

Parallel Analysis of Antimicrobial Activities in Microbial Community Using Single-Strand Conformation Polymorphism

정주희^{1,2}, 김진³, 박영섭⁴, 남명희¹, 오민규³, 김찬화²,
정규열^{4,5,*}

¹한국기초과학지원연구원 메타볼롬분석연구팀; ²고려대학교 생명공학원; ³고려대학교 화공
생명공학과; ⁴포항공과대학교
분자생명과학부; ⁵포항공과대학교 화학공학과
(gyjung@postech.ac.kr*)

Conventional antimicrobial activity analyses such as broth dilution method are demanding processes for new antimicrobial agent discovery and sensitive diagnosis on the infectious diseases. In this study, we developed a new antimicrobial activity analysis system based on single-strand conformation polymorphism (SSCP) combined with 16S rRNA gene specific PCR. By this method, population change of microbial community in response to the specific antimicrobial agents can be quantified with high sensitivity and accuracy from small amount of sample. Using a mixture of microorganisms containing *E. coli*, *C. glutamicum*, and *A. calcoaceticus*, it was found that the peak areas in 16S rRNA gene specific PCR-SSCP could quantify cell concentration. Subsequently, a comparison study with the broth dilution method using kanamycin, spectinomycin, and streptomycin showed that this method can be used for antimicrobial activity analysis. Results also demonstrated its high potential in the area of clinical diagnosis.