

183. Functional Genomics and Expression Maps of Human and Mouse

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Abstract

After the completion of the genomic sequences of man and mouse, the challenge will be to understand the function of all genes (about 30,000) and proteins and to reconstruct the complex networks of biological processes underlying organism development and maintenance. Information on the expression profiles of these genes in the different tissues and cell types at various stages of development provides key insights into gene function(s) and allows to identify genes involved in common molecular mechanisms.

As a pilot study for a systematic analysis in the mouse, we have analysed the patterns of gene expression of the mouse orthologues to the 240 genes located on chromosome 21 in man, using a combination of different experimental and "in silico" techniques [1]. One of these techniques, so-called EST mining, has proven particularly effective for identifying tissue-specific genes and clusters of functionally related genes. We have screened all public mouse EST libraries; EST counts for chr.21 orthologues were pooled in a non-redundant set of libraries and analysed by a method using the Pearson correlation coefficient. This approach is now being expanded to the analysis of all mouse and human genes based on the whole ENSEMBL reference set of genes. The profiles are being compared for identifying clusters of co-regulated genes present in both species.

As an additional powerful technique, we have designed a cDNA chip representing approximately 20,000 genes from the human ENSEMBL set (the mouse set is in progress) as a tool for analysing differential expression profiles for several well characterised human cell lines. These complementary approaches form the basis for building genome-scale gene expression maps as a first step towards identifying specific molecular phenotypes of cell lineages and tissues and give hints towards understanding gene function in complex biological networks. The current expression maps will be presented.

References

[1] The HSA21 expression map initiative. 2002. A gene expression map of human chromosome 21 orthologues in the mouse. *Nature* 420:586-590.