

79th Annual Report
Boyce Thompson
Institute for
Plant Research
2002



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LETTER FROM THE PRESIDENT

The Institute had an outstanding year.



In one measure of success, BTI scientists continued to garner significant external research support. Grant and contract revenue for 2002 reached an all time high of \$6.6 million, with more than two-thirds of the new research grants (\$4.7M) provided by U.S. government agencies, particularly the National Science Foundation.

The Institute also had a successful year of discovery, as measured by the publication of our scientists' research results in top-tier journals. A number of articles have or will soon appear in such respected publications as *The Proceedings of the National Academy of Science*, *The Plant Cell*, *The Plant Journal* and *The Journal of Biological Chemistry*. In addition, Greg Martin and Jim Giovannoni's teams have each published high profile/high impact research in the premier scientific journals *Cell* and *Science*, respectively. 2002 also was a year of transition with the departure of three faculty members and the hiring of three new scientists (see opposite page).

The Institute's 2001 Reallocation Process and a new Development Program, under Dorothy Reddington's direction, bore abundant fruit in 2002. We received a multi-million dollar grant from Atlantic Philanthropies to develop the new Molecular and Chemical Ecology Program in collaboration with Cornell University; a new Plants and Human Health Grant from The Park Foundation; a new postdoctoral fellowship program sponsored by the Francis Goelet Foundation; a major equipment grant from Monsanto, which is transforming the Institute's plant growth facilities; and a large NSF-sponsored multi-user equipment and instrumentation resource grant co-authored by Tom Brutnell and Greg Martin.

Renovation and upgrading in 2002 included a new central service area for glassware and media preparation and for lab supplies; a new library resource center for the digital age; the renovation of seven laboratory modules and accompanying offices; and a massive overhaul of the management and accounting system, including new hardware and software. Larry Russell, Director of Operations, and John Dentes, Vice President for Finance and Operations and Treasurer, continued to do a remarkable job in overseeing this extraordinary transformation of the Institute.

From an economic standpoint, the Institute also had a good year. Though the U.S. equity markets lost in excess of 22 percent in 2002, BTI's endowment declined by only 7 percent. The Institute's financial well-being is a result of the Investment Committee's expertise, led for many years by Chris Hohenlohe, Chairman. Chris, who served as a BTI board member for 31 years before his retirement in May, provided leadership, wisdom and judgment that will be greatly missed.

The Institute's scientific, administrative and support staff have exhibited remarkable cooperation, patience and tolerance during a somewhat difficult year. Their dedication and commitment to BTI were essential in making 2002 "a very good year" for the Institute and helped ensure an even brighter future.

A handwritten signature in black ink, reading "Ronel M. King".

Comings – 2002



Maria Harrison, Ph.D., assumed the position of Scientist at BTI in February 2003.

Dr. Harrison, who is a native of Great Britain, received her bachelor of science degree from the University of Newcastle Upon Tyne in England and her Ph.D. from the University of Manchester. She completed a postdoctoral

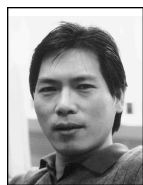
fellowship at the Samuel Roberts Noble Foundation in Ardmore, OK, where she has worked as a Staff Scientist in the Foundation's Plant Biology Division since 1990.

Dr. Harrison studies arbuscular mycorrhizal symbiosis and phosphate transport using the model plants *Medicago truncatula* and *Arabidopsis thaliana*.



Assistant Scientist **Georg Jander, Ph.D.**, was born in Koenigstein, Germany, and raised in Lawrence, KS. Dr. Jander received his bachelor's degree in computer science from Washington University in St. Louis and his doctoral degree in microbiology and molecular genetics from Harvard. He joined BTI from

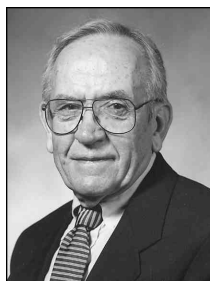
Cereon Genomics in Cambridge, MA, because, he said, BTI offered him "a unique combination of small town life and an excellent plant research environment." Dr. Jander studies plant/insect interactions using *Arabidopsis thaliana* (mouse ear cress) and *Myzus persicae* (green peach aphid).



Haiyang Wang, Ph.D., Assistant Scientist, came to BTI in July from Yale University, after completing a postdoctoral fellowship in molecular genetics. Born in Hangzhou, China, Dr. Wang received his bachelor and master's degrees from Zhejiang University and Northwest University of China, respectively,

and his doctoral degree in biology from the University of Michigan. He chose BTI because "it provides a super research environment and a reputation that will help to attract the top graduate and postdoctoral students." Dr. Wang studies light signaling transduction in plants.

In Memoriam



On August 17, 2002, **Dewayne C. Torgeson, Ph.D.**, died at the age of 76 in Ithaca, NY. Dr. Torgeson joined BTI in 1952 as a plant pathologist. Subsequently, he served as program director for bioregulant chemicals and then as corporate secretary until his retirement in 1990. He also served on the Board of Directors of both the Boyce Thompson Institute and the Boyce

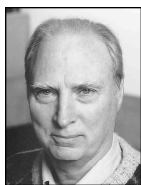
Thompson Southwestern Arboretum. Dr. Torgeson received a B.S. degree in botany from Iowa State University and a Ph.D. in plant pathology from Oregon State University.

Goings – 2002



After 38 years with BTI, **Robert R. Granados, Ph.D.**, virology, retired from the Institute in December 2002. Dr. Granados' recent research concentrated on novel methods of non-chemical insect pest control using baculovirus proteins. An integral member and director of BTI's Insect Biology Group, Dr. Granados developed cell

culture and insect control technologies at BTI that have received over 40 U.S. and international patents. His insect cell line, called High Five™, is used internationally for the production of proteins used in biological and pharmaceutical research.



Patrick R. Hughes, Ph.D., entomology, also retired at the end of December after 34 years with BTI. Dr. Hughes, who joined the Institute at its Grass Valley, CA, forest research laboratory, has spent his career studying various aspects of insect/plant, insect/environment and insect/virus interactions. Also an integral

member of BTI's Insect Biology Group, Dr. Hughes concentrated most recently on the development of methodology for isolating and culturing stem cells from insects.

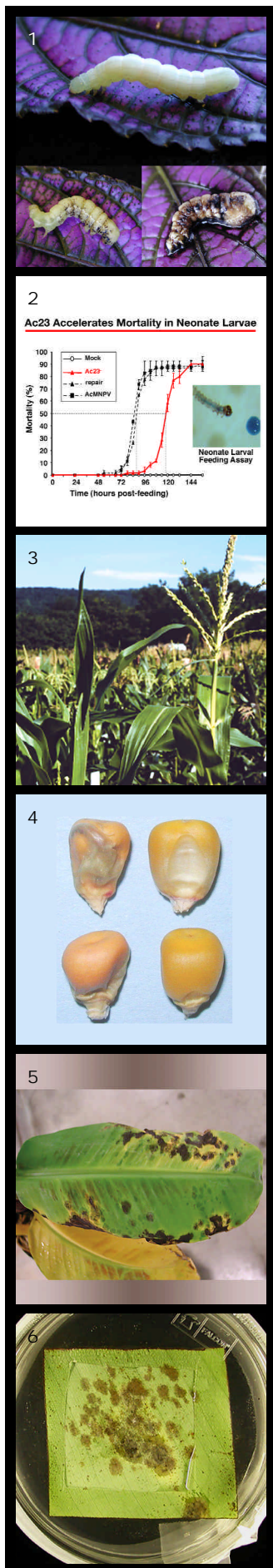


Hugh S. Mason, Ph.D., plant molecular biology, accepted a position as associate professor at Arizona State University to continue his research on plant-made vaccines with Charlie Arntzen, Ph.D., who joined the ASU faculty in 2000. Drs. Mason and Arntzen joined BTI in 1995; Dr. Arntzen is president emeritus of BTI

and a member of President George Bush's Council of Advisors on Science and Technology.

BTI Faculty & Staff





Studying the Genetic Basis of Infection by Baculoviruses (1, 2)

Like other viruses, baculoviruses infect insect cells by first attaching to the host cell's membrane. Once attached, they enter the cell, commandeer its genetic machinery and duplicate themselves in large numbers. Then, they exit the cell and repeat the process again and again. Understanding how viruses enter, exit and commandeer cells by studying baculoviruses could lead to innovative therapies for humans or targeted methods to control specific insect pests.



Gary Blissard works to understand the function of certain proteins found on the surface of the baculovirus membrane, or envelope. In earlier work, he proved that an envelope protein called GP64 enables baculoviruses to attach to

and enter host cells. Recent genomics research has revealed, however, that not all baculoviruses have a gene for the GP64 protein, but that all of them have an envelope protein gene called "F." In 2002, Blissard's group showed that in baculoviruses that do not contain GP64, the F protein functionally substitutes for the GP64 protein.

Because all baculoviruses contain an F gene, Blissard's group next investigated what role F proteins play in baculoviruses that also contain the GP64 protein. In those viruses, they discovered that the F protein is not essential, but that it does affect the virulence or aggressiveness of the viral disease. Blissard's group found that when the F protein was present, the virus was able to kill its insect host much more rapidly. Thus, these studies have shown that the F protein is an important virulence factor that probably contributes to the success of these viruses in nature.

Enhancing a Plant's Response to Light (3, 4)

Plants adjust their growth and productivity to the amount of light they receive, growing taller and yielding less when they are shaded – even minimally – by other plants. Understanding which genes control a plant's reaction to light could lead to crops that yield more under less than ideal light conditions.



Thomas Brutnell works to understand the light signaling pathway in crop plants. Previous work with the model plant *Arabidopsis* showed that the photoreceptor, Phytochrome B, is important in regulating the plant's growth response to shade produced by neighboring vegetation. In 2002, he confirmed that the phytochrome system is also important for the regulation of height and flowering time in corn.

Brutnell discovered a mutant line of corn that grows as if it is shaded even when it is not. In studying the mutant line, he discovered that its phytochrome system contains a defective gene, which causes the corn to flower early and "lodge" (the stalks tend to fall over). These physical manifestations of the defective gene confirm Brutnell's hypothesis that the phytochrome system is central to light signaling in corn, just as it is in *Arabidopsis*.

In parallel research, Brutnell discovered that another phytochrome gene, Phytochrome A, is linked to yield in rice. In collaboration with Dr. Ray Wu of Cornell, Brutnell and colleagues found that increasing Phytochrome A production in rice results in plants that are shorter and yield more than typical varieties. Brutnell's research could have important implications for increasing the productivity of staple food plants.

Understanding the Genetics and Chemistry of Bioactive Fungal Metabolites (5, 6, 1 on next page)

In nature, fungi produce chemicals with unknown biological activities. Some cause disease in plants and animals, while others have potential as human therapeutic drugs. Of the estimated 1.5 million fungal species on Earth, few have been analyzed for their potential to produce beneficial natural products.



Alice Churchill works to identify genes in fungi that produce the bioactive compounds – called secondary metabolites – that cause disease in plants and insects or can be used to treat disease in people. In 2002, her group completed a

1. A cabbage looper larva is infected with the baculovirus AcMNPV. The cabbage looper is an important agricultural pest.

2. The baculovirus F protein (Ac23) causes a dramatic acceleration of mortality in infected insect larvae.

3. The phytochrome deficient mutant, *elongated mesocotyl1*, flowers earlier and is taller than its wild-type sibling.

4. Mutant kernels, right, accumulate high levels of lycopene, resulting in pink endosperm and embryo tissues. Wild-type kernels shown at left.

5. Banana leaf infected with *Mycosphaerella fijiensis*, the most destructive pathogen of bananas worldwide.

6. Banana leaf disk assay to assess disease caused by *Mycosphaerella fijiensis*.

molecular screen of more than 150 fungi and found that many contain novel genes whose products could have potential pharmaceutical use. The next step is to understand how these genes are expressed in the fungi so that the compounds can be produced in quantity in the laboratory and screened for their bioactivity.

Churchill also is working to understand the roles of fungal natural products in host-parasite interactions, which could lead to novel strategies to control harmful insects or plant diseases. In one study, her group identified regions of the chestnut blight fungus genome predicted to encode genes for a family of bioactive pigments produced by this devastating tree pathogen. Churchill's group also is identifying disease-causing genes from a fungus that plagues bananas and plantains worldwide.

Determining the Genetic Basis of Plant Water Use Efficiency (2, 3)

Plants differ in their response to environmental conditions. Some species are physiologically specialized to tolerate drought or heat, while others are specially adapted to other environmental conditions. Determining the genetic basis of physiological specialization among species will yield important knowledge that, one day, could improve the productivity of crop plants.



Jonathan Comstock aims to understand why some plants use water more efficiently than others by comparing cultivated tomato and rice varieties to their wild relatives. His research interest is to discover whether the cultivated and wild varieties of a species differ in their water use efficiency and to identify the genes that direct that trait.

In 2002, 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. He also confirmed that all the varieties exhibit similar changes in their water use response when temperature or soil type changes.

Using genetic analyses, Comstock found two or three regions on the chromosomes of both rice and tomato that are critical to water use efficiency. The next step, which will take several years to complete, is to identify the specific genes in those regions that control water use in the plants.

Determining the Genetic Basis of Ripening in Fruit (4, 5, 6)

Ripening enhances the texture, color, flavor and nutrient value of fruit – traits that contribute to its healthfulness and desirability as a food choice. Understanding the principles of fruit ripening and the specific pathways that contribute to it may provide ways to enhance the ripening process and, therefore, the desirability and nutritional value of fruit.



James Giovannoni is studying the production of lycopene in tomatoes, which are the best source of this important antioxidant. Lycopene provides the red pigment characteristic of ripe tomatoes, but mounting data also suggests

that it inhibits degenerative diseases, such as cancer and heart disease, in addition to being a substrate for Vitamin A synthesis in the human body. Understanding how tomatoes accumulate lycopene in large quantity could enable scientists to provide these attributes to other fruits as well.

In 2002, Giovannoni's lab isolated two genes that activate ripening in tomatoes. As regulators of other genes involved in the process, the two isolated genes (RIN and NOR) are part of the fruit's master switch for ripening. At least one of the isolated genes (RIN) also appears to be a key ripening regulator in other species as well, including strawberries and bananas. Until this discovery, the best characterized cause of ripening was the production of ethylene by the plant (now known to be regulated by RIN and NOR).

In a new research project, Giovannoni's team is using genomics to explore lycopene production in tomato varieties that produce differing amounts of the antioxidant. Their goal is to determine whether genetic variation among the varieties correlates with their ability to accumulate higher



1. A germinated spore of the banana pathogen, *Mycosphaerella fijiensis*, just prior to penetration of a banana leaf stomate.

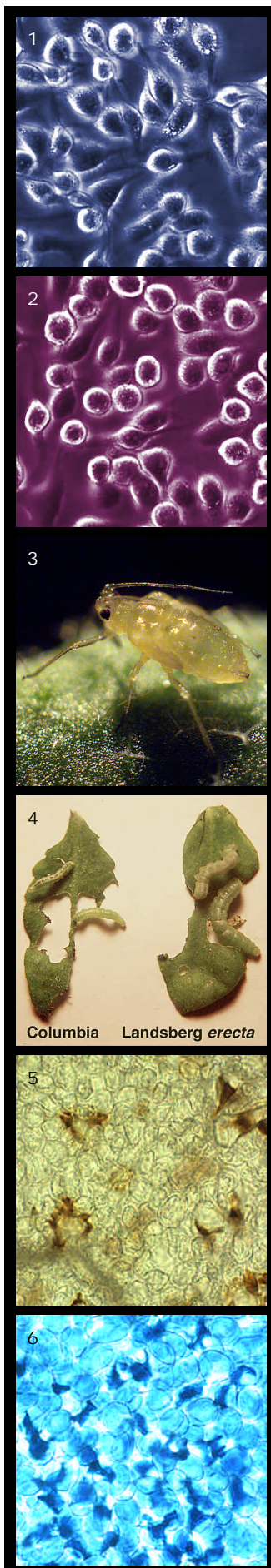
2. A tomato variety used in an NSF-funded project to investigate water use efficiency in plants.

3. A rice plant in full flower.

4. A cluster of high lycopene ripe tomato fruit.

5. Top: Developmental time course of a normal tomato. Bottom: A tomato carrying a mutation in the RIN gene does not ripen.

6. Antisense technology proves that a gene, LeMADS-MC, thought to regulate ripening actually regulates sepal development.



or lower levels of the nutrient, which might point to additional regulatory genes impacting levels of this important compound.

Using Insect Cells and Viruses To Benefit Agriculture and Human Health (1, 2)

Understanding, at the genetic level, how baculoviruses cause disease in insects can lead to new methods of insect control for agriculture that don't require the application of chemical insecticides. At the same time, developing cell culture systems for producing baculoviruses may lead to new production methods for human and animal pharmaceutical proteins.



Robert Granados has spent his career at BTI researching both applications. In the process, he has isolated a protein from baculovirus, called enhancin, that could be used to control insect pests that damage crops,

either by applying the protein to the crops in the field or engineering it into the crop plant itself. He also has developed a patented insect cell line, called High Five™, that is used to produce human and animal pharmaceutical proteins, such as enzymes, reagents and vaccines, for both research and commercial purposes.

In 2002, Granados and his colleagues improved on their extremely prolific High Five™ cells. They cloned single cells from the High Five™ line and then meticulously screened the isolates for protein production capability. In the process, the team identified two isolate clones that can produce pharmaceutical proteins at twice the level of the original High Five™ parent cells. Granados has applied for a BTI patent for the new cell line and currently is discussing licensing agreements with several companies for the use of the superior cells.

Understanding the Genetic Basis of Plant-Insect Interaction (3, 4)

Plants produce a wide variety of toxins and repellents in response to insect attack. Insects, however, often circumvent these barriers by developing resistance. In some cases, insects are even attracted by compounds that normally

provide plant defense. Understanding the complex signaling pathways that trigger plant-insect interactions is important for the future development of crops that naturally ward off insects more effectively.



Georg Jander is studying this interaction between a model plant, *Arabidopsis thaliana*, and two insect herbivores, the cabbage looper and the green peach aphid. He has identified mutant lines of *A. thaliana* that are defective in

the production of glucosinolates and serine protease inhibitors. These are, respectively, small molecules and proteins that help protect plants in nature from damage by cabbage loopers. Jander has identified *A. thaliana* lines with altered levels of protease inhibitors, or with a variety of qualitative and quantitative changes in glucosinolate production. In the next phase of his work, Jander will attempt to identify the genes that are responsible for the altered production of these defensive compounds.

Jander also is working with Marina Caillaud of Ithaca College to study genetic variation in the green peach aphid to determine the genetic and molecular basis of its interaction with *A. thaliana*. Because the majority of plant-insect interaction research has focused only on the plant side of the equation, Jander and Caillaud's work should add significantly to scientists' understanding of the complex interactions between plants and insect herbivores.

Understanding How Plants Protect Against Pathogens (5, 6)

Plants protect themselves from disease through an ancient system, called "innate immunity," that is also shared by people, insects and other animals. Understanding how this system works in plants at the molecular level could help scientists

improve plant immunity to pathogens. It also could provide important insights into the human immune system.



Daniel Klessig's laboratory is studying the signaling networks

1. The original High Five™ cells, which are widely used around the world for expression of recombinant proteins.

2. A new cell clone (clone F) derived from the original parental High Five™ cell line. This new clone is superior to the original cell line in producing recombinant proteins.

3. Green peach aphid feeding on *A. thaliana*.

4. Cabbage loopers feeding on *A. thaliana* leaves. The caterpillars on the right are larger due to biochemical differences in the plant lines.

5. A gain-of-function mutation (*ssi4*) in a resistance gene of *Arabidopsis* leads to spontaneous H₂O₂ generation, visualized by DAB staining.

6. Cell death, visualized by trypan blue staining.

that activate a plant's immune system in the presence of pathogens, such as bacteria or viruses. Recently, he and his colleagues identified a protein located in the chloroplasts of tobacco that plays a role in transmission of the defense signal, salicylic acid. The protein, called carbonic anhydrase, was previously thought to be involved primarily in photosynthesis. When the gene that controls the production of the protein was silenced, however, the plant's immune response was significantly altered. This surprising result has added important information to the knowledge base concerning plant defense signaling pathways.

Klessig and his colleagues also discovered a mutant *Arabidopsis* plant that exhibits higher resistance to disease than a normal plant. They found that the mutation is in a disease resistance gene, which makes the encoded protein continuously active, signaling the plant's immune response to turn on even in the absence of a pathogen. This important discovery now allows the team to study defense signaling mechanisms in *Arabidopsis* without the complicating presence of the pathogen – an advance that may simplify their understanding of the complete plant defense pathway.

Studying the Effect of Ozone on Plant Diversity (1, 2, 3)

Ozone is the most widespread air pollutant in the United States and the one most harmful to plants. Though its impact on the genetic diversity of sensitive native plants is not known, it could be significant.



Robert Kohut is developing a research project to assess the effects of ozone on the genetics of three sensitive plant species: spreading dogbane, big-leaf aster and quaking aspen. He plans to work at Cape Cod National

Seashore where plants are exposed to high levels of ozone, and at Acadia National Park in Maine and Roosevelt Campobello International Park on the U.S./Canada border where plants receive moderate and low levels of exposure, respectively.

Kohut's goal is to determine whether exposure to ozone has reduced the genetic diversity of these

plants. To do that, he will obtain leaf tissue from plant populations in the parks and analyze the tissue to determine genetic diversity. He will propagate whole plants from root sections collected in each park and expose them to ozone to determine their sensitivity. By comparing the genetic diversity of the populations and their levels of ozone sensitivity, he will determine whether higher ozone levels have had a negative impact on the genetic diversity of each species.

Identifying Genes Required for Disease Resistance (4, 5, 6)

All plants have an ancient immune system that helps them ward off disease. Identifying the genes that play a role in resistance and then understanding the function of the proteins they express is important to understanding how plant immunity works.



Gregory Martin is studying the immunity of tomato to a pathogen called *Pseudomonas syringae*, which causes bacterial speck disease. His work is funded by a grant from the National Science Foundation Plant Genomics Program. He

previously identified over 400 genes in tomato that are involved in the plant's response to the pathogen. In 2002, his laboratory discovered that expression of 230 of those genes increases significantly during resistance response (expression of the others decreases in the presence of the pathogen). Martin is now using a simple technique to "knock out" each of the 230 genes – one at a time – to see how resistance to speck disease is affected. His goal is to identify which of the 230 genes play the most important role in plant defense.

Once this smaller subset of genes is known, Martin will use biochemical analyses to understand how the proteins they encode provide resistance to speck disease in tomatoes. What he learns will have important implications for understanding exactly how immunity works in other plant species as well.



1. Ozone injury on big-leaf aster at Acadia National Park, Maine.

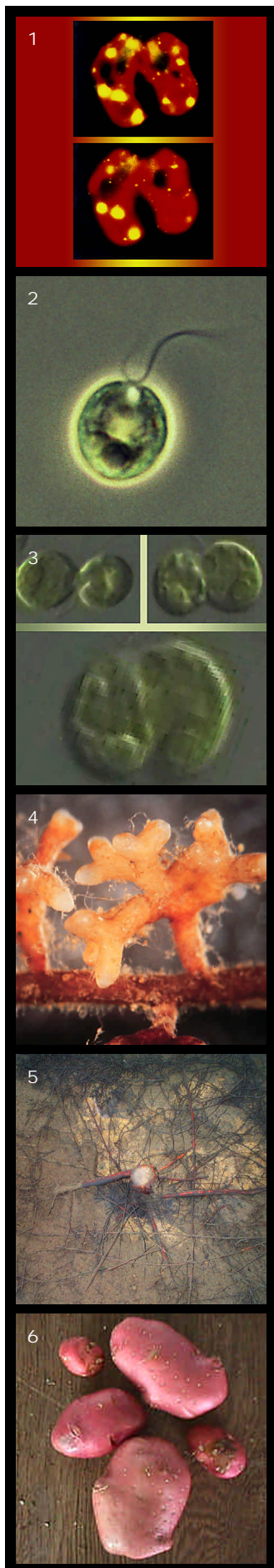
2. A woodland stream flowing through Acadia National Park, Maine.

3. Ozone injury assessment site of big-leaf aster at Acadia National Park, Maine.

4. DNA Microarray Spots. Computer generated image derived from confocal laser scan.

5. A visual representation of a microarray expression pattern.

6. Surface plot of microarray background intensities.



Defining the Genetic Basis of Intracellular Communication with Chloroplasts (1, 2, 3)

When plants are challenged by abiotic stresses, such as nutrient deficiencies in the soil, they respond through intracellular communication. When stressed, the plant's cells initiate defensive measures, such as using available nutrients more slowly, reducing their metabolic rates, or mobilizing internal nutrient stores. Plants also increase root growth, and secrete enzymes that break down elements in the soil into the nutrient components they require for survival and growth.



David Stern studies the chloroplasts of algae and plants to better understand intracellular communication at the genetic level. Chloroplasts are organelles that carry out photosynthesis and produce other substances needed

for plant growth. By understanding what happens in the chloroplast under environmental stress, Stern will be able to define the signaling networks that underlie intracellular communication.

With his colleagues, Stern sequenced the chloroplast genome of an alga, called *Chlamydomonas reinhardtii*, and proved that gene expression in the chloroplast changes significantly in response to abiotic stresses, such as phosphate and sulfur limitation. With a new \$3.8 million, five-year grant from the National Science Foundation, Stern and scientists from Cornell University and the University of Nebraska will study similar communication networks in corn, a major crop species.

Using microarray technology, proteomics (the study of all the proteins an organism produces) and a large collection of mutant plants, the collaborative research team aims to better understand intracellular communication in corn chloroplasts – knowledge that may one day enhance the agronomic performance of crops that are exposed to abiotic stress from the environment.

Identifying Fungal Communities that Enhance Tree Growth (4, 5)

Certain beneficial fungi, called mycorrhizas, colonize the roots of trees in a little understood

symbiotic relationship. The fungi appear to enhance tree growth while the tree provides much-needed carbon to the fungi. Improved understanding of this relationship could significantly add to the tree physiology knowledge base.



Mary Topa is studying the mycorrhizas that colonize the roots of several families of loblolly pine in North Carolina. Her study, which is funded by the National Science Foundation, aims to identify the mycorrhizal

species that colonize roots of fast- and slow-growing loblolly families to determine whether specific fungal communities significantly influence the rate of tree growth. One question Topa wants to answer is whether there is strong specificity between the tree host and fungal genotypes, and if so, which is in control.

To carry out her research, Topa and her collaborators at the U.S. Environmental Protection Agency laboratory in Corvallis, OR, are developing a new method to identify the fungal species in a particular community through DNA fingerprinting. Once available, the new method will enable her to identify and compare mycorrhizal community structure more quickly and accurately than was possible before.

Ultimately, Topa aims to understand how communities of mycorrhizas alter tree root function, and which fungal communities are most beneficial for tree growth. The results could speed the growth of loblolly pines, the most important tree crop in the U.S.

Understanding Disease Resistance & Nutrient Accumulation in Crop Plants (6, 1 on next page)

Making plants more productive or more nutritious depends on scientists' ability to better understand the genetic basis of plant processes, such as disease resistance or nutrient production. By identifying the genes that are responsible for certain processes and the proteins they produce, scientists may one day be able to adjust the plant's response using its own genetic resources.

Joyce Van Eck is collaborating with BTT's Gregory Martin to identify the genes involved in

1. Chloroplast DNA (yellow) is digested in the mating type minus gamete (right) shortly after mating. Red is chlorophyll fluorescence.

2. Using a phase-contrast microscope, *Chlamydomonas* is magnified about 1000 times.

3. Mating: Under nitrogen deficient conditions, the gametes form a pair with gametes of the opposite mating types and fuse into one zygote within 10-20 min after mixing.

4. The mycorrhizal pine root is colonized by an ectomycorrhizal strain of fungus.

5. Loblolly pine root in the ground after the topsoil was blasted away with air.

6. Greenhouse grown, Desiree potato tubers.

a plant's natural resistance to disease. Working with *Nicotiana benthamiana* as a model system, Van Eck has identified over 100 genes (in addition to the 400 Martin already has found) that may be involved in resistance to bacterial speck disease in tomato. The next step in this research is to discover which of these genes are most important to the plant's immunity.



Van Eck also is working with a unique line of potatoes that has potential for producing large amounts of beta carotene, the precursor of Vitamin A. Funded by a 2002 grant from the Helen Graham Foundation, Van Eck's goal is to genetically block the plant from converting the beta carotene it produces into a component with less nutritive value, called zeaxanthin. If her approach is successful, her work will lead to important new knowledge about ways to improve the nutritive value of crop plants.

Studying the Role of Light in Plant Development (2, 3)

Because of their sessile nature, plants have adapted a high degree of developmental plasticity to optimize their growth and reproduction in response to their ambient environments. Light is one of the major environmental signals governing plant growth and development, including seed germination, direction of growth, flowering time, circadian rhythms, and height. Consequently, light is a critical determinant of crop productivity.

Plants utilize specialized photoreceptors to detect almost all facets of light, including direction, duration, quantity and wavelength. Through distinct intracellular signaling pathways, these photoreceptors transmit the light signal to the nucleus to modulate the expression of photoresponsive genes, and, consequently, plant growth and development.



Haiyang Wang is studying light control of plant development in the model system *Arabidopsis thaliana*. Wang's group uses a variety of high technology approaches, such as forward and

reverse genetics, biochemistry, genomics and proteomics techniques to identify novel components of the light signaling pathways in plants and explore the molecular and cellular mechanisms that mediate the signaling process.

The results of Wang's research may lead to novel ways to modify crop plants by genetically fine-tuning their responsiveness to light – an advance that would enable the crop plants to achieve optimal growth and greater yield under varying ambient light conditions.

Using Computer Models To Study Nitrogen Pollution (4, 5, 6)

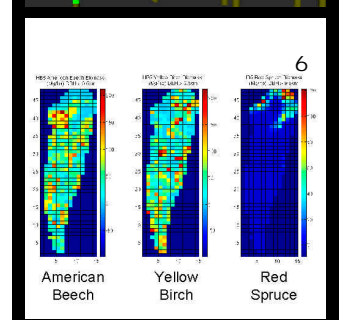
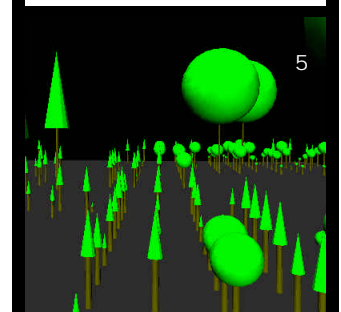
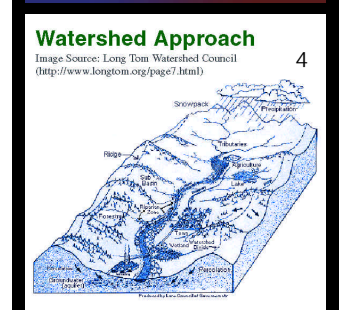
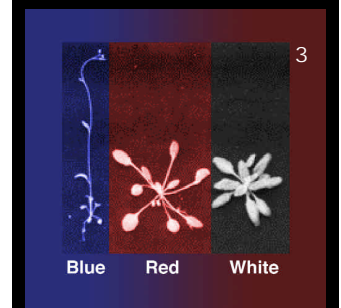
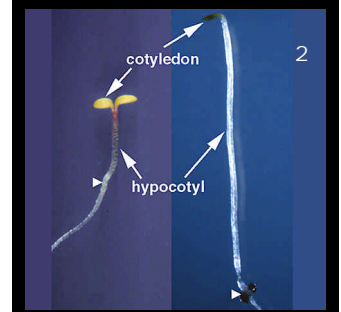
When nitrogen – in the form of nitrates – washes into streams and lakes from watersheds, it pollutes the water and endangers both fish and human health. It has been argued that nitrate pollution in streams in the U.S. northeast is a result of nitrogen deposition on forests from the atmosphere. Interestingly, nitrate pollution in the streams that drain these forests is lower today than in the 1970s, yet the amount of nitrogen in the air is about the same.



To explain this phenomenon, **David Weinstein** and colleagues developed a computer simulation model that enables them to artificially manipulate the nitrogen cycle in forested watersheds to identify the process

responsible for lowering the amount of nitrates in drainage stream water. By replacing current weather patterns with those of the 1970s in the computer model, the team has discovered that high nitrate production in watersheds occurs only when there is a specific combination of soil temperature and moisture.

Weinstein, who uses computer simulation to better understand how trees, forests and entire ecosystems respond to pollutants, has discovered that a reduction in atmospheric nitrogen in forested watersheds will have little or no effect on the amount of nitrates that pollute streams and lakes.



1. Potato plants in a culture box (a plastic container to grow plants under lab conditions).

2. 5-day old *Arabidopsis* seedlings. Wild-type on left. PhyA mutant on right.

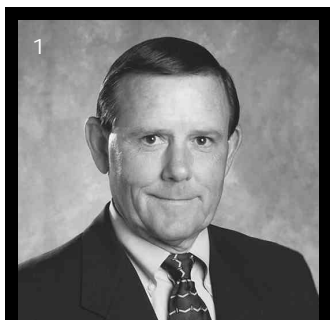
3. Effects of blue and red light on *Arabidopsis* flowering time.

4. A watershed is an area of land that drains into a common body of water, such as a river, a lake or an ocean.

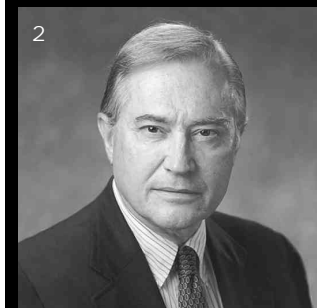
5. Computer simulation can help predict future forest conditions.

6. Spatial distribution maps of forest species at Hubbard Brook Experimental Forest in N.H.

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Arrivals and Departures: For the first time in BTT's history, there are no descendents of the Institute's founder on the Board of Directors. William Boyce-Thompson's great-grandsons, Charles Schulz and Chris Hohenlohe, stepped off the board in May, the latter after 31 years of service.



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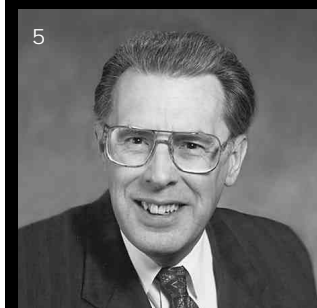
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New Directors are Ted Hullar, Director of Atlantic
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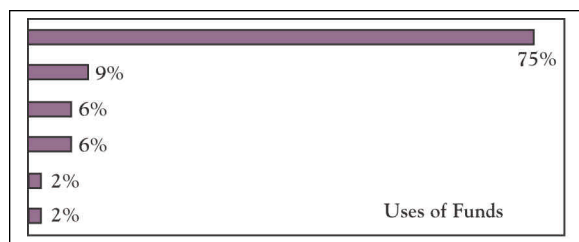
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Boyce Thompson Institute for Plant Research: FINANCIAL REPORT/GIFTS & GRANTS

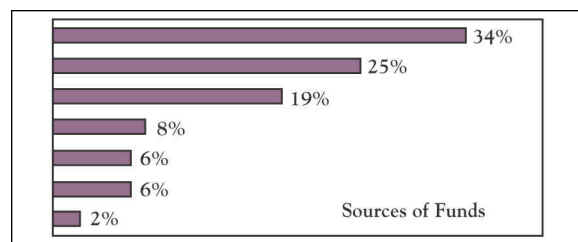
USES OF FUNDS

Research	\$ 10,437,000	75%
Administration	1,222,000	9%
Research support services	880,000	6%
Equipment & facility	820,000	6%
Non-research	256,000	2%
Fund raising	250,000	2%
	<u>\$ 13,865,000</u>	<u>100%</u>

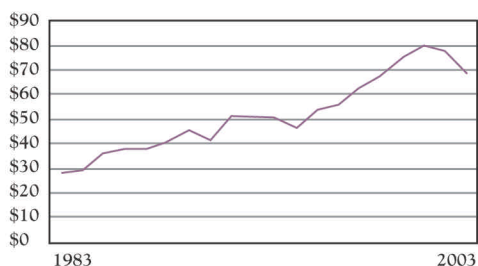


SOURCES OF FUNDS

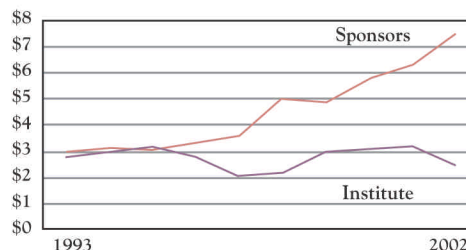
U.S. Government funding	\$ 5,038,000	34%
Institute endowment funding	3,739,000	25%
New York State funding	2,800,000	19%
Corporate funding	1,135,000	8%
Unrestricted revenues	930,000	6%
Foundation funding	948,000	6%
Other private funding	343,000	2%
	<u>\$ 14,933,000</u>	<u>100%</u>



Endowment (millions)



Research Funding (millions)



GIFTS AND GRANTS 2002

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Atlantic Philanthropies
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Anthony T. Gregig*
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The Charitable Lead Trusts Created Under the Will of Francis Goelet*
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