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Next-generation sequencing is a prerequisite for personalized lung cancer treatment

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Introduction. Non-small cell lung cancer (NSCLC) is characterized by a wide range of genetic abnormalities that impact the disease prognosis. However, the data on frequency of various genetic disorders in lung cancer in the Ukrainian population are limited. Our study aimed to evaluate the frequency of genetic alterations in NSCLC samples to identify potential candidates for personalized treatment. **Methods.** Tumor tissue blocks of NSCLC patients were used for the study. NGS technology was used to determine gene expression disorders and genetic alterations. The research was conducted in the CSD laboratory. **Results.** The tumor tissue of 117 NSCLC patients was studied. Among the total samples, 46 (39.3%) belonged to women and 71 (60.7%) to men. Eighty-seven patients were older than 50 years (66.7%), while 30 patients were ≤50 years old (33.3%). Lung adenocarcinomas predominated among the studied samples (95; 81.2%), and squamous cell carcinoma was present in 22 (18.8%). Genetic disorders were detected mainly in lung adenocarcinoma ($p < 0.001$). When assessing the frequency of genetic alterations in NSCLC, the EGFR mutations were found in 17 patients (14.5%), ALK rearrangement in 8 cases (6.8%), KRAS in 23 (19.7%), ROS1 in 2 (1.7%), MET — in 3 (2.6%), BRAF — in 3 (2.6%) cases, also in 23 cases (19.7%) registered alterations in other genes including PIK3CA, MAPK, ERBB2, TP53, FANCA, CDKN2A/B, NF1, CTNNB1. The presence of mutations in these genes can impact prognosis and determine sensitivity to targeted and immunotherapy. **Conclusions.** The high frequency and variety of genetic alterations in NSCLC determine the expediency of NGS testing to personalize the treatment of patients with NSCLC.

Keywords: non-small cell lung cancer, next-generation sequencing genetic disorders, EGFR, KRAS.