Effect of short-term storage of blood samples on gene expression in lung cancer patients

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From the journal Clinical Chemistry and Laboratory Medicine (CCLM)
https://doi.org/10.1515/cclm-2022-0738

Abstract

Objectives
The stability of gene transcripts associated with the presence of circulating tumor cells (CTCs) has been predominantly studied in cultured cancer cell lines added to blood samples under artificial conditions. In the present study the effect of storage on CTC-related transcripts was assessed in blood samples taken from patients with non-small lung cancer (n=58).

Methods
The blood samples were split in two equal parts to compare the gene expression with and without storage for 24 h at ambient temperature without preservative added. After enrichment using the microfluidic Parsortix® technology, the expression levels of selected genes were assessed using quantitative PCR following a gene-specific pre-amplification. The prognostic relevance of each gene in fresh and stored blood samples was evaluated using the R-package Survminer.

Results
Some genes were either not affected (TWIST1, CDH5, CK19) or upregulated upon storage (NANOG, MET, UCHL1) but still associated with poor prognosis. In contrast, ERBB3, PTHLH, EpCAM, and TERT were no longer associated with the overall survival of the patients.

Conclusions
The study demonstrates the surprising stability of CTC-related transcripts, which makes overnight shipping of native blood samples possible. Careful verification is required when using model systems – such as normal blood spiked with tumor cells – or other CTC-related markers, as individual transcripts may respond
differently to storage.

**Keywords:** blood storage; circulating tumor cells; liquid biopsy; molecular characterization; preservative; RNA stability

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**Research funding:** This study received support from Angle plc. in the form of an in-kind contribution of Parsortix® PR1 devices and microfluidic separation cassettes. ANGLE plc. had no influence on the design of the study, in the collection, analysis, and interpretation of data.

**Author contributions:** All authors have accepted responsibility for the entire content of this manuscript and approved its submission.

**Competing interests:** All authors declare no conflict of interest.

**Informed consent:** Informed consent was obtained from all individuals included in this study.

**Ethical approval:** The study was approved by the Ethic Committee of the Medical University of Vienna, Austria (EK366/2003 and EK2266/2018).

**References**


Supplementary Material
The online version of this article offers supplementary material (https://doi.org/10.1515/cclm-2022-0738).

Received: 2022-07-29
Accepted: 2022-11-07
Published Online: 2022-11-17

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