PREDICTIVE BIOMARKERS FOR THE TREATMENT OF NSCLC

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Purpose: The exact classification of lung carcinomas together with evaluation of molecular and cytogenetic changes plays a vital role in the optimization of treatment strategies, especially with respect to the dynamic development of new therapeutic methods. Non-small cell lung cancer (NSCLC) is characterised not only by variable clinical course of the disease, but also by differences in the histopathological findings and molecular-genetic characteristics of the tumours. New knowledge about these aspects led to fundamental changes in the approach to diagnosis and treatment especially for lung adenocarcinomas. The identification of specific genetic aberrations in a part of these tumours has enabled the use of targeted therapy, which has led to a significant improvement of the prognosis of these patients. Apart from these, the options of immunotherapy have also been expanding.

The algorithms for diagnosis and molecular testing differ between countries and are usually based on the recommendations of IASLC/CAP/AMP, ESMO, NCCN or ASCO. The main predictive markers evaluated in NSCLC include especially the mutation analysis of the genes *EGFR, ALK, ROS1, BRAF, RET, HER2, KRAS, MET, NTRK* and others. These biomarkers can be evaluated using a range of various methods which differ in their approach, demands on the tissue sample, sensitivity, specificity, and also in price. Concerning immunotherapy for NSCLC the main tested marker is the expression of PD-L1, and as of this year the FDA has also approved tumour mutational burden as a predictive marker for immunotherapy of unresectable of metastatic solid tumours.

The current trend of expanding the therapeutic options for tumour diseases however poses increasing demands on the number of evaluated predictors, which can sometimes be problematic given the often-limited amount of tumour tissue which is available for testing.

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