

POSTER PRESENTATION

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Microarray analysis reveals age-related differences in gene expression during the development of osteoarthritis in mice

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Background

Osteoarthritis (OA) is the most common form of arthritis and is the type most closely associated with aging. Joint injury is also a key risk factor in OA development. The mechanisms by which aging contributes to the development of OA are not completely understood. This study uses microarray analysis to compare the differences in gene expression in the joint tissues of young and old mice in a model of post-traumatic OA.

Methods

Young (12 weeks of age) and old (12 months of age) mice underwent surgery to induce OA, or underwent a control sham surgery. Mice were sacrificed eight weeks after surgery for RNA extraction. Three arrays (pooled RNA from three mice per array) were run for each DMM and sham surgery from each age group. Microarray data were normalized and filtered on detection *P*-value and signal log ratio. Filtered genes were assigned to expression patterns, followed by functional, pathway and network analyses.

Results

Significant expression differences in 541 genes were observed in either young or old mice post-surgery. Overall, old mice exhibited more up-regulation then young mice. Genes with no expression change in young but up-regulation in old mice (164 genes) included cell-cell adhesion genes, extracellular matrix genes, such as collagen, and carbohydrate-binding genes. Those genes down-regulated in young mice that showed no change (175 genes) or up-regulation (106 genes) in old mice are

components of the sarcomere or involved in carbohydrate metabolism. Additionally, genes not changed in young but down-regulated in old mice (30 genes) are involved in the immune response, and genes up-regulated in young but not changed in old mice (19 genes) are involved in the regulation of apoptosis and redox processes.

Conclusions

These results elucidate various biological systems that should be the subject of future research to determine the mechanisms by which OA development is affected by age.

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