PROTEOMIC COMPARISON THROUGH 2D-DIGE OF HUMAN MESENCHYMAL STEM CELLS FROM BONE MARROW AND UMBILICAL CORD VEIN.

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Mesenchymal stem cells (MSCs) are multipotent cells which are attractive candidates for clinical therapy due to their property if pluripotency. The usual source of these cells is bone marrow (BM), but other sources such as umbilical cord vein (UCV) have been evaluated. Since MSCs can be isolated from different tissues, it is important to establish how closely related these cells are in terms of gene expression (mRNA and proteins). A transcriptional study implied that despite the great similarity between MSCs from BM and UCV, differences between the two transcriptional profiles makes each cell appropriate for a different clinical application. In present work, our objective is to identify proteins differentially expressed in BM and UCV MSCs using the proteomic approach. MSCs were isolated from BM by separation of the mononuclear layer using Ficoll gradient and UCV by collagenase treatment. Cells were cultured and expand *in vitro* as well as immunophenotipically and functionally characterized. The proteins of these cells were extracted and quantified. We then used 2D-DIGE which allows us to compare both extracts in just one gel. Protein extracts were marked with CyDye (Cy3- UCV, Cy5- MO and Cy2- mix of both to de used as internal standard). For the IEF we used strips with pH range of 3 to 10, followed by 2nd dimension (SDS-PAGE). After scanning and analyzing the gel we found a total of 1010 spots. When we compared the volume of the spots we had that 465 were identical, 275 were decreased (UCV/BM = 0,5) and 270 spots were increased (UCV/BM = 1,5). The spots presenting significant differences will be identified by MS (MALDI TOF-TOF).

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