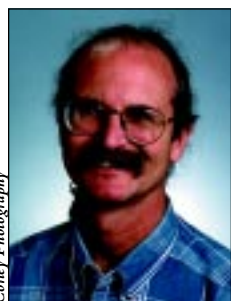


## New Director at the Biotechnology Center

Stanley Maloy, Professor in Microbiology, accepted the offer as the new director of the Biotechnology Center from Tony Waldrop, Vice Chancellor for Research, pending approval by the Board of Trustees. In his new role, Maloy is planning to work with interested faculty and the Biotechnology Center Advisory Committee to expand our existing capabilities in proteomics. Maloy will draw on the existing strength on campus in information, analytical and microelectronics technology and to work closely with researchers



Cortley Photography

Stanley Maloy

in the respective fields to improve collaborations with faculty in the biosciences. In order to increase the dialogue amongst faculty on campus Maloy is planning to organize an annual Biotech Symposium centered around a research theme. "Our campus could become a leader in technology development, if we provide the right climate that promotes close interactions. The 'north campus' with its many resources can develop the technologies to solve research problems in the biosciences," says Maloy. "We should work together to move the campus into a leading position." In addition, three areas in proteomics research are being considered: a protein expression/production facility that would support both of the other areas: research in protein identification and chemical characterizations, and protein interaction studies.

Another area that Maloy is interested in developing is training of our graduate and undergraduate students in relevant biotechnology methodologies to better prepare them for the job market. Maloy sees a role for the Biotech Center in facilitating

*continued on page 2*

## Evolution in an Illinois Cornfield?

Natural selection plays the central role in shaping the biological world, yet its glacial pace makes the evolutionary change occurring around us appear all but invisible. Occasionally, exceptional circumstances permit us to witness the process of natural selection. Such circumstances exist today in East Central Illinois; the behavior of the western corn rootworm, *Diabrotica virgifera virgifera* LeConte, an important pest of corn is changing under intensive selection by crop rotation circumventing the most cost effective and environmentally benign management tool. Western corn rootworm (WCR) rotation resistance is fundamentally a problem of movement. Normally, the mature beetle (see figure) deposits its eggs in August and September in corn fields only. The eggs overwinter in the egg stage, hatch the following spring, and the larvae feed on corn roots. However, if the farmer rotates to soybeans in the spring, the larvae will starve off, because there are only soybean roots to feed on. Now egg laying females disperse from cornfields to deposit their eggs in soybeans and other crops rotated with corn, effectively defeating crop rotation. Although the scientific literature is replete with examples of insects becoming resistant to insecticides, including corn rootworms, the adaptation to a cultural practice is exceedingly rare.

The debate within the entomological community rages regarding the fundamental explanation for the egg-laying shift of western corn rootworms away from the restrictive relationship with corn to include that of other crops, primarily soybeans. One theory suggests that the rigid cultural practice of crop rotation has placed selection pressure on the East Central Illinois population of western corn rootworms for at least the last two decades eventually triggering the behavioral abandonment of corn as the primary egg-laying site. Another contemporary theory suggests that the agronomic

*continued on page 3*



David Riecks, ACES-ITCS

Researchers believe a new strain of western corn rootworm that now lays eggs not only in corn, but in a variety of cropping systems began to evolve in East Central Illinois in the late 1980s.

## Summer 2001

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## New Director, continued from page 1

the development of laboratory courses using state-of-the-art instrumentation and techniques. Maloy comes well prepared for his new position as the following excerpt of his biosketch reveals.

B. Whitmarsh

### **Stanley Maloy** ([s-maloy@life.uiuc.edu](mailto:s-maloy@life.uiuc.edu)) Professor, Microbiology Department

I obtained my PhD in Molecular Biology and Biochemistry from the University of California at Irvine in 1981, did postdoctoral work in Genetics at the University of Utah, then joined the UIUC faculty in 1984. I have taught extensively, including a variety of classes at UIUC, the Cold Spring Harbor Laboratory summer course in Advanced Bacterial Genetics from 1990-1995, and international short courses. I have consulted for large companies and small, biotech start-up companies. I have served as a grant reviewer for funding agencies, and as a reviewer for numerous journals. I have organized several international scientific meetings. Research in my lab focuses on three topics.

**Membrane protein interactions.** Overproduction of membrane proteins causes a lethal imbalance in the proper ratio of protein to lipid in the membrane, which prevents other essential membrane proteins from assembling and functioning properly. However, it is not known how cells sense the proper ratio of membrane proteins to lipids or how they adapt to changes in this ratio. We have used the PutA protein from *Salmonella* to study the regulation of membrane protein synthesis. The *putA* gene encodes a membrane-associated enzyme that degrades proline to glutamate, and also autogenously regulates transcription of the *put* operon. Genetic and biochemical approaches elucidated the basic features of this process. In the absence of proline, the PutA protein exists as a dimer in the cytoplasm where it binds DNA and represses *put* gene expression. When substrate, electron acceptor, and membrane sites are available, PutA becomes compartmentalized at the membrane and is unavailable to bind DNA. Binding to the membrane depends upon a reduction

of the FAD cofactor and a subsequent conformational change in the protein that results in increased hydrophobicity and a transition from a dimer to a monomer. A combination of genetic and fluorescence-based screens allow the isolation of mutants that allow overexpression of PutA by a compensating increase in membrane biogenesis. Genome based approaches including microarrays and proteomics will facilitate the identification of additional gene products involved in the regulation of membrane biogenesis. Understanding the regulation of membrane biogenesis will facilitate the overproduction of membrane proteins for biotechnology applications.

**Host specificity of *Salmonella*.** *Salmonella enterica* are a large group of bacteria that are a major cause of food poisoning. *Salmonella* serovars produce distinct disease symptoms in different animals. Some *Salmonella* strains cause relatively mild disease, but pernicious new strains with unique virulence properties result in new, emerging diseases. Such new strains often seem to acquire changes in host-specificity that allow them to infect a different animal host. However, little is known about the genetic determinants of host-specificity in any bacteria. Identifying the genetic determinants of host-specificity may provide experimental approaches to limit the development and spread of virulent *Salmonella* strains in animals and the emergence of new infectious diseases. We have developed surrogate genetic approaches to identify genes responsible for the host specific virulence traits, and we are using these approaches to identify the relevant genetic differences in the broad host range *Salmonella* serovars Typhimurium and Enteritidis with host-adapted *Salmonella* serovars Typhi (human specific) and Pullorum (fowl specific).

**Comparative genomics of *Salmonella*.** We are sequencing multiple *Salmonella* serovars (Enteritidis, Dublin, Pullorum, and Choleraesuis) to gain insight into the evolution of closely related bacteria. In collaboration with Profs. Gary Olsen and Rob Edwards, we have begun comparative bioinformatic analyses with the other *Salmonella* genomes (see <http://salmonella.org>).

## Evolution in an Illinois Cornfield? continued from page 1

trend towards earlier corn planting dates has resulted in corn becoming a less attractive egg-laying target as compared with nearby soybean fields late in the summer. In such fields (see figure below) earlier maturing corn hybrids are starting to dry down during the egg laying season, and it is possible that the beetles move to soybean fields, because they prefer green soybean foliage over drying corn. This theory is strengthened by the fact that in the mid-1980s, WCR larval injury was confirmed in seed-production cornfields near Piper City, Illinois, located in Ford County. Seed production cornfields are generally harvested earlier than commercial cornfields. This area of Illinois may have served as the evolutionary cradle of this new WCR variant because of the intensity of crop rotation and the early-maturing characteristics of nearby seed-production cornfields.

A diverse group of researchers with expertise in entomology, atmospheric science, mathematical modeling, and genetics have been jointly funded by C-FAR to explore the collapse of crop rotation as a cultural control practice. Based on ecological and behavioral research conducted by Dr. **Michael Gray**, Professor, Department of Crop Sciences, University of Illinois and Dr. **Joseph Spencer**, Assistant Professional Scientist, Center for Economic Entomology, Illinois Natural History Survey, differences in flight, feeding, and ovipositional preferences occur in western corn rootworm populations. The movement of WCR between corn and soybean fields appears to be influenced by corn developmental stages and soybean leaf herbivory. Dr. Spencer and his graduate student, **Tim Mabry**, have observed increased activity and flightiness following even brief periods of soybean herbivory. Graduate research assistants, **Silvia Rondon** and **Chris Pierce**, with Dr. Gray have found western corn rootworms in East Central Illinois will lay eggs in a variety of cropping systems, and early-planted corn appears to be a less attractive ovipositional site. Microarray profiling will allow us to evaluate gene expression variation between the two populations and possibly identify the mechanisms controlling these behaviors. This research will provide insight into how gene expression is linked to environmentally induced behavior and provide guidance for effective measures to control this pest.

Drs. **Lei Liu**, Director of Bioinformatics, **Jose Pardinias**, former Director of High Throughput Sequencing and Genotyping at the W.M. Keck

Center for Comparative and Functional Genomics, **Susan Ratcliffe**, Assistant Professor, Department of Crop Sciences, and **Hugh Robertson**, Professor, Department of Entomology, plan to generate a western corn rootworm Expressed Sequence Tag (EST) database. Dr. Pardinias and **Rachel Schwartz**, Research Specialist, constructed the library from heads of gravid females exhibiting the shift in egg-laying behavior and from those not exhibiting the shift in behavior. Each population is tagged to preserve its population identity. Sequencing from the normalized library is currently underway and we estimate about 8,000 unique sequences will result from the sequencing of 12,000 clones. Dr. Liu will supervise gene annotation of the western corn rootworm EST and we predict many of the WCR ESTs will have high similarity with *Drosophila* and honey bee genes. Based on data from Dr. Gene Robinson's honey bee project, microarray profil-



David Riecks, ACES-ITCS

ing of the western corn rootworm EST should result in expression differences between the two population types. Dr. **Mark Band**, Director of Functional Genomics, W.M. Keck Center will collaborate with other members of the group on this portion of the project to identify candidate genes for future research based on gene expression.

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This project was supported by a Sentinel Grant from the Illinois Council on Food & Agricultural Research (C-FAR).



*Working with a new test organism, like the western corn rootworm, has presented challenges during RNA extraction and construction of the cDNA library, but through collaboration the group's members have overcome obstacles and streamlined protocols to provide high quality results.*

*On August 31, 1999, Dr. Mike Gray took this photograph in Iroquois County. The planting of early-maturing corn hybrids in early- to mid-April, along with crop rotation, may have contributed to the greater flexibility in oviposition (egg laying) by the new strain of western corn rootworm.*

## Campus Research Initiative in Biotechnology brings Affymetrix GeneChip Technology to the Keck Center

Research projects that look at the possibility of restoring sight and of fighting cancer are under way on the Chicago and Urbana-Champaign campuses because of a first-time research initiative aimed at encouraging top professionals in biotechnology from both campuses to work together.

About \$2.7 million is committed to the effort over the next five years through the offices of the vice president for economic development and corporate relations and the two vice chancellors for research, at Chicago and Urbana.

Vice President Chester Gardner proposed the idea to the vice chancellors to encourage researchers from both campuses to think of projects that could benefit from an inter-campus effort. Gardner says both campuses are among the finest in the country in biotechnology and biomedicine, but rarely

mittee with members from both campuses chose two.

The first project, being led by Dr. Carol A. Westbrook of the Chicago campus, will use the new genome technologies to look at all the genes in female uterus and breast tissue to see how the tissues change when exposed to estrogen, and how the response is different in normal and cancerous tissue. This research will look at as many as 40,000 genes at a time, resulting in so much information that computer scientists are needed to write programs for the findings.

“Although analyzing a large number of genes in cancer has been done before, combining the data from many different types of estrogen-sensitive tissues and cancers is a novel approach,” said Westbrook. “If we get it going as planned, and the computer scientists can make sense of this amount of data, it will be really impressive and we’re going to learn a lot about female cancers.”

The scientists are talking frequently by e-mail now, but will soon come together to meet, she said. Though collaboration among outside universities occurs frequently, Westbrook said she thinks this is the first time that an effort was made to partner with one of the other U of I campuses.

“It made us go out and look for people in Urbana who are working in this area,” Westbrook said. “That made it crystallize. And it’s really just clicked.”

Co-investigators in the research at Urbana-Champaign are **Benita Katzenellenbogen**, Swanlund Professor of Molecular and Integrative Physiology and Cell and Structural Biology; **Harris Lewin**, Professor and Director of the W.M. Keck Center for Comparative and Functional Genomics; **Romana Nowak**, Associate Professor, Animal Sciences; and **Mark Band**, Director of Functional Genomics at the W.M. Keck Center. **Lei Liu**, adjunct Assistant professor, Animal Sciences, is the computer scientist in charge of data analysis on the Urbana-Champaign campus, and his counterpart at UIC is **Jie Liang**, Assistant Professor, Bioengineering. Other co-investigators at UIC are doctors **Zarema Abbieva**, Hematology and Oncology, **Rajeshwari Mehta**, Surgical Oncology, and **Serdar Bulun**, Obstetrics and Gynecology.



Reproduced with permission by Affymetrix.

*Affymetrix GeneChip technology. The picture shows a wash station for 4 chips, a scanner and a computer with Affymetrix control software.*

do the scientists from the two campuses get the opportunity to work together.

“There is no doubt the U of I is a real powerhouse in academic research,” Gardner said. “The combined annual research expenditures at Chicago and Urbana-Champaign now exceed \$530 million, which ranks second in the nation to Johns Hopkins.”

“Unfortunately, the physical separation of the two campuses has impeded research collaboration,” he said. “With the Inter-Campus Research Initiative in Biotechnology, we hope to establish links between the faculty that will leverage the capabilities of the two campuses.”

Fifteen proposals were received last fall, and from those five finalists were selected. A faculty com-

cology. For more information about this technology go to <http://www.affymetrix.com/technology/>

The second, led by **David R. Pepperberg** of UIC's Department of Ophthalmology and Visual Sciences, will look at restoring the capacity for signaling between cells in damaged nerve tissue. An ultimate goal of the research is to restore the capacity for visual signaling within the retina of patients with retinal degenerative disease. The research may have uses in other diseases of the nervous system also.

One of the co-investigators on the project from Urbana is **Deborah Leckband**, an Associate Professor in the Department of Chemical Engineering. Others from Chicago are **Haohua Qian**, Assistant Professor, Department of Ophthalmology and Visual Sciences; **Tejal Desai**, Assistant Professor, Department of Bioengineering; **Miroslav Rezac**, Assistant Professor, Department of Medicinal Chemistry and Pharmacognosy; **Christoph Grein**, Associate Professor, and **Siva Sivananthan**, Distinguished Professor, both in the Physics Department.

"There is so much expertise on both campuses that when we began to identify the specifics of our project, it made perfect sense to seek the involvement of colleagues at both Urbana and Chicago on the research team," Pepperberg said.

Two such proposals will be funded each year, with each project receiving no more than \$450,000 over three years. One of the requirements for the projects is that they be able to sustain themselves with federal funds when the U of I funding ends.

"We see marvelous opportunities for fruitful collaboration," said Gardner of the initiative.

Both projects are slated to begin immediately. For information about the program, go to [www.vped.uillinois.edu/irib/](http://www.vped.uillinois.edu/irib/).

*B. Mabry and B. Galardy*

## Search for a Director for the Post-Genomic Institute underway

The position for the Founding Director of the Post-Genomic Institute (PGI) has been advertised in *Nature*, *Science* and other publications. As stated in the job description, the Director will be influential in creating and charting the focus of this Institute, which will provide an interdisciplinary research environment in which genomic information can best be exploited to drive fundamental advances in the biological sciences. The search committee is planning to identify a suitable candidate in early fall.

In addition to the search for a director, progress has been made towards beginning construction of the building. The institute will occupy an 110,000 sq ft facility and will be located immediately west of Bevier Hall. According to Vice Chancellor for Research (VCR), Tony Waldrop, design plans for the PGI will be presented at the July and September meetings of the Board of Trustees. Assuming that funding is approved by General Assembly, the PGI construction would begin next spring.

The Post-Genomic Initiative involves hiring of up to 40 new faculty. In collaboration with the Provost, the Vice Chancellor for Research committed to 18 faculty hires through the Post-Genomic Initiative this year with funds of \$1.6 million provided by the State of Illinois through Governor Ryan's VentureTECH Program. The Provost and Vice Chancellor held a campus competition for these recurring salary funds. Four out of eleven proposals were funded:

1. Microreactors, Microsensors and Microimaging: Technologies for the Post Genomic Era
2. Proteomics: Molecular Function in Biology and Macromolecular Assemblies and Machines as Determinants of Cell Function
3. Program in Mammalian Development
4. Genome-based Enhancement of Plant Functional Traits

A leader in plant functional genomics, Professor Hans Bohnert from the University of Arizona, has already been recruited and will join the University of Illinois/PGI faculty this coming fall.

*B. Whitmarsh*

## Biotechnology Center at the University of Illinois at Urbana-Champaign

**Stanley Maloy, PhD** • Director and Professor of Microbiology

**Robert Gennis, PhD** • Executive Associate Director and Professor of Biochemistry

**Bruce Chassy, PhD** • Executive Associate Director for Outreach, Assistant Dean, College of Agricultural, Consumer & Environmental Sciences

**Harris Lewin, PhD** • Director, W.M. Keck Center for Comparative and Functional Genomics and Professor of Immunogenetics

**Barbara Whitmarsh, PhD** • Associate Director and Editor

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*Please send comments on the newsletter, news, or questions to Barbara Whitmarsh at [b-whitmarsh@uiuc.edu](mailto:b-whitmarsh@uiuc.edu) or contact the Administrative Office.*

# Technical Note

## Intracellular and Multiple Cytokine Assays with Flow Cytometry

Cytokines are secreted regulatory proteins that control the maintenance, growth, differentiation, and effector function of immune system and tissue cells. Released cytokines interact with their target cells, which are often adjacent to the producer cells, resulting in the appropriate biological response. Frequently, these producer cells secrete very small quantities of cytokines. The role of cytokines in immunological processes, hematopoiesis, and inflammatory responses can be better understood by studying the intracellular processes involved in cytokine production.

Because of the interplay among cytokines and the cells that respond to their biological activity, the understanding of cytokine biology requires the monitoring of changes in the plasma levels of soluble cytokines, not only in cell-surface cytokine receptor expression, but also in the expression of intracellular cytokines by individual cell populations (2).

Techniques for analyzing individual cytokine-producing cells include immunochemistry, immunocytochemistry, ELISPOT, in situ hybridization, limiting dilution analysis and single cell PCR (2). While all of these techniques have their own advantages, they all have drawbacks (technical proficiency, labored data collection and analysis). Cytokine flow cytometry, how-

ever, is a simple and powerful analytical method in which individual cells can be simultaneously analyzed for many parameters, including expression of intracellular markers by fluorescent antibodies. It is possible to quantitate the cytokine secretion in serum or culture supernatant using a new methodology from BioErgonomics. Their MultiFlow-IFA assay system uses paramagnetic beads coated with specific monoclonal antibodies to capture desired analytes (3).

### General procedure for intracellular cytokine staining

Figure 1 shows the steps for intracellular cytokine staining for flow cytometry measurements. For a more detailed description of the method go to [http://www.biotech.uiuc.edu/flow\\_cytometry.htm](http://www.biotech.uiuc.edu/flow_cytometry.htm).

### Multiple cytokine method

Multiplexed flow cytometric analyses were developed by BioErgonomics to measure in addition to cytokine receptor expression and internal cytokine expression, the concentration of cytokine secreted into the fluid phase of a biological sample (1). Schematics of a Multiflow-IFA assay for cytokine secretion are shown in Figure 2. This system uses 7-mm paramagnetic beads labeled with a monoclonal antibody specific to a particular cytokine. These particles capture the target cytokines from the fluid phase of biological samples (2). After a short incubation period, the system is washed in the IFA provided buffer. A fluorochrome-labeled monoclonal antibody is added to the beads with the capture analyte. This results in the bound analyte becoming fluorescent, and the fluorescence intensity will be directly proportional to the sample analyte concentration (3). To quantitate cytokines, the standard curve has to be obtained with the beads incubated with known concentrations of cytokine (1).

### Conclusions

In this short technical note we briefly describe methods for the measurement of cytokines using

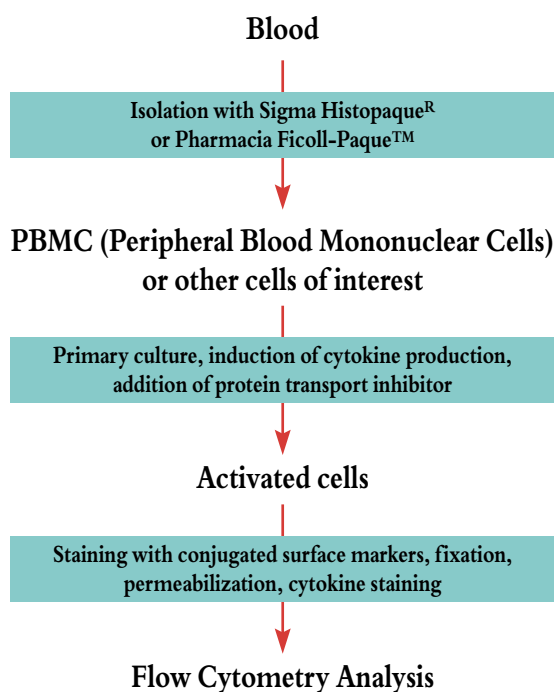
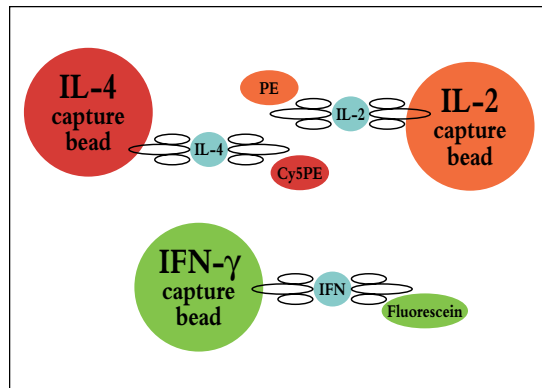


Fig. 1. Steps for intracellular cytokine staining for flow cytometry measurements

The most commonly used cells for cytokine induction are PBMC (Peripheral Blood Mononuclear Cells) or dendritic cells (DCs). Once the PBMC (or other cells of interest) are isolated, they need to be set up in a primary culture in order to induce cytokine production. Stimulation of cells with the appropriate reagent will depend on the cell type and experimental conditions. Unlike in ELISA where extracellular secreted cytokines are detected, the detection of intracellular cytokines requires the blocking of secreted cytokines. Immunophenotyping: the choice of the surface marker depends upon the type of cell to be selected. The intracellular staining procedure requires the fixation, permeabilization, and subsequent staining of the activated cell population with fluorochrome-conjugated or biotinylated anti-cytokine antibodies.

flow cytometry. The first assay can be used for simultaneous analysis of surface molecules and intracellular cytokines at the single cell level. This is a highly specific and sensitive method to measure several parameters for individual cells, and it has the capacity for rapid analysis of large number of cells. Some companies, like Pharmingen, offer ready kits containing fixation/permeabilization solution, antibody diluent/wash solution, a protein inhibitor, and also a intracellular cytokine positive control. Each component is also available individually. Multiflow/multiplexed cytokine immunoassay (BioErgonomics) offers an additional kit to measure secreted cytokines over a wide dynamic range (0.5–20,000 pg/ml) as compared to the smaller (15–2000 pg/ml) range obtained when using enzyme immunoassays, radioimmunoassays, or chemiluminescence assays (2).

B. Pilas



**Figure 2. Schematics of MultiFlow™ Multiplexed Cytokine Immunoassay.** Separate particles are coated with antibodies specific for a single cytokine. These particles then capture the soluble cytokines from biological fluids. Fluorescently labeled reporter antibodies allow detection of the captured cytokine. In this instance, IFN- $\gamma$  is

reported with a fluorescein labeled antibody resulting in green fluorescence. IL-2 is reported with a phycoerythrin-labeled antibody resulting in orange fluorescence. IL-4 is reported with a Cy5PE-labeled antibody resulting in a red fluorescence. The intensity of the fluorescence signal in each individual color range is directly proportional to the concentration of the cytokine in the sample.

## Facility Updates



During the last fiscal year several new employees joined the Biotechnology Center (BTC). The administrative office has a new secretary, **Rhonda Lipking**, who coordinates searches for all BTC positions, maintains inventory records, handles correspondence and many other duties in our office. In addition, **Marcia Dorsey-Watkins** was hired as a clerical assistant to support our Resource and Policy Analyst, Tom Bedwell.



The Flow Cytometry Facility hired two research programmers, **Chunlan Yao and Michael Lu**, for the development of bioinformatics tools to better manage and identify correlation among flow cytometry data, and for the development of sample tracking, scheduling and project management tools to more efficiently utilize laboratory testing resources in the flow cytometry area. This work is supported by a research grant with a private company.



The Immunological Resources Center hired **Theresa Holly** last fall. Theresa is taking on primary responsibility for the newly developed bioreactor method that is replacing ascites fluid pro-

duction. Steve Miklasz, former Director of the facility took a job with a leading biotech company. A search for his replacement is underway.



The Protein Sciences Facility added **Jennifer Fairgrieve** to its staff. Jennifer is working in peptide synthesis and purification and is also being trained on protein sequencing technologies.



The W.M. Keck Center for Comparative and Functional Genomics hired **Al Bari** to work as research specialist in the Functional Genomics Unit. **Garet Hunter** is working as a research specialist in the Bioinformatics Unit and primarily involved in DNA sequence analysis. **Alvaro Hernandez** and **John Moore** joined the High-throughput lab this April. Alvaro, who received his Ph.D. in Animal Sciences this spring, is working on cDNA library constructions and subtractions, and John is a research specialist working with the high-throughput sequencing team. Jose Pardinas, Ph.D., former Director of the High-Throughput Unit, decided to resume a research position with a leading biotech company. His position has been advertised.

# Coming Soon

## Oligos for \$0.30/base at the W.M. Keck Center

**Place your order on the web,  
receive your oligos via campus  
mail**

The Biotechnology Center Oligonucleotide Synthesis Facility at the W.M. Keck Center for Comparative and Functional Genomics is now producing oligos at the 10nmol scale for \$0.30/base. This very competitive price is available due to our new 96 well parallel oligonucleotide synthesizer: the **PolyPlex by Gene Machines**. Crude samples may be submitted as a full plate (10nmol at \$0.30/base), or submitted individually (10nmol scale at \$0.35/base). These oligos have been proven successful for PCR and sequencing, and are of comparable or better quality compared to those from leading oligonucleotide companies.

*Please look for this service to be available campus wide by July this year. For more information about turnaround times and ordering forms go to [www.biotech.uiuc.edu/oligonucleotide.html](http://www.biotech.uiuc.edu/oligonucleotide.html) #High-Throughput Oligo*

L. Hetrick

## Convenient Drop-Off Site for DNA Sequencing Samples in Room 315 Noyes Lab

Users of the DNA core facility, which is located at the W.M. Keck Center for Comparative and Functional Genomics, can now go to room 315 Noyes Lab, the Biotechnology Center Protein Sciences Facility, and drop off their samples.

*Samples will be picked up daily at 12 pm. Ready-to-load samples will be run the next day. Only samples that come with a completed DNA request form will be processed.*

**Notice the price drop for our economy option from \$20/sequence to \$17/sequence as of April 1, 2001.**



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