
BTI
Boyce Thompson Institute
for Plant Research
2011
ANNUAL REPORT

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MESSAGE FROM THE PRESIDENT

THE BOYCE THOMPSON INSTITUTE WAS FOUNDED ON THE BELIEF THAT BASIC RESEARCH WOULD UNDERPIN THE FUTURE SECURITY OF THE FOOD SUPPLY. William Boyce Thompson was visionary in this belief in the 1920s, and the same principle holds true today. But Thompson didn't know that by 2011, a substantial proportion of our corn crop would be converted to liquid fuel, that the world population would be approaching seven billion, or that fresh water supplies would be depleted or imperiled in many parts of the world. He would not have realized that globalization and climate change would result in the dispersal of plant pathogens far from their historical ranges. These are the types of challenges to which BTI is responding today.

As a producer of food, feed, fiber and raw materials, agriculture is a key component of the U.S. economy, and represents a vibrant export sector ($115B in 2010). The past six decades have seen a more than 260% increase in food production despite a slight reduction in inputs: a recent Department of Agriculture analysis found that U.S. farm productivity has increased nearly 50% in the past 30 years. While there are many factors that have allowed agriculture to flourish even as environmental and population pressures have grown, this ongoing "Green Revolution" clearly has some of its most important roots in the laboratory. Techniques to modify plant genomes, and molecular analytics for plant breeding that speed the integration of desired characters, are just two examples where basic research into plant functions has created new possibilities in the field.

Inside this report, you can read about the most exciting discoveries BTI scientists reported in 2011, including several related to plant diseases. For example, through protein structure analysis Greg Martin's lab gained new insights into the plant-pathogen "molecular arms race." Georg Jander's laboratory discovered a new plant defense compound, and Sorina Popescu led a team that identified a novel aspect of plant immune response receptors. BTI scientists also reported many advances in chemistry, genomics, molecular signaling and symbiosis, with the potential to generate new resources and tools for agriculture and human health. Such fundamental discoveries will allow the development of plants that more efficiently use nitrogen, tolerate drought, have improved nutritional qualities, and resist pathogens.

2011 was also a milestone year as the BTI Summer Internship program marked its tenth anniversary by selecting 27 undergraduates and five high school students from a national pool of nearly 250 applicants. Tiffany Fleming, Director of Education and Outreach, oversees this BTI and NSF-sponsored program that also serves Cornell and USDA scientists. The Plant Biology Curriculum Development Project for pre-college science teachers marked its sixth year, preparing 168 teachers to teach plant science in their classrooms, who went on to engage 883 students in Plant Science Experiment Kits relevant to biofuels. Finally, BTI Outreach, in collaboration with five other research institutes and USDA sponsorship, launched a new national effort to engage the next generation of plant scientists through Bioenergy and Bioproducts Education Programs. Indeed, communicating the excitement and importance of discovery is as integral to BTI's mission as the discoveries themselves.

Sincerely,

David B. Stern, Ph.D.
President

IN BRIEF

IN MEMORIAM

Leonard H. Weinstein

William B. Thompson Scientist Emeritus

Leonard Weinstein, esteemed Boyce Thompson Institute scientist, devoted writer, researcher and administrator, died of pneumonia at his home in White Plains, NY on November 6, 2011. He was 85.

Len was a staff sergeant in the US Army Corps of Engineers during World War II. He earned degrees from Penn State and University of Massachusetts, eventually earning his PhD in Plant Physiology from Rutgers University. Len came to BTI in1955 to work on a project sponsored by a consortium of rose growers supported by the Atomic Energy Commission and National Science Foundation.

Over his career he authored or co-authored over 175 scientific publications including journal articles, book chapters and books. He became an international authority on the effect of fluorides in plants from his work on the fluoride project with Percy Zimmerman and A. E. Hitchcock. Weinstein eventually became the project leader following their leadership. Len was named Program Director of the Environmental Biology Program in 1963, a position he held until his retirement in 1992. He was honored as the William B. Thompson Scientist in 1969, and in 1973 he was also elected to the BTI Board of Directors. He also served on the Board of Directors of the Boyce Thompson Southwestern Arboretum from 1969-1992. At Cornell University, he was an adjunct professor in the department of Natural Resources, served as Director of the Ecosystems Research Center and a graduate advisor in the fields of Environmental Toxicology and Natural Resources.

Weinstein served on the advisory boards for the U.S. Environmental Protection Agency and the Oak Ridge National Laboratory. He was a member of the joint Soviet-American Commission in the Field of Environmental Protection and testified on environmental funding for the U.S. Senate and House of Representatives. Len presented often on environmental pollution throughout China, where he and his wife Sylvia were guests of the Chinese government.

In his personal time, Len was a stained glass artisan and a writer of short stories. He was a creative and imaginative scientist with a first-class mind. He led an extraordinary life.

Our overriding goal for outreach in 2011 was to provide experiences that connect BTI's research portfolio to a broad audience.

TECHNOLOGY TRANSFER

The role of the Technology Transfer Office (TTO) is to increase the real-world impact of BTI discoveries by transferring technology to the private sector, or to foundations for humanitarian purposes. 2011 was an exciting year for technology transfer at BTI. We have begun to implement our five-year strategic plan. This plan included the addition of Karen Kindle as our new Principal Liaison for Technology Marketing and Licensing. Karen came to BTI from Monsanto, and she brings with her a wealth of experience in both commercial and academic settings. Donna Claes has also joined the TTO as a Patent and Licensing Specialist. This year Donna implemented our new TTO database system that has streamlined how the Institute manages all its technology transfer activities.

OTHER TECHNOLOGY TRANSFER HIGHLIGHTS

- Implemented a program to increase networking with new potential commercial partners. This included an overhaul of the TTO website to make it easier for potential partners to review BTI technology based opportunities.
- Initiated a program to increase IP awareness among research staff
- Nine new invention disclosures filed (an annual record for BTI)
- Eight new patents were issued; two in the US and six in other countries
- Five new patent applications were filed
- The Institute entered into 31 new materials transfer agreements with academic and commercial partners.

STUDENTS AND TEACHERS COLLABORATE WITH SCIENTISTS TO HELP SOLVE FOOD SECURITY, AGRICULTURE AND ENVIRONMENTAL PROBLEMS

BTI's Education and Outreach programs focus on linking students, teachers and scientists in plant research for a sustainable future. BrachyBio! is our newest program and combines plant research with citizen-science, teacher professional development and data sharing via online social networking.

BrachyBio! - named after the plant *Brachypodium distachyon* - a model grass species - engages students and teachers in the international effort to understand gene function in Brachy's agriculturally-important crop relatives, namely rice, wheat and barley. Developed by Scientist Tom Brutnell, whose research interests include gene function related to photosynthesis and Education Director Tiffany

Fleming, a former science teacher, the project's cutting-edge approach lies in tapping a new scientific community to do scientific research, high school and middle school biology students.

"We are essentially crowd-sourcing our genetics," notes Brutnell, "and in the process teaching kids about plants, genetics and how research can benefit society and promote a more sustainable future."

To date, 418 students across New York, Connecticut and Missouri are currently doing BrachyBio! research. Trained teachers teach students how to identify mutations in plant growth, development, leaf characteristics, flowering time and disease resistance. Students then go to Data Central, an online database developed by BTI and iPlant, to record and relay their findings to scientists around the world.

Dr. Richard Amasino, at the University of Wisconsin who specializes in plant flowering is the latest in a growing team of researchers to join forces with the project. "*Brachypodium* is a great model system, an approachable system, where we can understand the evolution of the regulation of flowering in grasses," he said, adding, "We're excited that the Brachy model came along. It is a network that extends from people who have done all the genomics to people doing screens in classrooms."

Creating networks and technologies for students, teachers and scientists to collaborate in plant biology research is the driving force behind BTI's Education and Outreach suite of activities. "BrachyBio! is an important program that truly enables students and teachers to contribute to the process of discovery beyond their classrooms" says Fleming. "It is so exciting that student work has the real potential to advance scientific knowledge in plant biology and that scientists are seeking out their results." This is a win-win situation where we all benefit.

OUTREACH SUMMARY

Over 2,050 people participated in BTI sponsored Education and Outreach programs in 2011.

- Science Teachers: 168
- Volunteers: 115
- 7-12 Grade Students: 1,153
- Undergraduates: 577
- Graduate and Postdoctoral Mentors: 72
- Faculty: 58

AWARDS

Jim Giovannoni receives Agricultural Research Service Award Jim Giovannoni was recognized for international leadership on tomato genomics research, including pioneering discoveries in fruit ripening, as well as leadership of the tomato genome sequencing efforts. http://my.aspb.org/members/blog_view.asp?id=700968&post=127332

Maria Harrison named William H. Crocker Scientist This chair was created in 1979 to be bestowed by the Board of Directors "on a Scientist whose outstanding contributions to the advancement of knowledge deserves singular recognition among the community in which she serves." Maria was recognized for her outstanding service to the BTI, Cornell and international communities, and for her high-impact research on mycorrhizal symbiosis.

Dan Klessig: APS 2011 Noel T. Keen Awardee for Excellence in Research Dan Klessig received the 2011 Noel T. Keen Award for Research Excellence in Molecular Plant Pathology from the American Phytopathological Society. Nominees for the award have made outstanding contributions and demonstrated sustained excellence and leadership in research that significantly advanced the understanding of molecular aspects of plant host-pathogen interactions.

Former BTI Postdoctoral Fellow Jiayang Li Elected to National Academy of Sciences Jiayang Li, a BTI postdoc in the early 1990's, has been elected as a Foreign Associate to the National Academy of Sciences. Jiayang worked in the laboratory of Rob Last (currently at Michigan State Univ.), and went from BTI to China, where his research on rice architecture and grain quality has flourished. He is also a Vice President of the Chinese Academy of Sciences. BTI is proud of its role in establishing Dr. Li's distinguished career. http://sourcedb.cas.cn/sourcedb_genetics_cas/yw/zjrc/pgr/200907/t20090721_2130992.html

Elaine Van Etten awarded the Brooks-Colavito Award for Distinguished Service Elaine Van Etten, a BTI staff member since 1997, was awarded the Brook-Colavito Award for Distinguished Service. This honor is awarded to an individual who personifies service and dedication to BTI, demonstrated by their diligence and perseverance, commitment to high standards, professional and gracious demeanor, flexibility, and integrity.

BIG BOOST FOR PLANT RESEARCH

Scientific leaders from BTI, The Carnegie Institution for Science, the Donald Danforth Plant Science Center and The Samuel Roberts Noble Foundation formed the Association of Independent Plant Research Institutes (AIPI) to facilitate scientific discovery in three core areas of plant research:

- Plants as sources of renewable energy
- Improving plants' abilities to provide an unparalleled range of "ecosystem services" to the planet.
- Development of sustainable agriculture practices.

GRANTS & GIFTS

NEW GRANTS AWARDED

Government

National Science Foundation	$	4,239,566
Health and Human Services	$	921,900
United States Dept. of Agriculture	$	676,370

Miscellaneous

International Human Frontier Science Program Organization	$	160,980

Foundations

Triad	$	250,000

Other

Corporate Grants	$	33,750
Other Support Services	$	1,400
TOTAL	$	6,283,966

GIFTS

William and Anne Thompson Society ($5000+)
The John and Magdolna Bank Family Trust
Chris & Nora Hohenlohe
Estate of Leonard Weinstein

William Boyce and Gertrude Thompson Society ($2000 - $4999)
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FINANCIAL REPORT

USE OF FUNDS

SOURCE OF FUNDS

LAB REPORTS

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 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 has recently 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 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 bud from the cell, some viruses elicit the aid of a complex of host cell proteins called ESCRT pathway proteins. To determine if baculoviruses use these proteins, Blissard's group inactivated a key regulator of the ESCRT pathway and examined the effect on virus infection. Their studies showed that when the cellular ESCRT pathway was disrupted, viral budding was interrupted as well, indicating that this virus uses the ESCRT pathway in its exit from the host cell.

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 Department 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 beta-carotene, Tom Brutnell's laboratory is working to enhance beta-carotene production — research that could lead to more nutritious varieties of corn, and healthier diets for some of the world's poorest people.

Brutnell's team previously proved that the enzyme lycopene beta-cyclase is required for the first step 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 Catalá, 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 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 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. This is the area of research that Carmen Catalá 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. **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 lab focuses on the discovery of genes and networks regulating tomato fruit morphology. 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. This research will help unravel the mystery behind the huge morphological differences among edible fruits and vegetables as well as provide new insights into mechanisms of plant development

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

How can 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.** 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 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 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 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.

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, TAGL 1, 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.** AP2a does not impact fleshy expansion but serves essentially as a braking system to prevent rapid over-ripening while ERF6 influences accumulation of two of the predominant nutritional compounds of tomato, lycopene and beta-carotene.

Current activities include efforts to discover 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 and then testing for similar activities 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.

Maria Harrison, Ph.D.
William H. Crocker 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, 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 the plant's 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.**

Through the analysis of *Medicago truncatula* mutants that are unable to develop symbiotic relationships with AM fungi, researchers in the Harrison lab were able to identify two transporter proteins, called ABC transporters, that are required for the symbiosis. These transporters are located in the periarbuscular membrane and they pump molecules out of the plant cell towards the fungus. These molecules are essential to enable the fungus to survive inside the plant cell and for the symbiotic partnership to be maintained. A major question is 'what is the molecule that is pumped out of the plant cell?' Identifying this molecule and why it is essential for survival of the fungal symbiont 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.

Georg Jander, Ph.D.
Associate Scientist, BTI

Adjunct Associate 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 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 gene expression to 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. While studying plant responses to aphid feeding, Dr. Jander's laboratory is identifying previously unknown toxic and deterrent plant metabolites, as well as their biosynthetic pathways, which are upregulated in response to insect feeding.** In a new research approach, members of the laboratory are studying natural variation in maize to identify novel aphid resistance mechanisms.

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 essential amino acids, whereas humans and most other animals can only produce half of these. In a new research approach, members of the Jander laboratory are studying regulatory mechanisms that increase plant amino acid production in response to drought or salt stress. Understanding the complex network of events involved in the synthesis of plant amino acids, particularly the discovery of new regulatory genes for amino acid biosynthesis, will help scientists to increase the nutritive value of crop plants. Another project, which combines the laboratory's two main research interests, Jander and his co-workers are identifying toxic non-protein amino acids, which some plants produce to deter feeding by aphids and other insects.

Dan Klessig, Ph.D.
Scientist, BTI

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

How do plants acquire immunity to disease?

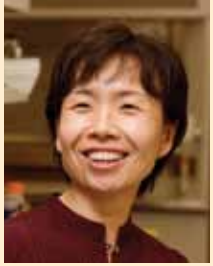
When we hear the phrase "acquired immunity", we usually think of humans, vaccinations, and our own disease protection system. **But plants also have acquired immunity (more often referred to as "resistance"), which is activated when a pathogen infects the plant. Understanding how this system works in plants could lead to crops that more effectively protect themselves from disease.**

Dan Klessig's lab studies the molecular basis of this resistance. In earlier work, his lab and others proved that an aspirin-like compound, called salicylic acid (SA), is produced at the site of pathogen infection. Some of this disease-fighting hormone activates the plant's local defenses and some is converted by an enzyme, SAMT1, into methyl salicylate (MeSA), an inactive form of SA. Studies by others subsequently showed that although SA was required in the uninfected systemic/distant tissue to develop systemic acquired resistance (SAR) against secondary infection, SA was not the mobile signal that had been sought after for almost half a century.

In an important breakthrough in 2007, Klessig's group discovered that MeSA is a mobile signal for SAR in tobacco plants. Their studies revealed that after pathogen attach some of the MeSA synthesized at the site of infection is transported through the phloem to distant, uninfected parts of the plant, where another enzyme, SABP2, converts it back into disease-fighting SA, which turns on the plant's defenses in those tissues. Their subsequent work in 2008-2011 showed that MeSA is also critical for SAR in Arabidopsis and potato, but that under certain light conditions MeSA is not required for SAR.

In addition to MeSA, one or more lipid-based mobile signals have been implicated in SAR by several groups. Recent studies in the Klessig group revealed that SAR is activated via the interplay between at least two mobile signals, MeSA and a complex formed between the lipid-transfer protein DIR1 and a lipid or lipid derivative. The function of this complex is to suppress expression of the *SAMT1* gene in the distal tissue to facilitate conversion by SABP2 of the translocated MeSA to SA.

The Klessig group's discovery of i) MeSA as a mobile signal, ii) the enzymes that regulate its level, and iii) the interplay between two mobile signals, provide key insights into how molecular information produced at the site of infection is communicated throughout the plant to provide it with acquired immunity.



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.

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. The movement of mobile microRNA 165/6 leads to a graded distribution of its targets, which are key transcription factors controlling xylem formation.** Recently, Lee's group also showed that this bidirectional signaling regulates the apical root growth by modulating the plant growth hormone cytokinin. The Lee lab is further investigating how key transcription factors in vascular stem cells drive xylem specification and root growth.

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.
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 pathogenesis 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.
Adjunct Scientist, BTI

Associate Professor, Université de Sherbrooke

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 disease resistance genes 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 happens and how it elicits a protective response in the plant.

Moffett's lab has discovered that the resistance proteins they study actually work in concert with another protein, called RanGAP2, which is present in all plants. They found that the RanGAP2 protein 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 the cell, but if the cell is attacked by a nematode, RanGAP2 activates a protein called Gpa2. 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.

More recently, the Moffett lab has shown that disease resistance proteins that specifically recognize pathogens function in concert with a class of proteins, known as CCR-NB-LRR proteins. The latter proteins are highly similar in structure to disease resistance proteins, but appear to function in inducing the defense responses that eliminate pathogens rather than immune receptors. This discovery will lend insights into how all disease resistance eliminate pathogens.

Lukas Mueller, Ph.D.
Assistant Scientist, 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 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 a number of genome sequencing projects, most notably the tomato genome project, which is the work of scientists in ten 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

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 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 pests 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 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. These findings could lead to a new understanding of how plant stress defense mechanisms work. It could also lead to new ways to protect plants from disease.

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

Adjunct Professor, Department of
Molecular Biology & Genetics,
Cornell University

Is there more to inheritance than genetics?

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), a process that can make the gene unreadable by the cell. The methylated gene can die out with the cell or it can be passed on to new generations of cells and, in some cases, organisms. Consequently, DNA methylation may play an important role in evolution, just as mutations do.**

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

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

Frank Schroeder, Ph.D.
Assistant Scientist, BTI

Adjunct Assistant Professor,
Department of Chemistry and
Chemical Biology, Cornell University

Missing pieces in the chemistry of life: what are the roles of biogenic small molecules?

The relevance of nucleic acids, proteins and carbohydrates for all aspects of biology is well established, but the varied and often unexpected roles of biogenic small molecules are just now emerging. Biogenic small molecules regulate development and immune response in plants and animals (for example as hormones) 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 building blocks. In contrast, biogenic small molecule 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 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 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 the entirety of its small molecules, usually referred to as the "metabolome." Recently, Schroeder's group identified several new compounds that influence various aspects of nematode behavior, as well as pathways involved in nematode development and life span regulation. These studies showed that *C. elegans* uses a modular "chemical language" to communicate a variety of different messages. The ultimate goal of this research is to identify the entire *C. elegans* metabolome for chemical structure and biological function.

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.

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 how the genes in plant chloroplasts are regulated in order to coordinate their expression with nuclear genes that encode other chloroplast proteins.**

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 – 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 more recent discovery has been the diversity 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 activation or repression of sense RNA expression, or to the destruction of the sense strand. The Stern laboratory has used high-throughput RNA sequencing to catalog more than100 new chloroplast antisense RNAs in Arabidopsis. Their functions remain to be uncovered.

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.
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. Preliminary analyses have shown that the enhanced carotenoid accumulation and stability during storage are associated with the formation of lipoprotein-carotenoid sequestering structures and possibly three major functional groups of proteins (heat shock proteins, glutathione-S-transferases, and carbohydrate metabolic proteins).**

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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Tower Road
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