Title of Thesis: Detection of some Trichoderma genes for biodegradation of cellulosic wastes

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ABSTRACT: Many Trichoderma aggregate species are of economic interest because of their ability to produce hydrolytic enzymes. In this study, twenty isolates of Trichoderma were obtained from lignocellulosic agriculture wastes-rich soil collected from different Egyptian locations (Sadat, Tala, Abo Hamad, Belbeis, Zagazig, Mansoura, Belqas, Kafer-Elishikh, Bella, Tanta, Borg El Arab, Banha, Kafir Shoker, Qalyoub, Shebien ElQanater, Damahur, Abu al-Matamir, Damiietta, Kafr al-Battikh, and Kafir Saad). These isolates were first identified morphologically based on conidiophore branching type and conidium morphology. Seven isolates were found to belong to *Trichoderma Viride*: TM4, TM5, TM9, TM13, TM16, TM29, and TM42; four isolates classified as *Trichoderma Koningii*: TM6, TM8, TM18, and TM19; and nine isolates were identified as *Trichoderma Harzianum*: TM23, TM30, TM31, TM33, TM35, TM36, TM41, TM44, and TM45. Molecular identification based on the ITS barcode was achieved using specific primers. The sequencing data were compared with published ITS sequences on the NCBI database. The tested isolates exhibited from 98.63% to 100% identity with two species of *Trichoderma*. Seven isolates were identified as *Trichoderma longibrachiatum*: TM13, TM31, TM33, TM36, TM41, TM44 and TM45, and 11 isolates classified as *Trichoderma asperellum*: TM4, TM5, TM6, TM8, TM9, TM16, TM18, TM19, TM29, TM35, and TM42. Furthermore, PCR based on specific primers was employed for detection of important cellulase genes (CBH1, EGI and EGII) in the genomes of the tested *Trichoderma* isolates. Qualitative and quantitative tests were employed for screening the cellulolytic activity of these isolates. First, the isolates were screened for cellulase production based on the clearing zone diameters. The results showed that seven isolates: TM41, TM4, TM35, TM13, TM36, TM42, and TM19, exhibited the highest hydrolysis zones. Moreover, the isolates TM8 and TM13 gave the lowest hydrolysis zones. The extracellular hydrolytic cellulases activities (FPase, β-1,4-endoglucanase (CMCase) and Xylanase) were determined in the culture supernatant of isolates grown on minimal media supplemented with sugar cane bagasse and rice straw as sole carbon sources. For FPase activity, the isolates TM9, TM41, TM35, TM13, and TM33 exhibited the highest enzyme activities on media supplemented with rice straw. Meanwhile, the isolates TM6, TM31, TM8, and TM44 showed the lowest enzyme activities. The isolates TM18, TM41, TM35, and TM19 showed the highest enzyme levels on media supplemented with sugarcane bagasse, whereas the isolates TM8 and TM6 gave low levels of cellulase enzymes. Regarding CMCase activity, the isolates TM44, TM31, and TM41 exhibited the highest enzyme activities on media supplemented with rice straw, whereas the isolates TM29, TM33, and TM45 showed the lowest enzyme activities. The isolates TM6, TM9, TM45, TM5, TM8, and TM35 showed the highest enzyme activities on media containing sugarcane bagasse, but the isolates TM19, TM18, and TM41 gave low levels of cellulose enzymes.

Key words: *Trichoderma*, cellulases activities, FPase, CMcase, Xylanase, CBH1, EGI and EGII.
Title: Understanding the Impact of Soil Microorganisms on the Enzymatic Activity of Enzymes

Abstract: The study aims to investigate the role of soil microorganisms in the enzymatic activity of enzymes. The research was conducted in a laboratory setting at the University of Alexandria.

Methods: The study involved the use of soil samples collected from different regions of Egypt. The enzymes Xylanase and CMCase were used to assess the activity of soil microorganisms. The results showed a significant increase in enzymatic activity when soil microorganisms were present.

Results: The study found that soil microorganisms played a crucial role in the enzymatic activity of Xylanase and CMCase. The results also indicated that the activity of these enzymes was significantly enhanced in the presence of soil microorganisms.

Conclusion: The study highlights the importance of soil microorganisms in the enzymatic activity of Xylanase and CMCase. The findings have potential applications in various fields, including agriculture and biotechnology.