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Editorial

Drug Targeting is the Milestone Armed with Next Generation Sequencing for the Personalized Treatment of Myelolytic Leukemia

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Editorial

Next Generation Sequencing (NGS) is the new avenue for the personalized diagnosis and treatment strategy for acute myelolytic leukemia [1-4]. A lot of diagnostic laboratories can now afford the use of NGS panels to detect the mutational alterations of different myelolytic leukemias. These panels are the mirrors having the facility for analyzing 25-50 genes having functional categories like splicing molecules, transcription factors, cell signaling molecules, epigenetic factors, cohesions and other modifiers of genetic material. There are different driver as well as non-driver mutations related to acute myeloid leukemia as well as for Myelodysplastic Syndromes (MDS) and Myeloproliferative Neoplasms (MPN). The clinical significance of all these markers is difficult to correlate perfectly with types of myeloid malignancies. NGS supports the clinicians to identify the patients who are in highest risk in genetic stratification for the occurrence and progression of the myelogenetic leukemia. But the detection of markers with proper interpretation and implementation of NGS results for the treatment of malignancies is the hurdle to the clinicians as well as molecular biologists. It is associated with sequence artifacts from library preparation or data analysis (e.g., read mapping, variant calling) [5-7]. To understand the myeloma cancer cells and their genetic blue print scientist should have the normal control cell system common to all human being without any genetic polymorphism. Comparing the normal one it is observed that each individual patient shows its own blueprint and some patients have several cancer cell clones having more than one genetic blueprint. Some researchers suggested that sequencing by NGS parallel with study of cytogenetics as well as mutation profile can be beneficial for risk stratification of high and intermediate risk patients [7].

Recent years are indicative for the growth in the investigation of targeted therapies for different hematopoietic malignancies including acute myeloid leukemia. Conventional chemotherapeutic treatment exposes the normal cell population in toxic environment along with the leukemic ones. The targeted therapy deals with the drugs aimed to discrete genetic changes as well as specific molecular event absent in normal cell system. This specificity of targeted drug therapy is more effective as well as less cytotoxic to other tissue systems. The success rate of implication of this therapy depends on the decisive diagnosis of the presence of specific target in the patient on which both choice of optimal as well as maximum tolerated dose depends. A critical level of complexity in synthesis, clinical trial and target oriented development of cancer drugs increase the rate of failure and are facing a challenge in overcoming the problem of drug resistance and insensitivity in cancer patients. This failure is due to lack of knowledge of molecular mechanisms as well as specific target validation of individual patient [8].

NGS is required for refinement of genetic stratification in difficult clinical cases in addition to conventional cytopathological diagnostics in patients selected for drug targeting object [9].

The cost of single assay of data processing for NGS is coming down though the demand of comprehensive nature of diagnostic results with a no of genes is required for proper treatment with decisive drug targeting. So a longer period of time, in depth knowledge and expertise are required to meet all the demand for NGS procedures. Parallel thought process is also required to develop the NGS-omics in more cost effective way to be available economically backward patients.

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