**UTILITY OF TUMOR GENOMIC PROFILING USING NEXT GENERATION SEQUENCING (NGS) IN METASTATIC LUNG CANCER MANAGEMENT**

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**BACKGROUND:** Next-generation sequencing (NGS) performs genomic profiling on tumor tissue and provides information on mutations on 300+ selected genes, with only a small percentage have targeted therapy options. This study examines the characteristics of mutations from lung cancer patients treated in a Brooklyn community hospital serving the local Chinese and other immigrant community. We evaluated the prevalence of driver mutations, their association with smoking, as well as the clinical usage of the information.

**METHODS:** This is a retrospective study for patients diagnosed between November 2011 and February 2018. Patients were identified from the data base of the NGS company and their clinical data was collected from electronic medical records at Maimonides.

**RESULTS:** 119 patients were identified, 55% had a history of smoking. 73% had adenocarcinoma, 4% had squamous cell cancer, the rest had non-small cell lung cancer not otherwise characterized. 31% of the tumors carried driver mutations, including: EGFR (n=21), RET (n=6), ALK mutation (n=3), MET amplification (n=2), and 1 each of ROS1 or NTRK mutation. 34 patients were Chinese, and 47% carried driver mutations. EGFR mutation was found in 16% of the adenocarcinoma, and 1 of the 5 squamous cell cancer patients; and in 17% of the smokers and 19% of the non-smokers.

All of patients with driver mutations received FDA-approved targeted therapy. In 70 patients, additional non-driver mutations were detected, with information suggesting that targeted therapy approved in a different tumor type can be used; but none was treated. 89 patients had a mutation being studied in a clinical trial, and 48 of them were eligible for an NCI sponsored basket trial (NCI-MATCH trial). The referral was rare.

**CONCLUSIONS:** NGS detected known targetable mutations in one platform facilitating prescription of targeted therapy. Information on the presence of other non-driver mutations was underused. Without solid clinical trial data, prescription of targeted therapy based on its potential effectiveness was rare. Future research should study barriers to enrollment in clinical trials, and barriers to using targeted therapy from different tumors.

**CONTENT CATEGORY:** patient care

**KEYWORDS:** *Next gene sequencing, Lung cancer, EGFR, smoking, clinical trials*