

## Comprehensive measurement of *C. elegans* gene expression

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We think the main targets in the post genomics era are; (1) to integrate the information on the expression and the function of all genes of the genome in the context of development, (2) to extract the rules that govern the molecular mechanisms of development that are carried out by a finite number of genes, (3) ultimately to reconstruct the developmental process in the computer.

The nematode *C.elegans* is an excellent system for the purpose, since the entire cell lineage from fertilized egg to adult is known and the entire genome sequence has been determined. We have identified about 10,000 cDNA species (more than a half of all genes) of the nematode *C.elegans* through our EST project. Out of them about 7,000 cDNA species have been analyzed for mRNA distribution throughout the life of worm by using of whole mount in situ hybridization. The mRNA patterns have been annotated for typical developmental stages and cell lineage/tissue. Based on the information, we are performing clustering analyses and finer analysis on subsets of the genes to elucidate the network of gene regulation. Currently we focus on the genes of maternal expression and embryogenesis. Here I will present the clustering results as together with the attempts for in silico reconstruction of embryogenesis.