European Review for Medical and Pharmacological Sciences 2018; 22: 580-581

Letter to the Editor

Correlation of CT indicators of NSCLC and pathological features and the expression level of p53 and c-myc. Positive example of the right way for translational diagnostics

Dear Editor,

we read with great interest the paper by Li et al[1], recently published on Eur Rev Med Pharmacol Sci and titled "Correlation of CT indicators of NSCLC and pathological features and the expression level of p53 and c-myc", very interesting and original, considering the correlation demonstrated between radiological indications and pathological features.

Lung cancer is the leading cause of cancer-related deaths yearly worldwide, with non-small cell lung cancer (NSCLC) accounting for about 80% of all cases of lung cancer. At presentation only 30% of all NSCLC are resectable[2,4]; the remaining 70% of all patients with NSCLC are affected by the advanced disease, and they are potential candidates for systemic treatment only.

To date, due to novel drugs and more pathological knowledge, the outcome in locally-advanced and advanced NSCLC patients is improved[5].

Also, diagnostic support is improved, i.e., spiral-CT and CT-Pet scan that can have more accurate information about staging, response to treatment and/or progression disease.

Li et al[6] reported the results of correlation of Computed Tomography (CT) and pathological features and the expression level of p53 and c-Myc and this kind of research represents a typical example of translational research.

The study published is very original and could open future scenarios in the staging and evaluation to response to treatment.

We know that tumor suppressor gene phosphoprotein 53 (p53) mutant and its downstream oncogene c-Myc are commonly seen in a variety of human tumors, and at present, they are indicators used in clinical tumor diagnosis and staging[7].

However, if the detection of p53 and c-Myc mutations are routinely incorporating into clinical practice, knowledge concerning the predictive value of test which will eventually enable of individual therapy not only for lung cancer, but also for any neoplasm involving these genetic variants in cancer patients[8].

Several approaches to consider the quality and cost-effectiveness of genetic tests now existed. Prominent is the Diagnostic Advisory Committee of National Institute for Health and Clinical Excellence (NICE) which excites Health communities to generate data for suitable cost-effective models into healthcare systems[9]

The early outline evaluation costs of the detection p53 and c-Myc gene expression could average about €20/per genes by Real-time PCR[10]. Meanwhile, confirmation method for mutation detection, require automated Sanger sequencing method; in this case, the cost is averaged €20/per exon[11].

Since these gene markers will be validated in international guidelines, is still open question the ability of physicians expertise to interpret the results of this genetic tests[12,13].

The authors, on 87 patients with NSCLC, found that the positive expression of p53 and c-Myc proteins were correlated with tumor diameter, speculation, and deep lobulation signs and lymph node metastases ($p < 0.05$), but not associated with spinous process, vacuole, and pleural indentation signs ($p > 0.05$). The results obtained are interesting, butthey need of

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more confirmation studies, considering the high incidence of lung cancer and it tissue heterogeneity. Probably, also a study with the use of CT-Pet scan related to pathological features and bio-molecular aspects could add interesting information in this setting.

We know that these translational studies are strongly recommended to have more and more information on cancer disease with the aim to improve the efficacy of treatment and quality of life of patients. Promising, this field of research might be able to accelerate the translational diagnostic of genetic into the routine imaging diagnostics.

Conflict of Interest

The Authors declare that they have no conflict of interests.

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