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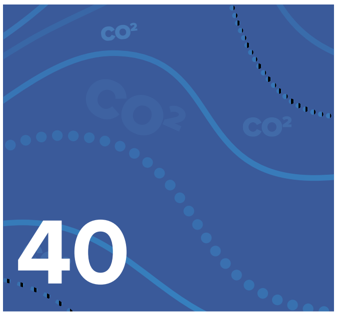
THE AUSTRALIAN AGRONOMIST MAGAZINE

Finding (microbial) pillars of the bioenergy community

Fungi could reduce reliance on fertilisers

Scratching beneath the surface of soil health

CONTENTS



THE AUSTRALIAN AGRONOMIST

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FINDING (MICROBIAL) PILLARS OF THE BIOENERGY COMMUNITY

STEMS, LEAVES, FLOWERS AND FRUITS MAKE UP THE BIGGEST CHUNK OF POTENTIAL LIVING SPACE FOR MICROBES IN THE ENVIRONMENT, BUT ECOLOGISTS STILL DON'T KNOW A LOT ABOUT HOW THE MICROORGANISMS THAT RESIDE THERE ESTABLISH AND MAINTAIN THEMSELVES OVER THE COURSE OF A GROWING SEASON.

In a new study in Nature Communications, Great Lakes Bioenergy Research Centre scientists at Michigan State University have focused on understanding more about the plant regions above the soil where these microbes can live, called the "phyllosphere."

Ashley Shade, MSU assistant professor of microbiology and molecular genetics, and her lab classified core members of this community in two bioenergy cropping systems: switchgrass and miscanthus. In so doing, the group made important distinctions about how these communities assemble - and how they're connected to microbes in the soil.

Microorganisms that dwell in the phyllosphere are thought to play a role in their host's growth and health. And, like their subterranean kin, the topside microbiome affects how much phosphorus, nitrogen and other nutrients bioenergy crops can keep out of our waterways and atmosphere.

Ashley says the first step in determining how to maximize production of these bioenergy crops is figuring out which taxa, or kinds of organisms, are long-term residents and which might just be passing through.

Pillars of the community

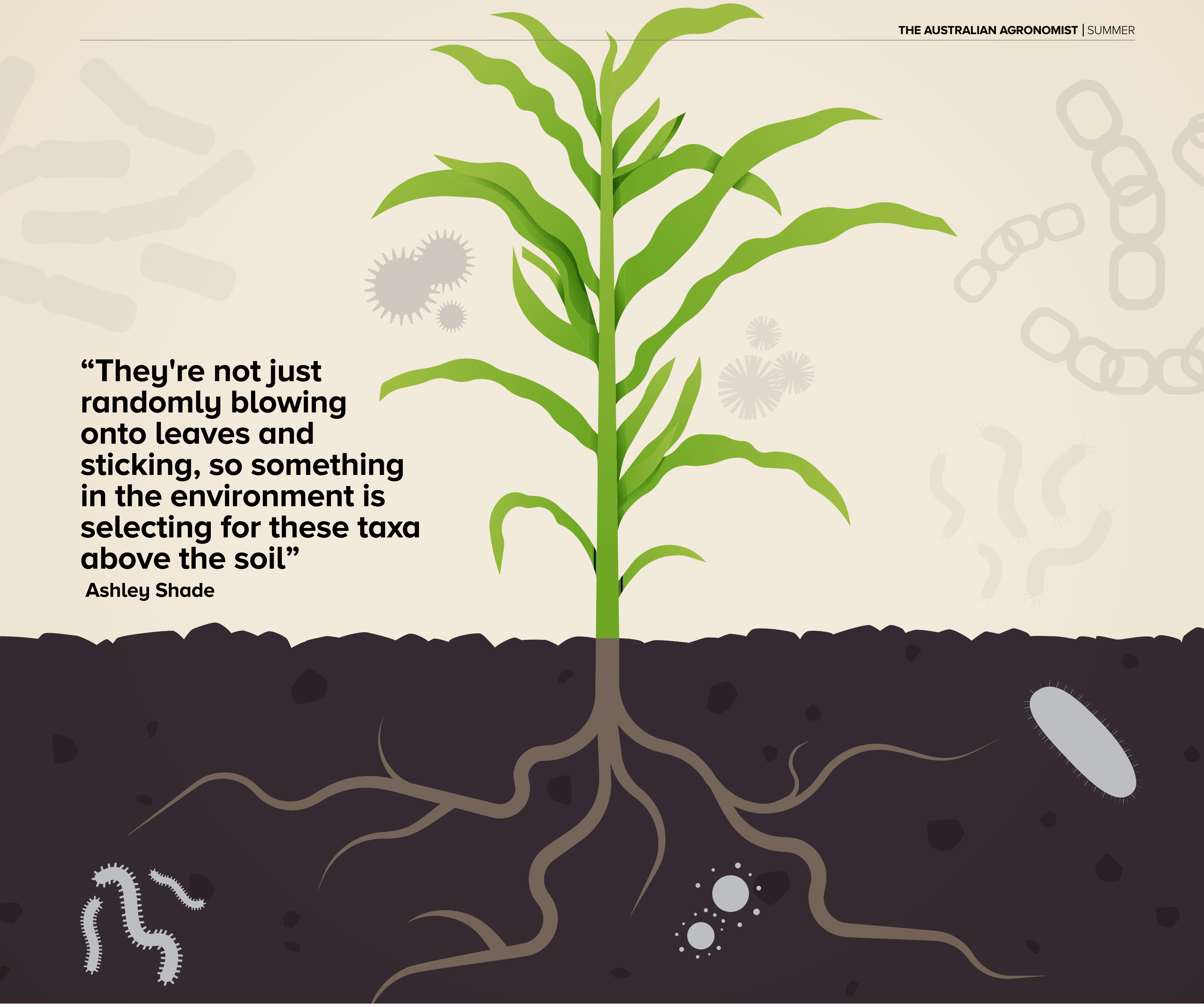
Ashley and her colleagues wanted to ask two questions: does the phyllosphere microbiome change across seasons; and, if so, what role does the soil play in the yearly dance between plants and microbes? To find out, they tapped miscanthus and switchgrass fields at MSU's Kellogg Biological Station in Hickory Corners, established in 2008 as part of a GLBRC biofuel cropping system experiment.

Ashley's lab members sampled microbial communities from bioenergy crop leaves every three weeks for one full growing season for miscanthus and two for switchgrass. They defined core microbes as those that consistently could be detected on leaves at the same time points across their fields, and that persistently appeared over sampling periods.

"If we found a microbe in one field, but not another, it couldn't be called a core member at that specific interval," she said. "We also expect these communities to change with the seasons, so we want to make sure we capture as many of those important taxa as possible."

It turns out that many core microbes on bioenergy plant leaves originate in the soil and are fairly consistent across seasons. This means the phyllosphere microbiome can be targeted for cultivation, just like the crops on which they grow.

The team identified hundreds of leaf microbiome members and compared them to thousands that live in the soil with a deep sequencing technique provided by the Joint Genome Institute,



"They're not just randomly blowing onto leaves and sticking, so something in the environment is selecting for these taxa above the soil"

Ashley Shade

a Department of Energy Office of Science user facility.

"Because of our relationship to JGI, we were able to get some really good coverage of the diversity in our soil communities, something we couldn't have done on our own," Ashley said.

Some microbes found at consistent but low levels in the soil turned out to be core members of leaf communities.

"This suggests that the leaf environment is a specific habitat where certain organisms fit," Ashley said. "The fact that we find them in the soil means the ground is a possible reservoir for these taxa."

To evaluate the idea further, Ashley and her team set up a statistical model to mimic results as if microbes were randomly distributed between a plant's leaves and the nearby soil, then compared the output to their real-life observations.

The models showed that, indeed, the microbial community on miscanthus and switchgrass leaves aren't distributed by chance.

"They're not just randomly blowing onto leaves and sticking, so something in the environment is selecting for these taxa above the soil," Ashley said. "Because the patterns on the ground are different than the ones we see on the leaves, there's reason to believe many of these core leaf members are there on purpose."

Whittling down the taxa

The next step will be to home in on which of the core microbiome members have important functions for the plant.

"Now that we have a whole bunch of community data from the microbiome that includes thousands of taxa," Ashley said, "we can understand which of these core members are just hanging out on the plant, and which ones have an impact on growth and health."

"If we can understand how that microbial community is changing its interactions with its host over a season, we might be able to leverage that to benefit the plant," she added.

Journal Reference:

Keara L. Grady, Jackson W. Sorensen, Nejc Stopnisek, John Guittar, Ashley Shade. Assembly and seasonality of core phyllosphere microbiota on perennial biofuel crops. Nature Communications, 2019; 10 (1) DOI: 10.1038/s41467-019-11974-4

GETTING TO THE ROOT OF HOW PLANTS TOLERATE TOO MUCH IRON

Iron is essential for plant growth, but with heavy rainfall and poor aeration, many acidic soils become toxic with excess iron. In countries with dramatic flood seasons, such as in West Africa and tropical Asia, toxic iron levels can have dire consequences on the availability of staple foods, such as rice.

Despite dozens of attempts in the last two decades to uncover the genes responsible for iron tolerance, these remained elusive until recently. Now, Salk scientists have found a major genetic regulator of iron tolerance, a gene called GSNOR. The findings, published in Nature Communications in August, could lead to the development of crop species that produce higher yields in soils with excess iron.

"This is the first time that a gene and its natural variants have been identified for iron tolerance," says Associate Professor Wolfgang Busch, senior author on the paper and a member of Salk's Plant Molecular and Cellular Biology Laboratory as well as its Integrative Biology Laboratory. "This work is exciting because we now understand how plants can grow in stressful conditions, such as high levels of iron, which could help us make more stress-resistant crops."

In plants such as rice, elevated soil iron levels cause direct cellular damage by harming fats and proteins, decreasing roots' ability to grow. Yet, some plants appear to have inherent tolerance to high iron levels; scientists wanted to understand why.

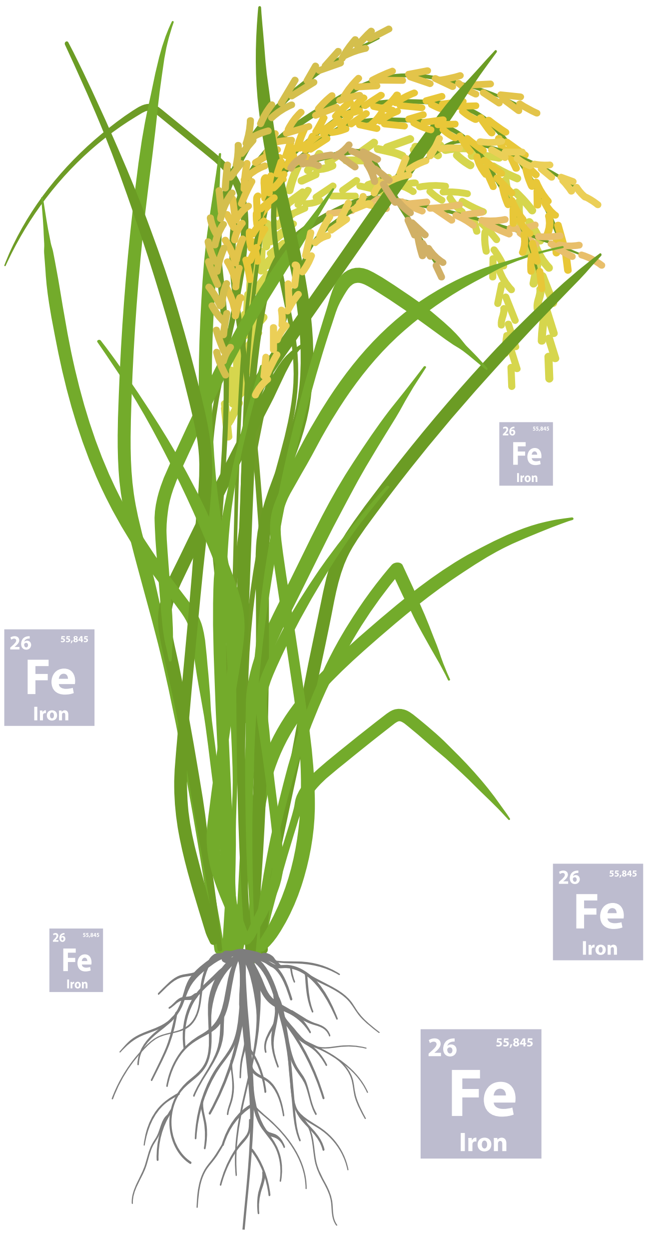
"We believed there were genetic mechanisms that underlie this resistance, but it was unclear which genes were responsible," says first author Baohai Li, a postdoctoral fellow in the Busch lab. "To examine this question, we used the power of natural variation of hundreds of different strains of plants to study genetic adaption to high levels of iron."

The scientists first tested a number of strains of a small mustard plant (Arabidopsis thaliana), to observe if there was natural variation in iron resistance. Some of the plants did exhibit tolerance to iron toxicity, so the researchers used an approach called genome-wide association studies (GWAS) to locate the responsible gene. Their analyses pinpointed the gene GSNOR as the key to enabling plants and roots to grow in iron-heavy environments.

The researchers also found that the iron-tolerance mechanism is, to their surprise, related to the activities of nitric oxide, a gaseous molecule with a variety of roles in plants including responding to stress. High levels of nitric oxide induced cellular stress and impaired the plant roots' tolerance for elevated iron levels. This occurred when plants did not have a functional GSNOR gene. GSNOR likely plays a central role in nitric oxide metabolism and regulates the plants' ability to respond to cellular stress and damage. This nitric oxide mechanism and the GSNOR gene also affected iron tolerance in other species of plants, such as rice (Oryza sativa) and a legume (Lotus japonicus), suggesting that this gene and its activities are likely critical in many, if not all, species of plants.

"By identifying this gene and its genetic variants that confer iron tolerance, we hope to help plants, such as rice, become more resistant to iron in regions with toxic iron levels," says Wolfgang. "Since we found that this gene and pathway was conserved in multiple species of plants, we suspect they may be important for iron resistance in all higher plants. Additionally, this gene and pathway may also play a role in humans, and could lead to new treatments for conditions associated with iron overload."

Next, Baohai will be starting his own laboratory at Zhejiang University, in China. He plans to identify the relevant genetic variants in rice and observe if iron-tolerance variants could increase crop yields in flooded Chinese fields.



Journal Reference:

Baohai Li, Li Sun, Jianyan Huang, Christian Göschl, Weiming Shi, Joanne Chory, Wolfgang Busch. GSNOR provides plant tolerance to iron toxicity via preventing iron-dependent nitrosative and oxidative cytotoxicity. Nature Communications, 2019; 10 (1) DOI: 10.1038/s41467-019-11892-5


Ag Leader

REDUCE, REUSE, RECYCLE: THE FUTURE OF PHOSPHORUS

When Hennig Brandt discovered the element phosphorus in 1669, it was a mistake. He was really looking for gold. But his mistake was a very important scientific discovery. What Brandt couldn't have realised was the importance of phosphorus to the future of farming.

Phosphorus is one of the necessary ingredients for healthy crop growth and yields. When farms were smaller and self-sufficient, farmers harvested their crops, and nutrients rarely left the farm. The family or animals consumed the food, and the farmer could spread manure from their animals onto the soil to rebuild nutrients. This was a fairly closed-loop phosphorus cycle.

But, as the world's population increased, so did food and nutrition needs. More of a farmer's harvest, and therefore nutrients, was sold off the farm. Agriculture adapted by developing many new growing methods, as well as fertilisers. Most phosphorus fertilisers use the world's supply of phosphate rock as a main ingredient. That main modern source is a finite resource and it's running out. Phosphate rock is also hard to mine and process.

"There is an urgent need to increase phosphorus use efficiency in agroecosystems," says Kimberley Schneider, a research scientist with Agriculture and Agri-Food Canada. "There are many chemical, physical and biological processes that affect the availability of phosphorus to crops." This is why farmers place great importance in having enough phosphorus for their crops.

Crop breeding and cultivar selection

Different plants can use phosphorus more efficiently than others. "Phosphorus use efficiency is the ability to yield more crop per unit of phosphorus taken up by the plant," explains Kimberley. "There is potential for crop breeders to develop new varieties that use phosphorus in even more efficient ways. They can also breed crops that work with mycorrhizal fungi in the soil to help increase their phosphorus absorption. Focusing on breeding plants that work well in low phosphorus soils will take an interdisciplinary approach."

Cropping system design and phosphorus use efficiency

Since some crops can increase soil phosphorus availability for future crops, growers could focus on crop rotations that take advantage of this. Cover crops and green manures can also contribute to phosphorus availability in many conditions. For example, one study found sorghum did well with phosphorus use after alfalfa or red clover, but not after sweet clover. Getting the right combinations for the right crops and fields will be important.

Soil organic matter's role in mineralizing phosphorus

Soil organic matter is known to indicate soil health. It can improve plant phosphorus availability by allowing for greater root access to phosphorus and by releasing plant available phosphorus. Currently, soil organic matter is not part of the soil fertility measurements on farms, so this is an area of future research potential.

Naturally occurring soil fungi to the rescue

Many soils contain one or more types of friendly fungus called arbuscular mycorrhizal fungi. They work with plant roots to exchange "life chores." The fungi help free up phosphorus and other nutrients, while the plants make sugar compounds that the fungi use for growth. Of course, the fungi and roots must be able to be near one another for this exchange to happen. Researchers are looking at the promise of building up and better utilizing mycorrhizal fungi populations in soils.

Recycling and recovering phosphorus

Phosphorus is the 6th most common element on earth. Yet, it is a limiting factor in crop yields. Excess phosphorus in the wrong place - streams, lakes and other waterbodies - causes pollution. How did this come to be?

Let's trace the "life cycle" of a phosphorus molecule. Most phosphate rock is mined on the continents of Europe and Africa, although some deposits are available elsewhere. After it is made into fertiliser, this phosphorus is then moved to farms. From there, the phosphorus is used by a plant to make a product, perhaps a soybean.

The soybean is removed from the farm and manufactured into tofu. It is then transported to your local grocery store, where you buy it and bring it home. If you live in a city, after you enjoy your meal of fried tofu, the waste your body produces flushes down the toilet. If you live in a rural area, it goes into the septic system.

Thus, the life cycle of this illustrative phosphorus molecule shows a broken cycle. The molecule originates far away from its final resting place. Because of modern day life, the phosphorus cycle that used to exist on farms is broken. The more urban society becomes, the more broken the phosphorus cycle is - unless scientists come up with answers to close the loops again.

Agricultural scientists are working with wastewater managers to develop ways to put those deserving phosphorus molecules back to work on the farm. "While most currently available phosphorus recovery technologies may not seem economically viable, the environmental and social benefits are important," says Kimberley. "There are also other valuable products of phosphorus recovery, such as organic matter, other nutrients, and even water."

"Increasing phosphorus use efficiency in agroecosystems must be a priority to reduce reliance on fertiliser and to minimize the effects on the environment," says Kimberley. "There are many possibilities for the agricultural system to improve the use of phosphorus. The outcome will be an agroecosystem that still feeds the world, while protecting the natural resources that help us grow our food and live healthy lives."

This article was recently published in a special section in the Journal of Environmental Quality called Celebrating the 350th Anniversary of Discovering Phosphorus - For Better or Worse.

Journal Reference:

Kimberley D. Schneider, Joanne R. Thiessen Martens, Francis Zvomuya, D. Keith Reid, Tandra D. Fraser, Derek H. Lynch, Ivan P. O'Halloran, Henry F. Wilson. Options for Improved Phosphorus Cycling and Use in Agriculture at the Field and Regional Scales. Journal of Environment Quality, 2019; 48 (5): 1247 DOI: 10.2134/jeq2019.02.0070

HARNESSING TOMATO JUMPING GENES COULD HELP SPEED-BREED DROUGHT-RESISTANT CROPS

Once dismissed as 'junk DNA' that served no purpose, a family of 'jumping genes' found in tomatoes has the potential to accelerate crop breeding for traits such as improved drought resistance.

Researchers from the University of Cambridge's Sainsbury Laboratory (SLCU) and Department of Plant Sciences have discovered that drought stress triggers the activity of a family of jumping genes (Rider retrotransposons) previously known to contribute to fruit shape and colour in tomatoes. Their characterisation of Rider, published in September in the journal PLOS Genetics, revealed that the Rider family is also present and potentially active in other crops, highlighting its potential as a source of new trait variations that could help plants better cope with more extreme conditions driven by our changing climate.

"Transposons carry huge potential for crop improvement. They are powerful drivers of trait diversity, and while we have been harnessing these traits to improve our crops for generations, we are now starting to understand the molecular mechanisms involved," said Dr Matthias Benoit, the paper's first author, formerly at SLCU.

Transposons, more commonly called jumping genes, are mobile snippets of DNA code that can copy themselves into new positions within the genome - the genetic code of an organism. They can change, disrupt or amplify genes, or have no effect at all. Discovered in corn kernels by Nobel prize-winning scientist Barbara McClintock in the 1940s, only now are scientists realising that transposons are not junk at all but actually play an important role in the evolutionary process, and in altering gene expression and the physical characteristics of plants.

Using the jumping genes already present in plants to generate new characteristics would be a significant leap forward from traditional breeding techniques, making it possible to rapidly generate new traits in crops that have traditionally been bred to produce uniform shapes, colours and sizes to make harvesting more efficient and maximise yield. They would enable production of an enormous diversity of new traits, which could then be refined and optimised by gene targeting technologies.

"In a large population size, such as a tomato field, in which transposons are activated in each individual we would expect to see an enormous diversity of new traits. By controlling this 'random mutation' process within the plant we can accelerate this process to generate new phenotypes that we could not even imagine," said Dr Hajk Drost at SLCU, a co-author of the paper.

Today's gene targeting technologies are very powerful, but often require some functional understanding of the underlying gene to yield useful results and usually only target one or a few genes. Transposon activity is a native tool already present within the plant, which can be harnessed to generate new phenotypes or resistances and complement gene targeting efforts. Using transposons offers a transgene-free method of breeding that acknowledges the current EU legislation on Genetically Modified Organisms.

The work also revealed that Rider is present in several plant species, including economically important crops such as rapeseed, beetroot and quinoa. This wide abundance encourages further investigations into how it can be activated in a controlled way, or reactivated or re-introduced into plants that currently have mute Rider elements so that their potential can be regained. Such an approach has the potential to significantly reduce breeding time compared to traditional methods.

"Identifying that Rider activity is triggered by drought suggests that it can create new gene regulatory networks that would help a plant respond to drought," said Matthias. "This means we could harness Rider to breed crops that are better adapted to drought stress by providing drought responsiveness to genes already present in crops. This is particularly significant in times of global warming, where there is an urgent need to breed more resilient crops."

Journal Reference:

Matthias Benoit, Hajk-Georg Drost, Marco Catoni, Quentin Gouil, Sara Lopez-Gomollon, David Baulcombe, Jerzy Paszkowski. Environmental and epigenetic regulation of Rider retrotransposons in tomato. PLOS Genetics, 2019; 15 (9): e1008370 DOI: 10.1371/journal.pgen.1008370

THE NEXT AGRICULTURAL REVOLUTION IS HERE

AS A GROWING POPULATION AND CLIMATE CHANGE THREATEN FOOD SECURITY, RESEARCHERS AROUND THE WORLD ARE WORKING TO OVERCOME THE CHALLENGES THAT THREATEN THE DIETARY NEEDS OF HUMANS AND LIVESTOCK. A PAIR OF SCIENTISTS IS NOW MAKING THE CASE THAT THE KNOWLEDGE AND TOOLS EXIST TO FACILITATE THE NEXT AGRICULTURAL REVOLUTION WE SO DESPERATELY NEED.

Cold Spring Harbor Laboratory (CSHL) Professor Zach Lippman, a Howard Hughes Medical Institute investigator, recently teamed up with Yuval Eshed, an expert in plant development at the Weizmann Institute of Science in Israel, to sum up the current and future states of plant science and agriculture.

Their review, published in Science, cities examples from the last 50 years of biological research and highlights the major genetic mutations and modifications that have fueled past agricultural revolutions. Those include tuning a plant's flowering signals to adjust yield, creating plants that can tolerate more fertiliser or different climates, and introducing hybrid seeds to enhance growth and resist disease.

Beneficial changes like these were first discovered by chance, but modern genomics has revealed that most of them are rooted in two core hormonal systems: Florigen, which controls flowering; and Gibberrellin, which influences stem height.

Zach and Yuval suggest that in an age of fast and accurate gene editing, the next revolutions do not need to wait for chance discoveries. Instead, by introducing a wide variety of crops to changes in these core systems, the stage can be set to overcome any number of modern-day challenges.

Dwarfing and flower power revolutions

To explain their point, the scientists reviewed research that focused on key moments in agricultural history, such as the Green Revolution.

Before the 1960s, fertilizing for a large wheat yield would result in the plants growing too tall. Weighed down with their grainy bounty, the wheat stems would fold and rot away, resulting in yield losses. It was only after Nobel laureate Norman Borlaug began working with mutations that affect the Gibberellin system that wheat became the shorter and reliable crop we know today. Borlaug's dwarfing was also applied to rice, helping many fields weather storms that would have been catastrophic only years before. This reapplication of the same technique to a different plant hinted that a core system was in play.

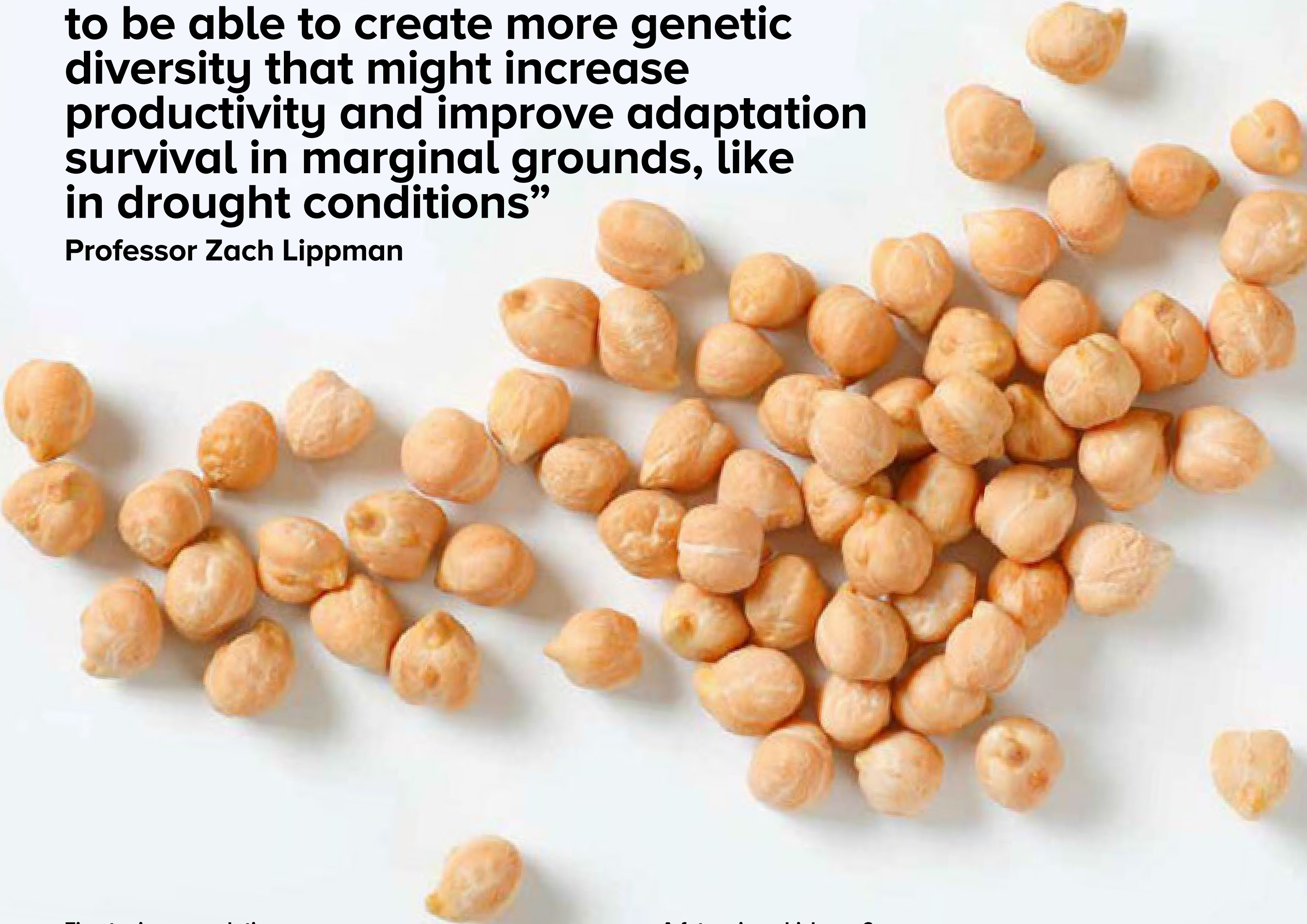
More recent examples Zach and Yuval mention include the changes undergone by cotton crops in China. There, growers turned the normally sprawling, southern plantation plant into a more compact, faster flowering bush better suited for China's northern climate. To do so, they took advantage of a mutation that affects Florigen, which promotes flowering, and its opposite, Antiflorigen.

This kind of change is related to Zach's works. He often works with tomatoes and explained that an Antiflorigen mutation in tomato was also the catalyst that transformed the Mediterranean vine crop into the stout bushes grown in large-scale agricultural systems throughout the world today. What's striking, Zach said, is that cotton is quite unlike any tomato.

"They're evolutionary very different in terms of the phylogeny of plants. And despite that, what makes a plant go from making leaves to making flowers is the same," he said. "That core program is deeply conserved."

"There's a lot more room for us to be able to create more genetic diversity that might increase productivity and improve adaptation survival in marginal grounds, like in drought conditions"

Professor Zach Lippman



Fine-tuning a revolution

As the review details, this has defined what makes an agricultural revolution. A core system - either Gibberellin, Florigen, or both - is affected by a mutation, resulting in some helpful trait. In a moment of pure serendipity, the plants boasting this trait are then discovered by the right person.

It then takes many more years of painstaking breeding to tweak the intensity of that mutation until it affects the system just right for sustainable agriculture. It's like tuning an instrument to produce the perfect sound.

Zach and Yuval note that CRISPR gene editing is speeding up that tuning process. However, they show that the best application of gene editing may not be to just tune preexisting revolutionary mutations, but instead, to identify or introduce new ones.

"If past tuning has been creating genetic variation around those two core systems, maybe we can make more variety within those systems," he said. "It would certainly mitigate the amount of effort required for doing that tuning, and has the potential for some surprises that could further boost crop productivity, or adapt crops faster to new conditions."

A future in… chickpeas?

More of that genetic variety could also set the stage for new agricultural revolutions. By introducing genetic variation to those two core systems that define most revolutions, farmers might get to skip the serendipitous waiting game. Chickpea is one example.

"There's a lot more room for us to be able to create more genetic diversity that might increase productivity and improve adaptation survival in marginal grounds, like in drought conditions," Zach said.

Drought resistance is just one benefit of under-utilized crops. Past revolutions have allowed crops to be more fruitful or to grow in entirely new hemispheres. Having a means to continue these revolutions with more crops and at a greater frequency would be a boon in a crowded, hungry, and urbanizing world.

"Given that rare mutations of Florigen/Antiflorigen and Gibberellin/DELLA mutations spawned multiple revolutions in the past, it is highly likely that creating novel diversity in these two hormone systems will further unleash agricultural benefits," the scientists wrote.

Journal Reference:

Yuval Eshed, Zachary B. Lippman. Revolutions in agriculture chart a course for targeted breeding of old and new crops. Science, 2019; eaax0025 DOI: 10.1126/science.aax0025

ADVANCED BREEDING PAVES THE WAY FOR DISEASE-RESISTANT BEANS

For many people in Africa and Latin America, beans are an important staple. Historically described as "the meat of the poor," beans are rich in protein and minerals, affordable and suitably filling. That is why they are served daily, often with several meals.

In many regions, however, plant diseases severely reduce bean yields. For example, the dreaded angular leaf spot disease can cause yield losses of up to 80 percent - especially in Africa, where smallholders rarely have the opportunity to protect their crops with fungicides.

Genomics-assisted breeding

Working with Bodo Raatz and his team at the International Centre for Tropical Agriculture (CIAT), ETH researchers from the group led by Bruno Studer, Professor of Molecular Plant Breeding, investigated the resistance of beans to angular leaf spot disease. Their findings are now enabling disease-resistant bean varieties to be bred more rapidly and selectively for the world's various bean-producing regions.

Their method is built upon genome analyses of those beans that are potentially suitable for breeding new, resistant varieties. The resulting genetic profiles provide information as to whether the progeny from crossbreeding two varieties will be resistant to the pathogenic fungus's different, locally occurring strains (known as pathotypes).

Genetic profiles created for 316 varieties

Michelle Nay, who carried out the project as part of her doctoral thesis in Studer's group, started by gathering as many different bean seeds as possible from CIAT's seed repository. In total, she collected 316 different varieties that displayed characteristics suitable for breeding resistance to the fungus that causes angular leaf spot disease.

Next, Michelle planted the beans from her collection in Uganda and Colombia, both in greenhouses and in the field. Her aim was to find out if and indeed how the different varieties react to the fungus's various pathotypes in each country, and then to identify the genetic basis of disease resistance.

Michelle also created a high-resolution genetic profile for each of the 316 bean types based on variations in their DNA known as genetic markers, and identified which markers occurred only in the disease-resistant beans. She subsequently used these markers to predict which progeny would be resistant to which pathotypes in a given country, and which ones would be susceptible to disease.

Improvement on conventional plant breeding

"Our method speeds up the breeding process considerably," Bruno says. It's a big step forward because crossbreeding had previously been a numbers game and involved testing every single plant for its resistance, he explains. Now, on the basis of a genetic test, it is possible to predict a plant's resistance without testing it in laborious field trials. "This is a huge help in bean breeding and great news for people who rely heavily on beans as a staple of their diet," Bruno says.

The group's work to provide disease-resistant beans will also help to cut down on global pesticide use. As things stand today, Studer explains, fungicide use is common for bean cultivation in Latin America, but almost non-existent in Africa because many farmers don't have access to pesticides, or don't know how to use them safely and efficiently "Disease-resistant beans are a double win: farmers in Latin America can reduce their pesticide use while farmers in Africa can increase their crop yield pesticide-free."

Simple, inexpensive and open-source technology

CIAT distributes the seeds from this project to various sub-organisations who then supply them to breeders. The analytical method for determining genetic markers is relatively simple and inexpensive to apply, making it viable for use in agricultural laboratories in the countries concerned. It costs less than 0.2 CHF to test a genetic marker, Nay explains, which is an affordable amount for laboratories in less affluent countries. What's more, all the findings from this study are available through open access.

> **"This way, our work reaches the people who really need these kind of resources," Michelle emphasises.**

Michelle and Bruno worked on this project in close collaboration with CIAT. The global research centre runs the largest breeding programme in the tropics and has several thousand varieties of bean in its seed repository. At its headquarters in Colombia, CIAT breeds new bean varieties, tests the seeds, and, in partnership with the Pan-Africa Bean Research Alliance, makes the seeds available to farmers for cultivation.

In collaboration with CIAT, Studer and his group will now conduct a follow-up project to refine their breeding method. While the researchers previously focused on markers for one specific disease, the new project will take a more holistic approach as they attempt to use such genome profiles to predict as many plant characteristics as possible.

Journal Reference:

Michelle M. Nay, Clare M. Mukankusi, Bruno Studer, Bodo Raatz. Haplotypes at the Phg-2 Locus Are Determining Pathotype-Specificity of Angular Leaf Spot Resistance in Common Bean. Frontiers in Plant Science, 2019; 10 DOI: 10.3389/fpls.2019.01126

GROWING ADAMA 2 - WHEEL TRIAL TOUR HITS THE MARK

IT APPEARS THE CONCEPT OF A SPRING CROP TRIALS TOUR ON MOTORCYCLES COMPLETE WITH SWAGS FOR CAMPING OVER SEVERAL DAYS, WHICH WAS ORIGINALLY DEVISED BY THE ADAMA TEAM IN WESTERN AUSTRALIA LAST YEAR, IS STRIKING A CHORD WITH GROWERS AND INDUSTRY.

The company's second 2-Wheel Trial Tour in WA this week, which moved from the state's Great Southern and South Coast regions last year up to the Avon Valley this season, attracted an increased number of motorcycle riders, including from across the Nullarbor.

A group of enthusiastic riders from New South Wales Elders agency, B&W Rural at Moree, and the wider area joined the tour, as well as another Elders agronomist and grower clients from Victoria. WA growers on the tour came from as far as Northampton around to Bremer Bay.

In addition to viewing a range of trials investigating weed and disease control, including showcasing the use of developmental products, as well as crop safety, soil health and frost management, participants enjoyed both open road and dirt riding as they travelled from near Brookton up to York, where they also took in a visit to WhiteGum Farm and its flight facility, before returning to Brookton.

Rather than inspecting only the company's trials, the Adama team also worked closely with a range of other companies and organisations, including SACOA, Australian Herbicide Resistance Initiative (AHRI), Department of Primary Industries and Regional Development (DPIRD) and consultancy groups, Farmanco, agVivo and Living Farm, to highlight a broad spectrum of research. Several trials are being coordinated with funding from the Grains Research and Development Corporation (GRDC).

Ben Cripps, who joined the tour from Northampton, said it was excellent Adama included trials on the tour from different organisations, while he also enjoyed meeting other like-minded people from across Australia.

Adama Market Development Manager - WA, Bevan Addison, said the weed control trials featured one of the company's new products due for release in 2021, Ultro 900 WG, a Group E herbicide for grass weed control in grain legume crops. It is being compared with existing products in lupin and field pea crops.

Bevan said Ultro 900 would provide excellent control of annual ryegrass, brome grass, barley grass and self-sown cereals in all grain legume crops.

"It will be a great rotational option, giving good weed control and helping to reduce the reliance on other pre-emergent herbicides such as Countdown, Sakura and propyzamide," Bevan said.

Post-emergent herbicide mixes are always of interest and another trial investigating grass and broadleaf herbicide options featured an experimental adjuvant product from SACOA code-named BEXA.

Bevan said this research, which was in its third season and showing some promising results, was targeting robust weed control and improved crop safety with some of the mixes that can sometimes damage crops.

The AHRI trial kicked-off the tour with a focus on a systems approach to weed control.

"Robust systems are critical for all aspects of our farming enterprises and we need to get the balance right between profitability and sustainability," Bevan said.

Disease was once again a strong component of the tour program in canola, field peas and cereals this season.

A GRDC trial in conjunction with Farmanco in canola is taking a closer look at blackleg disease, which has been on the rise both early and late with crops, while resistance has also been shown to some of the key fungicides being used.

"GRDC and plant breeders are looking at options and we are doing the same at Adama. We have had a blackleg project running for several seasons now and we are starting to see some promising options as an alternative to the traditional use

> **“We’re all in common in agriculture and we’re in common in riding bikes. It’s a wonderful thing - it’s great from that point of view.”**
> **Jonathan Boreyko**

Riders on the Adama 2-Wheel Trial Tour arrive at the post-emergent grass and broadleaf herbicide mixtures site in barley east of York. The trial included a novel surfactant product under development from SACOA code-named BEXA, which in this trial showed crop safety improvements with some of the more robust mixes.

of flutriafol fungicide, which is starting to come under pressure,” Bevan said.

He said field peas were starting to have a resurgence with some growers largely to help with management of soil-borne pathogen such as nematodes, as well as soil nitrogen supply.

“Tight cereal rotations on various farms have led to a build-up of soil-borne pathogen, which needs an effective break crop.”

“We now have better field pea varieties as well as a major component of the system, fungicide packages, available, such as Veritas, which can help reduce disease burdens and increase standability of crops, making harvest easier and hopefully capturing more grain.

“Veritas has become an important product for eastern states pea growers and while the area cropped in WA is much smaller, it is gaining momentum here as well. We showcased it in faba beans on last year’s crop trials tour and this season in peas.”

Bevan said strong barley rotations have also led to increased spot form net blotch as the major pathogen for many growers.

He said with resistance to triazole fungicides confirmed in many populations, a trial was being coordinated to assess SACOA’s Biopest product, in addition to commercial fungicides including the newly released Topnotch, which contained propiconazole and azoxystrobin.

“Propiconazole has been the backbone for net blotch control in WA and, combined with azoxystrobin in a unique formulation package, it will have a great fit for a full suite of wheat and barley diseases, but particularly in barley.”

“Similar trials last year showed excellent results from the combination of adjuvant and fungicides and this work will continue to help provide growers with another mode of action in the fight against cereal disease.”

The tour group also visited a long term soil amelioration project showing a range of interactions that have related effects on nutrition, weed and disease management, as well as a multi-year frost management site featuring various options designed to provide solutions to the sometimes devastating effects of frost.

Participants who joined the tour from interstate and local areas were pleased to attend the event.

The New South Wales group, who had scarcely seen a winter crop for the last three years, were happy to head west and view some nice crops.

Agronomist Brad Donald said learning about weed resistance and its management, particularly in annual ryegrass, which was becoming a bigger issue in the east, was highly beneficial.

Another fellow agronomist, Casey Onus, said WA growers “do things a little differently and it is very good to see”.

WA consultant and biking enthusiast Graham Laslett was quick to join the tour again this year and praised the event.

“We’re all in common in agriculture and we’re in common in riding bikes. It’s a wonderful thing - it’s great from that point of view.”

Meanwhile, as part of Adama’s local support toward the Blue Tree Project that is helping to raise awareness around mental wellbeing in rural areas, the company connected with the initiative for its latest tour group and heard from guest speakers during the event.

During the tour, Adama also announced the winner of its Quadrant product promotion, where a Yamaha Wolverine quad bike was up for grabs to growers who purchased the new multi mode of action broadleaf herbicide this season. Dalwallinu grower Paul Sutherland was the lucky winner.

MAPPING WHITE CLOVER HERITAGE

Four-leaved clovers may or may not bring good luck. What's indisputable is that all white clovers, whether with three or four leaves, have many benefits.

The United States Department of Agriculture calls white clover "one of the most important pasture legumes." In New Zealand, it is one of the main species, along with ryegrass, grown in pastures.

On farms, white clover provides multiple services. Bacteria in clover root nodules 'fix' atmospheric nitrogen and make it available to crops. White clover is a great source of protein for farm animals. In cities, white clover often accompanies the grass used in lawns and playgrounds.

Despite its many uses, white clover breeders in New Zealand did not have access to a comprehensive map of the population structure or genetic landscape of white clover diversity in the country. Now, researchers in New Zealand have created the first detailed map of white clover ancestry and genetics.

"This 'pedigree map' - achieved via pedigree analysis - will serve as an important resource to white clover breeders," says Valerio Hoyos-Villegas, lead author of the study. "It will also help make more informed decisions in the breeding of different white clover varieties."

For all crops, different varieties may be needed to grow in different environments for varying purposes. For example, some crop varieties might need to be drought resistant. Others may be bred to have high yields while growing on poor soils.

In addition to gaining a resource for breeding white clover varieties with desired traits, researchers also found information on the heritage of the species. Pedigree analysis provided this vital information.

For example, the researchers were able to confirm the genetic makeup of the plants initially used to establish white clover crops in New Zealand. They could trace how these initial group of plants, brought in by early plant breeders, were the basis for other varieties of white clover developed later.

"Understanding this genetic history of white clover will help maximize diversity in breeding populations," says Valerio. A diverse breeding population can help breeders develop varieties of white clover with more desired traits.

The researchers focused on a collection of white clover germplasm, maintained in the Margot Forde Germplasm Centre (seed bank) in Palmerston North, New Zealand. Germplasm refers to genetic resources or material maintained for breeding or conservation goals.

"Safeguarding germplasm is the most inexpensive and efficient method of genetic conservation for important plants," says Valerio. But, simply having a germplasm collection is of limited use. "We have created a curated resource of pedigree information," he says. "This resource can be used by any breeder or geneticist interested in using the white clover germplasm."

The study also provides a summary and results of white clover breeding efforts over the last 80 years. The historical nature of the research threw up some unique obstacles. "We were dealing with data from many different sources," says Valerio. "One of the main challenges was curating the data to reach a standard that gave us confidence in the results."

The researchers collected and analysed a lot of historical information in the study. Now, their results can serve as a launch pad for future research and breeding efforts. For example, researchers can use the pedigree analysis to associate traits of interest with specific genes.

"We can also cross populations of white clover based on data from the pedigree analysis," says Valerio. "We can test these populations to determine what sort of novel genetic variations we can create." These data can then be used to complement ongoing breeding efforts in the private sector.

Researchers are now thinking about expanding pedigree analysis into different species beyond clover. "It would be very useful to extend this analysis to other important forage species," he says. "Perennial ryegrass, which is often used as a companion species to clover in pastures, would be a great next choice."

CONTROVERSIAL INSECTICIDES SHOWN TO THREATEN SURVIVAL OF WILD BIRDS

New research at the University of Saskatchewan (USask) shows how the world's most widely used insecticides could be partly responsible for a dramatic decline in songbird populations.

A study published in the journal Science in September is the first experiment to track the effects of a neonicotinoid pesticide on birds in the wild.

The study found that white-crowned sparrows who consumed small doses of an insecticide called imidacloprid suffered weight loss and delays to their migration - effects that could severely harm the birds' chances of surviving and reproducing.

"We saw these effects using doses well within the range of what a bird could realistically consume in the wild - equivalent to eating just a few treated seeds," said Margaret Eng, a post-doctoral fellow in the USask Toxicology Centre and lead author on the study.

Margaret's collaborators on the research were biologist Bridget Stutchbury of York University and Christy Morrissey, an ecotoxicologist in the USask College of Arts and Science and the School of Environment and Sustainability.

Neonicotinoids are the most commonly used class of agricultural insecticides. They are often applied as a seed coating or as a spray on most major crops worldwide.

Although the toxic effects of neonicotinoids were once thought to affect only insects, most notably pollinators such as bees, there is growing evidence that birds are routinely exposed to the pesticides with significant negative consequences.

"Our study shows that this is bigger than the bees - birds can also be harmed by modern neonicotinoid pesticides which should worry us all," said Bridget.

Until now, researchers had not been able to assess what happens to pesticide-exposed birds in the wild. The USask and York University scientists used new lightweight tagging technologies and a collaborative research network called the Motus Wildlife Tracking System to track the effects in the sparrows' natural habitat.

The researchers exposed individual sparrows to small doses of the pesticide, imidacloprid, in southern Ontario, Canada during a stopover on the birds' spring migration. Each bird's body composition was measured before and after exposure, and a lightweight radio transmitter was attached to the bird's back to track its movements in the wild.

Birds given the higher dose of the pesticide lost six per cent of their body mass within just six hours. That one dose also caused birds to stay 3.5 days longer, on average, at the stopover site before resuming their migration compared to control birds.

"Both of these results seem to be associated with the appetite suppression effect of imidacloprid. The dosed birds ate less food, and it's likely that they delayed their flight because they needed more time to recover and regain their fuel stores," said Margaret.

Because the researchers used controlled dosing, they were able to confirm a cause and effect between neonicotinoid exposures and delayed migration, not just a correlation that is more typical of field studies.

In North America, three-quarters of bird species that rely on agricultural habitat have significantly declined in population since 1966. The results of the new study show a mechanism by which pesticides could be directly contributing to this drop-off.

"Migration is a critical period for birds and timing matters. Any delays can seriously hinder their success in finding mates and nesting, so this may help explain, in part, why migrant and farmland bird species are declining so dramatically worldwide," said Christy, senior author on the study.

The three researchers examined the effects of neonicotinoids in a previous study using captive sparrows. The new research reinforces the weight loss effect seen in that 2017 study. Captive birds in the earlier study were also found to become disoriented as a result of neonicotinoid exposure.

"We didn't see that result in wild birds here," said Margaret. "In the real-world, birds likely avoid migratory flight while recovering from the effects of the toxin."

Funding for the research published in Science was provided by the Natural Sciences and Engineering Research Council of Canada (NSERC) Discovery Grants Program, the Kenneth M. Molson Foundation, the NSERC Research Tools and Instruments Grants Program, and a Mitacs Accelerate Fellowship in partnership with Bird Studies Canada.

Journal Reference:

Margaret L. Eng, Bridget J. M. Stutchbury, Christy A. Morrissey. A neonicotinoid insecticide reduces fueling and delays migration in songbirds. Science, 2019 DOI: 10.1126/science.aaw9419

SOIL MICROBES PLAY A KEY ROLE IN PLANT DISEASE RESISTANCE

Scientists have discovered that soil microbes can make plants more resistant to an aggressive disease - opening new possibilities for sustainable food production.

Bacterial wilt disease caused by Ralstonia solanacearum infects several plants including tomatoes and potatoes. It causes huge economic losses around the world especially in China, Indonesia and Africa.

Researchers from the University of York working with colleagues from China and the Netherlands, investigated the effect of the soil microbiome on the plant-pathogen interaction. Infections are often 'patchy' in the field not affecting the whole crop and the cause for this is unknown.

Dr Ville Friman from the Department of Biology said: "Even though we have discovered that the pathogen is present everywhere in tomato fields, it is not capable of infecting all the plants. We wanted to understand if this spatial variation could be explained by differences in soil bacterial communities."

To study the effect of soil microbiome for disease development, the scientists used a newly developed experimental system that allowed repeated sampling of individual plants in a non-destructive manner. This allowed scientists to go back in time and compare healthy and diseased plant microbiomes long before visible disease symptoms.

The sampling method allowed them to compare the micro-organisms that were present in the soils of those plants that remained healthy or became infected. Their analysis showed that the microbiomes of surviving plants were associated with certain rare taxa and pathogen-suppressing Pseudomonas and Bacillus bacteria.

Ville added "We found that improved disease resistance could be transferred to the next plant generation along with the soil transplants analogous to fecal transplants used in medicine.

"Our results show that it is important to focus not only the pathogen but also the naturally-occurring beneficial micro-organisms present in the rhizosphere. While the beneficial role of microbes for humans and plants have been acknowledged for a long time, it has been difficult to disentangle the cause and effect and important bacterial taxa based on comparative data."

The team are currently developing and testing different microbial inoculants for crop production. The research has opened up the possibility in the future that bacteria could be used as 'soil probiotics' to protect plants from pathogens.

Journal Reference:

Zhong Wei, Yian Gu, Ville-Petri Friman, George A. Kowalchuk, Yangchun Xu, Qirong Shen and Alexandre Jousset. Initial soil microbiome composition and functioning predetermine future plant health. Science Advances, 2019 DOI: 10.1126/sciadv.aaw0759

PHOTOSYNTHESIS OLYMPICS: CAN THE BEST WHEAT VARIETIES BE EVEN BETTER?

Scientists have put elite wheat varieties through a sort of "Photosynthesis Olympics" to find which varieties have the best performing photosynthesis. This could ultimately help grain growers to get more yield for less inputs in the farm.

"In this study we surveyed diverse high-performing wheat varieties to see if their differences in photosynthetic performance were due to their genetic makeup or to the different environments where they were grown," said lead researcher Dr Viridiana Silva-Perez from the ARC Centre of Excellence for Translational Photosynthesis (CoETP).

The scientists found that the best performing varieties were more than 30 percent better than the worst performing ones and up to 90 percent of the differences were due to their genes and not to the environment they grew in.

"We focused on traits related to photosynthesis and found that some traits behaved similarly in different environments. This is useful for breeders, because it is evidence of the huge potential that photosynthesis improvement could have on yield, a potential that hasn't been exploited until now," says Viridiana .

During the study, published recently in the Journal of Experimental Botany, the scientists worked in Australia and Mexico, taking painstaking measurements in the field and inside glasshouses.

"The results that we obtained from our "Photosynthesis Olympics," as we like to call them, are very exciting because we have demonstrated that there is scope to make plants more efficient, even for varieties working in the best conditions possible, such as with limited water and fertiliser restrictions. This means for example, that breeders have the potential to get more yield from a plant with the same amount of nitrogen applied," says CoETP Director Professor Robert Furbank, one of the authors of this study.

Photosynthesis - the process by which plants convert sunlight, water and CO2 into organic matter - is a very complex process involving traits at different levels, from the molecular level, such as content of the main photosynthetic enzyme Rubisco, to the leaf, such as nitrogen content in the leaf and then to the whole canopy level.

"This work is an important result for the CoETP, which aims to improve the process of photosynthesis to increase the production of major food crops such as wheat, rice and sorghum. There is a huge amount of collaboration, both institutional and interdisciplinary, that needs to take place to achieve this type of research. Without the invaluable cooperation between statisticians, plant breeders, molecular scientists and plant physiologists, we would have never achieved these results," says co-author Tony Condon from CSIRO and the CoETP.

Journal Reference:

Viridiana Silva-Pérez, Joanne De Faveri, Gemma Molero, David M Deery, Anthony G Condon, Matthew P Reynolds, John R Evans, Robert T Furbank. Genetic variation for photosynthetic capacity and efficiency in spring wheat. Journal of Experimental Botany, 2019; DOI: 10.1093/jxb/erz439

HOW CAN WE FEED THE WORLD WITHOUT OVERWHELMING THE PLANET?

Sustainable Development Goal (SDG) 2 calls for ending hunger, achieving food security and improved nutrition, and promoting sustainable agriculture. The environmental challenges posed by agriculture are however massive, and many fear that they will only become more pressing as we try to meet the growing need for food worldwide. IIASA researchers and colleagues from Japan propose alternative hunger eradication strategies that will not compromise environmental protection.

Despite encouraging progress made in reducing the number of people that go hungry worldwide, one in nine people remain undernourished, more than 30 million children under the age of five are dangerously underweight, and poor nutrition is responsible for the deaths of nearly 3.1 million children under five each year. Across the globe, an estimated 821 million people were undernourished in 2017, and by 2050, the world will likely have two billion more mouths to feed. One approach to meeting the dietary needs of a rapidly growing world population is by increasing food production through agricultural intensification and expansion. This will however inevitably have negative effects on the environment such as air and water pollution, biodiversity loss, and increased greenhouse gas emissions. At the same time, it is well known that hunger is much more a result of unequal access to food across populations, even within single countries where undernourishment often coexists with obesity, rather than lack of agricultural production overall. This fact is however too often forgotten when hunger eradication strategies are being considered.

In their study published in the journal Nature Sustainability, IIASA researchers collaborated with colleagues from Ritsumeikan University and the National Institute for Environmental Studies (NIES) in Japan to explore different ways to end hunger by reducing the inequalities in access to food rather than increasing agricultural production, thus reducing the potential conflicts with environmental protection.

The first alternative hunger eradication strategy explored in the study, focuses exclusively on bridging the nutrition gap of the undernourished population, which can be realised through targeted government support in the short-term. Such a strategy would include food and nutrition programs that provide food in-kind transfers, school-feeding programs, vouchers for food, income support programs, and safety-nets, without the need to wait for economic growth. This more immediate strategy is termed, support-led security. In this scenario, eradicating hunger by 2030, means providing sufficient food to an additional 410 million people who would otherwise remain undernourished under a business as usual scenario. When focusing on the undernourished only, the additional global agricultural production necessary would only be 3%, with corresponding limited negative effects on the environment.

These negligible effects are in strong contrast with an alternative scenario, where hunger eradication is achieved through a general increase in food consumption typically associated with sustained economic growth leading not only to a reduction in the prevalence of undernourishment, but also to an increase in over-consumption. Apart from the fact that such a strategy would not allow the timely achievement of SDG2 (2030), as many decades of economic growth would be necessary, it would require a seven times higher (+20%) growth in food production. This would in turn require 48 Mha of additional agricultural land and also increase greenhouse gas emissions by 550 Mt CO_2eq/year in 2030.

"This paper demonstrates that providing enough food to the undernourished requires an only marginal increase in overall agricultural production and thus also has very limited trade-offs with the environment. Undernourishment is indeed not a problem of agricultural production capacity but of the current economic and political system. This means that there are no good excuses not to tackle it," says Centre Head for Environmental Resources Development and Deputy Program Director of the Ecosystems Services and Management Program at IIASA, Petr Havlik, who is one of the authors of the study.

Additional analysis shows that if equity of food distribution is accompanied by a reduction in over-consumption and food waste, as well as improved agricultural intensification, undernutrition can be eradicated while at the same time reducing agricultural production, thus leading to multiple benefits for environmental sustainability.

"The required amount of food for hunger eradication and the negative impacts on the environment are much reduced by combining hunger eradication with improved equity in food distribution such as reduced food waste and over-consumption, together with agricultural research and development to increase crop yields in developing regions," says study lead-author Tomoko Hasegawa, a researcher at IIASA, Ritsumeikan University and NIES. "Our research shows that to achieve multiple goals, only one policy is not enough. We need to combine different policies to avoid unintended negative impacts on others. This implies that to end hunger without pressuring the environment, we need not only policies that address hunger, but also policies related to food waste and over-consumption, as well as ones related to agricultural research and development to increase crop yields in developing regions."

Journal Reference:

Hasegawa T, Havlík P, Frank S, Palazzo A, Valin H. Tackling food consumption inequality to fight hunger without pressuring the environment. Nature Sustainability, 2019 DOI: 10.1038/s41893-019-0371-6

HOW A PROTEIN CONNECTING CALCIUM AND PLANT HORMONE REGULATES PLANT GROWTH

Plant growth is strongly shaped by environmental conditions like light, humidity, drought and salinity, among other factors. But how plants integrate environmental signals and the developmental processes encoded in their genes remains a mystery.

A new Tel Aviv University study finds that a unique mechanism involving calcium, the plant hormone auxin and a calcium-binding protein is responsible for regulating plant growth. Researchers say that a protein that binds to calcium regulates both auxin responses and calcium levels, creating an interface that determines how plants grow.

The study was led by Proffesor Shaul Yalovsky of TAU's George S. Wise Faculty of Life Sciences and published in PLOS Biology in July. Research for the study was conducted by TAU graduate students Ora Hazak and Elad Mamon and colleagues. It is the fruit of a collaboration with Prof. Joel Hirsch of TAU's Department of Biochemistry and Molecular Biology, Prof. Jörg Kudla of the University of Münster and Prof. Mark Estelle of the University of California, San Diego.

"Determining the mechanisms that underlie the developmental plasticity of plants is essential for agricultural innovation," Shaul explains. "It was believed for several decades that calcium and auxin interfaced during a plant's development, but the exact mechanisms underlying this 'cross-talk' were unclear.

"We have discovered that auxin communicates with calcium through a binding protein called CMI1. We believe our research will have long-term applications for farmers and agricultural experts, who will be able to harness this information to adapt future generations of plants to extreme environmental conditions such as high temperatures, drought and high salinity in the soil."

The levels of the plant hormone auxin determine where leaves develop on a plant, how many branches a plant has and how roots develop. Calcium levels change in plants in response to environmental signals like high or low temperatures, touch and soil salinity, as well as in response to auxin levels.

"Prior to our research, it was unclear how the interaction between calcium and auxin took place," adds Shaul. "Now we know that when auxin levels are high, the levels of the newly discovered binding protein CMI1 are high. We discovered that this protein regulates auxin responses and calcium levels and that it binds to calcium."

Plant responses to auxin are either slow or rapid. Slow responses take place over the course of hours and days and depend on gene expression pathways, whereas rapid responses take place within minutes. The characteristics of CMI1 enable rapid responses to auxin levels, which depend on the presence of calcium.

"We used a very wide collection of tools and approaches that allowed us to carry out our analyses starting from the level of the whole plant, down through the level of tissue and cells, and finally to the level of molecules," Shaul concludes. "The next step will be to identify the cellular components that interact with the protein that we discovered."

Journal Reference:

Ora Hazak, Elad Mamon, Meirav Lavy, Hasana Sternberg, Smrutisanjita Behera, Ina Schmitz-Thom, Daria Bloch, Olga Dementiev, Itay Gutman, Tomer Danziger, Netanel Schwarz, Anas Abuzeineh, Keithanne Mockaitis, Mark Estelle, Joel A. Hirsch, Jörg Kudla, Shaul Yalovsky. A novel Ca2 -binding protein that can rapidly transduce auxin responses during root growth. PLOS Biology, 2019; 17 (7): e3000085 DOI: 10.1371/journal.pbio.3000085

BIOLOGISTS UNTANGLE GROWTH AND DEFENCE IN MAIZE, DEFINE KEY ANTIBIOTIC PATHWAYS

Studying the complex layers of immunity in maize, a staple for diets around the world, scientists have identified key genes that enable surprisingly diverse antibiotic cocktails that can be produced as defensive blends against numerous disease agents. Biologists describe how they combined an array of scientific approaches to clearly define 6 genes that encode enzymes responsible for the production of key maize antibiotics known to control disease resistance.

In order to meet the demands of growing human populations, agricultural production must double within the next 30 years. Yet the health of today's crops and the promise of their yield face a rising slate of threats - from pests to chaotic weather events - leading to an urgent need to identify effective, natural plant defence strategies.

Biologists have access to a wealth of genomic and biochemical data, but rapidly deciphering entire biochemical pathways that protect key crops of global significance remains a significant challenge. Scientists are peeling away at the layers of immunity in maize, a staple for diets around the world, to determine if there are key genes that enable surprisingly diverse antibiotic cocktails that can be produced as defensive blends against numerous disease agents.

Now, a systematic and combined approach to identifying such genes in crop defence has been developed by Yezhang Ding, Alisa Huffaker and Eric Schmelz of the University of California San Diego and their colleagues and is described in Nature Plants.

"We need to know which crop defence mechanisms are effective and what we can do sustain or further improve them," said Eric.

"Co-authors and collaborators in China are already taking some of the maize genes we characterised and are using them to significantly improve disease resistance in rice."

Historically, defining a complete new biochemical pathway in crops has required stepwise progress and often the better part of an entire research career. In the new study, the UC San Diego biologists describe how they combined an array of scientific approaches to clearly define six genes that encode enzymes responsible for the production of key maize antibiotics known to control disease resistance.

Maize plants lacking small molecule antibiotic defences, derived from a skeleton of 20 carbon atoms known as diterpenoids, commonly suffer dramatic increases in fungal disease susceptibility.

"Most people appreciate that pine trees are heavily protected by sticky acid resins that kill or deter a majority of microbes and insects," said Eric. "We describe a complete maize biosynthetic pathway that also makes acid resins on-demand at the site of fungal attack. Interestingly, almost the entire pathway is derived from evolutionarily recent gene duplications from diverse hormone pathways related to plant growth and human testosterone metabolism."

One of the evolutionary steps was a comparatively recent gene duplication three million years ago from the hormone pathway responsible for plant growth called gibberellins. In a step not clearly borrowed from hormone biosynthesis, two highly promiscuous oxidative enzymes (with broad substrate and product specificity) termed cytochrome P450s were characterised to produce unique reactions different from known conifer pathways. In total, the effort leveraged more than 2,000 plant samples, each with 36,861 transcripts, spanning 300 different maize lines to systematically narrow candidates and define a maize pathway for antibiotics effective against fungal pathogens.

Journal Reference:

Yezhang Ding, Katherine M. Murphy, Elly Poretsky, Sibongile Mafu, Bing Yang, Si Nian Char, Shawn A. Christensen, Evan Saldivar, Mengxi Wu, Qiang Wang, Lexiang Ji, Robert J. Schmitz, Karl A. Kremling, Edward S. Buckler, Zhouxin Shen, Steven P. Briggs, Jörg Bohlmann, Andrew Sher, Gabriel Castro-Falcon, Chambers C. Hughes, Alisa Huffaker, Philipp Zerbe, Eric A. Schmelz. Multiple genes recruited from hormone pathways partition maize diterpenoid defences. Nature Plants, 2019; DOI: 10.1038/s41477-019-0509-6

FUNGI COULD REDUCE RELIANCE ON FERTILISERS

INTRODUCING FUNGI TO WHEAT BOOSTED THEIR UPTAKE OF KEY NUTRIENTS AND COULD LEAD TO NEW 'CLIMATE SMART' VARIETIES OF CROPS, ACCORDING TO A NEW STUDY.

Researchers at the University of Leeds have demonstrated a partnership between wheat and soil fungi that could be utilised to develop new food crops and farming systems which are less reliant on fertilisers, reducing their contribution to the escalating climate crisis.

It is the first time the fungi, which form partnerships with plant roots, have been shown to provide significant amounts of phosphorus and nitrogen to a cereal crop. The fungi continued to provide nutrients under higher levels of carbon dioxide (CO2) predicted for 2100, which has important implications for future food security.

The results were published in October in the journal Global Change Biology.

Lead researcher Professor Katie Field, from the University of Leeds' School of Biology and Global Food and Environment Institute, said "Fungi could be a valuable new tool to help ensure future food security in the face of the climate and ecological crises.

"These fungi are not a silver bullet for improving productivity of food crops, but they have the potential to help reduce our current over reliance on agricultural fertilisers."

Agriculture is a major contributor to global carbon emissions, partly due to significant inputs such as fertilisers. Whilst meat production contributes far more to global warming than growing crops, reducing the use of fertilisers can help lower agriculture's overall contribution to climate change.

Ancient plant-fungi partnership

Most plants form partnerships with fungi in their root systems, known as arbuscular mycorrhizas, which enable them to draw nutrients from the soil more efficiently. In exchange, the plants provide carbohydrates to the fungi as a form of payment, known as a symbiosis.

Plants can give 10-20% of the carbon they draw from the air to their fungal partners, in exchange for up to 80% of their required phosphorus intake. These fungi can also help plants increase their growth, nitrogen levels, water uptake, and defend the plant against pests and disease.

But over the last 10,000 years, crop plants have been domesticated through intensive breeding, which has inadvertently stopped some varieties from having such close relationships with beneficial fungi.

Across the globe, wheat is a staple crop for billions, and wheat farming uses more land than any other food crop (218 million hectares in 2017). Despite increasing the application of nitrogen and phosphorus fertilisers to boost yields, the amount of wheat that can be produced from a given area has reached a plateau in recent years.

Whilst some varieties of the wheat grown by farmers form these partnerships with beneficial fungi, many do not. The Leeds researchers therefore suggest there is potential to develop new varieties of wheat that are less dependent on fertilisers.

Sustainable food production

Co-author Dr Tom Thirkell, from the University of Leeds' School of Biology, said "For thousands of years, farmers have been breeding crops to increase productivity and disease resistance, but this has mainly been based on what can be seen above ground.

"We are starting to realise that some of the crops we have domesticated lack these important connections with fungi in the soil. Our results suggest there is real potential to breed new crop varieties which regain this lost relationship with beneficial fungi, and improve the sustainability of future food production systems."

Scientists allowed the fungi to colonise the roots of three different

"These fungi are not a silver bullet for improving productivity of food crops, but they have the potential to help reduce our current over-reliance on agricultural fertilisers." Professor Katie Field

varieties of wheat in the laboratory and grew them in one of two chambers - either mimicking current climatic conditions or those projected for 2100, when CO_2 concentration in the atmosphere is predicted to be double that of today if emissions are not curbed. They wanted to know what benefits the different varieties could gain from their fungal partners and how the relationships would be affected by increasing atmospheric CO_2.

By chemically tagging phosphorus and nitrogen in the soil and CO_2 in the air, the researchers were able to demonstrate that the different varieties of wheat absorbed the nutrients through their fungal partners, in both climate scenarios.

As expected, the three varieties of wheat underwent different levels of exchange with the fungi, with some varieties gaining much more from the relationship than others for a similar carbohydrate 'cost'.

In particular, the Skyfall variety of wheat took up far more phosphorus from the fungi compared to the other two varieties, acquiring 570 times more than the Avalon variety and 225 times more than Cadenza.

There was no difference in phosphorus or nitrogen exchange from the fungi to the wheat at the higher CO_2 level for any of the three crop varieties. It therefore appears that the fungi can continue to transfer nutrients to the crop even under future climate conditions.

The researchers suggest it could be possible to breed new varieties of wheat which are more accommodating to a fungal partnership. This could allow farmers to use less fertilisers, as it may allow the wheat to get more of its required nutrients through the fungi.

There is ongoing discussion about whether fungi are a net positive or negative to the growth of cereal crops, as some evidence suggests fungi can act as parasites to their plant hosts.

It has previously been predicted that higher CO_2 levels in the atmosphere will lead to fungi taking more carbon from their plant hosts, but this study found that not to be the case for these three varieties of wheat.

The researchers recommend that field-scale experiments are now needed to understand whether the fungi's beneficial effects on wheat demonstrated in this study are replicated in a farm setting.

Journal Reference:

Tom J. Thirkell, Daria Pastok, Katie J. Field. Carbon for nutrient exchange between arbuscular mycorrhizal fungi and wheat varies according to cultivar and changes in atmospheric carbon dioxide concentration. Global Change Biology, 2019; DOI: 10.1111/gcb.14851

LACK OF REPORTING ON PHOSPHORUS SUPPLY CHAIN DANGEROUS FOR GLOBAL FOOD SECURITY

Our global food production system uses 53 million tonnes of phosphate fertilisers annually, processed from 270 million tonnes of mined phosphate rock . Estimates show up to 90% phosphate loss from mine to fork. A considerable part of this loss is phosphate pollution in water, some of which creates "dead zones," areas where little or no marine life can survive. With an increase in food demand by 60% towards 2050, our food production system will need even more phosphate fertilisers. But where do the fertilisers come from and where do they go?

UN estimates a population increase to 9 billion by 2050, correlated with a 60% increase in food demand. In a world where almost a billion people are undernourished and where we waste up to half of all food we produce, this will pose new challenges to our global food supply chain and production system. A key variable for food production is the supply of phosphate fertilisers, most of which come from the mining and processing of phosphate rock. Only a handful of countries produce and export phosphate rock and phosphate fertilisers in a phosphate market that is tending towards a Moroccan monopoly. The later stages of the supply chain also see up to 90% losses and the transformation of phosphorus from a valued resource into one of the main causes for eutrophication.

A new study conducted at Stockholm University and the University of Iceland shows that while Phosphorus is a key element to global food security, its supply chain is a black box. This can lead to social, political and environmental issues, which in turn can create phosphorus supply crises. The results are published in the article "Opening access to the black box: The need for reporting on the global phosphorus supply chain" in Ambio, A Journal of the Human Environment.

"Cradle-to-grave reporting along the phosphorus supply chain can reveal the untold story about the social, environmental, ethical and economic price we pay for the food we see on our supermarket shelves. It can also help countries - most of which are dependent on phosphate imports - tailor better policies to decrease the vulnerability of their agricultural sector" says Eduard Nedelciu, researcher at the Department of Physical Geography at Stockholm University and main author of the study.

The study, which is part of a larger European research project called Adaptation to a new Economic Reality identifies four main challenges with reporting on phosphorus and phosphate fertilisers. First, terminologies and methodologies that are used to report on phosphate deposits are not harmonized and sometimes not transparent - this makes estimations of reserves and resources inaccurate and unreliable. Second, the phosphorus supply chain has up to 90% losses, which are poorly documented. Losses occur along all segments of the supply chain and this fragmentation of information makes it hard to accurately report on how much is lost and where.

Better reporting could help design methods to decrease losses and increase efficiency. Third, there are environmental and social consequences occurring along the supply chain of phosphorus. For example, mining and processing phosphate rock is polluting water bodies and is dangerous to human health. Moreover, the phosphorus that leaks from agricultural land and sewage systems into the water can cause eutrophication and the so-called "dead-zones": areas in our oceans and seas where life cannot be supported anymore.

But there is a social and ethical aspect to phosphorus too. Phosphate rock is increasingly mined from contested areas, such as Western Sahara, in what has been described by some as "illegal exploitation." Fourth, open access to data along the phosphorus supply chain is lacking. The authors reinforce the idea that public knowledge on phosphorus and its supply chain is necessary due to its direct link to food, a basic human right. Also, reporting on phosphorus can help better assess progress on a number of global indicators for sustainability, such as the Sustainable Development Goals.

Marie Schellens puts the study into perspective: "Phosphorus information is power. Reliable and regular data gathering can leverage corporate social responsibility as well as political action. Both are needed to tackle many of the issues identified along the supply chain. Transparency can foster a sustainable and socially just supply chain for decades to come."

Journal Reference:

Claudiu-Eduard Nedelciu, Kristín Vala Ragnarsdóttir, Ingrid Stjernquist, Marie Katharine Schellens. Opening access to the black box: The need for reporting on the global phosphorus supply chain. Ambio, 2019; DOI: 10.1007/s13280-019-01240-8

ENGINEERS PRODUCE WATER-SAVING CROP IRRIGATION SENSOR

A team of University of Connecticut researchers engineered a soil moisture sensor that is more cost effective than anything currently available and responds to the global need to regulate water consumption in agriculture.

Designed and tested on the university's farm, the sensors are small enough to insert into the soil with ease and less expensive to manufacture than current technology, the researchers write in the Journal of Sensors and Actuators.

"Advances in hydrological science are hampered by the lack of on site soil moisture data," said Guiling Wang, study author and professor of civil and environmental engineering at UConn. "It's really hard to monitor and measure things underground. The challenge is that the existing sensors are very expensive and the installation process is very labor intensive."

The sensors developed by the team of UConn engineers - environmental, mechanical, and chemical - are expected to save nearly 35% of water consumption and cost far less than what exists. Current sensors that are used in a similar way range from $100 to $1,000 each, while the one developed at UConn cost $2, according to the researchers.

An alternate monitoring option, soil moisture data collected from remote sensing technology such as radars and radiometers on board satellites, have suffered from low resolution. But the new technology developed by UConn Professor Baikun Li's group can provide high spatio-temporal resolution data needed for hydrology model development in Wang's group.

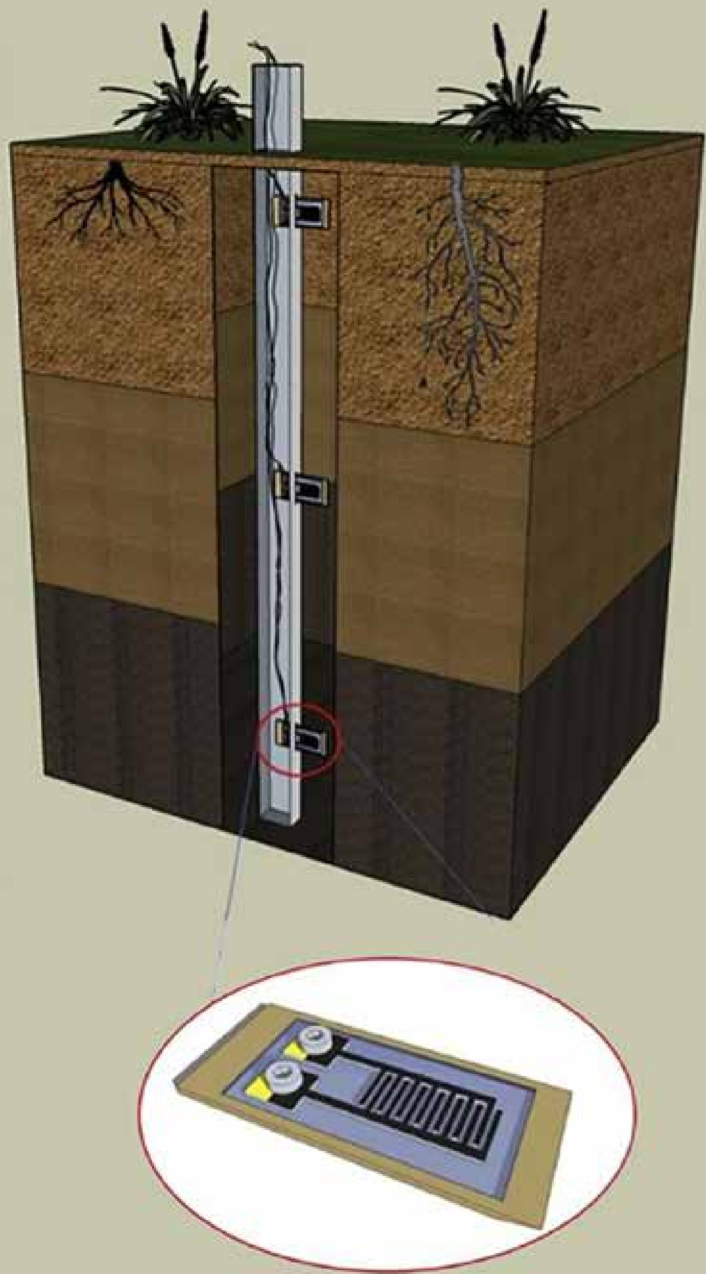
In the UConn prototype, wires are connected from the sensors to an instrument that logs data. Researchers conducted field tests of the sensors - performing side-by-side tests with commercial sensors under various environmental conditions throughout a 10-month period. The effects of the environmental variations on soil moisture throughout the period were clearly reflected.

Critically, the small sensors can also be easily sent around he world given the fact that soil moisture plays a fundamental role in agricultural decision-making globally.

Accurate soil moisture sensing is essential to ensure a water level that produces the most robust crops while not wasting the natural resource. In some states in the U.S. - Florida and California, for example - irrigation water usage has become tightly restricted.

The UConn researchers are also working on a nitrogen sensor that is the same model of the water sensors. These would help provide farmers with information on when fields need fertilizing. Currently, nitrogen sensors are not available using this type of technology.

"This is really an exciting start to a much larger scope of things we have in mind," says Baikun, a study author and professor of civil and environmental engineering.



The soil moisture sensor engineered at UConn is more cost effective than anything currently available and responds to the global need to regulate water consumption in agriculture.
Image Credit: UConn Engineering

Journal Reference:

Wangchi Zhou, Zhiheng Xu, Danny Ross, James Dignan, Yingzheng Fan, Yuankai Huang, Guiling Wang, Amvrossios C. Bagtzoglou, Yu Lei, Baikun Li. Towards water-saving irrigation methodology: Field test of soil moisture profiling using flat thin mm-sized soil moisture sensors (MSMSs). Sensors and Actuators B: Chemical, 2019; 298: 126857 DOI: 10.1016/j.snb.2019.126857

PINEAPPLE GENOME SEQUENCES HINT AT PLANT DOMESTICATION IN A SINGLE STEP

As their Latin name indicates, pineapples are truly "excellent fruits" - and thanks to a freshly completed genome sequencing project, researchers have gained a new understanding of how human agriculture has shaped the evolution of this and other crops.

An international team led by Ray Ming, University of Illinois Professor of Plant Biology and member of the Carl R. Woese Institute for Genomic Biology, published their analysis of the genome of the red pineapple, a plant grown for fibre production and as an ornamental, in Nature Genetics. They also examined new sequence data for other key cultivars of pineapple grown for fruit, leading to new insights into the genetic responses of the plant to centuries of domestication and cultivation. In particular, the work supported the hypothesis that domestication of crops that are propagated without using seeds, through cuttings or other means, can be domesticated in a single step.

"We have chosen major pineapple cultivars worldwide . . . to test our hypothesis of 'one-step operation' in domestication of clonally propagated crops," Ray said. He highlighted this aspect of the researchers' work as one of the primary goals of the study.

Pineapples are a little bit exotic yet pleasingly familiar; large, spiky fruits with sweet, juicy yellow flesh. The newly sequenced variety of this study, Ananas comosus var. bracteatus, is different from this standard grocery store variety. It produces a small fruit that is not suitable for consumption and is grown in gardens for decoration or to form a security hedge. Unlike many cultivars of pineapple, it is able to self-pollinate.

Ray and his colleagues sequenced and assembled the red pineapple genome, using the genome of previously sequenced fruit pineapple as a reference and comparator. They also re-sequenced the genomes of 89 pineapple accessions (samples of plant tissue) from multiple cultivars. By comparing similarities and differences in DNA sequence across different types of pineapple, they were able to trace how natural and artificial selection shaped key traits and established distinct varieties.

Pineapple plants can be grown from vegetative tissues, such as the leafy top of a fruit, a slip, or a sucker. The team hypothesised that for some cultivars, domestication might have been achieved in a single step - starting a variety with a cutting from a likely plant - rather than over years of breeding. They developed a novel bioinformatic method that looked for long strings of similar sequence at the ends of chromosomes.

"To our surprise and delight, extensive terminal runs of homozygosity [similarity] were detected in cultivar 'Singapore Spanish'," Ray said. He explained that this discovery was best explained by many years of exclusive clonal propagation: "One sexual recombination could interrupt terminal runs of homology formed over thousands of years. This novel method can be applied to study domestication history of other clonally propagated crops such as potato, sugarcane, cassava, banana, and many tree fruit crops."

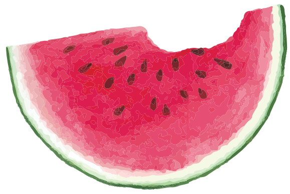
Comparison across genomes also allowed Ray and his coauthors to identify genes that support traits distinguishing different cultivars. For example, differing activity levels of multiple genes appear to support higher leaf fibre production in the red pineapple, and the sweetness of a particular cultivar of fruit pineapple is likely related in part to selection on a particular sugar transporter gene. The study also yielded additional evidence for the involvement of certain genes in allowing or prohibiting self pollination.

Overall, Ray said, he was most excited to find strong support for the idea that with clonal propagation, some plants were immediately and successfully domesticated.

"The co-existence of punctuated sexual reproduction and "one-step operation" in domestication of clonally propagated crops implies rapid domestication of clonally propagated crops is possible," he said. "One example is macadamia, and most macadamia cultivars in Hawaii were selected from seedlings of wild macadamia trees, just one generation away from the wild germplasm."

Journal Reference:

Li-Yu Chen, Robert VanBuren, Margot Paris, Hongye Zhou, Xingtan Zhang, Ching Man Wai, Hansong Yan, Shuai Chen, Michael Alonge, Srividya Ramakrishnan, Zhenyang Liao, Juan Liu, Jishan Lin, Jingjing Yue, Mahpara Fatima, Zhicong Lin, Jisen Zhang, Lixian Huang, Hao Wang, Teh-Yang Hwa, Shu-Min Kao, Jae Young Choi, Anupma Sharma, Jian Song, Lulu Wang, Won C. Yim, John C. Cushman, Robert E. Paull, Tracie Matsumoto, Yuan Qin, Qingsong Wu, Jianping Wang, Qingyi Yu, Jun Wu, Shaoling Zhang, Peter Boches, Chih-Wei Tung, Ming-Li Wang, Geo Coppens d'Eeckenbrugge, Garth M. Sanewski, Michael D. Purugganan, Michael C. Schatz, Jeffrey L. Bennetzen, Christian Lexer, Ray Ming. The bracteatus pineapple genome and domestication of clonally propagated crops. Nature Genetics, 2019; DOI: 10.1038/s41588-019-0506-8



HARVESTING GENES TO IMPROVE WATERMELONS

When many people think of watermelon, they likely think of Citrullus lanatus, the cultivated watermelon with sweet, juicy red fruit enjoyed around the world as a dessert. Indeed, watermelon is one of the world's most popular fruits, second only to tomato - which many consider a vegetable. But there are six other wild species of watermelon, all of which have pale, hard and bitter fruits.

Researchers have now taken a comprehensive look at the genomes of all seven species, creating a resource that could help plant breeders find wild watermelon genes that provide resistance to pests, diseases, drought and other hardships, and further improve fruit quality. Introducing these genes into cultivated watermelon could yield high-quality sweet watermelons that are able to grow in more diverse climates, which will be especially important as climate change increasingly challenges farmers.

"Unfortunately, as people made watermelons sweeter and redder, the fruit lost some abilities to resist diseases and other types of stresses," said Fei, who is also an Adjunct Professor in Cornell University's School of Integrative Plant Science.

As described in a paper published in Nature Genetics in November, the researchers made these insights using a two-step process. First, they created an improved version of a "reference genome," which is used by plant scientists and breeders to find new and interesting versions of genes from their specimens.

Fei co-led the creation of the first watermelon reference genome using an East Asian cultivated variety called '97103,' which was published in 2013.

"That first reference genome was made using older short-read sequencing technologies," Fei said. "Using current long-read sequencing technologies, we were able to create a much higher quality genome that will be a much better reference for the watermelon community."

The group then sequenced the genomes of 414 different watermelons representing all seven species. By comparing these genomes both to the new reference genome and to each other, the researchers were able to determine the evolutionary relationship of the different watermelon species.

"One major discovery from our analysis is that one wild species that is widely used in current breeding programs, C. amarus, is a sister species and not an ancestor as was widely believed," Fei said.

Indeed, the researchers found that cultivated watermelon was domesticated by breeding out the bitterness and increasing sweetness, fruit size and flesh colour. Modern varieties have been further improved in the past few hundred years by increasing sweetness, flavour and crispy texture.

The researchers also uncovered regions of the watermelon genome that could be mined to continue improving fruit quality, such as by making them bigger, sweeter and crispier.

In the past 20 to 30 years, plant breeders have crossed cultivated watermelon with the sister species C. amarus and two other wild relatives, C. mucusospermus and C. colocynthis, to make the dessert watermelon more resistant to nematode pests, drought, and diseases like Fusarium wilt and powdery mildew.

These types of improvements using wild relatives is what excites Amnon Levi, a research geneticist and watermelon breeder at that U.S. Department of Agriculture, Agricultural Research Service, U.S. Vegetable Laboratory in Charleston, South Carolina. Levi is a co-author of the paper and provided the genetic material for many of the watermelons used in the study.

"The sweet watermelon has a very narrow genetic base," says Levi. "But there is wide genetic diversity among the wild species, which gives them great potential to contain genes that provide them tolerance to pests and environmental stresses."

Levi plans to work with BTI to discover some of these wild genes that could be used to improve the dessert watermelon, especially for disease resistance.

"Watermelon is susceptible to many tropical diseases and pests, whose ranges are expected to continue to expand along with climate change," says Levi. "We want to see if we can bring back some of these wild disease resistance genes that were lost during domestication."

Other co-authors included researchers from the Beijing Academy of Agriculture and Forestry Sciences and the Chinese Academy of Agricultural Sciences.

The study was supported in part by funds from the USDA National Institute of Food and Agriculture Specialty Crop Research Initiative (2015-51181-24285), and the US National Science Foundation (IOS-1339287 and IOS-1539831).

In the same issue of Nature Genetics, Fei and colleagues also published a similar paper analysing 1,175 melons, including cantaloupe and honeydew varieties. The researchers found 208 genomic regions that were associated with fruit mass, quality and morphological characteristics, which could be useful for melon breeding.

Earlier this year, Fei, Levi and colleagues published a reference genome of the 'Charleston Gray' watermelon, the principle U.S. variety of C. lanatus to complement the East Asian '97103' genome.

Journal Reference:

Shaogui Guo, Shengjie Zhao, Honghe Sun, Xin Wang, Shan Wu, Tao Lin, Yi Ren, Lei Gao, Yun Deng, Jie Zhang, Xuqiang Lu, Haiying Zhang, Jianli Shang, Guoyi Gong, Changlong Wen, Nan He, Shouwei Tian, Maoying Li, Junpu Liu, Yanping Wang, Yingchun Zhu, Robert Jarret, Amnon Levi, Xingping Zhang, Sanwen Huang, Zhangjun Fei, Wenge Liu, Yong Xu. Resequencing of 414 cultivated and wild watermelon accessions identifies selection for fruit quality traits. Nature Genetics, 2019; DOI: 10.1038/s41588-019-0518-4

GAME CHANGER: NEW CHEMICAL KEEPS PLANTS PLUMP

A UC Riverside-led team has created a chemical to help plants hold onto water, which could stem the tide of massive annual crop losses from drought and help farmers grow food despite a changing climate.

"Drought is the No. 1 cause, closely tied with flooding, of annual crop failures worldwide," said Sean Cutler, a plant cell biology professor at UC Riverside, who led the research. "This chemical is an exciting new tool that could help farmers better manage crop performance when water levels are low."

Details of the team's work on the newer, more effective anti-water-loss chemical is described in a paper published in Science in October. This chemical, Opabactin, is also known as "OP," which is gamer slang for "overpowered," referring to the best character or weapon in a game. "The name is also a shoutout to my 10-year-old at home," Sean said.

An earlier version of OP developed by Sean's team in 2013, called Quinabactin, was the first of its kind. It mimics abscisic acid, or ABA, the natural hormone produced by plants in response to drought stress. ABA slows a plant's growth, so it doesn't consume more water than is available and doesn't wilt.

"Scientists have known for a long time that spraying plants with ABA can improve their drought tolerance," Sean said. "However, it is too unstable and expensive to be useful to most farmers."

Quinabactin seemed to be a viable substitute for the natural hormone ABA, and companies have used it as the basis of much additional research, filing more than a dozen patents based on it. However, Quinabactin did not work well for some important plants, such as wheat, the world's most widely grown staple crop.

When ABA binds to a hormone receptor molecule in a plant cell, it forms two tight bonds, like hands grabbing onto handles. Quinabactin only grabs onto one of these handles.

Sean, along with other collaborators from UCR and the Medical College of Wisconsin, searched millions of different hormone-mimicking molecules that would grab onto both handles. This searching, combined with some chemical engineering, resulted in OP.

OP grabs both handles and is 10-times stronger than ABA, which makes it a "super hormone." And it works fast. Within hours, Sean's team found a measurable improvement in the amount of water plants released.

Because OP works so quickly, it could give growers more flexibility around how they deal with drought.

"One thing we can do that plants can't is predict the near future with reasonable accuracy," Sean said. "Two weeks out, if we think there's a reasonable chance of drought, we have enough time to make decisions - like applying OP - that can improve crop yields."

Initial funding for this project was provided by Syngenta, an agrochemical company, and the National Science Foundation.

Sean's team is now trying to "nerf" their discovery.

"That's gamer speak for when a weapon's power is reduced," Sean said.

Whereas OP slows growth, the team now wants to find a molecule that will accelerate it. Such a molecule could be useful in controlled environments and indoor greenhouses where rainfall isn't as big a factor.

"There's times when you want to speed up growth and times when you want to slow it down," Sean said. "Our research is all about managing both of those needs."

Journal Reference:

Aditya S. Vaidya, Jonathan D. M. Helander, Francis C. Peterson, Dezi Elzinga, Wim Dejonghe, Amita Kaundal, Sang-Youl Park, Zenan Xing, Ryousuke Mega, Jun Takeuchi, Bardia Khanderahoo, Steven Bishay, Brian F. Volkman, Yasushi Todoroki, Masanori Okamoto, Sean R. Cutler. Dynamic control of plant water use using designed ABA receptor agonists. Science, 2019; 366 (6464): eaaw8848 DOI: 10.1126/science.aaw8848

IMPACT OF WATER DROPLETS ON LEAVES TRIGGERS STRESS RESPONSES IN PLANTS

In contrast to humans, plants cannot feel pain. However, so-called mechanical stimulation - rain, wind and physical impact from humans and animals - contributes to the activation of a plant's defence system at a biochemical level. This in turn triggers a stress hormone that, among other things, can lead to the strengthening of a plant's immune system.

The new study confirms the results of previous research. However, this time the researchers looked at molecular changes on a much larger scale - genome-wide - and focused on the role and regulation of the plant hormone jasmonic acid.

The researchers found that thousands of genes, hundreds of proteins and many growth hormones are affected within just ten minutes following water hitting the leaf surface of a plant. They also discovered a never seen before regulatory network that affects how the plant's defence hormones are strengthened by mechanical stimulation.

"This type of stimulation can lead to a delay in the flowering of plants and stunted growth. However, we can now show that the plant also has an increased immune response to certain pathogens and that the plant's biochemical changes are measurable after a very short period of time," says Olivier Van Aken, biology researcher at Lund University and leader of the study.

In experiments carried out in laboratory environments, the researchers used a common plant spray bottle set on a soft spray. The plants were showered once from a distance of 15 centimetres after which the researchers registered the molecular changes at the cellular level at several points in time after the treatment.

"Our results show that plants are very sensitive and do not need heavy rain to be affected and alerted at a biochemical level," says Olivier.

But why do plants react so strongly and quickly to drops of water? The research team says it may be a defence mechanism. When it rains heavily, water droplets that rebound from plants infected with bacteria, fungi and viruses can hit healthy plants.

"The sick leaves can act as a catapult and in turn spread smaller droplets with pathogens to plants several metres away. It is possible that the healthy plants close by want to protect themselves," says Olivier.

The research team says that mechanical stimulation plays a much more significant role than was previously believed, and that different kinds of physical impact can affect plants both positively and negatively depending on the plant's age and growing conditions. Which practical application could these new findings have then?

"We are currently studying an old Japanese agricultural technique that is based on treading down grains during the growth phase to achieve more abundant crop production. I think there is a lot more to learn about how mechanical stimulation affects plants, knowledge which may have significant consequences for agriculture in the future," says Olivier.

Journal Reference:

Alex Van Moerkercke, Owen Duncan, Mark Zander, Jan Šimura, Martyna Broda, Robin Vanden Bossche, Mathew G. Lewsey, Sbatie Lama, Karam B. Singh, Karin Ljung, Joseph R. Ecker, Alain Goossens, A. Harvey Millar, Olivier Van Aken. A MYC2/MYC3/MYC4-dependent transcription factor network regulates water spray-responsive gene expression and jasmonate levels. Proceedings of the National Academy of Sciences, 2019; 201911758 DOI: 10.1073/pnas.1911758116

CHEAP AS CHIPS: IDENTIFYING PLANT GENES TO ENSURE FOOD SECURITY

An international team of scientists led by the University of Goettingen has developed a new approach that enables researchers to more efficiently identify the genes that control plant traits. This method will enable plant breeders and scientists to develop more affordable, desirable, and sustainable plant varieties. The application will be most valuable for the fruit, vegetable and grain crops that not only end up on our dinner table, but are also critical for global food security and human nutrition. The research was published in BMC Plant Biology.

The new method is an extension of a tool known as GWA (Genome Wide Association). GWA studies use genetic sequencing technologies coupled with advanced statistics and computation to link differences in the genetic code with particular traits. When using GWA to study plants, researchers typically manage large sets of genetically identical plants. However, developing these sets of "inbred lines" is costly and time-consuming: it can take over six years of preparation before such a study can even begin. The new technique is modelled after an approach often used to study human DNA, in which DNA samples from thousands of individual people, who are certainly not identical, are compared.

The researchers wanted to discover whether this approach would be successful in plants. Since measurements of individual plants can be highly variable, the scientists developed a method that enabled them to combine the advantages of a GWA study with additional statistical analysis techniques. To test their idea, they investigated whether their combination of approaches could accurately detect genes involved in plant height, a trait that has been extensively studied in the scientific literature. The scientists planted four fields of an early variety of white maize (white corn) and measured the height of the plants. They identified three genes, from the potential 39,000 genes in the maize genome, which were controlling plant height. The effects of all three of these genes were supported by previous studies on other maize varieties. This showed that their method had worked.

"Scientists usually have to measure huge numbers of genetically identical plants in order to have a powerful enough study for finding genes," says Professor Timothy Beissinger, head of the Division of Plant Breeding Methodology at the University of Goettingen, "but we used a diverse maize population and showed that our approach was powerful without relying on identical plants at all."

Abiskar Gyawali, a University of Missouri (USA) PhD student who is the first author, went on to say, "This is great news for researchers interested in finding genes in crops where inbred lines are not available or are time-consuming to produce."

Timothy stated, "The exciting thing is that this study reveals the potential for our method to enable research in other food crops where research funding is not as high. Due to industry and government support, resources are already available to do large-scale studies in maize. But for scientists studying the countless vegetables, fruits, and grains that many communities rely on, funding for massive studies simply isn't possible. This is a breakthrough which will enable cheap and quick identification of trait-gene associations to advance nutrition and sustainability in food crops world-wide."

Journal Reference:

Abiskar Gyawali, Vivek Shrestha, Katherine E. Guill, Sherry Flint-Garcia, Timothy M. Beissinger. Single-plant GWAS coupled with bulk segregant analysis allows rapid identification and corroboration of plant-height candidate SNPs. BMC Plant Biology, 2019; 19 (1) DOI: 10.1186/s12870-019-2000-y

NEW MACADAMIA REGISTRATION PROVIDING EARLY IPM OPTIONS

The registration of Transform® Isoclast active insecticide, as an early season pest control option in Macadamias has helped enable growers to integrate Pest Management (IPM) techniques throughout the growing season.

Transform is now registered for the control of Macadamia Lace bugs (MLB), adding further value when used to control fruit spotting bug and banana spotting bug.

MLB is a small sap-feeding insect which attacks flower buds at early nutset stage. MLB feed directly on flower racemes, which causes flowers to desiccate resulting in significant crop losses.

Northern NSW Macadamia grower and consultant, Stephen McLean said the crop was important for the area but there was a lot of community scrutiny towards spraying chemicals.

“I think it is always good to be responsible and go the softer options, where you can. It is important to take on new chemistry along with cultural practices and other biological controls you can incorporate," he said.

“I've got a bit of hope for Transform. We've got Lace bug as a big flowering issue for us in the past. We've used things like diazinon as a pre-flower, which is quite effective, but it is a product that is up for review. It is pretty hard on beneficials as well and it is not really nice for the user.”

“I think Transform has got an opportunity there for a more friendly start to the season with Lace bug control,” Stephen said. “I am hoping that the use of it might reduce some of our spraying."

Corteva Agriscience Insecticide Development Manager, Rob Annetts said the registration of Transform to control Lace bugs was a significant development.

“This will result in growers using the product earlier, over flowering, which will set them up for a season of IPM by really conserving beneficial insects.”

He said the Macadamia industry has had to rely on some heavy chemistry to control these pests.

“For the first time, with the registration of Transform, they really do have an opportunity to practise IPM. If you use that in conjunction with some other soft products such as Prodigy® or Success® Neo, you can really have a season long control in these crops.”

“I think it is only until growers really start to embrace IPM with these new tools that they'll really see the potential of IPM in macadamias. Transform will round out that package for sap feeding insects and provides growers with a great IPM tool."

Rob said Lace bug was an important pest and attacks early in flowering with the potential to completely take the yield.

Corteva Agriscience Horticultural Manager, Nick Koch, said the new pest on the Transform label complemented the existing pests of fruit spotting bug and banana spotting bug.

“One of the most positive attributes of Transform is its selectivity to key beneficial insects.”

“The natural biological controls that exist in the orchard are conserved because Transform selectively controls the pests whilst preserving beneficial insects.”

“Biological control can help to keep invasive pests underneath the economic thresholds which in turn can reduce the dependency on insecticides.”

He said the three key pests on the label can all be very damaging early in the season and Transform presents an excellent option.

“We can also tie in our other portfolio offerings such as Prodigy, which is a highly selective insecticide for chewing pests particularly flower caterpillar and nut borer and Success Neo for thrips.”

“Growers can manage a season long IPM program where there is a interdependence on biological controls supported by cultural controls and careful management of selective chemical controls."

“Growers are investing significantly in IPM and introducing biological controls to the orchard. Beneficial insects such as trichogamma, a parasitic wasp that lays its eggs into macadamia nutborer work tirelessly for the farmer keeping the nutborers under control, the last thing a grower wants is to use is a broad-spectrum insecticide.”

“Transform has a fantastic fit early on in the season because it enables an Integrated Pest Management program to be successfully implemented in the orchard.”

Nick said an important aspect of all chemicals was to maximise spray coverage through the canopy.

“A lot of the new chemistry coming to market is highly selective and very targeted,” he said. “We need to be able to deliver the chemistry to where it is needed for it to work effectively.”

“There are differences in the way that new technology works, compared to some of the old chemistry like synthetic pyrethroids and organophosphates which are typically broad-spectrum insecticides. Having a targeted approach to crop protection means we can maintain healthier, more sustainable production for generations to come, and that’s a good thing for Australian agriculture.”

Northern NSW Macadamia grower and consultant, Stephen McLean said it was good to be responsible and go the softer options.

NO SOIL LEFT BEHIND: HOW A COST-EFFECTIVE TECHNOLOGY CAN ENRICH POOR FIELDS

Many farmers across sub-Saharan Africa try to coax crops out of sandy soils that are not ideal for holding water and nutrients. Their harvests are predictably poor. A traditional approach would have them apply more fertilisers and use irrigation, but both of these options require access to resources and infrastructure that many of them do not have. A relatively new technology modelled for eight African countries, and currently being tested in Zimbabwe, shows potential for substantially improving harvests through increased water retention and accumulation of organic material to make soils more fertile.

The technology consists of long strips of polyethylene membranes installed in a U-shape below and near the root zones of crops. Known as subsurface water retention technology (SWRT), these membranes have mostly been used in different soils in other regions of the world. Now for the first time, their impact was modelled for Africa. Projected results showed that the SWRT could increase maize yields in the eight African countries in the study by close to 50 percent and capture some 15 million tons of carbon in 20 years.

"With this new technology, sandy soil has the potential to lead a new green revolution," said George Nyamadzawo, a professor at Bindura University in Zimbabwe.

The researchers said this simple technology, if deployed and adopted at scale, could address major issues facing sub-Saharan African farmers, including food security and erratic rainfall patterns, while also helping countries meet climate change mitigation targets. The study was published in Frontiers in Sustainable Food Systems in in September.

"We should refuse to allow sandy soils to limit smallholder farmers from reaching their full potential," said Ngonidzashe Chirinda, a researcher at the International Centre for Tropical Agriculture (CIAT) who co-authored the research. "In arid and semiarid regions with poor soils, smallholder communities continue to suffer due to soil-based poverty. Our research shows SWRT has the potential to effectively change this without recurring to traditional and potentially expensive remedies."For the study, SWRT was modelled for the sandy soils of eight countries in Southern Africa and Eastern Africa: Angola, Botswana, Kenya, Namibia, Mozambique, South Africa, Tanzania, and Zimbabwe. The main objective of the study was to model scenarios of adoption of SWRT and estimate increases in maize yields, crop biomass, and soil carbon sequestration.

Co-authors include scientists at the Swedish University of Agricultural Sciences (SLU), in Sweden; Jomo Kenyatta University of Agriculture and Technology, in Kenya; Cape Peninsula University of Technology, in South Africa; Bindura University of Science Education, in Zimbabwe; and Michigan State University (MSU), in the United States.

"Potential benefits are obvious with new technologies such as SWRT, but there is a need to overcome non-technical barriers; this requires support from decision-makers who can put in place the necessary policies and financial mechanisms to support farmer adoption," said Libère Nkurunziza, the lead author and researcher at SLU. "Similar technologies should be tested and adapted to smallholder farmer conditions to solve productivity challenges on sandy soils."

Using data collected in other regions where SWRT has been tested, the authors made their projections for Africa. The technology is now being tested in Zimbabwe, through a new Swedish Research Council-funded project, called Productive Sands, that is being led by SLU.

"The new innovative, long-term SWRT will lead the way for modifying soils that best assist plant resilience to changing climates and associated weather patterns, enabling smallholder farmers of sandy soils to establish reasonable nutritious food supplies and annual income across all nations," said Alvin Smucker, a co-author from MSU and one of the pioneers of the technology.

"This fabulous contribution constitutes another great example of the need for increasing public and private investments in applied research on new agronomic practices and particularly those focusing on the management of soil fertility as an effective and efficient way of securing food production as well as sequestering carbon," said Ruben Echeverría, the Director General of CIAT.

"Congratulations to the authors for the research results and for building a great research partnership."

Journal Reference:

Libère Nkurunziza, Ngonidzashe Chirinda, Marcos Lana, Rolf Sommer, Stanley Karanja, Idupulapati Rao, Miguel Antonio Romero Sanchez, Marcela Quintero, Shem Kuyah, Francis Lewu, Abraham Joel, George Nyamadzawo, Alvin Smucker. The Potential Benefits and Trade-Offs of Using Sub-surface Water Retention Technology on Coarse-Textured Soils: Impacts of Water and Nutrient Saving on Maize Production and Soil Carbon Sequestration. Frontiers in Sustainable Food Systems, 2019; 3 DOI: 10.3389/fsufs.2019.00071

HERITAGE SEEDS TO BE KNOWN AS BARENBRUG

One of Australia's largest seed companies is changing names, with Heritage Seeds to be known as Barenbrug from 28th October 2019.

The name change to Barenbrug will bring Heritage Seeds in line with parent company The Royal Barenbrug Group, who part-owned Heritage Seeds from its inception in 1990 and have fully-owned Heritage Seeds since 1996.

The Royal Barenbrug Group operates globally with headquarters in The Netherlands and is recognised as the leading worldwide creator of forage and turf solutions. It has 18 operating companies and 22 research and development locations, creating grasses for different purposes in all major climate zones.

Barenbrug Managing Director Toby Brown said Barenbrug would provide the same service and products as Heritage Seeds, while embracing the 114 years of experience of its parent company and enjoying the advantage of its global network.

"Nothing changes but the name," he said. "We have a strong history with Barenbrug and the fourth-generation family business is well known globally so it will be a great advantage to strengthen that connection to Australia.

Toby said it is an exciting time for the company as the name change coincides with the opening of a new $15-million warehouse facility in Toowoomba.

"Supporting growth into northern Australia forms an important part of our strategic direction," Toby said.

"We believe there is a significant opportunity to increase engagement and support northern growers, so we've designed a new Toowoomba facility with capacity to expand as needed," he said.

Toby said the existing company structure and staff would continue. The company employs 110 people with representation across the country.

"We have been and will continue to invest in research and development to produce solutions for Australian conditions" Toby said.

Managing Director Toby Brown says the name change to Barenbrug marks a new era for one of Australia's largest seed companies.

CROP COMPETITION AS A WEED CONTROL STRATEGY

A new study featured in the journal Weed Science points to the formidable weed control challenges faced by growers today. Weeds have developed resistance to many existing herbicide options, and new herbicide discoveries have plummeted. As a result, non-chemical approaches are growing in importance.

Researcher Michael Walsh of the University of Sydney explored the impact that crop density might have on the biomass and seed production of four weed species found in Australian wheat crops.

When wheat was planted at the commercially recommended density of 120 plants per square meter, the biomass of rigid ryegrass, wild radish, ripgut brome and wild oat were reduced by 69, 73, 72 and 49 percent, respectively, compared to weeds grown in the absence of wheat. Weed seed production was reduced by 78, 78, 77 and 50 percent, respectively.

When wheat was planted more densely with 400 plants per square meter, there were additional reductions in both weed biomass (19, 13, 20 and 39 percent) and in seed production (12, 13, 17 and 45 percent). Grain yields remained the same.

Michael also found that crop competition causes weeds to grow more upright and retain significantly more of their seeds in the upper crop canopy.

"This modified growth pattern makes it possible for more weed seeds to be captured and destroyed as the wheat is harvested," Michael says.

Journal Reference:

Michael J. Walsh. Enhanced wheat competition effects on the growth, seed production, and seed retention of major weeds of Australian cropping systems. Weed Science, 2019; 67 (6): 657 DOI: 10.1017/wsc.2019.53

SORGHUM GRAIN YIELD COULD BE DOUBLED

Plant scientists at Cold Spring Harbor Laboratory (CSHL) and USDA's Agricultural Research Service (ARS), in their search for solutions to global food production challenges, have doubled the amount of grains that a sorghum plant can yield.

Sorghum, one of the world's most important sources of food, animal feed, and biofuel, is considered a model crop for research because it has a high tolerance to drought, heat, and high-salt conditions. Increasing the grain yield has become even more important to plant breeders, farmers, and researchers as they try to address and overcome food security issues related to climate change, growing populations, and land and water shortages.

Led by Doreen Ware, CSHL Adjunct Professor and research scientist at the U.S. Department of Agriculture, and USDA colleague Zhanguo Xin, Ph.D, the research team identified novel genetic variations that occurred in sorghum's MSD2 gene, increasing the grain yield 200 percent. MSD2 is part of a gene line that boosts flower fertility by lowering the amount of jasmonic acid, a hormone that controls the development of seeds and flowers.

"When this hormone is decreased, you have a release of development that does not normally occur," said Nicholas Gladman, a postdoctoral fellow in Doreen's lab and first author on the study, recently published in The International Journal of Molecular Sciences. "That allows for the full formation of the female sex organs in these flowers, which then allows for increased fertility"

MSD2 is regulated by MSD1, a gene discovered by Doreen's team last year. Manipulating either gene increases seed and flower production.

"Major cereal crops are very close to each other evolutionarily. A lot of the genes that they share have similar functions," said Yinping Jiao, a postdoctoral associate in the Doreen's Lab and an author on the study. "This gene that plays an important role controlling the sorghum yield may also help us improve the yield of other crops like maize or rice."

Doreen's lab uses this type of genetic research to understand how plants have changed over time.

"These genetic analyses actually give us the molecular mechanisms that provide more opportunities to engineer crops in the future," she said.

The team is now looking to work with collaborators, such as the United States Department of Agriculture, to see if one of the genes - MSD2 or MSD1 - can be used to improve sorghum yield in large field trials.

The left image shows the grains of a normal sorghum plant. The right image depicts how the amount of grains doubled in the genetic variant. CREDIT Ware lab/CSHL, 2019

Journal Reference:

Nicholas Gladman, Yinping Jiao, Young Koung Lee, Lifang Zhang, Ratan Chopra, Michael Regulski, Gloria Burow, Chad Hayes, Shawn A. Christensen, Lavanya Dampanaboina, Junping Chen, John Burke, Doreen Ware, Zhanguo Xin. Fertility of Pedicellate Spikelets in Sorghum Is Controlled by a Jasmonic Acid Regulatory Module. International Journal of Molecular Sciences, 2019; 20 (19): 4951 DOI: 10.3390/ijms20194951

EXPERTS UNLOCK KEY TO PHOTOSYNTHESIS, A FIND THAT COULD HELP US MEET FOOD SECURITY DEMANDS

Scientists have solved the structure of one of the key components of photosynthesis, a discovery that could lead to photosynthesis being 'redesigned' to achieve higher yields and meet urgent food security needs.

The study, led by the University of Sheffield and published in November in the journal Nature, reveals the structure of cytochrome b6f - the protein complex that significantly influences plant growth via photosynthesis.

Photosynthesis is the foundation of life on Earth providing the food, oxygen and energy that sustains the biosphere and human civilisation.

Using a high-resolution structural model, the team found that the protein complex provides the electrical connection between the two light-powered chlorophyll-proteins (Photosystems I and II) found in the plant cell chloroplast that convert sunlight into chemical energy.

Lorna Malone, the first author of the study and a PhD student in the University of Sheffield's Department of Molecular Biology and Biotechnology, said: "Our study provides important new insights into how cytochrome b6f utilises the electrical current passing through it to power up a 'proton battery'. This stored energy can then be then used to make ATP, the energy currency of living cells. Ultimately this reaction provides the energy that plants need to turn carbon dioxide into the carbohydrates and biomass that sustain the global food chain."

The high-resolution structural model, determined using single-particle cryo-electron microscopy, reveals new details of the additional role of cytochrome b6f as a sensor to tune photosynthetic efficiency in response to ever-changing environmental conditions. This response mechanism protects the plant from damage during exposure to harsh conditions such as drought or excess light.

Dr Matt Johnson, reader in Biochemistry at the University of Sheffield and one of the supervisors of the study added "Cytochrome b6f is the beating heart of photosynthesis which plays a crucial role in regulating photosynthetic efficiency. "Previous studies have shown that by manipulating the levels of this complex we can grow bigger and better plants. With the new insights we have obtained from our structure we can hope to rationally redesign photosynthesis in crop plants to achieve the higher yields we urgently need to sustain a projected global population of 9-10 billion by 2050."

The research was conducted in collaboration with the Astbury Centre for Structural Molecular Biology at the University of Leeds.

Researchers now aim to establish how cytochrome b6f is controlled by a myriad of regulatory proteins and how these regulators affect the function of this complex.

Journal Reference:

Lorna A. Malone, Pu Qian, Guy E. Mayneord, Andrew Hitchcock, David A. Farmer, Rebecca F. Thompson, David J. K. Swainsbury, Neil A. Ranson, C. Neil Hunter, Matthew P. Johnson. Cryo-EM structure of the spinach cytochrome b6f complex at 3.6 Å resolution. Nature, 2019; DOI: 10.1038/s41586-019-1746-6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NEW NORTHERN AGRICULTURE SEED HUB SET FOR TOOWOOMBA

Northern Australian agriculture is set to be boosted by the opening of a new $15-million facility in Toowoomba to provide growers with sub-tropical and tropical seed requirements.

The investment by Barenbrug (formerly Heritage Seeds) will see the latest equipment installed in the facility to allow for seed coating, bagging and distribution across the north, including to international customers. The seed company specialises in tropical and temperate pasture varieties, as well as fodder crops, forage cereals, field crops and turf and amenity grasses.

Toby Brown, Barenbrug Managing Director, says the new Toowoomba facility will support the growth of the northern market, while enhancing Barenbrug's market-leading service to growers.

"We believe there is a significant opportunity to increase engagement and support for northern growers, so we've designed a new Toowoomba facility with capacity to expand as needed," he says.

"Business growth has meant we've outgrown our current site in southern Queensland, so the new facility will help provide us with the ability to service the northern market more effectively."

Rory Richards, National Operations Manager for Barenbrug, explains the Toowoomba site will predominantly receive raw uncoated and untreated seed.

"We will then treat that seed in various ways, including using AgriCote, a tailored seed coating treatment, incorporating fertilisers, nutrients, insecticides and fungicides," Rory says.

"We can also film-coat the seed based on our customers agronomic requirements prior to planting, plus we have the capacity to coat seed with biological products."

The Toowoomba site also has a warehouse where the seed is re-bagged, re-labelled and then set up for distribution via sales networks.

"The site incorporates the latest technology, but more importantly has the ability to give us the verifiable quality we demand in our seed products," Rory says.

"Essentially this new site means consistency, volume produced and quality can now be taken one step further, which was more difficult at the old site."

Handover of the new building to Barenbrug took place early October, with the facility expected to become operational from the 18th November. Importantly, the old Toowoomba site will not be decommissioned until the new site is fully operational.

It's an exciting time for the business says Toby, with a range of activities planned to mark the expansion into northern Australia.

"We are holding the annual company conference in Toowoomba at the end of October," he says.

"Then there will be an official opening of the facility in early 2020, where dignitaries will be invited, as will representatives of the Dutch-based Royal Barenbrug Group."

To find out more about the new Barenbrug facility in Toowoomba, head to www.barenbrug.com.au.

Rory Richards, National Operations Manager for Barenbrug has overseen the construction of the new $15 million Barenbrug facility at Toowoomba.

The $15-million Barenbrug seed facility in Toowoomba is set to service the tropical and sub-tropical seed requirements of northern Australian growers

RISING OZONE IS A HIDDEN THREAT TO CORN

Like atmospheric methane and carbon dioxide, ground-level ozone is on the rise. But ozone, a noxious chemical by-product of fossil fuel combustion, has received relatively little attention as a potential threat to corn agriculture.

A new study begins to address this lapse by exposing a genetically diverse group of corn plants in the field to future ozone levels. The study, reported in the journal Global Change Biology, found that some members of the corn family tree are more susceptible than others to yield losses under high ozone air pollution. Discovering the genetic underpinnings of those differences could help plant scientists develop ozone-resistant corn, the researchers said.

"Ozone enters plants the same way carbon dioxide does: It diffuses from the atmosphere into the leaf," said Lisa Ainsworth, a U.S. Department of Agriculture scientist who led the research with University of Illinois plant biology professor Andrew Leakey; University of Florida molecular genetics and microbiology professor Lauren McIntyre; and University of California, Davis plant sciences professor Patrick Brown. Lisa and Andrew are affiliates of the Carl R. Woese Institute for Genomic Biology and the department of crop sciences at Illinois.

Carbon dioxide is a nutrient for plants, Lisa said. "All the carbon that ends up in the grain comes through the leaf first," she said. But ozone is a highly reactive molecule that damages biological tissues and impairs photosynthetic carbon capture in plant leaves.

"Basically, ozone accelerates the aging of the leaf," Andrew said.

Even background levels of ozone do some damage, Lisa said. "Our research suggests that current ozone levels decrease corn yields by as much as 10%," she said. "That's as much as drought or flooding or any single pest or disease, but this is a relatively unstudied component of yield loss in the U.S."

The researchers used the Free Air Concentration Enrichment facility at the U. of I. to track the real-world consequences of higher atmospheric ozone levels in an agricultural field. The FACE facility uses a sophisticated emission system that monitors wind direction and speed to dose a field with specific levels of a variety of gases, including ozone.

"The level that we're fumigating to in this study is a level that is commonly found today in China and India," Lisa said. "So, it's not excessively high, even though we're using a concentration that is 2 1/2 times the level of background ozone in central Illinois."

The researchers planted 45 hybrid corn plants representing all the major types of corn - popcorn, broom corn, dent, flint and others - to look for variation in their responses to high ozone levels. They found that some hybrids were more sensitive to ozone stress than others.

"We found two maize lines whose offspring were more sensitive to ozone pollution, regardless of which other types of corn we bred them with," Andrew said. "Their genetic deficiencies manifested in different ways when exposed to the high ozone conditions."

The genetics of commercial corn are a trade secret, so "we don't know if these corn varieties have the same Achilles' heels," Andrew said. "Breeders would not know about these differences since they are not apparent under clean-air conditions."

More genetic analysis and more experiments like those conducted at the FACE facility will be needed to determine how today's plants will respond to future conditions, Andrew said.

"It's important to understand how plants are going to respond to climate change before the climate changes," he said. "That is the only way we can find the solutions that will be needed in the future."

Journal Reference:

Nicole E. Choquette, Funda Ogut, Timothy M. Wertin, Christopher M. Montes, Crystal A. Sorgini, Alison M. Morse, Patrick J. Brown, Andrew D. B. Leakey, Lauren M. McIntyre, Elizabeth A. Ainsworth. Uncovering hidden genetic variation in photosynthesis of field‐grown maize under ozone pollution. Global Change Biology, 2019; DOI: 10.1111/gcb.14794

CARBON DIOXIDE AND WATER USE EFFICIENCY

BY DR. UWE STROEHER, MICROBIOLOGIST, NEUTROG AUSTRALIA

WITHOUT A DOUBT, THE CURRENT ECONOMIC AND CLIMATIC CONDITIONS ARE PRESENTING SOME NEVER BEFORE SEEN CHALLENGES TO AUSTRALIAN AGRICULTURE. THE MOST PRESSING ISSUE IS THE AVAILABILITY OF WATER, AND HOW TO EFFICIENTLY USE THIS LIMITED RESOURCE.

Perhaps surprisingly, carbon dioxide (CO2) and its availability plays a critical role in water use efficiency in plants, and to understand this we need to look at how CO2 is obtained and used by various plants.

As a rule, plants take up CO^2 via the stomatal pores in the leaves. These pores open and close according to various environmental signals, including the requirement for CO^2. Interestingly, not all plants use CO2 for photosynthesis in the same way - in essence, commercially important plants can be divided in C3 and C4 plants depending on how they use CO^2.

In C3 and C4 plants, the 'C' designates the carbon, whereas in CAM plants the 'C' stands for Crassulacean. These acronyms define the three ways in which plants fix CO2 during photosynthesis. Fixing carbon is the way plants remove the CO2 from atmosphere and turn it into organic molecules like carbohydrates *(Figure 1)*.

C3 plants are plants in which the initial product of the assimilation of CO^2 through photosynthesis is 3-phosphoglycerate, which contains 3 carbon atoms, whereas a C4 plant is a plant that fixes CO^2 initially into a four-carbon sugar. C4 plants are thought to have evolved more recently, and are very efficient in hot, dry climates.

The C3 group of plants (many of which have evolved in cool, wet climates) include cereal crops such as wheat, barley and rye, and important commercial crops such as rice and cotton, as well as many vegetable and fruit varieties. In these plants, the use of CO^2 occurs directly in the mesophyll cells of the leaves (mesophyll cells being the ones most responsible for photosynthesis), and the CO^2 that is taken up by the leaves is used directly in the Calvin cycle *(Figure 1)*.

Although this may sound efficient, it is only effective when the CO2 concentration is high within the cell. When the CO2 concentration drops below 50ppm, the plant may inadvertently uses oxygen instead of CO^2 in a process known as photo-respiration. This is extremely wasteful and can lead to a drop in yield of up to 30%. Therefore, the presence of oxygen becomes a major inhibitor for efficient photosynthesis in C3 plants. In order to overcome this inefficiency, C3 plants keep their stomata open in order to take in more CO^2, but this comes at a cost, as opening the stomatal pores allows water to escape, therefore leading to a drop in the water use efficiency of these plants[1].

As mentioned above, in C4 plants, the CO^2 is fixed in the mesophyll cells to form a four-carbon sugar (C4) in a pathway known as the Hatch–Slack pathway (which is not affected by oxygen). This C4 substrate is shuttled to the bundle cells within the plant where it is converted to C3, and the CO^2 is liberated and is ready to be used in the Calvin cycle away from any extraneous oxygen *(Figure 1)*. In this manner, these plants don't need to open their stomata to the same degree, as excess oxygen and lower CO^2 is not an issue, so as a result, these plants lose less water and have a higher water use efficiency.

Although there are a number of commercially important C4 plants such as corn, sorghum, sugar cane and millet, the vast majority of plants are C3 plants, and as such there is no ready alternative to these in agriculture. There is a third group of plants called the CAM plants (Crassulacean Acid Metabolism) which include pineapples and succulents these plants are the most efficient users of water, as they only open their stomatal pores during the night to take in CO^2. Similar to the C4 plants, these have a four-carbon intermediate which they produce at night. This is converted to a three-carbon substrate with the liberation of CO^2 during the day, and the CO^2 is then available for the Calvin cycle in a fashion similar to what occurs in the C4 plants *(Figure 1)*.

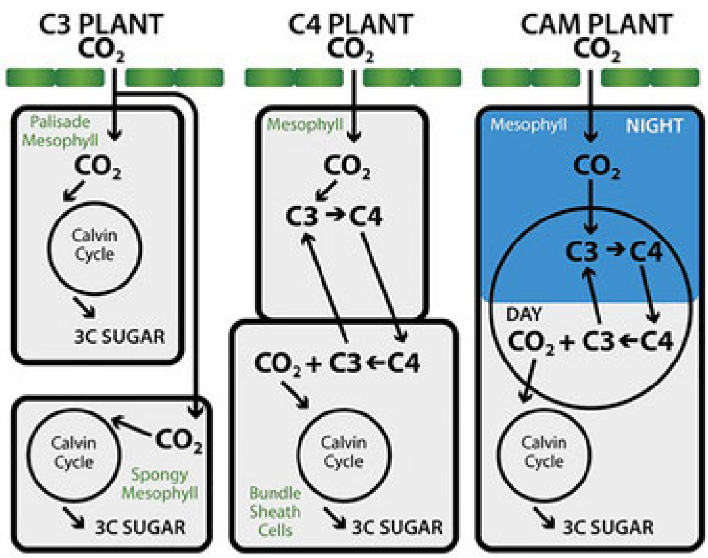


Figure 1.

An increase in the water use efficiency can benefit both C3 and C4 plants, so although C3 plants are the most affected by low CO^2, C4 plants are not immune to water loss due to the stomatal pore opening triggered by low CO^2 concentrations. In essence, the one way to overcome the issue of poor water use efficiency in plants is to increase the available CO^2 *(Figure 2).* [2]

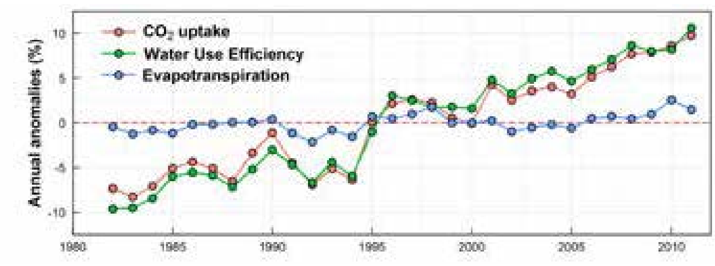


Figure 2. Source: https://phys.org/news/2017-07-carbon-dioxide-world-water-wise.html

Higher levels of CO^2 have been shown to significantly increase the growth of C3 plants and improve their water use - this is known as the 'CO^2 fertilisation effect', where the result on C4 plants is less obvious when it comes to plant growth and yield. Some increases in water use efficiency have come about by the increase of CO^2 in our atmosphere, which currently stands at about 400 ppm.[3] This increase in water use efficiency may be in part due to partial closure of the stomata as well as increased levels of CO^2, which results in fewer stomatal pores in the leaf. However, this increase in the greenhouse gas comes with its own problems, such as changing rainfall patterns, increases in average temperatures and drought, which negates much of the improvement in growth due to increasing CO^2 levels. This appears to be especially obvious in Australia. [3]

In essence, the ideal situation would be to see an increase of the CO^2 concentration in the vicinity of the plant, but not globally. The easiest and most cost-effective way to do this is to increase soil respiration rates by the use of organic inputs. Organic material (either plant or animal waste) consists of a significant proportion of organic carbon, which is carbon that is tied up in organic molecules, in substrates such as cellulose, lignin or oils, or more easily decomposed material such as starches, sugars and proteins.

When prokaryotic organisms such as bacteria and fungi metabolise these materials, they release CO^2 which is immediately available for plants to use *(Figure 3).* In effect, what then occurs is a localised but not a global increase in CO^2 concentration. The use of mulches or composts are ideal for this – we know that mulches will most obviously save water by reducing evaporative loses. We want to also increase the soil respiration rate, however using mulch with a high carbon to nitrogen ratio such as straw, woodchips and sugarcane tend to be biologically less active, and as such, will release much less CO^2 compared to a mulch which has a balance of carbon and nitrogen. A mulch such as 'Whoflungdung' from Neutrog (which is manufactured by screening out the bedding material (straw and shavings) from composted broiler/poultry manure) is much more biologically active, and will therefore release significantly more CO^2 than an inert mulch.

Composts incorporated into the soil will have a similar effect - during the breakdown of this material, CO^2 will stream out of the ground to be used by plants. As CO^2 is heavier than normal air, the plants which will benefit the most are those that are either low-growing such as vegetables and cereal crops, and obviously younger smaller plants.

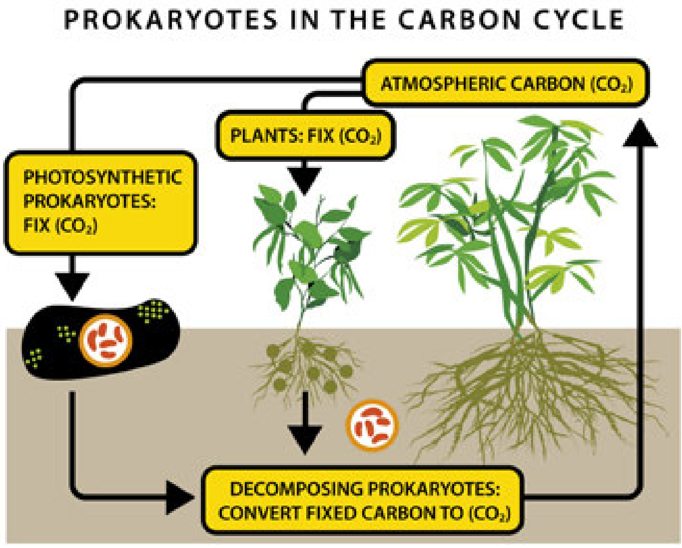
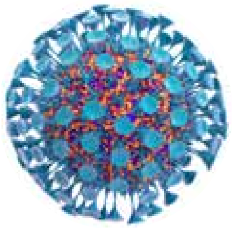


Figure 3.

Journal References:

1. CO^2 sensing and CO^2 regulation of stomatal conductance: advances and open questions. C. Engineer, M. Hashimoto-Sugimoto, J. Negi, M. Israelsson-Nordstrom T. Azoulay-Shemer,W-J. Rappel, K. Iba and J. Schroeder. Trends Plant Sci. 2016 (1):16-30. **2.** Benefits of CO^2 enrichment on crop plants are modified by soil water status. S. Kang, F. Zhang, X. Hu and J. Zhang. Plant and Soil. 2002 (238): 69-77. **3.** Recent increases in terrestrial carbon uptake at little cost to the water cycle. L. Cheng, L. Zhang, Y-P. Wang, J.G. Canadell, F.H.S. Chiew, J. Beringer, L. Li, D.G. Miralles, S. Piao and Y. Zhang. Nature Communications 2017 (8) Article #: 110

HELPING HANDS FROM WITHIN: LIVE-IN BACTERIA PROTECT PLANTS AGAINST INFECTIONS



Certain species of 'resident' bacteria can protect plant roots against fungal infections. Researchers from the Netherlands (Wageningen, Leiden, Rotterdam), Brazil, Colombia and the United States made this discovery using metagenomics: a form of DNA-technology that analyses genes from an environment to reveal the previously hidden diversity of the local microbial community.

"It's without precedent that we were able to reconstruct the composition and functions of this community in plant roots based solely on DNA-sequencing," says the study's last author and research leader, Jos Raaijmakers from NIOO-KNAW.

Sustainable crop production

"Bacteria are essential to the functioning of plants, animals and people," argues Jos. "Our main goal was to discover micro-organisms inside roots that are recruited by the plant when it's under attack from fungal pathogens. Our study represents a big step forward for developing more sustainable crop production systems, with fewer pesticides."

So what exactly happens in plant roots when they're on the verge of being infected? The researchers found out that 'helping hands' inside the roots begin producing all kinds of useful substances. Chitinases, for example: enzymes that break down the cell walls of attacking fungal pathogens.

This discovery allowed the researchers to develop tailor-made microscopic backup troops for plants, using Chitinophaga and Flavobacterium species. Experiments on sugarbeet consistently proved the effectiveness of this approach in suppressing fungal infections of the roots.

Genetic treasure trove

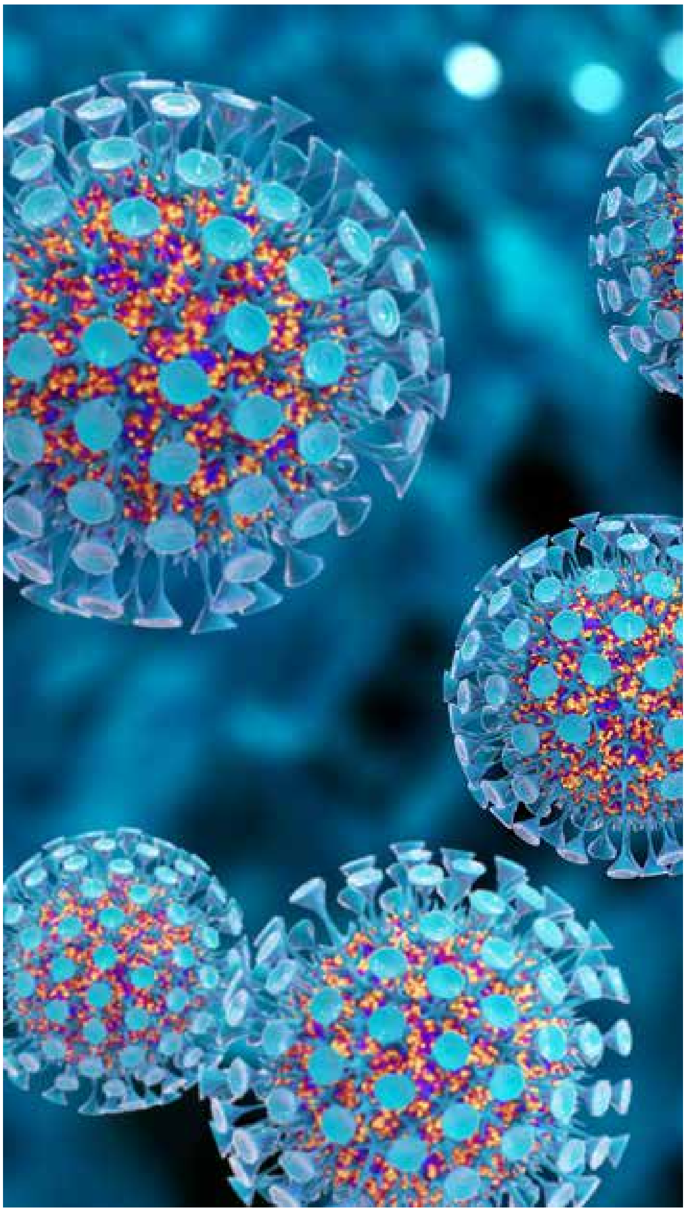
"The micro-organisms living in the roots also turned out to have a wealth of hitherto unknown genetic properties," says Jos . New software, developed by researchers at Wageningen University & Research (WUR), facilitates the comparison of the DNA of thousands of species at once.

Using this method, the researchers found more than 700 unknown gene clusters that produce unique substances. Only twelve had so far been recorded in worldwide databases. "We have discovered a real treasure trove of properties of which we do not even know the function yet. This is only the tip of the iceberg." says Jos.

The NIOO researcher stresses that these discoveries were only possible because of the study's multidisciplinary approach: "It included ecologists as well as microbiologists, molecular biologists, bio-informaticians and statisticians."

The team's research is part of the BackToRoots-project, which received funding from the Dutch Research Council's AES Domain (Applied & Engineering Sciences). BackToRoots aims to enhance plant growth and productivity by exploring beneficial microbial communities, including ones found in wild ancestors of our present-day crops.

With more than 300 staff members and students, the Netherlands Institute of Ecology (NIOO-KNAW) is one of the largest research institutes of the Royal Netherlands Academy of Arts and Sciences (KNAW). The institute specialises in water and land ecology. As of 2011, the institute is located in an innovative and sustainable research building in Wageningen, the Netherlands. NIOO has an impressive research history that stretches back 60 years and spans the entire country, and beyond.



Journal Reference:

Víctor J. Carrión, Juan Perez-Jaramillo, Viviane Cordovez, Vittorio Tracanna, Mattias de Hollander, Daniel Ruiz-Buck, Lucas W. Mendes, Wilfred F.J. van Ijcken, Ruth Gomez-Exposito, Somayah S. Elsayed, Prarthana Mohanraju, Adini Arifah, John van der Oost, Joseph N. Paulson, Rodrigo Mendes, Gilles P. van Wezel, Marnix H. Medema, Jos M. Raaijmakers. Pathogen-induced activation of disease-suppressive functions in the endophytic root microbiome. Science, 2019; 366 (6465): 606 DOI: 10.1126/science.aaw9285

TOO MUCH SUGAR DOESN'T PUT THE BRAKES ON TURBOCHARGED CROPS

Plants make sugars to form leaves to grow and produce grains and fruits through the process of photosynthesis, but sugar accumulation can also slow down photosynthesis. Researching how sugars in plants control photosynthesis is therefore an important part of finding new ways of improving crop production.

Recent research into highly productive turbocharged crops such as maize and sorghum, show the secret to their productivity could lie in their sugar sensing responses which regulate photosynthesis inside their leaves.

"By comparing rice and millet we found that crops that use the C4 photosynthesis path, such as maize, sorghum and millet, regulate photosynthesis using different sugar signal mechanisms than C3 crops, such as wheat and rice. This may be part of the reason why they are more productive," said lead researcher Dr Clemence Henry from the ARC Centre of Excellence for Translational Photosynthesis (CoETP).

"Plants can detect how much sugar is being produced and used through a complex set of sugar sensing mechanisms. These mechanisms can shut photosynthesis down if sugar accumulation is too high. However, to our surprise, we found out that unlike previously shown in some C3 plants, C4 plants are not so sensitive to high levels of sugars, which shows us that the feedback mechanism is not as simple as we previously thought" Clemence says.

"We are trying to understand how photosynthesis is regulated in C4 plants, which are some of the most important cereals in global food production. The regulation mechanisms have been well studied in C3 plants, but until now, we didn't know what happens in C4 crops and how this is related to their ability to produce more sugars," says Dr Oula Ghannoum, CoETP Chief investigator at Western Sydney University.

"One of the most exciting outcomes of this research is that if we understand how sugar signalling works in C4 crops, in the future when we transfer turbocharged photosynthesis mechanisms to crops like wheat and rice we will ensure we improve their yield," says Oula.

Improving photosynthesis, the process by which plants convert sunlight, water and CO2 into organic matter, is recognised as one of the best ways to increase crop production.

"The tricky part is to translate the results found at the molecular level to the crop level. For improved photosynthesis to give more yield we need to "take the brakes off" the crop. This is an essential piece of the puzzle to achieve improved yield through increased photosynthesis," says CoETP Director Professor Robert Furbank, one of the authors of this study.

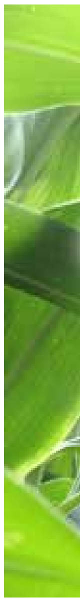
During the study, published recently in the Journal of Experimental Botany, the scientists used light intensity as a means to increase sugar production and identify the genes responsible for photosynthesis regulation. This is one of the few studies that are focusing on the source of sugar production where photosynthesis happens, rather than in the sinks where sugars are used by the plant. This is one of the few studies that are focusing on the source (leaves) where sugar production and photosynthesis take place, rather than in the sinks (grains, fruits) where sugars are used.

"We still have a lot of unanswered questions about how these sugar sensors work. Our next steps are to manipulate these sensors, which will help us to gather essential information we need to transfer them to C3 crops in the future," Oula says.

Journal Reference:

Clémence Henry, Alexander Watson-Lazowski, Maria Oszvald, Cara Griffiths, Matthew J Paul, Robert T Furbank, Oula Ghannoum. Sugar sensing responses to low and high light in leaves of the C4 model grass Setaria viridis. Journal of Experimental Botany, 2019; DOI: 10.1093/jxb/erz495

AI AND FARMER KNOWLEDGE BOOST SMALLHOLDER MAIZE YIELDS



Farmers in Colombia's maize-growing region of Córdoba had seen it all: too much rain one year, a searing drought the next. Yields were down and their livelihoods hung in the balance.

The situation called for a new approach. They needed information services that would help them decide what varieties to plant, when they should sow and how they should manage their crops. A consortium formed with the government, Colombia's National Cereals and Legumes Federation (FENALCE), and big-data scientists at the International Centre for Tropical Agriculture (CIAT). The researchers used big-data tools, based on the data farmers helped collect, and yields increased substantially.

The study, published in September in Global Food Security, shows how machine learning of data from multiple sources can help make farming more efficient and productive even as the climate changes.

"Today we can collect massive amounts of data, but you can't just bulk it, process it in a machine and make a decision," said Daniel Jimenez, a data scientist at CIAT and the study's lead author.

"With institutions, experts and farmers working together, we overcame difficulties and reached our goals."

During the four-year study, Jimenez and colleagues analysed the data and verified developed guidelines for increased production. Some farmers immediately followed the guidelines, while others waited until they were verified in field trials. Farmers that adopted the full suite of machine-generated guidelines saw their yields increase from an average of 3.5 tons per hectare to more than 6 tons per hectare. This is an excellent yield for rainfed maize in the region.

The guidelines also substantially reduced fertiliser costs, and provided advice on how to reduce risks related to variation in the weather patterns, with an emphasis on reducing the negative impacts of heavy rainfall.

Researchers from FENALCE co-authored the study, which is part of a Colombian government program aimed at providing farmers with options to manage both weather variability and climate change.

"If one farmer provides data to a researcher it is almost impossible to gain many insights into how to improve management," said James Cock, a co-author emeritus CIAT scientist. "On the other hand, if many farmers, each with distinct experiences, growing conditions, and management practices provide information, with the help of machine learning it is possible to deduce where and when specific management practices will work."

Year-on-year, maize yields in the study region vary by as much as 39 percent due to the weather. Small farmers in the past had to rely on their own knowledge of their crops and accept blanket recommendations often developed by researchers far removed from their own milieu. The study shows that combining farmers' knowledge with data on weather, soils and crop response to variables, farmers can, at least partially, shield their crops against climate variability and stabilize their yields at a higher level.

From farm to algorithm

In Córdoba, FENALCE, which compiles information on maize plantations, harvests, yields and costs, set up a web-based platform to collect and maintain data from individual farms. Local experts uploaded information on soils after visiting farms at various stages of the crop development, while IDEAM, Colombia's weather agency, supplied weather information from six stations in the region. This allowed researchers to match daily weather station information with individual fields and the various stages of the growing season.

The researchers used machine learning algorithms and expert analysis to measure the impact of different weather, soil conditions and farming practices on yields. For example, they noticed that improving soil drainage to reduce run-off likely reduces yields when rainfall is lower, whereas doing the same in areas with a lot of rain boosts yields. This shows advice on crops needs to be site-specific.

The study demonstrated that the amount of phosphorus applied, the seed rate, and field run-off capacity had a major impact on yield levels. Understanding the effects of the inputs on the crops allowed experts to guide small farmers towards the best practices to use in order to produce high, stable yields.

The upshot for farmers is that most of the management practices the study recommends do not require major investments, showing that food security and livelihoods can be improved - at least in this case - without major expenditures.

Human learning, too

Initially, CIAT and FENALCE designed a smartphone application for farmers to record soil and other data in the field but corn growers did not adopt the app. Although the web-based platform was used to compile the information, researchers and technical assistants had to visit the farms to help the farmers collect the data. This presents challenges for scaling up this type of exercise.

Nevertheless, researchers see opportunities for increased data collection by smallholders, both by directly working with farmers and through technology. Future projects could incorporate apps already developed and used by farmers.

Furthermore, data collection by a whole array of technologies ranging from satellites, drones and low-cost sensors, deployed in fields, coupled with combine harvesters that accurately record grain yield at a micro-scale are all becoming realities in the developing world.

"Much of the hardware and software for the future collection of data may well come when the private sector becomes involved in developing sustainable systems for capturing, analysing and distributing information," said Jimenez. "In the future we can envisage every field being carefully characterised and monitored, turning the landscape into a whole series of experiments that provide data which machine learning can interpret to help farmers manage their crops better."

Journal Reference:

Daniel Jiménez, Sylvain Delerce, Hugo Dorado, James Cock, Luis Armando Muñoz, Alejandro Agamez, Andy Jarvis. A scalable scheme to implement data-driven agriculture for small-scale farmers. Global Food Security, 2019; 23: 256 DOI: 10.1016/j.gfs.2019.08.004

NEMATODE FUMIGANTS HAVE VERY LOW LONG-TERM IMPACT ON SOIL HEALTH, STUDY SUGGESTS

It started with curiosity. How does a fumigant, commonly used for nematode management in potato cropping systems, influence soil microbial communities?

To explore this question, scientists at Colorado State University and Oregon State University used high-throughput sequencing techniques to investigate changes in soil bacterial and fungal community structure in response to the application of 1,3-Dichloropropene (1,3-D) in Pacific Northwest potato production fields. Their research found that the fumigant had very minor effects.

1,3-D is an organic compound used as a pesticide to control nematodes (roundworms) that reduce the yields of many plants. Despite its widespread use, little is known about the fumigant's effects on other organisms in soil. A recent paper published in the open access Phytobiomes Journal is one of the first to report on the effects of nematode management practice, specifically 1,3-D, on soil microflora.

"We found it interesting that only minor effects of 1,3-D were observed on both bacterial and fungal communities, suggesting that soil can be a robust ecosystem and fumigants may not have a long-term impact on the overall microbial community," said researcher Kenneth Frost. The research also showed that the average efficacy of 1,3-D was estimated to be 98% across all nematodes studied, which included root lesion and stubby root nematodes.

As a result of this research, the authors suggest there may be a greater impact on microbial community from other agricultural practices, such as tillage, use of cover crops, irrigation, and precipitation, than fumigant application in potato cropping systems.

There is still room for more studies of this nature, according to Kenneth, who says, "We think that investigating soil microbial community structure in response to different crop management strategies, including pesticide application, may eventually help farmers manage their communities in ways that will enhance crop health and productivity."

Journal Reference:

Yuan Zeng, Zaid Abdo, Amy Charkowski, Jane E. Stewart, Kenneth Frost. Responses of Bacterial and Fungal Community Structure to Different Rates of 1,3-Dichloropropene Fumigation. Phytobiomes Journal, 2019; 3 (3): 212 DOI: 10.1094/PBIOMES-11-18-0055-R

HELPFUL INSECTS AND LANDSCAPE CHANGES

We might not notice them, but the crops farmers grow are protected by scores of tiny invertebrate bodyguards. Naturally occurring arthropods like spiders and lady beetles patrol crop fields looking for insects to eat. These natural enemies keep pests under control, making it easier to grow the crops we depend on.

New research from Michigan State University by Nate Haan, Yajun Zhang and Doug Landis sheds light on how these natural enemies respond to large-scale spatial patterns in agricultural landscapes. These areas are made up of crop fields, forests and grasslands. It turns out their configuration, or spatial arrangement, can go a long way in determining how many natural enemies show up in a field to eat pests.

A new review article published in Trends in Ecology and Evolution summarises recent research into ways landscape configuration affects natural enemies and pest suppression.

"One of the take-homes from our review is that natural enemies can be more abundant when agricultural landscapes are made up of smaller farm fields," said Nate, MSU postdoctoral researcher in the Department of Entomology and one of the study's authors.

"Some natural enemies need resources found in other habitats or in crop field edges. We think when habitat patches are small, they are more likely to find their way back and forth between these habitats and crop fields, or from one crop field into another."

Nate emphasises that the exact effects of landscape configuration depend on the natural history of the critter in question.

"A predator that finds everything it needs to survive within a single crop field might not need natural habitats outside that crop field, but there are lots of other insects that need to find nectar or shelter in other places," Nate said. "For these insects, the spatial arrangement of crop fields and those other habitats can become very important."

This research will help scientists predict how future changes to farming landscapes will affect insect diversity and pest suppression, a service that is estimated to save farmers billions of dollars every year.

One expected change to landscapes in the Midwest will occur as farmers begin to grow more bioenergy crops. This is a key interest to the Great Lakes Bioenergy Research Centre, or GLBRC, which funded the study. Farmers are likely to grow more crops that can be processed and used as substitutes for petroleum; these crops could be traditional crops like corn, but switchgrass, poplar trees and native prairie are promising alternatives. Depending which crops are used and where they are planted, future landscapes will contain new habitats and will likely be in new spatial arrangements.

The next steps for this research include learning more about whether life history traits of beneficial arthropods predict how they will respond to landscape change. Insects have different food requirements and strategies for moving around the landscape, Nate and colleagues are excited to learn how these differences can be used to predict how the insects will respond to future landscape changes.

Journal Reference:

Nathan L. Haan, Yajun Zhang, Douglas A. Landis. Predicting Landscape Configuration Effects on Agricultural Pest Suppression. Trends in Ecology & Evolution, 2019; DOI: 10.1016/j.tree.2019.10.003

SCRATCHING BENEATH THE SURFACE OF SOIL HEALTH

THE TERM 'SOIL HEALTH' CAN MEAN DIFFERENT THINGS TO DIFFERENT PEOPLE, AND IN LOW RAINFALL SEASONS, WE HAVE EVEN MORE REASON TO QUESTION JUST HOW OUR SOILS ARE TRAVELLING. WHILE VISUAL EXAMINATION OF THE SURFACE CAN SOMETIMES TELL SO MUCH, LOOKS CAN BE DECEIVING TO THE MOST EXPERIENCED OF AGRONOMISTS AND GROWERS.

At a recent series of workshops in Queensland and New South Wales, Crop Consultants Australia (CCA) and CottonInfo sought to examine just what 'soil health' looks like in our current agricultural systems. Attendees at each of the forums were asked this question and the responses were wide and varied.

For some, it was defined in more holistic terms that encompass sustainability, longevity and 'good structure'. Others preferred to describe it via the functionality of the soil; its ability to be productive, suppress disease and hold water. Many attendees at the workshops however, delved further into the structure of the soil, highlighting the importance of balanced microbial activity.

The world view is that soil health is about a soil being 'fit for purpose' and for most of us that purpose is for food and fibre production. A healthy soil then becomes one from which we can derive a crop indefinitely and we have to be mindful of physical, chemical and biological aspects of our soils and maintain or improve them. One of the main speakers at the workshops, Dr Oliver Knox from the University of New England, explained that much of the research undertaken in soil health is based on European case studies.

"Our Australian soils and farming systems are not like those in other counties and so we need to be wary of comparing our biology against other parts of the world.'

"If we are testing biology, it is important we are mindful of when in the season we are taking our measurements, where in relation to the crops we are sampling and what we are comparing our data back to." Dr Knox highlighted the importance of looking to 'local' research when looking for answers in the area of improving our soils. It was for this reason, that CCA and CottonInfo chose to showcase some of the 'local' research in this area.

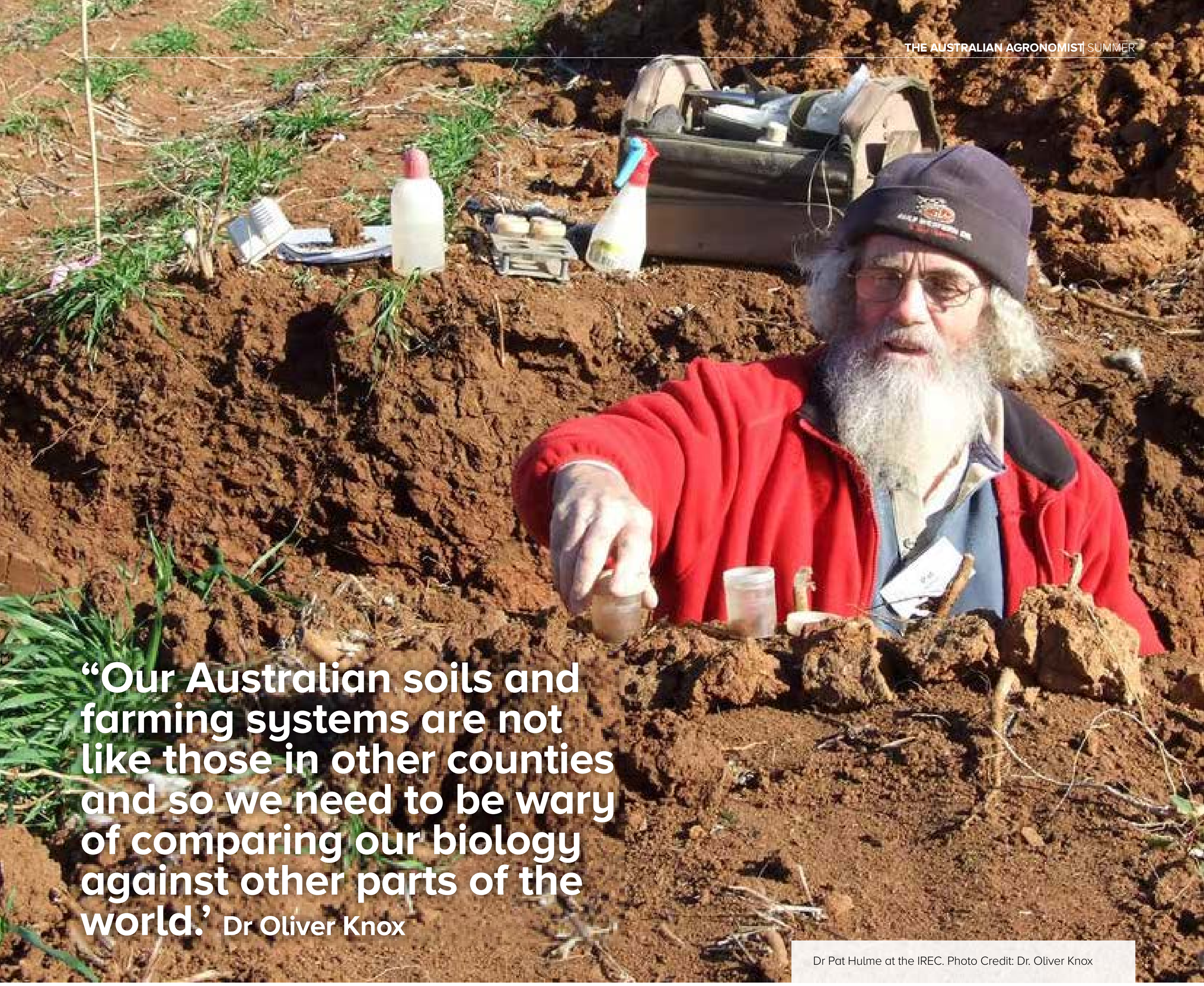
NSW DPI researcher Dr Guna Nachimuthu has been investigating aspects of soil condition in his project investigating yield variability in paired field sites. He has found that often there is not a lot of difference between the soil types studied as part of the project, however "occasionally changes in soil organic matter or an increase in sodicity appears to be the most obvious cause for a change in the harvested yield," said Dr Nachimuthu.

The discussion at the workshop therefore turned to the management techniques that can alter soil organic matter and impact on sodic constraints.

Dr Wendy Quayle from Deakin University has been examining the potential for the application of organic amendments to reduce fertility constraints. Dr Quayle's work has indicated that in the short term (over 2 seasons), it is possible to consider chicken manure as an alternative to mineral fertilisers.

"In a mixed fertility programme (manure and mineral) yield gains were seen from the organic amendment in the second year that could not be achieved with just mineral fertiliser." Dr Quayle said.

However, the limitations of the broadscale application of this approach due to the availability of suitable manures and composts are acknowledged. Another showcased research



"Our Australian soils and farming systems are not like those in other counties and so we need to be wary of comparing our biology against other parts of the world.' Dr Oliver Knox

Dr Pat Hulme at the IREC. Photo Credit: Dr. Oliver Knox

project, cover cropping, was of great interest due its broadscale application and availability to growers in a project that offers answers to new problems, with old fixes. Cover cropping is a technique which has used in cropping systems throughout generations to maintain sustainability and diversity. Recent research, however, by DAF QLD in conjunction with GRDC and CRDC has given much more insight into the benefits of considering including cover crop in a rotation.

Traditionally looked upon as an opportunity to reinvigorate nitrogen in the soil, the work of Dr David Lawrence and his SE QLD based team, which has travelled as far south as Parks and Wagga, has revealed even greater benefits including organic returns, improved rain recovery and of course, reduction in soil erosion.

Dr Lawrence says that one of the big issues and concerns around cover cropping is that of its requirement for water. His team's research has proven that these concerns are quite unfounded.

"The water needed to establish the cover crop was not insignificant, but subsequent rain in the cover crop quickly caught up with the fallow and eventually recharged the field above the fallow treatment," explained Dr Lawrence.

"In fact, the follow-on crop extracted more water from under the cover crop, returning a significant profit per hectare compared to the fallow."

Dr Lawrence also highlighted that cover crops, consisting of cereals or white French millet were superior to pulses, which failed to maintain the essential ground cover once sprayed out.

The results from this research have indeed shown great promise, but the need for ongoing work in this area is evident and future developments are funding dependant.

The CCA workshops incorporated a practical component at all locations, and it was here, that one of the main messages from the workshops became evident; basic visual examination and soil testing in isolation do not always give you an accurate snapshot of your soil health.

The results of soil tests on the blocks were discussed at length in soil pits within the same field. On paper, the lab results from one site would have suggested the block was completely unsuitable for future cropping. Examination of the soil pit, however, showed a healthy profile, which while constrained by a lack of surface water, was indeed 'fit for purpose'. Researchers and consultants at the site were quick to clarify that this did not indicate that soil tests are not a useful tool in agronomy. They are, however, no replacement for a thorough visual assessment of the field.

These messages are not new, but serve as a reminder that whatever your definition of 'soil health' may be, it is important that decisions are backed up by thorough visual assessment and the parameters that you place around that assessment are based on local data. The sub surface story may be very different to that which you expect.

AGRICULTURE OF THE FUTURE: NEURAL NETWORKS HAVE LEARNED TO PREDICT PLANT GROWTH

Scientists from Skoltech trained neural networks to evaluate and predict the plant growth pattern taking into account the main influencing factors and propose the optimal ratio between the nutrient requirements and other growth-driving parameters. The results of the study were published in the IEEE journal Transactions on Instrumentations and Measurements.

Over the past few years, multiple attempts have been made to use artificial intelligence (AI) in nearly all spheres of life. It did prove useful, helping people to make the right decisions and achieve the goal. Using AI to grow plants in artificial environments is no exception. Neural networks come in a broad variety of architectures, including their most prominent type, recurrent neural networks (RNN), that help efficiently process directional sequences of data, such as text, speech or time series, the latter being the most instrumental in describing plant growth over time.

In their study, the Skoltech scientists showed how RNN can be used in combination with computer vision algorithms to handle the plant growth prediction task in its entirety, while keeping an eye on the current status and main parameters of the plant growing system. The task was addressed using the data obtained in the study preformed in collaboration with the German Aerospace Centre (DLR), where the German scientists looked at additional stimulation for plant growth in artificial systems similar to those used on the International Space Station. The joint experiment yielded valuable results that helped find the optimal ratio of nutrients ensuring the best growth pattern under the existing constraints.

The scientists segmented and determined the total foliage area using computer vision algorithms and predicted plant growth using RNN of various architectures which coped efficiently with the task. They also proposed an embedded energy-efficient system for calculating and predicting the growth pattern in order to make real-life demo runs and tests of the dedicated software.

The system is based on Raspberry Pi, a popular single-board prototyping computer with an external Intel Movidius graphics card. The device uses a compact and powerful Myriad 2 graphics processor operating at 150 Gflops with a power of only 1 W, which is comparable to the supercomputers of the mid-1990s. A perfect solution for neural networks, these graphics chips will likely become the core of embedded AI-based systems in the future.

"The findings obtained in this study will help create portable systems for continuous monitoring and prediction of plant growth in artificial growing systems, which will ultimately be of invaluable benefit for man," said members of the authoring team, Dmitry Shadrin and Alexander Menshchikov.

This is the growing and data collection system CREDIT: Skoltech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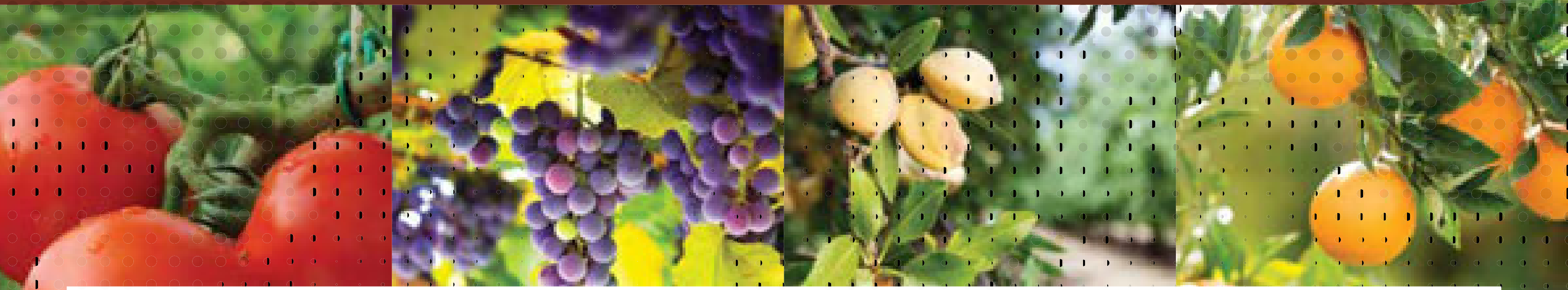

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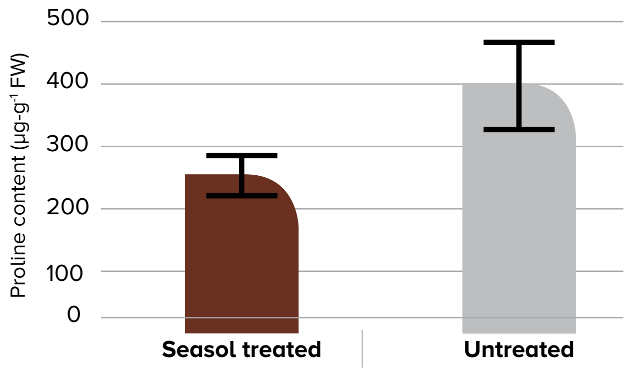

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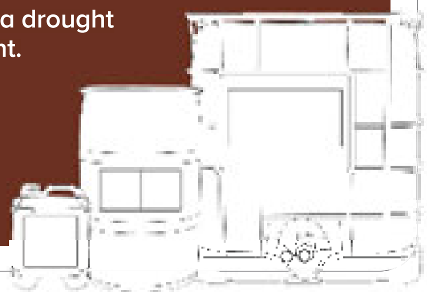
- Immediately after a drought or heat stress event.

* Proline amino acid is a reliable indicator of the environmental stress imposed on plants (Claussen 2005)



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