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RESEARCH ABSTRACT FORM

TITLE: Proteomic Analysis of the Human Synovium from Patients Clinically Diagnosed with Early and Late Osteoarthritis

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Osteoarthritis is the most common type of arthritis of over 100 different kinds, affecting over 20 million people in the US. The current methods of diagnosing osteoarthritis are subjective and cannot be quantified and initially the patient is not sensitive to damage as it progresses. There is need for quantifiable early detection of biomarkers or proteins involved. The overall goal of our study is to identify the proteome of the synovium, synovial fluid, and cartilage to look for the underlying molecular events and biological pathways occurring between these tissues. As a first approach to accomplishing this overall goal, my summer project focused on identifying the proteome of the synovium (synovial tissue). Using 3 samples of Early OA and 3 samples of Late OA with 1D Polyacrylamide Gel Electrophoresis, mass spectroscopy, and MASRAN software, we are able to make proteomic comparisons to establish trends in protein expression. All three synovium LOA samples exhibit approximately the same amount of different kinds of proteins. The synovium EOA individuals demonstrate individual variability in both the total number of expressed proteins and proteins commonly expressed. These observations suggest the possibility of different progressive stages of EOA. Future direction is to identify the metabolic and signaling pathways involved in osteoarthritis by comparing the proteomic profiles of the synovium, cartilage and synovial fluid from the same EOA or LOA subject. Using bioinformatics we plan to examine in more detail those proteins common to EOA and LOA in a particular tissue.