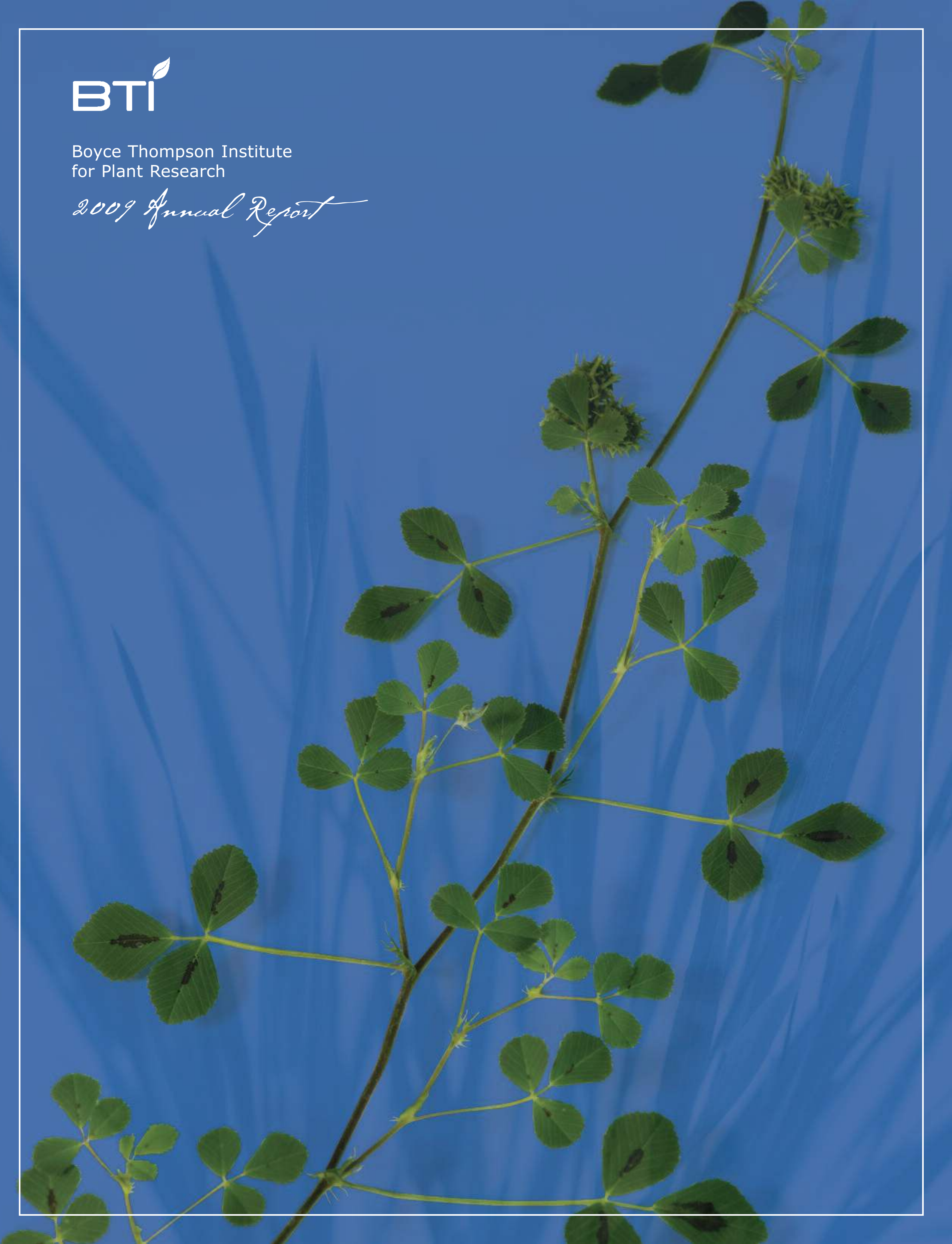
BTI

Boyce Thompson Institute for Plant Research

2009 Annual Report



LETTER FROM THE PRESIDENT

2009 Annual Report

Contents

We know that plants respond to changes in their environment. Too much light, too little water, not enough nutrients and plants either adapt or wither and die.

The past year has been a time for BTI to adapt, as well. In spite of a confining economic climate we continued to do what we do best: plant science research for the benefit of society. Last year presented a host of challenges, but, as you will read in this report, our grant portfolio is robust, our faculty research is thriving, and our supporters are many.

To guide BTI during the next five years, our exceptional staff has developed a comprehensive strategic plan, which includes new mission and vision statements and new values. You may want to read the key elements of the plan, which are posted on our web page at http://www.bti.cornell.edu/sp.pdf. Our new mission statement is rooted in the dreams of our founder and the needs of the future. We believe BTI exists *to advance and communicate scientific knowledge in plant biology to improve agriculture, protect the environment and enhance human health.*

We also completed our sustainability plan in 2009. When the plan is fully implemented, we will achieve further savings in energy use and become even more efficient in our operations. Not only will our efforts save BTI's resources, they will also help to save the earth's resources by continuing to reduce our carbon footprint.

To broaden the impact of our research, we continued our outreach, education and professional development efforts, which attracted teachers, undergraduate college students, high school students and other interested individuals to the Institute. One of the highlights of the year was a lecture by Jane Silverthorne, Ph.D., Acting Deputy Director, Division of Integrative Organismal Systems, at the National Science Foundation. Her talk, "Producing Food for a Hungry World," focused on how basic plant research can contribute to agricultural productivity, and drew a standing room only crowd of attendees. Programs like this would not be possible without our supporters, and we thank you for your continued encouragement.

When I wrote last year's introductory letter, I was hopeful that 2009 would bring positive changes to help us meet the many challenges facing both BTI and the world. I was not disappointed. We have seen bright glimmers of progress over the past year, and I am confident BTI is prepared to flourish in the face of any future challenges that may come our way.

Sincerely,

David Stern, Ph.D.
President

BTI Strategic Plan Completed 2010-2013

BTI's Strategic Plan, completed in 2009, is designed to guide the Institute for three to five years. The plan is the culmination of nine months of collaboration from a broad cross-section of BTI faculty and staff. Key elements of the plan are outlined below.

Mission Statement

To advance and communicate scientific knowledge in plant biology to improve agriculture, protect the environment and enhance human health.

Our Vision for 2013

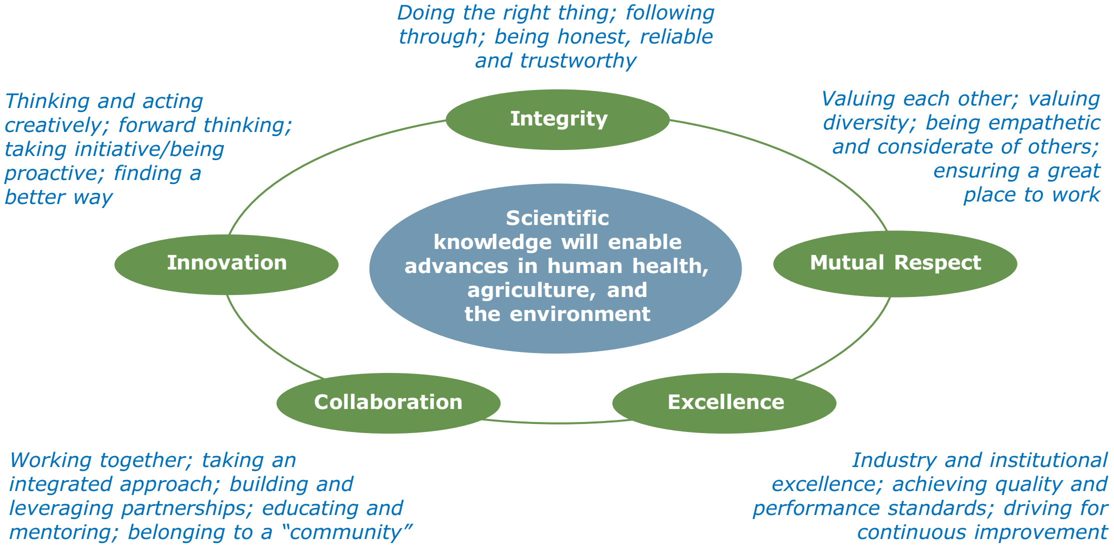
The Boyce Thompson Institute will be known worldwide for research excellence in the field of molecular and chemical plant biology. To accomplish this, BTI will:

- Ensure organizational integration and alignment around a common mission and a common set of goals.
- Promote and advocate for BTI in New York, the U.S. and internationally; attract and retain outstanding researchers, Board members, and staff.
- Be a partner of choice with academia, corporate entities and other research institutes.
- Formalize and implement a comprehensive intellectual property strategy.
- Stabilize long-term funding streams through diversification of funding sources.
- Achieve operational efficiencies and effectiveness.

To achieve this vision, BTI identified four key areas where results are essential:

- Ensure Institutional Alignment
- Develop and Manage the Research Portfolio
- Improve Operational Efficiency
- Develop Contingency Plans

Core Values of BTI Employees



Doing the right thing; following through; being honest, reliable and trustworthy

Integrity

Thinking and acting creatively; forward thinking; taking initiative/being proactive; finding a better way

Innovation

Scientific knowledge will enable advances in human health, agriculture, and the environment

Valuing each other; valuing diversity; being empathetic and considerate of others; ensuring a great place to work

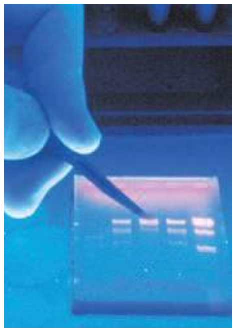
Mutual Respect

Collaboration

Working together; taking an integrated approach; building and leveraging partnerships; educating and mentoring; belonging to a "community"

Excellence

Industry and institutional excellence; achieving quality and performance standards; driving for continuous improvement



IN BRIEF

The Asia Connection: BTI, Asian Universities Collaborate

BTI has initiated research collaborations with universities in China and Taiwan. In one project, Institute scientists are working with scientists from Qingdao University (QU) in the People's Republic of China to develop new generations of insect cell lines which can be used to produce therapeutic proteins, such as vaccines, more economically. The research will take place at BTI and in an advanced culture center at QU, which was built with funds from BTI and the Chinese university.

The second agreement is with National Chung Hsing University (NCHU) in Taiwan. BTI and NCHU will collaborate on biofuels research projects of interest to both parties. The projects will begin in 2010 when two NCHU Ph.D. students travel to BTI to work with our scientists for six-month periods. The idea for the collaboration began in 2008 when David Stern, BTI president, visited NCHU's campus and met with its president.

Maximizing Resources: Establishing Goals for the Future

BTI's sustainability mission is to maximize the use of the Institute's resources without compromising the potential of future research. We have long been a proponent of environmental stewardship to save both the planet and BTI's resources, and we have already made good progress in reducing our energy consumption. Since 2003, our BTU consumption has declined nearly 60 percent.

In 2009, a BTI Sustainability Task Force, made up of a cross-section of BTI staff and faculty, identified several additional sustainable practices which will help the Institute become even more environmentally responsible and efficient. With the assistance of all Institute faculty and staff, the Task Force developed the goals and objectives listed below:

- Reduce printer and copier paper consumption.
- Increase volume of materials recycled.
- Reduce energy consumption by 10 percent more.
- Increase employee utilization and efficiency.

Postgraduate Society Sponsors Variety of Events

By sponsoring special events, speakers and workshops each year, the Postgraduate Society (PGS) facilitates professional development and fosters a sense of community among BTI's postdoctoral fellows, students and technicians.

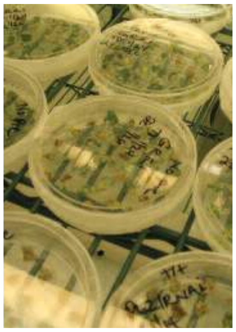
In 2009, the Society hosted Detlef Weigel, Ph.D., of the Max Planck Institute for Developmental Biology as a distinguished speaker. Herman Scholthof, Ph.D., a visiting scholar from Texas A & M University, also delivered a lecture to the PGS. In addition, the PGS hosted lectures by Cornell's Robert Raguso, Ph.D., Neurobiology and Behavior; Michael Scanlon, Ph.D., Plant Biology; Sylvia Lee, Ph.D., Molecular Biology and Genetics; and, Linda Nicholson, Ph.D., Molecular Biology and Genetics.

The PGS sponsored several career workshops in 2009 along with the annual PGS Career Day, which included various perspectives on how to choose a career path in academia or industry. During the annual off-site PGS retreat, members were given an opportunity to present their current research to the BTI community.

Technology Transfer Highlights

BTI's Technology Transfer Office is responsible for the management and maintenance of the Institute's growing portfolio of intellectual property. Intellectual property licensing revenue is an important source of income to the general research budget of the Institute.

- In 2009, we completed an audit of the Institute's intellectual property.
- The Institute was awarded three new U.S. patents in 2009, and filed three new patent applications.
- BTI has more than 20 licensing agreements with a broad range of commercial partners.
- The Institute's patented High-Five™ insect cell line is used in the manufacture of GlaxoSmithKline's Cervarix™ HPV vaccine, which was approved for use in the U.S. by the FDA in 2009.
- The Institute executed more than 40 Materials Transfer Agreements in 2009.



Outreach Broadens Participation, Expands Programs

Education and Outreach remained strong in 2009, reaching nearly 1,800 undergraduates, science teachers, K-12 students and local families. BTI faculty, students and staff educated diverse audiences about basic plant biology research and how this research relates to the environment, agriculture and human health.

- The Plant Genome Research Program Summer REU (Research Experience for Undergraduates), now in its eighth year, attracted 24 undergraduates from across the country and three local high school students to labs at BTI, Cornell and the USDA. The program included laboratory training, mentoring, weekly faculty-led science seminars and workshops, student poster sessions and student talks.
- One of BTI's core goals is to broaden the participation of under-represented groups in plant science research. To that end, Outreach Coordinator Tiffany Fleming exhibited at two national science conferences: Minorities in Agriculture, Natural Resources and Related Sciences (MANRRS) and the Society for the Advancement of Chicanos and Native Americans in Science (SACNAS). Her goal was to raise awareness about career and training opportunities in plant science research at BTI.
- BTI held its annual summer Curriculum Development Workshop in 2009. The program provided intense learning experiences for teachers from New York's large urban school districts, as well as teachers from rural districts. The teachers returned to their classrooms with new plant science curricula and materials. We also sent "Biomass to Biofuel" kits to participating classrooms to support inquiry-based learning.
- A variety of programs connected BTI and the local community. Science-After-School, BTI's hands-on plant biology curriculum, reached more than 120 elementary students, and 82 middle school students explored plant diversity through the "Expanding Your Horizons" and "Focus Day" events.

Honors and Awards

Chang-Sik Oh, a postdoctoral fellow in Greg Martin's laboratory, received the Lawrence Bogorad Molecular Plant Biology Award in 2009. The award was established to honor and celebrate Lawrence Bogorad, who was a scientist and longtime BTI Board member, for his accomplishments in science and his commitment to BTI. The Bogorad Award is given annually to an outstanding BTI postdoctoral fellow, following nominations by BTI faculty. The award, which recognizes research excellence in postdoctoral scientists at BTI, carries a modest cash prize.

Transitions

Peter Moffet, a native of Canada, accepted a position as Associate Professor at the Université de Sherbrooke in Quebec.

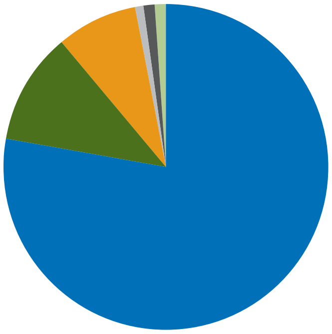
Haiyang Wang accepted a position at Yale University as a Research Scientist and Principal Investigator.

John Dentes, V.P. for Finance and Treasurer of the BTI Board of Directors, announced his retirement after 28 years of service. Working with four BTI presidents and meeting countless challenges, John has been a steady hand and a loyal member of the BTI team. In his "retirement" he will assume new finance responsibilities closer to home in Aurora, NY, at Wells College.

Larry Russell also announced his retirement in 2009. With nearly 11 years of employment at BTI, Larry was largely responsible for spearheading BTI's energy-saving programs and major building renovations during his tenure as Director of Facilities. Larry intends to refocus his energy on projects at his Saranac Lake vacation home.

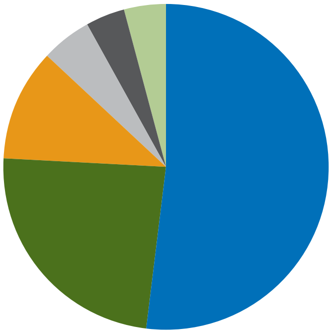
Carl Leopold, an eminent plant physiologist and nature lover, died on November 19, 2009, at the age of 89. Dr. Leopold joined BTI as a Research Scientist in 1977, and was named the William H. Crocker Scientist in 1979. Some of his most important work was in the area of seed physiology, particularly sugars that stabilize components in dry seeds. Dr. Leopold was a constant presence at BTI up to the time of his passing.

FINANCIAL REPORT
2009



USE OF FUNDS

🟦 Research	$12,306,000	78%
🟩 Administration	1,761,000	11%
🟧 Research Support	1,190,000	8%
⬜ Equipment & Facility	106,000	1%
⬛ Non-research	182,000	1%
🟩 Fund-raising	152,000	1%
	$15,697,000	100%



SOURCE OF FUNDS

🟦 U.S. Government	$ 8,121,000	52%
🟩 Institute Endowment	3,745,000	24%
🟧 New York State	1,804,000	11%
⬜ Foundations	764,000	5%
⬛ Other Private Sources	669,000	4%
🟩 Unrestricted Revenue	594,000	4%
	$15,697,000	100%

GIFTS AND GRANTS

GIFTS

William and Anne Boyce Thompson Society
($5000+)
Helen I. Graham Charitable Foundation
Christian and Nora Hohenlohe
William B. Thompson Fund
Triad Foundation

William Boyce and Gertrude Thompson Society
($2000 - $4999)
Philip and Anette Goelet
Carolyn Sampson

Chairperson's Circle
($1000 - $1999)
Greg Galvin
Mr. and Mrs. Paul H. Hatfield
Roy H. and Elizabeth P. Park, Jr.
Laura A. Philips
David and Karen Stern
Ruth Stern
Tompkins Trust Company

President's Circle
($500 - $999)
Anonymous
Evelyn Berezin
Mary E. Clutter
Ezra and Daphne Cornell
John M. and Marie Dentes
Dr. Ralph W.F. and Jacqueline M. Hardy
Susan and Gregory Martin
Sylvia and Leonard Weinstein

Alder Associates
($100 - $499)
Anonymous
Charles and Kathy Arntzen
Holly Beermann
Brian Bell
Tami and Paul Bogausch
Tom Brutnell and Mary Howard
Maria G. Bulis
Dr. Eleanor Storrs Burchfield
James J. and Terry R. Byrnes
Dr. and Mrs. Bruce Cahoon
Cayuga Landscape Co. Inc.
Charlie and Donna Claes
Luke and Greta Colavito
Richard and Joan Curtiss
Robert and Johanna Granados
Stephen and Elizabeth Howell
Ernest G. Jaworski
Lorraine S. and Stephen P. Johnson
Terry and Cathy Lauver
Anthony M. Marzullo Sr.
Dr. and Mrs. Robert C. Miller
Jay and Deborah Miller
Paxton and Cherie Payton
Alan and Anne Renwick
Andrew and Rosemary Sciarabba
Mark and Jane Siegwarth
Donald and Marcia Slocum
Richard and Mildred Staples
Boyce Thompson
Kathryn Torgeson
Lori A. Van Dusen
Mary Westlake
Fred A. (Ben) Williams
Jianjun Yang
Roy A. Young

Friend of BTI
($1 - $99)
Judith A. Bishop
S. Mark Henry
Andre T. and Jean W. Jagendorf
Helene Javot
Carl Leopold*
Robert T. Nelson
William G. Smith
Donald and Susan Waddell
*deceased

GRANTS AWARDED

Government	
Defense Advanced Research Projects Agency:	$ 6,023,083.00
National Science Foundation:	$ 7,931,385.00
Health and Human Services:	$ 1,497,214.80
United States Dept. of Agriculture:	$ 36,058.00
Miscellaneous	
Binational Agriculture Research and Development:	$ 53,500.00
National Engineering Research Center for Vegetables:	$ 35,000.00
International Human Frontier Science Program Organization:	$ 142,700.00
Foundation	
Triad:	$ 250,000.00
Other (Corporate)	
Monsanto:	$ 3,000.00
VILMORIN:	$ 3,000.00
Abbott and Cobb:	$ 3,500.00
Sakata Seed America:	$ 3,500.00
Syngenta Seeds:	$ 3,000.00
Total:	$ 15,984,940.80

BOARD OF DIRECTORS

Officers

Emeritus Directors

IN THE LABS

How do plants respond to environmental stress?

Klaus Apel, Ph.D.

Scientist, BTI

Plants can endure extreme environmental stress (heat, drought, cold or intense light) through genetically controlled defenses, such as wilting, loss of leaves or stunted growth, but these very defenses can also reduce yields, among other effects. As a result, one effect of global warming could be reduced food production just when the world's population is burgeoning.

Understanding how plants sense and respond to stress at the genetic level is the ultimate objective of **Klaus Apel's** laboratory at BTI. His findings could enable scientists to mitigate the negative results of stress, such as yield loss, or fine tune a plant's ability to survive climate change.

It turns out that chloroplasts — the tiny organs that contain chlorophyll and carry out photosynthesis — play an important role in a plant's ability to sense environmental stress. Conditions such as drought, heat, cold and intense light interfere with the normal photosynthetic process in the chloroplasts, which leads to over-production of sometimes toxic forms of oxygen, called reactive oxygen species (ROS).

High levels of ROS were previously considered detrimental to the cell. However, recent work with an *Arabidopsis* mutant by Apel and his research group indicates that the release of one ROS, called singlet oxygen, in the chloroplast actually triggers a variety of positive stress adaptation responses in the plant. These responses include slowed plant growth, cell death, and the activation of a broad range of defense genes, which normally are turned on only in the presence of pathogens.

In further work, Apel's group proved that certain genetic mutations in *Arabidopsis* eliminate the plant's stress responses without interfering with the release of singlet oxygen. It appears these mutations prevent the plant from sensing the presence of singlet oxygen, which, in turn, prevents symptoms of stress. Apel's group has identified these mutated genes, which is a first and crucial step toward understanding the genetic basis of the stress response in plants.

The results of Apel's work could lead to plants that cope better with the environmental stress of global warming. Ultimately, such a discovery could help increase food supplies or predict a plant's susceptibility to environmental changes.

How do viruses infect insect pests?

Gary Blissard, Ph.D.

Vice President for Research and Scientist, BTI

Adjunct Professor, Dept. of Microbiology and Immunology and Dept. of Entomology, Cornell University

Certain viruses are our allies in the fight against insect pests. Research that leads to a better understanding of these viruses could in turn lead to more environmentally friendly, natural insect control, and even to advances in human health.

Among other research projects, **Gary Blissard** is studying how certain viruses, called baculoviruses, infect insects. He and his colleagues have focused on how a particular baculovirus envelope protein, called GP64, enables the virus to invade an insect cell, multiply and then exit in massive numbers.

Blissard's group has found that GP64 has three major functions in the viral infection cycle. First, they showed that GP64 is an attachment protein — a protein that enables the virus to bind to receptors on the surface of the host insect cell, which is the first step in the process of infection. Blissard's laboratory identified the particular portion of GP64 that is necessary for this binding activity.

After the virus binds to the host cell, it enters the cell where it is surrounded by the cell's membrane. To cause infection, the virus must fuse with that membrane and deliver its DNA into the cell nucleus. Having proved that GP64 is independently able to fuse membranes, Blissard's team is now involved in a detailed investigation of how this process occurs.

The third step in the infection cycle calls for new virus particles to emerge or "bud" from the cell surface. To determine whether GP64 played a role in virus budding, Blissard's lab "knocked out" the gene for the GP64 protein, which severely limited virus budding, and the remaining new virus particles were not infectious. These studies show that GP64 plays a critical role in the assembly of the new virus particles. Current studies aim to understand these three major functions of GP64 in much greater detail.

Knowing how baculoviruses infect insect cells may enable scientists to improve the virus' insect control capabilities, which could reduce the use of chemical pesticides. This work also has other exciting applications, such as in gene therapy. Because baculoviruses cause disease only in insects and because they are highly effective at entering cells and depositing DNA in the cell nucleus, they may be excellent vehicles for inserting beneficial new genes into mammalian cells — an advance that could improve our ability to safely correct genetic disorders in humans.

How does maize produce beta-carotene?

Tom Brutnell, Ph.D.

Associate Scientist, BTI

Adjunct Associate Professor, Dept. of Plant Biology and Dept. of Plant Breeding and Genetics, Cornell University

Two BTI laboratories — Brutnell and Van Eck — are studying the genetic basis of beta-carotene production in certain staple foods (see Van Eck, page 14). Beta-carotene is a carotenoid and is the precursor to Vitamin A, which can prevent the eye disease and health disorders that currently plague hundreds of millions of children in the developing world. In their studies with maize, which is low in beta-carotene, **Tom Brutnell's** laboratory is working to enhance beta-carotene production — research that could lead to more nutritious varieties of corn, and healthier diets for some of the world's poorest people.

Brutnell's team previously proved that the enzyme lycopene beta-cyclase is required for the first step in beta-carotene production in maize. However, his laboratory recently showed that co-expression of the lycopene beta-cyclase enzyme with another enzyme, called lycopene epsilon-cyclase, leads to the accumulation of lutein rather than beta-carotene in seed tissues. This is because epsilon-cyclase is often expressed at high levels in seed tissues, where it competes with the beta-cyclase for the lycopene.

Next, Brutnell discovered rare alleles, or alternative forms of the epsilon-cyclase gene, that are associated with high levels of beta-carotene production. Brutnell's laboratory then used a polymerase chain reaction assay to monitor levels of the epsilon-cyclase enzyme transcripts during maize seed development. These studies confirmed that the gene's expression levels are consistently low in maize lines that produce high amounts of beta-carotene, and high in lines that produce high levels of lutein. Therefore, the ability to single out rare maize alleles with low epsilon-cyclase production could lead to the development of lines that produce more beta-carotene.

To that end, the team developed a polymerase chain reaction tool kit — currently being tested in Mozambique — that enables African corn breeders to identify these rare alleles in North American germplasm and then cross these plants to lines that have been adapted for optimal growth in Africa. The assay is relatively inexpensive, and will help African breeders generate high beta-carotene producing lines of corn.

How do plant hormones control fruit development?

Carmen Catala, Ph.D.

Adjunct Scientist, BTI

Senior Research Associate,
Dept. of Plant Biology,
Cornell University

When home gardeners or horticulturalists grow plants from stem cuttings, they often dip the cut end of the stem in a white powder that encourages the stem to develop roots. The white powder is a hormone, called an auxin, which plays an important role in plant growth and development. Auxins also influence cell division and differentiation, which is why the powder form used by gardeners helps the stem cutting to start growing root cells.

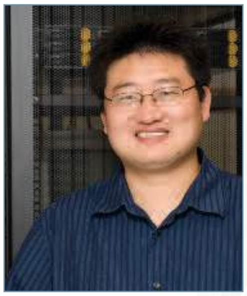
It's also known that auxins, particularly one called indole-3-acetic acid, are central to the development and ripening of fruit, such as strawberries and tomatoes. But very little is known about the molecular basis of auxin production, transport and signalling in fleshy fruit-producing plants. This is the area of research that **Carmen Catala** is pursuing at BTI.

Until now, the majority of research into auxins has been done in the model plant *Arabidopsis*, which is a flowering plant that only produces a dry fruit. Work on auxins has been conducted with strawberries, however, and has proven that the hormone is produced in the tiny seeds that speckle the outside of the berry, and that this auxin helps the fruit grow. It also has been found that when the berry is ready to ripen, the auxin is inactivated. A molecular explanation of how and why this happens in strawberries remains elusive.

Catala is applying knowledge gained about auxins in *Arabidopsis* and strawberries and using new molecular techniques to understand exactly how the auxin indole-3-acetic acid works in tomatoes. She aims to discover how and where this auxin is produced in the plant, how it is transported to the cells that will become fruit, and how it signals the cells in that tissue to grow, develop and ripen. What Catala learns in tomatoes will be applicable to other fleshy fruits as well, including strawberries.

Knowing at the molecular level how auxins help set fruit on plants and how they influence fruit development and ripening could one day lead to higher quality fruits. And, because auxins directly stimulate or inhibit the expression of specific genes, understanding how to control the production or transport of these hormones could lead to fruits with improved flavor, texture or other unique qualities.

How is massive plant genomics data organized and interpreted?



Zhangjun Fei, Ph.D.

Assistant Research Scientist, BTI

Consider that just one tomato plant contains about 35,000 genes that express thousands of different proteins. Then consider how many different plants are currently under study, and it's easy to understand the enormity of the data generated in biological research.

Organizing that data and making it accessible for further research is an area called bioinformatics. The interface between biology, statistics and computer science, bioinformatics develops computational tools and resources that organize massive amounts of data into usable sets so that the knowledge contained in them can be retrieved, analyzed and applied in biology research. **Zhangjun Fei's** laboratory at BTI develops both the databases and the interfaces needed to help scientists understand how genes work together and how they form functioning cells and organisms. He also has developed analytical and data-mining tools that allow scientists to efficiently extract biological information from the database for use in their research.

Fei has collaborated with the Giovannoni laboratory at BTI to develop databases that contain information on the expression of more than 10,000 tomato genes, as well as profiles of tomato fruit nutrition and flavor-related metabolites, during different developmental stages, upon various stresses, and in different genetic backgrounds.

As a part of International Cucurbit Genomics Initiative, the Fei lab has also developed a database, along with its corresponding interface and tools, for the organization of all the genomics information gathered to date on the cucurbit family of plants, which includes melon, watermelon, cucumber and pumpkins, among others.

Work in Fei's laboratory is providing tools and resources that organize genomics information about an organism into a form scientists can easily use to analyze and visualize the data they've gathered.

What is the genetic basis of fruit development and ripening?

Jim Giovannoni, Ph.D.

Adjunct Scientist, BTI

Plant Molecular Biologist, USDA-ARS Plant, Soil and Nutrition Laboratory

Adjunct Professor, Dept. of Plant Pathology and Plant-Microbe Biology, Cornell University

Fruit is a major source of nutrients and fiber in the human diet, so a better understanding of how fruit develops and ripens at the genetic level could significantly impact the quality and availability of food. This knowledge would be particularly useful in countries where food spoilage due to over-ripening is a root cause of hunger and in areas where people's nutritional requirements are not currently being met.

Jim Giovannoni's laboratory at BTI is working to understand fruit development and ripening by focusing on the genes and regulatory networks that control these processes in fleshy fruits, such as tomatoes, and in dry fruits, such as those produced by the *Arabidopsis* plant. The laboratory recently identified a gene, called *TAGL1*, which is necessary for both the fleshy expansion of pre-ripening fruit as well as the later ripening/seed dispersal process in dry fruits.

The seeds of dry fruits are spread by the wind or carried on the fur of passing animals, while the seeds of fleshy fruits are deposited far from the parent plant by animals that eat the fruit and excrete the seeds. Giovannoni and his group have shown that the gene, *TAGL1*, is a molecular bridge between fleshy fruit expansion and later ripening in tomato. Others have shown that this gene is necessary for silique (opening) in dry *Arabidopsis* fruit. These two discoveries prove that the process of silique rupture in *Arabidopsis* and fleshy fruit development and ripening in tomato, which are very different fruit types, are both controlled by a similar gene.

The next step in the research is to discover how the *TAGL1* gene functions with other fruit development and ripening genes which were previously identified and described by the Giovannoni laboratory and others. Results of this research may lead to new molecular strategies for improving fruit quality and shelf-life, which can, in turn, positively impact food security and human nutrition.

How do soil fungi supply plants with mineral nutrients?

Maria Harrison, Ph.D.

Scientist, BTI

Adjunct Professor, Dept. of Plant Pathology and Plant-Microbe Biology, Cornell University

In nature, certain plants and fungi have evolved a complex, symbiotic relationship in which the plants provide the fungi with carbon while the fungi provide the plants with phosphate needed for cell function and growth. Understanding this relationship could result in scientists' ability to develop plants that require fewer applications of phosphate fertilizers.

Working with a soil organism called arbuscular mycorrhizal fungi and a model legume, *Medicago truncatula*, **Maria Harrison's** laboratory is unraveling the mechanisms underlying mineral transfer from fungus to plant. The fungi, which are ubiquitous in soil, live in close proximity to the plant's roots. The fungal spores grow on the root surface and, in response to a signal from the plant, grow into the cells of the root. Once there, the plant forms a membrane, called the arbuscular membrane, through which the mineral exchange occurs.

Harrison theorized that a particular transporter protein in the arbuscular membrane mediates the movement of phosphorus from the fungus into the plant cell. In 2007, her team demonstrated that this theory was correct. When the plant gene that produces the transporter protein in question was "knocked out," or disabled, phosphate in the arbuscule did not cross into the plant cell.

Harrison's research yielded another, somewhat surprising result. She discovered that in the mutant plant, the arbuscules die very quickly. One interpretation is that the plant, on detecting that the phosphate transfer is not occurring, responds by triggering the death of the arbuscule. Understanding how and why this occurs will be a next step in her research.

Today, growers use fertilizers derived from rock phosphate to enhance plant nutrition, but rock fertilizer reserves are being depleted and at the current rate of use, they will last only an additional 90 years. Furthermore, excessive application of phosphate fertilizers contributes to the pollution of streams. Harrison's work may lead to plants that can use naturally occurring phosphate in the soil more completely and efficiently through enhanced symbiotic relationships with fungi — an advance that would lead to more environmentally friendly, sustainable agriculture.

How do plants ward off insects and produce amino acids?

Georg Jander, Ph.D.

Associate Scientist, BTI

Adjunct Professor, Dept. of Plant Biology, Cornell University

As the human population increases, so does the demand for food, yet there is a finite amount of arable land available for agriculture. To meet present and future needs, scientists are working to develop more efficient, more sustainable agricultural methods that may enable farmers to produce more, higher quality food on existing acres.

One way to do that is to reduce yield losses due to insects, which feed on the plants and spread plant diseases. In fact, insects reduce the average crop yield by 15 percent per year worldwide despite a variety of methods farmers use to control them. Therefore, understanding the interactions between plants and insects and how plants ward off insect attack is one way to increase yields. With that goal in mind, **Georg Jander's** laboratory is studying the biochemistry and molecular biology of plant-insect interactions.

Plants are not passive targets for insect herbivores. Rather, plants recognize that they are being attacked and respond by altering their gene expression to produce toxins that deter further insect feeding. Members of the Jander laboratory are studying how plants recognize feeding by phloem-feeding aphids, which cause relatively little overt damage, but can transmit numerous viral diseases to crop plants. Recent results show that certain components of aphid saliva activate certain defense responses within the plants that make them more aphid resistant. While studying these plant defense responses, Dr. Jander's laboratory identified previously unknown plant metabolites that deter aphid feeding. Ongoing research in the laboratory is directed at identifying plant enzymes that catalyze the formation of these aphid-deterrent molecules.

Dr. Jander's laboratory also studies the complex biochemical and biological systems that enable plants to produce amino acids. Plants are important in the mammalian diet because they produce all 20 amino acids essential for health, while humans and animals can only produce half as many. Understanding the complex network of events involved in the synthesis of plant amino acids can help scientists increase the nutritional value of crop plants. Dr. Jander has been working to understand the regulation of this network. Members of the laboratory have characterized the roles of enzymes involved in the production of two essential amino acids, threonine and methionine. Their work may help increase the nutritional value of potatoes, rice, and other crops. In a new project, which combines the laboratory's two main research interests, Jander and his co-workers have identified an enzyme that catalyzes the biosynthesis of an unusual non-protein amino acid that some plants produce to deter insect feeding.

How do plants protect themselves from pathogens?

Dan Klessig, Ph.D.

Scientist, BTI

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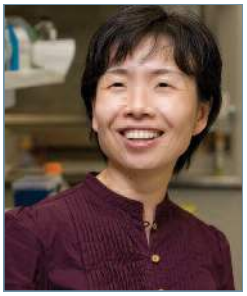
Plants have various ways to protect themselves against pathogens, including preformed physical and chemical barriers and induction of multiple defense responses. Perception of an invading pathogen often involves recognition of a pathogen-encoded factor by plant Resistance (R) proteins. Over the past 15 years, many R proteins have been identified in a variety of plants. They provide protection against diverse pathogens, including viruses, bacteria, fungi, and oomycetes.

Activation of R proteins by pathogens triggers an array of defense responses including production of the key defense hormone salicylic acid, activation of defense genes, and induction of host cell death at the site of infection. R proteins appear to exist in a repressed or inactive form in the absence of pathogens, due to inhibitory folding of the R protein or interaction of it with negative regulator proteins. Many R proteins are in stable complexes, which contain a small number of host proteins that facilitate proper folding of R proteins and are required for their activation.

To help understand how R proteins are activated and then transmit their information to the rest of the cell to induce defense, **Dan Klessig's** group in 2000 identified an R protein called HRT that confers resistance to Turnip Crinkle Virus (TCV) in the model plant *Arabidopsis thaliana*. They recently identified *Arabidopsis* mutants which are unable to effectively resist infection by TCV. One of these mutants called CRT1 (for comprised recognition of TCV) produces a defective ATPase, an enzyme that uses ATP as an energy source to perform various cellular functions. CRT1 interacts with HRT and a wide variety of other R proteins. In addition to its role in resistance to TCV, it is involved in resistance to bacterial and oomycete pathogens, indicating that CRT1 is an important mediator of defense signaling triggered by distinct classes of R proteins.

Recent studies indicate that CRT1 likely functions at an early step in defense signaling initiated by activated R proteins, but is not involved in their stabilization. CRT1's interaction with R proteins appear to be very dynamic since it is disrupted upon activation of the R proteins.

How do plant stem cells divide and differentiate?



Ji-Young Lee, Ph.D.

Assistant Scientist, BTI

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In response to certain genetic cues, stem cells in animals can differentiate into a wide variety of specialized cells. Understanding these cues at the molecular level is leading to new medical discoveries and cures for people. Plants, too, have stem cells that divide and generate specialized cells in response to currently unknown, genetically based, developmental cues. Understanding these cues is essential to understanding — and influencing — how plants grow.

Ji-Young Lee is studying the genetic factors that cause plant stem cells in procambium/cambium tissue to divide and generate specialized vascular tissues, using the *Arabidopsis* root as a model system. The generation of these specialized vascular tissues, composed of xylem and phloem, contributes to biomass production for renewable energy and for agricultural crops.

In *Arabidopsis*, a fast-growing plant commonly used in research, approximately 1,200 genes in the procambium/cambium tissue are highly expressed and potentially work in regulatory networks that cause stem cells to generate xylem and phloem. Lee is trying to unravel the underlying transcriptional regulatory networks using Systems Biology approaches. To this end, Lee's laboratory has generated genome-wide transcriptome data in the procambium/cambium and identified highly co-regulated groups of genes and their regulators in the procambium/cambium using computational approaches. These regulators include regulators known to be involved in the cell division and differentiation in animals. By systematically perturbing the activities of selected regulators, the Lee laboratory aims to elucidate their biological roles and the genetic relationships of selected regulators with other regulators.

The potential applications of Lee's work are far-reaching. Understanding the mechanisms that cause stem cells to develop into xylem and phloem in *Arabidopsis* will shed light on stem cell regulation in trees and other plants at the genetic level. With that knowledge, scientists may, one day, be able to influence the speed and/or rate of growth of trees and grasses, which could, in turn, increase the amount of biomass they produce for use as biofuel. Lee's research may even help advance knowledge of stem cell regulation in humans.

How do bacteria overcome a plant's disease defense system?

Gregory Martin, Ph.D.

Boyce Schulze Downey Scientist, BTI

Professor, Dept. of Plant Pathology and Plant-Microbe Biology, Cornell University

There's an arms race underway in the plant world in which plants and disease-causing bacteria are continually evolving ways to outsmart each other. Plants have developed a defense system that enables them to resist disease, but some pathogens have evolved survival methods that undermine this system. Understanding the details of this race for dominance could lead to crop plants with more effective, natural resistance to disease.

Gregory Martin's laboratory studies a bacterium called *Pseudomonas syringae*, which causes bacterial speck disease of tomatoes. When *P. syringae* invades a tomato plant, it injects a disease-promoting protein called AvrPtoB into the plant cells. However, the plant is ready and waiting with the protein Fen, which was recently discovered by Martin's team. Fen recognizes AvrPtoB and, in doing so, activates the plant's defense system.

Fighting back, *P. syringae* has cleverly engineered AvrPtoB to act as a tomato E3 ligase, a protein that tags other proteins to be destroyed. When AvrPtoB binds the Fen protein, Fen is tagged and the plant's own system takes Fen to the cell's garbage bin before Fen can activate the plant's defenses. This eliminates the plant's ability to resist speck disease and ensures the survival of the bacterium.

In further studies, Martin's laboratory found that the *Fen* gene is present in many wild species of tomatoes, suggesting it is an ancient plant defense strategy. But if the bacterial protein AvrPtoB is so effective at destroying the Fen protein, why would the *Fen* gene be so prevalent? Martin answers that there are some strains of *P. syringae* that produce a version of AvrPtoB that cannot destroy Fen, and, therefore, cannot turn off the plant's defense system. Consequently, he reasons that the bacteria have only recently evolved the version of AvrPtoB that can sabotage the plant's defenses.

Martin's work helps to explain how the plant/pathogen arms race works at the molecular level and sheds new light on how disease-resistant plants can suddenly become susceptible again. Understanding the strategies pathogens use to overcome plant defenses against disease may lead to crops that have more effective, longer lasting resistance — an advance that could lead to more productive varieties and less dependence on pesticides.

How do plants protect themselves from disease?

Peter Moffett, Ph.D.

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Cornell University

Though plants do not have an adaptive immune system like animals do, plants have evolved a defense mechanism of their own that protects them from disease. **Peter Moffett** is studying one such system using a disease resistance gene from potato.

All plants have a unique repertoire of several hundred disease resistance genes, each of which produces a resistance protein that protects the plant from specific pathogens. But this system works only if the resistance protein recognizes a protein from the pathogen, called an avirulence protein. Moffett is working to understand how this recognition event occurs and how it elicits a protective response in the plant.

Moffett's research team has discovered that the resistance protein they study actually works in concert with another protein, called RanGAP2, which is present in all plants. He found that RanGAP2 physically interacts with the appropriate resistance protein, and allows it to sense the presence of a particular pathogen. RanGAP2 activates a protein called Rx when a virus attacks a potato cell, but if the cell is attacked by a nematode, RanGAP2 activates a protein called Gpa2. Working together, RanGAP2 and the resistance protein initiate a programmed response that will kill the cell, and with it the pathogen.

Most recently, Moffett's laboratory discovered how the Rx protein interacts with RanGAP2 to signal the cell that a pathogen has invaded. This discovery is important because any plant can defend itself against most pathogens, but only if it can recognize the pathogen. Understanding how RanGAP2 works in concert with resistance genes like *Rx* and *Gpa2* to recognize a specific pathogen, may enable scientists to adjust a plant's defense system to mobilize against pathogens it couldn't previously recognize. This, in turn, may lead to a new way to transfer naturally occurring resistance to a particular pathogen from one plant into another — an advance that could have important agricultural implications.

How will researchers store and retrieve scientific information in the future?

Lukas Mueller, Ph.D.

Assistant Scientist, BTI

Consider that thousands of scientists are working worldwide to identify all the genes in a wide variety of plants. Then, consider that a plant like tomato has about 35,000 genes, some of which function in complex networks. And then consider that new genetic discoveries are being made each and every day about how these genes are regulated and how they interact. How can all this information be efficiently stored, updated and made accessible to scientists in a timely manner so they can use it and build on it?

This is the question that **Lukas Mueller's** laboratory at BTI is answering. Among other projects, Mueller's group coordinates the Solanaceae Genomics Network — a database of all the genetic information known about solanaceous plants, such as tomatoes and peppers. He's also involved in the tomato genome sequencing project, which is the work of scientists in 10 countries.

Mueller is developing software that will make it easier for scientists to access vast amounts of genomic data. He's also working to make it simpler for scientists to annotate, or update, the data as they make new discoveries. It's similar to the idea that gave rise to Wikipedia — an encyclopedia that can be added to or revised by anyone who reads it. The difference is that Mueller's software and the database it runs are specifically designed for complex biological data.

Until the advent of the Internet, scientists could only share the results of their research with others through personal communications and by publishing their work in scientific journals. But neither communication method enabled colleagues to access all the data that backed up the results. With the software Mueller is developing, scientists not only can see the results of others' work, they can also see and use the data the results were derived from.

Mueller's goal is to make these databases so easy to use that they will become the primary place for storing, sharing, updating and accessing genomics information. At that point, the practical applications of his work would multiply. For instance, plant breeders could use the database to more quickly develop new varieties of crop plants with innovative genetic characteristics, such as higher yield or enhanced nutritional quality.

Which proteins control which biological processes in plants?

Sorina Popescu, Ph.D.

Assistant Scientist, BTI

Proteins are the workers that participate in every process within cells, such as biochemical reactions (metabolism), structure (building and maintaining the shape of the cell) and defense mechanisms (disease or insect resistance), among others. Identifying all the proteins in a plant cell and determining the function of each is a major area of plant biology research.

Until recently, identifying and isolating these proteins and then using them to discover their specific function has been an arduous task. But as a result of discoveries made by **Sorina Popescu**, the work has become easier and more efficient. Popescu enhanced a technique called the microarray, which was previously used only to study gene transcription, and adapted it for the study of proteins.

Working with *Arabidopsis* proteins, Popescu discovered that she could "print" as many as 5,000 minute protein samples on one microscope slide (the microarray) and that these tiny amounts of protein could then be used in other research that would reveal the function of each. There are about 30,000 proteins in *Arabidopsis*, which means that the entire proteome (the complete protein library) of this plant could be stored on six standard microscope slides.

Using her technique, Popescu and other scientists will be able to more efficiently study protein function on a very large scale. Prior to the development of protein microarray technology, scientists were able to select only a few proteins at a time for study, which restricted their ability to identify which proteins are involved in which processes. Now, Popescu and others can easily study thousands of proteins — even those no one thought were involved in a particular process. As a result, her work has significantly expanded the universe of study involving proteins and their functions.

Popescu plans to use her protein microarray technology at BTI to identify proteins involved in protecting plants from various diseases. Her work could lead to the identification of proteins that were never before thought to be involved in disease resistance, which, in turn, could lead to a new understanding of how plant defense mechanisms work. It could also lead to new ways to protect plants from disease and enhance their yields.

How are genes turned off?

Eric J. Richards, Ph.D.

Scientist, BTI

Everyone knows by now that excessive exposure to the sun's radiation can cause skin cells to become cancerous. Cancer occurs because radiation causes changes (mutations) in the cell's DNA sequence. But cancer and other diseases can also occur when certain genes that might have protected the cell are "silenced" or turned off. In this case, the protective genes become unreadable by the cell and disease can result. Understanding how these genes become "unreadable" is the goal of a relatively new area of genetics research called epigenetics.

Eric Richards' laboratory studies epigenetics in the model plant *Arabidopsis*. "Epi-" means "on top of" or "in addition to," so epigenetic traits exist on top of or in addition to the cell's DNA sequence. Epigenetics research seeks to understand the molecular mechanisms that change the information contained in the DNA (making it unreadable) without changing the underlying DNA sequence. Richards focuses on one of these mechanisms, called "DNA methylation." In this process, a small chemical group is added to one of the DNA bases (cytosine) which can make the gene unreadable by the cell. The methylated gene can die out with the cell or it can be passed on to new generations of cells and, in some cases, organisms. Consequently, DNA methylation may play an important role in evolution, just as mutations do.

Richards is working to understand how, where and when DNA methylation occurs, its consequences on the organism, and to what extent variation in methylation is passed on to future generations. He is studying this process in plants because they can survive major epigenetic alternations that other organisms, like mice, cannot.

Understanding the basic biology of DNA methylation in plants could have applications to human health, such as the detection and prevention of disease. But it also has important applications in agriculture. Epigenetics controls important traits in crop plants, such as disease resistance and flowering time, so advances in this field of genetics could lead to higher quality food or increased yields.

How do secondary metabolites affect human health?

Frank Schroeder, Ph.D.

Assistant Scientist, BTI

Adjunct Assistant Professor, Dept. of Chemistry and Chemical Biology, Cornell University

The relevance of nucleic acids, proteins and carbohydrates for all aspects of biology is well established, but the varied and often unexpected roles of so-called "secondary" metabolites are just now emerging. Secondary metabolites regulate development and immune response in plants and animals (such as hormones) and also play an important role in the interactions of different organisms with each other.

Identifying secondary metabolites and determining their function is an important area of biomedical research that can help scientists better understand diseases such as bacterial infections, diabetes and cancer, as well as the phenomenon of aging.

Secondary metabolites are very different from proteins and nucleic acids. They constitute an extremely chemically diverse class of compounds, which have so far resisted systematic analysis.

Frank Schroeder's laboratory is developing new analytical methodology based on a technique called NMR spectroscopy, which promises to greatly simplify scientists' ability to identify the chemical structure of these compounds and find their biological functions. Using this approach, Schroeder's team is investigating the role of secondary metabolites in specific aspects of plant and animal biology.

In one area of research, Schroeder is investigating secondary metabolites produced by the nematode *Caenorhabditis elegans*. Nematodes are roundworms that are about 1 mm in length and ubiquitous in the soil. Scientists believe that many of the physiological pathways in *C. elegans* are analogous to corresponding pathways in higher animals, and as a result, nematodes have become an important model system for human disease and aging. Although the entire *C. elegans* genome — about 20,000 genes — was sequenced more than 10 years ago, little is known about its secondary "metabolome."

Recently, Schroeder's group identified several new compounds that influence mating behavior, as well as pathways involved in nematode development and life span regulation. The ultimate goal of this research is to identify the entire *C. elegans* secondary metabolome for chemical structure and biological function.

In other research, Schroeder and colleagues recently used his NMR-spectroscopic approach to identify a previously unknown human hormone that controls the excretion of sodium via the kidneys. This discovery may one day lead to a new approach for treating high blood pressure.

How do plants co-regulate genes?

David Stern, Ph.D.

President, BTI

Adjunct Professor, Dept. of Plant Biology, Cornell University

About two billion years ago, a bacterium capable of photosynthesis was engulfed by another single-celled organism, forming the first photosynthetic eukaryote. Eukaryotes differ from simpler bacteria because they have multiple genetic compartments within the cell. In modern plant cells, there are three genetically-active compartments: the nucleus, the mitochondria, and the chloroplasts. While the nucleus contains most of the plant cell's genes, the organellar (mitochondrial and chloroplast) genomes are essential, encoding proteins involved in respiration and photosynthesis, respectively. **David Stern's** laboratory studies how plant organellar genes are regulated, thus coordinating their expression with their nuclear counterparts.

One chloroplast protein that the Stern laboratory studies is called polynucleotide phosphorylase (PNPase). PNPase can either build or destroy RNA chains, depending on the phosphorus concentration in the cell. What was unknown until recently was that PNPase also has a role in phosphorus metabolism itself. Phosphorus is an essential nutrient for both plants and animals, and without an adequate supply they perish. The Stern laboratory created algae deficient in PNPase and found that these cells could not survive phosphorus starvation. When PNPase-depleted *Arabidopsis* plants were deprived of phosphorus, they proved unable to produce the additional roots which normal plants use to seek out new supplies. Such surprising findings illuminate unexpected physiological connections between different parts or compartments within an organism.

The laboratory also studies other ribonucleases, which are enzymes that break down RNA chains. RNases both create the correct forms of RNA chains, and recycle the chemical components of RNA. Chloroplasts contain a veritable "alphabet soup" of RNases, and the Stern laboratory is helping to untangle the web of enzyme activities. How do these enzymes divide their work, and why does their absence cause such enormous stress to the plant, even to the point where embryos and seeds are unable to develop? By using biochemical and genetic approaches, some of the answers are being discovered.

Chloroplasts are critical for life on Earth because they are the site of photosynthesis, which both removes CO_2 from the atmosphere and regenerates oxygen. They are also emerging targets from the production of biopharmaceuticals and biofuels. Understanding the basics of how chloroplasts operate underpins all of these practical applications.

How do potatoes produce and accumulate beta-carotene?

Joyce Van Eck, Ph.D.

Senior Research Associate, BTI

According to the World Health Organization, 100 to 140 million children in the developing world suffer from vitamin A deficiency, which can cause blindness and death. Finding ways to produce food with higher beta-carotene content — the precursor to Vitamin A — could significantly alleviate this serious health issue.

Working together, **Joyce Van Eck** and Li Li, a scientist with the U.S. Department of Agriculture, developed two lines of modified potatoes that accumulate more beta-carotene than conventional varieties. Van Eck knocked out, or "silenced," a gene in her line that converts beta-carotene into zeaxanthin, another carotenoid that is not converted into Vitamin A. She theorized and proved that silencing the gene would cause the potatoes to accumulate more beta-carotene. Li isolated a gene called *Or* from a naturally occurring mutant orange cauliflower. When Van Eck inserted the *Or* gene into potato, they found that the modified potatoes accumulated more beta-carotene than other potatoes.

In 2007, Van Eck's lab worked to better understand the molecular pathway involved in the production of carotenoids in potatoes. In analyzing the *Or* lines, the scientists discovered that early in the pathway (about four steps before beta-carotene is produced), certain genes caused the accumulation of some carotenoids, but limited the accumulation of others. As a result of this discovery, Van Eck's lab inserted certain genes earlier in the pathway to counteract the limiting effect she had found and increase carotenoid production.

Then, these genes were inserted into both the silenced lines and *Or* lines. Potatoes from these newly modified lines were harvested and analyzed. The results showed that the new plant lines do indeed produce significantly higher amounts of beta-carotene. The next step will be field trials to ensure that yield, plant health and other factors are not affected in the modified potatoes.

How do plants perceive and respond to far-red light?

Haiyang Wang, Ph.D.

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Plant growth and development are largely dependent on a plant's response to light. The color or wavelength of light, its intensity, direction and duration influence when, how fast, how tall and in what direction plants will grow, and when they will flower. But understanding fully how plants "see" and respond to light is an enduring mystery.

Haiyang Wang is studying how plants sense and respond to far-red light (light in the visible spectrum that we see at sunrise and sunset), using *Arabidopsis* plants as a model. When far-red light photons hit specialized protein photoreceptors in the cell called phytochrome A or PHYA, the receptors are activated. Activated PHYA molecules then move from the cytoplasm of the cell into the nucleus where they orchestrate the plant's physiological response to light by regulating gene expression. What causes the photoreceptor to move and how the process is regulated is not well understood.

Wang's laboratory is studying the biochemical function of two proteins, FHY3 and FAR1, that appear to be essential for the light response chain of events. They found through a series of biochemical, genetic and cell biological studies that these proteins can bind as transcription factors directly to the regulatory regions of two direct target genes, *FHY1* and *FHL*, and cause the genes to express products required for PHYA to accumulate in the nucleus.

This discovery, previously reported in *Science*, has important evolutionary significance because the two proteins appear to be related to certain enzyme products of transposable elements, which are residents of the genome that can "jump" from one place to another. Wang's research indicates these "jumping genes" may actually have evolved into important cellular genes, which, in this case, allow the plant to respond to its light environment.

The ability to fine tune a plant's response to light could significantly benefit agriculture. Such adjustments could lead to plants that yield more, produce more biomass or could be grown in higher density.

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