UNIVERSITI TEKNOLOGI MARA

PROTEOMIC CHARACTERIZATION OF *Corynebacterium pseudotuberculosis* BIOFILM

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ABSTRACT

Corynebacterium pseudotuberculosis is a pathogenic intracellular parasite causing caseous lymphadenitis (CLA) mostly in sheep and goats, thus, leading to significant economic losses. The morphology, biochemical composition, and antimicrobial susceptibility pattern of *C. pseudotuberculosis* biofilm have previously been addressed. However, little is known about the whole-cell proteome expression in *C. pseudotuberculosis* biofilm. The present study was performed to determine proteome profiles of planktonic and biofilm fractions of *C. pseudotuberculosis* using 1D-SDS-PAGE and to identify differentially expressed proteins during the biofilm formation by *C. pseudotuberculosis* using LC-MS/MS. The FESEM image showed that heterogenous *C. pseudotuberculosis* biofilm was successfully formed within 24h. The treatment with antimicrobials substantially inhibited the viability of the *C. pseudotuberculosis* biofilm. The percentage of biofilm inhibition was found to be in the range between 12.92% to 87.44%. Both planktonic and biofilm fractions showed the expression of nine protein bands ranging between 33.7 kDa and 150 kDa. However, a protein band of 48.3 kDa appeared in the planktonic fraction but not in the biofilm fraction. A total of 885 and 385 protein were successfully identified in planktonic and biofilm fractions, respectively while 264 proteins were detected at both stages. Most of them were found to be associated with transcription or translation pathways and cytoplasm. On the other hand, STRING analysis revealed a total of 1,206 functional interactions produced among differentially expressed *C. pseudotuberculosis* proteins. Sixty-five *C. pseudotuberculosis* proteins were considered as hub proteins because they showed more than 10 functional interactions in the protein interaction network. Furthermore, a total of 23 phosphoprotein in the biofilm fraction were also successfully identified and validated using gel-based phosphoprotein assay. In conclusion, biofilm formation by *C. pseudotuberculosis* involves multiple biological pathways and complex interaction network.

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