

CDB SEMINAR

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Wednesday, January 9, 2008 16:00~17:00 A7F Seminar Room

FANTOM and Genome-wide Technologies

Summary

The international FANTOM consortium was organized in 2000 and established the de facto standard of the full-length cDNA banks of mouse, human and several other species. Now, it is entering a new scientific phase dealing with functional genomics of the gene networks. A human monoblast cell line, THP-1, is used as a model for the development of a general-purpose pipeline for the elucidation of the gene expression regulatory network which consists of transcriptional factor proteins and functional RNA molecules. Large amounts of data such as promoter actitivites and RNA profiling by CAGE, chromatin structures and protein-DNA interaction by ChIP-Chip, small RNA profiling by sequencing and so on was obtained through PMA stimulation time coarse of THP-1, followed by extensive computational analysis. The analysis has showed that the differentiation of the cell was precisely controlled by concerted regulation of gene expressions. We have recently introduced a new concept called "Pond" for understanding cell function. A Pond is defined as a steady state of a cell with specific gene expression profile to autonomously maintain the cell function. Currently we are planning to expand our effort to establish a "Pond library", which is a collection of "Ponds" of all kinds of cells in the body.

We believe that our data and knowledge will make a great contribution for understanding cell as well as tissue engineering and regeneration medicine.

- 1) Pond analysis of each tissues and fetal cell could contribute to quick identification of key transcription factors that enable *in vitro* induction of an ES cell to a desired cell.
- 2) Comprehensive genome-wide survey with a massive-parallel shotgun sequencer of the iPS cell would provide with a safety assessment index

Effective use of the FANTOM database, technologies and resources could be a major source of the breakthroughs and advances in regenerative medicine.

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