44P Association of metastatic pattern and molecular status in metastatic lung non-small cell lung cancer adenocarcinomas

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Background: The recent identification of molecular alterations in some lung adenocarcinomas has led to the emergence of effective targeted therapies thus drastically improving their prognosis.The aim of our study was to investigate the association between driver oncogene alterations and metastatic patterns on imaging assessment, in a large cohort of metastatic lung adenocarcinoma patients.

Methods: From January 2010 to May 2017, 656 patients with stage IV lung adenocarcinoma with molecular analysis were studied retrospectively including 135 EGFR, 81 ALK, 47 BRAF, 141 KRAS, and 146 negative tumors for these 4 mutations (4N). After review of the complete imaging report by two radiologists (junior and senior) to identify metastatic sites, univariate correlation analyzes were performed.

Results: We found differences in metastatic tropism depending on the molecular alteration type when compared to the non-mutated 4N group: in the EGFR group, pleural metastases were more frequent (32% versus 20%; $p = 0.021$), and adrenal and node metastases less common (6% versus 23%; $p < 0.001$ and 11% versus 23%; $p = 0.011$). In the ALK group, there were more brain and lung metastases (respectively 42% versus 29%; $p = 0.043$ and 37% versus 24%; $p = 0.037$). In the BRAF group, pleural and pericardial metastases were more common (respectively 47% versus 20%; $p < 0.001$ and 11% versus 3%; $p = 0.04$) and bone metastases were rarer (21% versus 42%; $p = 0.011$). Lymphangitis was more frequent in EGFR, ALK and BRAF groups (respectively 6%, 7% and 15% versus 1%); $p = 0{,}016$, $p = 0{,}009$ and $p < 0{,}001$).

Conclusions: The application of these correlations between molecular status and metastatic tropism in clinical practice may lead to earlier and more accurate identification of patients for targeted therapy, savings in iterative biopsies, as well as improved and personalized imaging interpretation.

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