

Water quality assessment based on integrative community analysis of microorganisms in polluted aquatic systems

이예령¹, 송미영², 전태수², 전체옥³, 정영륜¹

¹경상대학교 응용생명과학부(BK21), ²부산대학교 생물학과, ³경상대학교 환경생명과학부

TEL : 055-751-5945 , e-mail : yrchung@gsnu.ac.kr

Microbial communities in polluted streams of Busan city area were analyzed in terms of organic matter degradation. Populations of bacteria which can degrade lipid, protein, cellulose and starch were determined on 0.1 tryptic soy agar(TSA) media supplemented with a 1%(w/v) tributyrin, skim milk, carboxymethyl cellulose and soluble starch, respectively. Various environmental factors affecting the community structures, concentrations of N, P, TOC and heavy metals were also analyzed statistically. The microbial community structures were identified with terminal restriction fragment length polymorphism (T-RFLP) analysis and denature gradient gel electrophoresis (DGGE) analysis. T-RFLP peaks and DGGE bands appeared in a diverse manner according to anthropogenic sources of pollution, and characteristically revealed the effect of pollution especially at the sites of industrial pollution. The populations of organic matter degrading bacteria were higher at sample sites polluted with more organic matters by SOM(self organizing mapping) analytical method.