

Real-time whole genome sequencing direct diagnosis of community-acquired bacterial meningitis

Morsli Madjid

IHU Méditerranée Infection, France

Community-acquired bacterial meningitis (CABM) is a life-threatening condition whose prognosis is partially depends on the causative bacteria genotype, which requires efficient diagnosis, patient management and adequate treatment. Current routine point-of-care multiplex real-time PCR diagnosis of CABM allowed to detect the presence of the pathogen genome in the cerebrospinal fluid (CSF). This assay requires additional in-vitro investigation for pathogen genotyping and antibiotic-resistance tests. Here we proposed one-shot **pathogen genotyping** in a case of deadly Haemophilus influenzae (H. influenzae) meningitis. Real-time PCR diagnosed H. influenzae meningitis in a 22-year-old male patient immunized against H. influenzae b serotype, during his hospitalization following a more than six-meter fall. Using metagenomics real-time sequencing in parallel to real-time PCR, we detected the H. influenzae genome directly from the CSF sample in six hours workflow, in-silico susceptible to the antibiotic panel used in routine. Furthermore, **BLAST analysis** of the sequence encoding for a partial DUF417 domain-containing protein diagnosed a non-b serotype, non-typeable H. influenzae belonging to lineage H. influenzae 22.1-21. The Oxford Nanopore metagenomic next-generation sequencing approach could be considered for the point-of-care diagnosis of infectious meningitis, by direct identification of pathogenic genomes and their genotypes/serotypes.

Biography

MORSLI Madjid, PhD, researcher at IHU Méditerranée Infection, Aix-Marseille Université, Marseille, France. The main research project focuses on the improvement of community-acquired meningitis diagnosis using both metagenomics next-generation sequencing and real-time metagenomics and its implementation at the Point-Of-Care laboratory.

mor_madjid@hotmail.com