

UNIVERSITI TEKNOLOGI MARA

**CHARACTERIZATION OF
N-ACETYLGLUCOSAMINIDASE GENE
FROM
*Staphylococcus aureus***

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MSc

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AUTHOR'S DECLARATION

I declare that the work in this thesis was carried out in accordance with regulations of Universiti Teknologi MARA. It is original and is the result of my own work, unless otherwise indicated or acknowledged as referenced work. This thesis has not been submitted to any other academic institution or non-academic institution for any degree or qualification.

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ABSTRACT

SACOL2666, which is known as an N-acetylmuramoyl-L-alanine in NCBI database is shown to be homologous with *atl* of *S. aureus*, a bifunctional autolysin gene. In this study, *in-silico* analysis of deduced amino acids sequence *SACOL2666* was characterized to confirm the protein from *S. aureus* SH1000 is an *N*-acetylglucosaminidase autolysin. Successful transformed gene in pBAD-sScaB and pQE60-xScaQ clones contain 1860 bp of the full gene and 1779 bp of gene without signal peptide sequence. An *N*-acetylglucosaminidase protein family (PF01832) of Lysozyme_like superfamily is found in *SACOL2666* domain architecture. The amino acid of *SACOL2666* gene demonstrated a high sequence similarity to characterized *N*-acetylglucosaminidases, AcmB (*L. lactis*) and Auto (*L. monocytogenes*) Group B in GH73 rather than bifunctional autolysins in Group A, Atl (*S. aureus*). *SACOL2666* has high relatedness in sequence similarity (46%) and structural alignment with *N*-acetylglucosaminidases Auto Chain A structure (3FI7_A). Residue E352, G356, E386, F399, Y455 and a tetrad YATD (Y449-D452) at *SACOL2666* hypothetical secondary structures are shown to be identical to Auto (3FI7_A) residues. As conclusion, this study reveals *SACOL2666* as a novel *N*-acetylglucosaminidase with high sequence similarity to *N*-acetylglucosaminidases in Group B of GH73. Moreover, structural similarity suggests the functional and enzymatic activity of *SACOL2666* is similar to Auto (3FI7_A).

TABLE OF CONTENTS

	Page
CONFIRMATION BY PANEL OF EXAMINERS	ii
AUTHOR'S DECLARATION	iii
ABSTRACT	iv
ACKNOWLEDGEMENT	v
TABLE OF CONTENTS	vi
LIST OF TABLES	x
LIST OF FIGURES	xii
LIST OF ABBREVIATIONS	xiii
CHAPTER ONE: INTRODUCTION	1
1.1 Background and Problem Statement	1
1.2 Significance of Study	3
1.3 Objectives of Study	4
CHAPTER TWO: LITERATURE REVIEW	5
2.1 <i>Staphylococcus aureus</i>	5
2.1.1 Pathogenesis of <i>S. aureus</i> Infection	5
2.1.2 The Peptidoglycan Structure of <i>S. aureus</i>	6
2.2 Peptidoglycan Hydrolase	8
2.2.1 Classification of Peptidoglycan Hydrolases	9
2.2.2 Physiological Function of <i>S. aureus</i> Peptidoglycan Hydrolases	10
2.2.3 Peptidoglycan Hydrolases from Other Gram-positive Bacteria	12
2.3 <i>N</i> -Acetylglucosaminidase Autolysins	14
2.3.1 Atl: An <i>N</i> -Acetylglucosaminidase in <i>S. aureus</i>	14
2.3.2 <i>N</i> -Acetylglucosaminidases in Glycoside Hydrolase 73 Family	15
2.3.3 SACOL2666: A Putative <i>N</i> -acetylglucosaminidase	21
CHAPTER THREE: MATERIALS AND METHODOLOGY	23
3.1 Cloning of SACOL2666 from <i>S. aureus</i>	23
3.1.1 Preparation of Genomic DNA	23

3.1.1.1	Pre-Treatment Lysis Solutions	23
3.1.1.2	Pre-Treatment of Isolation of Genomic DNA	24
3.1.1.3	Isolation of Genomic DNA	24
3.1.2	Preparation of Plasmid DNA	24
3.1.2.1	Isolation of Plasmid DNA	24
3.1.3	Agarose Gel Electrophoresis	26
3.1.3.1	10× Tris-Borate-EDTA (TBE) Stock Solution	26
3.1.3.2	Agarose gel	26
3.1.4	Amplification of <i>SACOL2666</i> from Genomic DNA	26
3.1.4.1	Designing Primers	26
3.1.4.2	Optimization of the Amplification	26
3.1.5	Digestion of DNA by Using Restriction Enzymes	29
3.1.6	Ligation of DNA	30
3.1.7	Transformation of <i>SACOL2666</i>	31
3.1.7.1	Preparation of Chemically Competent <i>E. coli</i>	31
3.1.7.2	Transformation by Heat Shock	33
3.1.7.3	Plasmid Stability	34
3.1.8	Confirmation of Recombinant Clones	35
3.1.8.1	PCR Colony	35
3.1.8.2	Restriction Enzyme Analysis	35
3.1.8.3	DNA Sequence Evaluation	36
3.2	Expression of Recombinant <i>SACOL2666</i>	37
3.2.1	Cell Density Concentration	37
3.2.2	Inducer Concentration	38
3.2.3	Post-Induction Time	38
3.2.4	Induction Temperature	38
3.3	Characterization of Nucleotide and Amino Acid Sequence from Recombinant <i>SACOL2666</i> Clone	39
3.3.1	Analysis of DNA Sequence	39
3.3.1.1	Analysis of Signal Sequence	39
3.3.1.2	Nucleotide BLAST Searches	39
3.3.2	Deducing Amino Acid of <i>SACOL2666</i>	39
3.3.2.1	Analysis of Protein BLAST	40
3.3.3	<i>In-silico</i> Studies of Deduced <i>SACOL2666</i>	40