PRODUCTION AND BIOACTIVITY CHARACTERIZATION OF PROTEIN HYDROLYSATE FROM PORTUGUESE OYSTER (*Crassostrea angulata*)

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A Master's Thesis Presented
to the Graduate Faculty of the
Institute of Fish Processing Technology
College of Fisheries and Ocean Sciences
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In Partial Fulfillment of the Requirements
for the Degree of
Master of Science in Fisheries (Fish Processing Technology)

JUNE 2019

ABSTRACT

It has been shown that oysters represent diversified peptides with a variety of biological importance. In the present study, the use of proteomics techniques and bioinformatics tool was carried out to predict the potential bioactivities of Portuguese oyster (*Crassostrea angulata*). Mascot database search have identified 8 proteins from *C. angulata* and 5 of which were selected for *in silico* analysis. Interestingly, BIOPEP-UWM database analysis predicted that pepsin (pH > 2) can theoretically release highest number of peptides with biological activities, predominantly angiotensin-1 converting enzyme (ACE) and dipeptidyl peptidase (DPP-IV) inhibitory activities, followed by stem bromelain and papain. To confirm the reliability of these predictions, *C. angulata* proteins were assessed *in vitro*. Results showed that all the hydrolyzed samples possessed inhibitory effect against ACE and DPP-IV, with pepsin hydrolysate (PEH) having the strongest activity of 78.18% and 44.34%, respectively. Further fractionation of PEH revealed that fractions with low molecular weight (MW) such as <1 kDa fraction (F1) and 1-5 kDa fraction (F2) can demonstrate higher ACE and DPP-IV inhibitory activity compared to crude PEH and >5 kDa fraction (F3), but not to a great extent. Overall, the results obtained from *in vitro* analyses corresponded with the *in silico* predictions. Findings of this study thereby suggest the applicability of *in silico* technique for rapid and reliable identification of bioactive peptides from food proteins and determination of suitable enzyme capable for the release of these peptides. Moreover, proteins from *C. angulata* can be considered as potential sources of peptides with potential pharmaceutical and nutraceutical application.

Keywords: *Crassostrea angulata, in silico*, BIOPEP-UWM database, bioactive peptides, proteomics