Southern Cross University
Research

Sejong University SCU Plant Science Symposium

Agenda

Sejong University SCU Plant Science Symposium

09:00-09:30	ARRIVAL	
9:30-10:00	Prof T. Carlin VC; Prof R. Joannes-Boyau DVCR; Prof Jon Hill Dean of FSE; Prof Tobias Kretzschmar; Prof Joong Hyoun Chin	Welcome and Opening Remarks
10:00-10:20	Prof Joong Hyoun Chin	Allele mining for economically important traits of milk thistle *(Silybum marianum)* genome through comparative genomics and association studies
10:20-10:40	Prof Kyung Do Kim	Chromosome-level genome assembly of milk thistle *(Silybum marianum)* reveals species-specific gene expansion and CYP450 variants associated with silymarin chemotypes
10:40-11:00	Prof Hyun Uk Kim	Functional characterization of *FAD2* and *FAD3* desaturases reveals the molecular basis of seed fatty acid composition in Milk Thistle (*Silybum marianum*)
11:00-11:40	MORNING TEA	
11:40-12:00	Prof Tobias Kretzschmar	New Crop on the Block - Tools for Cannabis Research and Development
12:00-12:20	Dr Jos Mieog	Maintaining the competitive edge for Australian tea tree oil production
12:20-12:40	Dr Jay Anderson	Plant pathology research for Northern Rivers crops: tea tree (Melaleuca alternifolia), blueberry and avocado

Our Partners:

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Southern Cross University Research
PDBL Plant Digital Breeding Lab

12:40-14:00	LUNCH BREAK	
14:00-14:20	Prof Hyun-Seung Park	Genome-to-Phenome Approaches for Chemotype Breeding in Milk Thistle
14:20-14:40	Prof Jinmi Yoon	Elucidating the Molecular Networks Underlying Early Seed Development in Rice
14:40-15:00	Prof Lae-Hyeon Cho	Internal nutrient signaling by sucrose in the molecular control of rice flowering
15:00-15:40	AFTERNOON TEA	
15:40-16:00	Dr Szabolcs Lehoczki-Krsjak	Climate Smart Black Rice development at SCU
16:00-16:20	Prof Bronwyn Barkla	Applications of plant proteomics to understand plant abiotic stress.
16:20-16:40	Dr Kwanho Jeong	Cluster root formation in Macadamia integrifolia seedlings: responses to phosphorus and variation among grafted scions
16:40-17:00	Prof Tobias Kretzschmar, Prof Joong Hyoun Chin	Wrap up and Closing Remarks
17:30 - 20:00	DINNER	

We acknowledge Widjabal Country as the Country where Southern Cross University originated and grew, and from where it continues to grow. It seeded the growth of our Gumbaynggirr Campus in Coffs Harbour, our Yugambeh Campus in Coolangatta and it planted the seeds to transform the Countries we are on.

Understanding our origins will make each step into the future a more purposeful one, leading all to transform tomorrow.

The Sejong University SCU Plant Science Symposium

Sustainable food systems and natural product innovation are key to improving human health, supporting resilient communities, and enhancing environmental wellbeing. These systems are increasingly vital as we face rising health challenges, climate pressures, and the need for more ethical, traceable supply chains.

Sejong University's PDBL (Phytochemical Digital Breeding Lab) delivers cutting-edge, cross-disciplinary research that spans plant genomics, multi-omics, and artificial intelligence-driven breeding. Our work advances the precision development of high-value medicinal crops, specifically Milk Thistle, by elucidating the genetic mechanisms behind phytochemical biosynthesis and environmental resilience. From genomic blueprints to field application, their researchers integrate standard genome assembly, single-cell transcriptomics and automated phenotyping to optimize key bioactive compounds such as silymarin and fatty acids. By converging agricultural biotechnology with digital innovation, we are establishing a new standard for global functional plant materials and securing sustainable bio-resources.

Southern Cross University's Harvest to Health research cluster (H2H) delivers cutting-edge, cross-disciplinary research that spans plant science, functional foods, and human health. H2H's work enhances the sustainable production of high-value foods and natural compounds, assessing their potential to optimise health outcomes and reduce disease risk. From soil to shelf, our researchers explore the full value chain, developing nutrient-rich crops, validating bioactive compounds, and investigating their effects on wellbeing. By integrating agricultural innovation with biomedical science, we're creating healthier futures for people, communities, and the planet.

Dr Joong Hyoun Chin

Associate Professor

Joong Hyoun Chin is an Associate Professor in the Department of Integrative Biological Sciences and Industry at Sejong University, Seoul, Republic of Korea. His research focuses on breeding and genetics of nutrient-efficient, climate-resilient rice and on smart production systems for phytochemicals from medicinal and functional plants. He has published over 80 peer-reviewed papers and contributed to the development of several phosphorus-efficient, multi-stress-tolerant rice varieties and patents, including IPS, IPSA and Sechanmi. Previously, he served for nearly a decade as a molecular breeder at the International Rice Research Institute (IRRI) in the Philippines. He currently leads national and international projects on phosphorus-use efficiency and low-input "green" rice systems, and seeks close collaboration with Australian scientists on sustainable cropping in marginal environments.

Allele mining for economically important traits of milk thistle (*Silybum marianum*) genome through comparative genomics and association studies

*Sunghan Kim, Trinh Minh Vu, Joong Hyoun Chin**

Department of integrative Biological Sciences and Industry, Sejong Univeristy, Seoul, Republic of Korea

Milk thistle *(Silybum marianum L.)* is widely recognized for its hepatoprotective and antioxidant properties, making it a focus of both traditional and modern pharmacological research. Our laboratory recently completed the first reference genome assembly for this species, enabling the identification of genes associated with economically valuable traits. Using QTL mapping, comparative genomics, and association studies, we have identified candidate genes involved in silymarin biosynthesis, involucre size, seed color, and heading date. Notably, unique allelic variants related to phosphorus homeostasis and stress response were found in accessions with elevated silymarin content, suggesting that phosphorus starvation and other abiotic stresses may influence flavonolignan accumulation. Additionally, many candidate genes for involucre size are predicted to regulate floral organ development, as supported by studies in other plant systems. Structural comparisons of these genes, as well as those involved in heading date control, with homologs in other plant genomes will also be discussed.

This work was supported by This study is supported by National Research Foundation of Korea (NRF) grant funded by the Korea government (MSIT) (No.RS-2024-00410854 and RS-2024-00343462)

Dr Kyung Do Kim

Associate Professor

Dr. Kim is a plant geneticist and biotechnologist developing innovative solutions for agricultural challenges in the climate change era. His research spans fundamental genomics to applied crop improvement, with particular expertise in legume crops, especially soybean.
His work focuses on identifying and characterizing novel genes conferring resistance to environmental stresses, including biotic threats like soybean cyst nematode, utilizing next-generation sequencing and molecular marker development to uncover genetic variations associated with stress resilience.

> *His research portfolio extends to medicinal crops, employing whole-genome sequencing to decode biosynthetic pathways for valuable phytochemicals. He is also democratizing plant breeding by developing cloud-based, low-cost genotyping platforms leveraging machine learning algorithms.*

With extensive experience in GMO risk assessment, molecular authentication, and standardized analytical methods, his interdisciplinary approach combines classical genetics with modern genomics, bioinformatics, and biotechnology, positioning him at the forefront of developing sustainable agricultural solutions for future food security.

Chromosome-level genome assembly of milk thistle (*Silybum marianum*) reveals species-specific gene expansion and CYP450 variants associated with silymarin chemotypes

Kyung Do Kim[1,2*]

[1]Department of Integrative Biological Sciences and Industry, Sejong University, Seoul, 05006, Republic of Korea

[2]Institute for Advanced Plant Breeding and Phytochemicals (IAPBP), Sejong University, Seoul 05006, Republic of Korea

Milk thistle (*Silybum marianum*), a member of the Asteraceae family, is valued for producing silymarin, a flavonolignan compound with potential hepatoprotective effects. Silymarin is synthesized through the oxidative coupling of coniferyl alcohol and taxifolin, which are derived from the flavonoid and phenylpropanoid pathways. However, the genetic mechanisms and subsequent pathways after oxidative coupling in silymarin biosynthesis are still unknown. Here we investigated the genomic features associated with silymarin production by constructing a high-quality chromosome-level genome assembly of milk thistle. We performed comparative genomics across Asteraceae species, revealing that milk thistle is most closely related to *Cirsium nipponicum*, with an estimated divergence time of 6.4 – 8.4 million years ago. Our analysis identified species-specific gradual substitution of paralogous genes in milk thistle, where genes involved in the silymarin biosynthesis pathway, were significantly expanded. Furthermore, a missense mutation (A91S) in the expanded CYP450-like gene, Smar07g031510, was associated with altered silymarin chemotype, specifically showing reduced silybin A/B and silychristin, but increased silydianin and isosilybin B content. These findings provide a valuable genomic resource and genetic evidence for the evolutionary basis of silymarin production, offering targets for phytochemical-integrated digital breeding of high-silymarin content milk thistle cultivars.

This work was supported by This study is supported by National Research Foundation of Korea (NRF) grant funded by the Korea government (MSIT) (No.RS-2024-00410854)

Dr Hyun Uk Kim

Professor

Professor Hyun Uk Kim is a plant molecular biologist whose work focuses on understanding lipid metabolism and seed oil biosynthesis in plants. He completed his B.S., M.S., and Ph.D. degrees in Agricultural Biology at Seoul National University, where he developed a strong foundation in plant genetics and biochemistry.

After earning his doctorate, Professor Kim continued his academic training through postdoctoral research appointments at the Plant Gene Expression Center (USDA/ ARS)/University of California, Berkeley, the Department of Botany and Plant Sciences, University of California, and later at the Institute of Biological Chemistry at Washington State University. These experiences allowed him to deepen his expertise in plant lipid metabolisms, gene regulation, and molecular biotechnology.

Before joining Sejong University as a faculty member, he spent many years as a Research Scientist at the National Academy of Agricultural Science (RDA), where he contributed to studies on seed development, fatty acid biosynthesis, and metabolic engineering approaches for crop improvement.

At Sejong University, Professor Kim's research continues to explore how plants produce and regulate fatty acids and triacylglycerols. His work has examined key enzymes such as desaturases, acyltransferases, and transcription factors involved in seed oil accumulation.
He has also applied molecular genetics, transcriptomics, and genome editing to understand lipid metabolism in various oilseed crops, including Camelina, Perilla, Physaria, and Brassica species.
Through these studies, Professor Kim aims to uncover fundamental mechanisms of plant lipid biology while also contributing knowledge that may support the development of crops with improved oil content or composition. He has published extensively in this field and remains engaged in collaborative research efforts focused on plant biochemistry, seed development, and metabolic engineering.

Functional characterization of *FAD2* and *FAD3* desaturases reveals the molecular basis of seed fatty acid composition in Milk Thistle (*Silybum marianum*)

Hyun Uk Kim[1,2]

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Milk thistle *(Silybum marianum)*, **a** diploid species of the Asteraceae, is valued for its high seed oil content and the hepatoprotective flavonolignan complex silymarin. Milk thistle seeds contain predominantly oleic (18:1) and linoleic acid (18:2) with almost no alpha-linolenic acid (18:3), yet the molecular basis for this unusual fatty acid profile has remained unclear. To investigate the genetic determinants underlying seed oil composition, we analyzed 22 accessions for fatty acid variation, seed developmental patterns, and desaturase gene function.

Substantial variability in 18:1 and 18:2 proportions was observed across accessions, while oil content increased sharply during the mid-developmental stages corresponding to active triacylglycerol accumulation. Genome and transcriptome analyses identified three FAD2 genes (SmFAD2a, SmFAD2b, SmFAD2c) and two FAD3 genes (SmFAD3a, SmFAD3b). SmFAD2a and SmFAD2c were highly expressed in developing seeds, whereas SmFAD2b and both FAD3 isoforms showed minimal seed expression. Tissue-specific profiling revealed that SmFAD2a is broadly expressed, SmFAD2c is seed-enriched, and SmFAD2b is restricted primarily to the involucre. Consistent with gene expression patterns, 18:3 accumulated in vegetative tissues but remained nearly undetectable in seeds.

Functional complementation in Arabidopsis mutants confirmed distinct enzymatic roles. SmFAD2a restored linoleic acid levels above wild-type in the fad2-1 mutant, and SmFAD2c restored near wild-type levels, whereas SmFAD2b exhibited negligible activity. SmFAD3a and SmFAD3b partially complemented the fad3-2 mutant, confirming their capacity to synthesize alpha-linolenic acid in non-seed tissues. Sequence substitutions near the His-box of SmFAD2b likely disrupt cytochrome b5 interaction and underlie its loss of activity.

Together, these findings demonstrate that SmFAD2a and SmFAD2c are the major contributors to seed desaturation in S. marianum, while repression of FAD3 during seed development accounts for the near absence of 18:3. This study provides a molecular framework for engineering milk thistle seed oil composition for nutritional or industrial applications.

This work was supported by This study is supported by National Research Foundation of Korea (NRF) grant funded by the Korea government (MSIT) (No.RS-2024-00410854 and RS-2024-00343462)

Dr Tobias Kretzschmar

Professor

Tobias Kretzschmar is a professor for plant breeding and genetics at Southern Cross University (SCU) where he co-leads of the Harvest to Health Research Impact Cluster. He researches value-added niche crops with focus on natural products and bioactive compounds. He currently supports the Australian industrial hemp, medicinal cannabis, coffee, rice and tea tree industries.

Prior to joining SCU he spent seven years at the International Rice Research Institute (IRRI), Philippines, as Senior Scientist in Molecular Genetics, supporting rice science for a better world.

Tobias Kretzschmar has a PhD from the University of Zurich, Switzerland (2009) and an MSc from the Technical University of Kaiserslautern, Germany (2005).

New Crop on the Block – Tools for Cannabis Research & Development

Tobias Kretzschmar

Southern Cross University, Australia

Cannabis sativa, is one of the oldest domesticated crops, cultivated for food, fibre and medicine. Its seeds are rich in protein and polyunsaturated fatty acids, while its stalks provide fibres for textiles, ropes, and sails. From the 17th to the early 20th century industrial hemp, i.e. non-psychoactive Cannabis sativa, was among the economically most valuable crops globally and a key driver of mercantilism, colonialism and imperialism.

However, a near global moratorium throughout most of the 20th century, largely due to confounded concerns around narcotic misuse, caused industrial hemp to miss out on the green revolution and the advent molecular breeding that enabled dramatic advances in performance of conventional crops.

Over the last decades there has been renewed interest in industrial hemp and medicinal cannabis. Relaxing regulation coupled with increasing market demand in the functional food and carbon sequestration space have created a thriving industry. To fast track the improvement C. sativa to its full agronomic potential for 21st century agriculture we are developing a suite of tools for Cannabis Research & Development (R&D), including a community-driven bioinformatics platform, an open-source SNP database, a mid-density genotyping platform, a quantitative proteomics library and a chemometric tool for cannabinoid quantification.

This presentation will highlight the utility of these tools and their applications in Cannabis R&D. In addition to supporting the improvement of modern Cannabis cultivars they can serve as a blueprint for the development of similar tools for other underutilized crops.

Dr Jos Mieog

Research Fellow

Jos Mieog is as a Research Fellow in Plant Breeding & Genetic Resources at the Faculty of Science and Engineering, Southern Cross University (SCU).
He earned his B.S. and M.S. in Biology from Radboud University Nijmegen, Netherlands and completed his Ph.D. focusing on coral bleaching responses at the University of Groningen, in partnership with the Australian Institute of Marine Science.

Prior to SCU, he spent seven years at CSIRO in Canberra, concentrating on improving grain quality in cereal crops through both GM and non-GM techniques. Since 2017, Jos mostly works on tea tree and Cannabis, focusing on pre-breeding research activities as well as achieving commercial outcomes.

He is leading an advanced breeding program for the Australian tea tree oil industry, with research activities focused on disease resistance, improving oil quality and moving the industry towards clonal deployment. On the Cannabis side, he conducts research into trichome biology, sex determination, tissue culture, pest management and QTL mapping for traits relevant to the hemp industry. He supervises HDR students on projects on tea tree, Cannabis and coral reef restoration.

Maintaining the competitive edge for Australian tea tree oil production

Jos Mieog, Ben Liu, Jay Anderson, Elisa Dalla Rosa, Regan Barker, Tobias Kretzschmar, Mervyn Shepherd*

Faculty of Science and engineering, Southern Cross University, Lismore, Australia

Tea tree oil (TTO) is an iconic Australian natural product marketed globally in healthcare, cosmetic, pharmaceutical and veterinary products. TTO is produced in specialised foliar oil glands, rich in terpenoid compounds that provide its antiseptic and antifungal properties. The entire shoot of the plant is harvested and steam distilled to produce a purified essential oil. Australian TTO production occurs in north-eastern NSW and far North Queensland, generating up to 1,000 tons of oil with ~90% of production sold overseas.

Domestication of tea tree began in the early 1980's as the industry transitioned from a reliance on natural stands for harvesting to purpose-grown plantations. A tea tree breeding program commenced in 1993 and underpinned the stabilisation and growth of the industry by developing a reliable source of seed cultivars with high oil quality that progressively increased in oil yields over the generations, allowing the industry to maintain a global competitive edge against increasing overseas TTO production in China, South Africa and Kenya,Southern Cross University has been leading the Australian tea tree breeding effort since 2017. The breeding program has continued the supply of improved germplasm to the Australian industry, introducing sophisticated methodologies and re-evaluating the data back to the start of breeding to maintain the desired rate of gain as the opportunities to easily make large advances, available in the early stages of domestication, have largely disappeared. Furthermore, the focus has progressively broadened to include pre-breeding activities on aspects such as leaf drop and emerging challenges related to oil quality and European regulations, guided by industry concerns. The approaches taken to address these challenges will be discussed.

Dr Jay Anderson

Senior Lecturer

Dr Jay Anderson is an experienced Plant Pathologist specialising in tropical and subtropical horticultural crops. She holds a Bachelor of Horticultural Science and a PhD in Plant Pathology from the University of Queensland.

Dr Anderson's research focuses on understanding pathogens and pathogen infection processes to develop integrated disease management strategies. Her work contributes to the University's "Harvest to Health" research cluster

Plant pathology research for Northern Rivers crops: tea tree (Melaleuca alternifolia), blueberry and avocado.

*Dr Jay Anderson, Dr Karina Griffin, Jean Page,
Dr MD Kamaruzzaman and Elisa Dalla Rosa*

*Faculty of Science and Engineering, Southern Cross University,
1 Military Road, East Lismore, 2480 NSW*

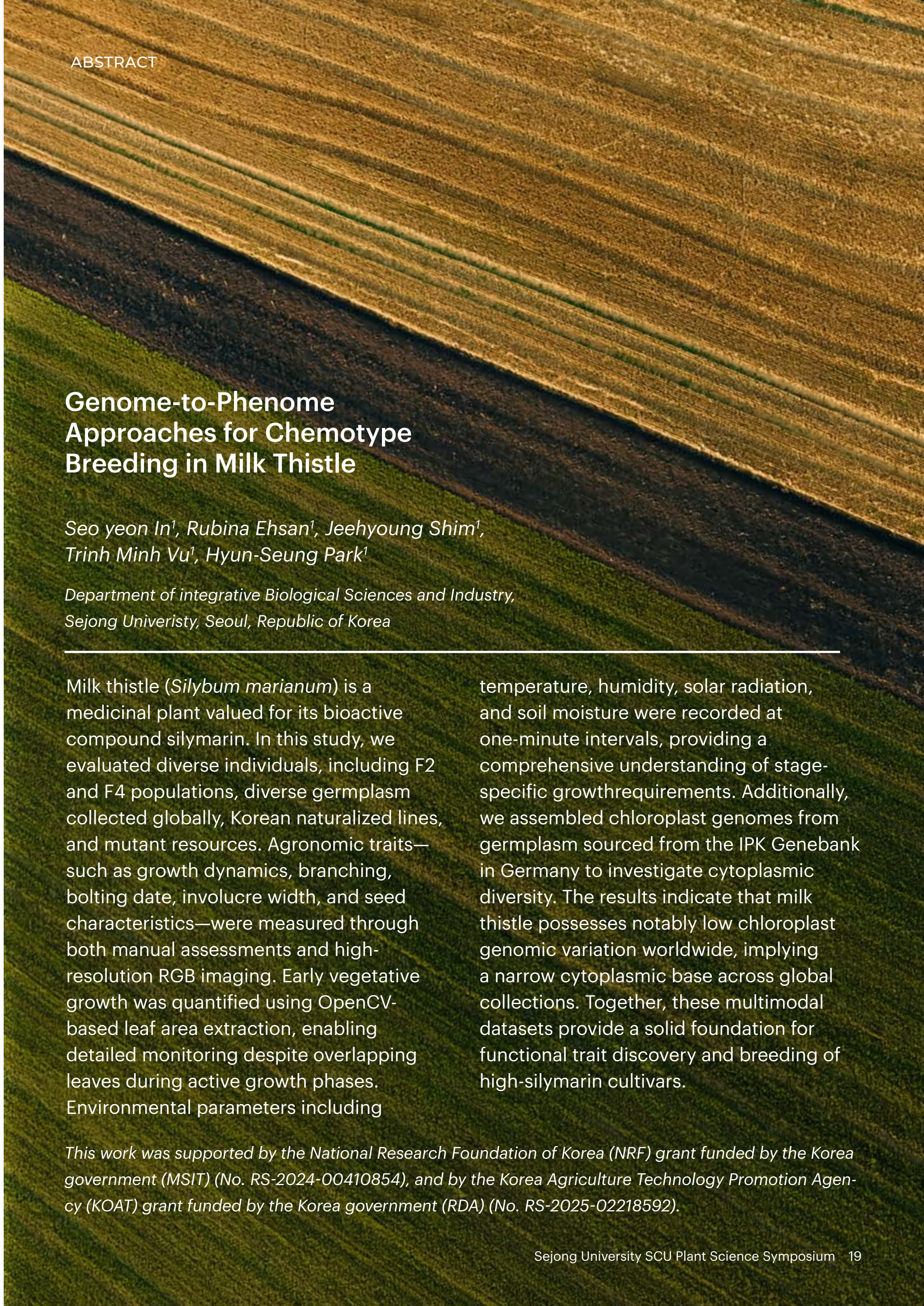
We work on understanding the organisms which cause diseases on our local crops, mostly blueberry, tea tree and avocado, but occasionally other crops too. We use field, glasshouse and laboratory studies to do this and we work closely with plant breeders, agronomists, NSW Department of Primary Industries and Regional Development, other university researchers, extension officers and farmers. The ultimate aim of our work is integrated management of diseases which is scientifically and environmentally sound, cost effective and easy for growers to apply.

Dr Hyun-Seung Park

Assistant Professor

Dr. Hyun-Seung Park is an Assistant Professor at Sejong University, Korea. He received his Ph.D. in Plant Science from Seoul National University in 2019, focusing on genomics and molecular breeding. His research explores the diversity of medicinal and resource plants, aiming to develop molecular markers for accurate species identification and functional trait analysis. He has published on the genome assembly of Korean mint (Agastache rugosa), discovery of plastid genes linked to albino phenotypes, comparative multi-omics in Panax species, and the impact of mitochondrial plastid DNA on DNA barcoding.

> *Recently, his work has expanded to breeding high-quality milk thistle (Silybum marianum) to enhance silymarin production integrating genomics, metabolomics, and digital phenotyping.*



Genome-to-Phenome Approaches for Chemotype Breeding in Milk Thistle

Seo yeon In[1], Rubina Ehsan[1], Jeehyoung Shim[1], Trinh Minh Vu[1], Hyun-Seung Park[1]

Department of integrative Biological Sciences and Industry, Sejong Univeristy, Seoul, Republic of Korea

Milk thistle (*Silybum marianum*) is a medicinal plant valued for its bioactive compound silymarin. In this study, we evaluated diverse individuals, including F2 and F4 populations, diverse germplasm collected globally, Korean naturalized lines, and mutant resources. Agronomic traits—such as growth dynamics, branching, bolting date, involucre width, and seed characteristics—were measured through both manual assessments and high-resolution RGB imaging. Early vegetative growth was quantified using OpenCV-based leaf area extraction, enabling detailed monitoring despite overlapping leaves during active growth phases. Environmental parameters including temperature, humidity, solar radiation, and soil moisture were recorded at one-minute intervals, providing a comprehensive understanding of stage-specific growthrequirements. Additionally, we assembled chloroplast genomes from germplasm sourced from the IPK Genebank in Germany to investigate cytoplasmic diversity. The results indicate that milk thistle possesses notably low chloroplast genomic variation worldwide, implying a narrow cytoplasmic base across global collections. Together, these multimodal datasets provide a solid foundation for functional trait discovery and breeding of high-silymarin cultivars.

This work was supported by the National Research Foundation of Korea (NRF) grant funded by the Korea government (MSIT) (No. RS-2024-00410854), and by the Korea Agriculture Technology Promotion Agency (KOAT) grant funded by the Korea government (RDA) (No. RS-2025-02218592).

Dr Jinmi Yoon

Assistant Professor

Jinmi Yoon is currently an Assistant Professor in the Department of Biological Sciences at Inha University, where research focuses on crop domestication traits and developmental genetics. Doctoral research at POSTECH centered on elucidating the molecular and genetic mechanisms underlying seed shattering in rice, leading to the identification of key regulators of abscission zone development.

Current research integrates genomics and multi-omics approaches, together with AI-driven genomic analyses, to identify critical genetic variants influencing seed development.

These efforts aim to develop precise molecular strategies for improving seed traits and enhancing crop productivity.

This work laid the foundation for a broader research program on early seed development, with particular emphasis on the hormonal and transcriptional networks that govern endosperm formation and seed quality.

Elucidating the Molecular Networks Underlying Early Seed Development in Rice

Hyeok Chan Kwon[1,2], Soo-Bin Hwang[1,2], Jang hyun Choi[2], Seong Kyu Han[1,2], Lae-Hyeon Cho[3], Jinmi Yoon[1,2]*

Improving crop productivity and resilience requires a precise understanding of the molecular mechanisms underlying seed development in rice (*Oryza sativa L.*).

Early seed development immediately after double fertilization remains poorly understood but represents a critical stage for determining grain yield and quality. To identify key regulators of early endosperm development, we analyzed the *endospermless2 (enl2)* mutant, which exhibits defective endosperm nuclear division. Transcriptome profiling of embryo sacs collected at 3 and 24 hours after pollination revealed a marked reduction in auxin-related gene expression in *enl2*, including the auxin biosynthesis gene *TAR2*, auxin transporters, and auxin-responsive genes. These findings indicate that auxin biosynthesis in the endospermis essential for early seed development. To further clarify the regulatory pathways controlling seed formation, we are identifying tissue-specific cis-regulatory regions through the integration of ATAC-seq and transcriptomic datasets, followed by functional validation to enable targeted regulation of gene expression in embryo and endosperm tissues. In addition, multi-omics approaches such as transcriptomics, epigenomics, and proteomics are being employed to define the hormonal and molecular networks active during the early stages of seed development.

This integrated framework provides new insights into the regulatory landscape of rice seed formation and offers molecular targets for precision improvement of grain traits.

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DR Lae-Hyeon Cho

Associate Professor

Lae-Hyeon Cho is an Associate Professor of Plant Bioscience at Pusan National University in Miryang, Republic of Korea. His work investigates how internal metabolic cues and external environmental signals are integrated to regulate flowering time and reproductive development in rice. Using genetic, biochemical, and chromatin-level approaches, his research has revealed post-translational and epigenetic mechanisms controlling key floral regulators, including recent insights into sucrose-mediated signaling pathways. His laboratory routinely employs genome-editing strategies such as CRISPR/Cas9 and prime editing to validate gene function and generate elite research lines. Through nationally funded projects and international collaborations, he aims to establish molecular frameworks for fine-tuning crop phenology and productivity under environmentally constrained and low-input agricultural systems.

Internal nutrient signaling by sucrose in the molecular control of rice flowering

Lae-Hyeon Cho

Department of Plant Bioscience, Pusan National University, Miryang 50463, Republic of Korea,

Rapid climate change is exposing plants to increasingly variable environmental conditions. Flowering time in rice is sensitive to external cues such as photoperiod, temperature, and abiotic stresses including drought, salinity, and nutrient deficiencies. Soil nutrient status and fertilizer inputs, particularly nitrogen, phosphorus, and potassium, further influence vegetative growth and reproductive timing by altering carbon–nitrogen balance, metabolic activity, and the expression of flowering regulators. Although many genes controlling flowering time have been identified in rice, how these diverse environmental and nutritional factors are translated into molecular changes that modulate the flowering network remains incompletely understood. Among various environmental and metabolic influences, sucrose has long been proposed as a candidate floral signal, yet its molecular role in flowering time regulation has been only partially defined. In this study, we investigated how sucrose acts as an endogenous metabolic cue that integrates external environmental conditions with internal developmental pathways. Exogenous sucrose application accelerated flowering, whereas genetic reduction of sucrose transport delayed floral induction. Mechanistically, sucrose promotes flowering by destabilizing the floral repressor Ghd7 through the action of the E3 ubiquitin ligase IPI1, resulting in enhanced activation of *Ehd1* and the florigen genes *Hd3a* and *RFT1*. These findings reveal how sucrose functions as a metabolic signal that connects environmental status with the core flowering-time network. Understanding the molecular basis of sucrose-mediated floral induction provides new opportunities for improving rice adaptation, yield stability, and resilience under rapidly changing climate conditions.

This work was supported by This study is supported by National Research Foundation of Korea (NRF) grant funded by the Korea government (MSIT) (No. RS-2024-00343462)2

Dr Szabolcs Lehoczki-Krsjak

Research Fellow

Dr Szabolcs Lehoczki-Krsjak is a Research Fellow in Rice Breeding and Genetics at Southern Cross University, working on a climate-smart rice breeding initiative aimed at transforming rice production in Australia. His research focuses on developing locally adapted pigmented rice varieties, particularly black rice for Northern New South Wales, with an emphasis on sustainable aerobic production systems.

Szabolcs brings strong commercial breeding and product development expertise to his work, ensuring research is aligned with farmer needs, industry requirements and practical variety development. He collaborates closely with industry partners and contributes to delivering resilient, climate-smart rice varieties for Australian environments.

His research integrates genetic resource characterisation, field-based speed breeding and quantitative genetics to address key challenges such as drought and cold tolerance, accelerating the development of climate-resilient rice germplasm. These efforts support the creation of high-yielding, climate-adapted varieties, including nutritionally valuable black rice genotypes.

Climate Smart Black Rice development at SCU

Szabolcs Lehoczki-Krsjak, Truong Duc Nguyen, Monaliza Magat,
Lei Liu, Tobias Kretzschmar

Rice is among the highest carbon footprint crops, due to the irrigation water required in traditional flooded production systems and the associated methane emission. Aerobic rice systems - such as the Northern Rivers dryland rice industry – use significantly less water and produce very low greenhouse gas emission. In aerobic systems, rice is grown in well saturated but not flooded conditions, demanding varieties with strong aerobic adaptation traits. Key traits include drought tolerance, which is essential in rainfed growing systems and cold tolerance, which currently limits broader adaptation of aerobic production by many growers.

To accelerate genetic improvement, we established a field-based speed breeding system allowing for selection of two generation a year under contrasting field environments. In our early nursery we select for reproductive stage drought tolerance and in our late season nursery we select for cold tolerance and resistance for rice blast, while in the normal season nursery and trial we select for agronomic traits and yield. This approach increases the number of genotypes evaluated, enhances the selection intensity and accuracy to reach higher genetic gain. We integrated this pipeline into our black rice breeding program, which focuses on developing high nutritional value whole grain black rice with outstanding anthocyanin content.

This field-based speed breeding system accelerates the identification of cold- and drought-tolerant genotypes with improved adaptability to aerobic conditions. It provides the foundation for a climate-smart black rice genetic pool that will enable the development of new water-saving low-carbon black rice varieties tailored for sustainable aerobic rice production.

Dr Bronwyn Barkla

Associate Professor

Prof. Bronwyn J. Barkla is Deputy Associate Dean of Research for the Faculty of Science and Engineering at Southern Cross University. Previous to that role she was Associate Dean of Research from 2021 to 2024 and Director of Southern Cross Plant Science from 2018 to 2021. She heads the Plant Biochemistry group in the Faculty. She received her Master's (1989) and Ph.D. (1994) in the Department of Botany at the University of Toronto and carried out Post-doctoral research in the Department of Plant Sciences (1994-1995) at the University of Oxford.

> *Her work has significantly contributed to shaping research in the field of plant membrane biology, particularly by advancing our understanding of plant salinity stress responses, membrane dynamics, and proteomics. Recent research interests include understanding the role of specialised plant cells, including trichomes and guard cells to identify key adaptive mechanisms for plant abiotic stress tolerance.*

Applications of plant proteomics to understand plant abiotic stress.

Bronwyn J. Barkla and Qi Guo

Faculty of Science and Engineering, Harvest to Health Research Cluster, Southern Cross University.

Sequestration of sodium is an important trait for plant salt tolerance. Using the halophyte Mesembryanthemum crystallinum as a model, we have been investigating the mechanisms employed by this plant to tolerate salt. Recent work has highlighted the role of endopolyploidy in most cell types including the mesophyll and modified trichomes called epidermal bladder cells. Using an Omics approach to gain insights into the processes involved; including transcriptomics, proteomics, metabolomics, and lipidomics, we have begun to map pathways and processes regulating cell enlargement, ion accumulation, DNA replication, membrane synthesis and cell wall loosening and growth that all contribute to enhanced sodium sequestration.

Dr Kwanho Jeong

Research Fellow

Dr Kwanho Jeong is currently a Research Fellow at Southern Cross University, where he leads research on phosphorus use efficiency in crops, with a particular focus on rice and macadamia. Dr Jeong holds a PhD in Plant Molecular Physiology from Southern Cross University, where he was awarded the Chancellors Medal for Outstanding
PhD Thesis.

He has extensive international research experience across Australia, France, Korea, the Philippines, and Senegal, including postdoctoral roles at INRAE and IRD in Montpellier, France. His career spans molecular biology, root development, and nutrient metabolism, with a strong emphasis on sustainable agriculture and crop improvement.

Cluster root formation in Macadamia integrifolia seedlings: responses to phosphorus and variation among grafted scions

Kwanho Jeong[1], Suzy Rogiers[2], Abraham J. Gibson[1], Jos Mieog[1], Manisha Thapa[1], Tobias Kretzschmar[1] Bronwyn J. Barkla[1] and Terry J. Rose[1]

1 Faculty of Science and Engineering, Southern Cross University, 1 Military Rd, Lismore, NSW 2480, Australia

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Cluster roots enhance phosphorus (P) acquisition in macadamia (Macadamia integrifolia), yet their development under different P levels and grafted scion/rootstock combinations is not well understood. This study examined cluster root formation in seedlings under varying soil P and evaluated differences among grafted scions on two rootstocks. Cluster roots first appeared at 42 days after planting (DAP), with low P promoting greater root number but without increasing biomass. High P application (800 mg P pot^{-1}) suppressed cluster root number by around 50%, corresponding to leaf P concentrations of ~1.05 mg g^{-1}. Root:shoot ratios increased with P supply, reflecting changes in resource allocation.

Grafted scions and rootstocks influenced cluster root development, with the H2 rootstock supporting more cluster roots than Beaumont, and scion-specific effects on leaf P observed. These results show that cluster root formation in macadamia is modulated by both P availability and genetics, offering guidance for optimising nutrient management in cultivation.

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