DIFFERENTIAL SHOTGUN ANALYSIS OF MESENCHYMAL STEM CELLS FROM OSTEOARTHRITIS PATIENTS

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Osteoarthritis (OA) is a chronic, degenerative disease with multifactorial etiology which constitutes the most common cause of pain and disability in older adults, as well as the leading cause of joint replacement surgery. The degradation of articular cartilage in osteoarthritis is related to changes in the composition of the extracelular matrix and the alteration of protein expression by chondrocytes, the only cell component of cartilage, along with well-defined changes in the subchondral and periarticular bone. Since the application of therapies based on cells with regenerative potential like mesenchymal stem cells (MSCs), progenitor cells with the capacity to differentiate into distinct connective tissues including cartilage, represent a promising strategy for the treatment of OA, we have searched in this work for altered proteins in bone marrow MSCs obtained from osteoarthritis patients using a shotgun approach.

MSCs protein extracts were prepared from bone marrow aspirates obtained from patients undergoing joint replacement as a result of OA as well as from healthy donors, without special radiographic signs of OA, in the surgery for the subcapital fracture of the hip. Samples were then digested with trypsin and analyzed by LC-MS. A variety of software tools (commercial, publicly available and home-made) enabled a comprehensive bioinformatic analysis based on the proteins identified. Results highlight distinctive functional categories and interaction networks which suggest a diminished differentiation and regenerative potential of MSCs in patients with OA.

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