



Text-mining network analysis of the response to osmotic stimuli in the intervertebral disc

X. Xu*, L. Liu* and Q.Y. Lu

Department of Trauma Surgery, East Hospital Affiliated to Tongji University, Shanghai, China

*These authors contributed equally to this study.

Corresponding author: Q.Y. Lu

E-mail: luqingyoulqy@163.com

Genet. Mol. Res. 12 (2): 1574-1581 (2013)

Received August 10, 2012

Accepted November 21, 2012

Published May 13, 2013

DOI <http://dx.doi.org/10.4238/2013.May.13.11>

ABSTRACT. Intervertebral disc cells experience a broad range of physical stimuli under physiologic conditions, including alterations in their osmotic environment. The purpose of this study was to construct a text-mining network of the genes induced during the response to osmotic stimuli in the intervertebral disc. We obtained a gene expression profile of human intervertebral disc cells from the National Center for Biotechnology Information, after culture under hyper- and hypo-osmotic conditions compared to iso-osmotic conditions, and we identified 65 differentially expressed genes of intervertebral disc cells. We constructed a text-mining network using Biblio-MetReS between the differentially expressed genes and other genes that were included in the same document as the differentially expressed genes. Then, we performed pathway-enrichment analysis to identify the most relevant pathways for the response to osmotic stimuli in intervertebral disc cells. Our data provide a comprehensive bioinformatics analysis of genes and pathways that may be involved in the response to osmotic stimuli in the intervertebral disc.

Key words: Text-mining network; Intervertebral disc; Osmotic stimuli