

“Isolation and Characterization of Proteins and Oligopeptides with potential Antimicrobial Properties”

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Continuous emergence of antibiotic-resistance microorganism has caused global panic. If not treated, the golden age of antibiotic will come to an end. A lot of other problems has arisen as a consequence to this issue. This includes increasing risk during surgical procedure and increase cost of treatment among others. Therefore, researchers of diverse discipline have come to work together to find solution to address this issue. Several approaches considered in addressing this issue are controlling the use of antibiotics, developing and producing more synthetic antibiotics and developing antimicrobial peptide as a new group of antibiotics. Among those approaches, antimicrobial peptide was considered as one with huge potential to resolve this issue. This small natural molecule was considered because of several appealing characteristics including cytotoxicity against a broad spectrum of microorganisms and most importantly, having low propensity to develop resistance against the peptide. Antimicrobial peptide has been showed to produce great result when combined with conventional antibiotics. However, with its huge potential, it is possible for antimicrobial peptide to completely replace conventional antibiotics in the future. In this study, eight plants selected from different locations were used to screen for the presence of antimicrobial peptide. Out of eight plant total protein extracts, only three were able to inhibit the growth of *B. subtilis*. However, none were able to demonstrate their antimicrobial property against *E. coli*. All three plants were identified as *Cassia alata*. Extracts were purified using a combination of heat-treatment and column chromatography (ion-exchange) techniques and visualized on Tricine-SDS-PAGE. Purification products were sent for LC-MS analysis which resulted in several matched proteins. These matched proteins were screened for antimicrobial regions using AMPA, a web server for prediction of protein antimicrobial regions. Based on several characteristics, the antimicrobial peptide of interest was identified as nucleoside diphosphate kinase, which is a commonly found enzyme. This is a compelling finding as this enzyme has never been reported with antimicrobial properties prior to this study. Furthermore, its different mechanism of action together with the low probability of developing resistance against the peptide may provide us winning formula in our concern against the ongoing emergence of antibiotic-resistance microorganisms. In addition, this enzyme was also shown to be thermostable as compared to other common enzymes. Even though with such huge potential, this enzyme still need to be optimized before utilizing them in medical field. Optimization is also necessary to maximize its potential. Therefore, further purification is needed which will enable a proper characterization of the antimicrobial peptide for development purpose.

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