6TH INTERNATIONAL SYMPOSIUM ON AGRICULTURAL SCIENCES

AgroReS
2017

BOOK OF ABSTRACTS

February 27 - March 2, 2017
Banja Luka, Republic of Srpska, Bosnia and Herzegovina

IDENTIFICATION OF FUNGAL COMMUNITIES FROM COMPOSTING HAZELNUT HUSK

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The objective of this study was to determine the fungi enabling the degradation of hazelnut husk and determine some chemical properties of decomposing hazelnut husk.Hazelnut husk picked from orchards was stacked on a land and left under aerobic conditions for fragmentation. The fungal strains were being detected in samples during 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 environments, five 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 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.

Keywords: hazelnut husk, fungi, compost, identification.