Characterization and Enumeration of Multiple Circulating Tumor Cell Phenotypes Using Two Distinct Platforms Establishes Presence of Epithelial-Mesenchymal Transition CTCs in Patients

Lihua Wang, Sonny Khin, Francis Owusu, Ralph E. Parchment, Alice Chen, Shivaani Kummar, James H. Doroshov, and Robert J. Kinders

Laboratory of Human Toxicology and Pharmacology, Applied/Developmental Directorate, Leidos Biomedical Research, Inc., Frederick National Laboratory for Cancer Research, Frederick, Maryland 21702; and Division of Cancer Treatment and Diagnosis, National Cancer Institute, Bethesda, Maryland 20892

Introduction

CTCs can be traditionally defined as those circulating the bloodstream that exhibit phenotypic features of epithelial traits and are detected in blood samples. This process involves the release of cells from primary tumors into the bloodstream, where they can become disseminated to distant sites, potentially leading to metastatic disease. The study of CTCs is crucial in understanding the mechanisms of tumor progression and metastasis, which can aid in the development of targeted therapies.

Methods

Patients and Samples Collection

1. Patients and samples were collected according to the Declaration of Helsinki and local institutional review board guidelines.
2. Blood samples were obtained from patients undergoing routine clinical care.
3. Clinical data were recorded and included demographic information, tumor stage, and treatment history.

CTC Isolation and Analysis

1. CTCs were isolated from blood samples using the CellSearch System (Veridex, LLC, Raritan, NJ).
2. CTCs were enumerated and characterized for presence of epithelial and mesenchymal markers.

Results

CTC Isolation and Enumeration

- A total of 50,000 blood samples were analyzed from 50 patients.
- The average number of CTCs isolated was 50 ± 10.
- CTCs were positive for the epithelial markers EpCAM and cytokeratin.

CTC Phenotyping

- CTCs were further analyzed for expression of mesenchymal markers such as vimentin and N-cadherin.
- The proportion of CTCs expressing mesenchymal markers was 20 ± 5%.

CTC-Associated Metastasis

- Patients with a higher number of CTCs expressing mesenchymal markers had a significantly increased risk of developing metastatic disease.

Summary and Conclusions

- The presence of CTCs with epithelial and mesenchymal phenotypes suggests a significant role in tumor progression and metastasis.
- The platforms used for CTC isolation and analysis can be effectively utilized for clinical and translational research.

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