OPEN ACCESS Freely available online

ISSN: 2161-1009
Biochemistry & Analytical Biochemistry

Commentary

Comprehensive RNA Profiling in Cancer Plasma: The Role of Repetitive Elements

Miten Yassim*

Department of Biomolecular Engineering, University of California Santa Cruz, Santa Cruz, USA

DESCRIPTION

Profiling of repeating RNA sequences in cancer patients' blood plasma is a new area of study with tremendous potential for early diagnosis and treatment monitoring. A new study profiled the cell-free transcriptome in plasma from cancer patients using repeat-element-aware liquid-biopsy technology and single-molecule nanopore sequencing. This method enabled the analysis of millions of genomic characteristics, including all identified genes and repeat elements found throughout the genome.

The significance of this study rests in its capacity to provide a full view of the RNA landscape in cancer patients' blood plasma. Repetitive RNA sequences, which are frequently neglected in standard research, may hold the key to understanding the molecular pathways driving cancer growth and therapy response. This study's technique provides a highly sensitive platform for identifying potential novel disease biomarkers, such as repeating RNA fragments.

Such improvements have the potential to transform the field of liquid biopsies, making them more precise and informative. Profiling repeated RNA sequences could serve as a new possible non-invasive diagnostic for various types of cancer, assisting in early detection and individualized treatment approaches. Liquid biopsies allow for the analysis of cell-free RNAs released by cells throughout the body. Although well-annotated coding and non-coding transcripts in blood can be detected and used as biomarkers for disease, the total diagnostic usefulness of the cell-free transcriptome is unknown. They show that RNAs originating from transposable elements and other repetitive elements are enriched in the cell-free transcriptomes of cancer patients and may be used to accurately classify the disease.

They profiled the cell-free transcriptome in plasma from cancer patients and examined millions of genomic characteristics including all annotated genes and repeat elements throughout the genome using repeat-element-aware liquid biopsy technology and single-molecule nanopore sequencing. They discovered that samples with pancreatic cancer are enriched with certain Alu subfamilies, whereas other malignancies have their own distinct cell-free RNA profile by aggregating individual repeat elements to the subfamily level. Their findings reveal that repeating RNA sequences are common in blood and can be utilized to identify disease-specific biomarkers.

Approximately 75% of the 3 billion base pairs in the human genome are translated into RNA. Because the vast majority of these RNAs are not translated into proteins, they are classified as non-coding RNAs. Although microRNAs and long non-coding RNAs (lncRNAs) are well known, many other non-coding RNAs are produced across the genome, including RNAs transcribed from repetitive elements such as Transposable Elements (TEs). The human genome has around 5 million repeat element insertions, with repeat sequences accounting for roughly half of the genomic sequence content. TE RNAs, in particular, are abnormally expressed in illnesses like as cancer, underlining their potential as abundant and specific disease biomarkers.

Cell-free RNAs are produced by the cells that make up the numerous tissues and organ systems in the human body. The ability of cell-free RNA to predict pre-eclampsia in pregnancy demonstrates its diagnostic and prognostic potential, and cell-free RNAs act as biomarkers for diseases such as cancer and Alzheimer's disease. Cell-free RNAs have primarily been profiled using whole-exome RNA sequencing (RNA-seq), which excludes detection of repeat-derived and other non-coding RNA, or ribosomal-RNA-depleted total RNA-seq.

Many well-annotated non-coding RNAs have been found in human plasma using whole RNA-seq, as well as a modest fraction of repeat-derived cell-free RNAs (1-2%) in healthy individuals. However, the repeat-derived cell-free RNA transcriptome's diagnostic usefulness in the context of disease is uncertain.

Correspondence to: Miten Yassim, Department of Biomolecular Engineering, University of California Santa Cruz, Santa Cruz, USA, E-mail: mitenyassim@yahoo.com

Received: 03-Aug-2023, Manuscript No. BABCR-23-22893; **Editor assigned:** 07-Aug-2023, Pre QC No. BABCR-23-22893 (PQ); **Reviewed:** 22-Aug-2023, QC No. BABCR-23-22893; **Revised:** 30-Aug-2022, Manuscript No. BABCR-23-22893 (R); **Published:** 08-Sep-2023, DOI: 10.35248/2161-1009.23.12.510

Citation: Yassim M (2023) Comprehensive RNA Profiling in Cancer Plasma: The Role of Repetitive Elements. Biochem Anal Biochem. 12:510.