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Perspective

Clinical Analysis and Genetic Mutations in Acute Myeloid Leukemia

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DESCRIPTION

Acute myeloid leukemia is a type of cancer and affect red blood cells. Gene changes its sequence and transmitted asprogeny it is known as a gene mutation. A single or a few nucleotides may be changed for others, or a single or a few pairs of nucleotides may be added or removed. The letters A, C, G, and T, respectively, stand in for the four nucleotide bases of DNA, adenine, cytosine, guanine, and thymine. Each section of three nucleotides-referred to as a triplet or codon-in a gene's sequence, which contains the instructions for building a protein molecule, codes for a specific amino acid in the protein. In which the viral genomes either contain DNA or RNA.

Recurrent gene mutations are characterized by the Acute Myeloid Leukemia (AML), a genetically diverse clonal cancer. The biggest challenges to the therapeutic effectiveness of AML patients include genomic heterogeneity, patient individuality, and recurrent gene alterations. An enormous variety of genetic mutations have been discovered to the use of DNA Next-Generation Sequencing (NGS) technology, which are both cost- and time-efficient. Various studies have been conducted on the recurring gene mutations and the significant roles they play in the pathogenesis of AML.

The failure of differentiation and unchecked proliferation of hematopoietic progenitor cells lead to a variety of clonal diseases of AML. Gene mutations and several cytogenetic abnormalities can assemble simultaneously.

It is now more feasible for clinical research to investigate cytogenetic analysis in many different disorders, including AML, to the recent improvements in NGS. After undergoing the recommended first-line chemotherapy regimen, the majority of AML patients can now achieve Complete Remission (CR) because to advancements in chemotherapy. Many patients can experience extended remission-free survival periods by combining chemotherapy, hematopoietic stem cell transplantation, immunotherapy, and molecular targeted therapy with conventional types of treatment. The preferred first-line treatment for AML is still acknowledged as the standard therapy of daunorubicin and cytarabine induction chemotherapy.

Prognostically different in cytogenetic subgroups were closely related with certain gene mutations. Additionally, multivariate analysis showed that patient age impacts on some mutations that are affected. We looked at patient subsets sorted by age and cytogenetics to make it easier to evaluate these results and see how co-occurring gene mutations affect survival together. The time from diagnosis to the end point, such as death or the last follow-up, is known as Overall Survival (OS). The term Relapse-Free Survival (RFS) was used to describe the time from the initial complete remission and the last follow-up, relapse, or death. Refractory response to chemotherapy was defined as primary induction failure or attaining CR through three or more cycles of induction of chemotherapy. Sensitive response to chemotherapy was defined as reaching CR status following one or two cycles of induction of chemotherapy.

CONCLUSION

The multistage hypothesis of tumour evolution states that diverse mutations might aid in the growth of tumours, accumulate, and it shows impact on various stages, increasing the number of genetic mutations. Patients with more mutations tend to be harder to completely cure, so this type of patient needs to be actively scheduled for allogeneic hematopoietic stem cell transplantation. In terms of the response to chemotherapy, the phenomenon of sensitive patients having significantly fewer genetic mutations than refractory patients exhibiting a strong relationship between mutation number and chemotherapeutic effect indicates that patients with more mutations tend to be harder to cure completely. AML is a very aggressive heterogeneous malignancy that is divided into subgroups by specific biological and clinical characteristics defined by genetic abnormalities.

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