

Roles of Metagenomics in Encephalitis Diagnostics

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Metagenomics, sequencing the total deoxyribonucleic acid (DNA) or ribonucleic acid (RNA) from cerebrospinal fluid (CSF) or brain tissue can identify genetic material of microorganisms present in the specimens. To date, the majority of available sequencing techniques are DNA based. Excluding detection of viruses with RNA genomes or RNA transcripts of microorganisms with DNA genomes would be sequenced only total DNA. This technique needs no assumptions of pathogenic microorganisms, thus, enabling detection of unexpected microorganisms that overcomes the limitations of targeted diagnostic techniques, such as polymerase chain reaction (PCR). Nevertheless, metagenomic data require careful analysis to identify microorganisms that represent true pathogenic organisms rather than environmental contamination. By consideration of the sensitivity of the next-generation metagenomic sequencing (NGMS) techniques, the authors suggest that individual laboratories will need to develop their own dynamic reference data sets for controlling contaminants.

In conclusion, knowledge of NGMS is critical for future development of increasingly rapid, low-cost, and fast point-of-care tests for screening CSF in unbiased manners for broad ranges of human pathogenic microorganisms and developing clinical algorithms that minimize the time to diagnosis and treatment.

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