



This preliminary clinical study aimed to examine whether next-generation sequencing (NGS) targeting 16S rDNA, which was PCR-amplified directly from the tip of a central venous catheter (CVC), can be used to identify causative pathogens in CRI, compared to the culture method” Okuda et al (2018).

Abstract:

BACKGROUND: Catheter-related infection (CRI) is one of the serious challenges in clinical practice. This preliminary clinical study aimed to examine whether next-generation sequencing (NGS) targeting 16S rDNA, which was PCR-amplified directly from the tip of a central venous catheter (CVC), can be used to identify causative pathogens in CRI, compared to the culture method.

METHODS: Hospitalized patients, from whom a CVC had just been removed, were prospectively enrolled and divided into the CRI-suspected and routine removal groups. DNA was extracted from the sonication fluid of CVC specimens derived from patients. For analysis of bacterial composition by NGS, the V3-V4 fragments of bacterial 16S rDNA were PCR-amplified, followed by index PCR and paired-end sequencing on an Illumina MiSeq device. Conventional culture methods were also performed in the CRI-suspected group.

RESULTS: Of CVCs collected from the 156 enrolled patients (114 men; mean age 65.6 years),

a total of 14 specimens were PCR-positive. In five patients with definite CRI, *Staphylococcus* was the most frequently detected genus by NGS (4/5 specimens), although no pathogens were detected by NGS in the one remaining specimen. The genera identified by NGS were consistent with those from conventional culture tests. There was high agreement between NGS and the culture method in the CRI-suspected group, with sensitivity and specificity values of 80.0% and 76.9%, respectively; meanwhile, the false-positive rate of NGS was as low as 4.0% in the routine removal group. Moreover, several genera, besides the genus identified by culture test, were detected in each patient with definite CRI and surgical site infection (SSI). Additionally, in one patient with SSI, Enterococcaceae were detected not only by NGS but also by abdominal abscess drainage culture.

CONCLUSIONS: NGS targeting 16S rDNA was able to analyze the bacterial composition of CVC specimens and detect causative pathogens in patients with CRI and was therefore suggested as a promising diagnostic tool for CRI.

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Okuda, K.I., Yoshii, Y., Yamada, S., Chiba, A., Hironaka, I., Hori, S., Yanaga, K. and Mizunoe, Y. (2018) Detection of bacterial DNA from central venous catheter removed from patients by next generation sequencing: a preliminary clinical study. *Annals of Clinical Microbiology and Antimicrobials*. 17(1), p.44.

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