Conclusions: The number of regional LNs examined did not correlate with the survival prognosis for stage IIA/II lung adenocarcinoma patients who underwent sublobar resection.

Legal entity responsible for the study: The authors.

Funding: Key Lab System Project of Guangdong Science and Technology Department-Guangdong Provincial Key Lab of Translational Medicine in Lung Cancer (Grant No. 2017B030314120), Project of National Natural Science Foundation (Grant Nos. 81673031, 81872510), Research Fund from Guangzhou Science and Technology Bureau (Grant No. 2019010121), High-Level Hospital Construction Project (Grant No. DFH201801), and Guangdong Provincial People’s Hospital Young Talent Project (Grant No. GDPHYPTP201902).

Disclosure: All authors have declared no conflicts of interest.

https://doi.org/10.1016/j.annonc.2020.10.353

361P Radiomic model predicting radiological response after thoracic stereotactic body radiotherapy regardless of tumor histology and staging

B.M.F. Cheung, J.K.S. Lau, M.Y. Luk, K.K. Yuen
Department of Clinical Oncology, Queen Mary Hospital, Hong Kong, China

Background: Thoracic stereotactic body radiotherapy (SBRT) is widely applied in both early and metastatic disease. Pathological CR rate after SBRT was quoted around 60%. Thus, it is important to predict responder and non-responder to SBRT. With advent of radiomics, textural features of tumor can be extracted from imaging. We propose a model to predict radiological response after SBRT based on tumor radiomics features regardless of histology and staging.

Methods: Patients receiving thoracic SBRT using active breathing control (ABC) were retrospectively recruited regardless of tumor histology/primary and staging. All patients received 50-54 Gy in 3-4 fractions equivalent to BED >100 Gy. All patients had regular contrast CT Thorax per protocol and PET/CT if indicated. Tumor response was assessed by an independent senior radiologist based on RECIST criteria. Responders are defined as complete response (CR) or partial response (PR). Non-responders were defined as those with stable or progressive disease. Gross tumor volumes (GTV) were contoured on the initial planning CT. 110 radiomics features including voxel intensities, textual and gray level features were extracted using pyradiomics module. The features were then analyzed using in-house software. A model using support vector machine (SVM) was trained to predict response based solely on the extracted radiomics features. 10-fold cross validation was used to avoid overfitting. ROC curves were constructed to evaluate model performance.

Results: 68 patients were recruited from 2008 to 2018. 54 patients had lung primaries while 14 patients had thoracic oligo-metastases. Secondaries include colorectal, head and neck squamous cell carcinoma and hepatocellular carcinoma. 85 tumors were analyzed, of which 31 tumors had CR and 11 tumors had PR. The radiomic model developed had an accuracy of 74.8%. The AUC for CR, PR and non-responders prediction was 0.865 (95% CI: 0.794 – 0.921), 0.946 (95% CI: 0.873 – 0.978) and 0.857 (95% CI: 0.789 – 0.915) respectively. Under the threshold, the sensitivity was 89% while the specificity was 64% for detecting non-responders.

Conclusions: Radiomic is a promising technique that can predict tumor response with good accuracy.

Legal entity responsible for the study: Department of Clinical Oncology, Queen Mary Hospital.

Funding: Has not received any funding.

Disclosure: All authors have declared no conflicts of interest.

https://doi.org/10.1016/j.annonc.2020.10.354

362P Integrative and comparative genomic analysis and immune microenvironment features of lung cancer patients with tuberculosis

X. Xu1, C. Bao1, D. Chen1, Y. Fan2
1Medical Oncology, Zhejiang Cancer Hospital - Cancer Research Institute, Hangzhou, China; 2Medi- cal Oncology, Shanghai Jiao Tong University, Shanghai, China

Background: High prevalence of tuberculosis (TB), is observed in China, and one of the etiological factors for lung cancer is TB. Our study was aimed to compare the differences of the tumor microenvironment (TME) based on tumor PD-L1 expression and CD3+/CD4+CD8+ T cells infiltration in patients with non-small cell lung cancer (NSCLC) who have ever/current suffered from TB to those lung cancer patients without TB.

Methods: Tumor samples from 69 patients with lung cancer who have ever/current suffered from TB were retrospectively collected at Zhejiang Cancer Hospital and Hangzhou Red Cross Hospital. The 21 samples of control group (lung cancer patients who never suffered from TB) is collected in Zhejiang Cancer Hospital. Tumoral PD-L1 expression (N = 68) and CD3+/CD4+/CD8+ T cells infiltration (N = 58) was determined by immunohistochemistry (IHC), based on which TME was categorized into different subtype. Proportion of four TME subtypes was determined, and overall survival with PD-L1 expression and TME was analyzed. The whole exon sequencing was used to characterize the different immune genomic landscape between 40 lung cancer patients who have ever/current/never suffered from TB.

Results: Patients with TB had a decrease of infiltration of PD-L1 expression and CD8+ T cells into tumors. In addition, a different prognosis was observed in patients with active TB. The WES test showed a significant difference in TP53 mutation, tumor mutation burden, neoantigen and mutation signature in lung patients with or without TB. Lung patients with TB had unique driver genes such as C1QB, CDKN2A and signaling pathways. After analyzing in TIMER database, TP53, C1QB, CDKN2A are closely related to various immune cells in NSCLC.

Conclusions: NSCLC patients with TB exhibited lower PD-L1 and CD8+ expression level in TME and have different genomic landscape compare to lung cancer patients. Immunotherapy may have less effective in patients with active or latent TB and is prone to re-ignition of TB because of the reduced expression of PD-L1 and CD8+. Novel C1QB and CDKN2A targeted therapies may be the future direction of treatment for these patients with lung cancer and TB.

Legal entity responsible for the study: Zhejiang cancer hospital.

Funding: Has not received any funding.

Disclosure: All authors have declared no conflicts of interest.

https://doi.org/10.1016/j.annonc.2020.10.355

363P Genetic predisposition for pre-invasive lung adenocarcinoma manifesting as ground-glass nodules with family history of lung cancer

B. Fu1, J.T. Zhang, R.R. Chen1, Z.X. Tai1, H.X. Lin1, J. Su1, X.P. Chu1, C. Zhang1, W.F. Tang1, J.T. Lin1, Q. Nie1, Y.L. Wu1, W.Z. Zhong1
1Guangdong Lung Cancer Institute, Guangdong Provincial People’s Hospital & Guangdong Academy of Medical Sciences, Guangzhou, China; 2Medical Center, Gen- ePlus-Beijing Institute, Beijing, China

Background: Lung cancer with family history have been increasing gradually of late years in East Asian, especially those presenting as pulmonary ground-glass nodules (GGNs). The genome predisposition of GGNs with lung cancer family history remains baffling.

Methods: This prospective study (NCT04220268) enrolled patients with pulmonary pre-invasive or invasive adenocarcinoma, which presenting as GGNs in computer tomography (CT) scans. We collected blood and tumor samples from 59 patients with GGNs and first-degree relative family history of lung cancer (FHLC) to investigated germline and somatic mutations by whole exon sequencing (WES). Pre-invasive neoplasia causal variants were detected by quality, classification, minor allele frequency (MAF), functional prediction, and family segregation filter. Validation was conducted in an external cohort of 669 healthy participants without cancer, and in 126 non-overlapping susceptibility loci for lung carcinogenesis identified by recent genome-wide association studies (GWAS).

Results: Eighty-five single nucleotide variants (SNVs) and 11 frameshifts were detected, which were rare, predicted as damaging, and presented in more than two families. Fifteen of them had been reported that were associated with high risk of lung cancer or deleterious function. The MAF of them were lower than 0.01 in a local health Asian cohort and human exome databases. Three of them were validated in 126 susceptibility loci for lung carcinogenesis. The number of the rare, damaging and repeatedly germline mutations in non-smoking patients were significantly higher than those in smoking patients (2436 vs 593, p<0.05). The number of these germline mutation showed no significant difference between the patients with pure GGNs and mixed GGNs (1298 vs 1333, p>0.05).

Conclusions: Patients with GGNs and FHLC may have inheritable carcinogenesis mutations. These variants may potentially contribute to the risk of pulmonary pre-invasive adenocarcinoma susceptibility in Chinese population.

Legal entity responsible for the study: The authors.

Funding: Guangdong Provincial Key Laboratory of Lung Cancer Translational Medicine (Grant No. 2017B030314120), National Natural Science Foundation of China (Grant No. 81673031&No. 81872510), High-level Hospital Construction Project (DFH201801), Guangdong Provincial People’s Hospital Young Talent Project (No. GDPHYPTP201902).

Disclosure: R.R. Chen, Z.X. Tai, H.X. Lin: Full/Part-time employment: GenePlus-Beijing Institute, Beijing, China. All other authors have declared no conflicts of interest.

https://doi.org/10.1016/j.annonc.2020.10.356