

Initial proteomic identification of secreted proteins of a white-rot fungus *Porodaedalea pini* grown on liquid medium

SUNARDI^{1,*}, AYANA NAKAMURA², FUTOSHI ISHIGURI², SHINSO YOKOTA^{2,*}

¹Faculty of Mathematics and Natural Sciences, Lambung Mangkurat University, South Kalimantan 70714, Indonesia

²Faculty of Agriculture, Utsunomiya University, Utsunomiya, Tochigi 321-8505, Japan

*Corresponding authors: E-mail: sunardi@unlam.ac.id; yokotas@cc.utsunomiya-u.ac.jp

Abstract

Porodaedalea pini is a white-rot fungus that attacks conifers and secretes different kinds of extracellular enzymes. This is the first report identifying the secreted proteome of *P. pini* grown on liquid medium. Some proteins involved in carbohydrate metabolism were identified by peptide mass fingerprinting (PMF) using matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI/TOF/MS). The identified proteins were classified according to their biochemical roles as: carbohydrate transport and metabolism, amino acid transport and metabolism, aromatic compound metabolism and oxidative stress responses, cellular processes and signaling, and hypothetical proteins. Furthermore, one spot of the proteins in the carbohydrate transport and metabolism categories may be correlated to the hydrolytic enzymes secretion. This protein was homologous to the glycoside hydrolase family 1 and seems to be a β -glucosidase.

Keywords: *Porodaedalea pini*; Cellulase; Proteomics; Peptide Mass Fingerprinting