Editorial

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Translational Biomarkers in Cancer Therapy

Adel Gouri[1], Aoulia Dekaken[2], Mohamed Chefrour[3], Arifa Aissaoui[1], Nihad Labed[1], Wissem Abdaoui[4] and Sadek Benharkat[1]

1 Laboratory of Biochemistry, College of Medicine, Annaba 23000, Algeria
2 Department of Internal Medicine, Pr EL OKBI Public Hospital, Guelma 24000, Algeria
3 Laboratoire de Biochimie, Hôpital de La Timone Enfant, Marseille, France
4 Department of Biology, Guelma University, 24000, Algeria

Corresponding author: Adel Gourii

pharmagor@gmail.com

Laboratory of Biochemistry, College of Medicine, Annaba 23000, Algeria.

Tel: 00213 666 088 226

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For decades, relevant improvements in cancer therapy have occurred, with a significant increase in the overall survival of patients. Nevertheless, with the recent emergence of highly selective molecular targeted agents and high-throughput genomic characterization technologies, robust and well-validated cancer biomarkers are increasingly needed.

Therefore, the new translational biomarker approach holds great promise for optimizing the safety and efficacy of pharmacotherapy and individualizing medical treatment to the patient. These biomarker approaches (including genetics, genomics, gene expressions, proteomics, and imaging) will facilitate evaluation of disease progression, drug efficacy, and drug-induced adverse reactions [1]. Translational medicine plays an important role in the research of malignant tumors and clinical treatment. Basic research on tumor biology has broadened our understanding of factors such as occurrence, metastasis, and drug resistance. Tumor biomarkers are of potential use in early cancer diagnosis, anticancer therapy development, and monitoring the response to treatment [2].

Rapid progress in the identification of these molecular targets in the cancer cell has led to a revolution of the "omic" in cancer care including (Whole) Genome (WGS), Exome (WES), methylome, transcriptome (including the miRnome), microbiome, metabolome, proteome and topome [3,4].

Recent studies have confirmed the utility of these biomarkers in early and accurate diagnosis and predict prognosis in cancers. A comprehensive approach based on detection of a panel of molecular alterations can give us a recognizable pattern of molecular alterations in the cancer cells which can serve as a "signature" specific for each tumor. Once such a "molecular signature" is identified in the tumor at the time of diagnosis, it can serve as a template for personalized onco-pharmacogenomics [4].

The use of this new approach has facilitated the selection of patients who would derive the most benefit from systemic therapy and a more personalised approach to treatment. However, only a few biomarkers for common solid tumours are currently routinely tested in the clinical setting. In the future, the development of less expensive and high-throughput sequencing methods will allow for the expansion of testing for genetic alterations to all tumours and patients and will lead to more tailored therapies. New and less invasive methods for obtaining tumour material such as measurement of circulating tumour cells in peripheral blood will enable more frequent monitoring of tumour response to therapy. Patients will benefit from this individualised approach to cancer care by receiving therapies modified to their unique molecular and cellular characteristics, leading to an improved therapeutic benefit to toxicity ratio. Ongoing biomarker development will allow the oncologist not only to better define prognosis and predict treatment response but also provide an early indicator of treatment efficacy [5].

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