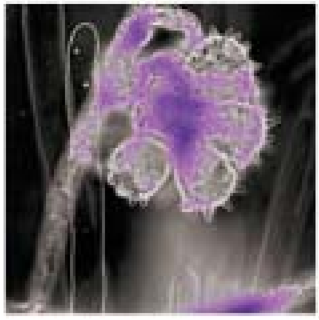
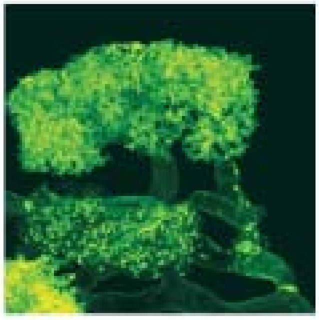
BTI

Boyce Thompson Institute for Plant Research





80th Annual Report 2003

From The Chairman

Overall, 2003 has been an excellent year for the Boyce Thompson Institute. As noted in the President's letter, the Institute's faculty has succeeded once again in attracting major sources of research funding. And, progress on our building renovations has helped create an environment that is more conducive to leading-edge science. We are squarely on the path to becoming a global leader in plant research, and, that, in large part, is due to the leadership of Dan Klessig.

The Board, therefore, regrets Dan's decision to resign as BTI's president. Though Dan will continue to head a significant research program at BTI, we will miss the diligent and self-less service he provided during his tenure as president. The Board greatly appreciates his efforts to improve the quality of the Institute's research programs and the effectiveness with which we use the Institute's resources. We know he will continue his tireless pursuit of scientific excellence as a member of our faculty.

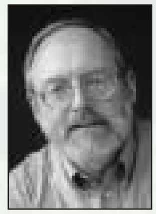
We have appointed a Search Committee, headed by Board member Ezra Cornell, to find a leading scientist in plant research who can provide the scientific and management expertise we need, and who shares our vision of BTI's future. I am encouraged by the committee's progress in its comprehensive search for the best possible successor, and I'm certain we will find a highly qualified candidate in coming months.

I want to thank BTI's faculty and staff for their patience during this time of transition. I also want to assure them and our many supporters that we will see a stronger institution that is better positioned for the future as a result of all our efforts.

Paul H. Hatfield
Chair of the Board

On the cover: *The arbuscular mycorrhizal symbiosis. Left Panel: Auxiliary cells of the arbuscular mycorrhizal fungus, Gigaspora gigantea (shown in purple), adjacent to a Medicago truncatula root hair. Middle Panel: Appressoria (shown in green) on the root surface (shown in red). The fungus develops appressoria to enter the root. Right Panel: Branched hyphae called arbuscules (shown in green) form within the root cells and transport phosphate to the plant.*

From The President



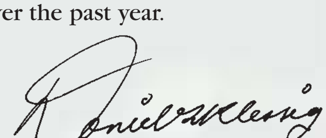
Over the past several years the Institute has undergone significant changes as it positions itself to play a leading role in plant sciences in the 21st century. This transition continued in 2003 on several fronts. Three new scientists joined our faculty, including Maria Harrison who moved here from the Samuel Roberts Noble Foundation in January; Peter Moffett who joined the Institute as an Assistant Scientist in August; and André Kessler who accepted a joint Cornell University-BTI appointment as an Assistant Professor/Scientist beginning in 2004.

We also made excellent progress on our plans to upgrade the Institute's infrastructure. Larry Russell, Director of Operations, and Larry Willard completed a massive renovation of our plant growth facilities. Installation of a new, vastly improved, flexible management and accounting system was completed, thanks to the tireless efforts of John Dentes, V.P. for Finance and Operations, and his team, including Lucy Pola, Director of Human Resources. We also continued major renovations of our research labs and support facilities that began about five years ago. Approximately 65 percent of the research areas on the 2nd, 3rd and 4th floors and 40 percent of these areas on the 1st and basement floors have now been renovated.

In 2003, BTI scientists published their research in a number of high-impact, top-tier scientific journals, which included such highly cited publications as *The Proceedings of the National Academy of Science*, *Genes and Development*, *EMBO Journal* and *The Plant Cell*. In addition, the premiere scientific journal, *Cell*, reported Meena Chandok's discovery of an enzyme (nitric oxide synthase) and its gene, both of which play a key role in plant disease resistance.

In another measure of success, BTI's scientists attracted $6.25 million in external research support. Grant and contract revenues in 2003 nearly equaled the all-time high reached in 2002 ($6.36M). On a per scientist basis, 2003 marked a new high in annual external research support, which has tripled to approximately $400,000 since 1996.

In closing, I wish to express my gratitude to the Institute's scientists, scientific staff, support staff, management team, and Board of Directors for their efforts to make 2003 another successful year. In addition, special thanks are due to David Stern, V.P. for Research, for his leadership and wise counsel in dealing with several difficult issues over the past year.



Daniel Klessig
President & CEO

Peter Moffett Appointed to BTI Faculty

Peter Moffett, Ph.D., joined BTI as an assistant scientist in August. A native of Canada, Dr. Moffett received his bachelor of science and doctoral degrees in biochemistry from McGill University. He joined BTI following three-and-a-half years as a postdoctoral fellow in the Sainsbury Laboratory at the John Innes Centre in the U.K. Dr. Moffett accepted the position at the Institute because, he said, "BTI is renowned in the plant research community. Here, I have the opportunity to do good science combined with the requisite resources. It's really a great atmosphere." Dr. Moffett studies the disease resistance pathway in plants, with tobacco and potato virus X as his model system.

Summer Research Students Vie for the Colonel's Cup

The 2nd Annual Summer Student Symposium, affectionately known as "The Colonel's Cup Challenge," took place on Friday, August 15, at the Institute. Seven undergraduates and one high school student gave talks on their summer research, and seven high school students presented posters. The event culminated the students' summer research experience in eight different BTI and Cornell laboratories.

Alyssa Wright, California State University – Fresno, won the Colonel's Cup for the best student presentation. Alyssa's talk was entitled "Ac transpositions in the pink scutellum gene." Her BTI mentor was Ling Bai, a graduate student in the Brutnell lab. 2003 judges were Drs. Carl Leopold, Alan Renwick and Dick Staples – all BTI emeriti faculty. Jonathan Lynch, Ithaca High School, won the Best Poster Award for elegantly answering the question, "What exactly is an Ac?" Jon's BTI mentor was Kevin Ahern, a technician in the Brutnell lab. The posters were judged by the undergraduate students.

Nicole Markelz, Outreach Coordinator for Plant Genome Projects at BTI and Cornell, organized this year's symposium and made introductory remarks. She was followed by the student presentations, one of which included a musical performance by Lisa Kennedy and Mhairi Lathe. Entitled "Silk Out!," the original composition captured the students' summer experience in the Brutnell lab and the maize nursery. Lunch in the Atrium preceded the poster session in the Biodiversity Conference Room. The Awards Ceremony capped off the event.

The students who gave talks were: Alyssa Wright, Lisa Kennedy, Mhairi Lathe, Johanna Smith and Kelly Dusinberre, (all from the Brutnell lab), Nicholas Licciardello (van Wijk lab), Liz Cirulli (Jahn lab), and Hannah Kohut (Kohut lab). Posters were presented by: Jon Lynch and Michael Martin (Brutnell lab), Rei Thompson and Ryan Brown (Comstock lab), Elana Maccou, Rebecca Fernandes and Joshua Esnard (all from the McCouch lab), and Teresa Rojas (Jander lab). Other participants included Dhruba Mukherjee (Stern lab) and Rachel Miller (Brutnell lab).

Thanks and kudos to all the BTI folks who helped make this event happen—our fantastic judges, Carl, Alan and Dick, Jude Tulla and Valleri Longcoy, our logistics experts, and Brian Gollands, for computer and video support.

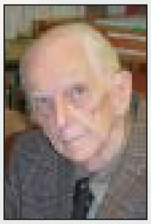
Martin Lab Helps Sequence Bacterial Genome

Collaborative research between Greg Martin's lab at BTI, Alan Collmer's lab at Cornell and The Institute for Genomic Research yielded the complete genome sequence of an agriculturally important plant pathogen, called *Pseudomonas syringae pv.* tomato (strain DC3000), in 2003. Sequencing the genome of *P. syringae*, which causes tomato speck disease and other plant diseases that depress crop yield, could lead to new ways of controlling plant pathogens in the field.

The research also may have important applications in human medicine because a related strain of the *Pseudomonas* bacterium causes fatal lung infections in people with cystic fibrosis. The project was funded by the National Science Foundation Plant Genome Research Project and the teams' results were published in the *Proceedings of the National Academy of Sciences (PNAS)* in August. The findings were the subject of an Associated Press article that was widely published last year as a result of a news release issued by Cornell.

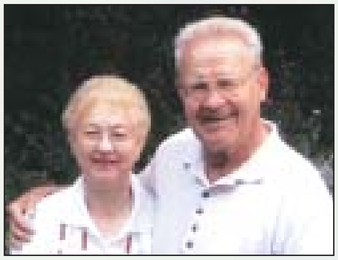
Anthony Grefig Makes Bequest to BTI

Anthony Grefig, who retired from the Institute in 1988, made the first gift to our planned giving program in 2003 when he designated the bulk of his estate to BTI. A graduate of Columbia University, Andy worked on the Manhattan Project early in his career. He joined BTI in 1962 to work with Lee Crisan, Ph.D., on thermophilic fungi and aflatoxins. Later, Andy transferred to Alan Renwick's analytical laboratory, which functioned as a service to the entire Institute. Andy moved with BTI to Ithaca in 1978. We are very grateful to him.



In Memoriam — George and Helen Kohut

George and Helen Kohut, long-time donors to the Institute, died as the result of an automobile accident in the Spring of 2003. Helen, who held degrees from Hartwick College and the University of Pittsburgh, was a social worker. One of her many accomplishments was helping to develop the first "Head Start" program. George earned both his bachelor and master's degrees from the University of Pittsburgh where he also played football. He was a Fulbright Scholar who taught for many years in Pennsylvania and Maryland schools. Helen and George were the aunt and uncle of BTI scientist Robert Kohut. The Kohuts' interest, support and kindness will be greatly missed.



Research Summaries

Gary Blissard

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Alice C. L. Churchill

Jonathan P. Comstock

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Daniel F. Klessig

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Gregory B. Martin

David B. Stern

Mary A. Topa

Joyce M. Van Eck

Haiyang Wang

David A. Weinstein



Gary Blissard
Ph.D., Scientist
Molecular Virology

How do viruses infect cells?

Viruses are highly successful organisms. They cause disease by entering a host cell and then commandeering the cell's genetic machinery to help them multiply. Afterwards, they exit the cell to carry out this process again and again. Gary Blissard, Ph.D., is working to understand how viruses enter, commandeer, and exit host cells at the molecular level.

Working on grants from the National Institutes of Health and the U.S. Department of Agriculture, Blissard and his colleagues study a common virus, called a baculovirus, that infects insects. They've found that certain proteins, called GP64 and F, on the virus' outer membrane enable it to fuse with and enter a host cell. Interestingly, the F gene was also found recently in the genome of the *Drosophila* fruit fly – a common research insect. Blissard's group cloned the *drosophila* F protein gene and are now working to discover where the protein is produced in the insect's tissues, what role it plays, and whether and how baculovirus may have acquired the F gene from its insect hosts. He's also trying to identify the host cell molecule that accepts the virus, which may help explain how the virus enters the cell's nucleus.

Blissard believes, however, that the GP64 protein may be more important than F in the virus/insect interaction because viruses with GP64 are more infectious than those with only F. In fact, Blissard recently discovered that when the GP64 gene is deactivated in the virus, it can no longer exit the host cell. Currently, Blissard is using mutations in the GP64 protein to better understand and define its function and molecular structure.

Blissard's research could one day lead to new biological control methods for insect pests and more effective gene therapy techniques for humans.

Thomas P. Brutnell
Ph.D., Assistant Scientist, Plant Molecular Genetics

How do plants know when to flower?

Plants can tell time and light sets their internal clock. They know the length of the day and the season of the year from the amount of light they receive. And when the time is right, they grow, flower and produce seeds. Thomas Brutnell, Ph.D., is working to understand the genetic basis of the plant's ability to respond to light with a long term goal of increasing yield by altering that response.

Funded by a three-year National Science Foundation grant, Brutnell and his colleagues discovered in earlier work that plant photoreceptors, called phytochromes, are involved in a number of light responses in corn. These responses include the regulation of flowering time, stem elongation and yield.

In 2003, Brutnell's group identified and sequenced the genes that control the production of three types of phytochromes in corn – A, B and C. They also discovered there are two functional copies of each gene: A1, A2, B1, B2, C1 and C2. Knowing this enabled the team to begin turning off each of the six genes, one at a time, to learn its individual role in the plant's response.

So far, they've discovered that of the two phytochrome B genes only phytochrome B2 is important in regulating flowering time in corn. When that gene is disrupted, the plants flower early. Deactivating phytochrome B1 does not appear to affect flowering time.

In future research, the team will deactivate each of the other phytochrome genes in corn to learn its unique effect on plant development. By understanding this complicated photoreceptor network, it may be possible to beneficially alter the plant's growth and yield by altering its response to light.

Alice C. L. Churchill
Ph.D., Center Scientist, Fungal Biochemistry

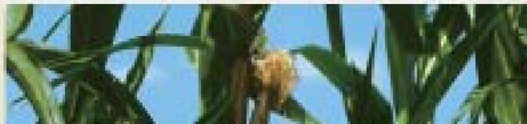
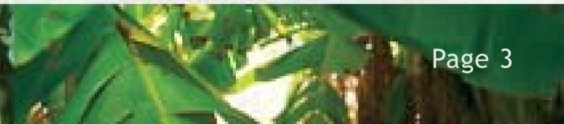
What is the genetic basis of secondary metabolite production in fungi?

There are about 1.5 million species of fungi on Earth. Some cause disease in plants or animals; others produce compounds – called secondary metabolites – that serve as valuable human therapeutic drugs. Alice Churchill, Ph.D., is investigating the genetic basis of secondary metabolite production in fungi to better understand how they cause disease in plants. She also works to identify fungi that make novel compounds for use in human medicine.

In 2003, Churchill's group cloned portions of the genome associated with the production of toxins from the chestnut blight fungus, a devastating tree pathogen. Currently, they are sequencing these genes and will use them to determine whether they play roles in the disease pathway.

In another project, Churchill is studying a pathogen that causes disease in bananas and plantains throughout the world. In commercial plantations, the fungus is controlled through weekly chemical sprays. Toxins produced by the fungus are predicted to be involved in the disease. Her group has cloned several putative toxin biosynthesis and transport genes. They are currently working to determine whether they are involved in causing disease.

Churchill also is working to find new fungal bioactive compounds that have medicinal potential. Her group has screened more than 160 fungi and cloned genes for the production of complex bioactive peptides from more than half. Currently, they are working to identify conditions under which the genes are expressed so that collaborators can screen for metabolites with anticancer and other activities.

Jonathan P. Comstock
Ph.D., Associate
Research Scientist,
Plant Ecophysiology

Why do some plants use water more efficiently than others?

Understanding why and how some plants use water more efficiently than others could one day lead to crop plants that are more tolerant of drought. Jonathan Comstock, Ph.D., is working to determine the genetic basis of this kind of physiological specialization among plants by comparing wild species of rice and tomato to their cultivated relatives.

In earlier research, Comstock hypothesized and confirmed that the rice and tomato wild relatives he selected exhibit better water use efficiency under variable environmental conditions than the cultivated varieties. By comparing the two through a variety of sophisticated genetic analyses, he found two or three regions on the chromosomes of both rice and tomato that appear to be critical to water use efficiency. He also confirmed that all the varieties exhibit similar changes in their water use response when temperature or soil type changes.

In 2003, which was the second year of a four-year National Science Foundation grant, Comstock and his colleagues continued research to confirm their earlier water use efficiency results in wild versus cultivated rice and tomato. Using stable isotope technology and molecular markers, they worked to verify that the chromosomal regions they found earlier are involved in water use efficiency and to identify the genes that control this trait. This step in the research will take several years to complete.

James J. Giovannoni
Ph.D., Scientist,
Plant Molecular Biology,
USDA-ARS PSNL

What is the genetic basis of nutrient accumulation in tomatoes?

Lycopene, an important antioxidant carotenoid, provides tomatoes with their red color and nutritive value. Mounting evidence suggests that lycopene inhibits degenerative diseases, such as cancer and heart disease. Jim Giovannoni, Ph.D., is studying the genetic basis of lycopene production in tomatoes with the long-term goal of increasing the amount of this important antioxidant they, and other, fruits produce.

In 2003, working on a grant from the U.S. Department of Agriculture, Giovannoni continued research to determine the genetic basis of lycopene production in a mutant, high pigment tomato (hp). The mutant tomatoes produce nearly twice as much lycopene as commercial varieties, so breeders have attempted to produce new tomato varieties with improved color and nutrition by crossing the hp mutants with commercial ones. Unfortunately, the mutation that provides color and health benefits also reduces yield and weakens the plants.

The detrimental effects of the hp mutation are commonly observed in plants that receive too much light; therefore, Giovannoni and others theorized that the hp mutation involved the plant's light sensing capabilities. Working on this theory, Giovannoni and his colleagues identified and cloned the gene responsible for the hp mutation. Their work proved that lycopene production is directly related to the plant's perception of and response to light in the environment. With the gene now in hand, scientists may be able to develop tomatoes and, possibly, other fruit crops that naturally produce twice as much lycopene and other health-promoting antioxidants without the negative agronomic side effects of the mutation.

Maria J. Harrison
Ph.D., Scientist,
Plant-Fungal Symbiosis

What is the genetic basis of a plant/fungal symbiosis?

Flowering plants form symbiotic relationships with certain root fungi that help the plant access phosphate – a key nutrient – from the soil. The fungi, in turn, receive carbon from the plant, which is critical to their survival. Maria Harrison, Ph.D., studies the relationship between certain fungi, called arbuscular mycorrhizal fungi, and a model legume, *Medicago truncatula*, in order to understand the genetic mechanisms that underlie it.

Supported by an on-going National Science Foundation grant, Harrison's goal is to understand how the plant and the fungus communicate with each other to form a symbiosis. Other goals are to explain how the fungus delivers phosphate to the plants, and how the plants distinguish, at a genetic level, between beneficial fungi, like arbuscular mycorrhizal fungi, and pathogenic soil fungi.

To do this, Harrison and her colleagues are using a variety of genomics techniques to monitor gene expression in the plant when it's roots are colonized by arbuscular mycorrhizal fungi. They've already discovered that an entirely new set of genes is activated when the mycorrhizal fungus invades the roots, and that genes associated with defense against pathogens are switched off. Identifying and cloning these new genes will provide important information about the relationship and how it works.

In the long run, Harrison's research may prove important for agriculture. By understanding the genetics of the mycorrhizal symbiosis, scientists may be able to enhance phosphate acquisition in crop plants and could reduce the amount of phosphate fertilizers used for agriculture.

Georg Jander
Ph.D., Assistant Scientist, Plant-Insect Interactions

How do plants and insects interact?

The relationship between plants and insect herbivores is extremely complex. Plants have developed a variety of physical and chemical defenses against insect attack, but insects, in turn, acquire resistance to plant defense systems. Georg Jander, Ph.D., is working to understand these interactions at the genetic level in both plants and insects.

Jander and his colleagues are investigating natural variation in insect resistance in the model research plant, *Arabidopsis*. At the same time, they are studying the peach-potato aphid, an insect pest, to identify natural variation in its growth and reproduction on different lines of *Arabidopsis*. Jander is using linkage to genetic markers on the chromosomes of both the plant and the insect to find genes that confer resistance or sensitivity. In the long term, such knowledge may lead to new ways of protecting crop plants from insects without the use of chemical insecticides.

In another project, Jander is studying the genetic basis of amino acid production in plants. Animals, including humans, are unable to make certain essential amino acids required for their health and growth, so these amino acids must be obtained from dietary sources. If crop plants could be altered to produce increased quantities of essential amino acids, food and feed would be more nutritious. Jander is working to discover genes in *Arabidopsis* that control the production of two essential amino acids, methionine and threonine. In the long term, the results from this research may help scientists enhance the nutritional quality of grain and reduce the need for additives.

Daniel F. Klessig
Ph.D., Scientist, Plant Pathology, President & CEO

What is the molecular basis of disease resistance in plants?

When a pathogen, such as a virus, attacks a plant, the plant activates its immune system. This ancient form of disease resistance, called “innate immunity,” is also shared by people, insects and other animals. Daniel Klessig, Ph.D., is working to understand the molecular basis of innate immunity in plants for both plant and human applications.

In 2003, Klessig and Meena Chandok identified the enzyme and the gene encoding it that is activated when a plant senses it is being attacked by a pathogen. This enzyme synthesizes nitric oxide (NO), a critical hormone that tells the plant to turn on its defense arsenal. This discovery, which was published in the journal *Cell*, provides new knowledge about the biochemical and genetic pathways in plants that enable them to protect themselves from disease.

Klessig and his colleagues also discovered another key component, called salicylic acid binding protein 2 (SABP2) that is involved in the plant defense pathway. SABP2 is an enzyme that Klessig believes may be the receptor for SA, which is another critical plant hormone involved in the defense response. Working with tobacco and tobacco mosaic virus (TMV) as a model system, Klessig and Dhirendra Kumar found that when the gene for SABP2 is silenced, the plant is less able to respond to SA and resist TMV infection. It appears, therefore, that without SABP2, the plant is unable to activate its immune response.

Understanding the biochemical/genetic sequence of events that occurs when a plant is attacked by a pathogen could provide new ways to enhance the plant’s ability to activate its natural defense system. These findings may one day lead to improved, natural disease resistance in crop plants.

Robert Kohut
Ph.D., Scientist, Plant Pathology

What is the ozone risk to plant species in our national parks?

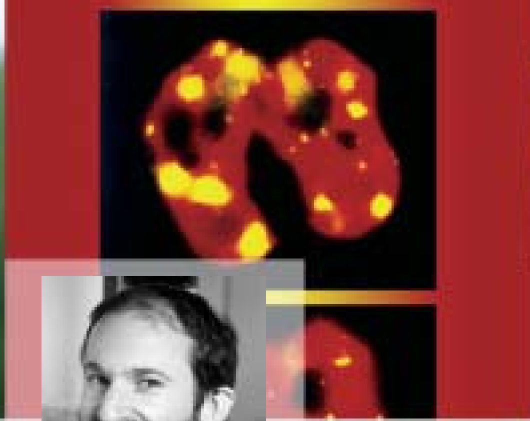
The plant communities in our national parks are treasures that the U.S. National Park Service strives to protect. However, many parks receive high levels of ozone, an air pollutant that can injure sensitive plants. To adequately protect its plant communities, the National Park Service must know which parks are at the greatest risk of ozone damage. Robert Kohut, Ph.D., is currently working on a U.S. Park Service grant to help determine the risk of ozone injury in 270 national parks.

To develop an assessment for each park, Kohut will analyze three sets of data: 1) ozone-sensitive species, 2) seasonal levels of ozone exposure, and 3) monthly soil moisture levels. Calling this the “injury triad,” Kohut explains that ozone injury to plants results from the interaction of the three data sets and their optimization.

To be injured, a plant first needs to be sensitive to ozone and then receive an exposure level that exceeds its threshold for injury. The sensitive plant must also take up the ozone, which occurs most readily under high soil moisture conditions. Most often, high ozone levels are associated with hot, dry conditions, so more moderate ozone levels coupled with moist soils actually can create the highest risk of injury.

Kohut’s assessments of risk will provide park managers with the information they need to understand the ozone hazard in each park and to decide what studies to conduct in order to determine whether ozone injury is occurring.

Gregory B. Martin
Ph.D., Scientist,
Plant Pathology



David B. Stern
Ph.D., Scientist, Plant
Molecular Biology,
V.P. for Research

Mary A. Topa
Ph.D., Associate
Scientist,
Plant Physiology

What is the relationship between plants and bacterial pathogens?

Plants have an ancient immune system that helps them ward off disease. But pathogens, such as certain bacteria, have evolved ways of circumventing the plant's natural resistance. Gregory Martin, Ph.D., is studying this interrelationship at the molecular level in both the plant and the pathogen.

Martin and his colleagues are working with tomatoes and a bacterium, called *Pseudomonas syringae*, that causes bacterial speck disease. He has discovered that tomatoes resistant to the disease recognize certain proteins (AvrPto and AvrPtoB) the bacteria injects into their leaf cells. Recognition of these proteins causes the plant to activate a variety of defense responses, ranging from the production of anti-microbial compounds to localized cell death in the parts of the leaf that have been infected. Identifying which tomato genes play the most important role in the disease resistance pathway is one of Martin's research goals.

In 2003, Martin's lab discovered that the bacterial protein, AvrPtoB, suppresses the plant's ability to cause the death of its own cells, which enables the pathogen to circumvent this plant defense response. Understanding how the AvrPtoB protein interferes with programmed cell death could contribute significantly to scientists' understanding of disease in plants as well as aging and disease in humans.

Also in 2003, Martin, in collaboration with researchers at six universities, sequenced the entire genome of *Pseudomonas syringae*, and identified where each of its 5,500 genes stop and start. The next step is to ascertain the function of each of these genes. To that end, Martin's lab designed software for the Web that enables any scientist, anywhere to note the function of each of the bacteria's genes as it is characterized.

How do plant cells communicate internally?

Plants need to react quickly when stressed by abiotic conditions, such as nutrient deficiencies. Phosphate is often a limiting nutrient, which is why it is heavily used in fertilizers. Root cells initially sense the deficiency, which is followed by complex responses that reduce use of available phosphate and mobilize additional internal stores. Understanding the systems plant cells use to sense, communicate and respond to abiotic stress is one research focus of David Stern, Ph.D.

Supported by a five-year National Science Foundation (NSF) grant, Stern studies responses to phosphate deficiency within the chloroplasts of an alga called *Chlamydomonas reinhardtii*, and in the model plant *Arabidopsis*. In 2003 research, Stern and his colleagues discovered that the activity of an important enzyme called PNP, found in chloroplasts as well as microorganisms, declines precipitously under phosphate stress. This finding indicates that both PNP and the chloroplast are part of the cell's phosphate-sensing, intracellular communication network in this alga.

Chlamydomonas is a unicellular organism, and in crop plants, response mechanisms may be distinctive. In *Arabidopsis*, Stern recently discovered that PNP is critical to plant survival, since mutant plants that did not produce PNP were also unable to carry out photosynthesis. Future work will focus on understanding the role of PNP in the phosphate limitation response, and why it is critical to plant survival even when phosphate is not limiting.

Stern also has two NSF grants with researchers at Cornell, Oregon and Nebraska, to study intracellular communication involving corn chloroplasts. Thus, abiotic stress responses will also be tested in a key crop species.

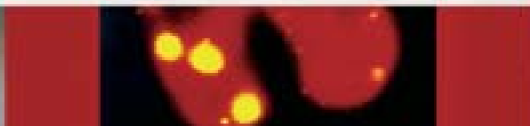
Do certain fungi benefit tree growth more than others?

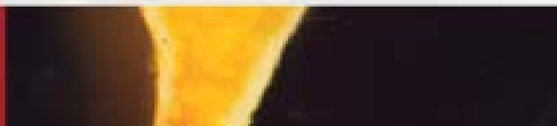
The biotic and abiotic interactions that occur between plant roots and the soil environment around the roots (the rhizosphere) are among the most complex and least understood interactions in plants. One example is the relationship between certain symbiotic fungi, called mycorrhizas, and the loblolly pines whose roots they colonize. Mary Topa, Ph.D., studies these fungi to better understand how rhizosphere organisms may alter root function and a tree's response to environmental stress.

The challenge to root biologists, like Topa, has been to find methodologies that will allow them to quickly and accurately characterize mycorrhizal diversity. This is because tree roots are colonized by communities of rhizosphere organisms that change with season, soil depth, age of tree, tree species and other factors.

Working on a National Science Foundation grant, Topa's lab is using novel molecular techniques to identify the mycorrhizal communities that colonize the roots of fast- and slow-growing loblolly pine families from different geographic regions of the southeast. Her theory is that different mycorrhizal species may colonize different loblolly pine families and that the tree's genetics may control which mycorrhizal species are able to colonize its roots. Preliminary data suggest that her theory is correct and that functioning of the mycorrhizal root and its overall effect on tree growth varies depending upon host/mycorrhizal genotype.

In the course of their 2003 research, Topa and her colleagues also found that nitrogen-fixing bacteria are associated with these mycorrhizal roots. This unique association has not been previously reported for southern pines, and may increase growth and survival of loblolly pines in nutrient-poor environments.





Joyce M. Van Eck

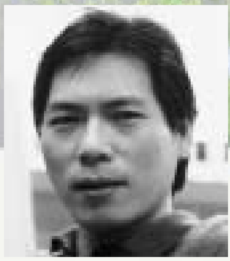
Ph.D., Senior Research Associate,
Plant Biotechnology

How do plants resist disease and accumulate nutrients?

Plants produce and accumulate nutrients important to human and animal health. Some plants also have a natural ability to resist disease. Joyce Van Eck, Ph.D., is working to determine the genetic basis of these important plant functions with an ultimate goal of increasing nutrient levels in crops and understanding their ability to ward off disease.

In 2003, funded by the Triad Foundation and the Helen Graham Foundation, Van Eck was able to enhance the amount of beta-carotene – the precursor of Vitamin A – produced by a yellow-fleshed variety of potato. The potatoes used in her research have the potential to produce large amounts of beta-carotene, but most of the beta-carotene they make is converted into a less nutritious component, called zeaxanthin. By blocking the gene responsible for the conversion, Van Eck produced potatoes with 8 percent more beta-carotene. Increasing beta-carotene production in potatoes even further will be the next step in her research.

Van Eck is also collaborating with BTI's Gregory Martin to identify the genes involved in a plant's natural resistance to disease. In 2003, Van Eck identified and partially sequenced two genes from the model plant, *Nicotiana benthamiana*, that may be involved in resistance to bacterial speck disease. As part of a continuing National Science Foundation grant, Van Eck is working to find the counterparts to these genes in tomato and determine whether they contribute to its protection from bacterial speck disease as well. Her work could have important implications for understanding plant immunity.



Haiyang Wang

Ph.D., Assistant Scientist, Plant Developmental Biology

How does light influence plant development?

Light is a major environmental signal that influences plant growth and development. By interpreting light, plants know when to germinate, how tall to grow and when to flower, among other responses. Understanding the genetic and molecular basis of this ability in the model plant, *Arabidopsis*, is the focus of research conducted by Haiyang Wang, Ph.D.

Plants utilize several photoreceptors to detect various aspects of their light environment, including its direction, duration, quantity and wavelength. Photoreceptors transmit light signals to the cell nucleus where photoresponsive genes are activated, leading to light-controlled plant development. One of these photoreceptors, called phytochrome A, is largely responsible for plant responses regulated by far-red light and is Wang's primary research interest. Over the past year, he has identified a number of mutants defective in phytochrome A signaling. Next, he will work to clone the corresponding genes and understand their function.

Working with Xing Wang Deng of Yale University, Wang is also studying the molecular and biochemical mechanisms underlying phytochrome A's ability to relay light information to target genes. They've found a molecule, called SPA1, that represses the plant's response to far-red light by interacting with another molecule, called COP1. They've also demonstrated that the COP1/SPA1 interaction defines a critical regulatory step in phytochrome A light signal transduction. Their work will be instrumental in scientists' ability to enhance food quality and yield in crop plants.

David A. Weinstein

Ph.D., Associate Research Scientist,
Plant Ecology

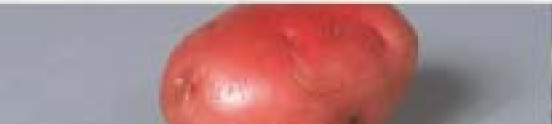
What are the signals that cause biological systems to change over time?

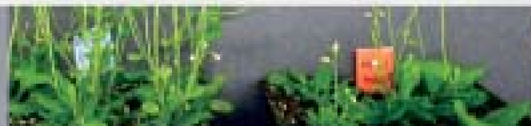
Every biological system, whether it is a single cell or an entire forest, changes over time in response to its environment. These changes are often subtle and minute, making them difficult to identify. David Weinstein, Ph.D., is developing computer software that uncovers the signals that tell cells and ecosystems to change based on patterns (clusters) in data gathered over time.

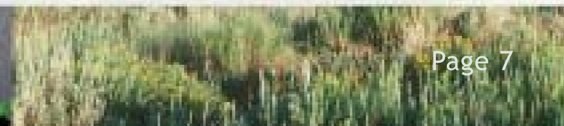
In previous work, Weinstein and his colleagues developed computer simulation software that enabled them to determine nitrogen pollution patterns in forested watersheds using data collected since the 1970's. The research revealed that changes in soil temperature and moisture, rather than atmospheric nitrogen levels, signaled changes in the ecosystem's overall nitrogen production.

In 2003, Weinstein began adapting this clustering software to detect biological signals over time at the cellular level. Working with other scientists at BTI, Weinstein is using existing data to track molecular processes within cells by analyzing the concentrations of certain proteins in the cells over time. The long term objective is to determine the signals, based on computer modeling, that tell the cell to turn certain processes on or off. Weinstein's research will provide biologists with an important tool for understanding the complex genetic pathways within cells that signal key physiological changes.

Weinstein also is testing the ability of his computer software to find biochemical pathways within cells with minimal data. The idea is to generate a list of alternative pathways and estimate the probability of their importance. The software will help other scientists understand the genetics of cellular systems through a more efficient use of their existing data.







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IN MEMORIAM: Lawrence Bogorad

We are very saddened by the death of Lawrence Bogorad on December 28, 2003 due to a stroke. Laurie was a strong supporter and dear friend of the Institute for nearly two decades. He joined the Board of Directors in 1988 and served as chair of the Research Oversight Committee (ROC) from 1988 to 2001. He continued as a Board Director and as a member of the ROC until his death.

Laurie was an exceptionally kind, gentle and thoughtful person, who was admired and highly respected by the Institute staff and his fellow Directors. His wise counsel, good judgment, and friendship will be sorely missed.

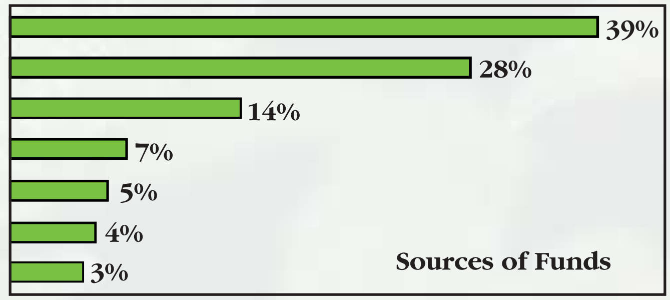
To honor and celebrate Laurie's extraordinary life and more than one-and-a-half decades of exceptional service to the Boyce Thompson Institute for Plant Research as a Board Director, the Institute has established the Lawrence Bogorad Molecular Plant Biology Fund in his honor to support postdoctoral fellows and distinguished lecturers at the Institute.

Uses of Funds

Research	$ 9.691,000	75%
Administration	1,393,000	11%
Research support services	861,000	7%
Equipment & facility	547,000	4%
Non-research	231,000	2%
Fund raising	181,000	1%
	$ 12,904,000	100%

Sources of Funds

U.S. Government funding	$ 4,636,000	39%
Institute endowment funding	3,389,000	28%
New York State funding	1,754,000	14%
Foundation funding	830,000	7%
Unrestricted revenues	554,000	5%
Corporate funding	455,000	4%
Other private funding	389,000	3%
	$12,007,000	100%



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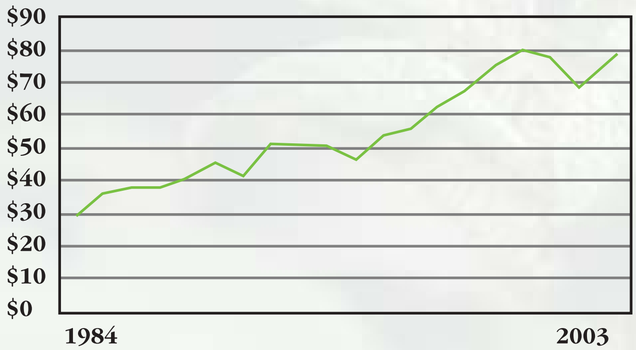
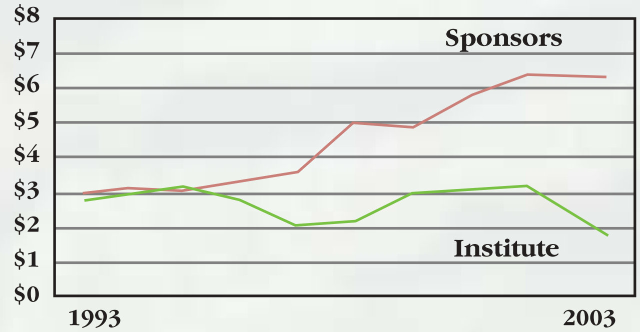


Research Funding (millions)



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