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Research Letter

Metagenomic next-generation sequencing for the detection of bacterial translocation in the blood of patients following liver, biliary tract or pancreatic surgery

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Dear Editor,

As an emerging, culture-independent, and unbiased technology for pathogen detection, metagenomic next-generation sequencing (mNGS) has been introduced to diagnose various infectious diseases, including surgical perioperative infections. Hepatopancreatobiliary (HPB) surgery is one of the most invasive abdominal procedures. Several studies have shown an increased risk of bacterial translocation (BT) into the blood following HPB surgery, which can contribute to the development of surgical site infections (SSIs)[1]. Therefore, monitoring BT is an important part of strategies to reduce the risk of SSIs. However, conventional microbial culture is inefficient at detecting BT[2]. This study aims to analyse the performance of mNGS in detecting BT and to explore the effects of BT on SSIs after HPB surgery based on mNGS results.

This retrospective study included 45 patients who underwent HPB surgery between March 2022 and March 2023 at the First Affiliated Hospital of Guangxi Medical University in China. Blood samples from these patients were analysed using both mNGS and culture. The patient recruitment criteria and flow diagram are provided in Supplementary Methods and *Fig. S1* respectively. A total of 12 bacteria, five viruses, and one parasite were identified through mNGS, whereas culture identified only six bacteria (*Fig. S2*). The bacterial detection rate for mNGS was significantly higher than that of culture (40.0% *versus* 13.3%, $P < 0.001$, *Fig. 1a*). The most common bacteria involved in BT were *Escherichia coli*. In addition, mNGS achieved a significantly higher identification rate of polymicrobial detection compared to culture (33.3% *versus* 2.2%; $P < 0.001$; *Fig. 1b*). Of the 45 patients, five had positive results for both mNGS and culture, whereas 17 had negative results for both methods. Additionally, 22 patients tested positive solely by mNGS, and one was positive exclusively by culture (*Fig. 1c*). Among the five double-positive patients, four showed partial consistency between mNGS and culture results, whereas one showed complete inconsistency (*Table S1*).

BT was observed in 40% (18/45) of the patients, and SSIs were observed in 31% (14/45) following HPB surgery. Univariate and multivariate analyses suggested that obstructive jaundice was an independent risk factor for BT (OR = 6.22, 95% c.i. 1.24 to 31.17; $P = 0.026$), whereas BT was an independent risk factor for SSI in patients who underwent HPB surgery (OR = 8.45, 95% c.i. 1.69 to 42.18; $P = 0.009$). Detailed data are provided in *Tables S2–S5*.

The mechanism underlying the association between the detection of BT in the bloodstream and the incidence of SSIs remains unclear. One possible explanation stems from the ‘Trojan Horse hypothesis’ of gut-derived remote infection, which suggests that certain microorganisms can be transmitted from the gut through the bloodstream to the wound by being captured by immune cells, resulting in SSI[3]. Another possible explanation involves the negative effects of intestinal microbial consortia on the gut barrier and host immune system following surgical injury[4]. In patients with BT and microbial dysbiosis, immune dysfunction may occur, a situation particularly evident in obstructive jaundice[5]; thus, these patients are more likely to develop SSI after surgery. In addition to the intestinal source, it is undeniable that part of BT may also originate from skin-colonizing and environmental bacteria.

Metagenomics NGS of blood samples represents a significant advancement in the diagnosis of BT. This diagnostic approach may guide more precise postoperative prophylactic treatments and facilitate the early identification and prevention of SSIs.

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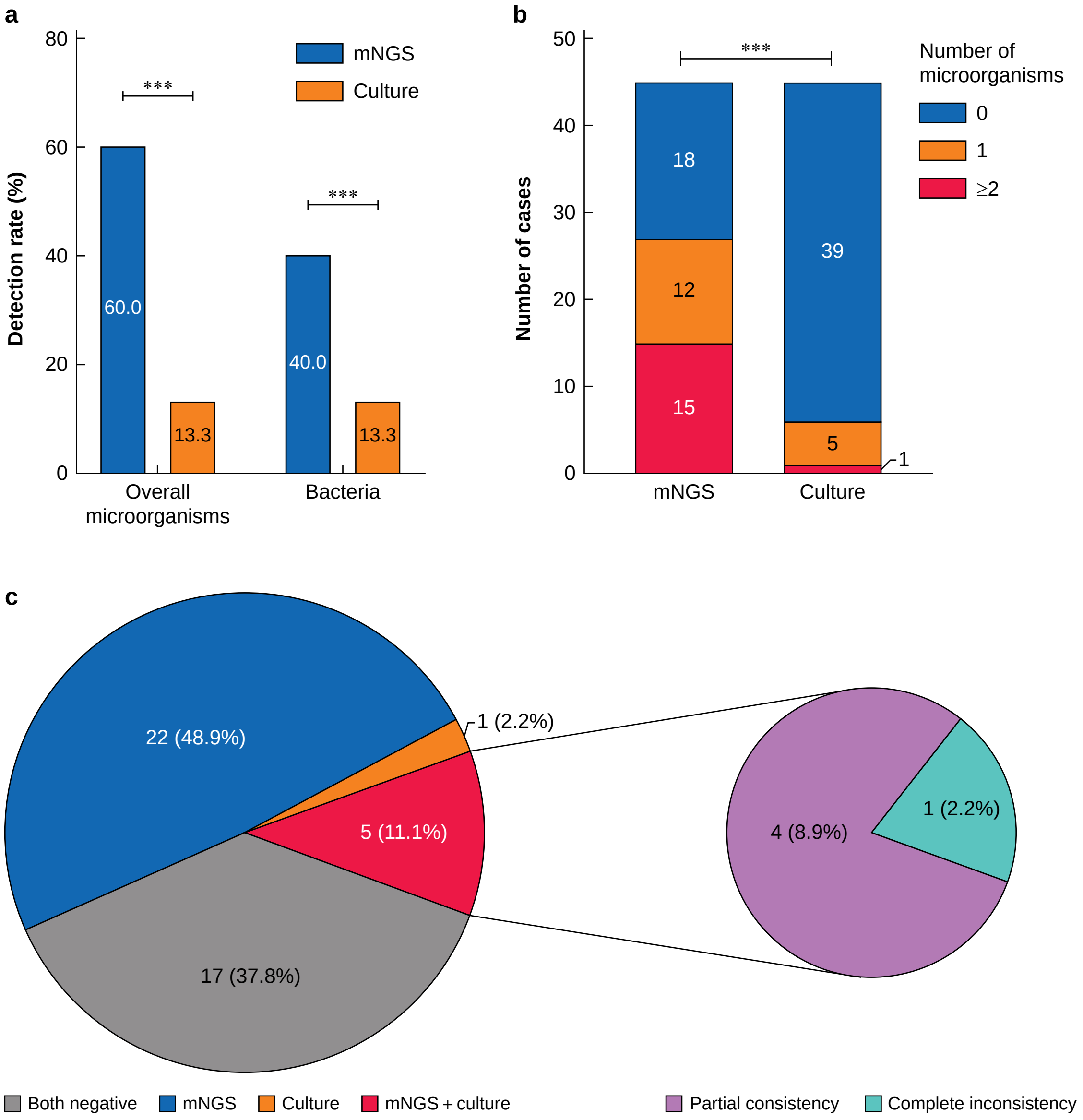

Fig. 1 Comparison of diagnostic performance between mNGS and culture
a The detection rates for overall microbes and bacteria were significantly higher with mNGS compared to culture (both $P < 0.001$). **b** mNGS yielded a higher incidence of polymicrobial results compared to culture ($P < 0.001$). **c** Positive results showed consistent agreement between mNGS and culture. mNGS, metagenomic next-generation sequencing

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Disclosure

The authors declare no conflict of interest.

Supplementary material

Supplementary material is available at *BJS* online.

Data availability

The study data are available on request. The mNGS sequencing data can be found at: https://www.ncbi.nlm.nih.gov/bioproject/PRJNA1139112.

Author contributions

Zhenfeng Deng (Writing—original draft), Zhujing Lan (Writing—original draft), Huaitao Zhu (Data curation, Investigation), Hongbing Ren (Data curation, Investigation), Zongrui Jin (Data curation, Investigation), Jiajun Jiang (Data curation, Investigation), Tiansheng Lan (Data curation, Investigation), Jinyuan Zhou (Data curation, Investigation), Jilong Wang (Data curation, Investigation, Visualization), Peiqi Wan (Data curation, Investigation, Visualization), Ya Guo (Data curation, Resources), Banghao Xu (Formal analysis, Investigation), Hai Zhu (Supervision, Visualization, Writing—review & editing), and Zhang Wen (Methodology, Supervision, Writing—original draft, Writing—review & editing)

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