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

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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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Supplementary Material

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