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HOTAIR and HOXD gene expressions in patients diagnosed with leukemia

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Dear Editor,

Leukemiassuch as acute myeloid leukemia and chronic myeloid leukemia are hematologic cancers characterized by a various cytogenetic abnormalities resulting from disrupted myeloid differentiation and a varying course. Various researches have been carried out to examine the genetic characteristics of the disease to improve outcomes in patients diagnosed with leukemia. These studies aim to understand disease pathogenesis and identify potential therapeutic targets.

The homeodomain-containing (HD) transcription factors play a significant role in leukemogenesis in leukemia patients. HOX genes belong to this gene family and are known to be expressed in healthy hematopoietic cells, human CD34+ stem cells, and leukemic cells [1,2]. While only HOX A, B, and C from the HOX gene family are expressed in normal blood cells, all subtypes are expressed in leukemic cells. On the other hand, HOXD genes are not expressed during hematopoietic development. Expression of HOXD3 genes is observed particularly in erythroleukemic cells [3]. Additionally, HOXD13, which fuses with NUP98 in acute myeloid leukemia, was found in a very few leukemic cells [4,5]. In these cases, HOXD13 secretion is in both bone marrow cells and leukemic cells, and it is thought that the expression of HOXD13 genes may lead to clonal development in leukemic cells.

In addition , long non-coding RNAs (lncRNAs) play an important role inregulation of hematopoietic stem cells at different developmental stages. One of the most well-studied long non-coding RNAs (lncRNAs) is HOX transcript antisense RNA (HOTAIR) transcribed from the HOXC gene on 12q13.13.

The HOTAIR gene suppresses HOXD gene expression on the second chromosome [6]. HOTAIR gene expression a diagnostic and prognostic biomarker in various cancers [7]. Several studies suggest that it could be a biomarker in patients diagnosed with leukemia. In a study evaluating HOTAIR gene expression in blood specimens from individuals diagnosed with acute myeloid leukemia (AML), no statistically significant difference was found between newly diagnosed AML and healthy control groups using real-time reverse transcription-PCR (qRT-PCR) from blood specimens, indicating that HOTAIR gene expression is not a reliable biomarker in the diagnosis of AML [8]. Nonetheless, several studies have shown that HOTAIR gene expression is significantly elevated in patients with leukemia compared to the control group, and they postulated that it could be a poor prognostic marker [9]. HOTAIR and HOXD gene expression in patients diagnosed with leukemia may affect proliferation in leukemic cells. Therefore,it could be used as prognostic markers, but further studies on gene function and mechanism are needed.

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