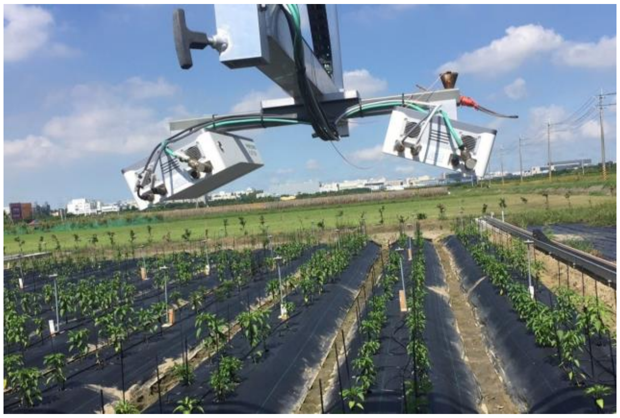
International Plant Phenotyping Symposium

‘PhenoVeg 2023’



Book of abstracts

26-27 September 2023, World Vegetable Center, Taiwan

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Sowing seeds, meeting needs
World Vegetable Center
1973-2023

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Cover photos
Top left: Automatic phenotyping and manual weeding of sweet pepper, WorldVeg HQ, Taiwan
Top right: Sweet pepper fruit phenotyping, Worldveg HQ, Taiwan
Bottom left: Manual phenotyping of amaranth at Worldveg experimental fields in Arusha, Tanzania
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Thanks are also offered to so many staff at World Vegetable Center headquarters in Shanhua, Tainan, for facilitating this event: to the logistical, administration and diverse support staff, and to scientists and their technical and field workers, without whose efforts the symposium would not have been possible. It takes true teamwork to build the foundations for progress to occur...

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FOREWORDS

Dr Marco Wopereis
Director General
World Vegetable Center

Welcome to the World Vegetable Center! We are delighted that you have decided to attend the first Phenotyping Symposium dedicated to vegetable biodiversity, breeding and precision horticulture (PhenoVeg 2023), at our Headquarters in Shanhua, Taiwan from 26-27 September.

This event will be a launch pad for experts from the public and private sectors to exchange ideas, insights, and advancements in the realm of phenotyping technologies, and their implications for the future of vegetable research and the vegetable sector at large.

At WorldVeg, we house the largest public collection of vegetable seeds in the world. Advancements in phenotyping technology will help us to better identify traits in that treasure box of vegetable biodiversity, that will be pivotal to enhancing crop productivity, abiotic and biotic stress resistance, shelf life, nutrition and health benefits, resilience in the face of climate change, and responding to evolving consumer demands.

The symposium's agenda spans an array of topics, from cutting-edge techniques in high-throughput phenotyping, to the integration of data-driven approaches for comprehensive trait analysis, phenomics enabled plant research and breeding, and phenomics in precision agriculture. By bringing together expertise from around the world, we hope to foster strengthened collaboration, accelerate knowledge dissemination, and cultivate new ideas.

We are proud to host this first symposium of its kind as we celebrate our golden Jubilee year. Over the last 50 years we have had huge impact around the world with new vegetable varieties and production and post-harvest technologies. However, much work remains to be done. Three billion people still suffer from malnutrition and many cannot afford a healthy diet. The way vegetables are produced is often not safe for the consumer, the farmer, or the environment.

We are convinced that advances in phenotyping will enable us to speed up vegetable breeding and enable greater precision and efficiency from seed to market, enhancing input use efficiency, reducing losses, and maintaining quality of vegetables and vegetable products. Such advances are critical to help make vegetables more accessible and affordable around the world.

Dr Marco Wopereis

Dr Junne-jih Chen
Deputy Minister
Ministry of Agriculture, Taiwan

Providing sufficient, safe, and nutritious food to all people is one of the major global concerns in the twenty first century, and the challenges posed by climate change to agriculture are also formidable. Resilient agriculture is crucial to adapting to these changing conditions, and utilizing state-of-the-art technology and innovation appropriately will enhance the practices and measures of resilient agriculture and achieve the goals of food security efficiently.

One of the great technologies that have been developed for the breeding of crops is high throughput phenotyping, which utilizes advanced sensors, imaging techniques, and data analysis to rapidly collect and analyze large amounts of phenotypic data. The big data collected by phenotyping, named phenomics, has been widely used for unveiling genes by incorporating genomics for molecular studies and breeding for crop improvement. Phenotyping involves the measurement and analysis of various plant traits, such as growth rate, yield and tolerance to environmental stresses. Thus, high through phenotyping is also applied to agricultural practice for precision and smart agriculture by incorporating internet of things (IoT) technology.

The implementation of high-throughput phenotyping technology will enable precise monitoring of crop phenotypes, facilitating crop research and production. To improve the research of the agriculture industry, Taiwan’s Ministry of Agriculture, committed to the adoption of high technology, has assisted the World Vegetable Center (WorldVeg) to set up the ‘PlantEye’ multispectral 3D scanner in the farm environment, and the National Taiwan University to set up the ‘Entoscan’ high throughput phenotyping equipment in the greenhouse environment. Furthermore, a National Plant Phenomics Center at the Taiwan Agricultural Research Institute will be established in 2024. It is expected that through the adoption of such high technology equipment, Taiwan and WorldVeg will enhance their recognized high status in the field of agricultural research.

I am pleased to know that the ‘International Plant Phenotyping Symposium – PhenoVeg 2023’ is one of a series of events celebrating the 50th anniversary of WorldVeg, highlighting WorldVeg’s commitment to this technology. This symposium will focus on three topics: sensors, cameras, and automation of phenotyping; big data, deep learning, and modeling; and phenomics enabled plant research and breeding. Experts in plant phenotyping from Taiwan and international institutions are invited to participate, and I believe that all participants can gain valuable insights into high throughput phenotyping, especially for promoting efficient breeding and practice to ensure sustainable crop production and enhance food security not only for Taiwan but also for other countries as well.

I am confident that the symposium will come up with constructive discussions and creative ideas. I wish the meeting great success.

Dr Junne-jih Chen

Dr Kuo-Chen Yeh
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Agricultural Biotechnology Research Center
Academia Sinica, Taiwan

Variation of plant phenotypes arises from the complex interplay between genetics and environmental conditions. While advances in high throughput sequencing have identified genetic diversities of many crop species, these discoveries have not always translated directly into crop improvements. This is largely due to a lack of high-quality phenotypic data, leading to what is often referred to as the 'phenomics bottleneck'. High throughput plant phenotyping (HTPP) has emerged as a solution to this challenge. Nevertheless, managing an HTPP system and analyzing the data it produces are not trivial tasks. They require a high level of expertise in hardware engineering, computer science, and plant growth and development to understand the associations of phenotypic variation in plants. Over the past decade, we have seen researchers from various disciplines develop a range of technologies and methods to tackle this issue.

In a collective effort to position Taiwan on the global stage, the World Vegetable Center, Taiwan Agricultural Research Institute, National Taiwan University, and our Agricultural Biotechnology Research Center at Academia Sinica, have dedicated our attempts to developing HTPP for both fundamental research and crop breeding. Currently, three large scale HTPP systems are being developed, and aerial based phenotyping is being intensively used in the rice fields in Taiwan. There are many exciting ongoing phenotyping developments for a wide range of crop species in various local universities and research institutes. We are on the verge of unleashing the potential of using HTPP to improve food safety and security.

In this symposium, we have invited international and domestic speakers to showcase progress in high throughput, field based, aerial, and unmanned platforms. Research in genomics, statistical modeling, plant physiology, and computer vision has illustrated the potential of integrating HTPP data to trait discoveries and functional studies. These research efforts have enabled HTPP to evolve from mere data collection to the development of breeding and farm management strategies.

As a plant biologist, I eagerly anticipate the advancements in HTPP and its potential to bridge the gaps from the laboratory to the field and back again.

Dr Kuo-Chen Yeh

Dr Yu-Pin Lin
Distinguished Professor and Dean
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Numerous complex and interrelated megatrends, such as climate change, environmental degradation, and stagnant crop yields, pose significant threats to global crop production and food security, especially given the expanding global population. These challenges necessitate the continuous development of climate-resilient and sustainable crop varieties to meet the increasing demand for both human and animal consumption.

In recent decades, plant phenotyping, a critical scientific tool, is playing a pivotal role in comprehending the intricate interactions between plants and their environment, spanning various levels of resolution, from cellular processes to the performance of the entire plant. While genotyping has become more efficient and cost-effective, the wealth of genetic data obtained must be complemented by quantitative analyses of crop performance concerning structure, function, quality, and their interactions with the environment. Recognized as a cornerstone of crop improvement, phenotyping has rapidly evolved over the last decade, driven by innovations in imaging and image analysis, automation, computing, and data analysis.

Phenotyping harnesses cutting edge non-invasive sensor technology, machine learning, and robotics to enhance efficiency, accuracy, and resolution. To further advance phenotyping towards sustainable plant production, it is crucial to integrate various components seamlessly. This integration involves bridging the gap between genetic information and plant performance data, allowing breeders to identify and select the most promising traits for crop improvement. By closely examining how crops respond to their environment and identifying traits associated with resilience, phenotyping enables the creation of climate-resilient varieties that can thrive under challenging conditions.

In conclusion, the urgency of breeding improved crop varieties to tackle global challenges such as climate change and food security cannot be overstated. Plant phenotyping, as a pivotal tool, continues to evolve and integrate cutting-edge technologies, ensuring that our agricultural systems can adapt to a changing world and provide sustenance for a growing global population.

Dr Yu-Pin Lin

Dr Hsueh-Shih Lin
Director General
Taiwan Agricultural Research Institute
Ministry of Agriculture, Taiwan

Phenotyping is a new technology that has emerged internationally in recent years. Its application in crop research includes gene exploration of important traits, the foundation of rapid and precise breeding platforms, and the foundation of smart farms, interaction between plant diseases and insect pests, plant stress physiology, etc. It is very meaningful to hold the international symposium related to phenotyping during the 50th anniversary of the establishment of the World Vegetable Center.

This symposium invited 18 experts from 8 countries. The lecture content ranged from introduction of phenotypic research progress in various countries, development of sensors, cameras, automation equipment, big data collection and analysis, deep learning, growth model establishment, the application for plant breeding, etc., the content is quite in-depth and worthy of reference.

Starting in 2022, the Agricultural Research Institute of Ministry of Agriculture of my country is preparing to build a national plant phenotype analysis center,

In the future, various advanced equipment attached to the greenhouse or outdoor overhead crane will be used, including: optical, multispectral or hyperspectral, fluorescence, thermal imaging, tomography and LiDAR laser scanners to conduct multi-dimensional phenotypes information collection, applied to the interpretation and analysis of various plant traits.

The World Vegetable Center established a phenotype system a few years ago. It has good equipment and good research results. I hope that there will be more opportunities for cooperation in the future.

Dr Hsueh-Shih Lin

INVITED PRESENTATIONS

Novel sensors to advance plant phenotyping

Onno Muller, Sven Fahrner, Roland Pieruschka, Uli Schurr

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Quantitative analysis of the structure and function of plants has become the major bottleneck in basic research and applied use of crop plants. Significant interdisciplinary approaches have been started in the recent years to establish research infrastructure that is able to quantitatively assess relevant traits under controlled and field conditions, complemented by data and modelling application. The overarching goal is to understand the dynamic interactions between genetic constitution, and molecular and biochemical processes with physiological responses leading to the development of phenotypes, and to translate this understanding into applications in breeding and agricultural management. To fully explore the potential of plant phenotyping, integrated concepts are needed that link the development and implementation of novel sensors under controlled and field conditions, to be able to measure the diversity of traits with high quality, under countless environmental conditions that are complemented with data management and modelling. Many ongoing developments in plant phenotyping are driven by advances in novel sensors, automation, robotics and computing capacity, leading to an increased quality and quantity of phenotypic data, as well as novel traits that can be measured. Advanced phenotyping facilities often include high resolution measurements, e.g. in tomographic measurements, and high throughput facilities that are equipped with specialized imaging systems that allow noninvasive trait assessment in fully automated facilities that can simulate complex environmental conditions. Intensive field sites provide opportunities to analyze crops in depth, e.g. by allowing simulation of future climate conditions. Mobile field systems, e.g. using unmanned aerial vehicles (UAVs) with a variety of sensors, have become available and allow breeders to monitor genotype performance in breeding plots, and that allow farmers to utilize these technologies for precision crop management and scale up advances from single plants to the agroecosystem level. This presentation provides examples that address sensor development and their applications across the entire phenotyping pipeline throughout the development of a plant above and belowground from single seeds under controlled and field conditions. Finally, we also address the need to integrate the community and advance plant phenotyping through joint developments, e.g. within EMPHASIS as the European research infrastructure in Europe, or the International Plant Phenotyping Network, a non-profit association that integrates the plant phenotyping community as a global communication hub.

ONNO MULLER, summary biography of presenter

Onno Muller, Deputy group leader shoot dynamics, Head Field Phenotyping, Institute for Bio-and Geosciences, IBG-2: Plant Sciences, Forschungszentrum Jülich GmbH, Jülich, Germany
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Onno Muller is a plant ecophysiologist interested in how and why plants respond to their environment, specifically plant leaves in their natural habitat. Experienced in field phenotyping, quantifying the relationship of photosynthesis to leaf nitrogen, rubisco, fluorescence, leaf and vein anatomy in laboratory and field conditions. Fascinated by noninvasive methods, he coordinates field phenotyping under elevated CO2 in BreedFACE, and photovoltaics in the APV 2.0. project. He uses light induced fluorescence among others, for photosynthetic phenotyping.

Employment/education

2016-	Institute for Bio-and Geosciences, IBG-2: Plant Sciences, Forschungszentrum Jülich GmbH, Jülich, Germany
2013-2015	Post-doc, German Plant Phenotyping Network, DPPN, Institute for Bio-and Geosciences, IBG-2: Plant Sciences,Forschungszentrum Jülich GmbH, Jülich, Germany
2011-2013	Post-doc, William Adams and Barbara Demmig-Adams at University of Colorado, USA
2008-2011	Visiting Assistant Professor/Post-doc, with Tsutom Hiura, Tomakomai Experimental Forest, Hokkaido
2005-2008	University Japan, Post-doc with Kouki Hikosaka Tohoku University, Japan
2001-2005	PhD Plant Ecology, Faculty of Biology, Utrecht University, the Netherlands

Selected publications

Watt M, Fiorani F, Usadel B, Rascher U, Muller O, Schurr U. 2020. Phenotyping: new windows into the plant for breeders. Annual Review of Plant Biology 71(1):689-712.

Zendonadi dos Santos N, Piepho H-P, Condorelli GE, Licieri Groli E, Newcomb M, Ward R, Tuberosa R, Maccaferri M, Fiorani F, Rascher U, Muller O**.** 2021. High-throughput field phenotyping reveals genetic variation in photosynthetic traits in durum wheat under drought. Plant, Cell and Environment 44(9):2858-2878.

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Morisse M, Wells DM, Millet EJ, Lillemo M, Fahrner S, Cellini F, Lootens P, Muller O, Herrera JM, Bentley AR, Janni M. 2022. A European perspective on opportunities and demands for field-based crop phenotyping. Field Crops Research 276:108371.

Acebron K, Salvatori N, Alberti G, Muller O, Peressotti A, Rascher U, Matsubara S. 2023. Elucidating the photosynthetic responses in chlorophyll-deficient soybean (*Glycine max* L.) leaf. Journal of Photochemistry and Photobiology 13:100152.

DIY plant phenotyping for application of digital phenotyping techniques in plant research and breeding

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Plant phenotyping technologies have been actively developed in recent years. However, introducing these technologies in research fields has not progressed as expected, with low flexibility and high costs being major factors. We therefore consider the concept of DIY (do it yourself) systems that are efficient in overcoming the obstacles. We defined DIY phenotyping as "phenotyping with a system that is built or rebuilt by users with shared or available software and hardware". The aims of DIY phenotyping are to reduce the building cost and increase the flexibility. Providing hardware and software, which can be rebuilt by users without needing to have full knowledge, is an important point for realizing and popularization of DIY phenotyping. Based on this concept, we have conducted the development of AGVs (automated guided vehicles) for transporting potted plants within greenhouses, and the creation of a system for constructing highly accurate 3D models of plants. These 3D models can be utilized for various applications, including the recreation of virtual fields in virtual spaces. The first step in applying digital phenotyping technologies in plant research and breeding, is to establish devices for data acquisition. Beyond that, there lies the more fundamental challenge of information extraction from acquired data in order to gain novel insights. By overcoming the barriers of phenotypic data acquisition through DIY approaches, we can anticipate advancements in plant science and breeding through leveraging large scale datasets.

SACHIKO ISOBE, summary biography of presenter

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Job/Academic title: Dr. Agr.

Research interests

Plant genome sequencing, molecular breeding, DB construction and digital phenotyping

Employment/education

2007-Present	Kazusa DNA Res Inst
2006	PhD degree, Kagoshima Federal Universities
1995-2007	NARO, Hokkaido Agric Res Cent, Forage Breeding
1993-1995	Graduate School of Okayama University (Master Course)
1989-1993	Okayama University

Establishment and application of crop phenotyping system in the National Crop Phenomics Center of Korea

Hyeonso Ji, Jeongho Baek, Song Lim Kik, In Sun Yoon, HwangWeon Jeong, Jae Il Lyu, Kyung-Hwan Kim

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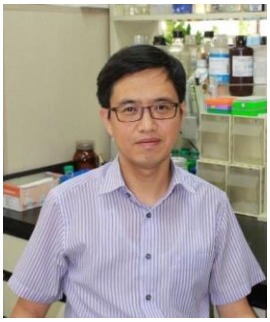
Plant phenomics has been realizing reliable, automatic, and high throughput plant phenotyping, and interests and demand has been growing sharply in Korean agricultural crop research. The National Crop Phenomics Center of the National Institute of Agricultural Sciences was established in 2017 as the first and largest plant phenomics center in Korea. Its infrastructure includes a high throughput screening greenhouse with a conveyor system that can hold 1,012 pots, image acquisition room with chambers equipped with red-green-blue, infrared and near-infrared cameras, a XYZ moving camera system, a fluorescence camera, a 3D laser scanner in a precision environment control room, and additional apparatus such as DroughtSpotter. We set up methods for measurement of growth and plant architecture traits such as plant area, height, width, compactness etc. in time series manner for the whole growth period of rice, soybean, sesame and maize. Also, we developed a high throughput phenotyping system for assessing drought tolerance in rice using RGB, IR, NIR, fluorescence images and DroughtSpotter. We apply this system in functional genomics studies including screening gene-edited rice lines for rice transcription factor genes conferring increased drought tolerance. We developed a high throughput seed phenotyping system for QTL mapping and GWAS studies for seed traits in soybean and rice, for seed phenotyping of various species in many universities and crop research institutions. We developed an image-based plant disease response assay system for QTL mapping for disease resistance, and a method for discriminating between haploid and diploid seeds based on fluorescence images for application of doubled haploid technology in maize breeding in collaboration with the Maize Research Institute. The National Crop Phenomics Center was approved as a national reference standards data center by the Ministry of Trade, Industry and Energy of Korea in 2022 which means that it provides highly reliable measurement data, while we are also increasing the precision in measuring crop traits based on plant phenomics. Currently, we are developing methods for high throughput phenotyping in various crops including mushroom, strawberry, apple, pear and groundnut, using various image sensors including RGB, IR, NIR, fluorescence, and hyperspectral in collaboration with crop research institutions, universities, agricultural companies, and local agricultural research institutions. These efforts will pave the way for digital innovation of agricultural research and contribute to developing crop varieties with increased resistance to various biotic and abiotic stresses and better quality and productivity to cope with climate change.

HYEONSO JI, summary biography of presenter



Hyeonso Ji, Researcher, National Institute of Agricultural Sciences, Gene Engineering Division, Dept. of Agricultural Biotechnology, National Institute of Agricultural Sciences
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Employment and education

2022-	Plant Phenomics Laboratory Director, Gene Engineering Division, National Institute of Agricultural Sciences
2008-2022	Researcher, National Institute of Agricultural Sciences
2002-2008	Researcher, National Institute of Agricultural Biotechnology
2004-2006	Visiting Scientist, Dept. of Plant Breeding, Cornell University
1998-2002	Researcher, International Technology Cooperation Center (ITCC), Rural Development Administration
1993-1998	Researcher, Kangwon-do Agricultural Research and Extension Services
PhD (2006), MSc (1998), BSc (1993)	Dept. of Agronomy, Seoul National University

Recent publications

Lee C, KS Cheon, Y Shin, H Oh, YM Jeong, H Jang, YC Park, KY Kim, HC Cho, YJ Won, J Baek, YS Cha, SL Kim, KH Kim, H Ji. 2022. Development and application of a target capture sequencing SNP-genotyping platform in rice. Genes (Basel) 13.

Kim MS, JK Yu, SR Ko, KJ Kim, H Ji, KK Kang, YG Cho. 2022. Marker-assisted backcrossing (MABc) to improve eating quality with thin seed coat and aleurone layer of non-glutinous japonica variety in rice. Genes (Basel) 13.

Ji H, Y Shin, C Lee, H Oh, IS Yoon, J Baek, YS Cha, GS Lee, SL Kim, KH Kim. 2021. Genomic variation in Korean japonica rice varieties. Genes (Basel) 12.

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Park SI, HJ Kwon, MH Cho, JS Song, BG Kim, J Baek, SL Kim, H Ji, TR Kwon, KH Kim, IS Yoon. 2021. The OsERF115/AP2EREBP110 transcription factor is involved in the multiple stress tolerance to heat and drought in rice plants. Int J Mol Sci 22.

Kim SL, N Kim, H Lee, E Lee, KS Cheon, M Kim, J Baek, I Choi, H Ji, IS Yoon, KH Jung, TR Kwon, KH Kim. 2020. High-throughput phenotyping platform for analyzing drought tolerance in rice. Planta 252:38.

Cheon KS, YJ Won, YM Jeong, YY Lee, DY Kang, J Oh, H Oh, SL Kim, N Kim, E Lee, IS Yoon, I Choi, J Baek, KH Kim, HS Park, H Ji. 2020. QTL mapping for pre-harvest sprouting resistance in japonica rice varieties utilizing genome re-sequencing. Mol Genet Genomics 295:1129-1140.

Leveraging artificial intelligence and machine learning to address critical challenges in plant phenotyping research

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In recent years the scientific community has witnessed extraordinary growth in the development and application of techniques from artificial intelligence and machine learning (AI/ML) to address pressing societal challenges. Contrary to more traditional linear models, some AI/ML approaches suffer from a general lack of interpretability and in disciplines and industries where understanding biological relationships among predictor and predicted is important, utility and trust in resulting predictions is a potential issue. Regardless, the plant phenotyping research community has shown considerable interest in the utilization of AI/ML methods, coupled with advanced cyberinfrastructure, to address large scale data challenges from the use of advanced imaging, sensors, and the internet of things (IoT) to solve problems related to trait quantification, genome-to-phenome, and climate change. The effective application of AI/ML to problems in plant phenotyping requires an understanding of what methods are available; the benefits and pitfalls of these methods; what resources are required including data and metadata, cyberinfrastructure, and interdisciplinary skills; best practices; and how AI/ML methods compare to alternative approaches. Awareness of the before mentioned items is critical to avoid reproducibility issues and the possibility of using overly complex models for simple tasks. Each of these topics will be addressed – including a introduction to AI/ML in the context of examples from phenotyping research, and a view towards future developments and application.

JENNIFER CLARKE, summary biography of presenter

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Jennifer Clarke, is Professor in Food Science and Technology, and Statistics, and the Director of the Quantitative Life Sciences Initiative at the University of Nebraska-Lincoln (https://bigdata.unl.edu). Dr Clarke received her undergraduate degrees in Mathematics and Psychology from Skidmore University, a MSc in Statistics from Carnegie Mellon University, and a Doctorate in Statistics from Pennsylvania State University. She is a founding member and past president of the North American Plant Phenotyping Network, and serves as co-chair of the Academic Section of the International Plant Phenotyping Network. She is leading a national effort on behalf of the United Stated Department of Agriculture (USDA) to develop a national agricultural producers' data framework. Her current interests include advanced statistical methodology, and training the next generation of interdisciplinary data scientists.

A deep learning model to detect the early drought stress status of tomato

Yuan-Kai Tu

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This study proposed a deep learning architecture, namely the 1D-SP-GC Net. By virtue of the Vis/NIR (visible to near infrared) spectral data obtained from tomato (*Solanum lycopersicum*) canopy leaves, a non-destructive model to detect the early drought physiological status was built by the 1D-SP-GC Net. In comparison with other commonly used model for spectral data, such as the PLS (partial least regression), RF (random forest) and the convolutional neural network (CNN), the 1D-SP-GC Net revealed higher prediction accuracy (>95%). Furthermore, by applying the Grad-CAM (gradient-weighted class activation mapping) on the proposed 1D-SP-GC Net architecture, spectral bands with high contribution to the discriminative capability for the model were identified. The proposed 1D-SP-GC Net was able to detect the occurrence of early drought status of tomato, and so can provide a warning method for farmers to conduct suitable agricultural practices in time, to reduce the impact of drought stress on the quality and yield of tomato.

YUAN-KAI TU, summary biography of presenter

Yuan-Kai Tu, Associate Researcher, Taiwan Agricultural Research Institute
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Special interest in applying diverse quantitative methods to genotyping and phenotyping analysis, deploying a deep learning model to predict drought stress of tomato, and developing phenomics research in TARI.

Employment and education

2023-	Associate Researcher, Crop Genetic Resources and Biotechnology Division, Taiwan Agricultural Research Institute, Ministry of Agriculture
2009-2023	Assistant Researcher, Biotechnology Division, Taiwan Agricultural Research Institute

PhD (2022) National Chung-Hsing University, Taichung, Taiwan; MSc (2007) National Taiwan University, Taipei, Taiwan; BSc (2005), University of Taipei, Taiwan.

2023: Image analysis for plant phenotyping. Wageningen University and Research. Netherlands

2018: Visiting scholar, Australian Plant Phenomics Facility (APPF), Australia.

2017: Machine Learning for Big Visual Data. IEEE International Elite School. Taiwan.

Selected publications

Kuo CE, YK Tu, SL Fang, YR Huang, HW Chen, MW Yao, BJ Kuo. 2023. Early detection of drought stress in tomato from spectroscopic data: A novel convolutional neural network with feature selection. Chemometrics and Intelligent Laboratory Systems. 239:104869.

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Tu YK, HW Chen, SL Fang, MH Yao, BJ Kuo. 2020. Establishment of early discrimination methods for drought stress of tomato grown in greenhouse by using environmental parameters and NIR spectroscopy. 2020. Acta Hortic. 1311:501-512.

Reducing the data analysis threshold for plant phenomics: a visual analysis tool for smooth extraction of traits for analysis

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Research in plant phenomics requires the integration of various basic research and interdisciplinary knowledge. However, the highly technical and resource intensive nature of phenomics may limit its applicability and technical dissemination. Specifically, equipment thresholds may limit research on specific crops and research fields. Nevertheless, with the advancement of equipment and affordable phenotyping technology, various phenotyping devices are gradually expanding into different areas of application. However, data analysis remains a major challenge because of the complexity of plant growth processes that often makes models complex and difficult to adapt. This requires high level statistical analysis skills and time consuming analysis processes, which are particularly challenging for agricultural breeding research, and that further limit the applicability and insights of phenomics. Therefore, reducing the data analysis technology threshold for plant phenomics has become an important issue for the development of phenomics applications. Phenotyping devices can measure the growth process of plants in detail, but also include short term transient deviations, which increase the burden of interpretability. To reduce the threshold for phenomics analysis, this study developed a visualization analysis tool using R software, and adopted a smooth extraction of traits analysis as the analysis framework to eliminate transient deviations as much as possible with a concise model for extracting effective traits, providing real-time feedback on the analysis results. The tool has been applied to phenotyping experiments of conservative long distance peptides in *Populus trichocarpa*, that effectively eliminated transient deviations and provided real-time growth rate analysis. As the tool is open source, it can be integrated with different statistical analysis models in the future for more extensive phenotyping studies, to reduce data analysis costs and improve the efficiency of phenotyping research.

CHENG-BIN LI, summary biography of presenter

Assistant Researcher, Taiwan Agricultural Research Institute, Taiwan

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Cheng-Bin Li is a researcher at the Taiwan Agricultural Research Institute, dedicated to the development and application of phenotypes in agriculture. He manages the phenomics facility and researches its applications, including experimental design and analytical methods. He has experience in R software analysis and its application development. In addition, he also studies how to establish core collections and genome analysis.

Employment and education

2023-	Assistant Researcher, Crop Genetic Resources and Biotechnology Division, Taiwan Agricultural Research Institute, Ministry of Agriculture
2021-2023	Assistant Researcher, Biotechnology Division, Taiwan Agricultural Research Institute, Council of Agriculture, Executive Yuan
2019-2021	Associate Technical Specialist, Agriculture Section, WaiPu District Office, Taichung City
2016-2019	MSc Major in Agronomy, National Chung-Hsing University, Taichung, Taiwan
2012-2016	BSc Major in Agronomy, National Chung-Hsing University, Taichung, Taiwan

Selected publications

Su YC, Lee CB, Yiu TJ, Kuo BJ. 2021. Incorporating the field border effect to reduce the predicted uncertainty of pollen dispersal model in Asia. Scientific Reports, 11(1):1-11.

Li CB. 2022. Establishment of the National Plant Phenomic Center in Taiwan. TropAg conference, 31 October 2022, Brisbane, Australia.

Li CB. 2022. Establishment of the pepper core collection in Taiwan. TropAg conference, 31 October 2022, Brisbane, Australia.

Li CB. 2021. Investigation methods of cold damage traits of soybean core-collection in seedling stage. Agronomy Society of Taiwan, 29 April 2021, Taichung, Taiwan.

Crop models assisted with drone spectral images for growth and yield prediction in broccoli

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Broccoli (*Brassica oleracea* var. *italica*), a widely grown Brassicaceae vegetable, is consumed both fresh and frozen. Planning the cultivation schedule in advance is essential for maintaining a stable supply and demand chain for its production. The AI dynamic predictive model developed for crop growth and harvested yield was initially conducted on collecting continuous parameters on plant growth traits, physiology, environmental factors through AIoT, drone spectral vegetative index, and final yield over six cropping cycles with 24 transplanting dates from 2020 to 2022. All collected data were pretreated by cleaning, fusion and transformation for further analysis. Trained models were subsequently validated using over 190 Taiwan Good Agriculture Practice (TGAP) recordings from around 50 hectares of broccoli farms from 2022 to 2023. Results demonstrated a 100% accuracy in prediction of flowering time, a 4-day difference in harvested time, and 94% accuracy in yield. The suitable planting time resulted in a 20.3% to 32.1% increase compared to the observed average during those cropping periods. Furthermore, the normalized difference red edge (NDRE) index measured before harvest also matches linear relationship with final yield (R^2=0.743). As the broccoli growth predictive model is optimized, the AI-based farm management SaaS platform was implemented to assist cultivation practices to improve yield and quality, as well as profits.

WEI-LING CHEN, summary biography of presenter

Wei-ling Chen (陳葦玲), Associate Researcher, Taichung District Agricultural Research and Extension Station, Taiwan
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Special expertise in vegetable physiology and cultivation, and greenhouse horticulture

Employment and education

2014-now	Associate Researcher/Taichung Agriculture Research and Extension Station, COA
2017/06-12	Visiting researcher/Wageningen UR, Greenhouse Horticulture BU
2015-2018	Society affair/Taiwan Society for Horticultural Science
2007-2014	Assistant Researcher/Taichung Agriculture Research and Extension Station, COA
2006-2007	Horticultural Technician/Tai-Sugar Orchid

PhD (2014) and MSc (2006), Department of Horticulture and Landscape, National Taiwan University
BSc (2004), Department of Horticulture, National Chung-Hsing University

Publications
(in 5 years) SCI Journals: 6, English peer-reviewed journals: 3, Chinese journals: 4, Symposium presentations: 7, Agricultural extension articles: 16
Journal reviewer Scientia Horticulturae, Elsevier, Netherlands (SCI), HortScience, American Society for Horticultural Science, U.S.A. (SCI), International Journal of Biometeorology, France (SCI)
Plant right and patents System of Crop seeding-information Management and Its Application in Automatic Sawing Machine (M632339)/MOEA, Taiwan
Common bean ‘Taichung No. 6’ (Plant Right No. A01973)/MOA, Taiwan
Radish ‘Taichung No. 2’ (Plant Right No. A01973)/ MOA, Taiwan
Common bean ‘Taichung No.5’ (Plant Right No. A01973)/ MOA, Taiwan
Cabbage ‘Taichung No. 2’ (Plant Right No. A01973)/ MOA, Taiwan
Technology transfer: 5 (Royalty: 1.8 million NTD)

Establish an evaluation system for thermotolerance in tomato under heat stress

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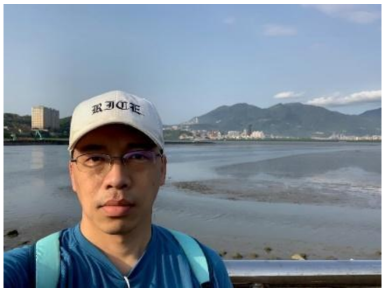
Tomato is one of the most important vegetables grown around the world. However, high temperatures reduce the net photosynthesis efficiency of plants, damage chloroplasts and inhibit plant growth. Many studies have shown the correlation between heat tolerance at the reproduction stage and yield production. However, the measurements of heat tolerance usually require destructive sampling and are labor intensive and time consuming. In this study, we used several non-destructive methods to evaluate the phenotypes of six tomato varieties at the vegetative stage in response to heat stress. We established correlation with the traits at the reproductive stage. These non-destructive methods included leaf chlorophyll fluorescence, canopy temperature, leaf angle, and the foliar reflection spectrum. In response to heat stress, most tomato varieties showed reduced chlorophyll fluorescence Y(II), quickly adjusted the canopy temperature to the environmental temperature, increased hyponasty response, and reduced vegetative indices. In addition, the correlation coefficient analysis between different indices showed that the vegetation indices significantly correlated with fruit setting number and rate under heat stress. Stepwise regression with fruit setting rate also showed that combining vegetation indices, canopy temperature, and leaf angle had the highest correlation. Combining these phenotyping indices can be used as alternative high throughput methods for evaluating complex heat stress tolerance.

YU-CHANG TSAI, summary biography of presenter



Yu-Chang Tsai (蔡育彰), Associate Professor, Department of Agronomy, National Taiwan University, Taiwan

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Research interests include Phytohormone signaling and abiotic stress tolerance regulation, root development in monocots, and application of phenome analysis

Employment and education

2013-	Associate professor, Department of Agronomy, NTU (assistant prof. 2013-2020)
2011-2012	Postdoctoral Fellow, University of North Carolina, USA
2010-2011	Postdoctoral Fellow, Rice University, USA
2004-2010	PhD in Biochemistry and Cell Biology, Rice University, Houston, Texas, USA
2002-2004	MS in Agronomy, National Taiwan University (NTU), Taipei, Taiwan
1996-2000	BS in Agronomy, National Taiwan University (NTU), Taipei, Taiwan

Selected publications

Fang HH, Lee W-L, Chiu K-T, Ma H-Y, Yang S-H, Hung C-Y, . . . Tsai Y-C. 2023. Irradiation with green light at night has great effects on the management of *Conopomorpha sinensis* and maintains favorable litchi fruit quality. Scientia Horticulturae, 312:111830.

Chen CY, Wu ZC, Liu TY, Yu SS, Tsai JN, Tsai YC, . . . Chung CL. 2023. Investigation of asymptomatic infection of *Phellinus noxius* in herbaceous plants. Phytopathology, 113(3):460-469.

Fu H, Liou C-C, Hong CY, Tsai YC. 2021. Recent progress of genome editing technology applied to improve tomato fruit traits. Crop, Environment & Bioinformatics, 17(3), 144-154.

Yue J-J, Hong C-Y, Wei P, Tsai Y-C, Lin C-S. 2020. How to start your monocot CRISPR/Cas project: plasmid design, efficiency detection, and offspring analysis. Rice, 13:1

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Wu T-M, Huang J-Z, Oung H-M, Hsu Y-T, Tsai Y-C, Hong C-Y. 2019. H2O2-based method for rapid detection of transgene-free rice plants from segregating CRISPR/Cas9 genome-edited progenies. International Journal of Molecular Sciences, 20: 3885.

Lee C-Y, Tsai Y-C. 2019. Light-regulated alternative splicing of pseudo-histidine phosphotransfer protein 3 in *Oryza sativa*. Journal of Plant Growth Regulation, 38:1215-1227.

Using advances in phenotyping technology to develop climate-ready crops for the future

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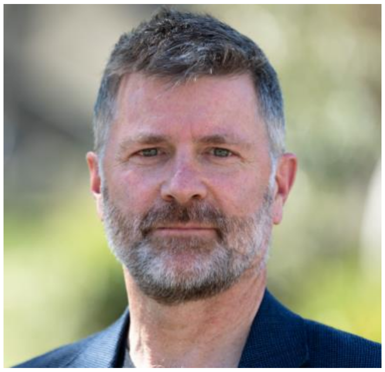
To keep pace with increasing global demand for food and to minimize the demand for arable land, grain yields per hectare need to increase by 2-2.5% each year. Yet, the actual annual increases delivered by crop breeding programs around the world fall markedly short of this figure, with recent increases in grain yields often being 0.5-1.5% per year. Reliance on business as usual crop breeding – with new varieties taking over a decade to develop - are unlikely, therefore, to deliver the increases needed. Contributing to the challenge of achieving global food security are the negative effects of climate change on crop yields, with rising day and night temperatures resulting in reduced yields of rice, wheat and other crops. This presentation outlines the importance of high throughput phenotyping of genetically diverse germplasm and applications of machine learning methods, to accelerate the breeding of climate-ready crops for the future. As a case example, it will show work being done to improve the efficiency with which light energy is converted into plant biomass. While the Green Revolution and more recent breeding has nearly maximized the harvest index and efficiency of light capture by crops, breeding has not maximized the efficiency with which solar radiation is converted into biomass. Two processes are crucial in determining the efficiency of biomass production from light: photosynthesis and respiration. This presentation will outline work in progress to improve these processes, including to identify genetic variants with reduced rates of respiratory carbon release per unit photosynthetic carbon uptake, and how we are screening for heat tolerance of these processes.

OWEN ATKIN, summary biography of presenter



Owen K. Atkin, Professor, Australian National University, Centre for Entrepreneurial Agri-Technology, Australian National University, Canberra, Australia.

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Owen Atkin completed his PhD in Toronto (1993) and BSc (Hons) at ANU (1987). Owen has been an editor for the New Phytologist journal since 2007, and Senior Editor for the journal's Environment Section from 2013-2019. He is based at the Australian National University, with three roles occupying his time. Prior to joining the ANU in 2008, Owen was a faculty member at the University of York (1999-2007), and post-doctoral fellow at ANU (1995-1998) and Utrecht University, the Netherlands (1993-1995).

He is Director of an ANU Innovation Institute (CEAT), tasked with harnessing the interdisciplinary expertise of the ANU and partners to address complex challenges facing the agriculture-food sector; and,

He is also Professor of Plant Science in the Research School of Biology, where his research focusses on the impact of environmental gradients on carbon uptake by photosynthesis and carbon use by respiration. From January 2022 to May 2023, he was also Director of the ANU node of the Australian Plant Phenomics Facility.

Automatic stomata detection and measurement for plant abiotic responses

Yao-Cheng Lin

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Stomata, the microscopic pores on the surface of plant leaves, play a pivotal role in plant physiology by serving as the primary conduits for gas exchange and temperature regulation. Despite their importance, the detection and analysis of stomata remain challenging because of their small size and variable morphology across different plant species. In this study, we developed computational methods to overcome these challenges, focusing on the detection of stomata and the calculation of their aspect ratios. This approach enabled us to determine whether the stomata were open or closed, thereby providing valuable insights into plant responses to environmental conditions. Our method was built on the YOLOv7-seg model, which is a state of the art object detection system known for its speed and accuracy. We leveraged the large dataset in the pretrained YOLOv7-seg model, and transferred it to support our specific tasks through model fine tuning. To fine tune the YOLOv7-seg model, we used five distinct datasets, each containing images of leaves with annotated stomata from different plant species. The model was adapted to segment stomata from the leaf background and calculate the aspect ratio of each detected stoma. Our fine tuned model demonstrated high segmentation accuracy, achieving a mask average precision of 84%. To test the generalization capability when the model was applied to images that were different from the training data, we tested the zero shot performance between models. The model could provide more than 80% accuracy, except in the maize dataset, where the original image resolution was low and the stomata size was small. Overall, our research represents a significant advancement in computational analysis of plant stomata. The ability of our method to work across different plant species broadens its applicability, making it a valuable tool for researchers in plant science.

YAO-CHENG LIN, summary biography of presenter

Yao-Cheng Lin, PhD (林耀正), Assistant Research Fellow, Biotechnology Center in Southern Taiwan, Agricultural Biotechnology Research Center, Academia Sinica, Taiwan

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His research is centered on understanding genetic variations in genome evolution, domestication, and genome engineering, with a special interest in exploring the genetic mechanisms that govern how plants interact with their environment, especially under stress conditions. A long term goal is to develop machine learning methods to integrate multi-omics and phenomics information, allowing us to predict complex biological traits and understand the underlying mechanisms.

Employment and education

2016-	Assistant Research Fellow, Biotechnology Center in Southern Taiwan, Agricultural Biotechnology Research Center, Academia Sinica, Taiwan
2011-2016	Staff Scientist, VIB-UGent Center for Plant Systems Biology, Belgium

PhD (2011), Plant Biotechnology and Bioinformatics, Ghent University, Belgium
MSc (2001), Anatomy and Cell Biology, National Yang-Ming University, Taiwan
BSc (1999), Agronomy, National Taiwan University, Taiwan

Selected publications

Huang C-J, Wu T-L, Zheng P-X, Ou J-Y, Ting C-L, Lin YC. 2023. Complete genome sequence resource of *Pectobacterium colocasium* strain F1-1 that causes soft rot disease of taro. Plant Disease, 107: 1911-1915.

Tu Y-L., Lin W-Y & Lin Y-C. 2022. Toward automatic plant phenotyping: starting from leaf counting. Multimed Tools Appl, 81, 11865–11879 .

Lin C-S, Hsu C-T, Yuan Y-H, Zheng P-X, Wu F-H, Cheng Q-W, Wu Y-L, Wu, T-L, Lin S, Yue J-J, Cheng Y-H, Lin S-I, Shih M-C, Sheen J, Lin YC. 2022. DNA-free CRISPR-Cas9 gene editing of wild tetraploid tomatoes *Solanum peruvianum* using protoplast regeneration. Plant Physiol, 188(4): 1917–1930.

Huang CJ, Wu TL, Zheng PX, Ou JY, Ni HF, Lin YC. 2021. Comparative genomic analysis uncovered evolution of pathogenicity factors, horizontal gene transfer events, and heavy metal resistance traits in citrus canker bacterium *Xanthomonas citri* subsp. *citri*. Front Microbiol, 12:731711.

Empowering breeders and researchers by leveraging automated plant phenotyping systems in vegetable crops

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With the vigorous development of genomic sequencing techniques, crop breeding has entered the era of high throughput and big data in genomic analysis. However, phenotyping techniques have not kept up with the development of genotyping techniques, and have become a bottleneck for breeding development. The development of a high throughput plant autophenotyping platform has become an important issue in crop breeding. For these purposes, a plant autophenotyping platform was established through the 3-dimensional laser scanner. First, the autophenotyping parameters of soybean, rapeseed and melons were validated by comparing them with the analysis of traditional manual phenotyping. The results displayed that the parameters of plant height, leaf area and biomass are all highly relevant between the autophenotyping platform and the traditional one ($r > 0.85^{***}$). This platform has been applied to the phenotyping of the cultivation of the two other vegetables. The first was conducted on the effects of different soil microbial agents on the growth of cucumber, the second on the effects of different nitrogen content formula for the growth of tomato. The results showed that four commercially available soil microbial products could improve the growth of cucumber and the formula with different nitrogen content significantly affected tomato growth. These results suggested that the autophenotyping platform established in this work can save labor and continuously collect phenotyping data. It can also be useful for users to analyze the diversities among plant growth stages as well as the treatments. This platform has the advantages of being fast, high throughput, objective and noninvasive for phenotyping analysis, and will be helpful for the development of crop breeding.

SSU-YU LIN - summary biography of presenter

Ssu-Yu Lin
Assistant Researcher, Taiwan Agricultural Research Institute, Taiwan

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Ssu-Yu Lin serves at the Crop Genetic Resources and Biotechnology division, Taiwan Agricultural Research Institute, as assistant researcher with expertise in molecular breeding. Her main research revolves around establishing core collection based on genetic backgrounds in melon and pepper. She explores crucial phenotypic traits of these core collections, particularly disease resistance, and improves variety through marker assisted backcrossing and gene pyramiding. Currently, she is also involved in using autophenotyping systems for vegetable cultivation management and stress tolerance research.

Employment and education

2023-	Assistant Researcher, Crop Genetic Resources and Biotechnology Division, Taiwan Agricultural Research Institute, Ministry of Agriculture
2016-2023	Assistant Researcher, Biotechnology Division, Taiwan Agricultural Research Institute, Council of Agriculture, Executive Yuan
2010-2016	BSc and MSc Major in Agronomy, National Taiwan University, Taipei, Taiwan

Selected publications

Lin SY, Wang JY, Li CB, Chen HW, Lin DG, Tu YK. 2023. The application of double-digest restriction-site associated DNA sequencing technology in pepper germplasm. J. Taiwan Agric. Res. 72(2):97–112.

Lin SY, Tu YK, You SC, Fu YY, Lin DG. 2020. Application of plant phenomics platform for automatic phenotyping in the vegetable crops. J. Taiwan Agric. Res. 70(1):11–23.

Lin SY, Huang JH, Wang YH. 2020. Morphological diversity and resistance to powdery mildew in melon (*Cucumis melo* L.) accessions. J. Taiwan Agric. Res. 69(2):169-183.

Lin SY, Tseng YH, Lin SF. 2017. Application of *Adh* genes in the identification of leguminous and gramineous species. Seed Nursery 19(1): 1-24.

Application of artificial intelligence on aerial images to identify rice growth and maturity

Ming-Der Yang, National Chung Hsing University, Taiwan

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Unmanned aerial vehicles (UAVs) which have been rapidly developed in the past few years, exhibit advantages of low cost and easy operation to provide broad area crop observations. UAVs fly at lower heights than planes or satellites and can instantly capture bird's eye view images with a high subdecimeter spatial resolution by flying designated routes according to requirements. Therefore, comprehensive and efficient assessment techniques for crop cultivation and agricultural damage using UAV imagery have a great potential and are highly demanded. Moreover, AI technology is employed to interpret UAV images for crop growth monitoring, yield prediction, and loss assessment. AI technology applied to UAV images with a fine spatial and temporal resolution is a promising tool for smart agriculture by providing in-time imagery and quantitative analysis. This presentation illustrates several cases of the application of deep learning in object detection on rice growth and maturity. Deep learning and UAV images make it possible to continuously follow crop growth on a paddy or single plant basis, especially the location and causes of poor crop growth, growth variation in a paddy, and growth differences of different paddies, so that the farming management strategy can be adjusted based on cultivation conditions.

MING-DER YANG, summary biography of presented

Ming-Der Yang, Distinguished Professor and Dean, Department of Civil Engineering, National Chung Hsing University, Taichung, Taiwan

mdyang@nchu.edu.tw, 886-4-22840440 ext 214

Ming-Der Yang received his BSc degree in Civil Engineering from National Chiao Tung University, Taiwan in 1990, and MSc and PhD degrees in 1993 and 1996, respectively, from the Department of Civil and Environmental Engineering and Geodetic Science, Ohio State University, USA. He is presently Distinguished Professor in the Department of Civil Engineering, National Chung Hsing University, and serves the Dean of College of Engineering. His expertise is geomatics and remote sensing, especially in image processing, geographic information system, environmental monitoring, and disaster assessment. He has authored 100 international journal and conference publications. In addition, he has patents on a street panoramic image preview system and gesture control. Recently, his research efforts are on developing artificial intelligence on remote sensing images for agricultural monitoring and disaster assessment, 3D scene reconstruction, and the applications of VR/AR and AI. He applied AI technology to UAV images for precision agriculture, and has been awarded prizes such as Tech Breakthrough Award in 2019, 2020 and 2022, Outstanding Research Award in 2021, and the Third Potential Investment Prize at the International Forum and Exhibition for AI Innovation Research Center Program in 2019.

Identifying the QTL of 3D multispectral traits for *Capsicum annuum* under heat stress

Ya-Ping Lin, Derek Barchenger, Roland Schafleitner

World Vegetable Center, Taiwan

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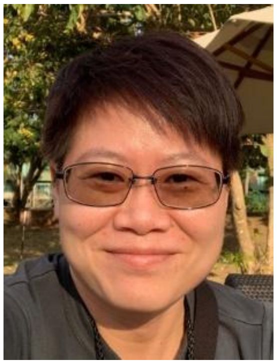
High throughput phenotyping opens the gate to more in-depth investigations of plant growth and development across different environmental conditions. The Phenospex PlantEye F500 can automatically capture 3D multispectral architecture in a nondestructive way across an entire field multiple times a day. In this study, we evaluated 300 *Capsicum annuum* accessions in one optimal and two high temperature stress seasons using the Phenospex platform. Each plot was measured two to three times every day on average throughout three growing seasons. Over half a million data points were collected and analyzed using a machine learning algorithm to evaluate the level of high temperature sensitivity of each accession, which can serve as a selection index for heat tolerance. In addition, we performed a genome-wide association study for the 3D multispectral traits across these three trials. One of these found marker-trait associations in a stable QTL on chromosome 11 for plant height and leaf area. Under elevated temperatures, these two traits were also associated with a QTL on chromosome 9. The results of the study not only advanced our understanding of the genetic mechanisms regulating the 3D multispectral traits under optimal and high-temperature stress, but also served as essential training data for future big data selection.

YA PING LIN, summary biography of presenter



Ya Ping Lin, Omics Breeder, Vegetable Diversity and Improvement,
World Vegetable Center, Tainan, Taiwan

ya-ping.lin@worldveg.org

Lin Ya-Ping Lin obtained her PhD from the Department of Agronomy at the National Taiwan University in 2019. Her passion lies in utilizing omics data to investigate genetic mechanisms underlying various agricultural traits. Her research focuses on exploring the genetic diversity of vegetable germplasm, deciphering genetic mechanisms governing responses to abiotic and biotic stresses, and developing selection methodologies to accelerate breeding programs. She joined the World Vegetable Center in 2020 after her work as a postdoctoral fellow at the Institute of Ecology and Evolutionary Biology, National Taiwan University.

PRESENTATIONS SELECTED FROM SUBMITTED ABSTRACTS

Automated chili phenotyping using deep learning approaches

Smita V Kurup[1], SP Shinde[1], S Agrawal[2], K Saddar[2], BR Char[1]

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Plant phenotyping is critical to streamlining selection processes in a breeding program. Progress in sensors and image processing methodologies have enabled the use of field rovers for high throughput phenotyping in small land holdings of India. In this study, we developed a rover prototype having real sense cameras and an AI stack for quantitative trait estimation in chili pepper. Focused traits were chili pepper leaf curl virus (LcV) disease severity indexing, fruit count, plant height and canopy temperature. Deep learning approaches such as fine tuned classification and object detection models were deployed on the imagery, and validated with ground truths provided by subject experts. The model is being further fine tuned by transfer learning from the deep neural network YoloV5 as the base detection and the classification model with darknet53 and resnet101 backbones as classifiers. The results indicated that image based phenotyping has immense potential in revolutionizing agriculture in a cost effective manner.

Drought-stressed or diseased? Using physiological indices to detect a disease infection in precision agriculture: Implications for phenotyping

Hyungmin 'Tony' Rho

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The use of UAV assisted thermal images to measure leaf temperature has become widely accepted in phenotyping stress responses of crops, particularly drought. However, accurately interpreting thermal images requires careful consideration of potential disturbances from other environmental factors, such as biotic agents like pathogen infections. We address this by investigating the evolution of physiological indices during disease infection under deficit irrigation in a semi-arid cropping system. Zebra chip disease (ZC) is caused by the fastidious, phloem-limited bacterial pathogen *Candidatus* Liberibacter *solanacearum*, transmitted by potato psyllids (*Bactericera cockerelli*). Understanding how ZC impacts potato physiology can aid growers in making informed management decisions. instantaneous leaf physiological responses were measured, e.g. photosynthetic CO2 uptake and transpiration, on infected potato plants subjected to different variable-rate irrigation (VRI) treatments (100%, 80%, and 60% of field capacity). Measurements were made each midday, weekly, from 25-50 days after plant infestation (DAI). The results revealed significant changes in several physiological parameters of photosynthesis and transpiration, with decreases in stomatal conductance, net CO2 assimilation rate, transpiration rate, quantum yields, and the normalized difference vegetation index were observed to be approximately 28-35 DAI. These changes worsened as the infection progressed. Reduced transpiration due to decreased stomatal conductance resulted in increased leaf temperature, especially under hot and dry conditions with high light intensity during the daytime. Consequently, elevated leaf temperature reduced photosynthetic light harvesting and damage to photosynthetic pigment formation and machinery. Our findings support previous reports indicating that increased leaf temperature in infected plants may result from closure of stomata in hypersensitive reactions to infection. These stomatal responses were detectable within 28 DAI, a week earlier than the differences in hyperspectral profiles observed at 35 DAI. These early disease detection strategies using leaf temperature measurements can be implemented to assess crop health more efficiently. Interestingly, increased leaf temperature of infected plants was also detected under low water availability (60%) as they were momentarily drought stressed during the daytime. However, the increased leaf temperature and stomatal resistance quickly recovered once re-irrigated. In conclusion, our research demonstrates the utility of physiological indices in detecting disease infections, but it implies that the cautious analysis could only differentiate infected plants from drought-stressed plants. Further, it highlights the importance of considering compounding environmental factors that may affect thermal imaging interpretations in precision agriculture or phenotyping in variety trials.

Using machine learning for early detection of heat responses: insights from natural sunlight hyperspectral imaging at the red edge

Po-Xing Zheng[1,2], Yu-Lin Wu[1,2], Jheng-Yang Ou[1,2], Tzu-Chiao Liao[1,2], Te-Chang Hsu[1,2], Yao-Cheng Lin[1,2*]

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[2] *Agricultural Biotechnology Research Center, Academia Sinica, Taipei, Taiwan*

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Climate change has intensified the importance of understanding plant responses to heat stress. To rapidly and remotely detect these responses, various high throughput phenotyping methods have been developed. In this study, we employed hyperspectral imaging to identify early heat responses in two cauliflower cultivars (*Brassica oleracea*). Despite no visible changes observed after 4 hours at 40°C, gene expression linked to heat responses was up-regulated in both roots and leaves. After 20 days of heat exposure, curd size decreased, indicating that short term heat not only impacts vegetative growth but also the reproductive stage. Using hyperspectral imaging with a halogen lamp, we captured temporal changes in reflectance spectrum. Machine learning and statistical analyses pinpointed reflectance at the red edge as a key feature that distinguished the control from heat treated plants. To validate these findings, we used hyperspectral imaging under natural sunlight. Our newly developed unsupervised method, hyU, effectively segmented plant regions at the canopy level, minimizing noise from shadows and leaf undersides. After noise removal, an overall increase in red edge reflectance was observed in heat treated plants. These findings underscore the significance of dimensional reduction and demonstrate the potential of hyperspectral imaging, even under natural sunlight, for early detection of heat responses in plants. The hyU tool is freely available at https://github.com/xavierzheng/hyU.

Phenomics approach for identifying superior rootstocks for drought tolerance of grafted tomato

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Drought poses a significant threat to the cultivation of economically and nutritionally important crops like tomato, as it is highly susceptible to water deficit stress. Climate change projections indicate an increase in the frequency and intensity of extreme events including drought, particularly in semi-arid regions. Hence, it is imperative to develop effective strategies to mitigate the negative impacts of drought on tomato production. One approach to improving drought resilience is the use of grafting, which allows the root system of cultivated tomato plants to be replaced with that of wild species, which offers the potential to modulate root system architecture and enhance water use efficiency. In the present study, we utilized a high throughput phenomics facility to assess the performance of tomato plants grafted onto rootstocks with different genetic backgrounds, under varying soil moisture regimes. The rootstocks consisted of tomato cultivars and hybrids derived from crosses involving wild relatives as donor parents (*S. pennellii* and *S. pimpenellifolium*). Our results revealed that an interspecific derivative rootstock, RF4A, derived from a wild parent species (*S. lycopersicum* × *S. pennellii*), exhibited high water use efficiency under drought stress. Tomato plants grafted onto the RF4A rootstock displayed more conservative water use patterns, maintaining higher plant water status even under water deficit conditions. Importantly, RF4A rootstock grafted plants exhibited enhanced stomatal regulation and better photosystem II efficiency, resulting in improved water use efficiency and biomass production under water deficit stress during early vegetative growth. This effect is attributed to an efficient root system from the wild parent (*S. pennellii*), facilitating enhanced water uptake even in drought stress conditions. The findings of this study demonstrate the efficiency of phenomics as a tool for evaluating and selecting superior rootstock-scion combinations in tomato for improving water use efficiency and drought tolerance. Overall, we demonstrated the efficient use of a phenomics platform and developed a protocol to identify promising rootstock–scion combinations of tomato for improving water use efficiency.

Stability and performance evaluation of *Brassica oleracea* germplasm for indoor vegetable breeding using high-throughput phenotyping approach (PlantEye)

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A total of 9,169 *Brassica oleracea* germplasm samples were collected worldwide from commercial seed companies and seed banks to undergo high throughput phenotyping of 34 traits using PlantEye. This assessment aimed to characterize the vegetables for breeding purposes under controlled indoor farming conditions. To simulate abiotic stress (nutrient and environmental stresses), the phenotypic traits of these samples were compared to their characteristics under optimal standard (non-stress) conditions. The coefficient of variation (CV) was calculated for all traits and genotypes under both standard and stress conditions to evaluate the stability of these traits. This preliminary study reports the pilot analysis of the first 100 accessions. The Wilcoxon signed-rank test of CV values revealed significant differences in traits for average greenness, height, leaf angle, leaf inclination, leaf penetration depth, and NDVI average, between stressed and standard conditions across all genotypes (p-value <0.05). For the digital biomass (yield trait) under both conditions, an analysis of variance (ANOVA) was conducted. It showed that the genotype factor had a highly significant effect on the digital biomass response variable (p<0.001), while the stress factor showed nominal effect (p~0.07). However, the interaction between genotype and stress factors was highly significant in explaining the variability in the digital biomass response variable (p<0.01). To identify genotypes with the highest yield stability, CV values were calculated across non-stress and standard conditions for each genotype, and a ranking was performed based on the magnitude of yield differences, from lowest CV values to highest CV values. The top 10 genotypes with the highest yield stability were identified as SMK7, KSK7, SGK3, BCK14, KSK8, MVK20, GPK2, WGK5, BLHK7, and MVK8. This information is valuable for researchers to select stable-performing *B. oleracea* genotypes across various growth conditions for further breeding work. These findings contribute to the advancement of vegetable breeding and will ultimately support sustainable agricultural practices.

POSTER PRESENTATIONS

Development of an autonomous vehicle for monitoring greenhouse asparagus growth conditions

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Asparagus holds significant economic importance in Taiwan. However, the mother stalk cultivation method, suitable for Taiwan's climatic conditions, demands a significant amount of labor to manage plant growth in the greenhouse. To address the current scarcity of agricultural labor, the development of automated tools becomes imperative. This research aims to develop an autonomous vehicle focused on a self -guided strategy and a real-time locating system (RTLS). The vehicle is capable of collecting plant growth data in the field, replacing manual inspections, and meeting labor saving needs. The experimental site for this study was situated at the Yizhu Branch Station of the Tainan District Agricultural Research and Extension Station. In terms of the self-guided strategy, the ENet model was applied to identify the driving lane from front view images. Subsequently, the centerline of the lane could be determined. Furthermore, the density based spatial clustering of applications with noise (DBSCAN) was utilized to cluster the point cloud acquired through LiDAR scanning and derive the reference line for navigation. By integrating the above results, the motor speed was adjusted to achieve precise movement along the center of the driving lane. As for the RTLS, ultrawideband (UWB) technology was applied to acquire instantaneous vehicle coordinates, allowing for precise recording of plant growth status at specific locations.

Singapore's Seeds Innovation Hub –unlocking opportunities for urban farms through seed R&D and deep phenotyping

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The need to secure access to sufficient, safe and nutritious food that meets human dietary needs and food preferences for an active and healthy life is a major global challenge because of the growing world population, changing climate, and increasing environmental degradation. As a land and resource scarce country, Singapore imports most of its food, including vegetables and fruits, which makes it vulnerable to global food supply shock. The degree to which food security in Singapore can be achieved depends on multiple factors, among which domestic supply provides an influential and stable foundation versus unstable supply through international trade. Urban farming in controlled environments provides a promising and feasible solution for Singapore to improve food self sufficiency, and its success depends on adapted crop varieties and optimized growth conditions with low environmental footprints. Currently food crops grown in indoor farms are not the ideal cultivars customized for controlled environments, causing unsustainable production of crops with low yield and limited quality despite high operation expenses. In Singapore's Seeds Innovation Hub, we aim to develop high efficiency breeding pipelines for achieving genetic improvement of popular or high value leafy vegetables and fruits that are better suited to controlled urban environments. Our strategies include deep phenotyping and the use of novel breeding technologies, such as genomic selection of complex traits and targeted modification of specific genes known to affect key plant traits for indoor farming, such as growth rate, crop yield, plant architecture, postharvest qualities, and nutrient level. This program will create novel leafy vegetable and fruit varieties with enhanced yield and nutritional values that are tailored for indoor production environments, and develop efficient breeding strategies that are applicable to breeding of a variety of food crops for urban farming systems. Achievement of these deliverables will contribute to boosting food security and creating sustainable urban farming industry in Singapore, and beyond.

From seed to success –preliminary phenotyping to unlock genetic improvement of winged bean

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Winged bean is an underutilized tropical legume with various edible plant parts, including young pods, seeds, leaves, stems, and even flowers. In the context of mounting challenges posed by climate change and food security, this versatile nitrogen fixing crop holds potential to enhance our existing food system and augment food diversity. Phenotyping is an essential tool for investigating variations in crucial agronomic attributes of winged bean. The study aimed to characterize 20 accessions for six major phenology and yield traits under field conditions, and to identify five promising accessions that exhibited high yield potential and early maturation, suitable for crossbreeding initiatives. A randomized block design was employed for the field experiment. Phenological traits including first flower (*DtFF*), first pod (*DtFP*) and first mature pod (*DtMS*) were recorded on initial observations, while postharvest lab measurements covered pod yield (*PY*), seed yield (*SY*), and harvest index (*HI*). Statistical analysis involving one-way ANOVA, Spearman's correlation, and Principal Component Analysis (PCA) was performed using GenStat 21st edition. Significant differences were found within the 20 accessions for all the traits measured. Strong positive correlations were observed between *DtFP* and *DtMS* ($r=0.874$, $p<0.001$) and between *PY* and *SY* ($r=0.965$, $p<0.001$). Although phenology traits showed weak negative correlations with yield components, they were not statistically significant. The PCA, encompassing a cumulative variance of 99.74%, elucidated the complex relationships within the dataset. The study concluded that seven accessions: a13, a15, a30, a6, i10, i17, and ma3 could be selected for early maturation and phenology in future winged bean enhancement.

How to calculate drought-related plant parameters from Phenospex data

Kevin Fernandes, Penospex

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With global warming on the rise, the agricultural industry is confronted with significant challenges in the form of drought, heat, and soil salinization. These conditions and trends significantly threaten agricultural productivity, necessitating the breeding of drought tolerant genotypes and the screening of agrochemicals that protect plants from abiotic stresses. Phenospex offers advanced high throughput and nondestructive plant phenotyping solutions, such as FieldScan and TraitFinder. These innovative products enable users to gather comprehensive data, including 3D imaging, multispectral analysis, gravimetric measurements, and environmental information, empowering users to analyze plants and identify traits that promote water use efficiency. By effortlessly extracting data from HortControl, users can calculate essential parameters associated with abiotic stress, such as drought, heat, and salinity. Furthermore, our methodology not only outlines the calculation of these parameters, but also provides a user-friendly, step by step guide on how to visualize them in R.

Phenotypic variation of worldwide germplasm of *Brassica oleracea* under controlled environment conditions

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Phenotyping presents a great bottleneck towards plant breeding for crop improvement, whereas the ability to assess many accessions effectively and quickly presents a key opportunity to improving plant breeding efforts. Noninvasive plant screening is performed with imaging technology including high throughput imaging devices, and other image analysis software. *Brassica oleracea* is a genus with extremely high phenotypic diversity. A study was performed to assess the phenotypic diversity of worldwide accessions of *B. oleracea*, exploiting indoor farming conditions to regulate growth environments and limit gene-environment interactions. High-throughput phenotyping and image analysis were used to characterize the accessions and identify genotypes of high performance in indoor farming conditions. A total of 403 *B. oleracea* accessions from seed banks and commercial sources, comprising of 2131 individuals, were evaluated for up to 27 characteristics. All traits exhibited significant differences ($p<0.05$) across accessions, indicating genetic variance available for breeding improvement. Multivariate statistical analysis clustered these accessions into four clusters. with ten genotypes selected as high performing accessions suitable for indoor faming conditions based on traits such as yield, leaf area index, light penetration depth and relative growth rate, using the rank summation index. They were all identified in the same cluster. These accessions may be selected as genotypes with useful traits for plant breeding, to be used for crop improvement for indoor farming. This study demonstrates the usefulness of high throughput and image analysis methods for efficient characterization of plant accessions in indoor farming environments.

Development of machine vision in muskmelon flower genders and stages identification

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Muskmelon (*Cucumis melo* var *reticulatus*) is a high value fruit. It is vulnerable to pests, diseases, and extreme weather conditions, so greenhouse cultivation has been adopted to overcome these limitations. While greenhouses effectively prevent pest infestations, they also hinder natural insect pollination. Manual pollination is time consuming and causes a drastic increase in labor requirements. Developing an automatic pollinator could be a potential solution, but integration of a wide range of domain knowledge is necessary. This study aims to apply machine vision and deep learning methods to develop an identification model for flower genders and stages, thereby facilitating the process of developing automatic pollinators. Muskmelon (Earl's summer line II) in this study was cultivated in the Intelligent Greenhouse of the Experimental Farm, College of Bioresources and Agriculture, National Taiwan University, from October 2022 to June 2023, using a vertical hydroponic system. Flower images were acquired by smartphones or Raspberry Pi camera modules with a minimum resolution of 3280 x 2464 pixels. A total of 1857 images were collected and annotated into two genders (male and female) and three flowering stages (before, during, and after flowering). Models were developed using the Faster Region-based Convolutional Neural Network (Faster R-CNN) deep learning architecture, combined with data augmentation methods for performance optimization. The developed identification model for muskmelon flower genders and stages achieved a mean average precision (mAP) of 0.759 and an average recall (AR) of 0.808, respectively. Model validation was performed on a dataset containing various types of images, including close ups (10-15cm), distant (>15cm), top view, and side-view images. The results of the current model demonstrate its capacity to identify muskmelon flowers in a greenhouse. It is expected to be integrated with robotic arms for broader applications.

A novel approach to high-resolution active multispectral imaging system development

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The accurate analysis of plant phenotypes the field is crucial in studying plant phenotypes and gene vs. environment interactions. The traditional phenotypic analysis relies heavily on time intensive visual observations and manual measurements, which not only increases labor costs due to the time required, but it also limits the obtainable phenotypic characteristics. Therefore, automated plant phenotyping technologies have gained high attention from research institutions worldwide, leading to investments in various technologies and equipment development in recent years. This study focuses on a novel active high resolution multispectral imaging system. Set a schedule by a central control system, this can automatically switch between 16 spectra for high resolution photography. After generating 3D images through image processing, post-image analysis yields plant growth physiological values, vegetation index, and area characteristics ratios. Taking an orchid and a gourd plant as examples, the study obtains 3D images of the orchid's height and area, as well as the area characteristics of severity levels of powdery mildew infecting the gourd plant. Since the nondestructive and rapid detection are advantages of continuing multispectral imaging, it can be well applied in crop breeding, quality assurance, and the differentiation and classification of plant diseases and pests.

Tracking rice root system architecture under early phase water stress through image-based phenotyping

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Rice productivity hinges upon the availability of soil moisture, directly influencing the growth and maturation of root systems. Identifying root phenes that optimize the utilization of moisture holds the potential to elevate biomass and augment grain yield. In this study we harnessed non-destructive gel-based phenotyping, coupled with an imaging-based monitoring system, to delve into the intricacies of root morphology, geometry, topology, and the dynamics of root system architecture (RSA). Two rice genotypes, IR64 and Kinandang Patong (KP) were subjected to contrasting water stress to investigate adaptive responses of their RSA. Rice plants typically develop a seminal root, nodal roots and lateral roots spanning various orders. Furthermore, lateral roots can be further subdivided into S-type (short and thin) and L-type (long, thick, and capable of further branching). Our analysis underscored higher production, and length of 1st-order L-type lateral roots on days 4-7, and 2nd-order L-type lateral roots from days 9-10 in variety KP. In contrast, IR64 demonstrated alterations through thinner and elongated nodal roots. Additionally, genotypes diverge in their preference for generating S-type or L-type lateral roots from the 3rd to 5th day. Furthermore, preference in KP for faster growth rates of shorter root types (S-type and 2nd-order L-type lateral roots) over longer root types (nodal root and L-type lateral roots) from days 6 to 8. Branching roots (1st and 2nd-order L-type lateral roots) emerged rapidly and exhibited significant variation, which indicated that this may play a substantial role over elongating roots in accessing moisture, as evidenced by higher shoot dry weight in KP. Moreover, topological aspects also varied with wider interbranch distances between lateral roots in KP. Interestingly, IR64 displayed a downward lateral root insertion angle, whereas a straighter trajectory was evident under controlled conditions. Overall, this study highlights the distinct early developmental adaptive strategies of both genotypes under stress. It emphasizes the pivotal role of lateral root development in facilitating efficient water uptake, ultimately leading to higher biomass accumulation.

Developing a high throughput plant phenotyping system in Academia Sinica

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High throughput plant phenotyping has transformed the plant science community into an unprecedented node of data-driven discovery and innovation. Such platforms offer a noninvasive, image based method to analyze complex traits, enabling efficient and continuous measurements of plant growth and development. In Academia Sinica, we have developed and maintain both the hardware, software, and analysis components of phenotyping platforms, both in field and greenhouse settings. Here, we present a highly customized high throughput plant phenotyping system developed in Academia Sinica Southern Campus. This system, with the latest off the shelf industry components, empowers us to fully understand and control the entire process, ensuring the highest quality of data for our research. To address diverse biological questions, we developed different methods based on various computational algorithms and models, to analyze the vast amount of imaging data. We developed various methods using deep learning models to extract crucial plant traits such as projected leaf area, number of leaves, leaf angles, and the time of curd induction. We also adapted large scale public datasets using transfer learning to improve prediction accuracy. Our work demonstrates the potential of using high throughput plant phenotyping to understand plant growth, interactions with the environment, and applications in plant breeding.

Evaluation and breeding of solanaceae vegetable crops in Armenia

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To increase production of vegetables, opportunities exist for expanding cultivation areas, creating high yielding varieties and hybrids, and improving cultivation technologies by integration of new scientific advances and best practices. High quality varieties and hybrids of the most used vegetable crops adapted to the Ararat valley and mountainous areas in Armenia are lacking. Experiments were carried out in 2006- 2022 at the Scientific Center of vegetables and industrial crops of village Darakert, Ararat region, using the worldwide collection of the World Vegetable Center. Source material of solanaceae vegetable crops with economically important properties was selected according to precocity, fertility, productivity, quality and product features, and disease resistance. A total of 70 varieties and hybrids of eggplant, chili, sweet pepper and tomato were tested for wide ecological adaptation and economically valuable properties and characteristics, from which were selected new varieties and hybrids of solanaceae vegetable crops which are promising for integration and cultivation in Armenia. The results from samples of solanaceae vegetable crops in the Ararat valley, revealed that varieties of sweet pepper (PBC-271, 0137-7020, 0137-7041), chili pepper (0337-7546), and tomato (CH 15H, CLN 2413D, CLN 1558B) showed good results. In addition, varieties obtained from WorldVeg, sweet pepper (Miles, Natalie, Emily), chile pepper (Gita, Zita), and tomato (Zeytun, Janna, Rubina, Renesans) have been tested since 2008m and licenses and authorship certificates are available. Studies also show convincingly that the eggplant species *Solanum undatu* subgenus *leptostemonum, Solanum macrocarpon (MA-134* and *S00052), Solanum aethiopicum (S00005),* and *Solanum insanium,* are notable for their growth, yields and wide adaptability.

Technology development for collecting temporal growth phenotypes for individual plants

Takanari Tanabata, Sachiko Isobe

Kazusa DNA Research Institute, Japan

In the research and development of crop breeding and cultivation technologies, it is necessary to develop varieties that best suit the production targets, optimize the planting environment, and develop disease and pest prevention techniques. Plants can survive by adapting to their environment, and the information obtained through the analysis of gene functions helps optimize the production environment and improve varieties that are resistant to climate change. To analyze gene function, it is essential to study various genotypes under diverse growing conditions, identify variations in their individual growth, and quantify these differences using large scale data sets. To address this need, acquiring individual growth information and previous environmental values throughout the plant's growth periods is essential. Thus, we are developing technologies aimed at obtaining trait information on individual plants that will be useful for understanding the function of genes. We will show the progress in developing a technology that acquires 3D point clouds to obtain morphological information, and an environmental sensor system capable of measuring temperature, humidity, sunlight, soil temperature, and soil moisture for each individual plant. 3D point cloud construction technology is an image analysis technology for acquiring 3D point clouds of individual plants. A plant’s structure tends to have thin stems and leaves that hide each other. This technology achieves point cloud construction that is optimal for these shape features. The environmental sensor system aims to obtain environmental values for each plant, then it realizes measurements using more than 100 environmental sensors at a time. The challenges are to reduce the cost of hardware production and to develop a system that integrates the measured values of many sensors. In addition, we will show automatic transport and small drone photography technologies, which we are developing for reducing measurement tasks.

StomaVision: stomata measurement using deep computer vision

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Measuring stomata traits, such as number, pore size and closure rate, provides direct insights into how plants respond to environmental signals. However, manual inspection and measurement of these traits is low throughput, in that it takes time and requires expert knowledge for accurate recording. We introduce StomaVision, a versatile tool for stomata detection and pore measurement. Developed from measurements on a diverse set of plant species (monocot and dicot), StomaVision can process 'dirty' images from field grown plants, significantly reducing the time researchers spend on processing microscope image data. StomaVision employs a progressive machine learning approach to enhance the accuracy of stomata inference and shortens the inference time. StomaVision provides an intuitive web interface with minimal need to modify parameters. It facilitates the investigation of stomatal traits and demonstrates the importance of plant physiological responses. Using StomaVision can successfully infer the negative correlation between curd initiation time and other features. Stomatal density, stomatal opening rates, normalized total stomata pore area, stomatal conductance related to water vapor (gsw) and assimilation rate, show a significant difference between heat stressed and control plants. Furthermore, normalized total stomata pore area and assimilation rate can also indicate significant differences between heat treatment lengths.

PhenoVeg 2023 symposium program

26-27 September 2023
World Vegetable Center, Shanhua, Tainan, Taiwan

Tuesday 26 September

09:30-10:00	*Registration and welcome coffee*	
10:00-10:20	Welcome, opening remarks and introduction	Junne-jih Chen (MoA), Yu-ping Lin (NTU), Ming-tsair Chan (Academia Sinica), Roland Schafleitner (Worldveg)
Sensors, cameras and automatization		
10:20-11:00	Novel sensors to advance plant phenotyping	Onno Muller, Forschungszentrum Jülich, Germany
11:00-11:40	DIY Plant Phenotyping: application of digital phenotyping techniques in plant research and breeding	Sachiko Isobe, Kazusa DNA Research Institute, Japan
11:40-12:10	Establishment and application of a crop phenotyping system in the National Crop Phenomics Center of Korea	Hyeonso Ji, National Institute of Agricultural Sciences, Korea
12:10-13:10	*Lunch break*	
Big data and deep learning, modeling		
13:10-13:50	Leveraging AI/ML to address critical challenges in plant phenotyping research	Jennifer Clarke, University of Nebraska - Lincoln, USA
13:50-14:20	A deep learning model to detect the early drought stress status of tomato	Yuan-kai Tu, Taiwan Agricultural Research Institute, Taiwan
14:20-14:50	Reducing the data analysis threshold for plant phenomics: a visual analysis tool for smooth extraction of traits for analysis	Cheng-bin Li, Taiwan Agricultural Research Institute, Taiwan
14:50-15:10	Automated chilli phenotyping using deep learning approaches	Smitha V. Kurup, Mahyco, India
15:10-15:50	*Coffee break and poster viewing*	
15:50-16:30	Application of artificial intelligence (AI) on aerial (UAV) images to identify rice growth and maturity	Ming-der Yang , National Chung Hsing University, Taiwan
16:30-17:00	Drought-stressed or diseased? Using physiological indices to detect disease infection in precision agriculture: Implications for phenotyping	Hyungmin “Tony” Rho, National Taiwan University, Taiwan
17:00-17:30	Establish an evaluation system for thermotolerance in tomato under heat stress	Yu-chang Tsai, National Taiwan University, Taiwan
18:00-21:00	*Symposium dinner*	

Wednesday 27 September

Phenomics enabled plant research and breeding		
09:00-09:40	Using advances in phenotyping technology to develop climate-ready crops for the future	Owen Atkin, Australian National University, Australia
09:40-10:10	Using machine learning for early detection of heat responses: Insights from natural sunlight hyperspectral imaging at the red edge	Po-xing Zheng, Academia Sinica, Taiwan
10:10-10:40	Phenomics approach for identifying superior rootstocks for drought tolerance of grafted tomato	Pratapsingh S Khapte, Indian Council of Agricultural Research, India
10:40-11:00	*Coffee break and poster viewing*	
11:00-11:40	Automatic stomata detection and measurement for plant abiotic responses	Yao-cheng Lin, Academia Sinica, Taiwan
11:40-12:10	Empowering breeders and researchers: Leveraging automated plant phenotyping in vegetable crops	Ssu-yu Lin, Taiwan Agricultural Research Institute, Taiwan
12:10-13:10	*Lunch break*	
13:10-13:40	Crop model assisted with drone-spectral image for growth and yield prediction in broccoli	Wei-ling Chen, Taichung District Agricultural Research and Extension Station, Taiwan
13:40-14:10	Phenomics as a breeding tool	Ya-ping Lin, World Vegetable Center, Taiwan
14:10-14:40	Stability and performance evaluation of *Brassica oleracea* germplasm for indoor vegetable breeding using high-throughput phenotyping approach (PlantEye)	Ting Xiang Neik, National University of Singapore, Singapore
14:40-15:00	Closing	Ming-che Shih, Distinguished Research Fellow, Academia Sinica, Taiwan
15:00-16:00	WorldVeg tour (facilities, demo garden, coffee)	

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The World Vegetable Center is an international non-profit institute for vegetable research and development. It mobilizes resources from the public and private sectors to realize the potential of vegetables for healthier lives and more resilient livelihoods.

WorldVeg’s globally important genebank, improved varieties, production and postharvest methods help farmers to increase their vegetable harvests, raise incomes in poor rural and urban households, create jobs, and provide healthier, more nutritious diets for families and communities. With headquarters in Taiwan, field operations are led from regional centers in Benin, India, Mali, Tanzania and Thailand, and through offices in other key countries.

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