Conference Abstracts

Circulating Tumor Cells(sCTCs): A Frontier for Multi-Omics and Active Management of Cancer Patients

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Background

Real-time determination of tumor mutational status enables precise optimization of therapy at diagnosis and during treatment. While next-generation sequencing (NGS) and circulating tumor DNA (ctDNA) are widely used, analysis of live circulating tumor cells (sCTCs) offers a more comprehensive approach, providing genomic (DNA, RNA) and proteomic data from intact cells. Obtaining viable sCTCs for multi-omics has been technically challenging.

Methods

We analyzed sCTCs from 2,062 patients across 25 cancer types using the OncoIncytes platform. The system employs ligand-conjugated 2 mm glass beads targeting EpCAM and/or transferrin receptors for selective capture, imaging, and live-cell release. sCTC stability was assessed over 0–6 days and up to 1 year. DNA mutations were profiled with a 1,080-gene panel and compared to matched patient samples. Analytical validation was performed using single A549 cells.

Results

Among 1,368 patients, 3,522 CTCs (2,891 single cells, 631 clusters) were isolated, with CTCs detected in 83.4% of samples. Analytical validation showed capture efficiency of 99%, sensitivity 97%, specificity 98%, positive predictive value 99.5%, and negative predictive value 93.5%. No CTCs were detected in 40 healthy volunteers. In a paired lung cancer cohort, 25% of patients had no mutations detected by ctDNA; however, sCTCs from the same patients revealed at least one pathogenic mutation in all cases.

Conclusions

The OncoIncytes platform enables precise isolation of live sCTCs from 10 mL of blood, supporting real-time DNA, RNA, and protein analysis with high accuracy and cost efficiency. This approach yields results comparable to or better than tissue biopsy or ctDNA profiling, providing a valuable tool for precision oncology and active cancer patient management.