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MEETING ABSTRACT

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The role of EGFR mutations in lung cancer: molecular basis of targeted therapy

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Background: The epidermal growth factor receptor (EGFR), a tyrosine kinase (TK) receptor, represents the crucial component of cell signalling pathways. In numerous malignancies, including non-small-cell lung cancer (NSCLC), the intracellular TK activity of EGFR may be deregulated due to somatic mutations of the EGFR gene, increased gene copy number and/or EGFR protein overexpression, thus representing a therapeutical target. EGFR mutation testing in advanced NSCLC nowadays is an essential step in decision on treatment with tyrosine kinase inhibitors (TKI).

Methods: During seven months (from June to December 2014), 175 patients were included in testing. Histological and cytological specimens were processed and genomic DNA was isolated using the Cobas® DNA Sample Preparation Kit. Measurement of DNA concentration was performed using the Qubit® dsDNA BR Assay Kit and the Qubit® Fluorometer. The target DNA was amplified and detected on the Cobas® z 480 analyzer using a real-time PCR test provided in the Cobas® EGFR Mutation Test Kit.

Results: All tested patients were of Caucasian descent and had the adenocarcinoma subtype of NSCLC, stage IIIb (27.4%) or IV (72.6%). Among 175 patients, 68% were males and 32% females, the median age was 61.5 (range 29–87 years). EGFR mutations were detected in 16 patients (9.1%), the wild-type gene was detected in 158 patients (90.3%) while in 1 patient (0.6%) the amplification was not achieved due to an inadequate sample. The types of detected mutations were as follows: deletions in exon 19 were detected in 9 patients (56.3%), exon 21 L858R point mutation was detected in 4 patients (25%), whereas exon 18 and exon 20 point mutations were found in 3 samples (18.7%).

Discussion: The prevalence of EGFR mutations in our patients with advanced lung adenocarcinoma is 9.1%. Regarding the type of mutations, deletions in exon 19 are the most frequent EGFR mutations, which is in concordance with previously published data. According to literature data, the EGFR mutation rate in the Caucasian population is approximately 10% for NSCLC, which corresponds to our results. We suggest that one of the strategies to improve the detection of mutations could be a better patient selection and stratification. The investigations of the molecular basis of cancer may bring better understanding of cancerogenesis and a further development of targeted therapies, thus providing a higher efficiency and lower toxicity compared to conventional treatment options.

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