

# Cancer Gene Panel Analysis of Cultured Circulating Tumor Cells Primary Tumor Tissue from Patients with Breast Cancer

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## Study Aim:

To determine if culturing circulating tumor cells (CTCs) from breast cancer patients is an effective method to obtain sufficient CTCs for molecular analysis, and to compare the genetic profiles of cultured CTCs to primary tumor tissue.

## Methods:

- CTCs were isolated and cultured from blood samples of 6 breast cancer patients
- Cultured cells were characterized by immunofluorescence staining for EpCAM
- Genomic analysis was performed on cultured CTCs and primary tumor tissue using the Ion AmpliSeq Cancer Hotspot Panel v2
- Mutations detected in cultured CTCs were compared to those in primary tumor tissue

## Key Findings:

- CTC cultures yielded 4-8 x 10<sup>5</sup> cells after 16-18 days, with 35-86% being EpCAM-positive
- COSMIC mutations were detected in genes including PDGFRA, MET, PTEN, HRAS in 5/6 CTC samples
- In one patient sample, an identical HRAS mutation was found in both CTCs and primary tumor
- 60-80% of novel mutations were shared between CTCs and primary tumor in analyzed samples

## Conclusions:

- The culture method successfully expanded CTCs to sufficient numbers for molecular analysis
- Cultured CTCs maintained genetic characteristics similar to primary tumor tissue
- This approach of culturing and analyzing CTCs may provide a novel method for breast cancer diagnosis and treatment monitoring via "liquid biopsy"

The authors suggest this technique could enable CTC-based prediction of effective treatments for breast cancer patients, though further validation is needed.