Asian Jr. of Microbiol. Biotech. Env. Sc. Vol. 21, No. (2) : 2019 : 335-338

ISSN-0972-3005

SCREENING OF ANTIBACTERIAL ACTIVITY FROM *ASPERGILLUS* SPECIES TREATED WITH SYNTHETIC ANTIFUNGAL AGENT

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(Received 18 September, 2018; accepted 21 November, 2018)

Key words : *Aspergillus sp., Secondary metabolites, Bioactive compounds, Pathogenic bacteria*

Abstract – The raising level of multi-resistant bacteria to antibiotics motivate the efforts over the countries to search for novel antibacterial source. Our study focused on preliminary screening for the antagonistic activity of four *Aspergillus* species belong to *A. niger, A. flavus, A. fumigates*, and *A. terreus* that chemically treated with antifungal chloro-traizine comparing with untreated (wild type) isolates against selected Gram positive and negative pathogenic bacterial strains including *Bacillus subtilis*., *Staphylococcus aureus*, *Escherichia coli*, *Proteus* sp., *Klebsiella pneumoniae*, and *Pseudomonas aeruginosa*. The antibacterial activity of *Aspergillus* species was varying based on the strain, and the tested bacteria. All the chemically treated and untreated *Aspergillus sp.* revealed high antibacterial activity against *Bacillus subtilis*, and *S. aureus*. Chemically treated *A. niger* was the only strain supress efficiently the growth of *E. coli*. In contrast, untreated *A. niger*, *A. flavus* and *A. fumigatus* inhibit the growth of *Proteus* sp. higher than the treated strains based on the zone of inhibition. Untreated *A. niger* reveals high antibacterial activity on *K. pneumoniae* in comparison with other untreated *Aspergillus* strains. *P. aeruginosa* exhibited notable resistance for treated and untreated *Aspergillus* strains. In conclusion, chemically treated *Aspergillus* species can be used effectively for production of a novel antibacterial compound that supress the growth of some common pathogens.

INTRODUCTION

Since the revolution of antibiotics discovery during the last century, the trend of pathogenic bacteria resistance to antibiotics has enhanced dramatically especially in the past few years (Fair and Tor, 2014). Therefore, there is an urgent need for screening of novel antimicrobial agents that can play a vital role to control and manage bacterial infections due to multi-resistant pathogens (Nikaido, 2009; Taylor, 2013).

Fungi has emerged as an ideal source for production of variety of natural metabolic compounds that can efficiently be exploited as bioactive materials. There are a wide range of primary and secondary fungal metabolites that are diverse in structures and functions (Keller *et al.*, 2005). The diversity of metabolic productions resulting from the ability of fungal adaptation within hetero-ecosystems on earth. It has been estimated that the fungal species number is between 1.5 to 5 million (Blackwell, 2011). Over the last decades, the development in molecular biology approaches have paved the way to discover several genes related to secondary metabolites in which further investigations of these genes that organised as gene clusters leads to screening new bioactive compounds through coding of proteins that are essentially involved in their biosynthesis of novel antimicrobial agents (Fisch *et al.*, 2009). It is obvious that that biosynthetic cluster genes of secondary metabolites are weakly expressed under normal growth conditions (cryptic genes). Therefore, many attempts have been conducted to activate these silenced genes (Nützmann *et al.*, 2011; Reyes-Dominguez *et al.*, 2012). Recently, many efforts have been pointed for using low molecular chemicals as an ideal tool to rearrange the secondary metabolites profile of fungi that is leading to enhance active antimicrobial agent productions (Cichewicz, 2008; Zutz *et al.*, 2013). The aim of this study is to preliminary screening of the antibacterial influence of fungal extract mycelia that derived from four treated *Aspergillus* isolates through using low molecular mass chemical is called Chloro-triazine(on several pathogenic bacteria and compare these influence with wild type (untreated) fungi.

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