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Commentary

Comparisons between transcriptional regulation and RNA and DNA

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Recent studies have focused on transcriptional regulation and gene expression profiling of Human Embryonic Stem Cells (hESCs). However, little information is available regarding relationship between RNA expression and transcriptional regulation, which is critical in complete understanding of pluripotency and differentiation of hESCs. In current study, we determined RNA expression of three different hESC lines compared to Human Universal Reference RNA expression (HuU-RNA) using a full genome expression microarray, and compared our results to target genes previously identified using ChIP-on-chip analysis.

"All genes are not expressed all time in all cells. Instead, each tissue type has its own epigenetic program that determines which genes get turned on or off at any moment," said co-senior author Thomas Cech, Nobel laureate and distinguished professor of biochemistry. "We determined in great detail that RNA is master regulator of this epigenetic silencing and that in absence of RNA, this system cannot work."

The results are consistent with RNA expression analyses that demonstrate these genes as differently expressed in our hESC lines, further substantiating their role across cell types and confirming their importance as embryonic signatures. Differential expression of Growth Arrest-Specific (GAS) family of genes in hESC. GAS2L1 and GAS3 members of this family appear to be transcriptionally regulated by OCT4, SOX2, or NANOG, whereas GAS5 and GAS6 are not; all of genes are differentially expressed, as determined by microarray and validated via quantitative (Q)-PCR. Collectively, these data provide insight into relationship between gene expression and transcriptional regulation.

The objective was to identify genes common between the two methods, and generate a more reliable list of embryonic signature genes. Even though hESCs were obtained from different sources and maintained under different conditions, a considerable number of genes could be identified as common between RNA expression and transcriptional regulation analyses. As an example, results from ChIP-on-chip studies show that OCT4, SOX2, and NANOG co-occupy SOX2, OCT4, TDGF1, GJA1, SET, and DPPA4 genes. hESCs.

DO ALL CELLS CONTAIN SAME DNA?

This demonstrated by fact that fully differentiated cell types are still capable, within right environment, of giving rise to an entire new animal. This capability was first shown by way of an experiment in which the nucleus of an adult frog skin cell was transplanted into an enucleated donor embryo, eventually leading to the development of a cloned adult frog. Later, intact complete genome of differentiated cell was used in cloning of famous sheep Dolly, showing that in mammals; genes are not lost during development, so they must therefore be regulated. Today, researchers understand that specialized, differentiated cell types of adult body contain genome as complete as any embryo's. This fascinating demonstration has led to proposal that changes in gene expression, rather than losses of genetic material, play key role in guiding and maintaining cell differentiation.

Several lines of evidence support proposal that all of cells within multicellular organism contain same genome. For instance, although you started as a single cell with half-genome from each parent, that single cell quickly divided and new cells began to differentiate, or become different from each other. While this process of differentiation established a wide variety of cell types (e.g., skin, liver, muscle, etc.), it was not accompanied by any permanent loss of genetic material.

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