THE PROTEOMIC APPROACH TO RESEARCH THE PATHOGENESIS, DIAGNOSTIC, PROGNOSTIC AND NEW THERAPEUTIC TARGETS IN OSTEOARTHRITIS

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Osteoarthritis (OA) is the most common rheumatic pathology. It is related with aging, and it is characterized mainly by cartilage degradation. Therefore, new diagnostic tests for OA are urgently needed, which also allow the efficient development of alternative therapeutic strategies. Considering that OA process implies different tissues and complex biological processes, the most promising diagnostic strategy seems to be the study of a combination of different biomarkers. Recently, using iTRAQ methodology (ABSCIEX), by two dimensional LC coupled to MALDI-TOF/TOF mass spectrometry and ProteinPilot 2.0 software (ABSCIEX, we have identified 349 proteins in serum and 113 proteins in synovial fluid of patients with Knee OA. This panel of proteins let us to find a pool of biomarkers with differential expression in OA patients and in healthy people with relevance to diagnostic and prognostic of OA. Significant advances have occurred in the symptomatic management of OA over the past several decades. The development of so called disease-modifying osteoarthritis drugs (DMOADs) is still in a formative stage. In this sense, to find new therapeutic targets to OA, we have carried out a pharmacoproteomic approach using DIGE and SILAC methodology in human articular chondrocytes treated with both Glucosamine Sulfate and Chondroitin Sulfate. Results showed that 31 different proteins were altered by GS or/and CS treatment when compared to control, 35% of the proteins modulated by GS are involved in signal transduction pathways, 15% in redox and stress response, and 25% in protein synthesis and folding processes.