Isolation of gene encoding xylanase from bagasse compost soil using sequence-based approach

Abstract

Hemicelluloses are among the most abundant biomasses on earth and represent a considerably immense source of fixed carbon in nature. Xylanases are one of the major hemicellulose-degrading enzymes that randomly cleave backbone xylans containing within the plant cell walls. Consequently, these enzymes have significant biotechnological potential applications in various industries. In this study, culture-independent approach using sequence-based technique was employed to isolate the xylanase genes from bagasse compost soil. To obtain the genes responsible for xylanase enzyme production, degenerate primers designed from the conserved regions of bacterial xylanase (glycosyl hydrolase family 10) genes were used. The degenerate primers were used in the PCR reaction to amplify the DNA previously extracted from bagasse compost soil. The obtained PCR products of approximately 160 bp. Sequence analysis of the partial xylanase gene exhibit 64% amino acid identity to *Geobacillus thermoglucosidasius C56-YS93.* The full-length gene determination was performed using the genome walking approach. The 3' and 5'ends were obtained. The results shown that a full-length xylanase gene contained 2,649 bp open reading frame encoding 883 amino acid residues which exhibited 43% amino acid sequences identity to Endo-1,4-beta-xylanase from *Thermotoga sp. RQ.* Additionally, a putative carbohydrate binding module family 9 was also present at the C-terminus of the gene sequence.