The Genetic Functional Matrix Theory

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Introduction

The human genome project "The ultimate triumph of genetics" demonstrated genomic controls of all developmental processes, at cellular, structural and organismal levels. Cartilage plays a critical role in condylar growth because it is the template onto which bone forms.

Objectives

1. To screen, using microarray, for the expression profile of genes related to chondrogenesis in the condyle.
2. To identify genes related to the "Mechanotransduction Theory" and are expressed in condylar cartilage.
3. To correlate such genes to genes that regulate condylar cartilage formation.

This way we can demonstrate the interplay between genetics and epigenetics factors involved in condylar cartilage growth.

Materials and Methods

280 rats were divided into 7 experimental (advancement) and 7 control groups.

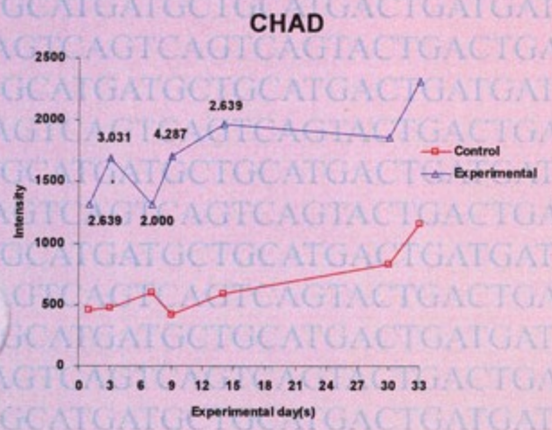
Rats were sacrificed on day 1, 3, 7, 9, 14, 30 and 33.

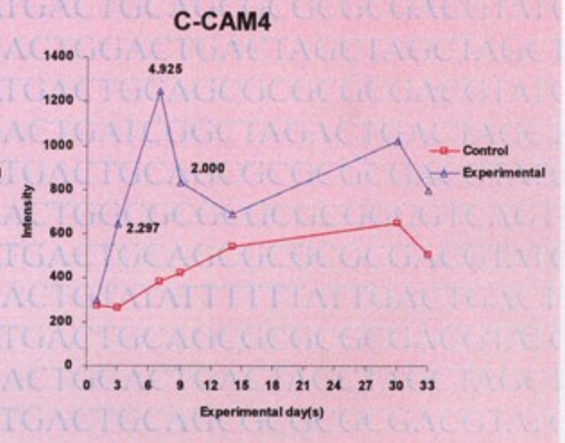
Total RNA was extracted for microarray analysis and confirmed with RT-PCR.

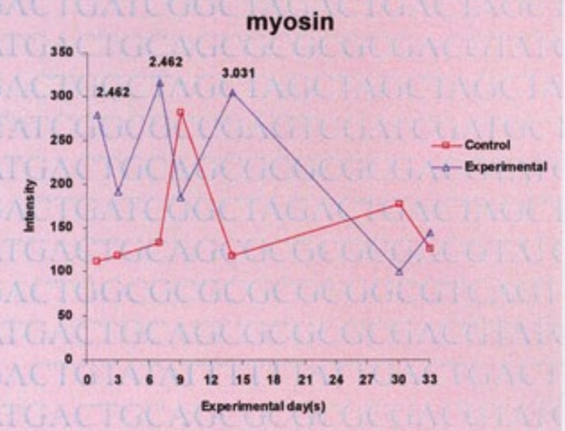
"Gene spring software" was used in analysis of microarray results and the search was limited to genes that showed a 2-fold or more change between groups.

Results

Out of 624 genes, only 25 genes were related to different aspects of cartilage development. **15** genes were up regulated while **10** were downregulated. Several genes were identified for the first time in the condyles and were cell-cell attachment genes (CHAD), cell-matrix attachment genes (C-CAM4), cellular movement genes (myosin)







Conclusion

Transmission of extra-skeletal stimuli to cells in condylar cartilage through mechanotransduction leads to expression of several genes that directly impact condylar growth. This demonstrates an orchestrated interplay between mechanotransduction and genetic regulation. Therefore we propose to re-name the theory into **"The Genetic Functional Matrix Theory".**