Title: PROTEIN PROFILE OF *Salmonella* Enteritidis EXPOSED AND NOT EXPOSED TO OREGANO ESSENTIAL OIL

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Abstract:

Salmonella is the major cause of foodborne illness which in turn are a serious public health problem. Therapeutic value of natural products has increased due to microorganisms capable of acquiring resistance to major classes of antimicrobial drugs. *Origanum vulgare* (oregano) essential oil has antimicrobial activity well documented in the literature. However, its use is still limited and the knowledge of mechanisms of action of this compound, poorly understood. The proteomics approach is a research tool to better understand the pathways of this product targets against micro-organisms. This study aimed was to evaluate the protein profile of *Salmonella* Enteritidis exposed and not exposed to oregano oil. Initially it was determined the maximum lethal concentration (CSM) oregano against *Salmonella* Enteritidis strain ATCC 13076. It was used microdilution method in Mueller Hinton Broth. Growth cells were harvested by centrifugation followed by extraction of proteins of *Salmonella* (control) and *Salmonella* exposed to CSM oregano (treatment). These proteins were quantified by Bradford method. The amount of 500 ug of each sample were subjected to the strip pI 4-7, 13 cm for the rehydration process for 18 hours. Then, isoelectric focusing was performed. To perform two-dimensional electrophoresis the strip coming from the first dimension was placed on top of a polyacrylamide gel (12.5% w/v). After separation in the second dimension, the proteins were visualized by staining with Coomassie Brilliant Blue. 2D gels were scanned using scanner ImageScanner III (GE Healthcare Life Sciences). The images were analyzed by the software Image Master 2D Platinun v 7.05 (GE Healthcare Life Sciences). The authenticity of each "spot" has been validated by visual inspection and edited when needed. In the control gel were found 193 spots and gel treatment 100 spots. The equivalence between them (match) was 73 spots. Analyses of the protein spots of the different experimental groups, considering the standardized volume (V%) revealed a correlation greater than 0.66. Thus, one can infer that there are both equivalent protein spots as different protein spots in the respective analyzed gels. The results allowed to characterize the samples and will inform the identification and study of proteins expressed differently in each profile.

Palavras-chaves: *Salmonella*, proteomic, antibacterial, natural products