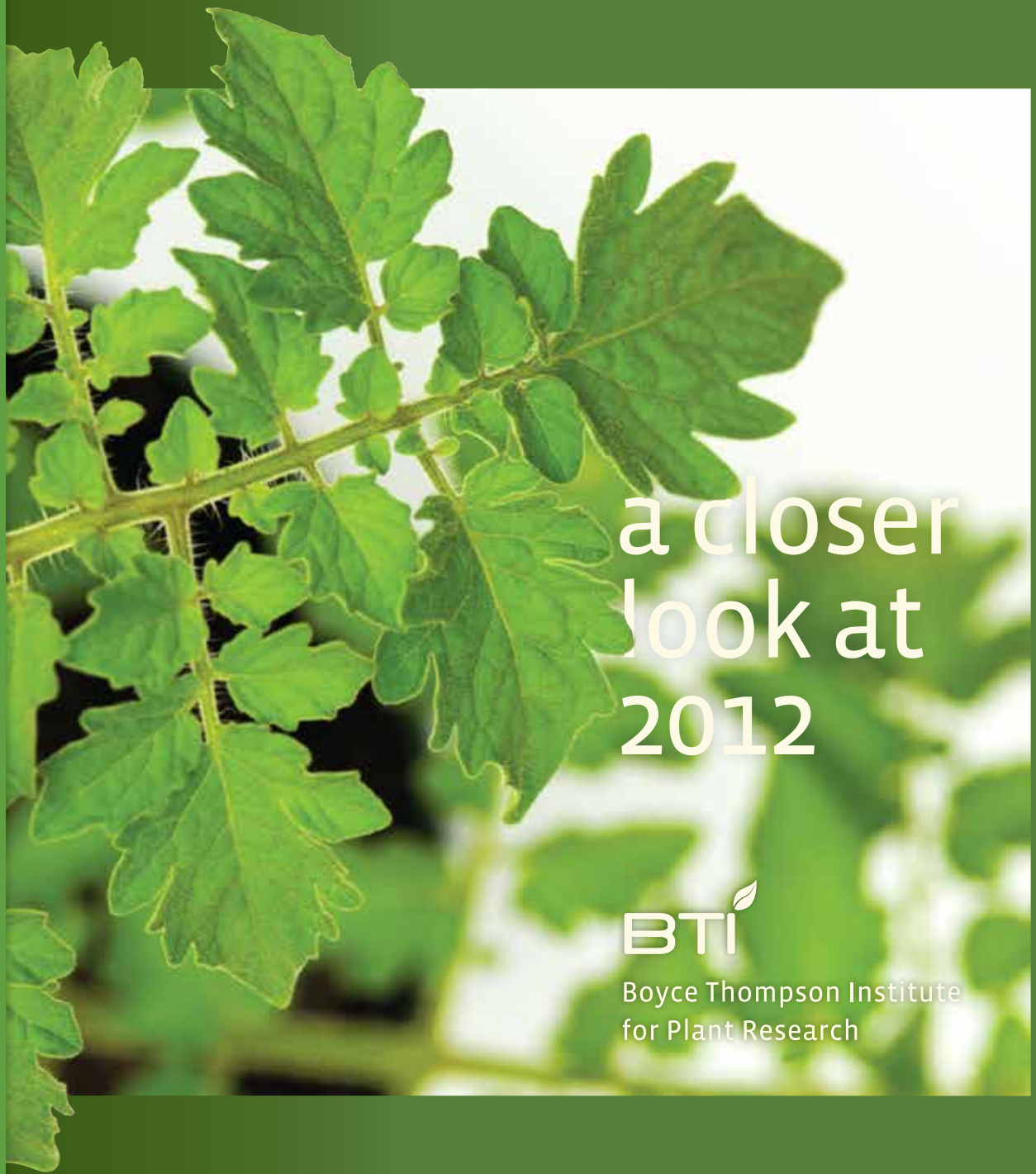

a closer look at 2012

BTI

Boyce Thompson Institute for Plant Research

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

officers

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WILLIAM BOYCE THOMPSON founded BTI in 1924 because he believed that basic plant research would lead to real benefits for human welfare. Today, BTI hosts 17 faculty-run laboratories, housing more than 150 researchers from 27 countries. Whether studying human health, plant nutrition, plant disease or environmental response, BTI scientists are bringing William Boyce Thompson's dreams to life every day. This work has the potential to improve food crops through increased yield and quality, to increase sustainability through reduced use of fertilizers and pesticides, to demystify plant and human immune systems, and to lower barriers to implementing alternative sources of energy. These discoveries are made possible because of one man's dream and the thousands after him, who believed in his vision.

board of directors

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president's message

Nearly 100 years after William Boyce Thompson founded BTI, the institute remains committed to basic research—the foundation genesis of virtually all real-world applications. In seeking the answers to fundamental questions about living things, plants, insects, microbes, and fungi, BTI scientists are building the foundations that make progress possible, whether in agriculture, human health, or bioenergy.

Since the discovery of DNA, scientists have longed to unravel the precise genetic codes, or genome sequences, of all living things. These sequences are the blueprints for life, but until recently, technological limitations and prohibitive cost made this dream unrealistic. In 2000, the first plant genome sequence was completed — a project that took more than four years and over $78 million. Since then, remarkable advances in laboratory and computing technologies have simplified the process to the point that an entire plant or human genome can be sequenced within days and for well under $1,000.

The plant science community as a whole, and many laboratories in BTI have taken advantage of the plummeting cost of DNA sequencing, resulting in an exponentially growing library of genetic information. The cumulative quantity of data is truly staggering, yet it must be easily accessed, and tools must be created to retrieve and analyze what is required for any given scientific question. This creates profound intellectual and computational challenges not just for plant biologists, but also across many scientific fields.

BTI is well positioned to profit from advances in informatics, because among its faculty are both computational and biological experts. In 2012, BTI scientists and their collaborators determined the complete genome sequences of several plants, with three "headline" accomplishments being tomato, watermelon, and a strain of tobacco used specifically for research.

A sequence is only a beginning: as you'll read in *the year in review* section of this report, everything from the flavor to disease resistance of fruits can be positively impacted by detailed genetic knowledge. Sequences provide ideas about plant characteristics that can be tested with further experiments. Ultimately, scientists would like to be able to predict a plant's growth and development from sequence alone, but this will also require equally deep knowledge of plant chemistry, gene function, and environmental interactions, which are also topics of intensive study at BTI. If predictive ability is achieved, it will usher in an era of research results contributing to society, and insights into plant functions will be made far more efficiently and quickly.

BTI's success in research depends on scientific creativity and excellence, but also on its state-of-the-art facilities. BTI is a first-class place to analyze small molecules, visualize structures within plant cells, and grow plants under precise conditions. BTI prides itself on providing a premier training environment, by investing in career-oriented activities for its postdoctoral associates and doctoral students, and by hosting a nationally-recognized education program that brings a diverse contingent of high school and undergraduate interns to BTI each summer, and develops plant biology and bioenergy curricula for New York state schools. BTI also provides its scientists support to identify and promote discoveries that have the potential for societal benefit, through its Office of Technology Transfer.

To stay in touch with the rest of world, BTI has increased its presence on the web: look for us on Twitter, Facebook, and through an all-new website. BTI not only makes discoveries, it communicates them to the world. After all, research is a truly international venture, just as our challenges in agriculture, health, and environment know no national boundaries. Thank you for your support and interest in the Boyce Thompson Institute.

Sincerely,

David Stern

year in review

With over 90 publications a year, BTI's halls are consistently filled with news and conversations on recent discoveries achievements, and collaborations. Here is a selection of stories from 2012 coming from the laboratories highlighting BTI research, awards, and outreach.

12.21.2012

SCHROEDER LABORATORY FOUND THAT WORMS HIJACK RNA BUILDING BLOCKS TO CONTROL DEVELOPMENT, CREATE UNIQUE SUGAR IN THE PROCESS

Assistant Professor Dr. Frank Schroeder and Dr. Ralf Sommer from the Max-Planck Institute reported that the roundworm *P. pacificus* regulates the morphology of its offspring through exposure to a potent cocktail of small-molecule signals, turning genetically identical juveniles into very different types of adults.

11.25.2012

BTI RESEARCHERS FIND CLUES INTO MORE DISEASE RESISTANT WATERMELONS, GENOME DECODED

An international consortium of more than 60 scientists, including Associate Professor Dr. Zhangjun Fei, published the genome sequence of watermelon *(Citrullus lanatus)*. This information could dramatically accelerate watermelon breeding towards production of a more nutritious, delicious, and resistant fruit.

10.22.2012

BTI INTERN PRESENTED AT SOCIETY FOR ADVANCEMENT OF CHICANOS AND NATIVE AMERICANS IN SCIENCE, INC (SACNAS)

Elena Cravens, a 2012 Plant Genome Research Program intern and winner of BTI's Best Scientific Presentation award, presented her summer research *Functional dissection of the VIM1 protein and its role in cytosine methylation in Arabidopsis* at the SACNAS conference in October. Elena talked about her BTI experience, "I know the skills and knowledge I gained at BTI over the summer will help me in future endeavors. The program exposed me to many different aspects of plant research separate from my project and gave me an accurate picture of what plant biology research entails." SACNAS awarded Elena a travel scholarship based on her 10-week research experience working in the BTI laboratory of VP for Research Dr. Eric Richards.

07.18.2012

DR. MARIA HARRISON, CO-PRINCIPAL INVESTIGATOR ON $6.5 MILLION NSF AWARD

Dr. Maria Harrison is a co-principal investigator on a research project that aims to understand and enhance symbioses between legumes and other plants that are crucial for sustainable agriculture. Many current agricultural practices require significant amounts of nitrogen and phosphorus fertilizers, which are restrictive, financially and environmentally. Understanding any possible beneficial symbioses between legumes and other plants could provide a more efficient use of these main fertilizer materials.

04.02.2012

SUGAR COULD BE A SWEET WAY TO CONTROL INSECT PESTS

Dr. Georg Jander worked with Cornell University's Angela Douglas to study the effects of sugar on insects, with the goal of controlling plant pests.

03.05.2012

AFRICAN SWEET POTATO DEVASTATION: BTI RESEARCH EXPANDED UNDERSTANDING OF VIRUSES

Dr. Zhangjun Fei was awarded a $700,000 grant to work with a team of researchers to explore viruses that devastate sweet potato crops in Africa.

11.30.2012

THREE RESEARCHERS HONORED AS AMERICAN ASSOCIATION FOR THE ADVANCEMENT OF SCIENCE (AAAS) FELLOWS

Dr. Maria Harrison, Dr. Georg Jander, and Dr. Daniel Klessig were awarded honors of distinction by AAAS. The three selected scholars brought the number of BTI fellows to nearly 50% of BTI's faculty.

11.13.2012

FACULTY WORK WITH USDA, ARS TO DEVELOP GLOBAL DISTRIBUTION MAP OF TOMATO VIRUS

Dr. Zhangjun Fei and his collaborators at USDA, ARS were awarded support from the The National Institute of Food and Agriculture's Specialty Crop Research Initiative (SCRI) to generate a comprehensive global virus distribution map for tomatoes and to develop breeders' tools to enhance virus resistance.

07.05.2012

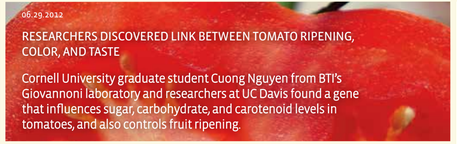
POWERFUL SCREENING EXPOSES THE ROLES OF SALICYLIC ACID

Dr. Zhangjun Fei, Dr. Daniel Klessig, and Dr. Sorina Popescu worked together to identify proteins that bind the plant hormone salicylic acid. This knowledge will potentially lead to a better understanding of the hormone—a close relative of aspirin—and its many physiological effects by unraveling its role in how plants respond to abiotic and biotic stresses.

06.29.2012

RESEARCHERS DISCOVERED LINK BETWEEN TOMATO RIPENING, COLOR, AND TASTE

Cornell University graduate student Cuong Nguyen from BTI's Giovannoni laboratory and researchers at UC Davis found a gene that influences sugar, carbohydrate, and carotenoid levels in tomatoes, and also controls fruit ripening.



05.30.2012

TOMATO GENOME FULLY SEQUENCED – PAVING THE WAY FOR HEALTHIER FRUITS AND VEGETABLES

Dr. James Giovannoni, Dr. Zhangjun Fei, Dr. Greg Martin, Dr. Lukas Mueller, and Dr. Joyce Van Eck played a major role in successfully decoding the genome of tomato *(Solanum lycopersicum)*, marking an important step toward improving yield, nutrition, disease resistance, taste, and color of the tomato and other crops. The project, highlighted as the cover article in the May 31, 2012 issue of *Nature*, was a joint effort by the Tomato Genomics Consortium, a group with members from 16 countries. BTI produced a short video highlighting the project, which can be found on our YouTube channel (BTI Science) and our website. To date, it has had almost 800 views.

02.25.2012

ASSOCIATION OF INDEPENDENT PLANT RESEARCH INSTITUTES (AIPI) ANNOUNCED FIRST ROUND OF COLLABORATIVE GRANT AWARDS

Leaders from BTI, the Department of Plant Biology at the Carnegie Institution for Science (Stanford, CA), the Donald Danforth Plant Science Center (St. Louis, MO), and The Samuel Roberts Noble Foundation (Ardmore, OK) formed AIPI to increase national awareness and support for plant research and to foster collaborations between the participating institutions.

An important initiative instituted by AIPI was a seed grant program that funds cooperative projects among scientists from the member organizations. Awards in this program occur twice a year and offer $10,000 to $50,000 to support innovative projects involving researchers from two or more member organizations. Eligible projects are designed to produce proof-of-concept data or planning activities to facilitate preparation of applications for larger grants from other sources. In 2012, three collaborative awards were granted.

01.09.2012

COMPARATIVE METABOLOMICS REVEALED BIOGENESIS OF ASCAROSIDES, A MODULAR LIBRARY OF SMALL MOLECULE SIGNALS IN *C. ELEGANS*

Dr. Frank Schroeder demonstrated the utility of applying MS/MS-based comparative metabolomics to a series of mutant strains for characterizing the biosynthetic pathway of small signaling molecules called ascarosides.

11.29.2012

BTI ASSISTANT PROFESSOR WORKING WITH CORNELL UNIVERSITY ON DATABASE FOR NEXTGEN CASSAVA PROJECT

BTI's Dr. Lukas Mueller began working on the NEXTGEN Cassava project at Cornell University in the fall of 2012. The project is an international consortium of seven institutions from the United States, Nigeria, and Uganda who are working together to improve cassava productivity and build human and technical capacity for plant breeding in sub-Saharan Africa. The Mueller laboratory is developing the central database, which will make the data accessible to all collaborators and plant breeders.

10.22.2012

HARRISON LABORATORY DISCOVERED INSIGHTS TO PLANT ROOT BEHAVIOR

Dr. Maria Harrison, BTI Professor and William H. Crocker Research Scientist, collaborated with researchers from Cornell University to image root growth using a 3-dimensional laser sheet imaging technique.

08.30.2012

BTI RESEARCHERS PUBLISHED A DRAFT GENOME OF AN EXPERIMENTALLY IMPORTANT STRAIN OF TOBACCO

BTI researchers Dr. Greg Martin, Dr. Lukas Mueller, Dr. Aureliano Bombarely, Dr. Hernan Rosli, Dr. Julia Vrebalov, and Université de Sherbrooke researcher Dr. Peter Moffett worked together to generate the sequence of *Nicotiana benthamiana*. The sequence contains information on more than 90% of the plant's genes and has been one the top downloaded articles on the website, Molecular Plant-Microbe Interactions.

BTI
Boyce Thompson Institute for Plant Research

outreach & education

TRAINING TOMORROW'S SCIENTISTS...

An important part of our mission entails communicating scientific knowledge to the public. To do so, BTI established a Center for Plant Science Teaching and Learning, which hosts an extensive education and outreach program that includes professional development for teachers, research experience for undergraduates, and educational involvement in the local community. The Center's overall goal is to engage students and teachers in authentic plant science research.

The center, directed by Tiffany Fleming, provides alternative models in plant science education that connect scientists to teachers and students. In 2012, over 125 science teachers attended seminars and field trips, conducted classroom lab activities, and designed inquiry-based lesson plans for their students. Participants also joined the BTI teacher network, an online community where teachers share student data, curriculum plans, and interests in science education while receiving reciprocal support for meeting their teaching goals.

In 2012, BTI's Plant Genome Research Program provided 27 students with an intensive 10-week research-based internship. Working alongside seasoned scientists, students acquired laboratory techniques, developed scientific writing skills, attended guest lectures by scientists, and presented their research at the annual BTI Student Symposium. In its 11th year, the program gave students an opportunity to participate in hands-on plant science research in our research laboratories.

2012 marked the second year of a $5 million USDA grant for Bioenergy and Bioproducts Education Programs (www.bioenergyed.org), collaboration between BTI and eight other institutions. The program provides educators with professional development tools to integrate information on bioenergy and bioproducts systems currently in use and under development in the United States. To this end, BTI—led by our Education Specialist Amanda Gurung—hosted educators at workshops, provided teaching fellowships and research internships, and gave post-program classroom support.

BTI brought plant science into the classrooms of over 3,500 middle and high school students in New York State with the distribution of Plant Experiment Kits, classroom visits and participation in local community educational events, such as Career and Focus Days with local middle and high schools and an Expanding your Horizons conference with the Cornell Center for Materials Research. BTI's education and outreach programs spark passion in students new to plant research, while arming teaching professionals with the skills they need to prepare the next generation of scientists.

outreach & education in numbers

Over 5,400 people paticipated in BTI sponsored education and outreach programs last year.

107 programs

27	Presentations and Trainings
10	Total Classroom Visits
70	Experiment Kits (distributed and explained)

5,441 participants

125	Teachers
3,589	K—12 Students
111	BTI and Cornell Faculty, PGS, Staff
1,616	Undergraduate Students

134 volunteers

21	Community Volunteers
72	University Faculty
41	Graduate and Postdoctoral Students

external relations

FOR THE ADVANCEMENT OF SOCIETY...

To help achieve BTI's mission of having a positive impact on society, the Office of Technology Transfer works to identify potential partners who are interested in commercializing technologies discovered or developed by Institute scientists. Paul Debbie, Director, Technology Transfer and Licensing and Karen Kindle, Principal Liaison for Technology Marketing and Licensing, showcased BTI technology to more than a dozen corporate partners. Our staff establish the following types of associations: 1) Licensing agreements, which allow licensees a fee-based usage of specific BTI technologies; 2) Collaborations, in which industry and institute scientists collaborate on industry-funded research to advance early technology to the point where it is ready to be developed into a product; and 3) Consulting agreements, which introduce potential partners to particular BTI scientists, where their expertise may be valuable to specific projects.

Technology development occurred at a brisk pace in 2012, with thirteen new invention disclosures submitted to the office and six new patent applications filed on BTI technology. In addition, BTI executed over forty materials transfer agreements, which govern the sharing of research resources.

RAISING AWARENESS AND SUPPORT...

Prior to the 20th century, most scientific research was performed and paid for by patrons or by individual scientists—usually through personal funds. In the United States, the Morrill Acts of 1862 and 1890 also brought essential funding to colleges and universities for agriculture education and research. Today, BTI still benefits from these types of funds. Since the early 1900s, corporations' research and development units, government programs, and private donations have provided additional funding for scientific research.

Despite the obvious benefits of investment in research, public funding has stagnated in recent years as the country endured a recession and became focused on deficit reduction. The result is missed scientific opportunities, low funding success rates (even for highly creative ideas) and discouragement among the next generation who might otherwise opt for careers in plant research. To mitigate these obstacles, it is becoming more important for organizations to have strong mechanisms to maintain and nurture diverse funding sources. To that end, in 2012, BTI reshaped its external relations and development department with the goal of increasing public awareness of our research programs and examining ways to expand support from foundations, corporations, and individuals.

Led by Director of Development and External Relations Bridget Rigas, the 2012 focus was building departmental infrastructure and enhancing awareness of BTI's research. We increased outreach to national and international media, established social media pages (Facebook, Twitter, LinkedIn, YouTube, and Tumblr), increased local knowledge on BTI through support of local public radio stations, and redesigned our website to be more engaging to the public, educators, and potential collaborators and to provide a sharper message on BTI.

communication in numbers

Below is a brief summary of activity for BTI's online presence. Facebook and Twitter accounts were activated in April of 2012.

WEBSITE BTI.CORNELL.EDU	104,861	Website visits
	52,528	Unique visitors
	306,067	Page visitors
FACEBOOK BoyceThompsonInstitute	160	Fans
	27,118	Content *likes*
	294,427	Viewers of *liked* BTI content
TWITTER BTIscience	250	Followers
	450	Tweets

charitable giving

GIVING TO THE BOYCE THOMPSON INSTITUTE

From William B. Thompson's cornerstone contribution in 1924 to the support we receive today, BTI science is made possible, in part, through the generosity of donors who appreciate the importance of basic research and its usefulness in solving larger global issues.

We take this opportunity to thank and recognize the following individuals and organizations who made gifts in 2012. To learn more about the benefits associated with giving to BTI, as well as designated opportunities, such as sponsoring a laboratory, specific research projects, or student interns, please call our development office at (607) 254-2923.

William and Anne Thompson Society
$5000 +
Anonymous
Estate of Anthony "Andy" Grefig
Estate of Leonard Weinstein

William Boyce and Gertrude Thompson Society
$2000 —4,999
Ithaca Garden Club
Mr. and Mrs. Roy H. Park, Jr.
Laura A. Philips and John A. Elliot
Carolyn W. Sampson

Chairperson's Circle
$1,000—1,999
Mary E. Clutter
Ezra and Daphne Cornell
Greg Galvin
Philip and Anette Goelet
Susan and Gregory Martin
David and Karen Stern

President's Circle
$500—999
Anonymous
Peter J. Bruns and Jennifer Shea
Rich and Joan Curtiss
Sophia and Nick Darling
Maria J. Harrison
Melissa and Eric Richards
Bridget M. Rigas
Donald and Marcia Slocum
Kathryn W. Torgeson

Alder Society
$100—499
Klaus Apel
Charles and Kathy Arntzen
Dr. Richard C. Back
Barbara Holowka Baird
Andrew Bass
Donald and Holly Beermann
Brian Bell
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Patti FitzPatrick
William and Barbara Fry
Shan Gao
Bob and Johanna Granados
Greg and Bev Hartz
Stephen and Elizabeth Howell
Dr. Andre T. Jagendorf
Patricia A. Johnson
Robert and Roberta Kohut
Terry and Cathy Lauver
Lynn B. Leopold
Anthony M. Marzullo, Sr.
Dr. Robert C. Miller
Kelli Monce and Rick Bayo
Charlie and Patricia Paucke
Anne Razer and Thomas J. Rice
Catherine Racer
Alan and Anne Renwick
Kira and Felix Sheinerman
Mark D. and Jane R. Siegwarth
Fred A. (Ben) Williams
Yi Zhang and Jianjun Yang

Friends of BTI
$2—100
Mrs. Joan M. Althaus
Thomas J. and Judith A. Burr
Anthony Carpi
John Dyba
Howard P. Hartnett
Dr. Betty Fong Zuzolo

Gift Designations
In Support of Research Programs
Dr. Richard C. Back
Maria J. Harrison
Kathryn W. Torgeson

In Support of Educational Programs
Dr. Richard C. Back
Maria J. Harrison

In Support of the Summer Internship Program
Carolyn Sampson
Ithaca Garden Club

For the President's Discretionary Fund
Barbara Baird Holowka
Bridget M. Rigas

Building a Legacy: Anthony "Andy" Grefig

Anthony "Andy" Grefig, who passed away in January 2009, began his BTI career in 1965 when the institute was still in Yonkers, NY. Hired as a research assistant with Dr. Lee Crisan, he worked on the biochemistry of fungi. In 1967, Andy took a position in Alan Renwick's analytical service lab, where he remained for the next 21 years, moving with BTI to Ithaca in the 1970s. After retiring in 1988, Andy continued to work as a volunteer for the institute for several years.

In small acts, like his daily kindness toward colleagues, and in grand gestures, like providing students free housing for over 25 years, Andy's life was dedicated to generously supporting BTI, its science, and its community. The depth of that generosity was proven by Andy's estate gift of $250,000 to BTI's endowment in 2012. His gift will allow scientists the freedom to perform research directed through curiosity—where many great discoveries are born.

Having a strong and healthy endowment is key to producing a robust research program focused on the fundamental discovery of plant functions, and providing the grounds for solutions—through BTI research—to many of our global and society issues. Planned gifts to our endowment can be established in ways that benefit BTI as well as you, your family, or another charity. If you are interested in learning more about how to include BTI in your estate plans, please contact Bridget Rigas, Director of Development and External Relations at (607) 254-2923.

memorials

In memory of Ralph E. Althaus
(gift from) Mrs. Joan M. Althaus

In memory of Donald G. Baird
Barbara Holowka Baird

In memory of Alan Bell
Brian Bell

In memory of Ursula Bruns, who loved plants of all kinds
Peter J. Bruns and Jennifer Shea

In memory of Dr. Harry P. Burchfield
Eleanor Storrs Burchfield

In memory of Dr. Horace G. Cutler
Mrs. Joanne S. Cutler

In memory of Irene Zachar Dyba
John Dyba

In memory of A. Carl Leopold
Lynn B. Leopold

In memory of Lawrence P. Miller
Dr. Robert C. Miller

In memory of Leonard Weinstein
Robert and Roberta Kohut
Sylvia Weinstein

financials

RESEARCH AND OTHER RESTRICTED SUPPORT

The Boyce Thompson Institute for Plant Research receives a substantial portion of their research funding through grants from the federal government, private foundations, corporations, and individuals. The following section lists new research awards received in 2012 and our fiscal year financial overview.

2012 research grants awarded

GOVERNMENT	
National Science Foundation	$ 2,762,589
US Department of Agriculture	$ 602,515
FOUNDATIONS	
Triad Foundation	$ 250,000
US-Israel Binational Science Foundation	$ 126,500
CORPORATIONS AND OTHER SUPPORT	
Binational Agricultural Research & Development Fund	$ 289,000
Next Generation Cassava Project	$ 1,817,136
Corporate Funding	$ 567,618
Other Support	$ 114,325
Total New Research Grants Awarded	**$ 6,529,683**

2012 annual financial report

INCOME SOURCES		%
Federal Government	$ 6,822,000	50
Institutional Endowment	$ 2,951,000	21
NYS Land Grant Provision	$ 1,580,000	12
Foundations	$ 222,000	2
Other Private Sources	$ 822,000	5
Unrestricted Revenues	$ 1,330,000	10
Total Operating Income	**$ 13,717,000**	

EXPENSES		%
Research Activities	$ 9,565,000	70
Research Support	$ 1,221,000	9
Research Facility Expenses	$ 388,000	3
Administration	$ 2,055,000	15
Intellectual Property	$ 305,000	2
Development & Communications	$ 183,000	1
Total Operating Expenses	**$13,717,000**	

scientific publications of 2012

Avila, J., Gregory, O.G., Su, D.Y., Deeter, T.A., Chen, S.X., Silva-Sanchez, C., Xu, S.L., Martin, G.B. and Devarenne, T.P. (2012) The beta-subunit of the SnRK1 complex is phosphorylated by the plant cell death suppressor Adi3. *Plant Physiology*, **159**, 1277-1290.

Barry, C.S., Aldridge, G.M., Herzog, G., Ma, Q., McQuinn, R.P., Hirschberg, J. and Giovannoni, J.J. (2012) Altered chloroplast development and delayed fruit ripening caused by mutations in a zinc metalloprotease at the lutescent2 Locus of tomato. *Plant Physiology*, **159**, 1086-1098.

Bennetzen, J.L., et al. (2012) Reference genome sequence of the model plant Setaria. *Nature Biotechnology*, **30**, 555-561.

Berger, F., et al. (2012) Reading the second code: Mapping epigenomes to understand plant growth, development, and adaptation to the environment. *Plant Cell*, **24**, 2257-2261.

Bombarely, A., Edwards, K.D., Sanchez-Tamburrino, J. and Mueller, L.A. (2012) Deciphering the complex leaf transcriptome of the allotetraploid species Nicotiana tabacum: a phylogenomic perspective. *BMC Genomics*, **13**, 406.

Bombarely, A., Rosli, H.G., Vrebalov, J., Moffett, P., Mueller, L.A. and Martin, G.B. (2012) A draft genome sequence of Nicotiana benthamiana to enhance molecular plant-microbe biology research. *Molecular Plant-Microbe Interactions*, **25**, 1523-1530.

Bose, N., Ogawa, A., von Reuss, S.H., Yim, J.J., Ragsdale, E.J., Sommer, R.J. and Schroeder, F.C. (2012) Complex small-molecule architectures regulate phenotypic plasticity in a nematode. *Angewandte Chemie-International Edition*, **51**, 12438-12443.

Cai, D.Y., Rodriguez, F., Teng, Y.W., Ane, C., Bonierbale, M., Mueller, L.A. and Spooner, D.M. (2012) Single copy nuclear gene analysis of polyploidy in wild potatoes (*Solanum* section *Petota*). *BMC Evolutionary Biology*, **12**, 70.

Cao, Y., Tang, X., Giovannoni, J., Xiao, F. and Liu, Y. (2012) Functional characterization of a tomato COBRA-like gene functioning in fruit development and ripening. *BMC Plant Biology*, **12**, 211.

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BTI

Boyce Thompson Institute for Plant Research

laboratory reports

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How do plants respond to 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 the Apel 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.

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How do viruses infect insects?

Certain viruses are our allies in the fight against insect pests. Research that leads to a better understanding of how viruses interact with insects will result in environmentally friendly and sustainable methods of insect control, and advances in human health. In one research project, Gary Blissard has been studying how certain viruses, called baculoviruses, infect and interact with 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 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 and they found that the virus can bind to artificial membranes that are devoid of protein, explaining how the virus gets into many diverse cell types.

After the virus binds to the surface of the host cell, it then enters the cell and 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. Blissard's group has recently identified critical amino acids in the GP64 protein, that are necessary for both the initial interaction between virus and host membrane, and fusion of the two membranes.

After the viral DNA is released into a cell, the virus takes over the cell and transforms it into a factory specialized for virus production. How does this occur? To answer this complex question, Blissard's group has performed a transcriptome analysis of the viral infection. This technique allowed them to simultaneously monitor the activity of approximately 156 viral genes in the entire virus genome, as well as the activity of the entire host cell genes. This has resulted in an unprecedented new appreciation of the complexity of interactions between the two DNA genomes (virus and insect cell) over the course of the entire infection cycle: from the first few hours through several days, when the cell has been completely conquered by the virus.

Knowing how baculoviruses enter and then take over 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 certain 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.

The Blissard group is also now applying technology developed for studies of baculovirus envelope protein GP64, to the study of an envelope protein of an important human pathogen, Dengue virus. Their goal is to understand how human viruses such as Dengue are able to interact with and move through the cells of the insect gut, a process that permits virus transmission through the insect and to the next human host. Studies of these virus-insect interactions will be important for understanding both plant and animal viruses that use insects as vectors for their dissemination.

Jim Giovannoni, Ph.D.
Professor, BTI
Plant Molecular Biologist, USDA, ARS Plant, Soil and Nutrition Laboratory
Adjunct Professor, Department of Plant 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 where 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 has focused on identification of genes necessary for regulation of the ripening process and has recently identified several new transcription factors essential to the process. These include 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, in addition to two negative regulators of ripening, AP2a and ERF6. In the last year we also reported a gene termed UNIFORM RIPENING that influences fruit pigmentation and defines a gradient of ripening along the longitudinal axis of the fruit.

Additional activities in the last year included cooperation with over 300 international researchers (including a number at BTI) to complete and publish the genome sequence of tomato. The laboratory then used this sequence as the basis of novel discoveries on the role of changes in the epigenome in controlling fruit ripening.

Current activities include efforts to discover how the epigenome may contribute to additional aspects of fruit biology and how the TAGL1, AP2a and ERF6 genes function in context with each other and additional fruit development and ripening genes previously identified and described by the Giovannoni laboratory and others. Work is also continuing in testing for similar genes and functions in species beyond tomato. 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.

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

How do bacterial pathogens undermine AND activate the plant immune system?

The Martin laboratory studies the molecular basis of bacterial pathogenesis, plant disease susceptibility, and plant immunity. Most of the research focuses on bacterial speck disease which is caused by the infection of tomato leaves with the pathogen *Pseudomonas syringae* pv. tomato. This is an economically important disease that can decrease both the yield and quality of tomato fruits. It also serves as an excellent model system for understanding plant-pathogen biology because much is known about the molecular biology of this pathosystem and many genomics resources are available for both tomato and *P. s.* pv. tomato.

In the tomato-Pseudomonas interaction, the bacterial type III secretion system delivers the virulence proteins AvrPto and AvrPtoB into the plant cell. Both proteins then act to suppress early host defenses and thereby promote plant disease susceptibility. Some tomato varieties express the Pto gene which encodes a protein kinase that detects the presence of AvrPto and AvrPtoB and confers resistance to bacterial speck disease. The Pto kinase is activated upon binding AvrPto or AvrPtoB and then acts in concert with Prf, a protein containing a nucleotide-binding site and a region of leucine-rich repeats (i.e., an NB-LRR protein). This recognition event activates a complex series of signaling events that leads ultimately to host defense responses, including transcriptional reprogramming and localized host cell death, that restrict growth of the pathogen. Currently, next-generation sequencing methods are being used to identify tomato genes whose expression increases in response to various *P. s.* pv. tomato strains. The genes identified are then being functionally characterized by using virus-induced gene silencing.

In related work, the laboratory has found that a C-terminal domain of AvrPtoB encodes an E3 ubiquitin ligase that, in certain tomato varieties, can interfere with activation of the host resistance response. Thus, some bacterial virulence proteins appear to have evolved to suppress both basal and resistance-gene mediated host defenses and plants have, in turn, evolved to interfere with both of these activities.

To further understand the molecular basis of bacterial virulence, plant immunity, and susceptibility in this pathosystem we are using various experimental approaches including: genomics, biochemistry, bioinformatics, cell biology, molecular biology, forward and reverse genetics, and structural biology. Our long-term goal is to use the knowledge we gain about plant-pathogen interactions to engineer plants for increased resistance to diseases and thereby lessen the need for synthetic chemical inputs.

Eric J. Richards, Ph.D.
Vice President for Research, BTI
Adjunct Professor, Department of Molecular Biology & Genetics, Cornell University

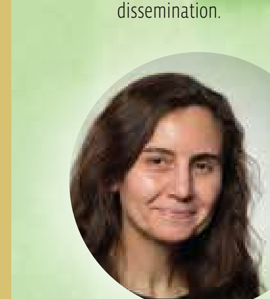
Is there more to inheritance than genetics?

As is widely known, excessive exposure to the sun's radiation can cause normal skin cells to become cancerous. In this case, cancer occurs because radiation causes changes in the cell's DNA sequence (mutations) within genes that regulate cell division. But cancer and other diseases can also occur when certain genes that might have protected the cell are "silenced" or turned off. Although the protective genes are still present, they can become "unreadable" and disease can result. Understanding how these genes become inaccessible 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 which a small chemical group is added to one of the DNA bases (cytosine). Both the gene and its new methylation state can be passed on to new generations of cells and, in some cases, organisms. Consequently, alterations in DNA methylation might play important roles in inheritance and adaptation, just as mutations do.

The Richards laboratory 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. Richards 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. Epigenetics also has important potential applications in agriculture, because epigenetic modifications such as DNA methylation can affect important traits in crop plants, such as disease resistance and flowering time. Consequently, advances in this field of genetics could lead to higher quality food and increased yields.



Carmen Catalá, Ph.D.
Adjunct Assistant Professor, BTI
Senior Research Associate, Department of Plant Biology, Cornell University

How do plant hormones control fruit development?

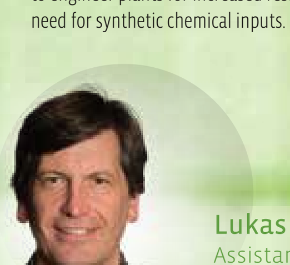
When home gardeners or horticulturalists grow plants from stem cuttings, they often dip the cut end of the stem in a white powder that encourages the stem to develop roots. The white powder is a hormone, called auxin, which plays an important role in plant growth and development. Auxins also influence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

It is also known that auxins, particularly indole-3-acetic acid, are central to the development and ripening of fruit, such as strawberries and tomatoes. Work on auxins conducted with strawberries 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. But very little is known about the molecular basis of auxin production, transport, and signaling in fleshy fruit-producing plants. Understanding these processes is the basis of Catalá's research 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. Catalá is applying knowledge gained about auxins in Arabidopsis 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 fruit, how it is transported to the different fruit tissues, and how it signals the cells in that tissue to grow, develop, and ripen. What Catalá learns in tomatoes will be applicable to other fleshy fruits as well.

Knowing at the molecular level how auxins help plants set fruit 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.

Another area of research in the Catalá laboratory focuses on the discovery of genes and networks regulating tomato fruit shape and size. In tomato domestication and extensive selection for fruit characteristics has given rise to large variations in fruit morphology. One of the objectives of this research is to gather information about genes that are expressed during tomato fruit development and that control fruit growth and shape. As part of this project the Catalá laboratory is generating maps of tissue and cell-specific gene expression in the developing tomato fruit using Laser Capture Microdissection, a technique that allows the isolation of specific cells or tissues from plant organs. This research is generating unprecedented data sets that will provide the basis for exploring key aspects of fruit biology.



Lukas Mueller, Ph.D.
Assistant Professor, BTI
Adjunct Assistant Professor, Department of Plant Breeding and Genetics, Cornell University

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

Consider that thousands of scientists are working globally 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 a number of genome sequencing projects, most notably the tomato genome project, which is the work of scientists in 16 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 source data. 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 to increase yield or enhance nutritional quality.

Frank Schroeder, Ph.D.
Assistant Professor, BTI
Adjunct Assistant Professor, Department of Chemistry and Chemical Biology, Cornell University

Can biogenic small molecules help us better understand development and aging?

The relevance of nucleic acids, proteins, and carbohydrates for all aspects of biology is well established, but the varied and often unexpected roles of small molecules produced by biological systems are just now emerging. Such biogenic small molecules regulate development and immune response in plants and animals (as hormones, for example) and also play an important role in the interactions of different organisms with each other.

Biogenic small molecules are very different from proteins and nucleic acids, which are polymers built from a limited set of building blocks. In contrast, biogenic small molecules are an extremely diverse class of compounds that 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 structures of these compounds and to find their biological functions. Using this approach, Schroeder's team is investigating the role of biogenic small molecules in specific aspects of plant and animal biology, including the phenomenon of aging.

In one area of research, Schroeder is investigating biogenic small molecules produced by the nematode *Caenorhabditis elegans*. Nematodes are roundworms that are roughly one millimeter 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 the entirety of its small molecules, usually referred to as the "metabolome." Over the past 5 years, the Schroeder group identified a library of several 100 compounds that regulate nematode lifespan, development, and several different social behaviors. These studies revealed that *C. elegans* uses a modular "chemical language" to communicate a large variety of different messages. The ultimate goal of this research is to characterize the signaling pathways that the identified *C. elegans* small molecules act in, including the identification of biosynthetic pathways, specific receptors, and downstream molecular targets.

In other research, Schroeder and colleagues recently used their NMR-spectroscopic approach to identify a large group of small molecules produced by a filamentous fungus, the human pathogen *Aspergillus fumigatus*. *A. fumigatus* is the causative agent of invasive aspergillosis and uses specific small molecules, called virulence factors, to overcome the immune responses of its mammalian hosts. Schroeder's research showed that this pathogenic fungus produces a much greater number of potential small molecule virulence factors than previously suspected. Knowledge of the structures and biosynthetic regulation of these small molecules provides insight in host pathogen interactions and may contribute to new approaches for the treatment of fungal infections.

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

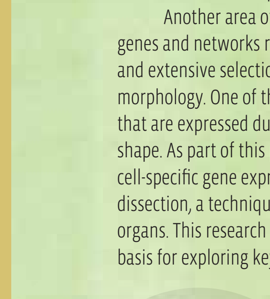
How do soil fungi supply plants with mineral nutrients?

In nature, plants and certain fungi, called arbuscular mycorrhizal (AM) fungi, have evolved a complex, symbiotic relationship in which plants provide the fungi with carbon while the fungi provide plants with phosphate needed for cell function and growth. Understanding this relationship may enable crop production with fewer applications of phosphate fertilizers.

Working with an AM fungus and a legume plant, *Medicago truncatula*, Maria Harrison's laboratory is unraveling the mechanisms underlying mineral nutrient transfer from the fungus to the plant. AM fungi are ubiquitous in soil and live in close proximity to plant roots. In response to a signal from the plant, the fungi grow into the roots and establish themselves inside the root cells. The plant surrounds the fungus in a membrane, called the periarbuscular membrane, and nutrients are exchanged across this membrane.

Several years ago, the Harrison laboratory identified phosphate transporter proteins that capture phosphate delivered by the fungus and move it into the root cell. The phosphate transporters are located exclusively in the periarbuscular membrane. Researchers in the Harrison laboratory were intrigued by the specificity of the location and carried out studies to determine how the phosphate transporters are sent to this specific location. Using proteins called green fluorescent protein (GFP), they were able to show that the timing of transporter protein production and changes in the direction of protein secretion in the cell, enable the proteins to be placed specifically in the periarbuscular membrane. Identifying the signals that trigger these cellular changes is the next step in her research.

Today, farmers 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 lakes and 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.



Michelle Cilia, Ph.D.
Assistant Professor, BTI
Research Molecular Biologist, USDA, Agricultural Research Service
Adjunct Assistant Professor, Department of Plant Pathology and Plant-Microbe Biology, Cornell University

How do viruses commandeer plants and insects to promote their own transmission?

Viruses cause millions of dollars of damage to food crops every year and are often at the root of food shortages in developing nations. Despite their importance to human wellbeing and the global economy, little is known about the relationships between plants, viruses, and the insects that spread these diseases.

Michelle Cilia, who recently joined BTI, holds a collaborative position between BTI and the Robert W. Holley Center for Agriculture and Health, US Department of Agriculture, Agricultural Research Service. She was hired by the USDA, ARS to develop a research program that tackles the fundamental biology of insect vectors and the plant viruses they transmit. Using a combination of traditional approaches and new, cutting edge mass spectrometry techniques, the Cilia laboratory studies the three-way relationships between virus, plant, and vector to develop a comprehensive understanding about how insects transmit viruses. Cilia hopes to identify ways in which the system might be manipulated to prevent infection, protecting crops and the communities that rely on them.

As an important first step towards achieving her goals, Cilia initiated a collaboration with the Bruce laboratory at the University of Washington to use advanced technologies to study how plant and insect proteins physically interact with viruses. Using a new technique called Protein Interaction Reporter (PIR) technology, Cilia and her colleagues mapped the structure of two key virus proteins and identified the surface features that are functionally important to the virus. The work is the first to provide these types of measurements on any infectious virus particle and the first structural insights into a virus in the family *Luteoviridae*, an economically important family of plant pathogens. The team will use these data to develop new ways to block the virus from infecting plants.

Cilia also holds an appointment as an adjunct Assistant Professor in the Department of Plant Pathology and Plant-Microbe Biology at Cornell University. Via her appointment at Cornell, Cilia is part of a team funded by the National Science Foundation's Basic Research to Enable Agricultural Development program. The team is working with scientists in Africa, where insect vectors are responsible for transmitting viruses to a variety of security crops. A major obstacle in vector management is that not all members of a vector species are able to transmit viruses. Cilia and her colleagues discovered a panel of protein biomarkers that can distinguish between insects that can transmit viruses and those that cannot. Cilia is exploring how to use these proteins in a simple assay to identify populations of insects that may threaten crops. In collaboration with scientists at USDA, Cornell, the University of Washington, and the International Institute for Tropical Agriculture in Africa, Cilia and her team are finding ways to expand the work to insect vectors that infest cassava, banana, and legumes so that farmers and scientists can identify the insect populations that transmit viruses before they strike. Cilia will host two visiting graduate students from Nigeria and Cameroon to work in collaboration on the project in 2013.

Cilia's long-term research plans will enable us to understand the co-evolutionary race between plants and viruses at the molecular level and to develop practical strategies that can be transferred to growers for virus and vector management.

Sorina Popescu, Ph.D.
Assistant Professor, BTI
Adjunct Assistant Professor, Department of Plant Biology and Department of Plant Pathology and Plant-Microbe Biology, Cornell University

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 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 standing 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 pests and growth and survival depend on it.

The Popescu laboratory studies the rich and complex system for signal sensing and intracellular transduction in tomato and the model plant Arabidopsis. The core of the cellular signaling mechanisms is represented by the protein kinases, a diverse class of enzymes that transfer a small phosphate tag onto proteins and other molecules. In her work with protein kinases, Popescu is employing special techniques that allow her to survey hundreds to thousands of proteins in parallel. 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. With another technique developed in her lab, she is able to screen interactions between tomato kinases and pathogen proteins directly in live tomato cells. 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.

Understanding how plants respond and acclimate to stress is a first step toward meeting agricultural and health challenges as the world faces increasing population, urbanization, and climate change. Popescu studies plant protein kinases to understand how they assemble in signaling pathways to activate the response to stress. She tries to understand how kinases orchestrate appropriate modification in the cellular proteome and gene transcription program of the cells, so that the final decision on how a plant will defend itself is reached. Her work has already led to the identification of proteins and cellular pathways that were never studied in the context of plant disease resistance and abiotic stress. These findings could lead to a new understanding of how plant defense mechanisms work. It could also lead to new ways to protect plants from environmental stress factors.

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

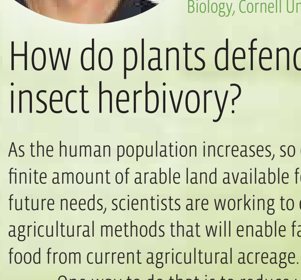
How do plants coordinate genes in different compartments?

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 also essential, because they specify proteins needed for respiration and photosynthesis, respectively. The Stern laboratory studies processes in plant chloroplasts, including carbon fixation and gene expression, and is also involved in projects seeking to adapt the chloroplast to bioenergy production.

One long-time interest 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 feature an "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 – to the point where embryos and seeds are unable to develop? By using biochemical and genetic approaches, as well as newer high-throughput methods, some of the answers are being discovered.

In another project, the Stern laboratory is attempting to solve the decades-old problem of how the enzyme Rubisco, which incorporates atmospheric carbon dioxide into sugar backbones, is assembled. Because Rubisco is both essential and the most abundant enzyme on Earth, plants invest a great deal of nitrogen and energy to synthesize it. Scientists have for many years wished for a "test-tube" method to optimize Rubisco, but because its assembly path isn't known, this is not yet possible. The Stern laboratory has now identified two previously unknown proteins that form part of this path, which could lead to a breakthrough in Rubisco biology.

As mentioned above, chloroplasts are the site of photosynthesis, where the sun's energy is used to create sugars, which in turn are incorporated into food, feed, and fiber. In one project, the photosynthesis machinery is being altered to create the potential for a "green battery" where chloroplast "juice" can be used directly to produce electricity. In a second project, genes from an alga that is very difficult to grow but makes unique hydrocarbons that can be very easily converted into diesel fuel, are being moved into other algae that are easily grown under controlled conditions, giving the potential for high-value bioenergy production. Both of these projects involve collaborations with engineers, whose ability to conceive and create devices can help to harvest the societal potential of plant biology.



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

How do plants defend themselves against insect herbivory?

As the human population increases, so does he 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 will enable farmers to produce more, higher quality food from current agricultural acreage.

One way to do that is to reduce yield losses due to insects, which feed on the plants and spread diseases. In fact, insects reduce annual crop yields by 15 percent per year worldwide, despite the implementation of a large variety of control methods by farmers. Therefore, understanding the interactions between plants and insects and how plants ward off insect attack is an attractive way to increase crop 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 metabolism to deter further insect feeding. Dr. Jander's laboratory is identifying previously unknown toxic and deterrent plant metabolites, as well as their biosynthetic pathways, which are up regulated in response to 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. Many plant viruses, which depend on aphids for transmission to new hosts, manipulate plant defenses so that aphids are attracted, are able produce more progeny, and transmit the virus more widely. In a new project, the Jander lab is investigating how a virus with only eleven genes is able to suppress aphid defense responses in plants that have more than 30,000 genes.

In another project, members of the Jander laboratory are using natural variation in maize to identify novel aphid resistance mechanisms. This approach has identified an interesting tradeoff in maize defenses: a biochemical switch that provides increased resistance to aphids makes the plants more sensitive to caterpillar feeding. Maize varieties grown in tropical areas, where there is often more damage from caterpillar feeding, have been selected to have elevated caterpillar resistance and relatively low aphid resistance.

George Popescu, Ph.D.
Senior Research Associate, BTI

How do computers help us undestand evolution?

The power of molecular methods and of computing technology has increased exponentially in recent years, empowering science to delve into new, unexplored questions in biology. Scientists can now apply computational approaches to studying complex phenomena, teasing apart dense networks of interactions in ways that would have been impossible only 10 or 20 years ago.

George Popescu's laboratory at BTI uses computational approaches to study biological networks and processes in order to understand evolution and dynamics at the molecular and cellular levels. Using the methods of systems biology, Popescu seeks to analyze and infer the properties of biochemical networks, signaling networks, and plant protein interactions. In DNA sequence-based work, Popescu's lab is developing methods for pinpointing networks of regulatory genes by comparing the conserved portions of many different plant genome sequences and integrating that information with data that shows when and to what degree plants use those genes. Popescu's work addresses fundamental questions in plant research using computational and analytic methods.

In recent work, Popescu and his colleagues identified proteins that interact with a critical immune receptor in *Arabidopsis thaliana*. The receptor, FLS2, acts like a surveillance system for the plant, sending out the alarm when it detects pathogens on the outside of the cell membranes. Using a functional protein microarray, a tiny chip with over 5,000 different *Arabidopsis* proteins arranged in a grid on the surface, the researchers identified specific plant proteins that interact with FLS2 and transport it to the cell membrane, where it can play its role in plant immunity. Their work indicates these transport proteins can fine-tune plant immunity by controlling the transport of FLS2 to the membrane, a new and important detail in our understanding of plant immune defense.

Joyce Van Eck, Ph.D.
Assistant Professor, BTI

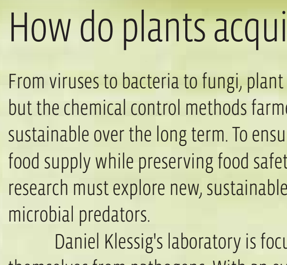
How do model plants help biotechnology projects?

In plant research, time is of the essence. That's one reason BTI's scientists use model systems as stand-ins for the real thing: model plants, that are smaller and quicker to mature and form seeds, are easier for researchers to grow and manipulate than the crops they represent. Model plants are particularly crucial to plant biotechnology, where they enable scientists to try out concepts and techniques that can be directly applied to solve real-world problems with crop plants.

Joyce Van Eck's laboratory is focused on applying the techniques of genetics and biotechnology to plant research, often using these model species to achieve their goals. Through metabolic engineering, Van Eck and her lab work on manipulating or inserting genes of interest into model species to investigate their potential for improvements in yield, vigor, and other measures of plant success.

Van Eck has recently been involved in an effort to enhance the utility of the model plant green millet (*Setaria viridis*). Like maize, sugarcane, and other grasses, green millet uses C4 photosynthesis to incorporate carbon into plant tissues, making it more efficient at using water and nitrogen than C3 plants. But unlike the economically important crops, green millet, a common weed, has a small genome, is relatively small in size, and has a rapid life cycle. Van Eck and her colleagues have successfully developed transformation systems by which temporary or permanent genetic changes can be introduced to the plant, making it a pliable system for learning about the features of C4 plants that enable their higher efficiency. Developing these and other techniques that enhance the usefulness of green millet as a model will enable Van Eck and her colleagues to further the effort to introduce C4 traits into C3 plants for the sake of improving the efficiency and yield of those crops.

Van Eck has also been involved in work with cell cultures from the Pacific yew tree, a species best known for its production of paclitaxel (Taxol®), which is used as a chemotherapy drug. Van Eck's laboratory has developed a consistent and repeatable transformation system for yew cell cultures that allows researchers to manipulate the plant's genes, making genetic engineering in yew cells possible. Moving forward, Van Eck and her collaborators are continuing work to explore the mechanisms by which the cells make paclitaxel, with the ultimate goal of enhancing the ability to manufacture the drug.



Dan Klessig, Ph.D.
Professor, BTI
Adjunct Professor, Department of Plant Pathology and Plant-Microbe Biology, Cornell University

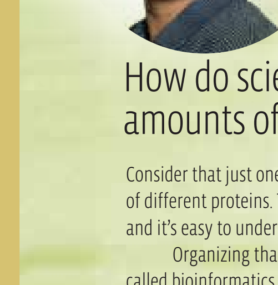
How do plants acquire immunity to disease?

From viruses to bacteria to fungi, plant pathogens are a constant in agriculture, but the chemical control methods farmers have long relied upon are not sustainable over the long term. To ensure the quality and reliability of the global food supply while preserving food safety and environmental quality, plant research must explore new, sustainable means for protecting plants from microbial predators.

Daniel Klessig's laboratory is focused on understanding how plants protect themselves from pathogens. With an eye toward developing sustainable control methods, Klessig and his colleagues apply a broad range of techniques to identify components of the plant immune system, including the key hormone salicylic acid, and determine how they work.

Recent work in Klessig's lab has focused on the CRT1 (Compromised for Recognition of Turnip Crinkle Virus) protein in the model plant Arabidopsis. Klessig's team first identified the protein in a search for signaling components of the plant's immune response. Sequencing of the gene for CRT1 shows that it belongs to the Microchidia (MORC) family of proteins, which are found in plants, animals, and microbes and are associated with DNA modification and repair. Using Arabidopsis mutants, Klessig and his colleagues showed that plants that lack a functional gene for CRT1 have compromised levels of resistance to pathogens. CRT1 is required not only for recognizing viruses, the results show, but functions in response to a broad spectrum of pathogens, including the bacterium *Pseudomonas syringae* and the fungus-like *Hyaloperonospora arabidopsidis*. What's more, CRT1 is involved in many different layers of plant immunity, including pathogen-associated molecular pattern triggered immunity, basal resistance, nonhost resistance, and systemic acquired resistance. Since CRT1 binds DNA and relocates to the nucleus of the cell upon pathogen attack, it likely carries out important nuclear functions during the plant's immune response. This work is the first evidence that a MORC protein plays a role in immunity.

Moving forward, Klessig expects that an understanding of CRT1 and its roles in multiple levels of immunity will lead to development of plant varieties that can fend off harmful microorganisms without the use of chemicals that can be harmful to humans and the environment. Work with several important crop species is already in progress.



Zhangjun Fei, Ph.D.
Associate Professor, BTI

How do scientists access and use massive amounts 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.

The Fei lab also uses next generation sequence technologies combined with bioinformatics tools to facilitate crop improvement. Fei co-led an international consortium to sequence watermelon genomes. By analyzing a high-quality reference genome and resequenced genomes of 20 watermelon accessions, Fei and others found that during watermelon domestication, a large portion of disease resistant genes had been lost while breeders were looking to improve fruit quality like sugar content. This information can help breeders to recover some of these natural disease defenses while retaining the high fruit quality of watermelon.

The laboratory is currently using a novel small RNA sequencing approach to define the pan-African sweet potato virome and global virus distribution of tomato. Using this approach, Fei and his USDA, ARS collaborators identified a novel tomato virus that had not been discovered using traditional approaches.

Fei often collaborates with the Giovannoni laboratory at BTI to investigate the role of epigenome in tomato fruit development and ripening using genomics and bioinformatics approaches. In 2012, they found a link between methylome dynamics and fruit maturation.

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"I am going to build a laboratory to study some of the fundamental things. I want to do something to get at the bottom of the phenomena of life processes and I think a good place to study them would be in the realm of plants. Any principles concerning the nature of life that you can establish for plants will help you understand man, in health, and in disease."

—COLONEL WILLIAM BOYCE THOMPSON

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The Boyce Thompson Institute will be known internationally for research excellence in plant biology and for discoveries that benefit society