UNIVERSITI TEKNOLOGI MARA

INVESTIGATION OF THE SECONDARY METABOLOME OF FUNGI FROM SVALBARD ISLAND

(MICROBIAL BIODIVERSITY IN SVALBARD ISLAND)

NURUL FATEEHA BINTI AHMAD

Dissertation submitted in partial fulfillment of the requirements for

Bachelor of Pharmacy (Hons.)

FACULTY OF PHARMACY

ACKNOWLEDGEMENT

First of all, I would like to thank Allah for giving me strength and patience to complete this final year project.

I would like to express my deepest appreciation and gratitude to my supervisor Prof Dr Jean Frederic Faizal Weber and Dr Nurhuda Manshoor for their ideas, guidance as well as support throughout this project.

Special thanks to post-graduates students, Miss Fatimah Bebe and Mrs Hajar for their help and support during laboratory process. All their advices are highly appreciated.

I also want to thank my parents as well as friends who give me support and motivation to complete this project.

Finally, I would like to express my appreciation to all people who were directly and directly involved all the way long in my process to complete the project.

Thank you.

TABLE OF CONTENT

TITTLE PAGE	PAGE
ACKNOWLEDGEMENT	ii
TABLE OF CONTENTS	iii
LIST OF TABLES	v
LIST OF FIGURES	vi
LIST OF ABBREVIATIONS	vii
ABSTRACT	viii
CHAPTER ONE (INTRODUCTION)	
1.1 Background of study	1
1.2 Problem statement	2
1.3 Research question	3
1.4 Objective	3
1.4 Hypothesis	3
CHAPTER TWO (LITERATURE REVIEW)	
2.1 Background	4
2.2 Fungi species	5
2.2.1 Asco- and Basidiomycetes	5
2.2.2 Lichens and lichenicolus fungi	6
2.2.3 Endopyhtic fungi	6
2.2.4 Phytopathogenic fungi	7
2.3 Bacterial species	7
2.4 Cyanobacteria species	8
2.5 Archaea species	8

ABSTRACT

Eight fungi which are E1PB, E10PB, E1LB, E1SB, E4SB, E5PB, E5PC and E6PA were isolated from a various parts of plants originated from Svalbard Island. In this study, investigation was carried out to obtain chemical profile for each of the fungi using HPLC analysis. All the fungi were cultured according to in-house protocols which are culture at microscale in 12 selected media consist of minerals and epigenetic elicitors and incubated in two different incubation times which were for three weeks and five weeks. Their cultures were then extracted and the extracts were subjected to HPLC for determination of their secondary metabolite profiles. All the fungi show significant chromatograms and each peak indicates the presence and concentration of different compound of their secondary metabolites.

CHAPTER 1

INTRODUCTION

1.1 Background of study

The term biodiversity is related to the variability among living organisms, number of species that exists, or species richness, along with the variability of activity each species undergoes during its existence through events in the life of its members in all sources of ecosystem (Colwell, 1997). In biodiversity, all types of ecosystems can be included, whether managed or unmanaged. Examples of unmanaged ecosystems are wild lands, nature reserves, or national parks, while examples of managed systems are plantations, farms, croplands, aquaculture sites and urban parks. All ecosystems have their own biodiversity.

Microorganisms which comprise of prokaryotes, viruses, filamentous fungi, yeast, microalgae, cyanobacteria and protozoans represent the biggest percentage in numbers of organisms on earth. New species of organisms evolved through their genomes with their environment giving rise to great microbial diversity and altered ecosystem functions (Indu Shekhar, 2006). Darwinian Principles state that mutations, genetic recombinant and natural selection all played roles in the evolution of microbial species. The bio-diversification of microorganisms has occurred over 3.85 billion years compared to only 600 million years for macroorganisms.