Investigation of potential new targets for the diagnosis and/or the treatment of osteoarthritis

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Purpose. Synovial membrane plays a key role in osteoarthritis (OA) pathophysiology. We have previously compared the gene expression pattern of synovial cells isolated from inflammatory (I) or normal/reactive (N/R) areas of a synovial membrane harvested from the same OA patient. We identified a large number of mediators belonging to key pathways involved in OA pathogenesis. The aim of this study was to validate different potential new targets for the diagnosis and/or the treatment OA.

Methods. Synovial cells (SC) were isolated from OA synovial specimens obtained from 12 patients undergoing knee replacement. The inflammatory status of the synovial membrane was characterized according to macroscopic criteria. The biopsies from N/R and I areas were cultured separately for a period of 7 days. Microarray gene expression profiling between N/R and I areas was performed. The biological relevance of up- and down-regulated genes was analyzed with Ingenuity Pathways Analysis. Western blot and immunohistochemistry confirmed the identified genes most differentially expressed in the key pathways.

Conclusion. Synovial membrane inflammation is a key target for OA treatments. In this work, we have identified proteins involved in the synovitis pathways like angiogenesis, cells infiltration and matrix remodeling. These proteins could be targeted by drugs and used as companion biomarkers for evaluating their efficacy. Although qualitative, our results could also yield to the identification of markers of the disease. This investigation has to be further pursued.