Acute Myeloid Leukemia gene co-expression networks and differential expression analysis in blood and bone marrow samples

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Acute myeloid leukemia (AML) is one of most aggressive hematological diseases, characterized by abnormal growth of immature myeloid hematopoietic cells inside the bone marrow (BM) and subsequent organ and tissue invasion via bloodstream. This causes a myriad of symptoms that goes from fever and shortness of breath to neurological manifestations and severe hemorrhage that could lead to death if there is no BM transplant or chemotherapy available or effective. Studies demonstrated that cancer cell environment is crucial to determine its growth and development. In this sense, the transcriptional profile of leukemic cells could allow to understand how these cancer cells are able to grow and disseminate quickly along the BM and the bloodstream. Thus, blood and BM RNA-seq data from AML patients were obtained from the Gene Expression Omnibus database, which were quality assessed and pre-processed using FastQC and Trimmomatic software. Trimmed reads were aligned to Ensembl reference transcriptome (version GRCh38.84) using Salmon software. Gene quantification were acquired based on transcripts count and used as an input to perform differential gene expression (DGE) and to build a co-expression network (CN) through DESeq2 and WGCNA R packages, respectively. Results showed a total of 1426 DEG (Blood x BM), which 416 and 1010 were over and underexpressed, respectively and they are mostly related to cell division, cell adhesion and also immune response and signaling processes mediated by immunoglobulins and cytokines. CNs showed, modules in both samples that have common biological processes, like immune response, cell cycle and DNA repair pathways. However, they differ in their composition and structure, as well as some of them are linked to different pathways. These preliminary results showed some possible insights about how these cells behave in different environments, although more analysis in these modules are required to understand, in a broad sense, how it can affect tumor biology.