

Pathogen Detection and Antibiotics Selection in Neurology Wards



주 건
서울대병원

Kon-Chu, MD, PhD.

Department of Neurology, Seoul National University Hospital, Seoul, South Korea.

Microbial diagnosis of various infections is basic to clinical antibiotic treatment. It depended on classical bacterial culture and antibiotic susceptibility testing, however unculturable bacteria or anaerobes could not be easily detected, and even if the bacteria was cultured, the timing was usually delayed. Recently, metagenomic analysis has been introduced to medical field, and been widely used in the microbial detection of clinical samples. Metagenomics is direct genetic analyses of genomes within a sample, made possible by modern genomic analytical tools. 16s ribosomal RNA (16s rRNA) genes are expressed in all bacteria and archaea and code for a component of the 30S subunit of ribosomes. As these genes are highly conserved, they are a valuable means of identifying bacteria. Multiple copies can exist within a single bacterium. Currently, sequencing-based approaches for pathogen identification are being applied. The MinION (Oxford Nanopore Technologies, Oxford, UK) is a nanopore sequencer that is gaining attention in metagenomics research because of its capability for long-read sequencing and real-time analysis, along with its small size. With the MinION sequencer, generated reads can be analyzed in real time, thereby making this approach more promising. In this lecture, I will present various examples of Metagenomic application on rapid diagnosis of bacterial infections. And, in the second part of the lecture, recent trends of etiologies of bacterial infections in neurology wards (bacterial meningitis, aspiration pneumonia, and urinary tract infection) will be presented.
