Poster abstracts

Jiang, Yuan

Evaluating altered levels of gene expression in cancer cellsYuan Jiang¹, Yidong Chen¹, Yan Su², Ena Wang³, Francesco M. Marincola³, Edward R. Dougherty⁴, Paul S. Meltzer¹, Michael Bittner¹ & Jeffery M. Trent¹¹Cancer Genetics Branch, National Human Genome Research Institute, National Institutes of Health, Bethesda, Maryland, USA²Lombardi Cancer Center, Georgetown University, Washington, DC, USA³Surgery Branch National Cancer Institute, National Institutes of Health, Bethesda, Maryland, USA⁴Computer Assisted Medical Diagnostic Imaging Laboratory, Department of Electrical Engineering, Texas A&M University, College Station, Texas, USA

A widely perceived opportunity for the use of microarrays is the examination of gene expression across collections of cancer cells derived from both tumour cell lines and tumours. Primary goals of such a cataloging effort will be to determine whether there are subtypes of cancer that can be identified on the basis of identifiable patterns of gene expression and whether these types can be correlated with susceptibility of the cancer to particular treatment regimes. While pursuing these primary goals, it will also be possible to examine some longstanding, basic questions about expression profiles in cancer. Our presentation will examine a large set of expression profiles of melanoma cells. It will furnish analyses of the extents of heterogeneity and homogeneity between individual tumour specimens and of differences in the extent and types of expression between tumours and cell lines derived from them. We will also provide examples of the coordinated changes in gene expression that result from experimentally imposed alterations of the expression of genes showing interesting patterns of expression in melanoma.

Johnson, Claire M.

Gene expression profiling of wound healing in keratinocytes using DNA microarrays

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Wound repair is a complex biological process involving cell migration, proliferation and differentiation of multiple cell types. A number of growth factors, receptors, matrix molecules and proteases have been shown to be important during wound healing. However, a detailed knowledge of the underlying gene expression changes occurring during wound healing would further improve our understanding of the repair process and how this may be disrupted in diseases of reduced or excessive wound healing.

To date discrete differential display or subtractive hybridization strategies have identified a small number of gene products that are upregulated in response to growth factor stimulation and wounding¹. To view gene expression changes on a much larger scale, we have applied DNA microarray technology to cell culture models of wound healing. The power of DNA microarray technology lies in its ability to collect gene expression data for tens of thousands of genes per study, enabling a comprehensive picture of gene expression changes to be built up². Our studies with human primary epidermal keratinocytes, either treated with growth factors or mechanically wounded *in vitro*, have identified several differentially expressed genes. These include previously identified wound related genes (for example stromelysin-2 and ADAM-TS) and a number of previously unreported or novel genes whose role in wound healing is currently under investigation. Data

will be presented which illustrates the common and unique transcriptional changes occurring upon mitogenic stimulus or mechanical injury to human keratinocytes *in vitro*.

1. Frank, S. & Werner S. *J. Biol. Chem.* **271**, 24337-24340 (1996).
2. Iyer, V.R. *et al. Science* **283**, 83-87 (1999).

Kalocsai, Peter

Visualisation and analysis of gene expression data

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Recent advances in microarray technology have led to the proliferation of experiments simultaneously measuring the transcriptional responses of massive amounts of genes to a variety of stimuli. The scale and complexity of the rapidly accumulating gene expression data presents numerous problems for experimental design, data interpretation and statistical analysis. At BioDiscovery, Inc. we are developing and implementing algorithms using various multivariate techniques that could provide solutions to many of the data analysis and visualisation needs of the microarray research community. We have implemented a variety of hierarchical and neural network-based clustering techniques and two-way Principal Component Analysis. With these tools it is possible to simultaneously search for patterns in gene expression profiles and across many different experimental conditions. Experiments analysing changes in expression pattern during the cell's life cycle can easily be visualised using our Time Series Analysis tool. The flexibility of our data analysis methods allow for analysis within one experiment, for comparative studies between two experiments or large scale analysis of any number of experiments. These techniques can help establish functional groupings of genes or predicting the biochemical and physiological pathways of previously uncharacterised genes and they are even becoming an invaluable aid in drug discovery. The usefulness of the aforementioned and other visualisation and data compression techniques for information integration and interpretation of expression data will be discussed, along with identification of key areas in statistical research where further developments are needed.

Kerkhoven, Ron

The use of DNA-microarray technology to research the cell cycle and tumour-specific expression profiles

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The Netherlands Cancer Institute is running a DNA microarray facility where this technology is used in fundamental research projects and studies on patient material. We are using the Unigene 40k human gene library (Research Genetics) to monitor tumour-specific expression profiles. We aim to find prognostic markers that predict treatment outcome. For these studies, we have available an extensive, well-documented tumour bank that has been collected over the past 20 years. Currently, large numbers of tumour samples and healthy control tissues are being prepared for analysis. To gain more insight into the significance of tumour-specific gene expression profiles, we are in the process of generating microarray data