

**B325** Microbial Degradation of 2,4,6-Trichlorophenol by a White-Rot Fungus  
*Phanerochaete chrysosporium*

Sung-Chan Choi, Mi-Sun Kim\*, Kwang-Keun Oh<sup>1</sup>, and Yeong-Kwan Kim<sup>2</sup>  
Division of Life Sciences, Hallym University

<sup>1</sup>Institute of Science & Technology, Cheiljedang Corporation

<sup>2</sup>Division of Biol. & Environ. Engineering, Kangwon National University

2,4,6-Trichlorophenol (TCP) is a hazardous pollutant causing environmental and health problems for mankind. *Phanerochaete chrysosporium* is one of the most studied fungus for bioremediation because of its high growth rate and lignin degrading capability. The purpose of this study was to determine the degradation characteristics of TCP by *P. chrysosporium*. The initial removal rates were measured to examine the degradation kinetics of TCP according to various TCP concentrations. TCP degradation did not reach to steady state at concentrations up to 4.4 mM, indicating that the solubility limit of TCP in water could be a limiting factor in the degradation process. The adsorption rate of TCP by heat-killed strain incubated at 30°C for 48 hrs increased as TCP concentration increased. The results showed that over 50% of TCP was mineralized, indicating that the degradation was the primary removal mechanism over adsorption. The initial rate determined in this study was found to be higher than the previously reported values.

**B326** Phylogenetic Analysis of Epiphytic Bacterial Communities on Plant Leaves  
in the Industrial Area and in the Clean Natural Forest Area

Pil-Mun Jeong<sup>1</sup>, Son-Hong Park<sup>1</sup>, U-Jin Kim<sup>1</sup>, Sook-Jin Bang<sup>2</sup>,  
In Soo Lee<sup>3</sup>, and Seong Ioo Park<sup>1</sup>

<sup>1</sup>Department of Microbiology, Taejeon University

<sup>2</sup>Water Supply & Sewerage Research Team, Water Resources Research Institute

<sup>3</sup>Department of Microbiology, Hannam University

Epiphytic bacterial communities on plant leaves (*Castanea crenata* S. et Z.) collected from the industrial area and the clean natural forest area were compared by phylogenetic analysis. PCR-amplified 16S rRNA genes from epiphytic bacteria were cloned, and a total of 39 eubacterial clones were obtained from both leaf samples. All clones were characterized by restriction fragment length polymorphism (RFLP) with the enzymes *Hae* III and *Hinf* I, and a total of 10 unique RFLP patterns (phylotypes) were identified. The phylotypes were slightly different each other, 6 phylotypes from industrial leaf samples and 3 from the clean samples but only 1 phylotype from both samples. By phylogenetic analysis, the partial sequences of all kinds of phylotype were placed into two major lineages of the *Bacteria* domain: the  $\gamma$  and  $\beta$  subdivisions of the phylum *Proteobacteria*. Analysis at the subphylum level revealed that the predominant group was *Pseudomonas* spp. of the subphylum of  $\gamma$ -proteobacteria (84.6% for industrial leaves and 81.8% for clean leaves), having the most diverse metabolic capabilities among microorganism. A distinct characteristics of epiphytic bacterial communities on industrial leaves is that no enteric bacteria were detected.