

In Silico* Analysis of Uncharacterized Proteins Expressed in *Bacillus Thuringiensis

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Structured Abstract

Background: *Bacillus thuringiensis* is a Gram-positive, aerobic, rod-shaped, and spore-forming bacterium. It is widely known as biopesticides due to its cry genes encoding for insecticidal proteins called cry toxins which when ingested, the toxin activated in pests' midgut due to the alkalinity of the midgut and cause osmotic shock and later, death. This bacterium can cause pulmonary infections and food poisoning although it is not a widely known fact due to this bacterium often mistaken as *Bacillus cereus*. There are still many uncharacterised proteins from *B. thuringiensis* that have yet to be studied and evaluated. This research is done in hopes to discover new information regarding *Bacillus thuringiensis*, especially in the medical and pharmaceutical field.

Methods: 150 of *B. thuringiensis* uncharacterized proteins sequence were retrieved from UniProtKB. The transmembrane proteins were identified and obtained the number of transmembrane domains for each protein through TMHMM. The next step, the protein sequences were input into ProtParam to obtain information of the proteins' physicochemical. Next, the transmembrane proteins were compared with 4 host organisms to search for homologous proteins for drug target purposes. After that, the essential genes were obtained by using DEG. Lastly, the potential proteins for vaccine target were identified using Vaxijen.

Results: The identified transmembrane protein were around 9%, which is 14. The physicochemical properties revealed that the amino acid length for the transmembrane proteins varies from 100 amino acids to 900 amino acids. The isoelectric point ranges from 5.00 to 10.00 whereas for molecular weight, the range is between 17kDa to 80kDa. 3 proteins were predicted to show homologous properties whereas 2 proteins were predicted to not show antigenic properties.

Conclusion: 14 of transmembrane proteins of *B. thuringiensis* were identified from 150 uncharacterised proteins. The proteins that are not suitable for drug target are A0AAX3HW35, A0AAX3HTG3 and A0AAX3HSV9. None of the proteins were predicted to be non-essential genes. The proteins that are not suitable for vaccine target are A0AAX3HL98 and A0AAX3HGW7. Further researches should be done to validate these findings and design high-quality drug and vaccine against *B. thuringiensis*.

Keywords: *Bacillus thuringiensis*, drug target, vaccine target, transmembrane proteins

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