

**CHARACTERIZATION OF EXTENDED SPECTRUM β -LACTAMASE
(ESBL) FROM *Staphylococcus aureus* RECOVERED FROM SURGICAL
WOUND PATIENTS**

BY

OLUTOLA, OLUSAYO TITILOPE

(SCP11/12/H/1848)

**BEING A THESIS SUBMITTED TO THE DEPARTMENT OF
MICROBIOLOGY, FACULTY OF SCIENCE, OBAFEMI AWOLOWO
UNIVERSITY, ILE-IFE, OSUN STATE IN PARTIAL FULFILMENT OF
THE REQUIREMENTS FOR THE AWARD OF MASTER OF SCIENCE
(M.Sc.) DEGREE IN MICROBIOLOGY**

2015

AUTHORIZATION TO COPY
OBAFEMI AWOLOWO UNIVERSITY, ILE – IFE, NIGERIA
HEZEKIAH OLUWASANMI LIBRARY
POSTGRADUATE THESIS

AUTHOR: OLUTOLA, OLUSAYO TITILOPE

TITLE: CHARACTERIZATION OF EXTENDED SPECTRUM β -LACTAMASE (ESBL)
FROM *Staphylococcus aureus* RECOVERED FROM SURGICAL WOUND
PATIENTS

DEGREE: Master of Science (M. Sc.) Microbiology

YEAR: 2015

I, OLUTOLA, OLUSAYO TITILOPE hereby authorize the Hezekiah Oluwasanmi Library to copy my thesis in part or in whole in response to request from individual and/or organization for the purpose of private study or research.

.....

Signature

.....

Date

CERTIFICATION

This is to certify that this research work was carried out by OLUTOLA, Olusayo Titilope of the Department of Microbiology, Faculty of Science, Obafemi Awolowo University, Ile-Ife, Osun state.

.....
DR. (MRS.) N. TORIMIRO
(Project Supervisor)

.....
DR. D.A. AKINPELU
(Head of Department)

DEDICATION

I dedicate this work to the Almighty God, the incomparable and unquestionable God for dealing graciously and mercifully with me.

ACKNOWLEDGEMENTS

My unending appreciation goes to God Almighty for everything He hath done in my life and for the grace He has given to me to successfully complete this programme. Lord I say thank you.

I am forever indebted to my supervisor Dr. (Mrs.) Nkem Torimiro who granted me the opportunity to tap from the reservoir of her knowledge. You took time amidst tight schedules to read through this work and provided me with illuminating ideas. May you enjoy promotion and long life in good health in Jesus name, Amen.

I also appreciate the Head of Department, Dr. D. A. Akinpelu who was also my experimental supervisor and a father who is worth commending. Thanks also go to all members of staff of the Department of Microbiology for their support.

I also appreciate the cooperation of staff and patients in adult and children orthopaedic wards, Department of Microbiology and Parasitology, Haematology and General out-patient Department (GOPD), Obafemi Awolowo University Teaching Hospital Complex (OAUTHC) for providing the necessary assistance for this work.

Thanks to Drs. Agboola, Adewale and Okonji of the Department of Biochemistry who provided me with some materials and the privilege to work in the Department, all for the success of this work. May God Almighty bless you all.

I am grateful to my loving parents Mr. and Mrs. Olutola, my elder sister Mrs Bose Oyedele, thanks for being there for me. I am also grateful to Rev. Odedele, Dr. and Mrs Afolabi Adegboyega, uncle Seyi, uncle Seye, for their financial support. Thanks to Adeniran Adeyanju for his assistance, Joshua, Kasang, Seyi, Mary, Niran, Kehinde, Christiana, Seun, Tosin, Amsat, Adekunle, other friends and colleagues.

TABLE OF CONTENTS

TITLE	PAGE
Title Page	i
Authorization to Copy	ii
Certification	iii
Dedication	iv
Acknowledgement	v
Table of Contents	vi
List of Tables	x
List of Figures	xi
List of Appendices	xii
Abstract	xiii
CHAPTER ONE: INTRODUCTION	1
1.1 <i>Staphylococcus aureus</i>	3
1.2 Pathogenesis of <i>S. aureus</i>	5
1.3 Justification of the Study	7
1.4 Objectives of the Study	8
CHAPTER TWO: LITERATURE REVIEW	9
2.1 Microorganisms Causing Wound Infection	9
2.2 Types of Wound	10
2.3 Consequences of Wound Infection	11
2.4 Prevention and Control of Wound Infection	11
2.4.1 Antibiotics Used in the Treatment of Wound Infection	12

2.4.2 Types of Antibiotics	12
2.4.3 Mechanism of Action	13
2.5 Management and Treatment of Wound Infection	14
2.6 Resistance to β -Lactam Antibiotics	16
2.6.1 Penicillins	17
2.6.2 Methicillin	18
2.6.3 Vancomycin	19
2.7 Action of β -Lactamase	20
2.8 Types of β -Lactamase	21
2.8.1 Extended Spectrum β -Lactamases	21
2.8.2 AmpCs	22
2.8.3 Sulfhydryl Variant (SHV)	23
2.8.4 TEM	23
2.8.5 Oxacillinase (OXA)	23
2.9 Class of β -Lactamase	24
2.10 Risk factor for β -Lactamase	26
2.11 Consequences of Drug Resistance	26
CHAPTER THREE: MATERIALS AND METHODS	27
3.1 Ethics Statement	27
3.2 Study Participants	27
3.3 Preparation of Media	27
3.4 Sample Collection	27
3.5 Isolation and Characterisation of Bacteria	28
3.6 Morphological Characteristics	28
3. 6.1 Gram Stain	28

3.7 Biochemical Test	28
3.7.1 Catalase Test	28
3.7.2 Coagulase Test	29
3.7.3 DNase Test	29
3.7.4 Latex Agglutination Test for the Identification of <i>S. aureus</i>	29
3.8 Antibiotic Susceptibility Test	29
3.9 Multiple Antibiotic Resistance (MAR) Indexing of Isolates	30
3.10 Beta Lactamase Test	31
3. 11 Induction of β -Lactamase	31
3.11.1 Preparation of Cell Lysates	31
3.11.2 Lowry's Method of Protein Determination	32
3.11.3 Lactamase Enzyme Assay	32
3. 12 Test for ESBL Enzyme Production	33
3.12.1 Screening for ESBL Producers-Double disk approximation method	33
3.13 DNA Analysis	33
3.13.1 DNA Extraction	33
3.13.2 Amplification of <i>nuc</i> Gene by PCR	35
3.13.3 Amplification of <i>mecA</i> Gene by PCR	35
3.13.4 Detection of PCR Product by Electrophoresis	36
3.13.5 Amplification of <i>blaSHV</i> Gene by PCR	36
3.13.6 Amplification of <i>blaTEM</i> Gene by PCR	37
3.13.7 Detection of PCR Product by Electrophoresis	37
3.14 Statistical Analysis	38
CHAPTER FOUR: RESULTS	39
4.1 Identification of <i>S. aureus</i>	39

4.2 Distribution of <i>S. aureus</i> with Respect to Age and Sex	39
4.3 Distribution of <i>S. aureus</i> in Various Wards	40
4.4 Antibiotic Susceptibility Profile of the <i>S. aureus</i>	44
4.5 Multiple Antibiotic Resistance Patterns of the <i>S. aureus</i> Isolates	47
4.6 Beta Lactamase Testing	49
4.7 Correlation between β -Lactamase Production and Resistance	52
4.8 Induction of β -Lactamase by Various Concentrations of β -Lactam Antibiotics	54
4.9 Detection of Extended Spectrum β -Lactamase (ESBL) in the <i>S. aureus</i> Isolates	57
4.10 Detection of <i>nuc</i> , <i>mecA</i> , SHV and TEM Gene of the <i>S. aureus</i> Strains	59
CHAPTER FIVE	64
5.1 DISCUSSION	64
5.2 LIMITATION OF THE STUDY	68
5.3 CONCLUSION	68
REFERENCES	70
APPENDICES	97

LIST OF TABLES

Table	Page
2.1 β -Lactamase Classification Schemes	25
4.1 Distribution of <i>S. aureus</i> with Respect to Age and Sex	42
4.2 Distribution of <i>S. aureus</i> in Various Hospital Wards	43
4.3 Frequency of Antibiotic Susceptibility Profile of the <i>S. aureus</i> Isolates	45
4.4 Multiple Antibiotic Resistance of the <i>S. aureus</i> Isolates	48
4.5 Distribution of β -Lactamase Production in the <i>S. aureus</i> Isolates	50
4.6 Frequency of Antibiotic Susceptibility Profile of β -Lactamase Producing <i>S. aureus</i> Isolates to β -Lactams	53
4.7 Profile of the ESBL Isolates	58

LIST OF FIGURES

Figure	Page
1 Antibiotic resistance Patterns of <i>S.aureus</i> Isolates from Nasal and Wound Swabs	46
2 Antibiotic Resistance Patterns of β -Lactamase Producing <i>S. aureus</i>	51
3 Induction of Isolates with Varied Concentration of Cefoxitin	55
4 Induction of Isolates with Varied Concentration of Penicillin	56
5 PCR Detection of the <i>nuc</i> and <i>mecA</i> Gene	60
6a PCR Detection of the SHV Gene	61
6b PCR Detection of the SHV Gene	62
7 PCR Detection of the TEM Gene	63

LIST OF APPENDICE

Appendice	Page
1 Questionnaire	97
2 Preparation of Media Used	99
3 Interpretative Chart of Zones of Susceptibility to Antibiotics	102
4 Preparation of Lowry's Reagent	103
5 Protein Standard Curve	105
6 Correlation between Nasal and Wound Resistance of Isolates	106
7 ANOVA Table Showing the Distribution of <i>S. aureus</i> with Respect to Sex	107
8 Statistical Table Showing the Distribution of <i>S. aureus</i> with Respect to Age	108
9 Antibiotic Resistance of Nasal and Wound Isolates	109
10 Correlation between Nasal and Wound <i>S. aureus</i> Resistance to β -Lactams	110
11 Correlation between β -Lactamase and Resistance	111

ABSTRACT

This study isolated and identified *Staphylococcus aureus* strains from surgical wounds; determined the antibiotic susceptibility pattern of the *S. aureus* isolates; evaluated the incidence of β -lactamase and extended spectrum β -lactamase (ESBL) production in *S. aureus*. This was with a view to characterizing the ESBL genes in *S. aureus* isolates recovered from surgical wound patients.

One hundred and ten and 107 samples were collected from wounds and anterior nares respectively of subjects at the Obafemi Awolowo University Teaching Hospital Complex (OAUTHC), Ile-Ife, Nigeria, using sterile cotton-tipped applicators. The primary isolation media were nutrient agar and mannitol salt agar. The isolates were identified as *S. aureus* based on standard methods. The antibiotic susceptibility typing was conducted using Kirby-Bauer disc diffusion method and interpreted using standard protocol. The acidometric method was used for β -lactamase detection. The induction of β -lactamase was carried out and the enzyme was assayed by the micro-iodometric method. The polymerase chain reaction (PCR) based technique was used for the detection of the resistance genes (*MecA*, SHV and TEM).

Forty seven (42.7%) *S. aureus* isolates were obtained from 110 wound samples collected while 34 (31.8%) *S. aureus* isolates were also obtained from 107 samples collected from the anterior nares. Forty seven (100%) of the *S. aureus* isolated from wound samples were multiple-resistant while 34 (100%) of the *S. aureus* isolates from anterior nares were also multiple-resistant. β -lactamase production was observed in 14 (41.2%) and 26 (55.3%) of *S. aureus* isolated from the

anterior nares and wounds respectively. The induction of β -lactamase test showed that the enzyme was both constitutive and inductive. *MecA* gene was detected in 2 (50%) of the methicillin resistant *Staphylococcus aureus* (MRSA) strains tested and Sulfhydryl variant (SHV) gene was detected in 13 (65%) of the strains tested. BlaTEM gene was not detected in any of the strains. There was no significant difference ($p > 0.05$) between the resistance patterns of *S. aureus* isolates from anterior nares and wounds.

The study concluded that the prevalence of multiple-resistant bacterial isolates among surgical wound patients was of epidemiological significance in the control of infectious agents.

CHAPTER ONE

INTRODUCTION

1.1 Background to the Study

The skin is the largest organ in the human body. It is a vital barrier against infection with many defenses to prevent invasion, yet many organisms thrive within the hostile environment (Chiller *et al.*, 2001). Human skin acts as an excellent barrier to infection, provided it is not breached. However, if this barrier is breached, bacteria usually regarded as non pathogenic on body surface may assume the role of opportunist pathogens, example some *Staphylococcus species*, *Micrococcus spp*, *Corynebacterium spp*, *Brevibacterium spp* and *Acinetobacter spp*.

A wound is a breach in the skin and exposure of subcutaneous tissue following loss of skin integrity, thus providing a moist, warm and nutritive environment that is conducive for colonization and proliferation of opportunistic and pathogenic microorganisms (Bowler *et al.*, 2001). Colonization of wounds by microorganisms is seen commonly in both the hospital and community settings (Bowler *et al.*, 2001). Wound infections are one of the most common hospital acquired infections and are an important cause of morbidity and account for 70-80% mortality (Wilson *et al.*, 2004; Gottrup *et al.*, 2005).

Development of wound infection depends on the interplay of many factors. Wound infections may occur following accidental trauma and injections, but post-operative wound infections in hospital are most common. Surgical wound infection is clinically defined as purulent discharge from the surgical wound, or spreading cellulitis from the wound (Bowler *et al.*, 2001).

The risk of developing surgical wound infection depends on the number of bacteria that colonize the surgical wound (Dohmen *et al.*, 2009). While the operating wound following surgery is

considered to be “clean”, the surgical wound may be contaminated by air-borne bacteria in the operating room and intensive care units or by bacteria from endogenous sources such as the patient’s mucous membrane, the hands of theatre personnel or by direct contamination by the patient’s normal skin microflora (Kühme *et al.*, 2007). The breaking of the host protective layer, the skin, and thus disturbing the protective functions of the layer, will induce many cell types into the wound to initiate host response (Bowler *et al.*, 2001; Collier, 2003). The severities of complications depend mainly on the infecting pathogen and site of infection (Terry, 1985; Garner *et al.*, 1988).

Staphylococci are Gram positive bacteria with diameter of 0.5µm and could divide in more than one plane to form grape-like clusters (Brock and Frazier, 1996; Harris *et al.*, 2002; Stapleton and Taylor, 2002). The Staphylococci are non- motile, non-spore forming facultative anaerobes that grow by aerobic respiration or by fermentation. Members of this genus are catalase positive and oxidase negative, distinguishing them from the genus Streptococci which are catalase negative and have a cell wall different from that of Staphylococci (Wilkinson, 1997). Staphylococci are tolerant to high concentration of salt and show resistance to heat (Kloos and Lambe, 1991; Wilkinson, 1997). They have a generally benign relationship with their host, however, if the cutaneous organ system is damaged by trauma, inoculation by needles or direct implantation of medical devices (foreign bodies), these organisms can gain entry into the host tissues and may develop life-style of a pathogen (Kloos and Musselwhite, 1975).

The genus *Staphylococcus* comprises of 41 known species and subspecies that are indigenous to human (Kloos and Bannerman, 1994). Among the 41 species, only five are common in causing human disease such as *Staphylococcus aureus*, *S. epidermidis*, *S. saprophyticus*, *S. haemolyticus* and *S. lugdunensis* (Trulzsch *et al.*, 2007). *S. aureus* is the most virulent specie of the genus *Staphylococcus* (Murray *et al.*, 2005). Coagulation of blood is used to distinguish *S. aureus* from

other members of the genus, which are collectively designated as coagulase-negative staphylococci (Ryan and Ray, 2004).

1.1 *Staphylococcus aureus*

Staphylococcus aureus forms part of the normal flora of the skin, intestine, upper respiratory tract and vagina (Lowy, 1998). It colonizes asymptotically the nasal mucosa of about 30% of humans and is responsible for a variety of diseases ranging in severity from mild superficial skin infections to life threatening infections (Lamikanra *et al.*, 1985; Lowy, 1998; Waldvogel, 2000; Yamamoto *et al.*, 2010). Colonization provides a reservoir from which bacteria can be introduced when host defenses are breached, and it clearly increases the risk for subsequent infections (Kluytman *et al.*, 1997; Wertheim *et al.*, 2005).

S. aureus has been reported to be the most common organism isolated from wound and is the leading cause of bloodstream, lower respiratory tract, skin / soft tissue infections in all regions surveyed (Gorbach, 1996; Diekema *et al.*, 2001; Maltezou and Giamarellou, 2006; Godon and Lowy, 2008). It is able to grow and persist in various ways once it adheres to host tissues or prosthetic materials. *S. aureus* can form biofilms (slime) on host and prosthetic surface enabling it to persist by evading host defenses and antimicrobials (Donlan and Costerton, 2002). The invasion of the tissues by *S. aureus* apparently involves the production of a formidable array of extracellular enzymes (invasins) which facilitate the actual invasive process. Some may occur also as cell associated proteins by breaking down primary or secondary defenses of the host which can facilitate the growth and spread of the pathogen (Deresinski, 2005; Godon and Lowy, 2008). The bacterium is a facultative anaerobe and has the ability to regulate its metabolism to withstand drastic changes in environmental conditions (Beaume *et al.*, 2010; Todar, 2011). *S. aureus* has evolved many mechanisms to overcome such changes particularly in an infection.