

PERMANENT REFERENCE

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

BY

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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.

TABLE OF CONTENTS

ABSTRACT	i
ACKNOWLEDGEMENT	iii
TABLE OF CONTENTS	iv
LIST OF TABLES	viii
LIST OF FIGURES	ix
LIST OF PLATES	x
ABBREVIATIONS	xi
CHAPTER 1	
1. Introduction	i
1.1. Objectives	6
CHAPTER 2	
2. Literature Review	
2.1. Mango (<i>Mangifera indica</i> L.)	7
2.2. Mango Production in Sri Lanka	8
2.3. Mango Varieties in Sri Lanka	9
2.4. Extent of loss	10
2.5. Current Constraints on Mango Production in Sri Lanka	10
2.6. Mango Anthracnose	11
2.7. Symptoms of the Disease	11
2.8. The pathogen; <i>C.gloeosporioides</i>	13

2.9. Host Range of <i>C.gloeosporioides</i>	14
2.10. Epidemiology	14
2.11. Infection	15
2.12. Quiescent Infection	16
2.13. Preformed Compounds in Mango Fruits	17
2.14. Conidial Characteristics	17
2.15. Morphological Variations of <i>C.gloeosporioides</i>	18
2.16. Pathological Variation of <i>C. gloeosporioides</i>	19
2.17. Molecular Variabilites of <i>C.gloeosporioides</i>	20
2.17.1. Molecular Characterization	20
2.18. Post Harvest Disease Control	25
CHAPTER 3	
3. Materials and Methods	29
3.1. Collection of <i>C. gloeosporioides</i> isolates	29
3.2. Isolation of <i>C. gloeosporioides</i> from Infected Plant Parts	32
3.3. Maintenance of <i>C. gloeosporioides</i> Isolates	32
3.4. Characterization of <i>C. gloeosporioides</i> According to Morphological Characters	32
3.4.1. Conidial Characteristics	33
3.4.2. Colony Characteristics of <i>C.gloeosporioides</i> on PDA	34
3.4.3. Data Analysis	34
3.5. Characterization of <i>C. gloeosporioides</i> Isolates According to Pathogenicity	35
3.5.1. Collection of fruits	35
3.5.2. Pathogenicity assays	35
3.5.3. Lesion Development	36

3.5.4. Cross Infection	37
3.5.5. Data Analysis	37
3.6. Characterization of <i>C. gloeosporioides</i> Isolates	
According to Mango Varieties	37
3.6.1. Selection of the samples	37
3.6.2. Isolation of the Pathogen	38
3.6.3. Confirmation of the Pathogenicity	38
3.6.4. Data analysis	39
3.7. Molecular Characterization of <i>C. gloeosporioides</i> Isolates	39
3.7.1. Production of Mycelial Mass	39
3.7.2. DNA Extraction and Amplification	40
3.7.3. Quantification of DNA	41
3.7.4. Polymerase Chain Reaction Amplification with Random Primers	41

CHAPTER 4

4.Results and Discussions	44
4.1. Isolation of <i>C. gloeosporioides</i> from Infected Plant Parts	44
4.2. Characterization of <i>C.gloeosporioides</i> According to Morphological Characters	46
4.2.1. Colony Characteristics (macro)	46
4.2.2. Conidial Characteristics	53
4.2.2.1. Cluster Analysis	54
4.3. Characterization of <i>C.gloeosporioides</i> According to Pathological characters	57
4.3.1. Cluster Analysis	62
4.3.2. Cross infectivity of <i>C.gloeosporioides</i>	63