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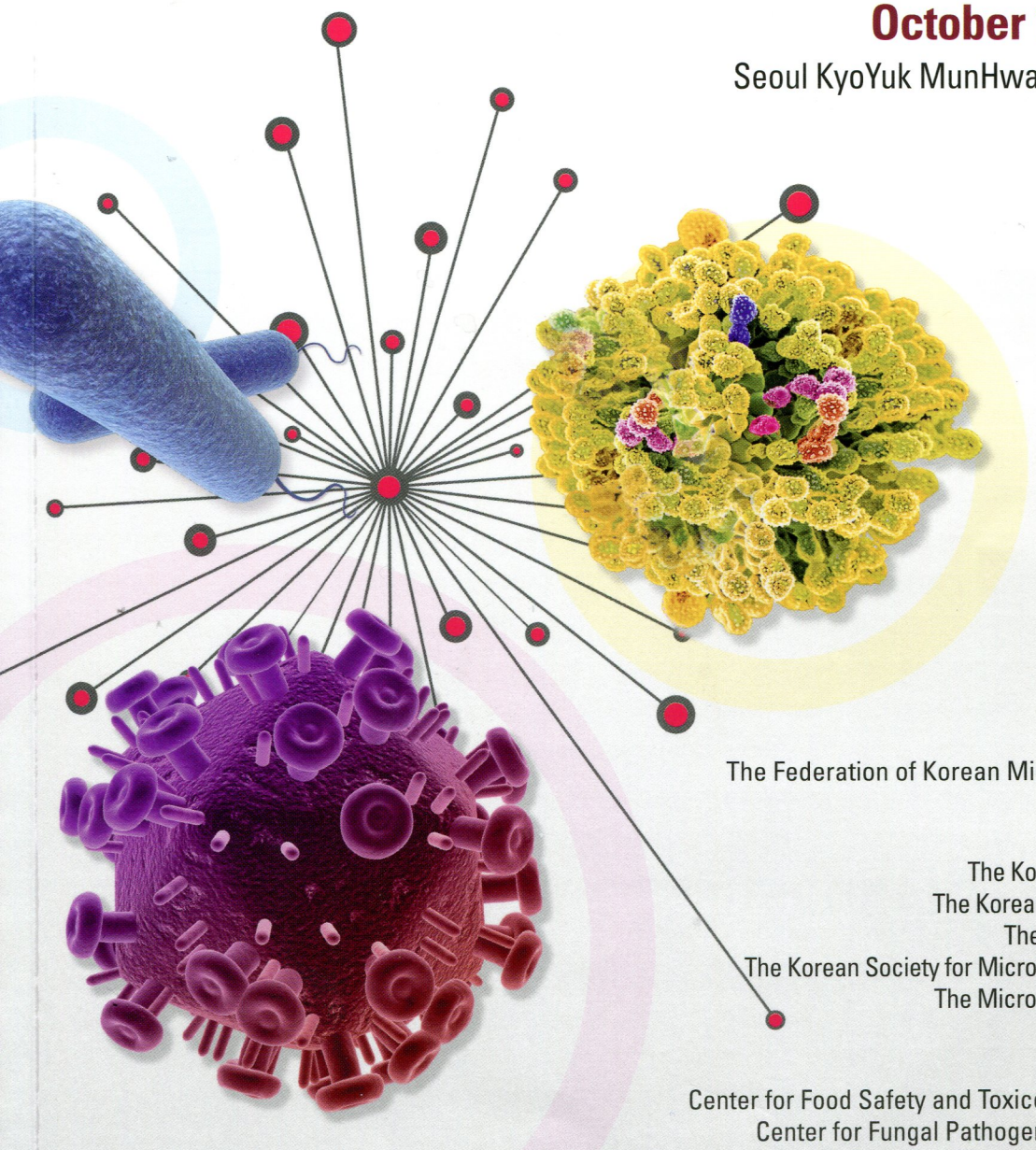

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B041

olar and Alpine Microbial Collection (PAMC): A Culture ollection Dedicated to Polar and Alpine Microorganisms

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croorganisms in polar areas may have important ecological roles in geochemical cycles and the food chain. Culture collections for polar alpine microorganisms can provide research resources for ecological physiological studies. The Polar and Alpine Microbial Collection MC) is a specialized culture collection for maintenance and ribution of polar and alpine microorganisms. A database system was eloped to share important data fields with DarwinCore2 and OBIS base schemas. Approximately 1,500 out of 5,500 strains maintained PAMC have been identified and belonged primarily to the phyla inobacteria, *Bacteroidetes*, *Firmicutes*, and *Proteobacteria*. Many of microbial strains can grow at low temperature and produce proteases, ses, and/or exopolysaccharides. PAMC provides search tools based keywords such as taxonomy, geographical origin, habitat and siological characteristics. Biological materials and information vided by PAMC will be important resources for ecological and siological studies on polar and alpine microorganisms.
pported by Korea Polar Research Institute (Grant PE06050, PE11030, E411060)]
ywords : polar and alpine microorganism, biodiversity, culture lection, physiological characteristics

B042

oduction and Characterization of Xylanase from *Aspergillus* -During Solid State Fermentation State Fermentation

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was produced from *Aspergillus niger* (MTCC 1344) rementation (SSF) using wheat bran as a low cost the major factors influenced on xylanase extraction mized. From the experimental results, maximum 50 U/g) was obtained from 14ml/g of extractant with ylanase was found to be active in a vast range of pH timum pH and temperature of xylanase were found pectively. The effect of metals ions and surfactants was studied. The metal ions such as Ca^{2+} and Mn^{2+} whereas, Mg^{2+}, Zn^{2+}, Fe^{2+} and Co^{2+} inhibited. On $^{2+}$ ions completely inhibited the activity of xylanase. rfactants, Tween 80 showed an increased trend. The nowed high specific activity to several xylans, of an yielding the maximum activity. It was concluded d in this study is very low-cost and also helpful in tries.
illus niger, xylanase, solid state fermentation, ns

B043

Apply to New Reclaimed Land of Salt Stress Using Halophilic Rhizobium and Hairy Vetch

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Newly reclaimed land has high salinity and low-organic-matter soil content as a result a severe environment to crop and plant growth. Hairy vetch is strong in the cold and can thus be grown on idle agricultural land in winter as a green manure crop. Rhizobium is made possible that fix nitrogen after becoming established inside nodules of hairy vetches, especially for crops grown without the use of chemical fertilizers. This study was screening to root nodule rhizobium for hairy vetch with halophilic and excellent nitrogen fixing ability, for application on newly reclaimed land containing high salinity. And investigate NaCl resistance, nitrogen fixation activity and growth promoting effect of hairy vetch by halophilic rhizobium. As a result, showed effect of growth promote of hairy vetch at 0.3% or more of the salt concentration. We suggest that apply to new reclaimed land of high salinity and low-organic to rhizobium inoculated with hairy vetch.
[This research was supported by Technology Development Program for Agriculture and Forestry, Ministry for Food, Agriculture, Forestry and Fisheries, Republic of Korea]
Keywords : Hairy vetch, Rhizobium, Newly reclaimed land, Plant growth promotion, Halophilic

B044

Bacterial Community of Sediments from the Australian-Antarctic Ridge Australian-Antarctic Ridge

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Benthic bacterial communities in the ocean environment play significant roles in the biogeochemical cycle and remineralization of organic matters. In this study, the bacterial community of surface sediments from Australian-Antarctic Ridge (AAR) was revealed by 454 pyrosequencing method. Bacterial communities inhabiting the sediments of AAR were highly diverse, covering 39 different taxonomic groups at the phylum level. Among 39 phyla and candidate phyla, *Gammaproteobacteria*, *Planctomycetes*, *Actinobacteria*, *Deltaproteobacteria*, *Acidobacteria*, *Alphaproteobacteria*, *Chloroflexi*, *Bacteroidetes*, *Chlorobi*, and *Gemmatimonadetes* were dominant comprising approximately 85~88% of bacterial community. 16S rDNA sequences of major OTUs with 1% or higher abundance showed high similarity (96.6% ~ 100%) with uncultured environmental sequences which were mostly recovered from sediments of various areas of Arctic Ocean, Southern Ocean, Atlantic Ocean, Indian Ocean, Pacific Ocean, etc, which implies that they represent taxonomically novel groups of bacteria and their function and physiology are mostly unknown and marine sediments were the most important source of the major OTUs.
Keywords : Benthic bacterial communities, Australian-Antarctic Ridge, Pyrosequencing