

UNIVERSITI TEKNOLOGI MARA

**SYSTEMIC BIOLOGY OF *Geobacillus
thermocatenuatus* UPON THERMAL
STRESS INDUCED BY HIGH
TEMPERATURE**

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NOORIZHAB**

Thesis submitted in fulfillment
of the requirements for the degree of
**Doctor of Philosophy
(Molecular Biology)**

Faculty of Pharmacy

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ABSTRACT

Thermophile is a group of microorganisms that are capable of growing at high temperature and the ability that allowed them to do so is termed as thermophily. *Geobacilli* is an example of thermophile which predominately lives in soils and hot springs. It is a well-known source of thermostable enzymes but very little is understood so far in term of the mechanisms that regulate or produce these enzymes. And there may be more hidden biological features of *Geobacillus* that contribute to better bioresources. This project aimed to investigate the genomic structures of *Geobacillus thermocatenulatus* A8 and the biological features associated with living in high temperatures. *G. thermocatenulatus* A8 was sequenced and gene sequences was annotated to biological properties like DNA repair genomics islands (GIs) and CRISPR repeats, preferences for hydrophobic and certain amino acids; and over-presentation of genetic features that are shared with other thermophilic bacilli were investigated. To investigate its thermophily trait, the bacteria were grown in two different temperatures (60 and 70°C) and the differential protein and metabolome profiles expressed were studied using SDS-PAGE and LCMS-QTOF. Through genomic analysis, the bacterial capabilities in producing protease and AMP were determined and the phenotypes were demonstrated on culture plates. Proteome profiles of *G. thermocatenulatus* A8 grown at optimum growth temperature (OGT) and under thermal stress were compared and different set of proteins were expressed from the bacteria to maintain regular cellular functions. The proteins which were expressed under thermal stress were found to perturbate the lipids and energy metabolisms of thermophile and signalling pathways for motility, membrane transport and amino acid tRNA. The metabolomics study identified 19 differentially expressed compounds which were involved in 5 pathways that were classified into lipids, energy, amino acid and secondary metabolite biosynthesis pathways. The biological properties of *G. thermocatenulatus* identified in this study highlighted its potential application as source of AMP in addition to other enzymes that were produced. Combination of omics platforms are useful to provide insights on bacteria characteristic to discover untapped biological resources.

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