**Intervertebral Disc Regenerative Therapy: Investigation of Cell Surface-Specific Markers via –omic Profiling and in silico Analysis**

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**Introduction**

According to the World Health Organisation, back pain is the leading cause of disability, affecting millions of people worldwide¹. One reason for axial back pain is the degeneration of the nucleus pulposus (NP) at the centre of the intervertebral disc, which is closely correlated to age. We have set out to associate NP cells with cell surface-specific markers different from the other closely related cell types, namely intervertebral disc annulus fibrosus (AF) cells and articular cartilage (AC) chondrocytes, in order to derive NP targets. These targets can be used to direct targeted therapies for cellular regeneration.

**Materials and Methods**

Human HG U133_2.0 Affymetrix arrays were used for all sixteen samples. The statistical environment R (http://www.r-project.org) and bioconductor (http://www.bioconductor.org) were used for data analysis²,³.

**Results**

We carried out a DNA microarray experiment on 16 human samples; 6 patients with 3 different cell types minus two AC samples. The global gene expression profiles, as assessed by both hierarchical clustering and principal component analysis, demonstrated a clear divide between the AC and AF and also between the AC and NP samples. However, the AF and NP samples did not separate out and displayed a greater inter-patient similarity over cell type transcriptomic profile.

With this information, transmembrane protein candidates unregulated at the transcript level in NP cells versus AF/AC have been identified (n=90; p<0.01) and are currently being investigated as suitable targets for phage display. RNA-sequencing of the 3 cell types is also an ongoing project, whereby a more in-depth coverage of the transcriptome may reveal more specific NP targets.

**Discussion and Conclusions**

Gene expression differences between cell types are key in discovering cellular targets, specifically for NP cells, and elucidating the necessary genes for therapeutic delivery. In short, this study will contribute to a larger, global aim of advancing the treatment of lower back pain.

**References**


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