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Isolation of *Exiguobacterium sp.* TYM-43 Containing Alginate Lyase and β-Agarase Activity from Estuarine Sediment

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We isolated an agar- and alginate-degrading bacterium, strain TYM-43 from Misu-Dong mud of Tongyoung-bay using M9 alginate agar plate and M9 agarose agar plate. When the strain TYM-43 was cultivated in marine broth containing 0.2% agar or 0.2% sodium alginate at 30℃, 250rpm. Strain TYM-43 produced extracellular and intracellular polysaccharide degrading enzymes, both agrase and alginate lyase. The subsequent BLAST analysis on sequence similarity and phylogeny analysis indicated that the closest relatives of the strain KLM-2 were *Exiguobacterium sp.* We characterized the optimum condition for the cell growth and the production of polysaccharide degrading enzymes of *Exiguobacterium sp.* TYM-43. 0.2% agar or 0.2% sodium alginate content in marine broth was appropriate as a carbon source better than glucose, fructose or mannose for the cell growth. The effects of temperature and pH on the cell growth and the depolymerization of the polysaccharide substrates were investigated. This work was finacially supported by the Region Innovation System Program, Ministry of Commerce, Industry and Energy , Republic of Korea.

Key Word : Alginate lyase, Agarase, 16S rDNA, *Exiguobacterium sp.* depolymerization

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Identification of a novel xylan degrading bacteria from East Sea, Korea

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At the previous study, we have isolated xylan degrading bacteria from East Sea sediment from East. This strain was identified as a member of the genus *Paenibacillus* on the basis of phenotypic and phylogenetic analyses. The isolated strain was growing optimally at 20 to 25℃. The rod-shaped strain showed Gram-negative staining and motile by means of peritrichous flagella. Whereas oxidase, catalase, urease, nitrate reduction, arginine dihydrolase, lysine decarboxylase, ornithine decarboxylase, indole production, H_2S production, and tryptophan deaminase test showed negative reaction, citrate utilization and Voges Proskauer showed positive reaction. Like other *Paenibacillus* species, it contained anteiso-$C_{15:0}$ as the major cellular fatty acid. 16S rRNA gene sequence analysis placed this strain within the *Paenibacillus* cluster, with a similarity value of 98% to *Paenibacillus wynnii* LMG 22176^T. Taken all our data together, our isolate is assumed as a novel species of genus *Paenibacillus.*