

Impact of Gene Expression Profiling using the 92-gene Assay on Management of Neuroendocrine Carcinoma of Unknown Primary Site

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Background: Neuroendocrine tumors (NETs) are slow growing and can be undetected until patients present with metastasis. Although pathologic examination is adequate for diagnosis, the identification of site of origin can be challenging. We aimed to retrospectively analyze the impact of the 92-gene assay on therapeutic decision making. Specifically, whether testing allowed for the use of molecularly targeted therapy, which otherwise may not have been utilized.

Methods: Forty patients from Louisiana State University and the University of Kentucky with metastatic neuroendocrine carcinoma of unknown primary site (NEC-UPS) after initial diagnostic evaluation were selected for retrospective analysis. Biopsy specimens were sent to bioTheranostics, Inc. (San Diego, CA) for molecular cancer classification with the 92-gene assay. Patient and tumor characteristics were collected and impact of the 92-gene assay results on clinical therapeutic decision making were evaluated.

Results: Twenty-one men and 19 women were included in the study, with an age range of 37-75 years and a median age of 63 years. Of the 40 patients, 55% presented with only liver metastases; 17.5% had disseminated metastases within the

liver and other sites, and 27.5% patients presented with metastases located outside of the liver. The most common presenting symptoms were non-specific: abdominal pain (n=14), and diarrhea (n=7). The most common positive serum biomarkers were 5-hydroxyindolacetic acid (n=17), chromogranin A (n=11), pancreastatin (n=11), neurokinin A (n=5), and serotonin (n=5). In all cases, the 92-gene assay predicted a site of origin with >90% certainty – 35% predicted to be gastrointestinal carcinoid, 27.5% pancreatic islet cell, 12.5% small/large cell, and 5% lung carcinoid.

Conclusion: In this retrospective analysis, patients identified with pancreatic islet cell tumors are most likely to benefit from gene expression profiling. Analysis of the impact of the 92-gene assay on survival should be evaluated in future studies.

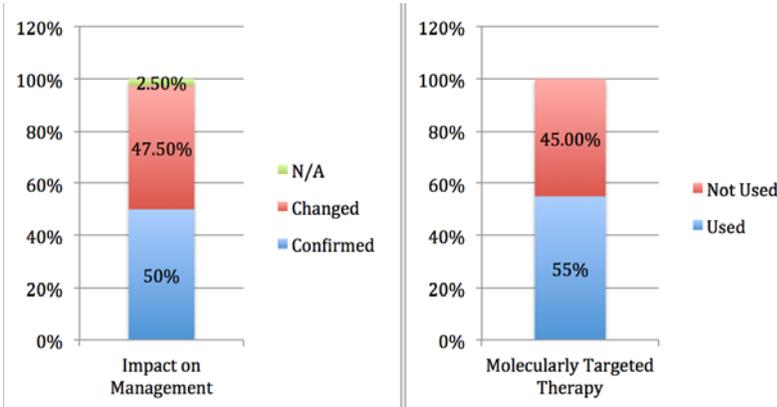


Figure: Results of the retrospective analysis. Identifying the site of origin with the 92-gene assay altered chemotherapy regimen in approximately half the patients, and provided molecularly targeted therapy options for more than half of that subgroup.