Proceedings International
Platinum Open Access Journal (ISSN 2668-6384)

Proceedings, Abstract
Volume 4, Issue 1, 2022, 3
https://doi.org/10.33263/Proceedings41.003

Assessment of Mutational Status in NSCLC - Histopathological and Molecular Aspects †

Florina Vasilescu [1,*], Laura Buburuzan [1], Maria-Anca Zamfir [1], Natalia Motas [2]

[1] Onco Team Diagnostic, 313A Splaiul Unirii, Bucharest, Romania;
[2] Oncology Institute of Bucharest, Alexandru Trestioreanu, Bucharest, Romania;
* Correspondence: florinapath@yahoo.com;
† Presented at 1st OncoHub Conference – Connecting Scientists for Next Generation Cancer Management (13-15 October 2021, virtual)

Received: 25.10.2021; Accepted: 5.02.2022; Published: 14.02.2022

Abstract: Despite the recent advances in NSCLC with drivable mutations, there are still variable differences in responses to targeted therapies. These may be explained by the association of more than one mutation that can be present from the beginning of treatment or gained during the therapy. Background: Our research project aimed to study and compare the mutational status in NSCLC-advanced stage, using either tumor tissue or circulating tumor DNA from the plasma. We enrolled in our study 57 patients diagnosed with advanced lung cancer. After performing IHC for histological subtyping, EGFR, ALK, and PDL-1 routine testing for selection targeted therapies, only 23 patients were eligible for our study; till now, nucleic acid samples isolated from plasma liquid biopsy of all these patients were assessed by Next-Generation sequencing (NGS). Only for a part of these patients, NGS analyses of DNA and RNA isolated from tumor tissue were made. Results: we find a wide spectrum of mutations, rearrangements, and gene amplifications involved in the development and progression of NSCLC cancer: EGFR, TP53, MET, FGFR, KRAS, PIK3CA, BRAF, FGFR1, CCND1, with some cases presenting more than 3 or 4 alterations. Because of the large and intermixed number of genetic alterations that can be met in NSCLC advanced stage, the utility of Next Generation Sequencing (both tumoral tissue samples and circulating tumor DNA samples) must be the future's choice analyses, either for the selection of targeted therapies or for prognostic evaluation.

Keywords: mutational status; next-generation sequencing; liquid biopsy; NSCLC;

Funding

This research was funded by a grant from the Ministry of Research and Innovation, CNCS-UEFISCDI, project number PN-III-P2-2.1-PTE-2019-0577 - ONCONGS, within PNCDI III.

Acknowledgments

Not applicable.

Conflicts of Interest

The authors declare no conflict of interest.