Proteomics guided study of Saccharomyces cerevisiae for the development of consolidated bioprocessing chasses

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Abstract

New approaches to increase productivity and reduce costs may improve the use of lignocellulosic biomass in biorefineries, benefiting the biobased economy and reducing political and environmental instabilities from fossil sources. The deletion of *MNN10* and *PMT5* genes, related to N- and O-mannosylation processes, in *Saccharomyces cerevisiae* BY4742 was performed by CRISPR/Cas9 to evaluate the effects on the enzymatic activity of a heterologous laccase. Next, the mutant with the higher laccase activity, *mnn10*Δ, in concert with expression of lignocellulolytic enzymes (*GH7*4 endoglucanase, *GH3* β-glucosidase) integrated in the *Ty1* locus was used to create a strain for a consolidated bioprocess. Proteomic analysis showed that several proteins related to the synthesis of the cell wall, vesicle formation, protein trafficking, and glycosylation had changes in expression levels after deletion of the *MNN10*. This mutant strain also showed increased extracellular activities of recombinant CAZYmes, which could be a result of changes in N- and O-glycosylation or extracellular secretion. Active heterologous enzymes can be expressed from genes integrated into the *Ty1* locus (transposon) of such industrial and laboratory *S. cerevisiae* chassis and provides a promising approach for the development of consolidated bioprocessing.

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