Use of Genomic Sequencing to Determine Genomic Alterations and New Therapeutic Opportunities in Spanish Lung Cancer Patients

Maria Rosario García Campelo, Edurne Arriola, Lola Isla, Reyes Bernabé Caro, Diego Pérez Parente, Borja Molf, Jesús Lavara, Sara Olson, Jorge García González

1 Medical Oncology, University Hospital A Coruña (XXIIAC SERGAS), A Coruña, Spain; 2 Medical Oncology, Hospital Universitari del Mar-CIBERONC, Barcelona, Spain; 3 Medical Oncology, Hospital Clínico Universitario Lozano Blesa, Zaragoza, Spain; 4 Medical Oncology, Hospital Virgen del Rocío, Seville, Spain; 5 Medical Affairs Department, Roche Farma S.A., Madrid, Spain; 6 Medical Oncology, Hospital Universitario de Santiago de Compostela, Santiago de Compostela, Spain

BACKGROUND

The therapeutic approach to advanced lung cancer has significantly changed with the identification of specific genetic alterations that drive tumor growth, and corresponding targeted therapies that demonstrate better effectiveness than traditional chemotherapy. Thus, the accurate determination of genomic alterations can provide valuable information to design the best therapeutic approach for each patient.

This study aimed to determine the genomic profile of Spanish lung cancer patients with no mutations previously identified by immunohistochemistry in clinical practice using Foundation Medicine services.

RESULTS

- A total of 508 samples were analysed: 209 (41%) with F1CDx and 299 (59%) with F1Liquid. Overall, the most prevalent histological diagnosis was adenocarcinoma (61%) (Table 1).

- The most common genomic alterations found in tumour tissue were high tumour mutational burden (TMB, 27%), EGFR (12%), ERBB2 (6%), and NFI (6%), while in ctDNA, the most common were high TMB (13%), EGFR (18%), ERBB2 (3%), and MET (3%) (Table 2).

- Actionable alterations with at least one sensitizing therapy recommendation were detected in 56% of the solid samples and 42% of the ctDNA samples. Actionable alterations with at least one clinical trial recommendation were detected in 89% and 68% of the tumour and ctDNA samples, respectively (Figure 1).

- Immunotherapies were recommended in 36.4% of patients and targeted therapies in 62.6%.

CONCLUSIONS

- To date, this is the largest study characterizing the genomic profile of Spanish patients with lung cancer in this setting.

- Our results show that patients without previously identified mutations in clinical practice and limited therapeutic alternatives could benefit from a more sensitive diagnostic tool and tailored therapeutic approaches.