CHARACTERIZATION OF BETA-GALACTOSIDASE CODING GENES OF *LICHTHEIMIA RAMOSA*

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Beta-galactosidase enzymes of Mucoromycota fungi are rarely studied, although this group of filamentous fungi is an excellent source of many industrial enzymes. In our recent studies, a *Lichtheimia ramosa* isolate proved to be an excellent beta-galactosidase producer, and the corresponding enzyme secreted by the fungus has also been purified and characterized. In connection with the enzyme production studies, we aimed to identify beta-galactosidase coding element(s) in the *L. ramosa* genome and investigate its/their expression level under different cultivation conditions. Two beta-galactosidase coding genes (*bgal1* and *bgal2*) were recognized in *L. ramosa.* The relative transcript levels of the coding genes were examined on malt extract agar and wheat bran via quantitative real-time PCR. In our study, *bgal1* gene showed a higher transcript level than *bgal2* gene. The relative transcript levels of *bgal1* and *bgl2* reached their maximum on the 6th day on wheat bran, while no significant changes in expression level were observed on malt extract agar. These observations are in agreement with the results of our former studies in which the highest overall enzyme activity was obtained in a wheat bran-based fermentation system. In an additional study, a plasmid-free CRISPR-Cas9 system was applied to create a *pyrG* auxotrophic mutant of *L. ramosa*. This strain is applicable as recipient strain in the future gene manipulation experiments (overexpression or gene disruption). Using this method, one-to-five nucleotide long-targeted deletions could be induced in the *pyrG* gene. This research was sponsored by NKFI FK 134886. B.V. was supported by ÚNKP-21-3.