

## Microevolution and Macroevolution of Antimicrobial Resistance Genes Identified in Korea

Dong Taek Cho

*Department of Microbiology, Kyungpook National University School of Medicine,  
Taegu 700-422, Korea*

Bacterial genomes are not static, monolithic structure but they are relatively variable, fluid structure. This plasticity is mainly the result of the rearrangement of genes within the genome and the acquisition of novel genes by horizontal transfer system, e.g. plasmids, bacteriophages, transposons or integrons.

Molecular gene evolutions of *Shigella sonnei* isolated in Korea so far have showed concerted changes in terms of microevolution and macroevolution. Microevolutions responsible for the rapid emergence of variants with novel virulence gene and antimicrobial resistance properties were revealed by genotyping methods. Evolutionary processes that proceed over longer time periods are termed macroevolution. As good example of microevolutions, novel genes of extended-spectrum  $\beta$ -lactamase producing Gram-negative organism

identified in Korea showed undergoing adaptation by point mutation led to the fittest survival genes. Methicillin resistant *Staphylococcus aureus*, a gram positive organism also rendered another examples of the emergence of variants with promoter or regulator genes of *mecA*.

Noteworthy is that *Sh. sonnei* species showed drastic changes of molecular structure of antimicrobial resistance genes as well as the newly generated genotype by adaptive mutations in virulence genes.

Large outbreak-related *Sh. sonnei* isolated recently revealed quite different genetic structure which carried horizontal gene transfer by plasmid and transposon. Loss of conjugal transferability of R-plasmid of *Sh. sonnei* was first detected and reported.