Extended Abstract Journal of Cancer Biology and Therapeutic Oncology 2021
Vol.5 Issue1

Bone marrow T-cell percentage: A novel prognostic indicator in acute myeloid leukemia

Nahla A. B. Abdulateef & Manar M. Ismail
King Abdullah Medical City, Kingdom of Saudi Arabia

Introduction
Acute myeloid leukemia (AML) is an aggressive malignancy for which overall disease-free survival is less than 50%. Manipulation of the immune system is an interesting and promising therapy for AML patients. We aimed to characterize the immune system of AML patients, highlighting the clinical relevance of total bone marrow (BM) lymphocytes and subpopulations. Sixty-six new AML cases diagnosed according to WHO criteria from King Abdullah Medical City, KSA. Analysis of BM lymphocytes and subpopulations was done by flowcytometry. Significantly, high percentages of BM lymphocytes, T cells, and natural killer (NK) cells were detected in the group that achieved complete remission (P values = 0.004, <0.001, and <0.001, respectively). Overall survival (OS) was significantly prolonged in patients with high BM lymphocytes and T cells (P values = 0.047 and P 0.002, respectively). Multivariate analysis indicated that BM T-cell percentage and cytogenetics were independent prognostic factors predictive of OS (HR 4.7, P value = 0.011). BM T-cell percentage constitutes a novel host factor that can be used in combination withcytogenetics to better predict OS. Large-scale multicenter studies are recommended to clarify its role as a predictor of OS and leukemia-free survival.

Keywords AML · BM lymphocytes · T-cells · Natural killer cells · Prognosis · OS.

Background of the Research

Acute myeloid leukemia (AML) is a fatal hematopoietic malignancy and has a prognosis that varies with its genetic complexity. However, there has been no appropriate integrative analysis on the hierarchy of different AML subtypes.

Natural killer (NK) function defects have been seen in many hematological malignancies, including acute myeloid leukemia (AML). AML is associated with deficient human leukocyte antigen (HLA) expression on leukemia blasts which become targets for killing by NK and natural killer-like T (NKT) cells. However, NK and NKT cells are not effective in killing autologous leukemia blasts, maybe due to number or functional abnormalities. The aim of the work was to detect the number and percentage of NK and NKT cells in patients with AML and the impact of their percentage on the prognosis, response to treatment and survival.

Current conventional chemotherapy for acute myeloid leukemia (AML) can achieve remission in over 70% of patients, but a majority of them will relapse within 5 years despite continued treatment. The relapse is postulated to be due to leukemia stem cells (LSCs), which are different from normal hematopoietic stem cells (HSCs). LIN28B is microRNA regulator and stem cell reprogramming factor. Overexpression of LIN28B has been associated with advance human malignancies and cancer stem cells (CSCs), including AML. However, the molecular mechanism by which LIN28B contributes to the development of AML remains largely elusive

Although the curative rate for acute promyelocytic leukemia (APL) has been improved over decades, long-term prognosis is still poor. The genetic pathways that regulated cell lineage fate during the development of APL remain unclear. Methods. We investigated the correlations of miR-146a expression with its target gene Smad4 and the biological behaviors of NB4 cells. We also analyzed their expression in clinical samples from APL patients. Results. miR-146a influenced apoptosis and proliferation in NB4 cells. miR-146a influenced endogenous Smad4 protein levels in APL cells. miR-146a expression levels were positively correlated with white cell counts and PML/RARα fusion protein expression. miR-146a expression levels were negatively correlated with Smad4 protein and the helper T cell (Th)/the suppressor T cell (Ts) ratio in these patients. Conclusions. These findings indicated that miR-146a played an important role in the development of APL in part through the repression on Smad4 protein expression. miR-146a functioned as an oncogene and may be a novel prognostic biomarker in APL.