B323 The Characterization and Isolation of Nitrate Reducing Bacteria and Denitrifying Bacteria Isolated from Activated Sludge in Plant

이한웅, 유경만, 이호정, 박용근
고려대학교 생명공학원

Thirteen bacteria were isolated from actived sludge in plant A deviced for removing nitrate. In the isolated 13 bacteria, 10 strains were isolated form sludge medium cultured under aerobic condition, and 3 strains were isolated form sludge medium culturded under anaerbic condition. In the result of nitrate reduction and denitrification test, AA7S4, AA8S2, and AAN2S29 were nitrate reducing ($NO_3^- \rightarrow NO_2^-$) bacteria, AA1S43 and AAN1S35 were denitrifying ($NO_3^- \rightarrow NO_2^- \rightarrow N_2O \rightarrow N_2$) bacteria. The isolated strains were identified by the VITEK system and the Bergey's Manual of Systematic Bacteriology. This study investigated for the characterization and the distribution of nitrate reducing bacteria and denitrifying bacteria in activated sludge of plant A.

B324 Waste Water Microcosms for Assesing Survival and Detection of Catechol-Biodegrading Strains

Soo Jin Choi and Yong Keun Park
Department of Biology, Korea University
Graduate School of Biotechnology, Korea University

Catechol-degrading bacteria, pIB1343 and KH1, were choosen as a model bacteria to estimate introduction of a catechol degrading ability into waste water microcosms. Prior to introduction into ecosystem, catechol degrading strains were experimented for their survival and catechol biodegradability in waste water miocrocosms. It was found that pIB1343 adapted and degraded more fastly in Namdong samples, on the other hand, KH1 more fastly in Sihwa samples. When catechol was added to microcosms, indigenous microorganisms in Sihwa samples used well catechol as a carbon and energy sources more than in Namdong samples. Under nonsterile conditions of microcosms, catechol was more fastly degraded than under sterile conditions because of existence of indigenous catechol-degrading microorganisms. A modified filter extraction technique was uesd for the high-yield extraction of purified DNA from 50㎖ of waste water samples and the extracted DNA (polymorphic DNA 〈20-23kb〉) was of a sufficient quantity and quality for PCR amplification. PCR was used to detect the *catA* gene encoding catechol 1,2-dioxygenase in waste water microcosms. PCR was performed with *catA* gene specific primer, C12U and C12L, and produced 320bp PCR products. PCR products were quantified of their intensities by densitometer, assumed CFU according to that intensity, and compared with CFU from plating counts. These results were correlated with the counts of microbes enumerated in the plates. The dominent strains of indigenous catechol-degrading bacteria in waste water environment were identified and classified into four groups based on the results of 16-23s rRNA intergenic spacer PCR (ITS PCR).