



Structural modelling the of fatty acid ester in *Rhizopogon luteolus* Mushroom

Farzane Kargar, Mojtaba Mortazavi, Masoud Torkzadeh Mahani

Department of biotechnology, graduate university of advanced technology and industrial, Kerman, Iran

Corresponding author: Mojtaba Mortazavi, mortezavimm@gmail.com

Abstract: Fungi are a group of eukaryotes, all of which are superficial heterotrophic. They need organic compounds to grow, reproduce, and receive energy. Mushroom *Rhizopogon luteolus* is a great known genus of mushrooms, so-called fungus, which was discovered in the early twentieth century. *Rhizopogon luteolus* is a source of carbohydrates, proteins, amino acids, fats, vitamins and minerals. Fatty acids are an important compound in the fungus. Phytochemical studies have led to the identification of a specific fatty acid called 3-hydroxy-2,4-dimethyl hepta-cocyl acetate from the *Rhizopogon luteolus* fungus. Unsaturated fatty acids have a positive effect on the human body, which are beneficial for human health and chronic diseases. In this study, two-dimensional and three-dimensional structure of 3-hydroxy-2,4-dimethyl-hepta-cocyl acetate fatty acid were determined using the Marvin Sketch and Gauss view software respectively. Also, the phylogenetic tree of this species was drawn by MEGA 7 software and the results show that this species has the 0.25% of proximity with the *Rhizopogon succosus* species.

Keywords: *Rhizopogon luteolus*; Protocatechuic acid; Phylogenetic tree; Bioinformatics study

References:

- [1] "A new fatty acid ester from an edible mushroom *Rhizopogon luteolus*", "Achyut Adhikari & Aziz Türkoğlu, G.T.-Ç., A.M., Mehmet Emin Duru, Mehmet Öztürk, 30(2016) 2258-2264 .
- [2] "Biology of the ectomycorrhizal genus *Rhizopogon*. VI. Re-examination of infrageneric relationships inferred from phylogenetic analyses of ITS sequences", "Lisa C. Grubisha, J.M.T., Randy Molina & Joseph W. Spatafora, (2002) 607-619.
- [3] "Systematics of the genus *Rhizopogon* inferred from nuclear ribosomal DNA large subunit and internal transcribed spacer sequences," Grubisha, L.C., (1998) 131.