EDITORIAL

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Endoscopic ultrasound-guided tissue acquisition for personalized treatment in pancreatic adenocarcinoma

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See "Clinical utility of endoscopic ultrasound-guided tissue acquisition for comprehensive genomic profiling of pancreatic cancer" by Nozomi Okuno, Kazuo Hara, Nobumasa Mizuno, et al., Clin Endosc 2023;56:221–228.

Pancreatic adenocarcinoma (PAC) is a complex and challenging disease with a low survival rate and limited effective treatment options. However, recent advancements in our understanding of PAC's biology have provided a roadmap for a more precise treatment approach.^{1,2} This has led to the development of therapies targeted at specific vulnerabilities in each patient's cancer. For example, a PAC that is deficient in homologous recombination and mismatch repairs should be identified in the clinic for a targeted approach. KRAS wild-type PAC, occurring in approximately 10% of patients, exhibit highly actionable alterations, including fusions; these alterations underscore the importance of integrative germline and somatic sequencing.

Endoscopic ultrasound-guided tissue acquisition (EUS-TA) has become an increasingly important tool in the diagnosis and staging of PAC and in obtaining tissue samples for genetic and molecular analysis.³ One of the advantages of EUS-TA is that it can be performed from early-stage disease to advanced metastatic disease. Next-generation sequencing (NGS) analysis is a powerful tool that analyzes genetic and molecular alter-

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Research Institute, Center for Liver and Pancreatobiliary Cancer, National Cancer Center, 323 Ilsan-ro, Ilsandong-gu, Goyang 10408, Korea **E-mail**: wsm@ncc.re.kr ations in cancer cells. NGS analysis of EUS-TA-derived material can significantly impact the management of PAC, leading to changes in therapeutic regimens and support of inconclusive or uncertain cytology results. However, the clinical utility of EUSfine-needle biopsy (FNB) has been hampered by concerns of low tissue quantities yielding suboptimal genetic material and sample contamination with non-malignant cells.

Although EUS-TA shows high diagnostic accuracy, the sample quantity obtained may be limited. This is particularly problematic when trying to obtain genetic information from rare or low-frequency mutations, which may be absent in the limited tissue sample obtained via EUS-FNB. Therefore, acquiring a large volume of good-quality samples via EUS-TA is integral for NGS. There is an ongoing debate regarding the optimal EUS-TA procedure, such as needle gauge (G) and type, number of passes required to acquire adequate samples, suction syringe vs. pull technique, and rapid onsite evaluation depending on lesion type.

Evidence suggests that FNB needles may provide higher specimen adequacy and DNA yield for NGS in PAC than fine-needle aspiration (FNA) needles. A tandem, randomized controlled trial, which included 50 patients with suspected or confirmed PAC, reported that specimen adequacy for genomic profiling and DNA yield was significantly higher with FNB needles than with FNA needles.⁴ Another large retrospective study, which included 190 patients with histologically proven PAC using EUS-FNA or FNB samples, determined that needles with a larger gauge (19 or 22 G) may be associated with higher NGS

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success rates than those with a smaller guage.⁵

In this issue of *Clinical Endoscopy*, Okuno et al.⁶ evaluated the adequacy rate of needles with different gauges for comprehensive genomic profiling (CGP) in PAC samples obtained via EUS-TA. They concluded that 19 G-FNB needles were the most effective in obtaining adequate samples for CGP. However, even using their optimal method with 19 G-FNB, the adequacy rate needed to be improved. The adequacy rate with 19G-FNB for CGP was 72.5% (29/40). The success of NGS analysis of the EUS-TA-derived samples can be influenced by several pre-analytical factors, including the input DNA threshold, DNA yield, and sample cellularity.⁷ Further studies are needed to identify the optimal EUS-TA-derived samples in NGS analyses. These factors need to be addressed to improve the performance of molecular testing for PAC.

Conflicts of Interest

The author has no potential conflicts of interest.

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