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The Screening of TEM Type Penicillinase Gene by Dot Blot Hybridization of *Klebsiella pneumoniae* Isolated from Patients

Jae sun Choi* and Yun Tai Lee
Department of Microbiology, Dankook University

Bacterial strains that cause nosocomial infections have their characteristic multiresistance against drug. *K. pneumoniae,* belonging to these strains, is also multiresistant. It is serious problem that the multiresistant strains cannot be controlled through the clinical therapy involving antimicrobial agents. This research concerns the TEM Type penicillinase gene which produces various types of β-lactamases. By investigating the *K. pneumoniae* which are isolated from clinical patients, this study aims at the molecular biological epidemical data which can be useful for a more effective antimicrobial therapy. 52(60%) of the *K. pneumoniae* 87 strains produced β-lactamase. In the resistance frequency test involving 5 kinds of β-lactam antimicrobial agents, 31 of 52 strains proved to be resistant to more than two agents, and 29(93.6%) of this 31 produced β-lactamase. Through the dot blot hybridization, 30 strains of the 52 β-lactamase producing strains which are 34.5% of the entire 87 strains, turned out to have TEM type penicillinase gene. Most of these strains also were found out to have more than one plasmid. The percentage of strains having penicillinase gene shown above requires a more careful consideration in choosing antimicrobial agents. Only when the antimicrobial agent is effectively used, the resistant strains haboring in hospitals can be reduced. Besides, it can also be prevented that the extended-spectrum β-lactamase spreads to the cephalosporin of third generation.

F315 Analysis of Nucleotide Sequence of alkane monooxygenase

Na-Ri Lee*, Chung-Il Cheon, and Kyung-Hee Min
Department of Biology, Sookmyung Women's University

The structural genes of the *Pseudomonas maltophilia alk* system, which are localized on the OCT plasmid were cloned as a 4.2-kilobase pair Hind III fragment. This fragment contains sequences for alkane hydroxylase gene (*alk*B) and rubredoxin reductase gene (*alk*A), respectively. The *alkB* sequence was composed of 1119 nucleotides, which exhibited 62.9% homology with the corresponding sequence for alkane hydroxylase of *Pseudomonas oleovorans.* The *alk*A region located downstream of the *alk*B gene was composed of 791 nucleotides, which showed 32.0% and 56% homologies to corresponding sequences of *alk*F and *alk*G coding for rubredoxin reductase in *P. oleovorans.* Thus the nucleotide composition of the *alk*A gene in *P. maltophilia* differs considerably from that of the *P. oleovorans* genome suggesting that the *alk* regulon may evolve indepenently in different organisms. The *alk*BA genes were complemented with alkane hydroxylation in both bacteria.