Differential Protein Profiles of the Lipolytic Yeast *Candida palmioleophila* under Different Growth Conditions

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This work aimed to establish the influence of different carbon and nitrogen sources, including vegetable oils, on the variability of the protein profiles of an oil and grease-degrading strain of *Candida palmioleophila*. Production of biomass and protein by *C. palmioleophila* strain SACL11 was evaluated under eight different culture conditions, which provided palm oil or sunflower oil as sole carbon source and ammonium sulfate as sole nitrogen source, during 48 h at 30 °C. Protein profiles from *C. palmioleophila* crude extracts were obtained by SDS-PAGE every 12 h and analyzed with bioinformatic programs. The results showed that treatments providing the highest concentrations of each of the carbon and nitrogen sources resulted in a higher biomass production, with sunflower oil being the carbon source that produced the highest values and an overall faster growth. Proteins of approximately 63 KDa and 28 KDa were detected only in protein extracts obtained from media containing palm or sunflower oil as carbon source, suggesting a key role of these proteins in the hydrolysis of oils. Furthermore, the molecular weights of these proteins were similar to several reported lipases and esterases from *Candida rugosa* and other related species, reinforcing their possible function. In conclusion, this work identified and reported for the first time differential protein profiles of the lipolytic yeast *C. palmioleophila* in response to different growth conditions, and found evidence of the involvement of lipase-like proteins during the metabolism of vegetable oils. This give insight about the enzymes involved in grease metabolism and reinforces the potential of this promising microorganism to be used as an excellent bioremediation agent in fat, oil and grease-polluted environments.

1. Introduction

*Candida palmioleophila*, formerly known as *Torulopsis candida*, is an ascomycetous lipolytic yeast related to *Candida famata* and *Candida saitoana*, with a remarkably ability to assimilate crude palm oil (Nakase et al. 1988). Even though there are only few reports on the biochemical and physiological characterization of *C. palmioleophila*, evidence points to a high potential of this yeast as bioremediation agent of effluents contaminated with fats and oils. Recently, Rodriguez-Mateus et al. (2016) reported the isolation and characterization of native strains of *C. palmioleophila* from solid and liquid wastes of a palm oil refining process, which showed high lipolytic activity and were successfully used to degrade up to 79% of palm oil in liquid medium. Agualimpia et al. (2016) also reported that microbial consortia composed of several strains of *C. palmioleophila* degraded more efficiently palm oil that individual strains, achieving up to 84% palm oil degradation and were successfully used for the bioremediation of Palm Oil Mild Effluents (POME). Even though the specific enzyme mechanisms and metabolic pathways used by *C. palmioleophila* to degrade oil and grease are not yet described, lipases and esterases are most likely involved in the first steps of this process. Lipases and esterases from *C. palmioleophila* could have a strong potential to be used as biocatalysts for bioremediation purposes. However, little is known about the structure and expression of *C. palmioleophila* lipases or esterases in response to different growth conditions and there is no reports about the characterization or purification of these enzymes for bioremediation purposes. Thus, this work aimed to establish the influence of different carbon and nitrogen sources, including vegetable oils, on the variability of the protein profiles of an oil and grease-degrading strain of *C. palmioleophila* in vitro.

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