INTRODUCTION

Biomarker testing in lung cancer is often limited by a lack of sufficient formalin fixed, paraffin embedded (FFPE) tissue for comprehensive genomic profiling. To promote personalized therapy for lung cancer, a multiplex FISH assay was developed to simultaneously assess aberrations in ROS1, RET, and MET on a single FFPE specimen slide.

METHODS AND MATERIALS

Specimens included lung primary tumor (N=47) as well as biopsies from a variety of metastatic sites (N=10) and 1 cell line.

- The hybridization of the fluorescently labeled DNA probes to the cellular DNA site was visible by direct detection using fluorescence microscopy on BioView imaging platform.
- BioView Duet scanning system was used to perform automated slide imaging and digital analysis.

There were 46 samples with ROS1 rearrangements, 15 samples with RET rearrangements, and 25 samples with MET amplification reported by a previously validated laboratory test method.

Specimens were considered positive for ROS1 rearrangement if ≥5% evaluated cells contained a break apart (rearranged) signal.

Specimens were considered positive for RET rearrangement if ≥5% evaluated cells contained a break apart (rearranged) signal.

Specimens were considered positive for MET abnormality if either criteria was met:

- ≥20% of cells were amplified, i.e. had MET/CEP7 ratio ≥2
- ≥20% of cells were highly polyclonal, i.e. had 5 or more MET signal copies per cell but MET/CEP7 ratio was <2

CONCLUSIONS

A newly developed 6-color FISH assay allows simultaneous detection of three genomic abnormalities using only 1 specimen slide.

This feature combined with rapid hybridization in IntellIFISH buffer and automated BioView slide imaging and analysis can significantly increase the yield of molecular testing on limited lung cancer tissue samples.

Careful pathologic correlation for tumor cell identification and careful assessment of hybridization quality are necessary to optimize the accuracy of this test method.