
ABSTRACT

Profitable biomass conversion procedures are extremely reliant on the use of efficient enzymes for lignocellulose degradation. Amongst the cellulose degrading enzymes, beta-glucosidases are necessary for efficient hydrolysis of cellulosic biomass because they relieve the inhibition of the cellobiohydrolases and endoglucanases by decreasing cellobiose buildup. Current study was carried out to isolate the fermentative microbes from soil that produce glycoside hydrolases (GHases) belonging to family 3 that is β -glucosidase. The DNA of those microbes was isolated by metagenomic technique which is a culture independent approach. The different isolated fermentative microbes were screened for β -glucosidase activity with carboxymethylcellulose (CMC) dye staining. The PCR amplification of those samples was conducted that have given positive result for the presence of β -glucosidase producing yeast. *Candida parapsilosis*, *Simplicillium obclavatum*, *Candida metapsilosis* and *Naganishia adeliensis* was amplified from metagenomic DNA sample. Out of four isolated strains amplified, *Simplicillium obclavatum* has shown maximum β -glucosidase activity by efficiently consuming substrate CMC during fermentation at temperature 30°C and pH 5. *Candida metapsilosis*, has also shown great β -glucosidase potential. Least efficient strain out of these four was found to be *Naganishia adeliensis* in comparison with others. The present data suggests that currently isolated yeast strains could be the great source for mining glycoside hydrolases obtained from orchards of cities Bhakkar, Sheikhpura, Chakwal and Faisalabad in order to enhance biofuel production. Moreover, additional research is needed to isolate more proficient glycoside hydrolases producing fermentative yeast in order to develop potential blend-in for cellulose hydrolysis.