Proteome of Precursor Hematopoietic Cells from Patients with Acute Myeloid Leukemia

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Proteomic datas can indicate detailed further studies in the pathogenesis of cancer. Acute myeloid leukemia (AML), an aggressive hematological neoplasia, is characterized by accumulating myeloid precursor cells in bone marrow and latter in peripheral blood. While cytogenetic and molecular diagnostics may contribute individualized therapy in certain subsets of AML, there is hope that proteomics of AML will identify new diagnostic or therapeutic biomarkers in the future. $CD34^+$ cells are a population of stem cells/pluripotents hematopoietic cells that self-replicates giving origin to all blood cells. Using this population, we compared the proteome of $CD34^+$ cells obtained from two AML patients with cells $CD34^+$ from healthy donors. After protein extraction, the proteins from $CD34^+$ cells were separated by 2DE gels. The proteins present in two or more times that in healthy donors or reduced in AML, were identified by mass spectrometry in a MALDI-TOF-TOF instrument. Among the proteins identified, Antioxidant Protein 1, Galectin 1 and Metastasin (S10A4) are involved in the control of the redox state, cell differentiation or involvement in the apoptosis and cell cycle control respectively, processes that are inexistent or at least much compromised in cancers. Future studies will extend this proteomic study to more patients in order to determine if these proteins are candidates for biomarkers or even molecular targets for more directed and less aggressive treatments for AML.

Key words: Proteome, Acute Myeloid Leukemia, Precursors Hematopoietic Cells

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