Geophysical Research Abstracts
Vol. 20, EGU2018-1172, 2018
EGU General Assembly 2018

A survey on the species diversity of cellulose and xylan hydrolysing soil bacteria in soil samples taken from agricultural areas, by culturing methods

Rózsa Máté (1), Ákos Tóth (2), Éva Kárpáti (3), József Kukolya (2), and József Kutasi (1)

(1) Biofil Microbiological, Biotechnological and Biochemical Ltd., Budapest, Hungary (materozsa91@gmail.com), (2) 2Department of Applied and Environmental Microbiology, Agro-Environmental Research Institute, National Agricultural Research and Innovation Centre, Herman Ottó u. 15., H-1022 Budapest, Hungary, (3) 3Saniplant Biotechnological Research and Development Ltd., Raktár u. 19, H-1035 Budapest, Hungary

The presence of crop residues is a major issue in soil management, due to the effect it has on soil structure and nutrient availability. Decomposing stalk residues can provide nutrient supply for both plants and soil microbes and improve the physical properties of the soil. Without treatment, however, large volumes of crop residues can cause problems in tilling and can temporarily disrupt nutrient supply. Undegraded organic matter has adverse effects on soil structure, water storage capacity, and hinders agrotechnical operations. The presence of cellulose and xylan (NSP, non-starch polysaccharide) hydrolyzing microbes can enhance crop residue degradation. The aim of our study was to identify the cellulase and xylanase producing microbial species in soil samples from agricultural lands with crop residues. Samples were taken from the Zala hills and the Great Plain regions in Hungary, from corn fields, following harvest. From the Great Plain region, both organically fertilized (stable manure) and unfertilized areas were sampled. Eight different culture media were used for isolation and the purification of cultures. A total of 250 isolates were tested for the presence of polysaccharidase enzyme activity by Congo-red staining. Incubation times and colony morphology were also recorded. 34 strains were positive in the Congo-red test. DNA was extracted for 16S rDNS PCR profiling for molecular taxonomy. 12 polysaccharidase positive strains were isolated from the Zala hills region and 20 strains from the Great Plains region. From areas without fertilization, 7 different genuses were identified, and the number of strains were double than those from fertilized lands, representing 3 bacterial genuses. Strains isolated from the Zala hills region belonged to 9 different bacterial genuses. When quantifying polysaccharidase activity of Congo red positive strains by the DNSA method, only a few of them showed considerable xylanase and cellulase activity. One of the bacterial strains was prominent in enzyme activity showing the highest xylanase (17742.03 IU/ml after 48h) and cellulase activity (540.261 IU/ml after 48 h). The observed variability in enzyme activity is either due to the differences in the use of xylan and cellulose substrates or that the Congo red test is primarily used qualitatively as a screening method, while the DNSA method is used for assessing actual enzyme producing capacity.

The project was supported by KFI_16-1-2016-0214 grant of the National Research, Development and Innovation Office, Hungary.