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Genetic Studies in Acute Myeloid Leukemia

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Abstract: Acute Myeloid Leukemia (AML) is a group of malignant diseases originating from clonal hematopoietic stem cells, with a prevalence of 2-3 per hundred thousand people all over the world every year, and whose incidence has not changed significantly for the last 20 years. This malignant change in hematopoietic cells causes loss of function in these cells and, if untreated, results in death within weeks or months depending on the clinical course. AML is a complex disease that shows heterogeneity as well as phenotypic and recurrent chromosomal aberrations are observed in most of the cases. AML-related translocations generally affect the CBF (corebinding factor), RAR α (retinoic acid receptor alpha) and ETS (E-twenty-six) family transcription factors and the HOX (Homeobox) gene family. There are various treatment examples and prognostic approaches as a result of genetic studies in AML. Recently, some molecules and molecular changes thought to be of prognostic and therapeutic importance have been identified and their importance in terms of treatment and prognosis has been investigated. In this study, genetic studies in AML were examined and new approaches and treatment processes in recent years were examined.

Keywords: AML, CRF, RAR α , ETS, HOX

Introduction

Cancer is defined as after uncontrolled cell proliferation after changes in the cell cycle due to environmental or genetic factors and mutations. (Jemal et al., 2009). Leukemia is a malignant disease arising from lymphopoietic or hematopoietic stem cells or precursor cells of the bone marrow. Although the etiology of leukemia, which is a blood disease characterized by the accumulation of neoplastic cells in the bone marrow and other tissues and accumulation in the peripheral blood as a result of pause and clonal proliferation in a specific stage of normal myeloid or lymphoid hematopoiesis, is not known exactly, it can result in death if not treated. (Biondi&McKenna, 2000 ; Lowenberg et al., 2003).

Acute myeloid leukemia (AML) is a hematopoietic stem cell disorder characterized by the cessation of differentiation during the hematopoiesis process, resulting in proliferation of the blast cell population. This malignant change in hematopoietic cells causes loss of function in these cells and, if not treated, results in death within weeks to months depending on the clinical course (Shiple et al., 2009). AML is a complex disease that shows heterogeneity both phenotypically and genotypically, and recurrent chromosomal aberrations are observed in most of the cases. Translocations related to AML generally affect CBF (corebinding factor), RAR α (retinoic acid receptor alpha) and ETS (E-twenty-six) family transcription factors and HOX (Homeobox) gene family (Dash et al., 2001).

Some generalizations are made about the molecular biology of leukemias. The first of these; It is the occurrence of chromosomal abnormalities that disrupt or interrupt gene control mechanisms, unlike normal cells in somatic tissues. A genetic defect that occurs at a certain point during normal hematopoiesis results in leukemia of a

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particular line of hematopoietic differentiation. Another generalization made about the molecular biology of leukemias is that leukemias develop from a single cell and proliferate clonal, as is the case with cancers in general. AML'de genetik çalışmalar sonucu çeşitli tedavi örnekleri ve prognostik yaklaşımlar bulunmaktadır. Son zamanlarda prognostik ve terapötik önem taşıdığı düşünülen bazı moleküller ve moleküler değişiklikler belirlenmekte ve bunların tedavisi ve prognoz açısından önemleri araştırılmaktadır (Gale et al., 2003).

Today, the methods applied in the fight against this disease; First of all, our aim is to determine the possible risk factors and genetic factors that play a role in the etiopathogenesis of these patients, and to apply appropriate treatment methods for these factors whose prognostic value is determined.

Etiology of AML

Although there is no risk factor to explain the etiology in all AML patients, many hereditary, acquired and environmental predisposing factors have been identified (Liesveld et al., 2006). Although the development of AML is associated with many risk factors, known risks explain only a small part of the identified cases. These risks include age, hematological diseases, genetic disorders caused by chemicals, viruses and radiation, chemotherapy or having a profession that will affect health, etc. can be counted as (Deschler & Lübbert, 2006).

Mutations in AML

Mutations that play a role in the pathogenesis of AML are generally defined in two subgroups. The first group activates the signal transduction system, resulting in increased proliferation or survival advantage. The second group affects transcriptional coactivation complexes via transcription factors, resulting in decreased differentiation or increased self-renewal capacity.

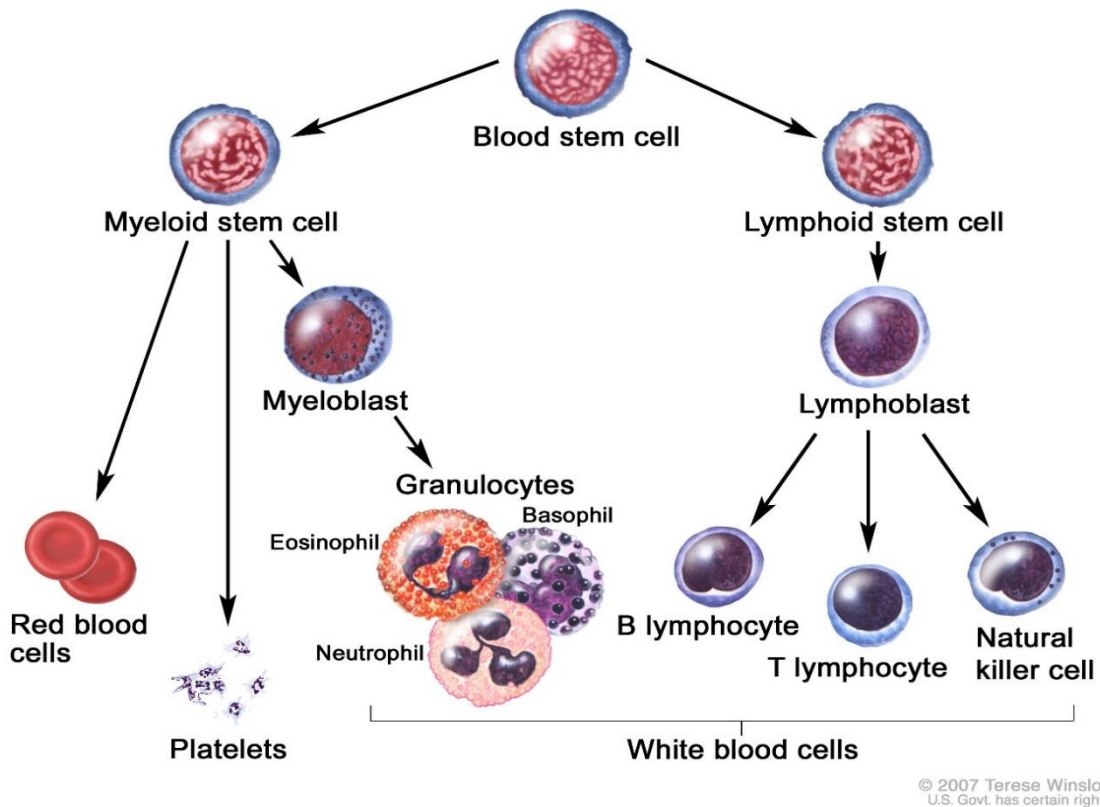


Figure 1. Blood stem cell proliferation

Cytogenetic studies have shown that frequently recurrent chromosomal abnormalities are found in approximately half of leukemias. When the genes affected by these structural chromosomal abnormalities in the form of translocations, inversions and deletions are examined, it has been shown that they play a role in the

development and normal function of the hematopoietic system. In addition to permanent structural changes (mutations) related to these genes, epigenetic changes have also been described.

Prognosis of AML

The response to treatment in AML is determined by various clinical and biological features. Being over 60 years old, poor pre-treatment performance status, AML occurring as a result of previous chemotherapy or a hematological disease such as MDS (Secondary AML), and high leukocyte count ($>20,000/\text{mm}^3$) or high lactate dehydrogenase level are unfavorable prognostic factors. . In addition, "multidrug resistance MDR1 protein" and immunophenotyping studies provide prognostic information, as well as cytogenetic analysis of leukemic cells, important information that is a prognostic indicator is obtained (T.H.D., 2011). When the patient's cytogenetic characteristics or some of the molecular alterations are taken into consideration together with the patient's age, it has been determined that they are suitable parameters that can be used in the follow-up of the disease, the prediction of recurrence, and the selection of appropriate treatment. (Ferrara et al.,2008). Nonrandom (non-random, previously described) clonal chromosomal abnormalities (eg, balanced translocations, inversions, deletions, monosomies, and trisomies) are alterations in leukemic blasts that occur in approximately 55% of adults with AML. These changes have been defined as the most important prognostic factors affecting the realization of complete remission, the determination of the risk of recurrence and the average life span in the past years. (Fröhling et al., 2005).

Conclusion

Cancer is defined as after uncontrolled cell proliferation after changes in the cell cycle due to environmental or genetic factors and mutations. According to the data of the Centers for Disease Control and Prevention (Centers for Disease Control and Prevention, CDC); While 12.7 million people worldwide get cancer annually, 6.7 million people die as a result of cancer-related diseases. It is extremely important that the data obtained to investigate the genetic origin of cancer shed light on the clinicians. Acute Myeloid Leukemia (AML) is a group of malignant diseases originating from clonal hematopoietic stem cells, with a prevalence of 2-3 per hundred thousand people all over the world every year, and whose incidence has not changed significantly for the last 20 years. Therefore, identification of mutations in AML is very important for early diagnosis. Therefore, we believe that both mutations and recent genetic studies in this study will be pioneers for clinicians.

Scientific Ethics Declaration

The authors declare that the scientific ethical and legal responsibility of this article published in EPHELS journal belongs to the authors.

Acknowledgements or Notes

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