



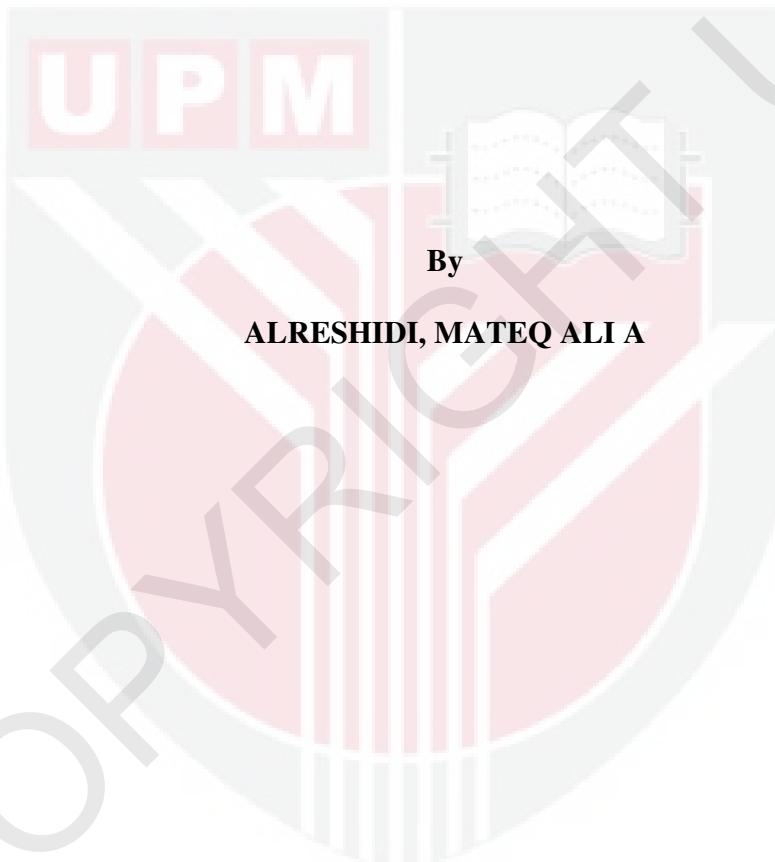
UNIVERSITI PUTRA MALAYSIA

**ELUCIDATION OF GENETIC DIVERSITY IN METHICILLIN-RESISTANT
Staphylococcus aureus ISOLATED FROM CANCER
AND NON-CANCER PATIENTS IN MALAYSIA AND SAUDI ARABIA**

ALRESHIDI, MATEQ ALI A

FPSK(p) 2013 1

**ELUCIDATION OF GENETIC DIVERSITY IN METHICILLIN-RESISTANT
Staphylococcus aureus ISOLATED FROM CANCER
AND NON-CANCER PATIENTS IN MALAYSIA AND SAUDI ARABIA**



**Thesis Submitted to the School of Graduate Studies, Universiti Putra Malaysia, in
Fulfilment of the Requirements for the Degree of Doctor of Philosophy**

February 2013



Abstract of thesis presented to the senate of Universiti Putra Malaysia in fulfilment of the requirements of the degree of Doctor of Philosophy

**ELUCIDATION OF GENETIC DIVERSITY IN METHICILLIN-RESISTANT
Staphylococcus aureus ISOLATED FROM CANCER
AND NON-CANCER PATIENTS IN MALAYSIA AND SAUDI ARABIA**

By

ALRESHIDI, MATEQ ALI A

February 2013

Chairman: Professor Mariana Nor Shamsudin, PhD

Faculty: Medicine and Health Sciences

Methicillin-resistant *Staphylococcus aureus* (MRSA) is a versatile pathogen capable of causing a wide range of human diseases and became a leading cause of nosocomial infections worldwide. Cancer patients are unique cohort with multiple risk factors for MRSA infection. Since a little is known about the characteristics of MRSA strains among the hospitalized cancer patients in Malaysia and Saudi Arabia, it is important to elucidate the phenotypic and genotypic characteristics of local MRSA clones for the efficient management of infection in cancer patients. In the current study, a total of 240 non-consecutive MRSA isolates were obtained from cancer and non-cancer patients in Malaysia and Saudi Arabia (60 each). The majority of MRSA isolates were multiresistant to more than four classes of antibiotics. Five and three antibiotic susceptibility profiles were observed among the MRSA isolates from cancer and non-cancer patients in

Malaysia. For the isolates from Saudi Arabia, five and 14 antibiotic susceptibility profiles were observed among the MRSA isolates from cancer and non-cancer patients, respectively. Three isolates were vancomycin-intermediate (VISA) however, all of them were susceptible to daptomycin. Although there was no statistical significance between the susceptibility of isolates from cancer and non-cancer patients, the high level of multiple drug resistance among MRSA isolated from cancer patients in both countries was observed. In addition, the susceptibility of all MRSA isolates against three antiseptics agents; benzalkonium chloride (BAC), benzethonium chloride (BZT) and chlorhexidine digluconate (CHG) were determined. All isolates were susceptible to all tested antiseptics with MIC ranging from 0.5-2 µg/ml. Antiseptic resistance gene *qacA/B* was detected in 98.3% and 83.3% of the isolates from cancer and non-cancer in Malaysia respectively. For the isolates from Saudi Arabia, *qacA/B* was detected in 46% and 35% from cancer and non-cancer, respectively. *Smr* gene was detected in one isolate each from cancer and non-cancer patients in Malaysia. The carriage of *qacA/B* highly correlated with reduced susceptibility to CHG and BAC.

Spa typing revealed four different *spa* types in the isolates from Malaysia. Eleven and 25 *spa* types were detected among isolates from cancer and non-cancer patients in Saudi Arabia, respectively including four new *spa* types identified in this study. All isolates from Malaysia belonged to ST239 whereas six and nine STs were detected among isolates from cancer and non-cancer patients in Saudi Arabia, respectively. Three *agr* types were detected in this study; the majority of MRSA isolates belonged to *agr* I. *Agr* III was detected in 25 and 17 isolates from cancer and non-cancer patients, respectively,

whereas *agr* II was detected in five isolates from non-cancer patients in Saudi Arabia. No *agr* type IV was detected in this study. Virulence genes profiling showed that all strains were commonly positive for adhesion genes except *ebps* and *bbp* genes which were not detected in any isolate. Although the presence of adhesion genes slightly varied among MRSA isolates from cancer and non-cancer patients, these variations were not found to be statistically significant. In contrast, the presence of toxin genes *seb*, *sec*, *seg* and *sei* was found to be significant between cancer and non-cancer patients, these significances were not consistent between isolates from cancer and non-cancer in both countries.

Relative quantitative real-time reverse transcriptase polymerase chain reaction (qPCR) assay was designed and applied in order to study the expression levels of selected genes encoding the adherence and toxins virulent factors. Relative quantification qPCR showed a significant higher expression level of common genes tested among strains isolated from cancer patients not only within the clone but also among different lineages.

In conclusion, this study demonstrated that although all MRSA strains studied from cancer and non-cancer patients possessed several virulence determinants, the isolates from cancer patients were more multiresistance to antibiotics with low susceptibility towards antiseptic agents and the expression rather than carriage of virulence determinants may mediate higher pathogenicity potential. These data will aid in developing more effective infection control strategy to improve the management of MRSA infection in cancer patients.

Abstrak tesis yang dikemukakan kepada Senat Universiti Putra Malaysia sebagai memenuhi keperluan untuk ijazah Doktor Falsafah

**PERUNGKAIAN KEPELBAGAIAN GENETIC *Staphylococcus aureus*
TAHAN METHICILLIN YANG DIPENCILKAN DI KALANGAN
PESAKIT-PESAKIT KANSER DARI MALAYSIA DAN ARAB
SAUDI**

Oleh

ALRESHIDI, MATEQ ALI A

Februari 2013

Pengerusi: Profesor Mariana Nor Shamsudin, PhD

Fakulti: Perubatan dan Sains Kesihatan

Staphylococcus aureus tahan methicillin (MRSA) merupakan satu patogen serba boleh yang mampu menyebabkan pelbagai penyakit di kalangan manusia dan menjadi punca utama jangkitan nosokomial di seluruh dunia. Pesakit kanser adalah satu kohort yang unik dan mempunyai pelbagai faktor-faktor risiko bagi jangkitan MRSA. Oleh kerana sedikit sahaja yang diketahui tentang ciri-ciri strain MRSA di kalangan pesakit-pesakit kanser di Malaysia dan Arab Saudi, satu kajian perlu dijalankan bagi menjelaskan ciri-ciri fenotip dan genotip MRSA klon-klon tempatan supaya pengurusan jangkitan MRSA pada pesakit kanser dapat dibuat dengan lebih berkesan. Di dalam kajian ini, sejumlah 240 pencilan MRSA telah diperolehi secara tidak berturutan daripada pesakit-pesakit kanser dan bukan kanser dari Malaysia dan Arab Saudi (60 setiap satu). Majoriti pencilan

MRSA adalah multiresistan terhadap lebih daripada empat kelas antibiotik. Lima dan tiga profil kerentanan antibiotik telah diperhatikan di kalangan pencilan MRSA daripada pesakit-pesakit kanser dan bukan kanser di Malaysia. Bagi pencilan dari Arab Saudi, masing-masing lima dan 14 profil kerentanan antibiotik telah diperhatikan di antara strain MRSA daripada pesakit-pesakit kanser dan bukan kanser. Tiga pencilan menunjukkan rintangan-pertengahan terhadap vancomycin (VISA), walau bagaimanapun, kesemua mereka adalah rentan terhadap daptomycin. Walaupun secara statistiknya tidak ada sebarang perbezaan terhadap kerentanan pencilan MRSA di antara pesakit kanser dan bukan kanser, tahap kerintangan yang tinggi terhadap pelbagai-bagai jenis antimikrob telah diperhatikan di kalangan pencilan MRSA dari kedua-dua buah negara.

Di samping itu, kerentanan pencilan MRSA terhadap tiga ejen antiseptik; benzalkonium klorida (BAC), klorida benzethonium (BZT) dan chlorhexidine digluconate (CHG) telah dapat ditentukan. Semua pencilan adalah rentan kepada semua antiseptik yang diuji dengan MIC antara 0,5-2 μ g / ml. Gen rintangan antiseptik qacA/B telah dikesan sebanyak 98.3% dan 83.3% pencilan masing-masing daripada pesakit-pesakit kanser dan bukan kanser di Malaysia. Bagi pencilan dari Arab Saudi, gen qacA/B telah dikesan, masing-masing sebanyak 46% dan 35% daripada pesakit-pesakit kanser dan bukan kanser. Pembawaan qacA/B adalah sangat berkait rapat dengan pengurangan tahap kerentanan terhadap CHG dan BAC.

Pengetian spa telah dapat mengasingkan empat jenis spa yang berlainan daripada pencilan dari Malaysia. Sebelas dan 25 jenis spa telah juga dikesan masing-masing di kalangan pesakit-pesakit kanser dan bukan kanser di Arab Saudi, termasuk juga empat

spa jenis baharu yang dikenal pasti di dalam kajian ini. Semua pencilan dari Malaysia tergolong di dalam ST239 manakala enam dan sembilan jenis STs telah dikesan masing-masing di kalangan pesakit-pesakit kanser dan bukan kanser di Arab Saudi. Tiga jenis kumpulan agr telah juga dapat dikesan di dalam kajian ini; secara majoritinya pencilan MRSA tergolong di dalam jenis kumpulan agr I. Jenis kumpulan agr III telah dikesan masing-masing sebanyak 25 dan 17 pencilan daripada pesakit-pesakit kanser dan bukan kanser, manakala kumpulan agr II telah dikesan pada lima pencilan daripada pesakit-pesakit bukan kanser dari Arab Saudi. Tiada jenis kumpulan agr IV dikesan di dalam kajian ini. Profil kevirulenan gen menunjukkan bahawa kesemua pencilan mempunyai gen-gen lekatan kecuali gen ebps dan bbp. Walaupun penemuan gen lekatan berbeza sedikit di dalam pencilan MRSA di kalangan pesakit-pesakit kanser dan bukan kanser, perbezaan ini adalah tidak signifikan secara statistiknya. Berbeza sekali, penemuan gen-gen toxin seb, sec, seg dan sei di antara pesakit-pesakit kanser dan bukan kanser adalah signifikan tetapi signifikasi tersebut tidak konsisten di antara pencilan-pencilan daripada pesakit kanser dan bukan kanser dari kedua-dua buah negara.

Relatif kuantitatif tindakbalas bersilang real-time (qPCR) asai telah direka dan digunakan untuk mengkaji tahap ekspresi gen-gen pengkodan yang dipilih seperti gen pelekatan dan toksin. Relatif kuantifikasi qPCR telah menunjukkan terdapat signifikasi tentang tahap ekspresi gen yang tinggi di kalangan strain-strain yang diperolehi daripada pesakit kanser bukan sahaja didapati di dalam klon tunggal tetapi juga di kalangan garis keturunan yang berbeza.

Kesimpulannya, kajian ini menunjukkan bahawa walaupun kesemua strain MRSA dikaji daripada pesakit kanser dan bukan kanser mempunyai beberapa penentu kevirulenan dengan latar belakang molekul yang sama, penciran daripada pesakit kanser mempunyai lebih multi kerintangan terhadap antibiotik dan berkecenderungan mempunyai kerentanan yang rendah terhadap agen antiseptik dan ekpresi gen bukannya pembawaan penentu kevirulenan yang berkemungkinan menyebabkan potensi kepatogenan yang lebih tinggi. Data-data ini dijangka dapat membantu di dalam merangka strategi kawalan jangkitan yang lebih berkesan bagi memperbaiki mutu pengurusan jangkitan MRSA pada pesakit-pesakit kanser.

ACKNOWLEDGEMENTS

Praise to **Allah** (Subhanahu wataala) as with his grace this study has been completed. Then, I would like to express my sincere thanks and heartfelt gratitude to the following peoples that has supported and help me to complete this study:

First of all, I am deeply grateful to my supervisor, Prof. Dr. Mariana Nor Shamsudin for giving me the great opportunity to join the Ph.D. program under her supervision, and for her outstanding guidance and dedication throughout the years of my Ph.D. study. Her open door policy and generosity in sharing knowledge is exemplary.

I would also like to express my deepest thanks and admiration to my Co-supervisors, Prof. Dr Ali Al salamah, Dr. Rukman Awang Hamat and Dr. VasanthaKumari Neela, who helped me from beginning to end without saying NO any single time. I am grateful for their positive approach and professional guidance over the five years with highest standard.

I would also like to acknowledge, Ministry of Higher Education, Saudi Cultural Mission for their financial support with a full scholarship from Government of Saudi Arabia.

Special thank to Mr. Hassan Al-Arossy, my academic advisor at Saudi Cultural Mission for his cooperative and contentious support during my study.

Special and personal thank to nice Juta-Park members Ahmad, Fahad, Mohammad, Abdullah, Abdul Aziz Alsharari. We spent together very nice years with non-forgotten stories.

My sincere thank to all members of the departments of clinical microbiology at Hospital Kuala Lumpur and Armed Forced Hospital for their help during the collection of samples used in this study.

I also want to take this opportunity to dedicate my appreciation to Mr. Yousef , Mr. Zinan Miss Hazliza and Miss Fara for giving me a helping hand whenever I needed it and for answering my questions regarding work-routines and such with great patience. In addition, I thank all all the former and current members of Medical Microbiology Laboratory for their kind support throughout my study and shared so many good times with me. I am extremely grateful for their ideas and efforts.

I also address my thanks to my beloved family in Motherland Saudi Arabia for their encouragements throughout my education life and continuously asked about the progress of my thesis. Finally, I express my deepest gratitude to my wife and children who kept the mood light and were both family and friends to me for their patience during my study. Their love, care and encouragement has given me a great inner strength to success.

Alreshidi Mateq Ali

Serdang, February 2013

This thesis submitted to the Senate of Universiti Putra Malaysia and has been accepted as fulfilment of the requirement for the degree of Doctor of Philosophy.
The members of the Supervisory Committee were as follows:

Mariana Nor Shamsudin, PhD

Professor

Faculty of Medicine and Health Sciences

Universiti Putra Malaysia

(Chairman)

Ali Abdullah Alsalamah, PhD

Professor

Faculty of Science

King Saud University

(Member)

Vasantha Kumari Neela, PhD

Associate Professor

Faculty of Medicine and Health Sciences

Universiti Putra Malaysia

(Member)

Rukman Awang Hamat, Medical Doctor

Lecturer Medicine

Faculty of Medicine and Health Sciences

Universiti Putra Malaysia

(Member)

BUJANG BIN KIM HUAT, PhD

Professor and Dean

School of Graduate Studies

Universiti Putra Malaysia

Date:

DECLARATION

I declare that the thesis is my original work except for quotations and citations which have been duly acknowledged. I also declare that it has not been previously or concurrently submitted for any other degree at Universiti Putra Malaysia or other institutions.

ARESHIDI MATEQ ALI A

Date: 15 February 2013



TABLE OF CONTENTS

	Page
DEDICATION	ii
ABSTRACT	iii
ABSTRAK	vi
ACKNOWLEDGEMENTS	x
APPROVAL	xii
DECLARATION	xiv
LIST OF TABLES	xix
LIST OF FIGURES	xxi
LIST OF ABBREVIATIONS	xxiv
CHAPTER	
1 INTRODUCTION	1
2 LITERATURE REVIEW	
2.1 The genus Staphylococcus	8
2.2 Morphological and Biochemical Characteristics	9
3.3 Emergence of MRSA	10
2.4 Genome	11
2.4.1 Core Genome	11
2.4.2 Accessory genome	12
2.5 Resistance of MRSA to Antimicrobial agents	14
2.5.1 Resistance to antibiotics	14
2.5.2 Resistance to antiseptics	16
2.6 Prevalence and rise of incidence of MRSA infection	18
2.7 Virulence factors of MRSA	20
2.7.1 Microbial Surface Components Recognizing Adhesive Matrix Molecules (MSCRAMMs)	21
2.7.2 Toxins	24
2.7.3 Accessory gene regulator (<i>agr</i>)	27
2.7.4 Biofilm associated proteins	28
2.8 Typing	29
2.8.1 SCCmec Typing	31
2.8.2 Multi-Locus Sequence Typing (MLST)	33
2.8.3 <i>Spa</i> Typing	35
2.9 Worldwide distribution of MRSA clones and status in Malaysia and Saudi Arabia	37

2.10	Gene Expression	40
	2.10.1 Quantitative real-time Polymerase Chain Reaction (qPCR)	40
2.11	MRSA and Cancer	45
3	MATERIALS AND METHOD	48
3.1	Bacterial isolates	48
3.2	Confirmation of isolates by conventional techniques	49
	3.2.1 Gram Stain	49
	3.2.2 Growth on Mannitol-salt Agar	50
	3.2.3 Catalase test	50
	3.2.4 Coagulase test	51
3.3	Antimicrobial susceptibility tests	51
	3.3.1 Disk diffusion test	51
	3.3.2 D-Zone test	53
	3.3.3 Minimum inhibitory concentration (MIC) test for vancomycin and daptomycin	54
3.4	Molecular identification of MRSA isolates	55
	3.4.1 DNA extraction	55
	3.4.2 DNA quality and quantity determination	56
	3.4.3 Detection of <i>mecA</i> and <i>pvl</i> genes gene	56
	3.4.4 Electrophoresis	57
3.5	Study I: Genotyping of MRSA	58
	3.5.1 SCC <i>mec</i> typing	58
	3.5.2 <i>Staphylococcus aureus</i> protein A (<i>spa</i>) typing	59
	3.5.3 Multi-Locus Sequence Typing (MLST)	62
	3.5.4 <i>Agr</i> typing	64
3.6	Study II: To investigate the virulence gene profiles of MRSA in cancer patients from Malaysia and Saudi Arabia	65
	3.6.1 Detection of adhesion (MSCRAMM) genes	65
	3.6.2 Detection of toxin genes	66
3.7	Study III: To determine the prevalence of antiseptic resistance genes and examine the efficacy of the selected antiseptic agents against MRSA	68
	3.7.1 Detection of antibiotic and antiseptic resistance genes	68
	3.7.2 Determination of MIC for antiseptic agents	69
3.8	Study IV: To establish a quantitative Real-Time PCR assay and investigate the quantitative gene expression in selected genes within strains isolated from cancer and non-cancer patients	70
	3.8.1 RNA extraction	70
	3.8.2 DNase treatment	71

3.8.3 Measurement of RNA concentration purity and integrity	71
3.8.4 cDNA Synthesis	72
3.8.5 Primer design	73
3.8.6 PCR efficiency	73
3.8.7 Determination of reference gene expression stability	73
3.8.8 Quantitative real-time Polymerase Chain Reaction (qPCR)	74
3.9 Statistical analysis	76
4 RESULTS	77
4.1 Description of samples and patient demographics	77
4.1.1 MRSA isolates from Malaysia	77
4.1.2 MRSA isolates from Saudi Arabia	78
4.2 Confirmation of isolates by conventional techniques	79
4.2.1 Culture media	79
4.2.2 Biochemical reaction	79
4.2.3 Oxacillin and Cefoxitin Susceptibility Test for MRSA Isolates by disc diffusion method	80
4.3 Antibiotic susceptibility test	81
4.3.1 Antibiotic resistance Profile	81
4.3.2 Detection of inducible clindamycin resistance (D-test)	84
4.3.3 Minimum inhibitory concentrations for vancomycin and daptomycin	87
4.4 Molecular identification of MRSA isolates	88
4.4.1 Total genomic DNA extraction	88
4.4.2 Detection of <i>mecA</i> and <i>pvl</i> genes	89
4.5 Study I: Genotyping of MRSA	90
4.5.1 SCC <i>mec</i> typing	90
4.5.2 <i>Spa</i> typing	92
4.5.3 Multi-locus sequence typing (MLST)	99
4.5.4 Determination of <i>agr</i> types	101
4.6 Study II: To investigate the virulence gene profiles of MRSA from two countries	103
4.6.1 Adhesion genes	103
4.6.2 Toxins genes	113
4.7 Association of virulence genes and clones	125
4.8 Study III: To determine the prevalence of antiseptic resistance genes and examine the efficacy of the selected antiseptic agents against MRSA isolates	128
4.8.1 Detection of antiseptic resistance <i>qacA/B</i> and <i>smr</i> genes	128
4.8.2 Minimum inhibitory concentrations for antiseptic agents	129

4.9 Study IV: To investigate the quantitative gene expression in selected genes among strains isolated from cancer and non-cancer patients	130
4.9.1 RNA concentration, purity and integrity	130
4.9.2 Validation of reaction specificity and efficiency	131
4.9.3 Identification of optimal reference genes	134
4.9.4 Relative expression of MRSA virulence genes by qRT-PCR	135
5 DISCUSSION	138
6 CONCLUSIONS	170
REFERENCES	175
APPENDICES	193
BIODATA OF STUDENT	207
LIST OF PUBLICATIONS	208