EDITORIAL COMMENT

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Prognostic factors in non small cells lung cancer

Lung cancer is the most common and deadly cancer worldwide, and its incidence is expected to increase with rising rates of smoking.[1] Considering the high incidence and the poor prognosis of this cancer, many oncological studies focus on a search for markers for diagnostic and prognostic purpose.

First of all, we aim to define prognostic factors, which are measurements that are associated with clinical outcome in the absence of therapy or with the application of a standard therapy that patients are likely to receive. It can be seen as a measure of the natural history of the disease. A control group from a randomized clinical trial is an ideal setting for evaluating the prognostic significance of a biomarker.[2,3]

There are numerous prognostic factors, which have been studied and known and which we take into account in our daily clinical practice when making a decision. Patient-related prognostic factors such as age, gender, performance status, nutritional, morphometric parameters, smoking, alcohol exposure, other comorbidities and symptoms at diagnosis. Histopathological prognostic factors related to the tumor such as tumor size, lymph node extension, metastatic invasion (TNM classification), histological type, histological subtype of adenocarcinoma and grade, pleural and lymphovascular invasion and spread through air spaces (STAS). Nowadays comprehensive molecular profiling showed a high degree of molecular heterogeneity in lung cancer and so the outcome largely depends on the identification of an addressable driver such as EGFR, ALK, ROS1, ERBB2, BRAF, MET, KRAS, RET, NRG1 and NTRK1-2-3, as mutations or gene fusions are highly predictive of response to combined targeted therapy. The detection of ctDNA post-surgery is a validated prognosis factor of high recurrence risk in multiple tumor localizations[4].

Prognostic biomarkers are an area of high interest in non-small cell lung cancer. Inflammatory blood markers can be routinely determined from complete blood counts, which are inexpensive and reliable. Many studies show us that the fast progression of a neoplastic process is perceived by an organism as an aggression and triggers an inflammatory reaction, which is accompanied by a release of different mediators of an inflammatory process. Laboratory tests reveal leucocytosis, neutrophilia, lymphocytopenia, and thrombocythemia[5,6]. Other example of that blood markers is preoperative serum uric acid and uric acid to albumin ratio, which seems to predict lymph node metastasis in non-small cell lung cancer undergoing thoracic surgery.[7] Although the results of these studies are encouraging, prospective randomized trials are needed, which may allow us to draw more robust conclusions.

It is necessary that we continue to investigate the prognostic factors that can guide us in daily clinical practice and that we can add to algorithms in use.

Understanding the prognosis, and finding easily reproducible and reliable markers, in non-small cell lung cancer is crucial to inform patients, guide treatment and plan supportive and palliative care. In addition, we need to continue to engage, validate, and facilitate the wide adoption of newly developed biomarkers, prioritizing their predictive value, cost-efficiency and reproducibility.

A final word focusing on the need for integration of information based on artificial intelligence. The development of these predictive models will improve the assessment, risk stratification, diagnosis and treatment of patients with NSCLC, but will also make the work of physicians easier, allowing an integrated analysis and practice of all patient characteristics.

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