ACKNOWLEDGEMENT

First and foremost, I want to thank GOD for allowing me to complete this thesis and for being by my side every step of the way.

I wish to express my sincere appreciation and heartfelt gratitude to my supervisor, Dr Geok Yuan Annie Tan for the guidance and supervision, assistance in directing this project, patiently enduring and improving all the drafts. Also the continuous interest and encouragement given throughout the course of this study and effort in getting me a comfortable lab to work in.

My special 'thank you' is also extended to Prof. Dr. S. Vikineswary for providing the fungal samples. I would also wish to extend my gratitude to all my labmates, Aaron, Lim Chew Theng, Lim Mei Sim and Shing Yi as well as En Hafiz and all staffs and students at Microbiology Department for their advice, assistance and guidance in doing the lab work.

Many thanks also go to my family, especially my parents, for teaching me how to love and respect my work and also for being there when I needed them most. Not to forget, thanks to all my friends, especially Imanina and Hanim.

Finally, my deepest and warmest gratitude is owed to all those who have helped me in many ways.

May happiness be a crown your wear for all days.

GOD BLESS

ii

ABSTRACT

Actinobacteria are well known for their production of an extensive array of chemically diverse and medically important secondary metabolites. Fifty two strains of actinobacteria used in this study were divided into 20 colour groups based on their aerial and substrate mycelium colour as well as diffusible pigment production on Yeast Extract Malt Extract (ISP) medium. Antifungal activity was determined against Candida albicans, Candida parapsilosis, Fusarium oxysporum, Ganoderma boninense, Schizosaccharomyces pombe and Saccharomyces cerevisiae by the agar plug-diffusion method. Ten of the fifty two actinobacterial strains showed strong antifungal activity. Two strains (MA04119 and RHRS) were active against S. pombe, four strains (9, A21, OPSa and RC3) against S. cerevisiae, two strains (OPSa and A21) against C. albicans, one strain (MA04020) against C. parapsilosis, one strain (H23) against F. oxysporum and two strains (9 and PDA4) against G. boninense. The identification of actinobacterial strains were done by using molecular approaches including enterobacterial repetitive intergenic consensus (ERIC)-PCR and 16S rRNA gene sequencing. By using the (ERIC)-PCR fingerprinting technique, all the tested strains have been de-replicated into three groups. The ten actinobacterial strains which showed antifungal activity were also screened for the presence of polyene-specific CYP genes and only four of them (strains H23, RC3, MA04020, and RHRS) showed the presence of the expected 350bp DNA fragment of the polyene CYP internal region. This suggests that these four strains might produce the cryptic polyene biosynthetic compound. 16S rRNA gene sequence analysis showed that nine of the strains, (H23, RHRS, MA04119, MA04020, OPSa, RC3, PDA4, A12 and OPSa) belong to the genus Streptomyces, while strain 9 was identified to be a Brevibacterium sp.

ABSTRAK

Aktinobakteria berkeupayaan untuk menghasilkan metabolit sekunder yang pelbagai dan mempunyai keupayaan dari segi perubatan. Lima puluh dua strain aktinobakteria yang dikaji dalam eksperimen ini telah dikategorikan kepada 20 kumpulan, berdasarkan warna miselium dan penghasilan pigmen pada media Yeast Extract Malt Extract (ISP). Aktiviti antikulat telah dikenalpasti ke atas Candida albicans, Candida parapsilosis, Fusarium oxysporum, Ganoderma boninense, Schizosaccharomyces pombe and Saccharomyces cerevisiae dengan menggunakan kaedah penyerapan agar. Daripada lima puluh dua strain yang dikaji ini, sepuluh daripadanya telah menunjukkan aktiviti antikulat yang kuat. Dua strain (MA04119 dan RHRS) adalah aktif ke atas S. pombe, empat strain (9, A21, OPSa dan RC3) ke atas S. cerevisiae, dua strain (OPSa dan RHRS) ke atas C. albicans, satu strain (MA04020) ke atas C. parapsilosis, satu strain (H23) ke atas F. oxysporum dan dua strain (9 dan PDA4) ke atas G. boninense. Pengenalpastian strain aktinobakteria telah dilakukan dengan menggunakan teknik molekul termasuk enterobacterial repetitive intergenic consensus (ERIC)-PCR dan amplifikasi PCR ke atas gen 16S rRNA. Melalui teknik amplifikasi (ERIC)-PCR, semua strain actinobacteria yang diuji telah direplikasikan kepada tiga kumpulan. Kehadiran gen CYP yang spesifik kepada polyene turut dikaji ke atas sepuluh strain tersebut. Daripada strain-strain tersebut, empat daripadanya (strain H23, RC3, MA04020, dan RHRS) menunjukkan kehadiran fragmen DNA bersaiz 350 pasang bes seperti yang dijangka. Ini menunjukkan bahawa keempat-empat strain tersebut kemungkinan menghasilkan sebatian biosintetik polyene. Analisis turutan gen 16S rRNA menunjukkan bahawa sembilan strain (H23, RHRS, MA04119, MA04020, OPSa, RC3, PDA4, A12 dan OPSa) tergolong dalam genus Streptomyces, manakala strain 9 dikenalipasti sebagai Bevibacterium sp.

TABLE OF CONTENTS

| ACKNOWI | LEDGEMENT | ii |
|---------------------------------------|--|------|
| ABSTRACT | ſ | iii |
| ABSTRAK | | iv |
| TABLE OF | CONTENTS | V |
| LIST OF AI | BBREVIATIONS | vii |
| LIST OF TA | ABLES | viii |
| LIST OF FIGURES | | ix |
| LIST OF APPENDIX | | xi |
| | | |
| CHAPTER | ONE : INTRODUCTION | 1 |
| 1.1 | Objectives of research | 4 |
| | | |
| CHAPTER | TWO : LITERATURE REVIEW | 5 |
| 2.1 | General characteristics of Actinobacteria | 5 |
| 2.2 | Habitats of Actinobacteria | 12 |
| 2.3 | Fungal infections | 17 |
| | 2.3.1 Fungal infections of humans | 17 |
| | 2.3.2 Fungal infections of plants | 22 |
| 2.4 | Antifungal activity of Actinobacteria | 25 |
| 2.5 | Molecular characterization of Actinobacteria | 33 |
| | | |
| CHAPTER THREE : MATERIALS AND METHODS | | |
| 3.1 | Sources and storage of the strains | 37 |

| 3.2 | Charae | cterization and KOH String Test | 37 |
|-----------|------------------|---|----|
| 3.3 | Antifungal assay | | 39 |
| 3.4 | Molec | ular studies | 40 |
| | 3.4.1 | DNA extraction | 40 |
| | 3.4.2 | Polyene CYP-specific fragment PCR amplification | 40 |
| | 3.4.3 | ERIC PCR | 42 |
| | 3.4.4 | Partial 16S rRNA gene analysis | 43 |
| | 3.4.5 | Purification and partial sequencing of 16S rRNA gene | 44 |
| | 3.4.6 | Sequence analysis | 44 |
| | | | |
| CHAPTER F | FOUR | : RESULTS AND DISCUSSION | 45 |
| 4.1 | Morph | nology and cultural characteristics of actinobacteria | 45 |
| 4.2 | Antifu | ingal assay | 54 |
| | 4.2.1 | Antiyeast assay | 54 |
| | 4.2.2 | Antagonistic activities against filamentous fungi | 55 |
| 4.3 | Molec | ular characterization | 64 |
| | 4.3.1 | DNA extraction | 64 |
| | 4.3.2 | Polyene CYP-specific fragment PCR amplification | 65 |
| | 4.3.3 | ERIC PCR | 70 |
| | 4.3.4 | Amplification of 16S rRNA gene | 74 |
| | 4.3.5 | Partial 16S rRNA gene analysis | 75 |
| | | | |
| CHAPTER F | FIVE | : CONCLUSION | 86 |
| CHAPTER S | SIX | : REFERENCES | 89 |

CHAPTER SEVEN : APPENDIX

vi

110

List of abbreviations

| % | percentage |
|--------------------|------------------------------------|
| sp. | species |
| et al. | et alia (~and others) |
| μm | micrometer |
| mm | millimeter |
| rRNA | Ribosomal Ribonucleic Acid |
| PCR | Polymerase Chain Reaction |
| bp | base pair |
| NaHCO ₃ | Sodium bicarbonate |
| EDTA | Ethylene diaminetetraacetic acid |
| μl | microliter |
| TBE | Tris/Borate/EDTA |
| UV | Ultraviolet |
| dNTPs | Deoxyribonucleotide triphosphate |
| ISP | International Streptomyces Project |
| rpm | revolutions per minute |
| w/v | weight per volume |
| mM | millimolar |
| °C | degree Celcius |
| ml | milliliter |
| μg | microgram |
| MgCl ₂ | Magnesium chloride |
| v/v | volume per volume |
| V | Voltan |

List of tables

| Table | Description | Page No. |
|-----------|--|----------|
| Table 2.1 | Cell wall chemotypes with representative families | 7 |
| Table 3.1 | Reaction micture for Polyene CYP-specific Fragment | 41 |
| | PCR Amplification | |
| Table 3.2 | Reaction miture for ERIC-PCR | 42 |
| Table 3.3 | Reaction mixture for Partial 16S rRNA Gene Analysis | 43 |
| Table 4.1 | Characterization of strains based on aerial and substrate | 46 |
| | mycelia colour and diffusible pigment on ISP2 media | |
| Table 4.2 | Antifungal activity of the actinobacterial strains, grown in | 54 |
| | ISP2 media after ten days, against S. pombe, S. cerevisiae, | |
| | C. albicans and C. parapsilosis | |
| Table 4.3 | Actinobacterial strains showing antifungal activity against | 56 |
| | F. oxysporum and G. boninense | |
| Table 4.5 | Closest matches from the GenBank using BLAST | 76 |

List of figures

| Figure | Description | Page No. |
|------------|---|----------|
| Figure 4.1 | Colony morphology of selected actinobacterial strains | 48 |
| | grown on ISP2 at 28°C for ten days | |
| Figure 4.2 | Gram stain of selected actinobacteria showing CM3, | 49 |
| | MA04020, H23 and OPSa strains. All strains were | |
| | observed under 100X magnification with a light | |
| | microscope | |
| Figure 4.3 | Spore chain morphology of actinobacterial strains on | 50 |
| | coverslip. All strains were observed under 100X | |
| | magnification with a light microscope | |
| Figure 4.4 | Inhibition of yeast (a-d) and filamentous fungi (e and f) | 57 |
| | by actinobacterial strains | |
| Figure 4.5 | DNA isolated from selected actinobacterial strains; lane | 65 |
| | 1, 100bp ladder; lane 2, negative control; lane 3, strain | |
| | H23; lane 4, strain A21; lane 5, strain MA04119; lane 6, | |
| | strain 9; lane 7, strain MA04020; lane 8, strain RHRS; | |
| | lane 9, strain PDA4; lane 10, strain A12; lane 11, strain | |
| | RC3; lane 12, strain OPSa | |
| Figure 4.6 | Polyene CYP specific fragment amplified from selected | 66 |
| | actinobacterial strains; lane 1, strain H23; lane 2, strain | |
| | RC3; lane 3, strain MA04020; lane 4, strain MA04119; | |
| | lane 5, strain 9; lane 6, strain 9; lane 7, strain RHRS; | |
| | lane 8, strain A21; lane 9, strain OPSa; lane 10, strain | |
| | OPSa; lane 11, strain A12; lane 12, strain A12; lane 13, | |
| | strain PDA4; lane 14, 100bp DNA ladder | |

Figure Description

71

74

- Figure 4.7 ERIC-PCR fingerprinting patterns of selected actinobacterial strains; lane 1, strain RHRS; lane 2, strain MA04020; lane 3, strain RC3; lane 4, strain PDA4; lane 5, strain A12; lane 6, strain OPSa; lane 7, strain H23; lane 8, strain MA04119; lane 9, strain 9; lane 10, strain A21; lane 11, negative control; lane 12, 100bp DNA ladder
- Figure 4.8 Partial 16S rRNA gene fragment amplified from selected actinobacterial strains; lane 1, negative control; lane 2, strain 9; lane 3, strain H23; lane 4, strain RHRS; lane 5, strain MA04119; lane 6, strain MA04020; lane 7, strain OPSa; lane 8, strain RC3; lane 9, strain PDA4; lane 10, strain A12; lane 11, strain A21; lane 12, 100bp DNA ladder
- Figure 4.9 Neighbour-joining phylogenetic tree showing 76 relationship between the tested actinobacterial strains and closely related validly described *Streptomyces* spp. and *Brevibacterium linens*

Х

List of appendix

| Appendix | Description | Page No. |
|------------|---------------------|----------|
| Figure 7.1 | Media Preparation | 110 |
| Figure 7.2 | Source of Isolation | 111 |
| Figure 7.3 | Antifungal Activity | 112 |
| Figure 7.4 | Strain Sequence | 113 |