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Microarray analysis after adipose derived mesenchymal stem cells injection in monosodium iodoacetate-induced osteoarthritis rats

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Osteoarthritis (OA) is a degenerative joint disease characterized by abrasion, and ultimately, destruction of the articular cartilage and trabecular bone loss. OA is still considered a devastating disease, which requires an aggressive therapeutic approach. Despite the therapeutic potential of human adipose-derived mesenchymal stem cells (AD-MSCs), the molecular parameters needed to define the stemness remain largely unknown. Using high-density oligonucleotide microarrays, the differential gene expression profiles between a fraction of human adipose-derived (AD) mononuclear cells and its MSC subpopulation were obtained. Of interest, a subset of 58 genes preferentially expressed at 7-fold or higher in the group treated with human AD-MSCs. This subset contained numerous genes involved in the inflammatory response, immune response, lipid metabolism, cell death, cell proliferation, and DNA repair. Additionally, four protein networks were constructed. The interaction network consisted of 46 proteins encoded by up-regulated genes. However, the interaction network also consisted of 38 proteins encoded by down-regulated genes. My results provide a basis for a more reproducible and reliable quality control using genotypic analysis for the definition of human AD-MSCs. Therefore, these results will provide a basis for studies on molecular mechanisms controlling the core properties of human MSCs.

Biography

Jae Chul Lee, Department of Biology, School of Life Sciences, Chungbuk National University, Cheongju, Korea & has many research publications & attended national & international conferences

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