ABSTRACT

Xylan is the primary hemicellulosic part of plant biomass, xylanase plays significant role for its degradation. The current research work was done to increase the xylanase production from fungal isolates. 21 soil samples were collected, 16 fungal isolates were purified and characterized on morphological basis. From these, 6 fungal isolates were found to be good producer of xylanase. ZGCL22, ZGCL49, ZGCL18, ZGCL44, ZGCL51 and ZGCL12 were good xylanase producer fungal isolates. Mutation of three of these fungal isolates was done through UV light for increase production of xylanase. ZGCL22, ZGCL49 and ZGCL12 show increase of xylanse production after exposure of 5 minutes UV. Positive fungal isolates were screened by qualitatively by congo red staining and quantitatively by DNS method. 30 °C temperature and 5.0 pH was found to be optimum for most of the xylanase producer fungal isolates except ZGCL44 strain which was found to be optimum at 9.0 pH for 5 days of fermentation period. Xylanase maximum activity was observed at 50 °C, at 30 minutes of incubation with 1% substrate concentration. On the basis of 18S rRNA sequencing using ITS primer, ZGCL22 was 100% homologous to *Aspergillus niger* isolate SUMS0061 FJ011541.1, ZGCL49 was 99% homologous to *Aspergillus flavus* strain 176.1B2 KP784374.1, ZGCL18 showed 100% similarity with *Fusarium oxysporum* isolate FoxySIN8 KJ466113.1, ZGCL44 was 100 % homology with *Pencillium digitatum*, strain FRr 1313 AY373910.1, ZGCL51 showed 100% homology with *Trichoderma harzonium* strain HEND AF055216.1and ZGCL12 showed 100% homology with *Aspergillus oryzae* NRRL 506. AF459735.1. XynB gene was detected in *Aspergillus niger* wild and mutated fungal isolate. It was found to be 97% homology with *Aspergillus niger* culture-collection CICC:40616 xylanase B (xynB) gene. Comparison of wild and mutant of xynB gene was observed.