B306 Degradation of Dimethylamine Salt of 2,4-Dichlorophenoxy-acetate by a Mixed Bacterial Culture in Stirred Tank Reactors

Min-Seok Cha* and Kye-Heon Oh
Department of Life Science, Soonchunhyang University

An aerated microbiological process was tested in 1.5-L stirred tank reactors for the treatment of dimethylamine salt of 2,4-D (2,4-dichlorophenoxyacetate). A mixed bacterial culture was used within the concentration range of 54 to 216 mg 2,4-D/L. The highest concentration was slightly enhanced by pH control to neutralize of hydrochloric acid formation resulting from the dechlorination reaction. 2,4-DCP (2,4-dichlorophenol), the first intermediate of the degradative pathway, accumulated transiently in the growth medium. HPLC and GC were used to measure and confirm 2,4-D and it also resolved 2,4-DCP, the corresponding phenol as intermediate. UV scans of spent cultures showed that the maximum absorption of 2,4-D at the wavelength of 283 nm was decreased toward the end of incubation, but the culture displayed no detectable spectral changes or peak shifts in the UV absorbance.

B307 Identification of Microorganisms Responsible for Anaerobic Degradation of Pentachlorophenol Using RFLP Analysis of PCR Amplified 16S rDNAs

Chang-Soo Seoung*, Soo-Woong Lee, O-Seob Kwon[1], and Young-Shik Park
Department of Microbiology, Environmental Sciences[1], Inje University

Chlorophenols are widespread toxic compounds. Reductive dechlorination of pentachlorophenol (PCP) was observed in PCP-adapted enrichment cultures derived from anaerobic sewage sludge and leachate of lanfill site. To identify the enriched microbial population by molecular techniques total genomic DNAs were PCR amplified from time-dependent culture broth of both sites. Total genomic DNA was isolated from the centrifuged precipitates. Amplified 16S rDNA products from six individual PCRs were pooled, purified, and ligated into pGEM-T vector. The whole ligation reactions were used for transformation. Total 47-50 positive clones were prepared from each of the samples and subjected to RFLP. After third round of restriction analysis two most prevalent kinds of clones were revealed in both active samples. The homogeneities of the whole clones classified to them by RFLP were confirmed by partial DNA sequencing. Both clones harboring 16S rRNA genes of microorganisms which are presumed to be responsible for the reductive dechlorination of PCP were identified by searching the most similar sequence in rRNA database.