Lemkin, Peter

MAExplorer – microarray exploratory data analysis

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MAExplorer is a Java applet that runs in a user's Web browser. It allows the exploratory data analysis of quantitative cDNA expression profiles across multiple microarrays. Data may be viewed and directly manipulated in images, scatter plots, histograms, expression profile plots, cluster analysis and so on. A key feature is the clone "Filter" for constraining a working set of clones passing a variety of user specified tests. Reports may be generated with Web access to UniGene, GeneBank and other Internet databases for sets of clones found to be of interest. Reports may also be exported to MS-Excel. MAExplorer is being developed in a collaboration between the Laboratory of Genetics and Physiology (LGP, NIDDK) and the Laboratory of Experimental and Computational Biology (LECB,NCI). LGP has established a program designed to identify and understand genetic pathways operative during normal mammary gland development and tumorigenesis. One arm of this program focuses on the use of cDNA microarrays to profile gene expression patterns. For this purpose, cDNA (EST) libraries are generated, sequenced and clone inserts are spotted on nylon membranes. These membranes are used to monitor expression profiles under various physiological conditions. At this point, expression profiles have been obtained from several stages of normal mammary gland development and different tumour models. With this program, you may: (i) analyse the expression of individual genes; (ii) analyse the expression of gene families and clusters; (iii) compare expression patterns. Data is downloaded as required to the user's Web browser to perform real-time analyses on the user's computer. However, the user has access to the entire database and may save and share their explorations in a groupware environment. The MAExplorer may be accessed through the MGAP web site at http://mammary.nih.gov/mgap

Lennon, Greg

Challenges and opportunities in constructing comprehensive gene expression databases

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Gene Logic is using microarrays (including the Affymetrix GeneChip™) to construct a comprehensive gene expression database for pharmaceutical, biotech and academic users. We are determining thousands of expression profiles of normal and diseased mammalian tissues, experimentally manipulated animals and cell lines, and tissues and cells treated with pharmacologic and toxic doses of a diversity of compounds. The technical issues in generating this data as well as the complex challenges of storing, analysing and integrating it with public data will be presented. In addition, the biological relevance of data generated from this approach will be demonstrated as an example of the type of functional information that can be derived and applied to pharmaceutical and diagnostic research and development.

Levy, Shawn

DNA microarrays as a method to monitor changes in mitochondria-related gene expression during development and mitochondrial dysfunction

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Mitochondria produce most of the cellular ATP by the process of oxidative phosphorylation (OXPHOS) and generate most of the endogenous oxygen radicals as a toxic by-product. In addition, mitochondria are central in the regulation of apoptosis, calcium homeostasis and cytoplasmic redox state. The 16-kb mitochondrial genome encodes only 13 of the more than 100 proteins involved in OXPHOS. Most mitochondrial proteins are encoded by the nuclear genome. Although the role of mitochondria in various cellular processes is becoming more and more apparent, little is known about the regulation of mitochondria-related gene expression. We have begun to use DNA microarray technologies to both identify genes related to mitochondrial function as well as characterize changes in mitochondrial gene expression during development and mitochondrial dysfunction. Working in the mouse system, we have chosen a preliminary set of 300 genes that are related to various aspects of mitochondrial function. Using a standard two-colour fluorescent system, we are analysing the temporal regulation of mitochondrial gene expression during early development. Experiments are also underway to analyse the changes in gene expression caused by genetic models of mitochondrial dysfunction. Through these experiments, we hope to better understand the complex interaction between nuclear and mitochondrial DNA gene expression in mitochondrial biogenesis and bioenergetics.

Li, Haochuan

Profiling expression patterns of 2,214 unigenes in mouse craniofacial development by cDNA microarray analysis

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The recent development of cDNA microarray technology enables parallel expression monitoring of thousands of genes simultaneously, which provides a powerful tool for characterizing transcriptional activities of genes in various developmental stages and pathological states. We initiated the Oral and Craniofacial Genome Anatomy Project (OC-GAP) to identify genes important for craniofacial development and disorders. As part of this genome project, we have examined gene expression patterns during mouse craniofacial development. Fluorescently labelled probes prepared using mRNA from mouse embryonic craniofacial tissues at embryonic day (E) 9.5, E13.5 and E16.5 were hybridized to microarray slides printed with 2,214 mouse unigenes. A microarray quantitative analysis revealed that 10% of these genes were expressed in different levels during craniofacial development, whereas the rest showed no significant differences in expression throughout the different developmental stages. We found that 41 genes, such as those encoding Wnt-1, retinoid receptor and Brca1, showed higher expression lev-