacao*), and *C. truncatum* (from *Ficus religiosa* and *Durio zibethinus*). Twelve new geographical records of *Colletotrichum* species were also discovered in this research viz. *C. endophyticum* (from *Persea americana*), *C. fructicola* (from *Persea americana*), *C. gigasporum* (from *Mangifera indica*), *C. musae* (from *Mangifera indica*), *C. plurivorum* (from *Mangifera indica*), and *C. siamense* (from *Anthurium andraeanum*, *Artocarpus heterophyllus*, *Bauhinia* sp., *Ficus* sp., *Litchi chinensis*, *Piper nigrum*, and *Psidium guajava*).

This study was also the first comprehensive study documenting and illustrating species diversity of *Diaporthe* associated with crop diseases in Thailand. Thirteen species were obtained and identified using a morpho-molecular approach viz. *D. arecae*, *D. capsicicola*, *D. discoidispora*, *D. durionis*, *D. lansii*, *D. perseae-americanae*, *D. pterocarpi*, *D. rosae*, *D. siamensis*, *D. sojiae*, *D. tamarindi*, *D. thunbergiicola*, and *D. tulliensis*. The species were associated with leaf blight, die back, canker, and fruit rot of crops viz. *Mangifera indica*, *Durio zibethinus*, *Capsicum annum*, *Lansium domesticum*, *Psidium guajava*, *Persea americana*, *Ziziphus mauritiana*, *Dimocarpus longan*, *Tamarindus indica*, *Nephelium lappaceum*, *Litchi chinensis*, and *Solanum lycopersicum*. *Diaporthe* was the second most frequently obtained genus, representing 49 (19%) strains.

The present study revealed a high species diversity of *Neopestalotiopsis* associated with major tropical crops, namely: *Cocos nucifera*, *Lansium domesticum*, *Mangifera indica*, *Persea americana*, *Nephelium lappaceum*, *Garcinia mangostana*, *Psidium guajava*, and *Litchi chinensis*. Thirteen species of *Neopestalotiopsis* were identified in this study viz. *N. chrysea*, *N. rosicola*, *N. cubana*, *N. dendrobii*, *N. hydeana*, *N. iridicola*, *N. litchii*, *N. litchiicola*, *N. mangiferae*, *N. mangifericola*, *N. mangiferigena*, *N. psidii*, and *N. rhododendri*, associated with leaf spots, leaf blight, and fruit rot. *Neopestalotiopsis* was the third most frequently obtained genus, representing 39 (15%) strains. This study represented fifteen new host records of *Neopestalotiopsis* species viz. *N. chrysea* (from *Mangifera indica*), *N. cubana* (from *Lansium domesticum*, *Nephelium lappaceum*, *Garcinia mangostana*, *Mangifera indica*, *Nyssa sylvatica*, *Persea americana*, *Psidium guajava*), *N. dendrobii* (from *Mangifera indica*), *N. hydeana* (from *Persea americana*), *N. neomaricae* (from *Casearia lasiophylla*), *N. psidii* (from *Mangifera indica*), *N. rhododendri* (from *Mangifera indica*), *N. rosicola* (from *Cocos nucifera*), and *N. samarangensis* (from *Garcinia mangostana*).

Lasiodiplodia was obtained with 18 (7%) strains and *Fusarium* with 15 (6%) strains, majority reported from important tropical crops for the first time worldwide. Different *Lasiodiplodia* species viz. *L. brasiliensis*, *L. chonburiensis*, *L. pseudotheobromae*, and *L. theobromae* were discovered from different symptoms such as dieback, canker, leaf blight, and fruit rot. The present study expand our knowledge on species diversity of *Lasiodiplodia* in Thailand, discovering six new host reports from *Durio zibethinus*, *Morinda citrifolia*, *Iris pseudacorus*, *Elaeagnus pungens*, *Litchi chinensis*, and one new geographical record of *Lasiodiplodia theobromae* associated with *Musa* sp. fruit rot. *Fusarium* species were discovered for the first time worldwide associated with symptomatic tissues viz. *F. coffeibaccae* (*Psidium guajava*), *F. endophyticum* (from *Citrus* sp., and *Dimocarpus longan*), *F. fujikuroi* (from *Persea americana*), *F. hainanense* (from *Mangifera indica*), *F. pernambucanum* (from *Persea americana* and *Carica papaya*), *F. pseudocircinatum* (from *Citrus* sp., *Spathiphyllum* sp., and *Carica papaya*), *F. sulawesiense* (from *Dimocarpus longan*, and *Carica papaya*), and one new geographical record of *F. sacchari* from *Musa* sp.

Other species and new records revealed in This study include *Botryosphaeria fabicerciana* (from *Mangifera indica*), *B. scharifii* (from *Mangifera indica*), *Neocosmospora diminuta* (from *Durio zibethinus*), *N. metavorans* (from *Persea americana*), *Neofusicoccum parvum* (from *Persea americana*), *N. sinoeucalypti* (from *Mangifera indica*), *Phyllosticta capitalensis* (from *Diospyros virginiana*, *Brassica oleracea*, *Psidium guajava*, and *Dimocarpus longan*), *Pseudocercospora terengganuensis* (from *Hymenocallis littoralis*), *Pseudoplagiostoma perseae* (from *Persea americana*), *Neoscytalidium dimidiatum* (from *Mangifera indica*), *Pestalotiopsis humicola* (from *Mangifera indica*), and *P. menhaiensis* (from *Mangifera indica*).

These results underscore the need for comprehensive surveillance and targeted management strategies to mitigate the potential impact of these fungi on agriculture and horticulture. The study's outcomes enhance understanding of fungal distribution, species diversity, pathogenicity, and potential threats to plant health, aiding in future diagnostic and control efforts.

Keywords: Agriculture, Anthracnose, Multi-gene Phylogeny, Pathogenicity, Phytopathogenic Fungi, Post-harvest Disease, Taxonomy