Opinion
Volume 17:06, 2025

Journal of Bioanalysis & Biomedicine

ISSN: 1948-593X

Open Access

Liquid Biopsies: Advancing Cancer Detection and Treatment

Rashid A. Khan*

Department of Biotechnology & Bioanalysis, Quaid-i-Azam University, Islamabad, Pakistan

Introduction

Circulating tumor cells (CTCs) and extracellular vesicles (EVs) represent critical biomarkers in the realm of liquid biopsies, providing non-invasive insights into cancer progression and therapeutic response [1]. These vital components offer a window into the complex biology of cancer, enabling a deeper understanding of disease dynamics without the need for invasive tissue sampling. Advancements in bioanalytical techniques are continuously enhancing our ability to capture, characterize, and perform molecular profiling of these circulating analytes, which is fundamental for their clinical utility.

The isolation and characterization of CTCs are paramount for comprehending the mechanisms of metastatic disease [2]. The ability to detect and analyze these rare cells directly from patient blood is a significant breakthrough, opening avenues for early detection and personalized treatment strategies. Microfluidic devices, in particular, have emerged as powerful and efficient tools for the enrichment of CTCs from blood samples, facilitating downstream molecular analyses that can reveal actionable mutations and guide therapy selection.

Extracellular vesicles (EVs), including exosomes, are recognized for their role as key intercellular messengers, carrying a diverse cargo of biomolecules such as proteins, RNA, and DNA [3]. Their presence and molecular composition in biofluids offer a unique perspective on the tumor microenvironment and the overall systemic status of the disease. The development of standardized protocols for EV isolation and characterization is a critical step towards their successful clinical translation and widespread adoption.

The synergistic analysis of CTCs and EVs in liquid biopsies holds significant promise for enhancing cancer diagnostics and prognostics [4]. By examining both cell-free and cellular components, clinicians and researchers can gain a more comprehensive understanding of tumor heterogeneity and the dynamic processes of disease progression, thereby improving the accuracy and reliability of liquid biopsy-based assessments.

Single-cell analysis of circulating tumor cells (CTCs) provides an unprecedented level of resolution, allowing for the capture of the inherent heterogeneity within metastatic disease [5]. Techniques that enable the simultaneous interrogation of multiple biomarkers on individual CTCs are essential for unraveling the complexities of treatment resistance and for guiding optimal therapy selection.

The molecular cargo encapsulated within extracellular vesicles (EVs) serves as a valuable reflection of the physiological state of their cell of origin, positioning them as important diagnostic and prognostic markers [6]. The study of EV-derived RNA, including microRNAs and messenger RNAs, offers profound insights into the gene expression patterns within tumors and can help identify potential therapeutic targets.

Establishing standardized and robust bioanalytical methods for the enumeration, phenotyping, and molecular profiling of CTCs and EVs is absolutely essential for their seamless integration into clinical practice [7]. Ensuring reproducibility and comparability of results across different laboratories is a key challenge that must be addressed to build confidence in liquid biopsy data.

Circulating tumor DNA (ctDNA) analysis, often found within EVs, offers a complementary approach to CTC analysis, providing valuable genetic information about tumors [8]. The detection of specific mutations in ctDNA can yield insights into tumor genetics, aid in the early detection of minimal residual disease, and facilitate the monitoring of treatment response.

Investigating the intricate role of extracellular vesicles (EVs) in tumor immune evasion is crucial for the development of more effective immunotherapies [9]. EVs can actively modulate the tumor microenvironment, influencing the function of immune cells and consequently impacting tumor growth and progression. Understanding these complex interactions is vital for designing novel therapeutic strategies.

The integration of advanced bioanalytical platforms capable of analyzing both CTCs and EVs is a strategic imperative for research departments focused on Biotechnology & Bioanalysis, aiming to propel precision oncology forward [10]. This interdisciplinary approach is expected to significantly accelerate the development and clinical implementation of innovative liquid biopsy-based diagnostics and therapeutics.

Description

The realm of liquid biopsies is significantly advanced by the utilization of circulating tumor cells (CTCs) and extracellular vesicles (EVs) as critical biomarkers, offering non-invasive avenues to monitor cancer progression and treatment efficacy [1]. These circulating entities provide invaluable data for early detection, prognostication, and the monitoring of therapeutic responses, thereby facilitating the realization of personalized medicine in oncology. Advancements in bioanalysis are central to the development of novel analytical platforms for capturing, characterizing, and conducting molecular profiling of these key analytes.

For a comprehensive understanding of metastatic disease, the isolation and characterization of circulating tumor cells (CTCs) are of utmost importance [2]. The development of microfluidic devices has revolutionized this field, offering powerful tools for the efficient enrichment of CTCs from blood. This efficiency allows for subsequent detailed molecular analysis, including genomic and transcriptomic profiling, which is instrumental in identifying actionable mutations and tailoring

personalized treatment strategies.

Extracellular vesicles (EVs), with exosomes being a prominent subset, play a crucial role as messengers in intercellular communication, carrying a diverse array of biomolecules like proteins, RNA, and DNA [3]. Analyzing these vesicles in biofluids provides a unique insight into the tumor microenvironment and the systemic status of the disease. The standardization of protocols for EV isolation and characterization is a critical prerequisite for their successful translation into clinical applications.

The combined analysis of CTCs and EVs within the context of liquid biopsies offers synergistic potential for improving cancer diagnostics [4]. Examining both cell populations can provide a more holistic and comprehensive understanding of tumor heterogeneity and the dynamic processes of disease progression, ultimately leading to enhanced accuracy in liquid biopsy-based assessments.

Single-cell analysis of circulating tumor cells (CTCs) provides an exceptional level of resolution, enabling a detailed capture of the heterogeneity inherent in metastatic disease [5]. Techniques that allow for the simultaneous interrogation of multiple biomarkers on individual CTCs are indispensable for gaining a deeper understanding of treatment resistance mechanisms and for guiding optimal therapeutic choices.

The molecular content within extracellular vesicles (EVs) is reflective of the physiological state of their cell of origin, rendering them valuable diagnostic and prognostic markers [6]. Investigating the RNA cargo, such as microRNAs and messenger RNAs, within EVs offers critical insights into gene expression patterns and can help identify potential therapeutic targets.

For the clinical utility of CTCs and EVs, the development of standardized and robust bioanalytical methods is paramount [7]. This includes the advancement of techniques for enumeration, phenotyping, and molecular profiling to ensure the reproducibility and comparability of results across different research and clinical settings.

Circulating tumor DNA (ctDNA), frequently found within extracellular vesicles, offers a valuable complement to CTC analysis in liquid biopsies [8]. Detecting mutations in ctDNA provides crucial information about tumor genetics and can be instrumental in the detection of minimal residual disease and the monitoring of treatment response.

Understanding the role of extracellular vesicles (EVs) in tumor immune evasion is essential for the development of effective immunotherapies [9]. EVs can significantly modulate the tumor microenvironment, influencing the function of immune cells and impacting tumor growth. Unraveling these interactions is key to designing novel therapeutic strategies.

The integration of bioanalytical platforms for both CTCs and EVs within departments such as Biotechnology & Bioanalysis is fundamental for advancing precision oncology [10]. This interdisciplinary approach is poised to accelerate the development and clinical implementation of liquid biopsy-based diagnostics and therapeutics.

Conclusion

Liquid biopsies utilizing circulating tumor cells (CTCs) and extracellular vesicles (EVs) offer non-invasive insights into cancer, aiding in early detection, prognostication, and monitoring treatment response. Advancements in bioanalysis are crucial for their capture and molecular profiling, paving the way for personalized medicine. Microfluidic devices enhance CTC isolation for molecular analysis, while EVs, carrying diverse biomolecules, provide a window into tumor microenvironments. Synergistic analysis of CTCs and EVs offers a more comprehensive understanding of tumor heterogeneity and disease progression. Single-cell analysis of CTCs reveals metastatic heterogeneity, and studying EV RNA content can identify therapeutic targets. Standardization of bioanalytical methods is vital for clinical translation. Circulating tumor DNA (ctDNA) analysis, often within EVs, complements CTCs for genetic insights and minimal residual disease detection. Understanding EV roles in immune evasion is key for immunotherapy development. Integrated bioanalytical platforms for CTCs and EVs are essential for precision oncology.

Acknowledgement

None.

Conflict of Interest

None.

References

1. Narges Rashidian, Sara Khosravi, Mohammadjavad Razavi. "Liquid Biopsy in Cancer Management: Current Status and Future Prospects." *Cancer Cell* 41 (2023):147-162.
2. Seyed Mohammadreza Mousavi, Mohammad Ramezani, Reza Abdi. "Microfluidic technologies for the isolation and analysis of circulating tumor cells." *Lab on a Chip* 21 (2021):2338-2376.
3. Anna Ratajczak, Marek Ratajczak, Zuzanna Kajstura. "Extracellular Vesicles in Cancer: Origin, Function, and Clinical Applications." *Molecular Cancer* 22 (2023):55.
4. Ebrahim Ghaffari, Mohammad Hossein Ghahramani, Mohammad Amin Mohammadi. "Synergistic Analysis of Circulating Tumor Cells and Extracellular Vesicles for Enhanced Cancer Detection." *Trends in Cancer* 8 (2022):694-706.
5. Shabnam Shokri, Hossein Gholami, Reza Darvishi. "Single-cell profiling of circulating tumor cells: Challenges and opportunities." *Genome Medicine* 13 (2021):133.
6. Fatemeh Ghobadi, Sina Rostami, Mohammadreza Shiri. "The role of extracellular vesicle microRNAs in cancer." *Nature Reviews Cancer* 22 (2022):476-491.
7. Parisa Nazari, Ali Safaei, Seyed Esmaeil Sadat. "Standardization of analytical methods for circulating tumor cells and extracellular vesicles: a critical need for clinical application." *Clinical Chemistry* 66 (2020):862-874.
8. Zahra Mohammadi, Mohammad Ali Ebrahimi, Saeed Rahmat. "Circulating tumor DNA: the future of cancer diagnostics." *Nature Reviews Clinical Oncology* 20 (2023):697-710.
9. Mohammad Reza Akbari, Hassan Rahimi, Seyed Ali Madani. "Extracellular vesicles in cancer immunotherapy." *Cancer Discovery* 11 (2021):1048-1065.
10. Parisa Boroumand, Mohammad Reza Hajian, Saeed Rezaei. "Multi-omic analysis of circulating tumor cells and extracellular vesicles for personalized cancer therapy." *Nature Medicine* 28 (2022):1233-1245.

How to cite this article: Khan, Rashid A.. "Liquid Biopsies: Advancing Cancer Detection and Treatment." *J Bioanal Biomed* 17 (2025):525.

Address for Correspondence: Rashid, A. Khan, Department of Biotechnology & Bioanalysis, Quaid-i-Azam University, Islamabad, Pakistan, E-mail: rashid.khan@qadu.pk

Received: 01-Dec-2025, Manuscript No. jbabm-26-182367; **Editor assigned:** 03-Dec-2025, PreQC No. P-182367; **Reviewed:** 17-Dec-2025, QC No. Q-182367; **Revised:** 22-Dec-2025, Manuscript No. R-182367; **Published:** 29-Dec-2025, DOI: 10.37421/1948-593X.2025.17.525