A novel, antibody-independent platform, ApoStream™, successfully isolated CTCs from the blood of patients with advanced NSCLC. In a side-by-side comparison, ApoStream™ isolated more EGFR/C443 deletion NSCLC CTCs compared to the CellSearch® platform in 3 out of 5 NSCLC patient samples with detectable CK+/CD45− cells, neither system detected CTCs in 1 patient sample.

Phenotypic immunofluorescence analysis of cells isolated by ApoStream™ revealed the presence of CK+/CD45− cells, which are not detected by the CellSearch® platform. This is consistent with previously reported data indicating that ApoStream™ is able to isolate cells with CK expression, a potential advantage for this technology.

The use of ICE COLD-PCR coupled with standard Sanger sequencing allowed detection of EGFR Exon 19 mutations in CTCs isolated by ApoStream™. Method modifications led to increased sensitivity in detecting EGFR Exon 19 mutations in CTCs from tissue samples.

For EGFR Exon 21: two mutations were observed in the tumor tissue from this set of patients. Using standard ICE COLD-PCR followed by Sanger sequencing on the targeted DNA extracted from the CTCs isolated by ApoStream™, both mutations were found in an exonic region for which the Sanger analysis was EGFR Exon 19-13bp deletion.

For the EML4-ALK fusion protein, both methods demonstrated high sensitivity and specificity. In some cases, the ICE COLD-PCR was able to detect the fusion protein in samples that were negative by standard methods.

Summary & Clinical Significance

A novel, antibody-independent platform ApoStream™ successfully isolated CTCs from the blood of patients with advanced NSCLC. In a side-by-side comparison, ApoStream™ isolated more EGFR/C443 deletion NSCLC CTCs compared to the CellSearch® platform in 3 out of 5 NSCLC patient samples with detectable CK+/CD45− cells, neither system detected CTCs in 1 patient sample.

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For the EML4-ALK fusion protein, both methods demonstrated high sensitivity and specificity. In some cases, the ICE COLD-PCR was able to detect the fusion protein in samples that were negative by standard methods.

References:

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