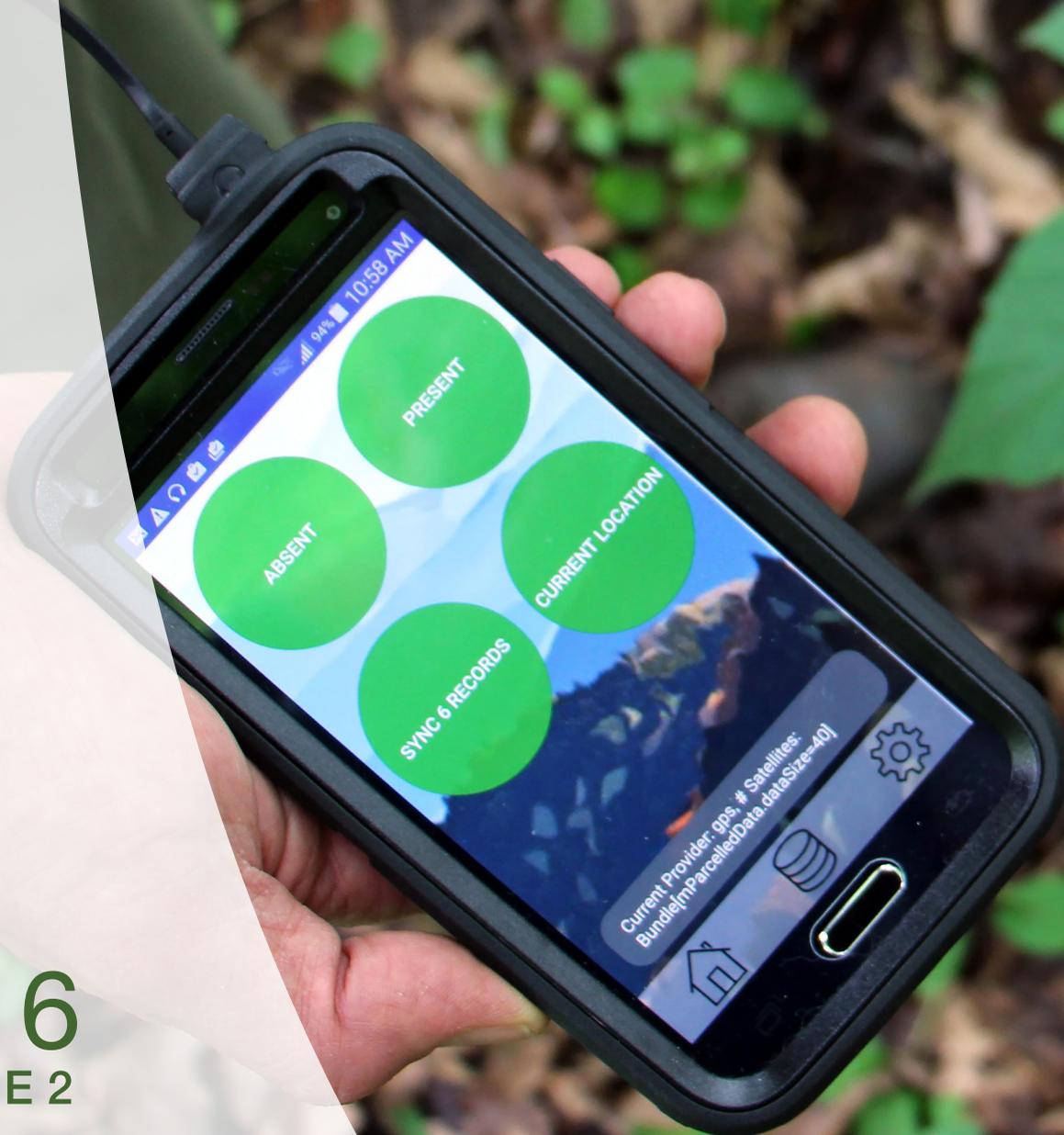


GROWING TPS

ANNUAL MAGAZINE OF THE
TRANSLATIONAL PLANT SCIENCES
PROGRAM AT VIRGINIA TECH



2016
VOLUME 2

TRANSLATIONAL PLANT SCIENCES

WELCOME



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The first year has passed after the complete transition from Molecular Plant Sciences (MPS) to Translational Plant Sciences (TPS) and after successful rebranding. As any successful venture, it could not have been done without team effort and sufficient funding, particularly prospective student recruiting efforts, annual TPS Minisymposium, TPS Student Grant Competition, and many other activities organized by students and faculty with ample support of our outstanding staff. It is tempting to think that the hard part is over and we can continue in our mentoring and research efforts. However, as a community, we need to generate new strategies on how to foster integration of basic and applied plant research, which was the basis for rebranding.

Forming the new School for Plant and Environmental Sciences (SPES) is exciting as it will provide an opportunity to unify both graduate and undergraduate curricula and foster multidisciplinary collaborations, but it will also generate

new challenges. We have to start thinking about how the activities of the newly rebranded TPS Graduate Program will fit the scopes of various Destination Areas formed within the new School. With three Colleges and seven Departments at VT, TPS is translational by nature, with research opportunities ranging from basic to applied research, including, but not limited to, plant-organism interactions, plant evolution, metabolism, crop improvement, plant-soil microbiome interactions, and stress physiology. This translational nature can be expanded at the “environmental” part as we should consider integrating other related, but currently underrepresented areas within TPS that are part of the School.

To faculty, TPS provides means of recruiting prospective students. To students, TPS provides opportunities to sample different research programs through rotations and find home labs. Although the students remain TPS students until they graduate through various TPS activities organized within our community, they get their degrees from the home departments of the respective faculty and TPS remains a non-degree graduate program. Perhaps it is the time to change it and form an official degree giving program under the umbrella of SPES as part of the Graduate Curriculum development within the SPES Working Groups.

We pride ourselves as being diverse, progressive, and translational within TPS, which is evident not only from wide range of technologies and methods used in our research, but also from collaborations among TPS faculty and also students. Keeping up with the current state-of-the-art instrumentation will aid in attracting excellent prospective students. As a metabolomics expert, I can say that we have state-of-the-art instruments in our Mass Spec Incubator. However, there is something missing. Recent progress in high-resolution mass spectrometry imaging (MSI) now enables visualizing metabolite distribution in single cells, which is the “holy grail” in the metabolomics field. Ability to spatially separate metabolite signals within

distinct tissues or cell types facilitates addressing specific questions about regulation of metabolism in cell-specific manner. Acquisition of a MSI instrument would increase our competitiveness with the top graduate programs. But that is not all... just see what this baby can do.

Translational collaborations are even more important than fancy instruments as they foster brainstorming leading to generations of new ideas coming from scientists of different mind sets that would not see the light otherwise. Having more options is especially attractive to prospective students. For example, while it was very rare in the past for a scientist to be both a biologist and a computer scientist, dual majors of such nature are currently offered at an undergraduate level. Leveraging experiments with computational predictions is regarded as a preferable approach by funding agencies and multidisciplinary training is paramount in better career opportunities in sciences in general. TPS students already have an opportunity to collaborate with students from other labs, including collaborations with Computer Science or Genomics, Bioinformatics, and Computational Biology students. Activities such as these could be encouraged as part of the TPS Student Grant Competition and through appropriate coursework.

Overall, TPS as a truly translational program has had many successes, which, I think, are a result of the excellence of TPS students, faculty, and supporting staff. The infrastructure is important, but the ideas that are the cornerstone of high-quality research come from people, not machines.

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NEWS



David Haak developed a bioinformatics program using deep sequencing data to test whether his team's editing of the genome of the Arabidopsis plant was both efficient and specific in its targeting. Photo by Cris Thompson.

NEW STUDY OF CRISPR-CAS9 TECHNOLOGY SHOWS POTENTIAL TO IMPROVE CROP EFFICIENCY

A team that includes a Virginia Tech plant scientist recently used life sciences technology to edit 14 target sites encompassing eight plant genes at a time, without making unintended changes elsewhere in the genome.

The technology, a genome-editing tool called CRISPR-Cas9, revolutionized the life sciences when it appeared on the market in 2012. It is proving useful in the plant science community as a powerful tool for the improvement of agricultural crops.

The ability to alter several genes at once promises to advance researchers' understanding of how genes interact to shape plant development and responses to environmental changes. However, a challenge of this technology has been identifying the impact of editing on genomic regions that were not targeted. David Haak, an assistant professor of plant pathology, physiology, and weed science in the College of Agriculture and Life Sciences, developed a bioinformatics program using deep sequencing data to test whether the team's editing of the genome of the Arabidopsis plant was both efficient and specific in its targeting. The team's finding that CRISPR-Cas9 is a reliable method for multi-gene editing of this particular plant species was published in PLOS ONE on Sept. 13.

"We were surprised to see that we had targeted gene editing efficiencies ranging from 30-85 percent with no detectable off-target editing," said Haak, who is also affiliated with the university's Fralin Life Science Institute and the Global Change Center.

"The ability to edit gene function in a specific manner using CRISPR-Cas9 has the potential to really change how we study plants in the lab and improve crop efficiency," said co-author Zachary Nimchuk, an assistant professor of biology at the University of North Carolina. "But, there have been concerns about the potential for undesired off-target effects. We tested this in plants, targeting 14 sites at once, and found no off-target events in a large population of plants. Our data expands on previous work to suggest that, at least in Arabidopsis, off-target events are going to be extremely rare with Cas9."

Other paper co-authors were: Brenda Peterson, a lab technician at the University of North Carolina; Marc T. Nishimura, a post-doctoral fellow at the Howard Hughes Medical Institute; Paulo J.P.L. Teixeira, a post-doctoral fellow at the Howard Hughes Medical Institute; Sean R. James, a graduate student at the University of North Carolina; and Jeffrey L. Dangl, a professor of biology at the University of North Carolina

- Lindsay Key

SCIENTISTS DISCOVER WAY TO POTENTIALLY TRACK AND STOP HUMAN AND AGRICULTURAL VIRUSES

Viruses are molecular thieves that take from their hosts under the cloak of darkness. But now a Virginia Tech scientist has found a way to not only track viral hijackers, but also potentially stop them from replicating.

The discovery has broad ranging applications in stopping viral outbreaks such as Hepatitis C in humans and a number of viruses in plants and animals because it applies to many viruses in the largest category of viral classes — positive-strand RNA viruses.

The findings were recently published in the Proceedings of the National Academy of Sciences.

"Even though these viruses infect very different hosts, they all replicate similarly across the board, so what we learn from one virus can potentially be translated to control viruses in agricultural production as well as human health," said Xiaofeng Wang, an assistant professor of plant pathology, physiology, and weed science in the College of Agriculture and Life Sciences.

Wang's findings could target any number of plant viruses. One virus Wang has studied — the cucumber mosaic virus — affects pumpkin, squash and gourds in

1,200 species in over 100 plant families. Potentially, sprays could be developed to halt the virus on plants, saving millions of dollars in agricultural sectors.

Wang, who is associated with the Fralin Life Science Institute, used bromovirus to study how viral infections start. He found that the bromovirus stimulates synthesis of host lipid cells called phosphatidylcholine at the sites where viral replication occurs, and that by inhibiting its synthesis, the viral replication stopped.

Wang also collaborated with researchers to study how human viruses like Hepatitis C virus and poliovirus regulate host lipid synthesis and found that viral replication behaved in the same way as using plant viruses. The ramifications for human health mean that developing a drug delivery system to combat the Hepatitis C virus would be much more nimble in treating viral outbreaks than slow-moving vaccines, and could play a crucial role in halting the debilitating infection which affects 3-5 million people in the U.S. according to the Centers for Disease Control.

Viruses can't replicate by themselves. They are essentially thieves that break into cells and multiply by hijacking the machinery of the host cells and proliferating and remodeling lipid-containing membranes such as phosphatidylcholine — one of the most prominent lipids in host membranes. Wang and his collaborators were able to see where exactly the virus replications started and how they managed their hosts to meet their needs. Based on the finding of Wang and his collaborators, new ways can be developed to stop

phosphatidylcholine synthesis for viral replication, but leave the host undamaged.

"The better we understand the mechanisms of a biological process, the better are our options to rationally design tools that can control it," said George Belov, a collaborator of Wang's and an assistant professor of virology at the University of Maryland. "In the case of viral replication it may provide us with novel ways to control infection without causing host toxicity and a generation of viral-resistant mutants."

- Amy Loeffler

PESTICIDES USED TO HELP BEES MAY ACTUALLY HARM THEM

Pesticides beekeepers are using to improve honeybee health may actually be harming the bees by damaging the bacteria communities in their guts, according to a team led by a Virginia Tech scientist.

The discovery, published in the journal *Frontiers in Microbiology*, is a concern because alterations can affect the gut's ability to metabolize sugars and peptides, processes that are vital for honeybee health. Beekeepers typically apply pesticides to hives to rid them of harmful parasites such as *Varroa* mites.

"Although helpful for ridding hives of parasites and pathogens, the chemicals in beekeeper-applied pesticides can be harmful to the bees," said Mark Williams, an associate professor of horticulture in the College of Agriculture and Life Sciences and lead author. "Our research suggests that pesticides could specifically impact the microbes that are crucial to honey bee nutrition and health."

Mark Williams, an associate professor of horticulture in the College of Agriculture and Life Sciences, led a team that extracted genomic data from honeybees.

Honeybees from chlorothalanyl-treated hives showed the greatest change in gut microbiome, said Williams, who is also affiliated with the Fralin Life Science Institute.

Looking ahead, the team plans to investigate the specific changes in gut microbiota activities that affect honeybee survival. Honeybees are the foundation of successful high-value food production.

"Our team wants to better describe the core microbiota using bioinformatics to help best characterize the microbes that support healthy honeybees and thus stave off disease naturally," said co-author Richard Rodrigues, a postdoctoral researcher at Oregon State University and formerly a graduate student in Williams' lab.

Other authors include Troy Anderson, a former assistant professor of entomology at Virginia Tech; Madhavi Kakumanu, a postdoctoral scientist at North Carolina State University and former Virginia Tech graduate student in Williams' lab; and Alison Reeves, a former graduate student in Anderson's lab.

In Virginia, the approximate rate of hive loss is more than 30 percent per year, and continued losses are expected to drive up the cost for important crops that bees make possible, such as apples, melon and squash.

- Lindsay Key



Xiaofeng Wang looks at yeast cells to study how viruses overtake their host's cellular machinery to replicate. Photo by Amy Loeffler.

For the project, the team extracted genomic data from honeybees that lived in hives that were treated with pesticides (three different kinds) and compared with those that were not. Samples were pulled from hives in three separate Blacksburg locations.



In general, honeybee health has been declining since the 1980s, with the introduction of new pathogens and pests. Photo by Rob Flynn.

THE BEAUTY AND

Trees are vital. They are one of Earth's most important renewable resources, providing numerous ecosystem services worldwide.

They also offer us shade in summer, colorful leaves in fall, firewood in winter, and of course, fresh air to breathe year-round.

But, with an increased demand for forest products and land use for urbanization and food production, there are now fewer trees on Earth. And, since changing climates are disrupting seasonal temperature regimes as well as the distribution of rainfall, understanding how trees adapt is key to protecting them – and, ultimately, us.

Virginia Tech researchers Amy Brunner and Jason Holliday study how trees adapt and protect themselves in the face of climate change. Here's some of that story.

PREPARING FOR WINTER

As seasons change, trees, like all plant life, change too. During the fall, leaves turn from green to shades of orange, yellow and red, before falling to the ground as part of a greater process by which trees prepare for the cold.

In Appalachian forests surrounding Blacksburg, broadleaf trees shed their leaves to prepare for winter. These trees are also known as deciduous, meaning "falling off," for the autumn behavior of their leaves, which change color so the plant can conserve resources as days become shorter and cooler.

As autumn days grow shorter, trees use the decreased daylight to begin developing dormancy – a process by which they stop growing and make metabolic changes to protect against winter's freezing temperatures.

But a few shorter days are not enough for trees to complete this transition. Rather, trees initially transition into ecodormancy, a temporary state that can be quickly reversed if temperatures increase. Trees can prematurely grow again when



temperatures are not consistent, which prevents them from transitioning into endodormancy, the deepest stage that protects trees during the winter.

"In the fall, there are still some warm days, so if there's a transient warm day or period of days, plants can start growing again if they're not fully dormant," said Amy Brunner, an associate professor of molecular genetics in Forest Resources and Environmental Conservation in the College of Natural Resources and Environment.

"Dormancy really is about timing, as trees depend on temperature and daylight cues. If they perceive warmth, they can leave dormancy. This can become an issue with climate change because the plants may be in a state in which they cannot respond to changes," she said.

Brunner studies when and how poplar trees, commonly known as cottonwoods or aspens, transition from the partial to full state of dormancy. The availability of soil nutrients, which fluctuate with the seasons, plays a role in this.

"This response in trees happens over long periods of time, weeks, when various changes happen in various tissues, so we observe various parts of the tree, including leaves, shoot and meristem, the tip of the tree, the roots and stem," said Brunner, who has always been attracted to the complexity of the tree life form.

"There's this assumption that plants are so much simpler than animals, but this



isn't the case, especially since they don't tend to move on their own."

Her ultimate goal is to map the underlying genes that regulate how trees transition into dormancy in order to better understand how they can adapt under differing climatic conditions.

"Many trees require an extended period of cool temperatures to develop a full tolerance to freezing, and all require a period of warm temperatures to resume growth. One issue with climate change is that trees may not receive these cool temperatures during fall because it doesn't get cold enough anymore, which may lead them to resume growth if there is a mid-winter warm spell," said Jason Holliday, an associate professor of forest genetics in the same college. Holliday studies this same underlying genetic variation across tree species, namely lodgepole pine and interior spruce.

Spruce and pine are found in northwestern parts of the United States and Canada, and also use decreased day length and consistently cooler temperatures to transition in the fall. These trees have needles in place of the larger, flat leaves, and are called gymnosperms, or conifers, because they bear cones rather than fleshy fruits.

Like Brunner, Holliday also studies how and when these species transition to dormancy and acquire cold hardiness against the extreme temperatures of winter.

SCIENCE OF TREES

In Appalachia, trees tend to develop cold hardiness around September or October. As trees become cold hardy, transitioning to dormancy, they use a couple of different strategies to keep from freezing, he explained.

"If the inside of a tree cell freezes because there's lots of water, then the cell is dead, and if this happens across a whole tree, then the tree is dead. So, one strategy trees use is super cooling," said Holliday.

"One of the things that trees do is they make solutes, like amino acids and sugars, which lowers the freezing temperature of water much in the same way as applying salt to your driveway in winter melts the ice."

Another way trees prevent themselves from freezing is by removing water from their cells. Trees will purposely dehydrate their cells so that ice can't form.

The trick is that if trees haven't been able to transition into an effective dormant or cold hardy state because of fluctuating seasonal temperatures, then they may not be able to employ one of these

strategies to avoid freezing when those extreme winter temperatures come around.

AN ENDURING BEAUTY

In literature and film, trees have long held beauty as a representation of life and the process of change. Even Charles Darwin in 1859 adapted the tree as a metaphor in "The Origin of Species" to organize how species descend and relate to each other through evolution. A tree's young "twigs" can represent living species, he wrote, and older ones can represent those that have gone before, now extinct.

Darwin ultimately developed this metaphor by making sense of his observations, an empirical process that continues in evolutionary biology today. Since Darwin, developments in genomics have paved the way to better correlate observable traits with underlying species function, especially that within genes. Brunner and Holliday's work is no exception, and offers us clues to how trees have endured in the past for the sake of their future.

In a paper recently published in Science magazine, Holliday and a team of colleagues from Canada found that pine and spruce use the same suite of only 47 genes out of a possible 23,000 to adapt to variation in regional climate across the species ranges. These genes were specifically developed for those involved in cold hardiness. This finding was unexpected because pine and spruce have been evolving independently for about 140 million years (about the same amount of time between humans and kangaroos), and suggests that there are genetic constraints on how trees adapt to their environment.

At the same time, Brunner is working to build an overall framework of how poplar trees work genetically as they transition to endure these seasonal changes. Together, then, Holliday and Brunner work to map genetic responses to seasonal changes, both within a large individual genome and across species, so as climate patterns change, they can teach us how trees respond – and adapt to (hopefully) endure.

- Cassandra Hockman

Background photo by Jack Woods



Engelmann spruce.
Photo by Sally Aitken.

ITCHING TO

VIRGINIA TECH RESEARCHERS STUDY POISON IVY ON THE APPALACHIAN TRAIL

John Jelesko was hiking along the Appalachian Trail when he saw his quarry — one which other hikers would think of as their nemesis.

“Careful,” he said as he and David Haak stopped at a white blaze marker and pulled out his bag of scientific tricks. Though many people want to avoid poison ivy, the thick wall of poison ivy plants bordering the trail is just what the team of Virginia Tech researchers were after.

While scientists know about poison ivy’s ability to cause an all-consuming itch and even spawn terrible rashes, little is known about the plant itself or how it grows.

Jelesko and his team are out to change that.

Jelesko, associate professor of plant pathology, physiology, and weed science in the College of Agriculture and Life Sciences, Haak, an assistant professor in the same department, and Lynn Resler, an associate professor in the College of Natural Resources and Environment, are mapping and surveying the growth patterns of poison ivy where it lives in order to glean more information about how it grows and its genetic make up.

The trio recently set out on the Appalachian Trail to perform some preliminary research about the geolocation of the plant as well as collect DNA samples starting near McAfee Knob in Southwest Virginia.

“In many ways this plant is the familiar stranger,” he said, “We’re all told ‘leaves of three, let it be,’ and that’s all very sensible, but beyond that there is remarkably little specific scientific knowledge about poison ivy.”

In order to collect geolocational data of the plant the team used a smartphone app that enables users to tag where they find poison ivy. Jelesko, a Fralin Life Science Institute-affiliated faculty



member, and his team stopped at every “white blaze” marker along a 60-mile segment of the Appalachian Trail to catalogue and tag samples. The project was funded by a College of Agriculture and Life Sciences Proposal Development grant.

Though poison ivy is native to the United States, it’s known as a neo-invasive species because it tends to overtake landscapes. The plant has an uncanny knack to cozy up to human populations but it is also found in forests.

“Poison ivy has an ability to cohabitate with humans and we think that those plants will show different signatures of adaptations than those found in a natural forest, its native habitat,” said Haak.

One aspect of the plant’s behavior that has been proven is poison ivy’s affinity for greenhouse gases. A 2006 study showed that as the planet warms, poison ivy is predicted to grow faster, bigger, and more allergenic, causing much more serious reactions to urushiol – the rash-causing chemical found in the plant’s oils. Urushiol is extremely potent. Only one

nanogram is needed to cause a rash, and the oil can remain active on dead plants up to five years.

“Water, light, and carbon dioxide are poison ivy’s bread and butter,” said Jelesko, who originally became interested in studying poison ivy after a day of yard work and a bout with the plant that left him with a nasty rash.

Jelesko hopes to eventually hike the entire Appalachian Trail and extensively catalogue the poison ivy samples he finds along the way, as well as enlist the help of citizen scientists in geotagging poison ivy populations.

Though he didn’t experience any itching on this research trip, he did pick up a nickname by fellow hikers, as is custom on the AT.

The name?

“Rash.”

- Story and photos by Amy Loeffler

LEARN MORE



STUDENT SPOTLIGHT



BEN WEBB

One bacterium's devotion to finding its host plant is nothing to sniff at.

Thanks to years of evolution, *Sinorhizobium meliloti* bacteria have developed super-noses that allow them to sniff out alfalfa plants underground and swim to them through the soil.

Ben Webb, a Ph.D. student in the department of biological sciences in the College of Science, has devoted his graduate career to pinpointing exactly which molecules are involved in the underground union.

Without the bacteria, alfalfa plants—one of the most popular foraging crops for livestock in the United States—cannot fix nitrogen or grow very well. In turn, the bacteria rely on alfalfa for food and nourishment.

To attract the bacteria, the plant sends out attractants such as sugars, amino acids, betaines, and other undiscovered molecules underground, through its germinating seeds.

To determine which molecules play a crucial role, Webb—with guidance from his advisor Birgit Scharf—used liquid chromatography and mass spectrometry to analyze the alfalfa seed exudate. By observing molecule masses, they were able to identify the molecules and measure their relative abundance. Webb tested the most promising molecules

with a chemotaxis assay to determine which are attractants for *S. meliloti*.

Webb also investigated the bacterial side of the connection. To identify which of the bacterium's chemoreceptors are used to sense attractants, he knocked out single chemoreceptor genes creating 'mutant' bacterial strains. Each strain was tested for its ability to sense an attractant molecule.

Lastly, Webb purified the individual receptors, and then mixed the receptor and the attractant molecule together, watching for a change of heat that indicates a chemical reaction, and direct binding.

Based on this series of experiments, Webb concluded that certain betaines are the strongest attractants for the bacteria, and that the bacterial McpX chemoreceptor is most effective at sensing the attractant. This sort of scientific matchmaking and its resultant strong bond could greatly inform and benefit agricultural practices in the future.

"Matching the strong attractants with their cognate chemoreceptors will help us in designing *S. meliloti* strains with a more preferential chemotaxis towards the host alfalfa, which would propagate the symbiosis more efficiently," said Webb, who defended his dissertation in August. "In essence, these chemoreceptors are to

bacteria as noses are to humans, except *S. meliloti* has eight of these noses," said Webb.

Webb was a sophomore in college when he looked down a microscope and found his calling in the form of a plate full of bright, squirming bacteria.

"My mind was blown," Webb said. "I couldn't believe that there was this whole other universe under my nose this whole time, complete with a vast variety of species portraying similar ecological principles yet on a scale invisible to the naked eye."

As an undergraduate at Virginia Tech, Webb was mentored by then-graduate student Sean Mury in the lab of David Popham, a professor of biological sciences in the College of Science. When Webb graduated with a bachelor's degree in Biological Sciences in 2010, he entered the Interdepartmental Microbiology Graduate Program, where he rotated between three different labs, ultimately matching with Scharf, an assistant professor of biological sciences in the College of Science and a Fralin Life Science Institute affiliate.

"Ben contributed greatly to the success of my lab, not only because of his scholarly accomplishments, but also due to his engaging personality," said Scharf. "I am extremely thankful that Ben shares my passion for mentoring. It was wonderful

BEN WEBB

to watch the seed that I planted to germinate and fully develop, and I am looking forward to see Ben continuing our devotion for nurturing future seeds.”

Webb has five first author publications, and won the award for 'Outstanding Talk by a Graduate Student' at the Bacterial Locomotion and Signal Transduction meeting in 2015, according to Scharf.

“His excellent presentation skills are just one reflection of his dedication to teaching. Ben has advised seven undergraduate researchers in my lab by enabling them to grow and succeed,” said Scharf.

In 2015, Webb received the Noel Krieg Graduate Fellowship for excellence in teaching and research from the Department of Biological Sciences at Virginia Tech. He is one of the first recipients of the fellowship, which honors Noel Krieg, an Alumni Distinguished Professor Emeritus of Biological Sciences.

“Ben has the kind of teaching style that helps you grow as you learn. He helps you use the tools and abilities you already have to solve problems, which ends up yielding an understanding of both your work and yourself,” said Karl Compton, Webb’s former student. “He is exceptionally friendly and personable to everyone who comes into lab. If I had to use one word to describe him, it would be nurturing. In the future, it is my hope (though it may not necessarily be his own) that he does something that at least in part involves helping and teaching others - it is something of a gift he has.”

In 2016, he received the John Johnson Award for Excellence in Microbiology, also from the Department of Biological Sciences at Virginia Tech. He received a Fralin Life Science Institute Research Assistantship, a GSDA fellowship from the department of biological sciences, and is actively involved with the newly revised Integrated Microbiology Program (IMP) and the Translational Plant Sciences (TPS) program at Virginia Tech.

- Lindsay Key

MEET BEN WEBB

Hometown: Richmond, VA

Major/Year: Biological Sciences/2016

Fralin Advisor: Birgit Scharf

Other Degrees/Schools: BS in Biological Sciences with Biotechnology at Virginia Tech

Why do you want to be a scientist? When did you know?

There are many great reasons for me to be a scientist. One of the reasons I value the most is how being a scientist allows me to open my mind and understand new perspectives. Interestingly, I knew this about two years into my Ph.D. studies, *not before* I started my studies.

What attracted you to your particular field of science?

I was attracted by ability to actually see bacteria and watch them swim through their environment. This behavior was shown to me in Virginia Tech’s Microbiology laboratory class.

Your best Eureka! Moment (when something cool happened in your research):

This happens often... When I stay up late hypothesizing with colleagues. The ideas formed during those impromptu brain-storming events lead to great “Aha!” “of course!” “duh!” “Eureka!” moments. But then I get to test those ideas and if everything goes as planned, great. If not, then it’s back to hypothesizing.

What are your ultimate career goals?

Find ultimate freedom (a sign of the times, perhaps?)

Favorite hobby outside of school?

Exploring the woods



Q&A: COFFEE BREAK



AURELIANO BOMBARELY ASSISTANT PROFESSOR, HORTICULTURE

Educational Background:

B.S. in Chemistry at
University of Malaga, Spain

Ph.D. in Plant Molecular Biology at
University of Malaga

Postdoc, Bioinformatics at Boyce
Thompson Institute

Postdoc, Plant Systematics and Evolution
at Cornell University

Hometown:
Malaga, Spain

Hobbies:
Plant collecting, writing short stories, and
cooking

Favorite place to visit:
El Palmar, Cadiz, Spain

A quote to live by:
"So long, and thanks for the fish." – From
The Hitchhiker's Guide to the Galaxy by
Douglas Adams

What is the focus of your current research?

My research is focused on the study of plant domestication using genomic tools. Domestication is the process of modifying a species to make it useful for humans. For example, teosinte, the wild relative of maize, has a hard coat kernel that needs to be broken to be able to eat the seed. During the domestication of maize, the corn selected a form (phenotype) that makes a soft coat kernel. I ask, how are these phenotypes produced to make this selection possible? Are these the same genetic mechanisms that are involved in a natural selection process?

We know that transposons found in all living organisms are genetic elements that are able to reproduce in a genome by inserting copies of themselves into random places. When they are inserted into a gene, the gene's function may be disrupted, which happens for the maize gene *TB1*, responsible for short eared branches.

Another common mechanism for natural selection is the single nucleotide mutation that can change an amino acid or introduce an early stop codon, impacting protein function. These single nucleotide mutations are usually produced by errors in DNA replications, but they also can be produced when the DNA is damaged and repaired by the

other copy in a hybrid, such as in gene conversions. I am interested to know how important transposons and gene conversions are in the disruption of gene functions during the domestication process in order to increase phenotypic diversity, which would give us the possibility of selecting useful phenotypes.

To do this, I am using ornamental plants, specifically begonias, sinningias and petunias, as models to study plant domestication. They have several advantages compared to other crops, such as recent domestication history, small genomes and are compact in size.

Ultimately, the study of plant domestication can give us more information not only about how we can domesticate new plants and how much time it can take to develop a new crop, but also how flexible modern crops are to producing new phenotypes that can adapt to new conditions and new pathogens.

How did you become interested in your line of research?

I always have been interested in plant domestication, about how we artificially select phenotypes to make plants useful to us. During my PhD I worked in strawberry ripening, and what caught my attention was how different are the wild strawberries (usually not bigger than a quarter) compared to the cultivated

strawberry (the fruit can reach sizes of a small fist). Nevertheless it was during my postdoc under the supervision of Professor Jeffrey J. Doyle at Cornell when this idea started to have its current shape, when I incorporated polyploidy (when an organism has more than two sets of chromosomes) and evolution into my knowledge. I started to ask myself if the domesticated plants follow the same evolutionary mechanisms as other organisms or if there are some specific mechanisms that are more important than others.

What fascinates you about plants?

Everything from their genomes to their ecology, and the more that I learn, the more that they fascinate me. You only need to take a look at the world that surrounds you.

Just some examples: You can find species closely related to species that have been in this world for 270 million years, such the Ginkgo biloba ancestor; these plants started to be domesticated only around 15,000 years ago in several parts of the world.

In addition, today our species depends on plants such as maize, wheat or potato for surviving and, at the same time, these domesticated accessions depend on us to reproduce and survive. In the wild, plants are attacked by some insects, but they need other ones for reproduction. Plants

WITH A SCIENTIST

such as *Nicotiana attenuata* developed complex defense mechanisms to defend themselves against predators such as *Manduca sexta*, a caterpillar. At the same time, they use other insects such as moths for pollination.

What are some of the most significant challenges facing scientists today?

Funding their research. Also, administrative support is limited, especially for research without direct application. Additionally the increase of overheads and publication fees in the last ten years makes it even more difficult to support the research system. Other challenges are education and communicating science to the non-scientist population. Surprisingly, in the age of information, with amazing resources such as the Internet, there is a lot of misinformation. For example, the misinformation about GMOs, genetically modified organisms. There are some social communities that believe that GMOs are dangerous for the environment and human health without any evidence. More than a thousand research projects have not shown any evidence that GMOs can be dangerous. Still, these anti-GMO

communities have enough influence on public opinion to make countries ban GMOs (just in case those thousand independent research projects are not enough to prove that they are not dangerous).

Do you teach? If so, how does teaching inform your research, and vice versa?

Yes, I do. I co-teach one course in the fall semester, Introduction to Genomic Analysis and another one in the spring semester, Plant Genomics. The teaching of some topics can help you to understand a part of your research. For one hand, students may have questions that you may not have and that can help to reach new ideas. For another hand, there is room to develop some research during the classes by assigning small projects. For example, I am working in collaboration with my colleague Dr. Song Li and three excellent graduate students on a piece of software to study some evolutionary properties of plant genomes, such as gene duplications. This project comes from a problem-solving project assignment from Dr. Song's class. We expect to publish a small article as a result of this class project.



These flowers are part of our Sinningia collection in Bombarely's labs : Virginia Tech Greenhouse. Photos by Aureliano Bombarely.



SCIENTISTS USE 'INSECT PERFUMES' TO LURE STINK BUGS TO EXPENDABLE CROPS



DOROTHEA THOLL

When a stink bug finds a plant to eat, it produces a pheromone that alerts other stink bugs to the food source, similar to the ringing of a dinner bell.

A team of Virginia Tech researchers is studying the biosynthesis of this pheromone in order to mimic it and attract the pests to expendable food plants—also called 'trap crops'—rather than cash crops.

With funding from the USDA, researchers Dorothea Tholl and Tom Kuhar in collaboration with colleagues at the USDA ARS in Beltsville, Maryland, are just beginning the four-year project that they hope will save farmers millions of dollars.

"By understanding the biosynthesis of these volatile pheromones in stink bugs, we will be able to assemble gene tools to cost-effectively produce these chemicals, via synthetic biology, for their application in the field to trap stink bugs," said Dorothea Tholl, an associate professor of biological sciences in the College of Science and a Fralin Life Science Institute affiliate. "In addition, we plan to design chemically-modified trap crops that directly release the pheromones to attract and re-route the bugs away from commercial crops."

In Virginia, crops like sweet corn, wine, grapes, and apples have been under attack by the invasive brown marmorated stink bug since 2004 and cabbage has been affected by its similarly stinky cousin, the harlequin bug.

If successful, the genetic engineering technique would be an environmentally friendly alternative to using insecticides.

"Currently, most growers combat these difficult pests with applications of broad-spectrum insecticides," said Kuhar, a professor of entomology in the College of Agriculture and Life Sciences and a Virginia Cooperative Extension specialist. "These insecticide applications have been shown to have negative non-target impacts on natural enemy populations and pollinators and alternative strategies for stink bug management are badly needed."



Doctoral student Jason Lancaster examines a harlequin bug infestation on collards at Kentland Farm last August. Photo by Tony Dimeglio.

JASON LANCASTER OF KNOXVILLE, TENNESSEE

A biological sciences doctoral candidate working with Tholl, recently used next-generation sequencing to identify the first enzymatic step in the biosynthetic pathway of the harlequin bug pheromone compound.

"Our work targets the production of the bug's pheromone and not its defense compound (the stink)," said Lancaster. "The enzyme I'm studying is only one step in the biosynthetic pathway but has already provided some very valuable information."

So far, Lancaster has determined that the harlequin bug makes the pheromone on its own, without using microbes or the host plant. Meanwhile, early work on the brown marmorated stink bug suggests it has a very similar enzyme to the harlequin bug and both differ significantly from other insect enzymes of this type.

"This divergence, along with the similarity between stink bug pheromones, suggests an evolutionary event that led directly to a unique pheromone biochemistry," said Lancaster. "We assume that similar events have occurred in other insects allowing exciting future discoveries in the biosynthesis of pheromones and their application."

- Lindsay Key

Mating harlequin bugs. Photo by Tom Kuhar



AROUND TPS



*TPS students went for a day hike to Cascade Falls.
Photo by Kasia Dinkeloo*



*Kasia Dinkeloo works with a student to prepare the beds for planting.
Photo by David Haak*

*TPS students get their hands dirty working with a local child development center.
Photo by Kasia Dinkeloo*



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ABOUT TPS

The Graduate Program in Translational Plant Sciences (TPS) at Virginia Tech allows students interested in pursuing a Ph.D. degree in this discipline to work in a wide variety of research areas ranging from plant genomics to disease resistance, metabolic engineering, bioproduction and bioprocessing, and forest biotechnology.

TPS degree candidates who enroll in the program participate in several rotations through laboratories of interest. The program of study includes selections from a range of course offerings, tailored to the background and interests of each student. At the end of the first or second semester of enrollment, a permanent advisor is selected in whose laboratory the dissertation research will be conducted.

The diversity in the TPS program is evident by looking at the federal agencies that fund them: National Science Foundation, United States Department of Agriculture, Department of Energy, and National Institute of Health.

Moreover, many laboratories are also supported by various Virginia and US grower organizations and industry.

