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심포지움

Molecular Strain Typing in Clinical Microbiology Laboratory

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Several molecular techniques has been introduced recently for the differentiation of microbial isolates: plasmid profiles, restriction fragment length polymorphism of chromosomal DNA or plasmids, ribotyping, arbitrarily primed PCR, pulsed-field gel electrophoresis(PFGE), and phylogenetic analysis. Molecular strain typing became an essential tool for epidemiological investigation. And conventional serotyping or phage typing methods are so time-consuming and labor-intensive that molecular fingerprinting methods are used as a substitute. Clinical microbiology laboratory cannot help doing strain typing for infection prevention and control, and should make a good choice among them in respect of efficiency and cost effectiveness.

PFGE, compared with other methods, can provide a high level of discrimination and is used as a method of choice for strain typing of a wide variety of organisms. For example, bacteriophage typing is not used but PFGE is recommended for the classification of methicillin- resistant *Staphylococcus aureus* isolates. Results are reproducible and easy to interpret. Guideline has been proposed for evaluating whether PFGE patterns represent the same or different strains. But other genotyping methods such as plasmid profiles or arbitrarily primed PCR occasionally may be useful for further evaluation of isolates. The major disadvantage is that the method is more complicated and expensive than other genotyping methods.

The introduction of diagnostic procedures based on nucleic acid sequences, in particular PCR, has recently increased the need for precise classification of microorganisms in accordance with their molecular characteristics. Statistical methods in molecular phylogenetics have been developed and amenable to use in the clinical microbiology laboratory for the classification of some microorganisms. Currently used methods such as neighbor joining, minimum evolution, likelihood, and parsimony methods produce reasonably good phylogenetic trees when a sufficiently large number of nucleotides or amino acids are used. For example, clinically significant serotypes of enteroviruses, which are presently composed of 67 individual serotypes and distinguished on the basis of the neutralization tests with restricted amount of antisera, can be identified by the phylogenetic approach based on RT-PCR and nucleotide sequencing of the 3′ half of genomic region encoding VP1.

In the near future, the number of microorganisms available for molecular strain typing will be increased and the molecular techniques for strain typing will be a routine test in clinical microbiology laboratory. It is essential to keep a close communication between the clinical microbiology laboratory and the hospital epidemiologists for the efficient and appropriate use of molecular strain typing results.