

**MORPHOLOGICAL, PATHOLOGICAL AND MOLECULAR
CHARACTERIZATION OF *Colletotrichum gloeosporioides*
ISOLATES FROM DIFFERENT AGRO ECOLOGICAL
REGIONS OF SRILANKA.**

BY

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Thesis

Submitted in the partial fulfillment of the requirements
for the degree of

MASTER OF PHILOSOPHY

in the

POST GRADUATE INSTITUTE OF AGRICULTURE

of the

**UNIVERSITY OF PERADENIYA
SRI LANKA.**

July 2002

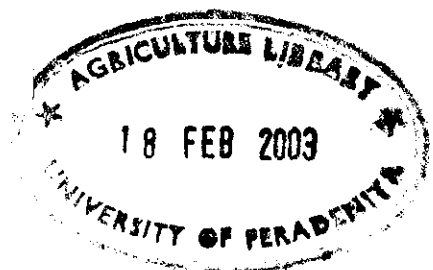
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ABSTRACT

Anthranose caused by the fungus *Colletotrichum gloeosporioides* (Penz) Penz and Sacc. which is extremely variable in its morphology, is a major post harvest disease of mango (*Mangifera indica* L.) in Sri Lanka. A research was carried out to evaluate and to identify the variations in *C.gloeosporioides* from different Agro Ecological Regions (AER) of Sri Lanka in order to understand the degree of pathogenicity. Isolates were obtained from infected fruits, leaves and inflorescence from 45 locations in Sri Lanka which fall into 15 AER (Anuradhapura, Vavuniya, Trincomalee, Dambulla, Batticaloa, Ampara, Puttalam, Gampaha, Polgahawela, Colombo, Kandy, Kurunegala, Chilaw, Badulla and Matale).

After seven days on PDA at 28°C under continuous white light, morphological characters of the culture (colour, appearance and growth rate) were closely examined. The lengths of at least 30 conidia per isolate were measured microscopically and were subjected to cluster analysis in SAS statistical package. Pathogenicity of each isolate was tested with the commercially available variety *Petti amba*. Ten isolates were obtained from ten mango varieties commonly grown in Sri Lanka and their colony characteristics and length of conidia were studied. RAPD – PCR with twenty random operon primers (OPA 01 to OPA 20) was done for all forty five isolates obtained, to test the genetic variability of these isolates.

Out of forty five isolates examined in this study, twenty-seven were characterized as fast growing colonies (FGC) and eighteen were slow growing colonies (SGC). Significant variations were observed within the two types of colonies. Conidia were divided into two types: cylindrical, with both apices of the conidium rounded; or

fusiform, with one apex rounded and the other fusiform. Cluster analysis based on the lengths of spores divided the forty-five isolates into three distinct clusters (cluster I, II and III) at the Median Normalized Distance less than 1.00, and subdivided into several sub clusters delineated at the Median Normalized Distance less than 0.6. Since cluster II have been grouped with isolates mostly from dry zone, climatic conditions may have an effect on the prevalence of different conidial lengths in each isolate. Pathogenicity test revealed that all the *C.gloeosporioides* were virulent on mango. Highly aggressive isolates of *C.gloeosporioides* (Amp 1, Bat 1, Col 2, Vav 2, Kur 2,) infecting the commercial variety *Petti amba* were detected from samples collected from a number of field sites in Sri Lanka. One aggressive isolate, Amp1 from Ampara (DL 2) was identified by DMRT from anthracnose lesion diameter produced. Cluster analysis based on the anthracnose lesion diameter produced by *C.gloeosporioides* isolates divided the forty five isolates into three distinct clusters (Cluster I, II and III) at the Median Normalized Distance less than 1.00. Isolates from Gampaha, Dambulla, Matale, Polgahawela, and Puttalam were characterized into cluster I by both conidial length and pathogenicity test. Isolates virulent on mango showed cross infectivity under the laboratory conditions. Isolates of *C. gloeosporioides* from ten varieties of mango grown in Sri Lanka, showed variations in the colony characteristics (colour, growth rate and growth habit), length of conidia and pathogenicity. Cross compatibilities of these isolates over the mango varieties have been noticed.

Operon primers used in RAPD-PCR, failed to detect any genetic polymorphism that might be present between the different isolates from different AER of Sri Lanka. Therefore, further molecular analysis is necessary to establish the genetic diversity of this pathogen.