FROM OSTEOARTHRITIC SYNOVIUM TO SYNOVIAL-DERIVED CELLS CHARACTERIZATION: OBESE VS NON-OBESE

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Introduction: Obesity is one of the important risk factors in the development of knee osteoarthritis (OA). Studies focused on well-characterized clinical samples to investigate the cellular and molecular effects of chronic inflammation and obesity on OA are limited. Focussing specific sites on OA synovium membrane (SM) may provide clues to possible pathophysiological processes that can be targeted for therapeutic purposes. This study was thus conducted to: (i) Characterize histopathological changes of OA SM and (ii) To determine the cellular and molecular changes in OA SM derived fibroblast (SDF), demonstrate changes in patients who are and are not obese (BMI>27.5kg/m2).

Methodology: OA synovium were collected from subjects who underwent arthroplasty and arthroscopy procedures (MREC reference no: 20164-2398). Groups include Non-OA and non-obese (G1, n=3), Non-OA and obese (G2, n=3), OA and non-obese (G3, n=3) and; OA and obese (G4, n=3). SMs underwent histopathology analysis and primary SDF culture. The changes in the OA SMs were scored using Krenn synovitis score and morphological differences in primary SDF were recorded. Total RNA extracted from SDF were used for microarray gene expression profile analysis.

Results: OA SM histopathology analysis showed apparent changes in G1 to G4. Synovial hyperplasia and inflammatory cells infiltration were observed in G2, G3 and G4. Interestingly, lymphocytes were observed in G3 and the presents of macrophages were more apparent in G4. Immunofluorescence staining showed a positive expression of VCAM1 in OA SDF, which may play a role in the inflammatory cells infiltration in SM. SDF global gene expression profiles analysis showed upregulation of focal adhesion-PI3K-AKT-mTOR-signaling pathways, calcium signalling pathways and protein-protein interactions in podocytes signalling pathways.

Conclusion: Obesity appears to be associated with inflammatory process in SM, and is involved in specific OA pathogenesis pathways.