



to improve agriculture, protect the environment, and enhance human health

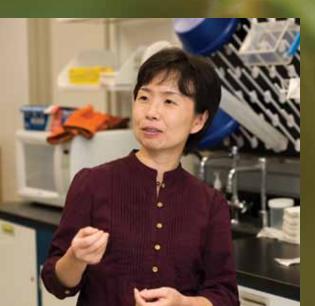






What drives BTI staff in their pursuit of new knowledge? The answer is that our faculty, postdoctoral fellows, graduate students and research assistants all share a passion

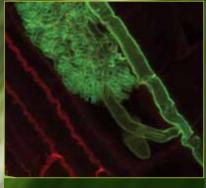
for discovery. This excitement, along with a deep-seated belief in BTI's mission, pervades our entire staff, including those that operate our research facilties and our business operations. This confluence of purpose gives BTI its energy and identity, and creates an environment where success is frequent, and is celebrated.











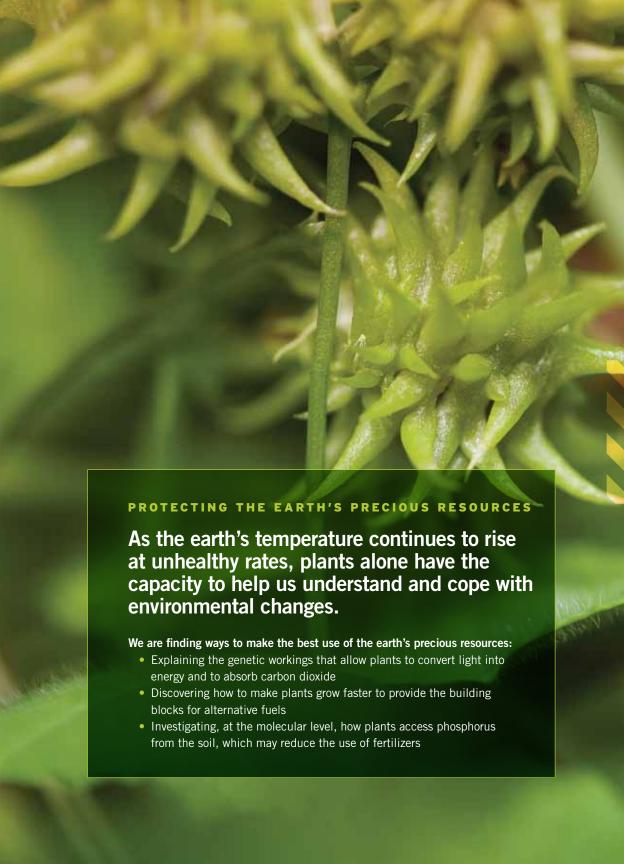
Arabidopsis root

#### LEADING THE WAY TO A HEALTHIER WORLD

Plants offer a window into life processes at the most basic level and provide essential treatments for many diseases and chronic illnesses.

What we are doing to help lead the way to a healthier world:

- Discovering new methods to fortify staple foods that prevent diseases common in developing nations
- Learning how viruses interact with DNA molecules, which could improve human gene therapy
- Researching genetic cues that cause stem cells to specialize, which could lead to new treatments for diseases like Parkinson's and cancer
- Developing a new approach to analyzing complex mixtures of small molecules, which could lead to new treatments for conditions like high blood pressure



BRINGING THE BEST SCIENTIFIC MINDS TOGETHER

# Innovative tools and technologies allow scientists to collaborate across disciplines and produce breakthroughs with wide-ranging effects.

#### How we are bringing the best scientific minds together:

- Creating innovative tools to organize enormous amounts of data generated in genomics and making it easily available to researchers across the globe
- Using novel research methods to identify new compounds that influence biological phenomena, which create a knowledge base for medical researchers looking for new approaches to the treatment of human diseases

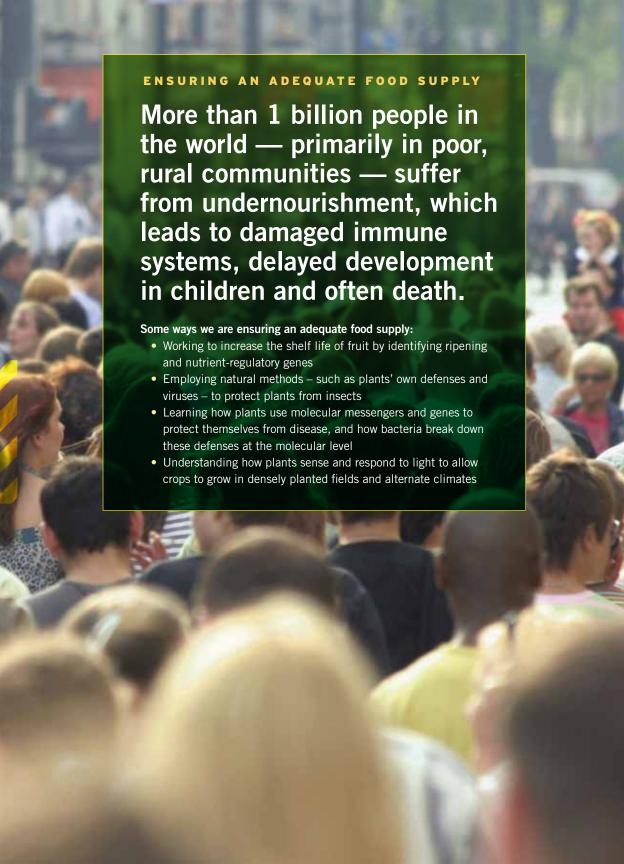
#### REACHING OUT ACROSS THE GLOBE

### BTI is committed to championing the field of plant science around the world.

#### BTI scientists are:

- Collaborating with researchers at Qingdao University in China to create new generations of insect cell lines that can be used to produce new vaccines at lower cost.
- Teaching students of all ages from school children to undergraduates about the wonders of plant science.
- Helping educators from across the state of New York create science curricula.
- Building a network of researchers, educators and government officials to share information on scientific issues.







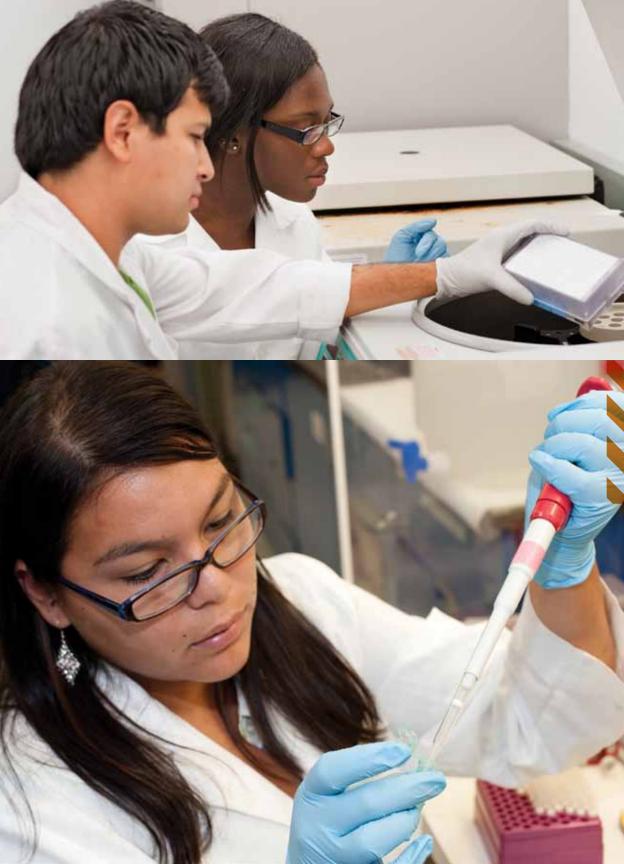


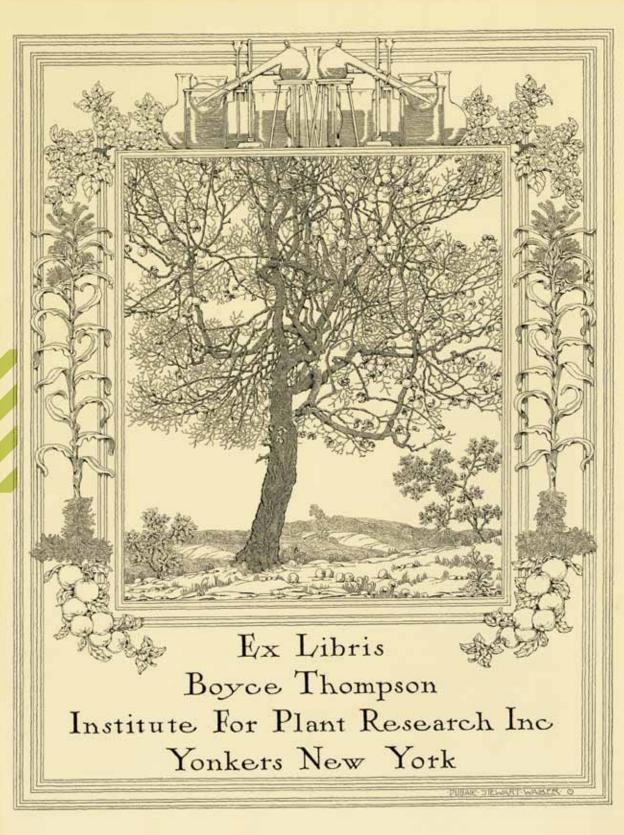
Our Plant Genome Research Project summer internship program recruits

 The BTI seminar series brings bright minds in plant science and biology from across the globe to share their expertise with the BTI community.

genetics and offer genuine scientific research opportunities.

high school and undergraduate students to teach a broader knowledge of plant





#### A TRADITION OF INNOVATION

William Boyce Thompson – a businessman and layman scientist – founded the BTI in 1924 with the vision that basic plant research was an essential foundation for increasing food production. Since

Thompson's insightful undertaking, the institute has made dozens of scientific discoveries. Today, in partnership with plant scientists in the US and the world, BTI is advancing the field of plant biology in areas that were inconceivable more than 80

For example, BTI scientists have:

years ago.

- Developed modified plants that deliver "edible vaccines."
- Discovered and developed the first selective herbicide.
- Developed an insect line that led to the production of the cervical cancer vaccine.
- Created a technique for identifying plant viruses that is used worldwide.
- Discovered natural ways to control insects.



### THE BOYCE THOMPSON ARBORETUM

The Boyce Thompson Arboretum in Superior, Arizona, our sister institution, also founded by William Boyce Thompson, contributes to botanical education and research. You can learn more at http://ag.arizona.edu/bta.



### POTENTIAL OF PLANTS

As a non-profit research institute, gifts from private foundations and individuals help strengthen BTI's influence in the field of plant science.

Your investment in BTI helps to:

- Lay the foundation for research that will improve our world.
- Develop young scientists, talented undergraduates and school children.
- Upgrade our facilities.
- Attract promising postdoctoral fellows.

Please consider supporting BTI with your gift. We welcome your annual gift of cash, check and stock as well as your planned gifts through an insurance policy, bequest or one of the many financial instruments available for charitable donors who wish to leave a legacy to BTI.

#### **ACCOMPLISHMENTS**

BTI scientists have, for example:

- Discovered the role of a naturally occurring substance that stabilizes dry, stored seeds and led to an insulin aerosol spray.
- Created the first computer models to test the impact of acid rain and ozone on mature forests.
- Formulated worldwide air quality standards.

More than 85 years ago BTI was born of a vision that fundamental research related to plants would ensure the food supply. Today's world is far more complex and interdisciplinary, but then, as now, BTI's success has been sustained by an intense curiosity of the natural world and the thrill of discovery.



### BEADERSHIP

### INSIDE BTI

2 In Brief

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- 4 Financial Report
- 5 Lab Reports
- 15 Publications



#### **BOARD OF DIRECTORS**

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#### MESSAGE FROM THE PRESIDENT

**2010 MARKED 86 YEARS SINCE THE FOUNDING OF BTI** and while much has changed since then, one feature of the Institute remains the same: we continue to push the boundaries of plant science discovery. The recipe for this success? Top-flight scientists, a talented and dedicated support staff, excellent facilities, and access to some of the best minds in the field at BTI, Cornell and across the world.

It is in this environment that our scientists carry out foundational, hypothesis-driven research that we believe will ultimately contribute to solutions for some of the planet's most pressing problems. Over the next 10-15 years, as BTI prepares to celebrate its centennial, we expect societies to grapple with several complex and intertwined problems, including the nutritional quality of food and its relationship to obesity, the sustainability of our energy needs and the contributions of bioenergy, agricultural yields and their link to food security, and changing climate patterns, with their own impact



on agriculture. BTI also recognizes a broader link between its research mission and human health, ranging from chemical signals involved in determining lifespan, to insect cells that are used to produce therapeutics.

Some of the specific research projects related to these larger-scale issues are detailed in the reports from individual laboratories. For example, the Brutnell and van Eck laboratories have developed new tools for *Setaria*, a small grass whose similarity to corn allows it to be used as a simple, rapid model to test ways to improve crop yield. The Harrison laboratory has uncovered new details of how the beneficial mycorrhizal fungi help plants absorb the nutrient phosphorus, findings that could one day improve the efficiency of fertilizer absorption. The Blissard laboratory created a test-tube cell line from the Black Witch moth which expresses proteins at an unprecedented level, creating a platform with excellent potential for the production of diagnostics, vaccines, or other enzymes. Other BTI laboratories seek to understand how plants resist diseases or insects, capture carbon, or communicate internally. Two faculty, Zhangjun Fei and Lukas Mueller, use computational tools and web interfaces to help scientists sort through and interpret the blizzard of data that is being created through genome sequencing projects. Overall, BTI is a scientifically diverse institute that prizes scientific and human innovation.

Flourishing during challenging economic times is not easy, but BTI has been fortunate to attract generous funding from federal agencies, foundations and corporations. This enables us, in addition to pursuing the boundaries of knowledge, to offer educational and mentoring opportunities, deliver content through our outstanding web site, and foster career development. BTI also endeavors to act responsibly through pragmatic steps such as reducing paper usage, converting to energy-efficient fixtures, expanding recycling, and facilitating electronic transactions and communication. Together, these actions all support our mission "To advance and communicate scientific knowledge in plant biology to improve agriculture, protect the environment, and enhance human health."

Sincerely,

David B. Stern, Ph.D.

President

### IN BRIEF

### OUTREACH HELPS BTI REACH A BROAD AUDIENCE Why?

Our overriding goal for outreach in 2010 was to provide experiences that connect BTI's research portfolio to a broad audience. Nearly 1,700 people participated in BTI outreach activities in 2010.

#### Who?

101 science teachers 734
undergraduates 505 K-12 students
185 Volunteers Mentors and Faculty

#### What?

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Symposia Teacher Workshops
Volunteer and Mentor Training Class
presentations Recruitment Poster
sessions Student seminars BTI
Tours Student Workshops

#### Where?

- K-12 classrooms BTI conference rooms greenhouse and laboratories
- Kohut Teaching Laboratory
   Minorities in Agriculture, Natural Resources and Related Sciences Conference
   Society for the Advancement of Chicanos and Native Americans in Science Conference
- Science Teachers Association of New York State Annual Conference

#### Support

National Science Foundation
 Northeast Sun Grant Initiative
 United
 States Department of Agriculture
 Helen Graham Foundation

#### Collaborations

Cornell Institute for Biology Teachers
 New York State Agricultural Experiment Station
 Cornell Plantations
 Cornell Center for Materials Research
 Cornell Laboratory for Accelerator-based Sciences and Education
 Cornell Center for Nanoscale Systems
 Cornell Center for Radiophysics and Space Research
 Department of Horticulture

Cornell University • Department of Plant Breeding and Genetics, Cornell University • Guilderland High School • Ithaca City School District • STEM Outreach Group, Cornell University • Tompkins Cortland Community College • TST BOCES • Wheatland-Chili Central Schools

#### **TECHNOLOGY TRANSFER**

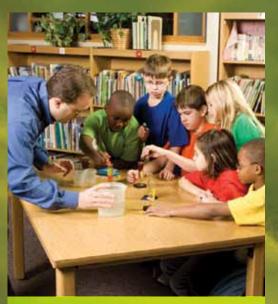
The role of the Intellectual Property Department (IP) is to transfer

the technology developed at BTI to the private sector and to other academic partners.

In 2010 we developed a new IP strategic plan that will better protect and commercialize BTI technology in the years to come while we work with BTI scientists and potential commercial partners to broaden the reach of our efforts.



- Reorganization and expansion of IP staff and function including an important focus on marketing BTI technology and working closely with new commercial partners to develop new technology
- Nine new invention disclosures filed; a record number
- Eight new patents were issued; two US and six in other countries
- Four new patent applications filed
- Entered into forty-one new materials transfer agreements vwith academic and commercial partners.



Our overriding goal for outreach in 2010 was to provide experiences that connect BTI's research portfolio to a broad audience.

#### ORANGE TREES ON FAST TRACK

More than one thousand 2 ½ foot orange trees made their way to Frostproof, Florida to replace trees decimated by "greening" disease. RPM Ecosystems, (RPM) a company in Dryden, NY and BTI, carried out a pilot project in the BTI greenhouses using a special root propagation method in the hope they can grow trees faster and thus decrease the length of time the groves are idle. "Citrus Greening" is probably the most serious of all afflictions of the citrus species, killing every tree it infects and causing losses of millions of dollars. BTI's greenhouse staff grew the seedlings under the strict growing conditions they require. If

the time growing an orange tree to maturity can be shortened it means groves can be planted and become productive sooner.

#### STRENGTHENING PLANT BIOLOGY

BTI has teamed up with three centers that focus primarily, though not exclusively, on plant research. The purpose of the linkage is to develop a stronger presence for plant biology on a national level and for scientists at the institutes to collaborate on a joint project. The collective is in its nascent stage and includes The Donald Danforth Plant

Center, The Noble Foundation and The Plant Biology Department of the Carnegie Institute of Washington at Stanford.

#### **AWARDS**

Gregory Martin, Ph.D., was named the recipient of the Noel T. Keen Award for Research Excellence in Molecular Plant Pathology by The American Phytopathological Society (APS). The award recognizes an outstanding research scientist in the field of plant molecular pathology. Dr. Martin is a research scientist at BTI, holds The Boyce Schultz Downey Chair, and is Professor of Plant Pathology and Plant-Microbiology at Cornell University.

**President David Stern, Ph.D.** was awarded the Fellow of the American Society of Plant Biologists (ASPB). The award is granted to

current ASPB members in recognition of direct service to the Society and distinguished and long-term contributions to plant biology. In addition to his position at BTI he has an adjunct faculty appointment in Plant Biology at Cornell University.

The Lawrence Bogorad Molecular Plant Biology Award established to honor scientist and long-time BTI Board member Lawrence Bogorad is given annually to an outstanding BTI postdoctoral fellow. The recipient for 2010 is **Pinghua Li** from Dr. Tom Brutnell's lab. Pinghua has been instrumental in establishing and executing transcriptomics

work in the Brutnell lab which has been central to several recent publications, including the maize leaf transcriptome study (Li *et al.* (2010) *Nature Genetics* 42:1060). She has also provided transcriptomic data for refinement of the maize genome annotation, and worked on specialized annotation of the Brachypodium genome sequence. Pinghua has been an energetic and dedicated lab citizen, colleague and mentor.

### **OUR VISION**

The Boyce Thompson
Institute will be known
worldwide for research
excellence in the field
of molecular and
chemical biology.

#### TRANSITIONS

Sofia Darling was appointed Chief Financial
Officer. She is a native of Ithaca, NY and before
joining BTI was Chief Financial Officer for Vanguard Press of Ithaca.

**Joan Curtiss** was appointed Chief Operating Officer. Originally from Richford, NY, she is a 13-year BTI employee and continues her responsibilities as Information Technology Manager.

**Eric Richards** is the new Vice-President for Research and also leads a laboratory in the study of epigenetics. Before coming to BTI two years ago he held a faculty position at Washington University at St. Louis.

Jane Calder was promoted to the position of Human Resources Manager. She is a native of Canada and formerly BTI's HR assistant.

#### **GRANTS & GIFTS**

#### **GRANTS AWARDED**

#### Government

Defense Advanced Research Projects Agency (DARPA)	\$ 21,123
National Science Foundation	\$ 3,096,593
Health and Human Services	\$ 2,083,963
United States Dept. of Agriculture	\$ 1,182,809

#### Miscellaneous

Binational Agriculture Research and Development (BARD)	\$ 135,000
The International Human Frontier Science Program Organization	\$ 160,980

#### **Foundations**

Binational Science Foundation	\$ 88,000
Gates Foundation	\$ 177,850
Triad	\$ 250,000

#### Other

British American Tobacco (Investments) Limited	\$ 326,360
Bench fees for Sarah Collier	\$ 1,650
Bench fees for Nate Pumplin	\$ 1,650
Bench fees for Muhammad Naeem	\$ 3,500
Tompkins Cortland Community College	\$ 2,818

TOTAL \$ 7,532,296

#### **GIFTS**

#### William and Anne Thompson Society (\$5000+)

Helen I Graham Charitable Foundation Chris & Nora Hohenlohe Triad Foundation

#### William Boyce and Gertrude Thompson Society (\$2000 - \$4999)

Carolyn Sampson

#### Chairperson's Circle (\$1000 - \$1999)

Ling Bai Mary E. Clutter Greg & Betsy Galvin Kathleen P. Mullinix, Ph.D. Mr. & Mrs. Roy H. Park Jr. Laura A. Philips & John A. Elliott David & Karen Stern Wm. B. Thompson Fund

#### **President's Circle** (\$500 - \$999)

Anonymous (2)
Dr. & Mrs. Ralph W.F. Hardy
Susan & Gregory Martin
Donald & Marcia Slocum
Ruth Stern
Sylvia & Leonard Weinstein

#### Alder Society (\$100 - \$499)

Anonymous
Holly Beermann
Kishor K. Bhattarai
Gary Blissard & Elizabeth Mahon
Thomas Brutnell & Mary Howard
Maria G. Bulis
Dr. Eleanor Storrs Burchfield
James & Terry Byrnes
Bruce & Tricia Cahoon

Jane Calder
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Charlie & Donna Claes
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Rich & Joan Curtiss
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Dr. & Mrs. Robert C. Miller
Jay & Deborah Miller
Kelli Monce
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Nancy Ray
Alan & Anne Renwick
Kira S. Sheinerman
Mark & Jane Siegwarth
Richard & Mildred Staples
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Mary Westlake
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Jianjun & Li Yang
Brian Bell

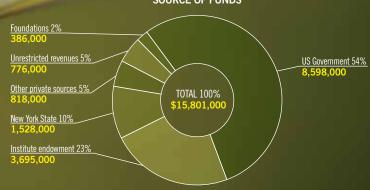
#### Friend of BTI (\$1 - \$99)

Anonymous
Judith A. Bishop
Dr. S. Mark Henry
Mrs. Evelyn Mehlhop
Lisa Meihls
Sorina Claudia Popesc

#### FINANCIAL REPORT



#### SOURCE OF FUNDS







Klaus Apel, Ph.D. Scientist, BTI

### How do plants respond to environmental stress?

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 overproduction 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.



Gary Blissard, Ph.D.

Scientist, BTI

Adjunct Professor, Department of Microbiology and Immunology and Department of Entomology, Cornell University

#### How do viruses infect insect pests?

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 plays 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.



Tom Brutnell, Ph.D.
Associate Scientist, BTI
Adjunct Associate Professor, Department of Plant Biology and Dept. of Plant
Breeding and Genetics, Cornell University

### How does maize produce beta-carotene?

Two BTI laboratories — run by scientists Tom Brutnell and Joyce Van Eck — are studying the genetic basis of beta-carotene production in certain staple foods. (Also see Van Eck, page 14). Beta-carotene is a carotenoid and is the precursor to Vitamin A, which can prevent an eye disease and other health disorders that plague hundreds of millions of children in the developing world. In studies with maize, which is low in betacarotene, 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 of 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.



**Carmen Catala, Ph.D.**Adjunct Scientist, BTI
Senior Research Associate, Department of Plant Biology, Cornell University

### How do plant hormones control fruit development?

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



**Zhangjun Fei, Ph.D.**Assistant Research Scientist, BTI

### How can scientists access and use the massive amonts of plant genomics data?

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.



Jim Giovannoni, Ph.D.

Adjunct Scientist, BTI

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

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

### What is the genetic basis of fruit development and ripening?

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 and 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.



Maria Harrison, Ph.D. Scientist, BTI Adjunct Professor, Department of Plant Pathology and Plant-Microbe Biology, Cornell University

### How do soil fungi supply plants with mineral nutrients?

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 periarbuscular membrane, through which the mineral exchange occurs.

Harrison theorized that a particular transporter protein in the periarbuscular 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.



**Georg Jander, Ph.D.**Associate Scientist, BTI
Adjunct Professor, Department of Plant Biology, Cornell University

### How do plants ward off insects and produce amino acids?

As the human population increases, so does the demand for food, yet there is a finite amount of arable land available foragriculture. 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.



Scientist, BTI

Adjunct Professor, Department of Plant
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Dan Klessig, Ph.D.

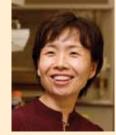
### How do plants protect themselves from pathogens?

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 research group 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. CRT1 localizes to endosome-like vesicles, suggesting a key process in resistance protein activation and signaling occurs in this subcellular compartment.



Ji-Young Lee, Ph.D.
Assistant Scientist, BTI
Adjunct Assistant Professor, Department of Plant Biology, Cornell University

### How do plant stem cells divide and differentiate?

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 human disease. Plants, too, have stem cells that divide and generate specialized cells in response to genetically based, developmental cues. Understanding these cues is essential to understanding — and influencing — how plants grow.

Ji-Young Lee's lab 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 the biomass production for renewable energy and agricultural crops.

Recently Lee's group and collaborators discovered a novel cell-cell signaling mechanism that is critical for proper xylem development in the root. This cell-cell signaling is achieved by the intercellular movement of a transcription factor SHORT ROOT in one direction and microRNA 165/6 in the other. Mobile microRNA 165/6 forms gradual distribution of its targets, which are key transcription factors of the xylem formation. The Lee lab is further investigating how these key transcription factors drive xylem specification from vascular stem cells and maintain vascular stem cell population.

In Arabidopsis, 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. The Lee lab is trying to unravel the underlying transcriptional regulatory networks at a global level using systems biology approaches. To this end, the Lee lab has generated genome-wide transcription data in the procambium/cambium and identified highly co-regulated groups of genes and their regulators in the procambium/cambium. These regulators include regulators involved in cancer suppression in animals. By systematically perturbing activities of selected regulators, the Lee lab is heading to clarify their biological roles and the genetic relationships among regulators.

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 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.



Gregory Martin,
Ph.D., Genetics
Boyce Schulze Downey Chair, BTI
Professor, Department of Plant Pathology
and Plant-Microbe Biology, Cornell

### How do bacterial pathogens manipulate plant immune responses?

The Martin laboratory studies the molecular basis of bacterial patho genesis and plant immunity. Bacterial pathogens of both plants and humans use a type III secretion system to inject virulence proteins ('effectors') into the cells of their hosts. As many as 30 or more different effectors can be delivered by an individual pathogen and, once inside the host cell, they manipulate various processes to promote bacterial virulence.

The great diversity of type III effectors, and the fact that their amino acid sequences offer few clues to their function, has been an impediment to understanding how they manipulate the host. One host process, the attachment of ubiquitin to a protein in order to regulate its function or to cause its degradation, plays an important role in host immunity and has been shown to be a vulnerable host target for type III effectors.

To study how pathogens exploit the host ubiquitination system, the Martin lab has focused on the characterization of a type III effector, AvrPtoB, from the plant pathogen Pseudomonas syringae. In previous work, it was discovered that the C-terminal domain of AvrPtoB is a structural mimic of the U-box class of E3 ubiquitin ligases — a type of host protein that facilitates the attachment of ubiquitin to other proteins. The AvrPtoB E3 ligase is able to use host E2 conjugating enzymes to cause ubiquitination and degradation of a host protein kinase, Fen, required for immunity.

Despite these recent discoveries, much remains to be learned about how the AvrPtoB E3 ligase binds and ubiquitinates its host substrates in order to subvert their normal functions. Recently virulence proteins from human pathogens such as Legionella pneumophila and Escherichia coli have also been found to express proteins of the U-box class of E3 ligases. Therefore, structural mimicry of this type of host protein appears to be a common strategy for undermining host immunity. The long-term objective of this project in the Martin lab is to increase our understanding of the underlying mechanisms that bacterial E3 ligases use to manipulate host ubiquitination. This knowledge will be useful for the development of novel strategies for interfering with these virulence proteins in order to lessen the impact of pathogen infection in both plants and humans.



Peter Moffett, Ph.D.

Assistant Scientist, BTI

Adjunct Assistant Professor, Department of Plant Pathology and Plant-Microbe Biology, Cornell University

### How do plants protect themselves from disease?

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.



**Lukas Mueller, Ph.D.**Assistant Scientist, BTI

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

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



**Sorina Popescu, Ph.D.** Assistant Scientist, BTI

#### How do plants sense their environment?

Although plants lack eyes, ears, nose and toes, they are continuously attuned to their surroundings. Plants are able to "see", "hear" "smell" and "feel" as well as us humans if not better. Plants can sense environmental factors such as heat, cold, humidity and the presence of enemies. Special proteins in plant cells called receptors have a sentinel function, continuously surveying the environment and ready at the smallest provocation to alert an orchestra of second tier sentinels located inside the cells. Plants are dependent on this surveying and response system, called signal transduction, because their defense mechanisms against bests and growth and survival depend on it.

Popescu Lab studies the rich and complex system for signal sensing and intracellular transduction in the model plant Arabidopsis. The core of the cellular signaling mechanisms is represented by the protein kinases. In her work with protein kinases, Popescu is employing a special technique called protein microarray analysis. 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 one. Using this technique, Popescu and other scientists will be able to more efficiently study protein function on a very large scale. Now, she 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 protein microarray technology to understand how protein kinases assemble in signaling pathways in response to plant pathogens. She tries to understand how kinases orchestrate appropriate modification in the gene transcription program of the cells, so that the final decision on how a plant will defend itself is reached. 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.



Eric J. Richards, Ph.D. Vice-President, Research Scientist, BTI

#### How are genes turned off?

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,

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.

organisms. Consequently, DNA methylation may play an important role in

evolution, just as mutations do.

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.



Assistant Scientist, BTI

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Frank Schroeder, Ph.D.

### How do secondary metabolites affect human health?

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.



**David Stern, Ph.D.** President, BTI Adjunct Professor, Department of Plant Biology, Cornell University

### How do plants co-regulate genes?

As long as 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 the case of modern plant cells, there are three genetically-active compartments: the nucleus, the mitochondria, and the chloroplasts. While the nucleus contains most of the plant's genes, the organellar (mitochondrial and chloroplast) genomes are essential encoding proteins involved in respiration and photosynthesis, respectively. The Stern laboratory studies how the remnant genes in plant organelles are regulated, thus coordinating their expression with their counterparts in the nucleus.

One major focus of the laboratory is enzymes that break down RNA chains, which are called ribonucleases (RNases). RNases both create the correct forms of RNA chains such as the RNA components of ribosomes, and also are required to recycle RNA to recover the embedded phosphorus, nitrogen and carbon. 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, when do their activities overlap, 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.

A second emphasis in the past two years has been to explain the presence and function of so-called antisense RNA, in the chloroplast. Sense RNA is predominantly studied, since its code specifies the proteins that accumulate in cells. However, antisense RNA can specifically bind to its sense RNA counterpart — they are coded on opposite sides of the same DNA strand — leading to repression of sense RNA expression. The Stern laboratory has studied the particular case of a chloroplast antisense RNA called AS5, showing that it can regulate protein synthesis rates in the chloroplast. This is the first time a chloroplast antisense RNA has been functionally characterized.

Finally, the Stern laboratory is investigating the assembly pathway for the enzyme Rubisco, which incorporates atmospheric carbon dioxide into sugar backbones. Because of its indispensable function, but its slow reaction speed, Rubisco is the most abundant enzyme on Earth. Therefore plants invest a great deal of nitrogen and energy to synthesize Rubisco, which consists of 16 protein subunits. Scientists have for many years wished to manipulate Rubisco to increase its catalytic rate, but testing mutant versions has been difficult because the plant enzyme can't be assembled in the test tube. The Stern laboratory project, if successful, will enable rapid tests of many Rubisco forms, and also reveal the still-unknown steps in its assembly pathway.



Joyce Van Eck, Ph.D.
Plant Breeding and Genetics
Senior Research Associate. BTI

### How do potatoes produce and accumulate beta-carotene?

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. The most recent findings have
shown that during long-term storage under cold conditions, the stored
Or potatoes accumulate an even greater amount of beta-carotene as
compared to Or potatoes that are not stored. Analyses are underway to
determine the mechanisms responsible for this increase in accumulation
during storage.

Van Eck's lab has also 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.

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