

Isolation, characterization and genetic identification of natural fungal strains from decomposing hazelnut husk

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Abstract

The goal of this study was to determine the fungi enabling the degradation of hazelnut husk and awkward some chemical properties of decomposing hazelnut husk which is an agricultural organic waste. For that purpose, an amount of hazelnut husk picked from hazelnut gardens was stacked on a land and left under aerobic conditions for fragmentation. The fungal strains which use hazelnut husk were detected by molecular techniques in samples which were taken periodically for 2 years.

Efficient Cellulase-producing fungi were isolated from different sampling time in hazelnut husk composting process decayed lignocellulosic waste etc using different isolation strategies. Among the various isolates obtained from different environment, five different fungi were selected depending upon the diameter of clear zone produced in Carboxy methyl cellulose agar for further screening in liquid media and one potent strain NASC3 was identified as efficient cellulolytic fungi. Molecular identification of strain NASC3 was done by PCR amplification of 18s rDNA region using primers ITS4 and ITS5. The amplified products were sequenced and analyzed using ClustalW. The phylogenetic analysis of strain NASC3 showed and identified as *Penicillium piceum* IMI 392509^T, *Penicillium citrinum* C1-1^T, *Emericella rugulosa* 14^T, *Penicillium brasilianum* KUC1433^T, *Acremonium* sp. ATT196^T, *Penicillium verruculosum* 101119^T, *Penicillium piceum* IMI 392509^T and *Aspergillus tubingensis* SAB-B3C-T^T.

Key words: hazelnut husk, fungi, decomposing, compost, identification

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