

**PA19) T-RFLP 분석 및 실시간 정량 PCR 법을 이용한 도시지역
대기 중 세균 및 진균 군집구조의 시간적 변이 조사**

**Monitoring of Temporal Variability of Airborne
Bacterial and Fungal Community Structure in Urban
Area by T-RFLP Analysis and Quantitative Real-time
PCR**

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This study explores the bacterial and fungal communities of total suspended particulates(TSP) in atmosphere by using molecular methods. Samples of TSP have been collected on glass-fiber filter at urban locations in the middle of Korean Peninsula(Seoul) at 7 times for a period between middle autumn and early winter in 2007. From filter aliquots loaded with about 400 milligram of air particulate matter, DNA could be extracted and DNA sequences could be determined for bacteria and fungi. Terminal restriction length polymorphism(T-RFLP) analysis was applied to analyze the community structure of bacteria and fungi. To estimate the concentration of DNA originated from bacterial and fungal communities, we used the quantitative real-time PCR(Q-RT-PCR). Sequence analyses were also used to determine the identity of biological organisms. We found that large shifts in the community structure of bacteria and fungi present in our TSP samples collected on different dates. The number of bacteria and fungi for air in this study were determined to range from 5.19×10^1 to 4.31×10^3 cells m^{-3} and from 9.56×10^1 to 4.22×10^4 cells m^{-3} , respectively and bacterium/fungus ratios ranged from 0.09 to 0.76 across the seven sampling dates. Through T-RFLP and sequence analyses, we observed that most of the bacterial sequences found in our TSP samples were from *Proteobacteria*, *Actinobacteria*, *Firmicutes*, and *Bacteroidetes*. The fungal sequences were characteristic for *Ascomycota*, *Basidiomycota*, and *Glomeromycota* which are known to actively discharge spores into the atmosphere. The plant sequences also could be detected. The results demonstrated that in our TSP samples collected at urban site, i) there are very diverse bacteria and fungal group including potential pathogens and allergens and ii) there are temporal shifts in both bacteria and fungal community in terms of both diversity and abundances across a mid-term time period.