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Pathologists identify patterns of mutations to help inform design of future trials

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Molecular driven therapeutic targets have resulted in a paradigm shift in the treatment of advanced lung adenocarcinoma. However, in early non-small cell lung cancer (NSCLC), surgical resection remains the treatment of choice with adjuvant chemotherapy. In a recent study published in the April 2013 issue of the International Association for the Study of Lung Cancer's (IASLC) *Journal of Thoracic Oncology*, researchers identified patterns of mutations in early stage node negative lung adenocarcinoma.

They retrospectively reviewed 204 patients with stage IB primary lung adenocarcinoma who underwent surgical resection between January 1990 and May 2008. Patients who received neoadjuvant or adjuvant treatments were excluded.

The study demonstrates that mutations are common in resected early node-negative, treatment-naive lung adenocarcinoma with 54 percent of patients having tumors which harbor at least one biologically relevant mutation. Although mutations in KRAS, EGFR and ALK were mutually exclusive, some tumors harbored synchronous mutations within a single oncogene such as double EGFR mutations or within two different oncogenes in the case of comutations.

The researchers unexpectedly found that there were also mutations associated with drug resistance despite the fact that this was a cohort of early stage disease patients who had not been treated with chemotherapy or targeted agents.

They concluded that their data provides, "compelling evidence for comprehensive tumor mutation profiling as an essential element of adjuvant trial design as DNA changes present in advanced cancer cohorts do not necessarily match those from early stage disease."

Provided by International Association for the Study of Lung Cancer