



***METABOLOMICS ANALYSIS ON ANTIFUNGAL ACTIVITIES PRODUCED  
BY *Penicillium oxalicum* T3.3 GROWN ON DIFFERENT TYPES OF  
CARBON SOURCES***

**NURLIYANA BINTI SALIKIN**

**FBSB 2015 176**



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By

**NURLIYANA BINTI SALIKIN**

**Thesis Submitted to the School of Graduate Studies, Universiti Putra Malaysia,  
in Fulfillment of the Requirements for the Degree of Master of Science**

**July 2015**

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Abstract of thesis presented to the Senate of Universiti Putra Malaysia in fulfilment of the requirement for the degree of Master of Science

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**July 2015**

**Chairman : Associate Professor Umi Kalsom Md Shah, PhD**  
**Faculty : Biotechnology and Biomolecular Sciences**

Anthracoze is a disease caused by a fungal *Colletotrichum gloeosporioides*. It is a common disease to dragon fruit plant and has caused a great loss to this industry. This pathogenic fungus can cause damage to most parts of plants including roots, stems, leaves, flowers and fruits. One of the potential microorganisms that able to produce antimicrobial activity against this plant pathogen is the endophytic fungus. However, research carried out on metabolomics of cellular metabolites produced by endophytic *Penicillium oxalicum* against *C. gloeosporioides* is very limited. Thus, this study was conducted with the aims to evaluate the antifungal activities produced by *Penicillium oxalicum* T3.3 against *Colletotrichum gloeosporioides* by using different types of carbon sources in fermentation medium and to identify the possible compounds produced by this strain through metabolomics approach.

Preliminary study on locally isolated; *P. oxalicum* T3.3 had shown a promising antagonism through antifungal secondary metabolites which suppressed the growth of *C. gloeosporioides*. Disc diffusion test was conducted in order to determine the inhibition zone on the growth of *C. gloeosporioides*. Among the six carbon sources tested, glucose exhibited the highest percent inhibition of radial growth (PIRG) of 75% and producing inhibition zone ranges from 4 to 7 mm. The minimum inhibition concentration (MIC) and minimum fungicidal concentration (MFC) of the glucose crude extract was the highest with 78 µg/mL and 2500 µg/mL, respectively. Meanwhile, starch and xylitol crude extracts gave the lowest MIC value of 1250 µg/mL and no MFC can be recorded. The compounds were extracted with ethyl acetate and <sup>1</sup>H NMR analysis was carried out to identify candidate compounds that had been produced. Metabolomics studies were conducted by analyzing the spectrum using SIMCA P+, Principal Component Analysis (PCA) and Partial Least Square

(PLS) multivariate statistical method. The conducted metabolomics study showed that sugar crude extracts (glucose, sucrose and maltose) tend to produce more threonine, 2-heptanone, lactate, valine, butyrate, *O*-phosphoserine. Meanwhile complex sugar substrates (xylitol, starch and *Undaria pinnatifida*) produced more acetic acid, methionine and leucine. From this analysis, different metabolites produced by *P. oxalicum* T3.3 were clustered according to the carbon sources used. This research demonstrates the potential of using a combination of  $^1\text{H}$  NMR spectroscopy and multivariate data analyses in differentiating the effect of carbon sources used based on the identification of possible metabolites contributing to their differences.



Abstrak tesis yang dikemukakan kepada Senat Universiti Putra Malaysia sebagai memenuhi keperluan untuk ijazah Master Sains

**ANALISIS METABOLOMIK KE ATAS AKTIVITI ANTIKULAT YANG DIHASILKAN OLEH *Penicillium oxalicum* T3.3 YANG TUMBUH DI ATAS PELBAGAI JENIS SUMBER KARBON**

Oleh

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Antraknos adalah penyakit yang disebabkan oleh kulat *Colletotrichum gloeosporioides*. Ia adalah penyakit yang biasa untuk tanaman buah naga dan telah menyebabkan kehilangan besar kepada industri ini. Kulat pathogen ini boleh menyebabkan kerosakan pada kebanyakan bahagian tumbuhan termasuk akar, batang, daun, bunga dan buah. Salah satu mikroorganisma yang berpotensi dapat menghasilkan aktiviti anti-mikrob terhadap patogen tumbuhan ini adalah kulat endofitik. Walau bagaimanapun, penyelidikan yang dijalankan ke atas metabolomik metabolit selular yang dihasilkan oleh *Penicillium oxalicum* terhadap *C. gloeosporioides* adalah sangat terhad. Oleh itu, kajian ini dijalankan dengan tujuan untuk menilai aktiviti anti-kulat yang dihasilkan oleh *P. oxalicum* T3.3 terhadap *Colletotrichum gloeosporioides* dengan menggunakan pelbagai jenis sumber karbon dalam medium fermentasi dan untuk mengenal pasti sebatian yang mungkin dihasilkan oleh strain ini melalui pendekatan metabolomik.

Kajian awal mengenai isolat tempatan; *P. oxalicum* T3.3 telah menunjukkan penentangan yang menjanjikan melalui anti-kulat sebagai metabolit sekunder yang boleh menyekat pertumbuhan *C. gloeosporioides*. Ujian cakera penyebaran telah dijalankan untuk menentukan zon perencatan pada pertumbuhan *C. gloeosporioides*. Antara enam sumber karbon yang diuji, glukosa mempamerkan peratus perencatan pertumbuhan tertinggi (PIRG) sebanyak 75% dan menghasilkan zon perencatan antara 4-7 mm. Kepekatan minimum perencatan (MIC) dan kepekatan minimum berhubung dgn kulat (MFC) daripada ekstrak mentah glukosa adalah yang tertinggi dengan 78 µg/mL dan 2500 µg/mL, masing-masing. Sementara itu, kanji dan xylitol ekstrak mentah memberikan nilai MIC yang paling rendah dengan 1250 µg/mL dan tiada MFC boleh direkodkan. Sebatian ini diekstrak dengan etil asetat dan analisis <sup>1</sup>H NMR telah

dijalankan untuk mengenalpasti calon sebatian yang telah dihasilkan. Kajian metabolomik telah dijalankan dengan menganalisis spektrum menggunakan SIMCA P +, Analisis Komponen Utama (PCA) dan “Partial Least Square” (PLS) kaedah statistik multivariat. Kajian metabolomik yang telah dijalankan menunjukkan bahawa ekstrak gula mentah (glukosa, sukrosa dan maltosa) cenderung untuk menghasilkan lebih treonina, 2-heptanina, laktat, valina, butirat, dan *O*-fosfoserina. Sementara itu sampel gula kompleks (xylitol, kanji dan *Undaria pinnatifida*) menghasilkan lebih banyak asid asetik, metionina dan leusina. Daripada analisis ini, metabolit berbeza yang dihasilkan oleh *P.oxalicum* T3.3 dikelompokkan mengikut sumber karbon yang digunakan. Kajian ini menunjukkan potensi menggunakan gabungan <sup>1</sup>H NMR spektroskopi dan data multivariat analisis dalam membezakan kesan sumber karbon yang digunakan berdasarkan pengenalpastian metabolit yang mungkin menyumbang kepada perbezaan mereka.



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I certify that a Thesis Examination Committee has met on (10<sup>th</sup> July 2015) to conduct the final examination of Nurliyana Binti Salikin on her thesis entitled “Metabolomics Analysis on Antifungal Activities Produced by *Penicillium oxalicum* T3.3 Grown On Different types of Carbon Sources” in accordance with the Universities and University Colleges Act 1971 and the Constitution of the Universiti Putra Malaysia [P.U.(A) 106] 15 March 1998. The Committee recommends that the student be awarded the Master of Science.

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## LIST OF ABBREVIATIONS

NMR	Nuclear magnetic resonance
GC-MS	Gas chromatography-mass spectrometry
LC-MS	Liquid chromatography-mass spectrometry
FTIR	Fourier transform infrared spectroscopy
<sup>1</sup> H-NMR	Proton nuclear magnetic resonance
MIC	Minimum inhibition concentration
MFC	Minimum fungicidal concentration
spp.	Species
pH	Potential of hydrogen
DNA	Deoxyribonucleic acid
α	Alpha
β	Beta
mRNA	Messenger RNA
TLC	Thin layer chromatography
GS	Gas chromatography
MS	Mass spectrometry
<sup>1</sup> H	Hydrogen-1
<sup>13</sup> C	Carbon-13
<sup>19</sup> F	Fluorine-19
<sup>31</sup> P	Phosphorus-31
1D	One-dimensional
2D	Two-dimensional
COSY	Correlation spectroscopy
HMBC	Heteronuclear multiple bond correlation
NOESY	Nuclear overhauser effect spectroscopy
R&D	Research and development

PCA	Principal components analysis
PC	Principal components
PLS-DA	Partial least squares-discriminant analysis
OPLS-DA	Orthogonal projection to latent structures-discriminant analysis
DCW	Dry cell weight
FF microplates	Filamentous fungi microplates
nm	Nanometer
rpm	Rotation per minute
min	Minute
µg	Microgram
PIRG	Percent inhibition of radial growth
µl	Microliter
TMS	Tetramethylsilane
Hz	Hertz
ppm	Parts per million
δ	Chemical shift
PDB	Potato dextrose broth
MEB	Malt extract broth
par	Pareto
YMDB	Yeast metabolome database

# CHAPTER 1

## INTRODUCTION

### 1.1 General Background

In Malaysia, the first report on the occurrence of anthracnose disease in dragon fruit (*Hylocereus* spp.) caused by *Colletotrichum gloeosporioides* was reported by Masyahit *et al.* (2009). The infected stem and fruit had reddish-brown lesions or black spots symptoms where it can expand and merge to cover the whole affected area. At present, the great potential health benefit (Ching and Yusof, 2005), physico-chemical characteristics (Chuah *et al.*, 2008) and nutritional value (Rebecca *et al.*, 2008; Ariffin *et al.*, 2009) of dragon fruit had been a great interest among the researchers, however the exploitation of natural organism as biological control and the potentialities of these microorganisms in production of bioactive metabolites and bio-control agents in controlling the pathogenic fungi has not receive any further investigations yet.

*Colletotrichum gloeosporioides*, known as one of the world's most plant pathogenic fungi can cause a serious damage to most parts of plants including stems, fruits, roots, leaves, and flowers but are often highly specific to individual tissues (Bailey *et al.*, 1992). This pathogenic fungus attacked an extremely wide range of plants growing in both temperate and tropical environments. In Korea, *C. gloeosporioides* had been identified as the cause of anthracnose disease that attack tulip trees as the necrotic lesions became black as the spots expanded on the leaves of that trees (Choi *et al.*, 2012). The first report of anthracnose of *Pisonia alba*, commonly called lettuce tree was reported in India described the *C. gloeosporioides* as the fungus that produced white mycelia, which became dark grey with later formation of numerous salmon pink colored spore masses (Vidyalakshmi and Divya, 2013).

There is no agreement on which media are the optimal for metabolite production. However, according to Mathan *et al.* (2013), the growth media and incubation conditions have a very great influence on secondary metabolites production. The ability of microorganisms to produce their metabolites would depend on their ability to modulate their metabolic composition according to their environment. By understanding the metabolites produced, researchers are able to study the unique cellular process of certain microorganisms which may be influence by physiological and also environmental signals (Jensen *et al.*, 2006). Fingerprinting these chemical constituents that present in the microorganism may helps to further understand the microorganism antibiotic pathway. Some of the physical and chemical parameters like pH, temperature, carbon and nitrogen sources play a major role on fungal growth and production of bioactive compounds and antimicrobial agents (Gunasekaran and Poorniammal, 2008; Mathan *et al.*, 2013). The availability and type of carbon and nitrogen source give effect on polyketide production whereby carbon source such as

glucose and sucrose have been found to increase the fungal growth and sporulation along with the high aflatoxin production (Keller *et al.*, 2002).

Metabolomics can be described as a comprehensive quantitative and qualitative analysis of holistic metabolites present in a biological organism, which are the end-products of its gene expression (Van der kooy *et al.*, 2009). Microbial metabolomic, focus on the low molecular mass metabolites which would indicate certain specific regulator or pathway mechanisms (Azizan *et al.*, 2012). Microbial profiling of extracellular metabolites had proved to give a better idea on the overall metabolites produced by the microorganisms compared to the used of intracellular metabolites (Kamenik *et al.*, 2010). Major benefit of profiling extracellular metabolites obtained from the fermentation broth, was the ability to determine the present of overall chemical properties that was produced during the fermentation process (Azizan *et al.*, 2012).

With the new development of tools for metabolomics study, it has allowed researchers to analyze broad range of metabolites (Fatma *et al.*, 2012). There are many tools that can be used to analyze large number of metabolites simultaneously such as nuclear magnetic resonance (NMR), gas chromatography-mass spectrometry (GC-MS), liquid chromatography-mass spectrometry (LC-MS) and Fourier transform infrared spectroscopy (FTIR). Some of them rely on chromatographic separation step and others do not require any in which represent a global view of the sample (Ulrich-Merzenich *et al.*, 2007). Among these tools, NMR method is able to provide a wide range of many molecular classes including sugars, amino acids, organic acids, alcohols or polyols, amine and ketones (Wishart, 2008) and allowed the detection of metabolites either from biofluid, tissue, whole organisms or even cell extract (Fernie *et al.*, 2004). For NMR analysis, <sup>1</sup>H-NMR has been the most frequently used tool for the metabolomics study due to the highly reproducible method, rapid and robust of the technique (Kim *et al.*, 2010; Ward *et al.*, 2010).

In this study, the endophytic *P. oxalicum* T3.3 was subjected to fermentation and the impact of medium composition (specifically by using different carbon sources) was valued by using disc diffusion test, minimum inhibition concentration (MIC) and minimum fungicidal concentration (MFC) against the pathogenic fungi, *C. gloeosporioides*. Metabolomics study was performed to determine the metabolites responsible for the antifungal production. It is hypothesized that metabolites produced were an extracellular compounds and these compounds inhibited the growth of *C. gloeosporioides* through the mode of antibiosis.

## 1.2 Objectives

The specific objectives of this study were:

- 1) Screening of fermentation media for optimum growth and carbon sources for antifungal activity.
- 2) To evaluate the antifungal activities produced by *P. oxalicum* T3.3 against *C. gloeosporioides* by using different types of carbon sources in selected fermentation medium.
- 3) To identify the possible metabolites produced by the strain T3.3 through metabolomics approach.



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