

Unique Gene Expression Patterns in Hematopoietic Stem Cells from Various Sources

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KEYWORDS CD34+ Hematopoietic Stem Cells. Genespring. Unique Gene Expression. Cord Blood. Bone Marrow. Liver. Peripheral Blood

ABSTRACT Hematopoietic stem cells are involved in the production of blood cells. These cells are derived from various origins. In this study, we examined, using microarray software GeneSpring GX, whether HSCs derived from four different origins i.e., cord blood, liver, bone marrow and peripheral blood, exhibit unique gene expression pattern. A total of 23 individual normal hematopoietic cell expression profiles were identified in NCBI's GEO database -10 normal CD34+ bone marrow sample, 4 normal CD34+ liver sample, 5 normal CD34+ cord blood sample and 4 normal CD34+ peripheral blood sample. These studies were performed using U133A array platform. The data analysis was done by GeneSpring GX Microarray software 7.3 version. Our results indicated that HSCs derived from various origins exhibited unique gene expression patterns. We also determined the specific biological function of HSCs using upregulated genes that are uniquely expressed in each origin. We observed the following results - cord blood HSCs play an important role in development of embryos; Liver HSCs play an important role in apoptosis, angiogenesis and neural transdifferentiation; Bone marrow HSCs play an important role in cell proliferation, cell migration and cell retention and peripheral blood HSCs play an important role in nucleosome assembly. These HSCs genes present in peripheral blood, when altered, get involved in Systemic Lupus Erythematosus Pathway.