P71

Production of Oligoalginates from a Novel Alginate Lyase, *Streptomyces sp.* ALG-5

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Streptomyces sp. ALG-5 with an alginate lyase activity was isolated from seaweed. The gene of alginate lyase of *Streptomyces sp.* ALG-5 was cloned by PCR with specific primer designed from homologous nucleotide sequences. The alginate lyase gene (GenBank ID : ABS59291) was successfully expressed in Escherichia coli BL21. The recombinant ALG-5 was purified using Ni-Sepharose affinity chromatography. We investigated the optimum pH and temperature conditions on the alginate lyase activity. ALG-5 lyase preferred to degrade poly-guluronate block rather than poly-mannuronate block. Unsaturated oligoalginates were obtained from sodium alginate solution by incubation of purified enzyme and purified to 6 oligo-alginates, including di-, tri-, tetra- and pentasaccharides, by using Bio gel P-2 chromatography gel-filtration. (2.5 × 234 cm) [This work was supported by the 2007 Busan Techno Park program (BTP) and 2006 Region Innovation System Program (RIS), Republic of Korea.]

P72

The Superoxide Dismutase Gene from the Isolated Organic Solvent Tolerant *Pseudomonas* Strain is Highly Conserved in the *Aeromonas* Species

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The incomplete reduction of O_2 in the respiration process brings out the generation of active oxygen species. For instance, univalent reduction of O_2 yields superoxide anion (O_2^-) to allow the conversion to hydrogen peroxide (H_2O_2). Such reactive molecule, superoxide becomes detoxifying by role of a superoxide dismutase gene. The *sod* gene (*sodB*) from an organic solvent tolerant *Pseudomonas* stain was cloned into the pGEM-T easy vector and sequenced for phylogenetic analysis. As a result, the *sodB* sequence showed more than 80% identity, compared with that of many *Aeromonas* species including *A. bestiarum*, *A. hydrophila*, *A. bestiarum*, *A. media*, and *A. bestiarum*, respectively. In addition, the nucleotide sequence of *sodB* from the isolate was significantly homologous to that of *P. putida*, *P. entomophila*, *P. fluorescens*, *P. aeruginosa*, *P. mendocina*, and *P. syringae*, respectively. This finding may derive the significant phylogenetic relationship among the *sodB* sequence of the *Pseudomonas* strain and *Aeromonas* species. High level expression and purification of the protein, superoxide dismutase B using an expression vector system is under the study.

Key words: Superoxide dismutase, *Pseudomonas* strain, *Aeromonas*, phylogenetic analysis