

Biotechnology Gets a Boost

The Illinois General Assembly allocates planning and initial construction support for the Post Genomics Institute at the University of Illinois in Urbana-Champaign

The budget passed by the Illinois General Assembly endorses the Governor's budget that recommended construction of the Post Genomics Institute at the Urbana-Champaign campus. This 110,000-square-foot biotechnology research facility will house about 45 scientists, their research teams and support staff who will focus on creating new technologies for understanding and utilizing genomic information to improve human health, the environment and food production systems. The addition of this building and new biology faculty, along with the present strengths in information technology, engineering, agriculture and life and chemical sciences, will enable the University of Illinois to be a leader in the Post-Genomics era.

Planning of the building will begin in FY01, with \$7.5 M in funds allocated for this stage. Also included in the budget is a substantial commitment for the addition of faculty lines in biotechnology and in information technology. \$1.6 million will be used to fund new positions in the Post Genomics Institute, \$900,000 for information technology and \$4.3 M for the faculty excellence program to recruit and retain top-level faculty members on this campus. The state budget also includes planning funds for a new building for NCSA and a research incubator to be constructed in the South Center of the University of Illinois Research Park.

—Tony Waldrop, Vice Chancellor for Research

How does a common soil bacterium transfer genes into plants?

The completed genetic code of the Ti plasmid of *Agrobacterium tumefaciens* provides clues to the puzzle

With agricultural biotechnology in the forefront of the news these days, it is important that we, as scientists and citizens, understand the technologies that are involved in bringing to the consumer the products of this new biology. Nowhere is this more evident than in the production, marketing, and utilization of genetically-engineered plants. We now have the technology available to us to insert genes into plants and express genes from any source. The first-generation efforts from this technology have given us Round-Up Ready soybeans, and insect-resistant corn and cotton. The future promises, among other benefits, crops tailored for

higher nutritional value, and better adaptability to marginal growing conditions.

The soil bacterium, *Agrobacterium tumefaciens*, has been and continues to be the workhorse for the plant genetic engineer. This bacterium has a trick; it can transfer DNA to plants, and direct this DNA to the nucleus where it is integrated and becomes part of the plant genome. In nature, the bacterium does this for its own purposes; this DNA transfer process by *A. tumefaciens* causes plant overgrowth called crown galls. These galls, in turn, provide a

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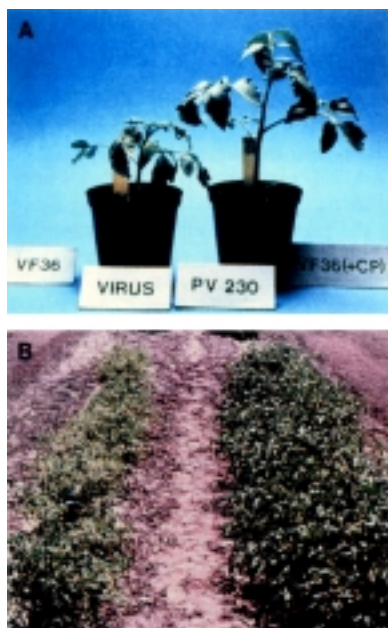
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Clues to the puzzle, continued



Resistant and Virus Infected Tomato plants. The plants on the left are wild-type plants with stunted growth and yellow leaves due to an infection with the tobacco mosaic virus. In comparison, the plants on the right are genetically engineered plants, carrying a gene for the viral coat protein that induces resistance against the infection. The disease resistant gene had been introduced into leaf discs using *Agrobacterium tumefaciens* mediated transformation. Plants carrying the gene were selected and regenerated.

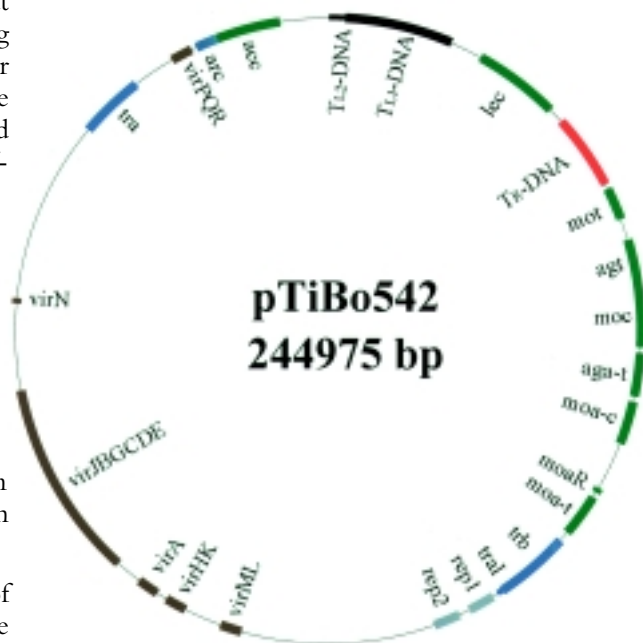
place where the bacterium can live successfully when in competition with other soil microbes. Over the past decade, plant biologists have successfully developed strains of *A. tumefaciens* that transfer only genes of interest, making it possible to develop plants that differ from their parents only by the single gene of interest. *Agrobacterium*-mediated gene transfer technology is extremely effective with many plants. However, the bacterium is much less useful with others. Among these so-called recalcitrant plants are included corn and soybeans, crops of particular interest to the farmers of Illinois. Given these limitations, and the economic importance of such recalcitrant plants, there is considerable interest in determining why *A. tumefaciens* does not transform plants like corn and soybeans with high efficiency.

The plant transformation properties of *A. tumefaciens* are associated with a large circular DNA element, called the Ti plasmid, present in the bacterium. This plasmid contains the genes specifying the machinery required to transfer DNA to plants. Among the different Ti plasmid types, the element present in one strain, Bo542 is of more than usual interest. Unlike most strains of *A. tumefaciens*, Bo542 is particularly effective on soybeans, raising the possibility that pTiBo542, the Ti plasmid of this

strain, could be used to genetically transform this plant. Unfortunately, why pTiBo542 is so effective, is not completely understood.

A research group here at the University of Illinois led by **Prof. Stephen K. Farrand** in Crop Sciences and **Prof. Gary J. Olsen** in Microbiology set about to dissect this Ti plasmid using the power of genomics analysis. They reasoned that by knowing the DNA sequence of this plasmid, that is, the complete genetic blueprint of the element, they might gain clues as to why pTiBo542 is so effective on soybeans. Funded by a grant from C-FAR (Council for Agricultural Research), the team, including **Drs. Philippe Oger** and **Claudia Reich** determined the complete 244,975 bp nucleotide sequence of pTiBo542. The clone banks, constructed by Dr. Reich, were sequenced using automated dye chemistry by the University of Illinois

W.M. Keck Center. In the initial stages, 1200 clones were sequenced from both ends in 2400 sequencing reactions. This phase, lasting about five weeks, generated almost the entire sequence. The



The structure of an *Agrobacterium* Ti plasmid

As assessed by the nucleotide sequence, pTiBo542 found in *Agrobacterium tumefaciens* Bo542 is a circular DNA molecule composed of 244,975 base pairs. Informatical analysis of this sequence defined 229 genes organized into groups as shown on the map. Color coded regions correspond to: **BLACK**, the two TL-regions and **RED**, the TR region, which contain the 15 genes transferred to the plant during infection by the bacterium; **BROWN**, the 33 vir or virulence genes that are involved in processing the T-regions and transferring these segments of plasmid DNA to the plant during infection. Some of these genes are required for transfer while others may be required for survival of the bacterium when in association with the plant; **GREEN**, the 44 genes specifying the uptake and catabolism by the bacterium of opines (*acc*, *lec*, *mot*, *agt*, *moc*, *aga-t*, *aga-c*, *moa-c*, *moa-t*) which are specialized substrates produced by the crown gall tumors that the bacterium can use as sources of nutrition; **BLUE**, the 22 genes required for the transfer of the entire Ti plasmid from one bacterium to another by conjugation; **GREY**, the 3 genes required for replication of the Ti plasmid in the bacterium. Interestingly, this Ti plasmid contains two complete sets of replication genes (*rep1* and *rep2*) organized in tandem. The large segments at 6 o'clock and 9 o'clock denoted by the thin lines represent the two spacer regions. These regions are full of genes of unknown function.

sequencing phase was completed and the information was assembled over another three months period.

Since completion of the sequencing and assembly phase of the project, the four members of the team have been annotating the information and determining the genetic composition of this DNA element. They have identified a minimum of 229 genes, of which 15 to 25 are believed to be involved in the transfer of DNA to plants. This portion of the work gives a view of this DNA molecule as a composite of gene modules, each associated with a different function (Figure). Some have to do with transferring DNA to plants, while others are necessary for this plasmid to replicate in its host bacterium. Still other gene sets allow the bacterium to take advantage of the environment provided by the crown galls on the plants. Having the complete sequence of this Ti plasmid will allow the team to focus on genes that are likely candidates for transformation of soybeans.

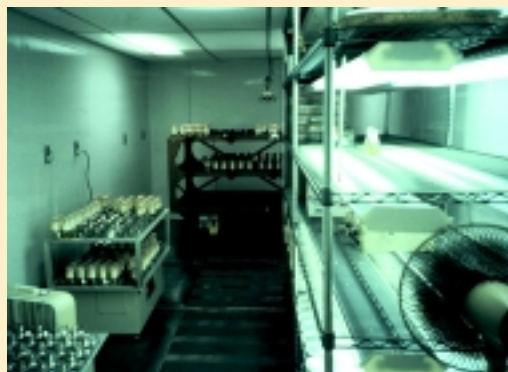
In addition to the practical aspects of improving plant transformation technology, knowing the complete sequence of this Ti plasmid contributes to our understanding of how these elements work, and the roles they play in the natural biology of *Agrobacterium tumefaciens*. The sequence already has provided surprises, including two large regions populated with genes of completely unknown function. These genes serve a purpose to the bacterium, and learning their functions will help to understand the habitat in which this bacterium lives, and how the bacterium copes with its environment. The sequence also provides clues concerning the evolutionary history of this element, and by inference, other Ti plasmids. This sort of information is not just of academic curiosity. The molecular phylogenists are telling us that genes transfer horizontally from one organism to another, and this transfer accounts for much of the diversity we see in evolution. Already we can see the evidence of such horizontal gene flow in the structure of pTiBo542. Furthermore, this element not only transfers DNA to plants, but also can transfer itself to other bacteria. Thus, pTiBo542 is the product of horizontal gene transfer, and can conduct horizontal gene transfer. Understanding the nature of this plasmid and its various gene components will be made easier now that we know its complete sequence.

—Edited by B. Whitmarsh

Plant Tissue Facility

The Plant Tissue Culture and Gene Transfer Facility is available to the research community for plant tissue culture and for gene transfer by particle bombardment. The facilities consist of a media preparation lab, autoclaves, laminar flow hoods and constant temperature rooms with shakers and shelves with lights. The facility has a Bio-Rad Model PDS-1000/He Biolistic Particle Delivery System and a PIG (particle inflow gun) for particle bombardments. A fluorescence dissecting microscope is also available.

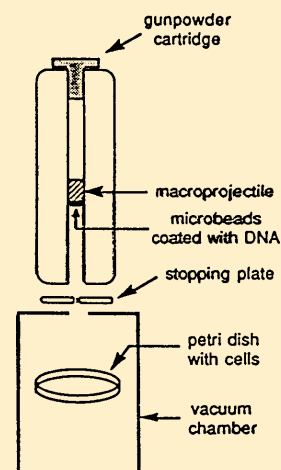
The facility is available for use to all on campus researchers for a fee to cover maintenance and supplies and is located in room 280 at the Edward R. Madigan Laboratory. For further information contact the Manager, Ms. Therese Eggett at 333-0822 or either of the faculty coordinators, Dr. S.S. Korban at 333-8298 or Dr. J.M. Widholm at 333-9462.



Plant Tissue Culture and Gene Transfer Facility. *The culture room (Room 280 in the Edward R. Madigan Laboratory) has shakers and shelves with lights, and a media preparation lab. Adjacent rooms are temperature and light controlled to provide constant growing conditions.*



Plant Tissue Culture and Gene Transfer Facility. *Bio-Rad Model PDS-1000/He Biolistic Gene Gun.*



Schematic of a microprojectile delivery system. *Microbeads (usually tungsten) are coated with the DNA of interest and deposited on one face of a macroprojectile. The macroprojectile is inserted into a barrel mounted above a vacuum chamber that contains the cells to be bombarded. The gunpowder cartridge is then set off with a firing pin, and the macroprojectile is accelerated against the stopping plate that has a hole, to allow the microbeads to continue and bombard the cells in the vacuum chamber.*

Food Poisoning: Tracking Down the Microbes

With a new instrument arriving in the **Laboratory of Veterinary Diagnostic Medicine** in February, the search for food-borne pathogens will get a boost. The instrument, called a RiboPrinter, will be used to develop a rapid screening test for pathogenic bacteria that may contaminate foods.



The RiboPrinter® microbial characterization system is the only fully automated instrument for fingerprinting the DNA of bacteria. It is made by Qualicon, a subsidiary of DuPont.

This new technology can shorten the time for identification of disease causing microbes from several weeks to a few days, which is critical in the case of a food borne disease outbreak to prevent the spread of further illness. For example, in the 1998-1999 *Listeria* outbreak from hot dogs, riboprinting was used to quickly identify the source of contamination that led to a recall of the product and procedures to reduce further risk.

The RiboPrinter has been optimized to categorize known microbes that may contaminate fresh-cut produce, meats, animal feed and other agricultural products. These pathogens belong to the following microbial species: *Campylobacter*, *Listeria*, *Salmonella*, *E. coli* and *Staphylococcus*. The fully automated instrument, available on the market since 1995, performs molecular genotyping of bacteria based on differences in ribosomal RNA, and generates highly reproducible fingerprints. The instrument performs DNA extraction, followed by a restriction enzyme digest and subsequent identification of fragments by probing with a region of the rRNA operon to reveal the patterns of rRNA genes. Subspecies identification is based on comparisons of fragment sizes and intensities. The instrument comes with a large database of characteristic patterns, for example over 250 for *Staphylococcus* and close to 100 for *Salmonella* have already been catalogued. With each new subspecies identification, the database continues to grow daily.

Funding for acquisition of the RiboPrinter and for initial testing was made possible by C-FAR (Council for Agricultural Research). The purpose is to provide a resource for the State of Illinois to identify pre- and post harvest food-borne diseases and to improve the speed and quality of food safety research in Illinois. Placing the instrument into the Laboratory of Veterinary Diagnostic Medicine will provide access on a fee-for-service basis to in-state veterinarians and U of I researchers. Several researchers in the College of ACES (Agricultural, Consumer and Environmental Sciences) and in the College of Veterinary Medicine will use the instrument for their research on cattle, swine and in food sciences.

—B. Whitmarsh

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The Laboratory of Veterinary Diagnostic Medicine (LVDM) at the University of Illinois, College of Veterinary Medicine

The College of Veterinary Medicine at the University of Illinois at Urbana-Champaign provides a unique service to the citizens of Illinois through the referral diagnostic laboratory known as the **Laboratory of Veterinary Diagnostic Medicine (LVDM)**. The LVDM is a part of a four-laboratory system that serves the entire state of Illinois. These include full-service diagnostic laboratories at Galesburg, Centralia and the UIUC and a serology laboratory at Springfield.

In addition to providing full service, all-species diagnostic assistance to practicing veterinarians and their clientele in the central and eastern portions of Illinois, the laboratory at the University of Illinois also utilizes the latest technology derived from research activities at the University in its diagnostic laboratories, teaches graduate students and veterinary students diagnostic methods and supports the research community of the college and university with its laboratory services. It is a unique blend of public service, teaching and research that serves both the citizens of the state and the university research and teaching communities.

The LVDM at the UIUC provides a faculty and staff composed of discipline specialists, including pathologists, clinical pathologists, histotechnologists, microbiologists, virologists, immunologists, toxicologists, chemists, microscopists, parasitologists, and serologists. Many also have one or more particular species and/or organ specialties to offer a well-rounded approach to diagnostic medicine with considerable depth. A team approach for in-laboratory consulting often provides the best possible diagnostic service.

The LVDM at UIUC works closely with the laboratories at Galesburg, Centralia and Springfield and with the State Veterinarian's office to insure that essential services are provided at one or more of the laboratories in the state. In addition the multi-laboratory system has established uniform labora-

tory fees to insure that clientele using the laboratory of their choice, will be charged the same fees for the same services at any of the laboratories. During 1999, fees for Illinois swine accessions to the laboratory were waived from January 1, 1999 to December 31, 1999 and laboratory fees for all food-producing animals (cattle, swine, sheep, goats, poultry, etc.) were waived from July 1, 1999 to December 31, 1999 at all four of the laboratories including the UIUC LVDM.

Over the last few years the LVDM has continued to add new tests to better serve the animal industries. Some of those tests include a test to detect cattle which are persistently infected with BVD (bovine virus diarrhea) virus, a more sensitive serologic test for Johne's disease (Johne's ELISA) in cattle, sheep and goats, a sensitive test for detection of rotavirus infection in diarrhea animals (rota ELISA), a series of sensitive detection methods for use in formalin-fixed sections of animal tissue (immunohistochemistry tests) for such diseases as *Neospora* abortion in cattle, toxoplasmosis abortion in sheep, leptospirosis abortion and infection in many species, PRRS virus infection in swine, circovirus (so called post-weaning multi-systemic wasting disease) infection in swine, and swine influenza infection. Also serology tests for four types of APP (*Actinobacillus pleuropneumoniae* 1, 3, 5, and 7) and *Mycoplasma hyopneumoniae* infection in swine have been added. The UIUC LVDM is also one of the few laboratories in the USA that can analyze for the toxins of white snake root in animal tissues and has added a test called the ICP which can analyze for up to 30 elements in samples of blood, tissue or feed in a single run.

The increased diagnostic capabilities of the LVDM have resulted in a steady increase (10-15% per year) in the number of specimens submitted from investigations that are made on livestock, poultry, equine and companion animal problems.

—J. Andrews



Phylogenomics

A New Initiative to Explore the Fundamentals of Life

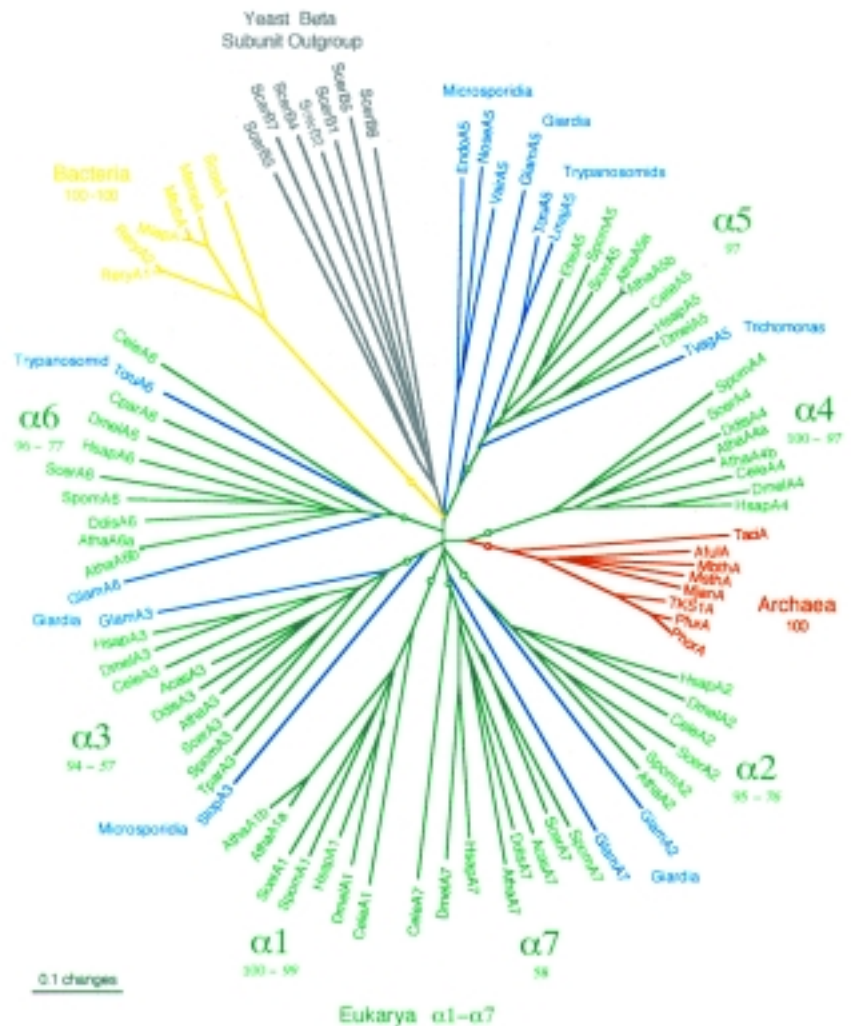
The late 20th century will be remembered as the dawn of the age of genome science. The massive large-scale sequencing of representative species of the three major life domains, *Bacteria*, *Archaea* and *Eukarya* is resulting in an exponentially growing number of whole genome sequences. Today, 31 genomes are completed and sequences of 200 genomes are in progress. These include not only unicellular prokaryotes with relatively small size genomes but also complex multicellular eukaryotes such as those of the nematode, *Caenorhabditis elegans*, the fly, *Drosophila melanogaster* and the human genome.

The determination of complete genome sequences provides scientists with a unique opportunity to study the origin and evolution of whole genomes. Since species and their genomes are products of history, knowledge of their phylogenetic relationships (i.e., of their common evolutionary histories) is essential for understanding their origin and evolution. Ultimately, the knowledge gained from comparing the organization and function of genes across distantly related phyla will provide new insights into the evolutionary processes resulting in the diversity of life on our planet.

A group of University of Illinois researchers has built upon the rapid growth in the characterization of genomes and the associated bioinformatics techniques to foster advancement of a new discipline they called *Phylogenomics*. This new discipline results from the combination of two major fields in the life sciences: *Genomics*, i.e., the study of the hierarchical organization and evolution of genes and genomes; and *Molecular Phylogenetics*, i.e., the study of evolutionary relationships among organisms or genes.

The research project in *Phylogenomics* is an interdisciplinary project directed by **Prof. Harris Lewin** (Professor of Immunogenetics and Director of the Biotechnology Center), **Prof. Shankar Subramanian** (Department of Bioengineering, University of California at San Diego) and **Prof. Carl Woese** (Department of Microbiology). The research was supported by a grant from the University of Illinois Critical Research Initiative. **Juan L. Bouzat**, a post-doctoral associate and **Leslie K. McNeil**, graduate research assistant in the Department of Molecular and Integrative Physiology, selected the 20S proteasome gene family to test the validity and power of the proposed approach.

Proteasomes are large protein complexes responsible for intracellular protein degradation and, thus, they play a key role in many



Phylogenetic tree of proteasomal genes from 29 species sampled from the Tree of Life. The three major domains of life are colored in yellow (Bacteria), red (Archaea), and green (Eukarya). Microsporidia, Giardia, Trypanosomids and Trichomonas are considered early branching eukaryotes as shown by analysis of ribosomal RNAs (shown in blue). Numbers indicate percentage bootstrapping values of 100 replicates (neighbor-joining in regular text and maximum parsimony in italics) at the nodes marked with a circle.

Scer-, *Spom* = Yeast; *Endo-*, *Nose-*, *Vair-*, *Slop* = Microsporidia; *Tcru-*, *Lmaj* = Trypanosomids; *Glam* = Giardia; *Tvag* = Trichomonas; *Ehist* = Entamoeba; *Atha* = Arabidopsis thaliana (plant); *Cele* = Caenorhabditis elegans (worm); *Hsap* = Homo sapiens (human); *Dmel* = Drosophila melanogaster (fly).

cellular processes. These catalytic complexes are found in representative species from the three domains of life (*Bacteria*, *Archaea* and *Eukarya*). The number of proteasomal genes in different species varies from a single alpha and beta gene in *Archaea* to up to seven alpha and seven beta genes in higher eukaryotes. The variable number of alpha and beta proteasome genes present in

different species and the levels of sequence similarity among them suggest that this gene family originated by a series of duplications of a single gene followed by subsequent sequence divergence.

In collaboration with **Mitchell L. Sogin** of the Marine Biological Laboratory at Woods Hole, UIUC researchers performed an extensive comparative analysis of whole genomes as well as a systematic sampling of proteasomal genes from the three domains of life. DNA sequencing was performed at the W.M. Keck Center for Comparative and Functional Genomics. A phylogenetic analysis of proteasomal genes from 29 species including *Bacteria*, *Archaea* and *Eukarya* showed that the extensive diversification of the proteasomal genes occurred prior to the emergence of currently existing eukaryotes (Figure). The deep branching patterns observed among the 7 alpha proteasome genes characteristic of *Eukarya* (branches shown in green) suggest that the duplications that originated this gene family were ancient events. The identification of most of the alpha proteasomal genes in the complete genome database of *Giardia lamblia*, considered one of the earliest branching eukaryotes, supports this idea and suggests that the duplication events occurred during the early evolution of *Eukarya*. Although the proteasome quaternary structure is highly conserved, probably because of a functional constraint on the proteolytic activity, the increase in the number of genes encoding proteins of the proteolytic core may have allowed the extensive diversification of the subunits. This process may have provided a source of variation for novel functional adaptations associated with the highly conserved quaternary structure.

The study of molecular phylogenetics has a long tradition on the UIUC campus. In 1977 Carl R. Woese, Professor of Microbiology, and member of the National Academy of Sciences, revolutionized biology by changing our view of the diversity of life (Woese 1977). Using sequence analysis of ribosomal RNA (rRNA) Woese identified a new group of microbes, the *Archaea*, as a third kingdom of life, adding to the two kingdoms originally believed to encompass all existing organisms (*Bacteria* and *Eukarya*). The recent advances in genomics are painting a clearer picture of the major life domains originally characterized by Woese, allowing biologists, for the first time, “to attack the greatest of evolutionary problems, how cells evolve” (Woese 1998). The combination of molecular phylogenetics and genomics, referred to as Phylogenomics, will play a key role in addressing fundamental questions in the life sciences. Following this tradition, the University of Illinois is committed to be at the front line of this emerging field that will ultimately yield important clues about the origin and evolution of genes and genomes.

—Edited by B. Whitmarsh

Woese quotation:

Woese, C.R. and Fox, G.E. *Proc. Natl. Acad. Sci. USA* **74**:5088-5090 (1977)

Woese, C.R. *Proc. Natl. Acad. Sci. USA* **95**: 11043-11046 (1998)

The Certificate in Business Administration for Scientists

A Joint Effort of the Biotechnology Center and College of Commerce

The Certificate in Business Administration for Scientists was first offered by the Biotechnology Center, in cooperation with the College of Commerce in the spring of 1999, prompting rave reviews from the 22 participants.

The program is designed to provide the essential management knowledge and skills necessary to running an academic or industrial research laboratory and to provide the strategic framework for making informed business decisions about current and future issues. It covers the basic concepts of strategic management and marketing, accounting, financial management, interpersonal and organizational skills, managerial types and preferences, negotiating, conflict management, and personal financial management. The instructors each present in her/his area of expertise.

Companies, too, participate in the program, not only as participants at times, but also as presenters. The first session of this semester, held February 15, included Dr. Michael Rothgeb of Procter and Gamble, explaining the ways in which industrial employees are evaluated, using the same criterion for hiring as for evaluating performance. This included a great deal of information about the values, culture, and practices of research and development departments of corporations. The final session features a panel of industry representatives who “tell it like it is” and answer myriad questions posed by the participants. Companies also participate, in a manner of speaking, by funding new hires participation.

The participants in the program become involved for a variety of reasons. Directors of university service laboratories, wish to enhance all of their managerial and people skills; graduate students who will seek employment in industry and wish to have a leg-up on the industrial climate; professors wishing to improve their laboratory management and understanding of budgets; owners of local biotech start-ups seeking all these skills as well as techniques for recruiting. And in all cases, the solid grounding in concepts used in all teamwork, industrial, and managerial situations well serves those who receive The Certificate in Business Administration.

—C. Connor

Facility Updates

Welcome to Our New Employees



Michelle (Holly) Tiffin transferred from the Department of Continuing Education in Music to the Administrative Office of the Biotechnology Center in February to serve as our new secretary. Her job experience and knowledge of the campus has already become a great asset to our office. The Bioinformatics unit of the W.M. Keck Center for Comparative and Functional Genomics expanded its staff. **George Gong** joined us in January as our new database administrator and designer. During his previous employment as software engineer with ERES Consultant, George gained extensive experience in Oracle database design and development which he is now employing to DNA sequencing databases. Two graduate students from the Department of Computer Sciences, **Zhifang Liu** and **Jian Sun**, support the unit as research programmers. Zhifang works primarily on automating a DNA sequencing data pipeline for high-throughput sequencing projects. Jian is developing a pilot project to analyze and visualize microarray data in three dimensions and time resolved.

BioInteractive Analysis (BIA) Instrumentation Update



The first faculty user experiments using the new BIAcore 3000 are now underway, and the Immunological Resource Center (IRC) is beginning the process of fine-tuning the administration of BIA services on the UIUC campus.

By working to solve the research problems of the major users involved in the BIAcore grant, the IRC staff will acquire competence in the effective utilization of this new tool. The instrument comes with many sophisticated software resources that when learned will enhance the value of this instrument to UIUC research investigators.

Although it is still premature to open the doors for campus wide service, the establishment of protocols and methods has begun. Investigators who may be interested in making kinetic measurements are encouraged to begin discussing their research interests with either Liping Wang or Steven Miklasz. It may also be useful for potential BIAcore users to familiarize themselves with the sample preparation methods needed to measure BIA. A useful Internet resource, describing sample preparation (as well as other useful information) can be found at the University of North Carolina at Chapel Hill web site: <http://macinfac.bio.unc.edu/biaprep.html>

Protein Sciences Facility Update



Peptide Synthesis: Small scale peptide synthesis is now available in addition to half scale and full scale synthesis. This allows the user to order peptide quantities from 5-120 mg or more (crude/desalted peptide) and 1-25 mg or more (purified peptide).

Peptides between 6-20 amino acids are guaranteed (no charge in case of failure). Guarantees for all other peptides and special projects will be given based on the peptide sequence. Please talk to Dr. Remmer (3-3841, remmer@uiuc.edu). The facility offers a variety of special syntheses e.g. cyclic and cold-labeled peptides.

Protein Identification Services/Proteome Analysis: The Protein Sciences Facility is expanding its protein identification services. 2D electrophoresis, in-gel-digestion, peptide mass fingerprinting and sequencing by mass spectrometry will soon be available. These new services complement the already existing Edman sequence analysis and also allow for proteome analysis. Guidelines for sample preparation and handling are available. Please discuss your projects with Dr. Remmer.



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