

Epigenetic biomarkers for human cancer: The time is now

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The importance of epigenetic processes in the development of cancer is clear. The study of epigenetics is therefore bound to contribute to the improvement of human health. Aberrations in DNA methylation, post-translational modifications of histones, chromatin remodelling and microRNAs patterns are the main epigenetic alterations, and these are associated with tumorigenesis. Epigenetic technologies in cancer studies are helping increase the number of cancer candidate genes and allow us to examine changes in 5-methylcytosine DNA and histone modifications at a genome-wide level. In fact, all the various cellular pathways contributing to the neoplastic phenotype are affected by epigenetic genes in cancer. They are being explored as biomarkers in clinical use for early detection of disease, tumor classification and response to treatment with classical chemotherapy agents, target compounds and epigenetic drugs. Encouraging results have been obtained with histone deacetylase and DNA methyltransferase inhibitors, leading the US Food and Drug Administration to approve several of them for the treatment of hematological malignancies and lymphoproliferative disorders, such as myelodysplastic syndrome and cutaneous lymphoma.

However, many tasks remains to be done, such as the clinical validation of epigenetic biomarkers to allow the accurate prediction of the outcome of cancer patients and their potential chemosensitivity to current pharmacological treatments. implications.