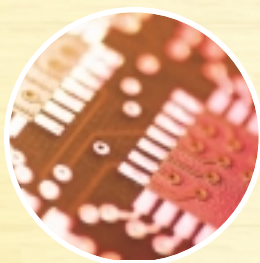


# BIOCHIPS

FROM NOVEL TECHNOLOGY TO LATEST APPLICATIONS

July 14-15, 2003

Sheraton Woodbridge Place Hotel - Iselin, NJ



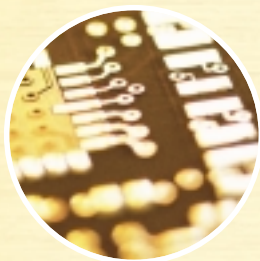
## SECTIONS INCLUDE:

- Microarray Experimental Design & Data Analysis
- System Biology/In Silico Approaches
- Biomedical/Pharma Applications
- Antibody Arrays/Protein Profiling
- Protein Arrays/Phenotype Profiling

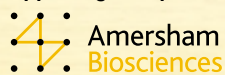


## FEATURING:

- CodeLink Three Dimensional Bioarrays for Gene Expression and SNP Analysis  
**John D. Burczak, Ph.D.**, Vice President, R&D  
AMERSHAM BIOSCIENCES
- Microarray Data Management and Analysis for Drug Discovery  
**Soheil Shams, Ph.D.**, President & CEO  
BIODISCOVERY INC.
- Protein Biochips: Micro-Scale Analysis in the Post-Genomic Era  
**Peter Wagner, Ph.D.**, Senior VP & Chief Technology Officer  
ZYOMYX INC.
- Strategies Toward Reproducibility in a High-Throughput DNA-Microarray Environment  
**Andrew Carmen, Ph.D.**, Manager of Genomic Operations  
JOHNSON & JOHNSON PHARMACEUTICAL R&D, L.L.C.
- Microarray Biomedical Applications in Drug Discovery  
**Gianfranco de Feo, Ph.D.**, Associate Director, Genomic Collaborations  
AFFYMETRIX INC.



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Dear Colleague,

Microarrays, or biochips, are powerful tools allowing scientists to harness the wealth of genomic information now available. DNA microarrays, now rising from their infancy, are standard and widely applied in various areas of drug discovery. Similarly, many emerging technologies, such as protein arrays, tissue arrays, or cell-based arrays, are quickly making their marks and will soon be integrated into different areas of pharmaceutical R&D.

In this intensive two-day conference, you will be exposed to the latest developments and great diversities of microarray technology. Here you will see these technologies integrated at the very cutting edge. Dozens of leading scientists in this field will present exciting new applications, as they strive forward, utilizing these tools to create a successful impact on drug discovery and development.

Come join us for a great opportunity to network and discuss with peers the latest trends, both technology and business, in microarray industry!

Sincerely,



**Jing Xu, Ph.D.**

President

**BIOMINERVA GROUP**



**Andrew Carmen, Ph.D.**

Genomic Operations Manager

**JOHNSON & JOHNSON PHARMACEUTICAL R & D, L.L.C.**

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**VENUE: Sheraton at Woodbridge Place**

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**PAYMENTS:** The conference registration fee is \$1195 until May 20, 2003 and \$1395 thereafter. The registration fee includes all breakfasts, lunches, refreshments, receptions, breakfast workshop and the conference documentation workbook. Payments may be made by company check, American Express, Visa, Mastercard, or Diner's Club. Please make checks payable to Strategic Research Institute, L.P. and be sure to write the registrant's name on the face of the check along with the conference code CS259 to ensure proper credit. **PAYMENTS MUST BE RECEIVED BY JUNE 27, 2003.**

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**BREAKFAST WORKSHOP**

7:15 - 8:00

**Mergen's Prokaryotic Arrays**

Mergen's core business is based on providing the highest quality DNA microarray and services. DNA microarray technology is a high-throughput method for gene expression analysis, gene discovery, genotyping, and functionality investigations. Microarrays have been successfully applied to the study of cancer and other diseases where certain genes are up or down regulated. The technology can also be used to study how cells respond to chemicals or other treatments by observing the changes in expression patterns. Mergen manufactures pre-spotted arrays of human, mouse, rat, and bacterial genomes using publicly available, well-annotated sequences. Mergen has recently expanded its offering in bacterial genomes to include arrays for studying the transcriptional profiles of *Staphylococcus aureus* (2674 genes), *Helicobacter pylori* (1565 genes), *Haemophilus influenzae* (1697 genes) with more to come. This presentation will provide an overview of Mergen's technology platform and provide information on our prokaryotic arrays.

**WORKSHOP LEADER:****Jaime Love, Ph.D., MBA***Director of Business Development***MERGEN LTD.**

8:00 - 8:10

**Chairpersons' Opening Remarks****Jing Xu, Ph.D.***President***BIOMINERVA GROUP****Andrew Carmen, Ph.D.***Genomic Operations Manager***JOHNSON & JOHNSON PHARMACEUTICAL R & D, L.L.C.****MICROARRAY EXPERIMENTAL DESIGN & DATA ANALYSIS**

8:10 - 8:40

**CodeLink Three Dimensional Bioarrays for Gene Expression and SNP Analysis**

CodeLink is an oligonucleotide bioarray platform which utilizes a three dimensional surface. For gene expression analysis, 30mer oligonucleotide are used on the bioarray, the limited oligonucleotide length imparts high specificity. The three dimensional surface promotes hybridization kinetics similar to those in solution, and thus imparts high sensitivity. For analysis of gene expression, mRNA sequences are amplified and turned into complement RNA (cRNA). cRNA hybridization to the expression bioarray is detected by the presence of incorporated labeled ribonucleotides. For SNP analysis, allele extension is done using oligonucleotides attached to the bioarray.

**John D. Burczak, Ph.D.***VP, Research & Development***AMERSHAM BIOSCIENCES**

8:40 - 9:10

**Microarray Data Management & Analysis for Drug Discovery**

Over the past five years, microarrays have rapidly become an integral part of the drug discovery process. From their initial applications to target identification to their growing list of applications in toxicological prediction and pharmacogenomics application, microarray data management and analysis has loomed as a significant challenge for practitioners. The analysis of microarray data is highly dependent on both the experimental set up as well as the aim of the research process. Nevertheless, a common theme for all array experimentation is data management. A microarray experiment involves a complex multi-step process. These steps include probe selection, array design, sample preparation (extraction, RNA preparation, labeling), hybridization, scanning, image processing, and data analysis. A key factor in ensuring the downstream analysis is to track all data associated with the experiment and effectively remove the process noise in order to mine and extract useful data about experimental variations of interest. In this presentation, we will discuss the rationale and highlight the need for such data management systems and demonstrate the utility of an integrated management and analysis system through a specific drug discovery application.

**Soheil Shams, Ph.D.***President & CEO***BIODISCOVERY INC.**

9:10 - 9:40

**Novel Data Visualization Tools Integrating Biological Information for the Enhanced Interpretability of Microarray Results**

We have developed two novel analytical tools that integrate biological information with expression profiling data to greatly enhance the biological interpretability of microarray experiments. With both tools, predefined categories of genes (e.g., biochemical pathways or biological processes) are analyzed for over-representation of genes whose expression values change during an experiment. In the Hierarchical Category Viewer™, changes in gene expression are visualized in a 2-D format with the expression levels of individual genes color-coded and superimposed on a hierarchically-organized representation of the input biological pathways. The software dynamically adapts to the hierarchical structure of the input categories making it easy to modify or create visual representations. In the Activation States Analysis software, co-developed with Compugen Ltd., algorithms are used to statistically rank the predefined categories based on the over-representation of altered genes contained within the groupings. The results are output graphically as lists that retain the hierarchical information underlying the biological function of the group. Different statistical criteria can be used to rank the categories and the results are linked dynamically to scatterplot representations of the data. Both of these complementary approaches allow for the facile identification of perturbed pathways and gives insights into the underlying biology of the experimental perturbation.

**Ron Blackman, Ph.D.***Senior Scientist II, Functional Genomics***MILLENNIUM PHARMACEUTICALS**

9:40 - 10:10

**Experimental Design & Statistical Analysis for Microarrays**

The majority of microarray experiments are conducted without the benefit of a statistically sound experimental design. In order to make valid discoveries with microarray technologies, proper experimental design procedures and appropriate statistical methodologies must become standard practice. This talk will cover the fundamental design types for microarray experiments, and how analysis of variance (ANOVA) can be used to identify sources of variability in the data, e.g. finding genes which are differentially expressed due to treatment.

**Thomas J. Downey***President***PARTEK INC.**

10:10 - 10:50

**Refreshments, Networking & Exposition**

10:50 - 11:20

**High-Throughput Target Synthesis for MicroArrays Leads to Increased Capacity and Reduced Variability**

Systemic variability introduced during MicroArray experiments makes data analysis complex and difficult to interpret. The design of biological experiments is critical for building statistical power and reducing variability in the experimental protocol. Through controlled experiments and statistical tools, we have identified and controlled most sources of experimental variability. We have identified target synthesis as a significant source of MicroArray experimental variability. Targets synthesized on different days will contribute more to variability than even treatment effects in an experiment. The critical need to reduce variability and the demand of large experiments has led to the development of high-throughput target synthesis procedures for MicroArrays. Based on a 96 well format, we have used this procedure to isolate RNA and synthesize hundreds of targets rapidly. We will describe the key considerations for the design of these protocols and show how they improve the quality of MicroArray experiments.

**Suzanne Torantali, Ph.D.***Senior Researcher, Corporate Biotechnology***PROCTER & GAMBLE**

11:20 - 11:50

### Analyzing Gene Expression Data: Knowing When to Stop

One of the primary challenges in microarray data analysis is "knowing when to stop" analyzing the raw data, and how to effectively focus on the biological interpretation of the results. With the proliferation of tools and approaches for raw analysis, there is a tendency to dwell on the numbers before getting back to the biology. Reaching a useful, biologically meaningful end-point in microarray data analysis requires a focused, hypothesis-driven approach to data analysis, plus tools for annotation mining, pathway visualization, and knowledge integration. Solutions to this challenge are being developed; some will be illustrated in this presentation using recent data sets from ongoing collaborations, together with freely available tools such as NetAffx, Gene Ontologies, and GenMAPP.

**Tarif Awad, Ph.D.**

Senior Investigator, Genomic Collaborations  
AFFYMETRIX INC.

11:50 - 12:15

### System That Enables Processing Standardization of Microarray Applications

Current manual methods for microarray hybridizations are often inconsistent, non-standardized, labor intensive and time-consuming. Variable signal intensities, non-uniformity due to diffusion limitations, extended hybridization times, and requirements for high probe concentrations all affect reproducibility and sensitivity of the assay. The Ventana Discovery™ system, with its air vortexing and patented liquid coverslip technology, individual temperature-controlled thermopads, and built-in quality control features, provides improved uniformity in a faster, less labor-intensive manner, appropriate for both experimental and industrial standardization. Furthermore, optimized reagents minimize nonspecific binding while providing quality results with high signal-to-noise ratios and exceptional specificity. Uniform hybridization on the entire microarray surface yields greater consistency, eliminates slide-to-slide variation and improves reproducibility and reliability.

**Anis H. Khimani, Ph.D.**

Director, MDS  
VENTANA MEDICAL SYSTEMS INC.

12:15 - 1:30

### Luncheon

## SYSTEM BIOLOGY/IN SILICO APPROACHES

1:30 - 2:00

### Application of Genomics to Drug Discovery

A priority for pharmaceutical drug discovery and development is to improve the quality of drug candidates both through better decision-making and a reduction in candidate attrition. Towards these goals, we are applying functional genomics to drug discovery and development through the use of DNA microarrays to provide global views of biology that will be utilized to improve the quality of our drug candidates. Microarrays enable a systems biology approach to drug discovery that complements the conventional reductionist approach. Systems biology can be defined as the analysis of all components (genes, transcripts, proteins) in a complex biological system to predict biological function. The unbiased quantitative analysis of a large number of biological pathways simultaneously enables hypothesis generation related to disease pathophysiology, drug mechanism of action, mechanisms of toxicology, biomarker discovery, and allows for product differentiation. Knowledge of genome-wide transcription changes can therefore be applied and have a positive impact throughout the various stages of drug discovery and development from target identification/validation to product support. In my talk I will present several examples of our systems biology approach, and its impact on drug discovery and development.

**Shawn Estrem, Ph.D.**

Senior Biologist  
ELI LILLY & COMPANY

2:00 - 2:30

### In-silico Identification of Cellular Processes Implicated in Cancer Using Expression Array Data

The cancer state of a cell is characterized by alterations of important cellular processes such as cell proliferation, apoptosis, DNA-damage repair, etc. Some of these alterations involve modifications of the expression of genes that participate in the pathways responsible for these processes. From this simple observation it follows that the expression of genes associated with cancer related pathways should exhibit differences between the normal and the cancerous states. We explore various means to find those differences. Interestingly, these differences can only be identified when groups of genes, as opposed to isolated genes, are considered. In typical studies of cancer using gene expression arrays all the genes participating in a DNA array are used when comparing cohorts of cancer patients with control subjects. In our study sets of genes associated in some manner with a specific pathway are considered, thereby allowing for a considerable increase of the signal to noise of the analyses, while preserving the biological information contained in the pathways. We analyze 6 different sets associated with 6 different pathways (p53, Ras, Brca, DNA damage repair, NFkb and b-catenin) and 4 different types of cancer: colon, pancreas, prostate and kidney. Our results are in agreement with existing knowledge of the involvement of these pathways in different cancers, suggesting that it is possible to identify pathways that are specifically involved in given cancers using a reduced set of genes defined on the basis of past knowledge about the pathway. Our analysis constitutes proof of principle that it may be possible to identify pathway involvement in cancers whose biology is poorly known, using gene expression data.

**Gustavo A. Stolovitzky, Ph.D.**

Manager, Functional Genomics  
IBM T.J. WATSON RESEARCH CENTER

2:30 - 3:00

### Application of Proteome-wide Computational Analysis to Enhance Protein Function Information

Our research has been focused on *in silico* methods for extending the amount of information that can be extracted from the proteome in order to identify & characterize potential targets for drug discovery. Because our analyses are performed proteome-wide we have been able to generate a vast amount of data that enables us to characterize variations in protein biochemical function that relate to biochemical features such as the shape of the binding pocket and the chemistry within it. This data can be utilized to a) confirm which proteins in a given system are actually capable of binding the substrate of interest b) understand what features in the protein are important for drug-binding and c) how those features vary across isoforms, splice variants and other protein family members that may be expressed in different tissues. The better understanding of protein function and specificity gained from this information can be used to design new protein arrays and functional assays. The *in silico* methods that have been applied include a variety of 3D-based functional assignment and annotation technologies that have been combined to form an automated analysis pipeline, GeneAtlas, the resulting information is captured in a relational database environment, DS AtlasStore, and protein-drug interactions are further characterized using virtual high-throughput screening algorithms. Additionally, data from Mass Spectrometry (MS) experiments can be used directly to search DS AtlasStore thus enabling the researcher to more rapidly identify proteins of interest for further analysis.

**David J. Edwards, Ph.D.**

Director, Computational Proteomics  
ACCELRYS

3:00 - 3:40

### Refreshments, Networking & Exposition

## NOVEL ARRAY TECHNOLOGIES SHOWCASE

3:40 - 4:00

### A Platform Biochip Technology for Pharmaceutical Applications

Miniaturized, spatially addressable microchips of peptide/peptidomimetics are powerful tools for high throughput biomedical and pharmaceutical research and advancement of proteomics. Herein we present an efficient and flexible method for the parallel synthesis of individually addressable peptide arrays on a microfluidic platform (XeoChip™). Digital photolithography and photogenerated acid deprotection of the Boc group from an amino moiety are used to create peptide arrays containing one's desired sequences. All 20 amino acids as well as synthetic monomers are readily incorporated in the synthesis. We demonstrate the use of these peptide/peptidomimetic arrays for rapid screening of high affinity binding molecules.

**Xiaolian Gao, Ph.D.**

*Professor, Department of Chemistry*

**UNIVERSITY OF HOUSTON**

*Co-Founder & Chief Scientific Officer*

**XEOTRON CORPORATION**

4:00 - 4:20

### Cell-On-Chips Technologies in the 'BioPuces' Lab at the CEA

Cell-On-Chips are microsystems integrating live cells dedicated to individual multiparametric analysis and manipulation. These devices hold great promise in high throughput phenotypic screening, and in elucidating biological processes in general. We will present some Cell-On-Chip microsystems which are developed in our laboratory. In particular, the 'Phenopuce' device is an array of virtual wells allowing parallel phenotypic cell screening in response to different types of molecules (such as nucleic acids, peptides and small chemical derivatives). The technological and biological challenges of 'Phenopuce' will be illustrated with the automation of recombinant gene expression as well as gene silencing using RNAsi.

**Béatrice Schaack, Ph.D.**

*Cellular Responses and Dynamics Department (DRDC)*

**CEA GRENOBLE FRANCE**

4:20 - 4:40

### Phenotype MicroArrays: A New Technology Platform Useful in Multiple Stages of the Drug Discovery Process

Phenotype MicroArray (PM) technology allows a biologist to test 2,000 properties (phenotypes) of a cell simultaneously. The phenotypic assays are designed from a physiological perspective to survey *in vivo*, the function of diverse biological pathways, including both metabolic and regulatory pathways. A unique aspect of PM technology is that cellular pathways can be monitored in real time, in living cells, without having to break the cells open and thereby destroy the system that is being monitored. Included in the phenotypes are basic cellular nutritional pathways for C, N, P, and S metabolism (800 tests), pH growth range and regulation of pH control (100 tests), sensitivity to NaCl and various other ions (100 tests), and sensitivity to chemical agents that disrupt various biological pathways (1,000 tests). The testing protocol is very simple. The arrays are inoculated with a cell suspension and then loaded into the OmniLog instrument, an automated incubator/reader, which monitors and records the cellular responses directly to computer files. PM technology can be used in multiple stages of drug development to compare cell lines, to determine the function of genes by assaying cell lines with gene knockouts, and to fingerprint the biological effects of chemicals (i.e., drugs) on cells. A unique advantage of PM technology in fingerprinting drugs and drug leads is that it measures the effect of a drug on the cell under hundreds or thousands of different physiological states of the cell. A drug's effect can be substantially different depending upon the physiological state of the cell. Examples will be discussed from a variety of model microbial cells such as *Escherichia coli* (prokaryotic) and *Saccharomyces cerevisiae* (eucaryotic). Prototype PMs have also been developed for human cells, including both blood cells and liver cells. With recent data we can demonstrate uses of the technology in mode of action as well as toxicology studies.

**Larry Wiater, Ph.D.**

*VP, Drug Discovery*

**BIOLOG INC.**

4:40 - 5:00

### Protein Microarray Manufacturing Technologies

Protein and DNA microarrays are a precision out technology. Precise engineering must be employed in the tools, devices and reagents used to produce high quality microarrays. The printing technology used to manufacture microarrays represents only 1/5 of the variables that need to be controlled. The other key microarray manufacturing components that must be tightly regulated are robotics, surface chemistry, sample preparation and environment. In addition to a detailed overview of various printing technologies, each of the key areas with accompanying examples will be discussed in detail in this talk. Also, the 12 rules that determine how microarray printing technologies should be used and interpreted will be presented.

**Todd Martinsky**

*Executive Vice President*

**TELECHEM**

5:00 - 7:00

### Cocktail Reception

## TUESDAY JULY 15, 2003

7:00 - 8:00

### Breakfast, Networking & Exposition

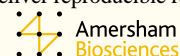
## BREAKFAST WORKSHOP



7:15 - 8:00

### CodeLink Bioarray System

The CodeLink™ Bioarray System offered by Amersham Biosciences consists of bioarrays, reagents, hardware and tools for gene expression and SNP analysis. It is an open system designed to deliver reproducible results at higher sensitivity and quality.



**WORKSHOP LEADER:**

**Abhay Patki, Ph.D., MBA**

*Marketing Manager for Genetic Variation, North America*

**AMERSHAM BIOSCIENCES**

8:00 - 8:05

### Co-Chairs' Recap of Day One

## BIOMEDICAL/PHARMA APPLICATIONS

8:05 - 8:35

### The Use of Microarrays in Drug Discovery

The development and increased use of microarrays to study expression patterns of samples relevant for the study of disease and therapies has led to a wealth of knowledge previously unavailable to the drug development scientist. The use of microarrays to better understand the molecular mechanisms of disease, and in the identification of potential therapeutic targets is well established and has been shown to be extremely fruitful. However, more recently, many pharmaceutical companies are moving the use of microarrays, for expression monitoring or large scale genotyping, to later stages in the drug development process. The use of arrays in target validation, toxicological investigations (or pre-clinical safety studies), and in clinical trials is growing and there are now examples demonstrating the advantages of using microarrays in downstream drug development processes. Published examples from the literature as well as examples from collaborations will be discussed in order to explore the uses of microarrays in target validation, toxicology and clinical trials.

**Gianfranco de Feo, Ph.D.**

*Associate Director, Genomic Collaborations*

**AFFYMETRIX INC.**

8:35 - 9:05

### Strategies Toward Reproducibility in a High-Throughput DNA-MicroArray Environment

Pharmaceutical research has found many applications for DNA MicroArray in all areas of drug discovery and drug development. This, in

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effect, causes increased demands on array processing while at the same time tighter acceptable tolerances. In order to address these issues an effort has been placed on automating all processes of MicroArray, from chip production through image and data analysis. This system allows for the preparation and analysis of an excess of 200 slides per day. Through automation we have removed many elements of variation and subjectivity, which have previously made comparative data analysis between data sets difficult. Here we present strategies, which we have put in place to increase overall throughput and concurrently markedly improve data quality.

**Andrew Carmen, Ph.D.**

*Genomic Operations Manager*

**JOHNSON & JOHNSON PHARMACEUTICAL R & D, L.L.C.**

**9:05 - 9:35**

### **Characterization of Compound Toxicity Using DNA Microarray**

**Jian Xu, Ph.D.**

*Safety Assessment*

**MERCK RESEARCH LABORATORIES**

**9:35 - 10:05**

### **High-Throughput Transcriptional Profiling for Novel Drug Discovery & Optimization**

The interaction of small molecules with their targets produces specific changes in RNA expression profiles within cells following treatment. Rapid identification and selection of exciting new lead compounds can be driven by the molecular definition of desirable transcript patterns at the whole genome level. Avalon Pharmaceuticals is discovering novel drug candidates by screening chemical libraries for their effects on proprietary drug activity markers across a broad selection of pathways and processes within the cell. This approach permits the evaluation of compounds against many different targets - both known and unknown - in parallel within a single assay. The Avalon approach can be applied to a number of drug discovery challenges, including the screening for hits against intractable protein targets. Comprehensive transcriptional fingerprints can be determined for hit compounds within days of their discovery, providing quick definitions of MOA, specificity, efficacy, and possible toxicity. Promising leads are immediately linked to specific gene biomarkers that provide direct feedback on therapeutic effectiveness and that can be used throughout lead optimization, in vivo testing, and clinical trials.

**Reinhard Ebner, Ph.D.**

*Principal Scientist*

**AVALON PHARMACEUTICALS**

**10:05 - 10:35**

### **Refreshments, Networking & Exposition**

## **PROTEIN ARRAYS/PHENOTYPE PROFILING**

**10:35 - 11:05**

### **Identification of Peroxisome Proliferator-Regulated Biomarkers by Proteomics Approach**

Proteomics is rapidly expanding field encompassing both broad-based screening and strategies focused on analysis of discrete subproteoms. In an effort to understand the mechanism of peroxisome proliferator-induced hepatocarcinogenesis and to identify biomarkers for drug safety evaluation, mouse liver homogenates of control (wild type), ACOX  $-/-$ , and wild type treated with Wy-14,642 were analyzed by two different proteomics approaches: SELDI and 2-D DIGE/MS. Results from these analysis will be presented and the usefulness of SELDI and 2-D DIGE/MS in biomarker discovery will be discussed.

**Ruiyin Chu, Ph.D.**

*Group Leader, Functional Genomics*

**AVENTIS PHARMACEUTICALS**

**11:05 - 11:35**

### **Phosphoprotein Antibody Arrays: The Tools Required to Interpret the Language of a Cell's Signals**

The ink wasn't dry on the genome project before it was realized that in order to fulfill its promise for drug discovery, a protein project was needed. The problem is that the protein project is 10-30 times larger than the genome project. To make this project manageable PhosphoSolutions focuses on a

subset of proteins known as phosphoproteins. Phosphoproteins represent only 10-20 percent of the proteome, but they regulate almost all cell signaling processes from cell division (cancer) to neuronal communication (Alzheimer's). Phosphoproteins can be studied with a revolutionary antibody known as a phospho-specific antibody. These antibodies bind to their target proteins only when the protein is in the phosphorylated state. However, there is overwhelming evidence that intracellular signaling involves multiple messengers that activate complex arrays of pathways which intersect each other at many sites in a web-like fashion. Dissection of these phosphorylation networks is simply not possible with currently available technologies. To address this issue we are developing phosphoprotein cluster arrays that permit us to interpret a cell's signaling language. A focus on phosphoproteins (the verbs of the proteomics language) cuts the proteomics project down to a manageable size. Consequently, arrays focused on phosphoproteins can translate the language of a cell's signals.

**Michael D. Browning**

*Professor of Pharmacology and Neuroscience*

**UNIVERSITY OF COLORADO**

*President*

**PHOSPHOSOLUTIONS INC.**

**11:35 - 12:05**

### **Quantitative Assessment of Protein Phosphorylation in Cultured Cell Arrays and Reverse Phase Protein Arrays by Near Infrared Detection and Imaging**

Protein phosphorylation and dephosphorylation are critical processes regulating cellular signal transduction. Abnormal expression and enzymatic activity of kinases and phosphatases are involved in many diseases including cancer, diabetes, rheumatoid arthritis, and Parkinson's disease. Cell-based assays for protein phosphorylation tend to give more biologically relevant results. We have developed technology based on detection of antibodies labeled with near infrared dyes for assessment of protein phosphorylation in cultured cell array and protein array formats. We have demonstrated that the technology is accurate and reproducible. Furthermore, using the cultured cell array technique, we can accurately assess the  $IC_{50}$  of a known phospho-inhibitory compound. These methods should find wide utility in assessing protein phosphorylation and characterizing drugs aimed at inhibiting phosphorylation.

**D. Michael Olive, Ph.D.**

*VP of Research & Development*

**LI-COR BIOSCIENCES**

**12:05 - 12:30**

### **Development of Flow-thru Chip™ Proteomics**

We are developing protein microarrays on the Flow-thru Chip™ (FTC) platform. FTC is a uniformly porous substrate, where microchannels at a diameter of 10  $\mu$  m connect the upper and lower faces of the chip in such a manner that fluid can flow through the chip. Antibody or antigen spots are dispensed over the surface of the microchannels to create a protein microarray. The 3-dimensional Flow-thru Chip™ provides higher surface area to volume ratio, better wetting properties and faster mass transport within the microchannels than flat substrate. FTC technology has been proved of its successful application in assessment of plasma markers of congestive heart failure and other proteomic analysis.

**YongYi Yu, Ph.D.**

*Manager, Assay Development*

**METRIGENIX**

**12:30 - 1:45**

### **Luncheon**

## **ANTIBODY ARRAYS/PROTEIN PROFILING**

**1:45 - 2:15**

### **Protein Profiling for Biomarker Discovery: Biologically Significant Protein Pattern Relationship to Phenotypic variations and identification**

Physiological changes from internal and external perturbations (disease, drug treatment) result in changes in the protein expression pattern. Detecting these biomarker signatures will aid in early prediction of the disease, diagnosis and development of effective treatments. CIPHERGEN's ProteinChip® technology provides an enabling tool for protein biomarker discovery, validation and assay development as a direct approach to classification according to phenotype. Such classifications include early detection of disease, monitoring of disease progression, monitoring of therapeutic effects of drugs,

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drug responses/toxicity studies and clinical stratification of patient populations. Using ProteinChip® Arrays and Surface Enhanced Laser Desorption Ionization (SELDI) based technology allows rapid generation of "protein patterns" from matched sets of biological samples. The analyses are rapid and done directly from small amounts of complex biological fluids and tissue samples in clinical and research environments.

**Anju M. Dang Ph.D.**

*NJ/PA Program Manager*

**CIPHERGEN BIOSYSTEMS**

2:15 - 2:45

### High-Throughput Protein Technology Applications

**Yan-Hui Liu, Ph.D.**

*Senior Scientist*

**SCHERING PLOUGH**

2:45 - 3:15

### Protein Biochips: Micro-Scale Analysis in the Post-Genomic Era

Proteomics is increasingly dependent on analytical tools that focus on quantification of protein expression, biomolecular-protein interactions, and functional activity. Zyomyx is a multi-faceted technology company uniquely positioned to address the complex problems associated with protein detection and characterization. Using proprietary biochip-based tools Zyomyx has developed several novel platforms for proteomic research. The first commercially launched Zyomyx product offering is a novel protein biochip platform that facilitates rapid, precise, highly multiplexed analysis with minimal sample requirements.

**Peter Wagner, Ph.D.**

*Senior Vice President & Chief Technology Officer*

**ZYOMYX INC.**

3:15 - 3:45

### Gene-Specific IgY Avian Antibodies as "Content" for Multiplex Protein Assays

Antibodies are gene-specific and have several distinct advantages over conventional IgG antibodies. Besides being useful in conventional immunoassays, such as Western blot, immunoprecipitation, immunohistochemistry, immunocytochemistry, cell sorting, serum depletion, etc., IgY antibodies are also particularly suitable for applications in multiplex assays due to their higher surface stability, lower cross-reactivity, stronger avidity, and greater detection sensitivity. This approach is particularly well suited for the specific and sensitive detection of target proteins, often in conjunction with conventional monoclonal IgG capture antibodies. We have produced hundreds of antibodies and is applying them on antibody arrays, microspheres, and tissue arrays for high-throughput screening of biomarkers and drug targets. These gene-specific antibodies are also applicable for proteomic mapping and protein expression profiling.

**Jerry Feitelson, Ph.D.**

*VP of Technology & Business Development*

**GENWAY BIOTECH**

3:45

### Conference Concludes

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## ATTENDEES OF THE 2001 INAUGURAL BIOCHIPS (MICROARRAY TECHNOLOGIES) MEETING COMMENTED:

"Learned some new product information."  
**GENOME THERAPEUTICS CORPORATION**

"Gained knowledge about new technologies/methodologies & made valuable contacts."  
**PROCTOR & GAMBLE**

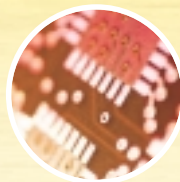
"Established more contacts and learned what technical needs array users have."  
**ROCHE**

"Coming from the protein arrays field, the conference provided complete information from start to finish."  
**CIPHERGEN BIOSYSTEMS**

"A great conference. Learned about how different methodologies apply to microarrays."  
**UNIVERSITY OF OTTAWA**

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