16S ribosomal RNA

16S ribosomal RNA (or 16S rRNA) is the RNA component of the 30S subunit of a prokaryotic ribosome (SSU rRNA). It binds to the Shine-Dalgarno sequence and provides most of the SSU structure.

The genes coding for it are referred to as 16S rRNA gene and are used in reconstructing phylogenies, due to the slow rates of evolution of this region of the gene.

Carl Woese and George E. Fox were two of the people who pioneered the use of 16S rRNA in phylogenetics in 1977.

Multiple sequences of the 16S rRNA gene can exist within a single bacterium.

Jang et al. performed nanopore 16S amplicon sequencing from cerebrospinal fluid (CSF) to evaluate bacterial meningitis in patients who underwent neurosurgery.

Among the patients who visited the neurosurgery department of Seoul National University Hospital between July 2017 and June 2020, those with clinically suspected bacterial meningitis were included. 16S rDNA PCR was performed from the CSF, and nanopore sequencing was performed for up to 3 h. The reads were aligned to the BLAST database. In each case, the culture and the 16S rRNA gene amplicon analysis were simultaneously performed and compared with each other, and they retrospectively reviewed the medical records. Genuine infection was determined by the identical results between conventional culture study and the sequencing, or clinically determined in cases with inconsistent results between the two methods.

Of the 285 samples obtained from 178 patients who had 16S rDNA PCR, 41 samples (14.4%) were diagnosed with genuine infection. A total of 56.1% (23/41) of the samples with genuine infection showed a false-negative culture test. In particular, 16S amplicon sequencing was useful in evaluating patients at the initial tests who had infection with intraventricular hemorrhage (Culture false-negative rate = 100%), subarachnoid hemorrhage (Culture false-negative rate = 77.8%), and systemic cancer (Culture false-negative rate = 100%), which are risk factors for central fever. Moreover, 16S amplicon sequencing could suggest the possibility of persistent bacterial meningitis in empirical antibiotic use.

CSF nanopore 16S sequencing was more effective than conventional CSF culture studies in postoperative bacterial meningitis and may contribute to evidence-based decisions for antibiotic maintenance and discontinuation [1)]

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Jang Y, Kim S, Kim N, Son H, Ha EJ, Koh EJ, Phi JH, Park CK, Kim JE, Kim SK, Lee SK, Cho WS, Moon J, Chu K. Nanopore 16S sequencing enhances the detection of bacterial meningitis after neurosurgery. Ann Clin Transl Neurol. 2022 Feb 6. doi: 10.1002/acn3.51517. Epub ahead of print. PMID: 35124895.