Performance of a high-intensity 508-gene circulating-tumor DNA (ctDNA) assay in patients with metastatic breast, lung, and prostate cancer

Pedros Bazhen, Beo T.L., Westin Almida, Alex Arzouan, Bregganak Jung, Roufii Shieh, Chelsea Hsu, Jie De-Bo Li, Santse Greiner, Raymond S. Lin, Carl Hollub, Gucia Reale, Tara Madalit, Michael F. Berger,1, 4, Gregory J. Rieky, Howard I. Scher,2, 5

1. Department of Medicine, Memorial Sloan Kettering Cancer Center, NY, 2. University of California, San Francisco, 3. Department of Radiotherapy, Memorial Sloan Kettering Cancer Center, New York, NY, 4. Department of Radiation Oncology, Memorial Sloan Kettering Cancer Center, New York, NY, 5. Department of Radiation Oncology, Memorial Sloan Kettering Cancer Center, New York, NY

Methods

Objectives

- To determine the performance of a high-intensity 508-gene ctDNA assay in patients with metastatic cancer
- To evaluate the concordance of ctDNA results with tissue-confirmed results
- To identify actionable mutations and their clinical implications

Methods

- Sample Workflows and Analyses
- Performance of a high-intensity 508-gene circulating-tumor DNA (ctDNA) assay in patients with metastatic breast, lung, and prostate cancer

Results

- Concordance is calculated as positive percent agreement (PPA) with tissue as a reference (cfDNA/tissue).
- Eligible patients with established cancer diagnoses.
- Blood and tissue were analyzed independently and blinded to the results of each.
- Analytical Metrics
- Female
- Median Age at enrollment
- 39 (100.0%) 28 (68.3%)
- Median Age
- 26 (66.7%) N/A N/A
- 4 (10.3%) 13 (31.7%)
- 15 (38.5%) 4 (9.8%)

Conclusions

- This novel, high-intensity cell-free DNA sequencing assay incorporates unprecedented high number of panel. A number of panels can improve the precision of the assay, resulting in high intensity levels in the proportion of concordance for both clinical and non-clinical levels between plasma and tissue.
- By interpreting concordance on strong evidence for tissue DNA, we aim to use high level of tissue DNA detection in plasma to determine clinical implications.
- Tissue calls detection rate by cfDNA was determined for the majority of patients, at least one mutation detected in tissue was also detected in plasma DNA of 70% (65%, 78%), 73% (65%, 79%), 72% (65%, 78) for breast, lung, and prostate cancer patients.
- The majority of tissue reports, subclonal mutations detected in tissue were also detected in plasma (25%, 79%, 70%, 90%, 70%).

Summary

- This novel, high-intensity cell-free DNA sequencing assay incorporates unprecedented high number of panel. A number of panels can improve the precision of the assay, resulting in high level of tissue DNA detection in plasma to determine clinical implications.
- Tissue calls detection rate by cfDNA was determined for the majority of patients, at least one mutation detected in tissue was also detected in plasma DNA of 70% (65%, 78%), 73% (65%, 79%), 72% (65%, 78) for breast, lung, and prostate cancer patients.

References


- This novel, high-intensity cell-free DNA sequencing approach incorporates unprecedented high number of panel. A number of panels can improve the precision of the assay, resulting in high level of tissue DNA detection in plasma to determine clinical implications.
- Tissue calls detection rate by cfDNA was determined for the majority of patients, at least one mutation detected in tissue was also detected in plasma DNA of 70% (65%, 78%), 73% (65%, 79%), 72% (65%, 78) for breast, lung, and prostate cancer patients.
- The majority of tissue reports, subclonal mutations detected in tissue were also detected in plasma (25%, 79%, 70%, 90%, 70%).