stress-induced over-expression of caveolin-1 in the cellular aging. Our recent study revealed that angiogenic growth factors, especially vascular endothelial growth factor (VEGF), downregulate catabolic activity and cellular aging, and also maintain anabolic viability in chondrocytes. We also review the underlying signal transduction pathways. Finally, we show that newly developed antioxidant C60 is a useful as a therapeutic agent to reduce articular cartilage degeneration in the OA rabbit model.

**Conclusions:** Our studies reported here sought to demonstrate in the OA model in vitro and in vivo that oxidative stress is closely involved in the cartilage/chondrocyte aging and degeneration and that angiogenic growth factors may at least in part participate in the pathogenesis of OA. Also, we demonstrate that water-soluble C60 fullerene, a strong free-radical scavenger, can function as a protective agent against the catabolic stress-induced degeneration of articular cartilage.

**Results:** Our studies reported here sought to demonstrate in the OA model in vitro and in vivo that oxidative stress is closely involved in the cartilage/chondrocyte aging and degeneration and that angiogenic growth factors may at least in part participate in the pathogenesis of OA. Also, we demonstrate that water-soluble C60 fullerene, a strong free-radical scavenger, can function as a protective agent against the catabolic stress-induced degeneration of articular cartilage.

**THE APPLICATION OF PROTEOMICS IN THE STUDY OF OSTEOARTHRITIS**

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**Purpose:** For a highly complex, multifaceted disorder such as osteoarthritis, proteomic approaches have much to offer. Biomarker "fingerprints" which indicate disease outcome, networks of molecular pathology and therapeutic targets can be filtered out from background signals with proteomic techniques.

**Methods:** Following closely on the heels of genomic screening, proteomic platforms have the potential to provide additional levels of understanding to the leading edge of osteoarthritic disease. Proteomic tools have the significant advantage in not precluding biomarker identity, so research strategies can be formed in an objective, "unsupervised" fashion.

**Results:** This talk aims to give the uninitiated an overview of the technologies currently available, highlighting their assets and pitfalls. A brief history of findings to date from published proteomics studies of synovial fluid, cells and tissue will be reviewed from a variety of arthritides. The importance of formulating clinically relevant questions will form a major focus and novel strategies and sufficient powering of studies will be discussed.

**Conclusions:** This workshop gives the opportunity to learn of the skills now available, giving inspiration and expanding on existing knowledge. The content is pitched at scientists and clinicians with limited knowledge of global proteomic technologies and strategies and an interest in applying them in the study of osteoarthritis.

**COMBINED TRANSCRIPTOME AND PROTEOME APPROACHES TO ELUCIDATE GENE EXPRESSION PATTERNS OF SYNOVIAL TISSUES AND SYNOVIAL FLUIDS FROM PATIENTS WITH RHEUMATOID ARTHRITIS VERSUS OSTEOARTHRITIS**

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**Purpose:** With the availability of the human genome sequence and those of animal models, data driven research for unravelling the molecular grounds of Rheumatoid Arthritis (RA) and Osteoarthritis, respectively, can be considered a realistic challenge to the scientific community.

**Methods:** A comprehensive research strategy is presented for studying multifactorial polygenic (autoimmune) diseases, enabling the integration of multiple research efforts by so called proteomics and systems biology approaches. An integrative scientific concept is discussed of how to elucidate molecular mechanisms of complex diseases using state-of-the-art methodologies in functional and comparative genomics.

**Results:** RNA, protein, and peptide microarray profiles are currently obtained in cutting edge research projects producing gene signature read-outs rather than single DNA and/or protein markers. A continuous interchange of data-driven and hypothesis-driven research has been enhanced in order to investigate the tissue of such marker signatures.

**Conclusions:** Currently, a comprehensive study of the RNA and protein regimes is undertaken that eventually will lead to a "holistic" view of signalling pathways that are expected to reveal how the respective molecules and the cells themselves interact with each other; hopefully leading to new diagnostics and therapeutics in the future.