UNIVERSITI TEKNOLOGI MARA

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

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MSc

September 2014

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 homologuos with a*tl* 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).

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