Sixth International Joint Meeting on THORACIC SURGERY

Barcelona - 20th, 21st and 22nd November 2024
Auditorio Foment del Treball Nacional. Barcelona (Spain)

11th International Meeting on General Thoracic Surgery
Clínic Barcelona | Universitat de Barcelona | Hospital Universitari Sagrat Cor

5th Meeting of the Thoracic Oncology, Thoracic Surgery, Techniques & Transplant, Respiratory Nursing and Respiratory Physiotherapy Areas of the Spanish Society of Pneumology and Thoracic Surgery (SEPAR)
Sociedad Española de Neumología y Cirugía Torácica (SEPAR)

10th International Workshop on Surgical Exploration of the Mediastinum and Systematic Nodal Dissection
Hospital Universitari Mútua Terrassa | Universitat de Barcelona

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3rd Joint Meeting of the Spanish Society of Thoracic Surgery (SECT)
SECT Sociedad Española de Cirugía Torácica

30th Congress of the "Asociación Iberoamericana de Cirugía Torácica" AIACT

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NEXT-GENERATION SEQUENCING GENOTYPING AND CIRCULATING TUMOR CELL ANALYSIS IN RESECTABLE NON-SMALL CELL LUNG CANCER

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Objectives

Next-Generation Sequencing (NGS) and Circulating Tumor Cells (CTCs) analysis could help identify heterogeneity and stratify high-risk patients in resectable Non-Small Cell Lung Cancer (NSCLC). This study evaluates the mutational profile with a customized panel of 50 genes and CTCs status in stage I-III NSCLC patients. Methods In this single-centre prospective study, blood samples for CTCs analysis were obtained from 76 stage I-III NSCLC patients who underwent surgical resection. Targeted NGS was performed using customized 50-gene panel on matched tumoral/peritumoral tissue biopsies from a subset of patients.

Results

The most highly mutated genes were: TP53, FLT1, MUC5AC, EGFR and NLRP3. Pair of genes that had mutually exclusive mutations was TP53-RIN3, and pairs of genes with co-occurring mutations were CD163-TLR4, FGF10-FOXP2, ADAMTSL3-FLT1, ADAMTSL3-MUC5AC and MUC5AC-NLRP3. The number of somatic variants detected from tissue biopsies were 143. Regarding clinical significance 9.8% were benign/likely benign (B), 83.2% of uncertain significance (VUS) and 7.0% pathogenic/likely pathogenic (P). Most variants were VUS. We studied their impact on recurrence by grouping them in P+VUS and VUS+B, observing a significant association between P+VUS and recurrence (p=0.0404). We also evaluated a possible correlation between CTCs status and VUS in the studied genes. There were 67% patients without CTCs in the follow-up and with VUS in ADAM19 that locally recurred, but no statistical differences were found.

Conclusions

Integrating molecular profiling of tumors and CTC analysis could provide valuable insights into tumor heterogeneity and improve patient stratification for resectable NSCLC. Further research is warranted.