KJCO Korean Journal of Clinical Oncology
Korean Journal of Clinical Oncology 2023;19:43-44
https://doi.org/10.14216/kjco.23008
pISSN 1738-8082 · eISSN 2288-4084
Editorial

Integrating ctDNA and tumor tissue analysis in gastric cancer: a synergistic approach unveils prognostic insights

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Article: Concordance of circulating tumor DNA and matched formalin-fixed paraffin-embedded tumor tissue in gastric cancer as a predictor of recurrence **(Seo SH, et al. Korean J Clin Oncol 2023;19:45-51)**

Gastric cancer, a formidable global health challenge, ranks as fifth most frequently diagnosed cancer and as the third highest leading causes of cancer-related mortality worldwide [1]. Despite advances in diagnostic and therapeutic strategies, the high mortality rates associated with gastric cancer underscore the critical need for innovative approaches to enhance early detection and precision medicine interventions. Gastric cancer, with its complex genomic landscape, poses a formidable challenge in the realm of oncology [2]. Precision medicine is gaining prominence in improving treatment outcomes for gastric cancer, with circulating tumor DNA (ctDNA) emerging as a key player in this paradigm shift [3].

ctDNA, fragments of tumor-derived DNA circulating in the bloodstream, offers a noninvasive window into the genomic landscape of gastric cancer [4]. Recent strides in liquid biopsy techniques have propelled the field forward, and among these, ctDNA emerges as a promising player in revolutionizing the diagnostic landscape [5]. Its potential to reflect the dynamic alterations in the tumor genome provides a unique opportunity for real-time monitoring and personalized treatment strategies [6].

In recent years, the exploration of ctDNA has burgeoned, with compelling evidence supporting its pivotal role in solid cancers. Pioneering studies, such as the landmark work by Bettegowda et al. in 2014 [7], have illuminated ctDNA's prowess as a noninvasive diagnostic tool [7]. This seminal research, centered on colorectal and breast cancers, demonstrated the sensitivity of ctDNA in detecting somatic mutations, opening avenues for early cancer detection. Moreover, the prognostic value of ctDNA has been underscored in investigations like the study by Abbosh et al. in 2017 [8] on non-small cell lung cancer. By unraveling the dynamic genomic landscape through ctDNA analysis, the research unveiled its potential to prognosticate disease progression and guide treatment decisions [8]. These findings catalyzed a paradigm shift in our approach to solid cancer management.

The study [9], titled "Concordance of circulating tumor DNA and matched formalin-fixed paraffin-embedded tumor tissue in gastric cancer as a predictor of recurrence," published in this issue of the *Korean Journal of Clinical Oncology*, introduces a pioneering approach to understanding gastric cancer dynamics. By concurrently analyzing ctDNA and tumor tissue, the research uncovers compelling correlations, revealing that higher concentrations of cell-free DNA (cfDNA) are associated with advanced tumor stages and larger tumor sizes.

This groundbreaking investigation involved 46 gastric cancer patients, employing targeted deep sequencing on both cell-free plasma and formalin-fixed paraffin-embedded tumor tissue samples. The study's findings unveil a nuanced genetic landscape, where only a subset of tumor tissue mutations aligns with those identified in ctDNA samples. Notably, actionable variants found in concordance were predominantly observed in later-stage gastric cancer, showcasing the clinical relevance of preoperative ctDNA analysis.

Received: Dec 15, 2023 **Accepted:** Dec 26, 2023
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Beyond diagnostic implications, the study positions the concordance between preoperative ctDNA and tumor tissue mutations as a robust prognostic indicator. The association of preoperative ctDNA positivity for actionable variants with clinicopathological parameters, including cfDNA concentration, lymphatic invasion, N stage, and TNM stage, underscores its potential as a comprehensive prognostic tool.

Moreover, the study establishes a significant link between cancer recurrence and the concordance of ctDNA and tumor tissue mutations, reinforcing the prognostic value of this integrated approach. The collective parameters of tumor size, lymphatic/vascular invasion, TNM stage, and the alignment of ctDNA-tumor tissue variants provide a comprehensive prognostic framework for gastric cancer patients.

In conclusion, the study marks a significant milestone in precision oncology. The integration of ctDNA and tumor tissue analysis not only enhances diagnostic accuracy but also equips clinicians with a powerful prognostic tool. This synergistic approach offers a holistic understanding of the genetic landscape of gastric cancer, laying the foundation for personalized interventions and improved outcomes at the intersection of technology and oncology.

CONFLICT OF INTEREST

Jong Hyuk Yun is an editorial board member of the journal but was not involved in the peer reviewer selection, evaluation, or decision process of this article. No other potential conflicts of interest relevant to this article were reported.

FUNDING

This work was supported by the Soonchunhyang University Research Fund.

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