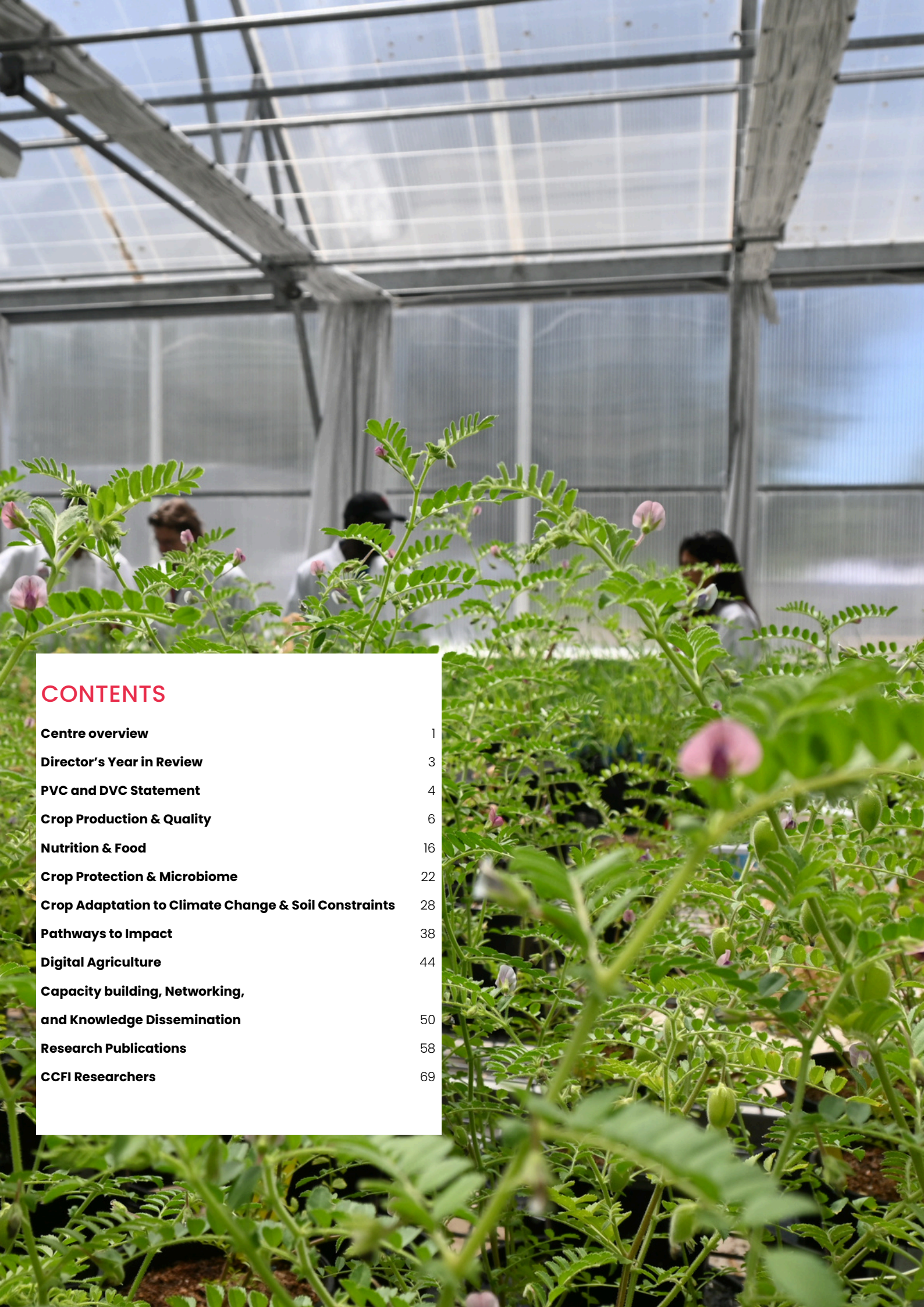




Annual Research Report

2025 Delivering research with global reach



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About the Centre for Crop and Food Innovation (CCFI)

We are focused on empowering farmers, revolutionising agriculture and securing a sustainable food future.

The Centre for Crop and Food Innovation (CCFI) at Murdoch University's Food Futures Institute is a centre of excellence for research and development in crop improvement and food technologies.

We craft cutting-edge solutions that address current and future agricultural challenges, improve farmer profitability, contribute to food security and promote environmental sustainability for future generations.

At CCFI, our research focus is grouped under six major research themes.

CCFI Research Focus

Crop Production and Quality (Led by Prof Chengdao Li)



Our research spans molecular technologies to field agronomy, encompassing molecular and physiological studies aimed at improving crop and fruit resilience, tolerance, and adaptability to biotic and abiotic stresses.

Nutrition and Food (Led by Dr Wendy Hunt)



Our research is devoted to developing technologies that extend the shelf-life of exports, identify and reduce antinutritional compounds found in foods, enable nutritional profiling of emerging foods and replace animal proteins with plant proteins to enhance the value of food products.

Crop Protection and Microbiome (Led by A/Prof Kirsty Bayliss)



We use new technologies to improve our understanding of the interactions between crop pests, diseases and their respective host plants. This research enables us to develop strategies and novel methods of improving disease and pest resistances.

Crop adaptation to climate change and soil constraints (Co-led by Prof Richard Harper and Emeritus Prof Richard Bell)



Our expertise in soil, water and biodiversity management enables us to find and implement innovative solutions to the challenges of climate change and poor arability.

Pathways to impact (Led by Prof Michael Jones)



We routinely collaborate with key sector stakeholders to advance agricultural outcomes. This includes engaging with community, advocating for vocational training and contributing to sound, evidence-based government policy that delivers best practice.

Digital Agriculture (Co-led by Prof Ferdous Sohel and Dr David Berryman)



Through the use of predictive modelling, data analytics and process automation, we anticipate changes in weather patterns, plant/animal behaviours and streamline production processes to increase yield and profitability.

Capacity building, networking and knowledge dissemination (Led by Anu Chitikineni)



We share knowledge and actively seek international collaboration and partnerships that benefit global, national and local research systems. CCFI and SABC routinely

“

I am proud to lead a Centre which is dedicated to developing cutting-edge technological solutions that address the agricultural challenges of the future.

Our pioneering research has an international reputation for embracing new technologies and securing investments in crop agriculture and we will continue to diligently pursue our primary goals of empowering farmers, revolutionising agriculture and securing a sustainable food future.”

”

Professor Rajeev Varshney FRS FAA

Our Approach

Ingenious genomics research

CCFI is dedicated to empowering farmers and enhancing their competitive edge in the global market. Our world-class facilities are leading the way towards improved crop genomics, genetics, molecular biology, and bioinformatics.

Our state-of-the-art sequencing and high-performance computing facilities enable the development of extensive genomic resources, including reference genomes, pangenomes, markers, superior haplotypes, candidate genes and genotyping platforms.

These tools are crucial for both fundamental and applied research aimed at crop improvement. Our multidisciplinary approach enables in-depth exploration of trait biology and offers genetic solutions and advanced pre-breeding technologies to breeders.



Innovative agricultural biotechnology

Our extensive expertise and multidisciplinary approach empower us to address critical challenges faced by Australian farmers, devising innovative solutions to enhance crop yield, improve quality, and increase tolerance to biological and environmental stresses.

Using cutting-edge genetic engineering methods, we employ recombinant DNA technology to develop improved crop varieties.

Our research also focuses on non-GM enhancements in yield and quality, as well as on reducing losses from pests, diseases, and environmental conditions.

We work towards harmonising Australian genetic engineering regulations while promoting consumer awareness and acceptance of genetically engineered crops to ensure better food outcomes for all.



Inventive agri-tech and food technologies

Our teams of scientists, engineers, and industry experts collaborate to unlock crop potential, employing advanced techniques, such as remote sensing, robotics, and real-time sensors for crop and soil monitoring.

Digital technologies, supported by advanced analytics, are providing practical solutions for Australian growers, aiding informed decisions on agricultural inputs, pest and disease management.

Precision agriculture, guided by real-time data and integrated systems, is revolutionising Australian farming, leading to increased yields, optimised input efficiency, reduced costs, and enhanced environmental protection.

Advances in food and nutrition science add value to products through research on extending export shelf life, minimising anti-nutritional compounds, and substituting plant proteins for animal proteins.



Director's overview



As Director of CCFI and SABC, I am proud to present the 2025 Annual Research Report and reflect on what has been an especially productive year across both Centres.

Through the work of our researchers and collaborators, CCFI and SABC continue to deliver translational agricultural research that increases crop productivity, addresses some of the most significant stresses on our crops, and ensures we play an active role in Australia's continued agricultural success story.

While this has been a year of many highlights, one area of focus that I believe will have lasting significance has been our development of comprehensive genomics resources for key commercial crops. In 2025, our researchers led efforts to construct pangenomes for five leading Australian crops, namely wheat, barley, oat, chickpea and peanut.

Given that pangenomes provide a complete set of genes found across all individuals of a species, these resources significantly enhance our ability to improve the actionable traits underpinning productivity, nutrition, climate resilience, and pest and disease resistance.

The pangenome tailored for Australian chickpea varieties is a resource I'm especially excited about, as it is the first of its kind and has already delivered important insights for breeders. Building on this resource, we have started introgressing the "QTL hotspot" into elite Australian chickpea cultivars to improve acid soil tolerance. This innovation is expected to facilitate the expansion of chickpea cultivation into acid soil environments, particularly across Western Australia, increasing the adoption of chickpea while contributing to more resilient, productive, and sustainable farming systems.

In terms of publications, CCFI has contributed significantly to the global research landscape, publishing more than 150 peer-reviewed papers in 2025, seven of which appeared in *Nature* and its sister journals. For a Centre of our size, this represents an extraordinary level of output covering a vast array of research themes, ranging from genomics and AI in agriculture to soil management and post-harvest food security.

Our researchers also took their work well beyond the page, organising four national and international conferences and presenting at dozens of seminars, symposia and conferences across the globe.

A particular highlight was hosting the Genome Data Analysis & Integration Workshop at Murdoch University, which brought together leading researchers from America, Canada, China, Germany, France, India, and Australia to discuss reference genome development across diverse crop species, advanced methodologies for understanding plant complexity, pan-genome exploration and analysis, and emerging bioinformatics approaches.

CCFI generated positive press in 2025, with 151 pieces of earned media in mainstream and trade press publications. From interviews with Science to coverage of our research in MSN, our work reached consumers, breeders and industry leaders in Australia, China, India, the US, and across Europe.

The SABC has also had an incredibly busy year and continues to play a pivotal role in enabling WA's biotechnology research capability. In 2025, SABC saw the number of Centre users climb to 163 in total: 39 are now full-time resident researchers, 108 are external non-resident researchers, and 16 are commercial researchers.

Our close relationship with the WA Department of Primary Industries and Regional Development (DPIRD) continues, and we're glad to have DPIRD researchers embedded at the SABC and using our facilities for their work.

To ensure that our researchers are working with the most up-to-date technology, we invested in brand new equipment in 2025, including two Thermo Fisher freezers, a QuantStudio 3 qPCR system with thermal shift software, an Absolute Q digital qPCR system, and a BMG VANTASTAR plate reader.

On the funding front, I am thrilled that CCFI has secured six new grants and investments. These include new projects focusing on pulses, canola, barley, oats, and wheat, as well as an exciting partnership with the Joint FAO/IAEA Centre of Nuclear Techniques in Food and Agriculture, in which CCFI will provide training to enhance the scientific and technical capabilities of researchers in FAO/IAEA Member States.

We are sincerely grateful to all of our investors, including the Grains Research and Development Corporation, Hort Innovation, the Australian Research Council and the WA Agricultural Research Collaboration, for their confidence in our ability to deliver research with impact.

It would be remiss of me not to highlight the people behind CCFI and SABC's success, and we are fortunate to have such a passionate and dedicated team of researchers and administrative staff. Special mention goes to Emeritus Professor Richard Bell, who celebrated an incredible 40 years at Murdoch University in 2025, and to Dr Wendy Hunt, who was inducted as a Fellow of the Australian Institute of Food Science and Technology, a recognition reserved for members who have dedicated themselves to advancing the food industry.

I'd also like to congratulate Dr Vanika Garg and Dr Rutwik Barmukh, who received the Murdoch University Mid-Career Researcher Award and the Crawford Fund Scholar Program Award.

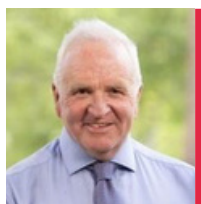
Looking ahead, CCFI has immersed itself in new approaches, tools and research techniques that we believe will be pivotal in supporting Australia's agricultural sector and enhancing global food security.

These include leveraging AI and machine learning in our genomics work, creating new open-access platforms for our genomic resources, and leading international efforts to deploy spatiotemporal omics in plant research.

In closing, I would like to thank my team for their hard work and dedication, our investors and collaborators for all their continued support, and Murdoch University's Senior Leadership Team, including the Vice Chancellor; Deputy Vice Chancellor, Research and Innovation; Pro-Vice Chancellor Food Futures Institute; and Director for Research and Innovation, for enabling all that we do at CCFI and SABC.

Professor Rajeev Varshney FRS FAA
Director, Centre for Crop and Food Innovation
Director, WA State Agricultural Biotechnology
Centre
International Chair – Agriculture & Food Security

PVC and DVC Statement



Prof Peter Davies
Pro-Vice Chancellor,
Food Futures Institute

2025 has seen CCFI embark on new research approaches, deliver outstanding science, and forge new connections across the global research community.

In January, I joined CCFI Director Professor Rajeev Varshney on a week-long visit to India, where we met senior officials at several of the nation's leading research institutes.

As one of Australia's most significant trading partners and the source of one of the University's largest international student cohorts, India offers real scope for mutually beneficial collaboration and a chance to build on our already strong bilateral agricultural, research and education relationships.

With that in mind, I am pleased to have signed MoUs with the National Institute of Plant Genome Research and Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir. We look forward to working with their respective senior leadership teams to deliver research that propels both our agricultural sectors forward.

It is one thing to publish in the world's leading journals, as CCFI researchers have done many times this year. It is another to see that science leave the lab and reach the people who can use it. The Centres' work on chickpea genomics is a fitting example, with real potential to strengthen Australia's pulse crop sector and Western Australia's contribution to it.

It is also pleasing to see research reaching well beyond our shores. From on-the-ground projects in Bangladesh to shaping GEd policy in Europe, CCFI's researchers are making their mark across Africa, Asia, the Americas and beyond.

In a year of such achievement, it is fitting to acknowledge Professor Varshney's own recognition. Following his election as a Fellow of the Royal Society in 2023, in 2025 he was elected a Fellow of the Australian Academy of Science — the only Western Australian among the 26 elected this year.

He was also named Australia's leading plant scientist in The Australian's Research Magazine, whose Top 250 Researchers list rewards research quality, impact and volume.

In closing, CCFI's defining quality this year has been its determination to ensure research delivers genuine impact. That outlook, more than any single result, is what keeps Murdoch University at the forefront of Australian agricultural research.



Prof Peter Eastwood
Deputy Vice Chancellor,
Research and Innovation

Murdoch University is committed to interdisciplinary research of global significance, guided by three strategic priorities: Sustainability; Equity, Diversity and Inclusion; and First Nations.

Few areas of our research embody the first as fully as the work of the CCFI, and few enable it as effectively as the SABC. And few challenges are as consequential, or as global, as securing the food supply of a warming world.

This report demonstrates not only the scale of CCFI's research output, considerable as it is, but the determination to ensure that science reaches the growers, breeders and consumers who can put it to use.

That determination is matched by genuinely groundbreaking work. Whether developing the first pangenome for Australian chickpea, joining a global consortium to build an open-access, whole-life-cycle single-cell atlas of wheat, or unveiling the first chromosome-scale genome of a wild barley species, CCFI has continued to prioritise research that matters on both a local and global scale.

I am also pleased to see CCFI not only embrace but lead the adoption of pioneering approaches in plant science. Spatial omics, for example, has predominantly been confined to medical and clinical research; CCFI is now at the forefront of bringing this revolutionary technique to crop research.

I would also like to acknowledge the people whose talent makes this possible. I warmly congratulate Professor Rajeev Varshney on his election as a Fellow of the Australian Academy of Science (AAS) and on his recognition as Australia's leading plant scientist.

I am equally proud of our early- and mid-career researchers, and of long-serving colleagues such as Emeritus Professor Richard Bell, whose forty years at Murdoch embody the continuity on which lasting research depends.

These researchers continue to be recognised nationally and internationally, whether presenting to learned societies such as ATSE and the Australian Academy of Science or being selected for programs run by organisations that support international agricultural research, such as the Crawford Fund.

A common thread throughout this report is the conviction that good science is measured by what it changes. That conviction is what keeps Murdoch University going from strength to strength, and I extend my sincere thanks to every researcher, collaborator, stakeholder and investor who shares this vision.





Crop Production and Quality

Building a global genetic blueprint for climate-resilient and high-yielding wheat

Murdoch project team:

Prof Rajeev Varshney (Project coordinator).

Collaborating Organisations:

Australia:

Adelaide University, UWA, Australian Grain Technologies, InterGrain, LongReach Plant Breeders.

International:

IPK Leibniz, Helmholtz Munich (Germany); Peking University Institute of Advanced Agricultural Sciences (China); University of Saskatchewan, University of Alberta, University of Manitoba, McGill University (Canada); Chinese Academy of Agricultural Sciences, China Agricultural University; INRAE (France); University of Bologna (Italy); Kyoto University (Japan); CIMMYT (Mexico); KAUST (Saudi Arabia); Earlham Institute, NIAB (UK); University of Maryland, USDA-ARS (USA); and many others.

Acknowledgements:

This initiative is governed by a Memorandum of Understanding among consortium partners from more than 12 countries. The authors acknowledge the generous contribution of unpublished genome assemblies and sequencing data from all participating groups.

Project Overview:

The International Initiative on Wheat Pangenome and Haplotype Catalogue (IIPGHCW) is a landmark global collaboration coordinated by Prof Rajeev Varshney, Dr Martin Mascher (IPK Leibniz), and Prof Manuel Spannagl (Helmholtz Munich).

The initiative brings together leading wheat scientists and major breeding programs from more than 12 countries, including Australia, Germany, Canada, China, Italy, Japan, Switzerland, Mexico, Saudi Arabia, the USA, the UK, and France. The overarching goal is to develop a comprehensive pangenome, global variation atlas, and haplotype catalogue for hexaploid (AABBDD) bread wheat, and to use these resources to reveal the genetic determinants of wide adaptation, climate resilience, and key agronomic traits across diverse breeding programs and environments worldwide.

To achieve this, the consortium has generated two major datasets: nearly 150 high-quality chromosome-scale genome assemblies from 26 countries.



IIPGHCW Consortium members met to discuss progress and next steps

The team used long-read PacBio HiFi, Hi-C and Omni-C technologies to deliver whole-genome resequencing data at 15x depth for 1,200 diverse wheat lines originating from 46 countries across six continents.

Australia has led the largest national contribution, delivering all 28 genome assemblies and the entire 1,200-line resequencing dataset.

Key Highlights:

- 146 high-quality chromosome-scale wheat genome assemblies from 26 countries, representing the most comprehensive wheat genomic resource ever assembled.
- Whole-genome resequencing data generated for 1,200 wheat lines from 46 countries at 15x depth, organised across five panels covering elite cultivars, landraces, pre-breeding materials and introgression lines, with over 62 to 95 million SNPs and indels identified per panel.
- Pangenome construction under way to capture core and dispensable gene space, structural variants, presence-absence variants, copy number variants, and transposable element insertions across all 146 assemblies spanning the A, B and D subgenomes of hexaploid wheat.
- Pan-GWAS analyses planned to incorporate SNPs, orthogroup presence-absence variation, copy number variation, and structural variant haplotypes to dissect adaptation, yield stability, and disease resistance across global germplasm.
- A publicly accessible visualisation portal and data resource will be developed to deliver breeder-ready markers, haplotype catalogues, genome browsers, and analysis tools to the global wheat community.

Impact and Applications:

This initiative will deliver the most powerful and comprehensive genomic resource ever built for the world's most widely grown cereal crop.

By capturing the full scope of genetic diversity across elite cultivars, landraces, pre-breeding lines, and introgression materials from every major wheat-growing region, the pangenome will transform the ability of breeders and researchers to identify and deploy genes for climate resilience, disease resistance, yield stability, and end-use quality.

For Australia specifically, the initiative positions Murdoch University and Australian wheat research at the forefront of global genomics-enabled breeding.

The 1,200-line resequencing panel, which includes two years of phenotypic data for up to 51 traits collected at Australian field sites, will directly inform genomic selection and marker-assisted breeding in Australian wheat programs.

Breeder-ready markers and haplotype catalogues derived from pan-GWAS will accelerate variety development, reduce breeding cycle times, and support the identification of adaptation architectures suited to Australian environments.

The open-access data portal will ensure that all resources are freely available to the global community, maximising long-term impact for food security and agricultural resilience in the face of climate change.

Increasing wheat nitrogen use efficiency through improved genetics

Murdoch project team:

Prof Rajeev Varshney (Project lead), A/Prof Reyazul Mir, Dr Vanika Garg, Anu Chitikineni, Dr Vikas Kumar Singh, Devshree Singh, Saliah Gul Jabeen.

Collaborating Organisations:

WA Department of Primary Industries and Regional Development, The University of Western Australia, Australian Grain Technologies, Analytics for the Australian Grains Industry – Curtin University.

This research is supported by the Grains Research and Development Corporation (Project code: UMU 2404-003RTX) and the WA Agricultural Research Collaboration.



Prof Rajeev Varshney inspects progress of NUE glasshouse trials at Murdoch University

Project Overview:

Nitrogen fertiliser is essential for achieving high wheat yields and grain protein content, yet much of the applied nitrogen is not efficiently used by the crop.

Cereal crops take up less than 40% of applied nitrogen, and only about one-third ends up in the grain. This inefficiency increases production costs and contributes substantially to greenhouse gas emissions in global and Australian grain farming systems.

This five-year, multi-partner project, supported by GRDC and WAARC, is addressing this challenge by identifying, validating, and deploying genetic factors that improve nitrogen use efficiency without compromising yield. It is designed to both identify the genetic basis of improved nitrogen use efficiency (NUE), and convert that knowledge into practical tools and pre-breeding material for Australian wheat breeders.

The multidisciplinary research team brings together complementary strengths in genetics, genomics, field phenotyping, physiology, biochemical analysis, and statistical genetics.

A major foundation for the work is earlier GRDC-supported research that developed six doubled-haploid wheat populations and identified 37 QTLs linked to NUE, grain yield, and grain protein content, grouped into 14 QTL clusters across 10 chromosomes. These prior findings provide the platform for selecting major-effect loci that improve NUE and/or grain protein content without reducing yield.

From there, the current project aims to discover causative alleles, understand their biological function, and develop breeder-ready molecular markers and improved germplasm.

Key Highlights:

During 2025, the project made substantial progress in both field validation and pre-breeding deployment.

Field trials were expanded across key Australian wheat-growing environments, including Northam and Eradu in Western Australia, Roseworthy in South Australia, and Collingullie (Wagga) and Sunville (Narrabri) in New South Wales.

These sites were selected to represent a broad range of production conditions and to test the consistency of nitrogen use efficiency-related traits across environments.

In addition to multi-location testing, selected trials were conducted under two nitrogen regimes, NI00 and N50, enabling evaluation of wheat responses under contrasting nitrogen supply and strengthening validation of target loci under realistic agronomic conditions.

Earlier field datasets had already demonstrated strong environmental effects on grain yield and grain protein content, and the expanded 2025 trials added further depth to this multi-environment validation platform.

Progress in 2025 also extended to the physiological and biochemical dissection of nitrogen efficiency.

Detailed studies on selected wheat lines generated data on nitrogen assimilation, nitrogen remobilisation, enzyme activity, biomass production, canopy nitrogen and grain protein composition.

These results added an important mechanistic layer to the project by helping explain why some lines perform better than others under varying nitrogen conditions. At the same time, high-throughput phenotyping approaches, including canopy-based measurements, were further developed to improve the efficiency of NUE assessment in the field.

A major breeding milestone in 2025 was the continued introgression of two priority QTL clusters into five elite Australian wheat backgrounds: Ironbark, Leverage, Shotgun, Sunmaster, and Sundancer. These included QTL Cluster 1_2B on chromosome 2B and QTL Cluster 2_2D on chromosome 2D. Cluster 1_2B was prioritised because it contains six QTLs associated with NUE, grain protein content and grain yield, with relatively strong phenotypic effects. Cluster 2_2D was selected because it carries two QTLs linked to NUE and grain yield and has also shown stable performance across relevant environments.

Together, these two clusters represent some of the most promising genomic regions identified in the project for improving nitrogen-related performance without compromising agronomic value.

Increasing wheat nitrogen use efficiency through improved genetics

In parallel, genomics-based analyses, such as QTL-Seq, helped refine candidate genomic regions, while gene validation strengthened confidence in the biological significance of selected targets. These advances represent an important step toward breeder-ready markers, improved germplasm, and a clearer biological understanding of nitrogen-related traits.

Overall, the 2025 progress shows that the project has matured into a fully integrated pipeline in which field data are used to validate genetic effects, physiological studies clarify trait function, genomic analyses refine candidate regions, and breeding activities translate these discoveries into applied outcomes.

Impact and Applications:

The main application of this project is in wheat breeding. By generating validated QTLs, candidate genes, physiological knowledge, and breeder-friendly markers, the project is building the foundation for wheat varieties with improved NUE.

For breeders, this means more precise selection tools. For growers, it could mean varieties that maintain strong yield and grain protein with the same or lower nitrogen input, improving both profitability and resilience.

The project also has environmental significance.

Improved NUE can reduce nitrogen losses and help lower the environmental footprint associated with fertiliser use.

More broadly, the project provides a strong example of how genetics, physiology, phenotyping, and molecular breeding can be integrated to address complex agronomic traits in modern crop improvement.



Towards developing a pangenome and haplotype catalogue for yield and yield-related traits in wheat under rainfed conditions in Australia

Murdoch project team:

Anu Chitikineni (Project lead),
Prof Rajeev Varshney, A/Prof Reyazul
Rouf Mir, Prof Richard Harper, Dr Liu Xin
Dr Yan Huang.

Collaborating Organisations:

AAGI, Adelaide University,
BGI Genomics, Australian Grain
Technologies.

Project overview

Understanding the genetic basis of yield and adaptive traits under rainfed conditions is critical for developing resilient wheat cultivars suited to increasingly variable Australian rainfed production environments.

This project aims to develop a comprehensive wheat pangenome and haplotype catalogue to enable the identification and deployment of superior alleles for yield and yield-related traits.

A diverse panel of 300 wheat genotypes were selected and evaluated under rainfed conditions across three drought-prone Australian locations: Lake Grace (Western Australia), Pinery (South Australia), and Pinnaroo (South Australia). Extensive phenotyping was conducted for key agronomic and physiological traits, including days to flowering, NDVI, grain yield, thousand grain weight (TGW), grain protein content (GPC), hectolitre weight, and screenings. Substantial phenotypic variation across all traits at all sites highlighted the panel's broad genetic diversity and its suitability for dissecting complex yield-related traits.

To complement field phenotyping, all 300 genotypes were subjected to whole-genome resequencing (WGRS) at ~15× coverage. Population structure and genetic diversity were assessed using principal component analysis, multidimensional scaling, and phylogenetic analyses, revealing clear genetic stratification.

Based on these analyses, a subset of 11 representative genotypes, capturing ~90% of the total genetic variation, was selected for high-resolution sequencing. PacBio HiFi and Omni-C sequencing (~20× coverage) has been completed for all selected lines, and genome assemblies are currently in progress to support wheat pangenome construction.

2025 Field Trial Highlights

During the 2025 season, 272 genotypes per site were evaluated in replicated trials across the three locations, generating high-quality phenotypic datasets under realistic conditions.

Grain yield and protein varied markedly by site:

Pinery (yield: 0.32–1.36 kg/plot, mean 0.90 kg/plot; protein: 10.20–15.60%),

Pinnaroo (yield: 0.17–1.19 kg/plot, mean 0.62 kg/plot; protein mean 12.90%), and Lake Grace (yield: 0.12–1.54 kg/plot; protein: 8.80–14.50%).

A classic yield–protein trade-off was evident across sites, with Pinnaroo showing the highest protein despite the lowest yield.

Pinery offered the strongest balance of yield and protein consistency, while Lake Grace showed the greatest genotype × environment variability.

Impact:

Two-year, multi-location phenotypic data will be integrated with WGRS-derived SNPs and pangenome-based structural variants for genome-wide association studies (GWAS).

Candidate genes will be prioritised through functional annotation and haplotype mining to define superior haplotypes for yield-related traits. The resulting pangenome and haplotype catalogue will provide genomic resources for Australian breeding programs, accelerating development of high-yielding, resilient wheat varieties adapted to rainfed environments.



Achieving improved genetic gain for yield in chickpea, faba bean and lentil using genetic diversity

Murdoch project team:

Prof Rajeev Varshney (Project lead),
Dr Rutwik Barmukh, Dr Vanika Garg,
Anu Chitikineni, Dr Oluwaseun Akinlade

Collaborating Organisations:

Australia:

The University of Queensland;
Department of Energy, Environment
and Climate Action; Agriculture
Victoria Research; NSW Department of
Primary Industries; Chickpea Breeding
Australia; Australian Grains Genebank;
Adelaide University; The University of
Sydney; Analytics for the Australian
Grains Industry.

International:

International Center for Agricultural
Research in the Dry Areas.

Acknowledgements:

This research is supported by Grains
Research and Development
Corporation (Project code: UMU2403-
009RTX).

Project Overview:

Australia's pulse production systems
face ongoing profitability challenges,
largely due to limited genetic gains and
a narrow genetic base in cultivated
varieties.

This project addresses these
constraints by integrating diverse
germplasm with advanced genomic
and breeding technologies to
accelerate yield improvement and
enhance climate resilience.

Led by Murdoch University, this \$11.02
million multi-partner initiative aims to
achieve up to a 1.5% annual increase in
genetic gain through the application of
genomic selection, speed breeding,
and AI-assisted breeding, while
leveraging both domestic and
international genetic resources.

In 2025, significant progress was made
in developing and evaluating diversity
panels for chickpea, lentil, and faba
bean. Chickpea and faba bean
diversity panels were consolidated to
include landraces, elite breeding lines,
and wild introgression lines, ensuring
both agronomic relevance and
enhanced genetic diversity.

These panels now serve as core
resources for phenotyping, genomic
analyses, and haplotype-based
breeding. Multi-environment field trials
were conducted across five Australian
sites for chickpea and faba bean, and
three sites for lentil, capturing a wide
range of agro-climatic conditions.



CCRI drone footage of chickpea field trial at Mingenew conducted as part of the Pulses Genetic Gains Project.

The trials revealed strong
environmental influences on crop
performance, reinforcing the
importance of environment-specific
breeding strategies.

Substantial advances were also
achieved in genomics research and
germplasm enhancement. Whole-
genome resequencing generated
high-density datasets for chickpea and
faba bean, enabling genome-wide
association studies, genomic
prediction, and haplotype discovery.

These datasets will support the
identification and stacking of superior
alleles for yield and adaptation using AI
and advanced breeding approaches.

In parallel, over 750 new accessions of
chickpea, lentil, and faba bean were
imported in Australia through
collaboration with the International
Center for Agricultural Research in the
Dry Areas, significantly expanding the
genetic base available to the program
and supporting the discovery of novel
traits for productivity and stress
tolerance.

Progress was also made in building
digital infrastructure through the
development of PulseBase, a multi-
species genomics and phenomics
platform designed to integrate and
analyse diverse datasets. By combining
phenotypic data from multi-location
trials with genomic and haplotype
information, PulseBase will enable more
efficient, data-driven breeding
decisions and accelerate crop
improvement.

Impact and Applications:

By 2028, the project will deliver new
tools, knowledge, and germplasm to
Australian pulse breeding programs.

By 2032, growers across northern,
southern, and western regions are
expected to benefit from improved
pulse varieties with higher yields,
enhanced disease resistance, and
better adaptation, supporting more
profitable and resilient farming
systems.



Ultimately, we want to
develop high-yielding,
climate-resilient chickpea,
faba bean and lentil
varieties that can deliver
greater profitability to
growers across Australia.

With this investment, we can
implement modern genomic
approaches coupled with
huge genetic diversity.

Prof Raveev Varshney



Mapping oat genomes to accelerate the development of climate-resilient and high-yielding oat varieties

Murdoch project team:

Prof Chengdao Li (Project lead), Dr Tefera Angessa, Dr Viet Dang, Dr Brett Chapman, Dr Tianhua He, Dr Yong Jia, Dr Haifei Hu, Dr Penghao Wang, Dr Xiao-Qi Zhang, Dr Gaofeng Zhou.

Collaborating Organisations:

Australia:

WA Department of Primary Industries and Regional Development.

International:

IPK Leibniz (Germany); Helmholtz Munich (Germany); Technical University of Munich (Germany); (Germany) German Research Center for Environmental Health (Germany); Natural Resources Institute Finland (Finland); Brigham Young University (USA); Agriculture and Agri-Food Canada (Canada); University of Helsinki (Finland); Université Laval (Canada); Institute for Sustainable Agriculture (Spain); University of Manitoba (Canada); ETH Zurich (Switzerland); University of Arizona (USA); General Mills (USA); USDA-ARS (USA); Julius Kuehn Institute (Germany); Aberystwyth University (UK); CBGP, UPM-INIA (Spain); Cornell University (USA); McGill University (Canada); Lund University (Sweden); University of Life Sciences in Lublin (Poland); University of Toronto (Canada); University of North Carolina (USA); Viikki Plant Science Centre (Finland); University of California (USA); Martin Luther University (Germany); Canadian Grain Commission (Canada); PepsiCo (USA); Shandong Agricultural University (China); German Centre for Integrative Biodiversity Research (Germany).

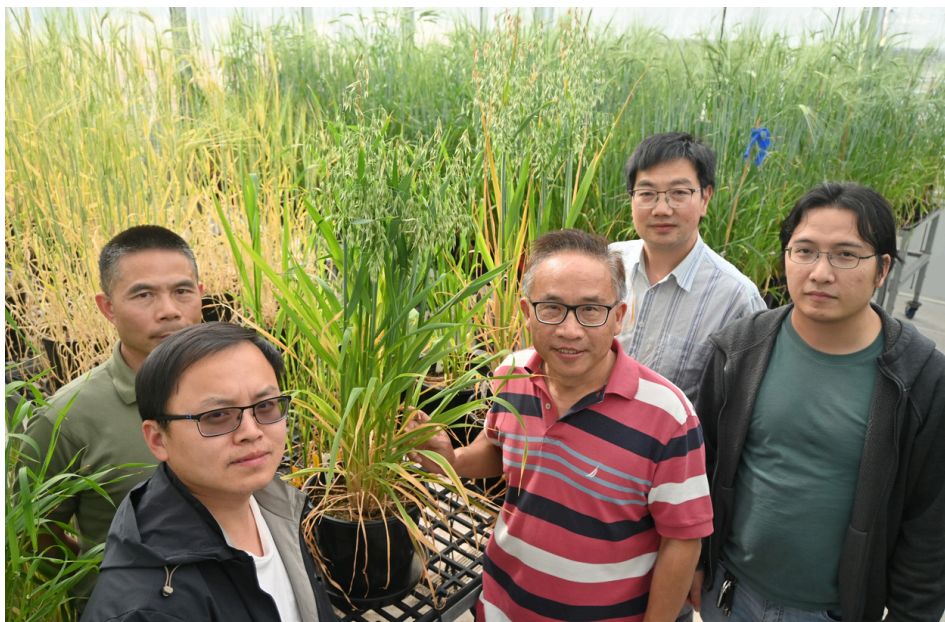
Acknowledgments:

This research is the result of a joint effort by research teams in the PanOat Project, including the Western Crop Genetics Alliance (WCGA). The Australian arm of the project is jointly funded by the GRDC (Project code UMU2003-002RTX), the WA Oat Industry partnership, and DPIRD.

Project Overview:

Oats are an important crop with many health benefits and diverse applications.

However, their complex genetic structure, featuring six sets of chromosomes derived from three ancestral species, has made oats especially challenging for researchers to analyse.



WCGA researchers Dr Tianhua He, Dr Yong Jia, Prof Chengdao Li, Dr Gaofeng Zhou and Dr Viet Dang inspect oat crosses in the GRDC Grains Precinct glasshouse at Murdoch University

An international research team has successfully decoded the pan-genome of 33 oat lines, mapping their full genetic diversity.

The findings offer unprecedented insights into oat genetic diversity in Australia and abroad, identifying key traits responsible for oat yield, plant health, and environmental adaptability, and provide leverage to breed more resilient, higher-yielding oats facing pressures from a changing climate.

The Western Crop Genetics Alliance (WCGA), led by Director and Murdoch University's Centre for Crop Innovation Research Theme Leader, Professor Chengdao Li, revealed the genomic composition of the Australian oat and uncovered the genomic mechanism for oat adaptation to Australia's unique environment.

Key project highlights:

The research team mapped the full genetic diversity of 33 oat lines, including cultivated, landrace, and wild species.

This led to the identification of genes responsible for yield, environmental adaptation (drought/heat tolerance), and health benefits (high fibre, gluten-free), which will enable the development of superior varieties.

The team also found that structural variations in the genome affect genes controlling flowering time and that gene loss in one subgenome is often compensated for by other gene copies.

Importantly, the project has highlighted that wild oat species hold untapped potential for disease resistance and stress tolerance.

Impact and Applications:

The project provides invaluable insights to accelerate the development of climate-resilient and high-yielding oat varieties.

By integrating genomic data with breeding innovations, it equips researchers and breeders with tools to address future challenges in food security and sustainable agriculture.

The findings are already being used to transfer elite traits into new, high-performance Australian oat varieties.

This research was presented in *Nature*. DOI: 10.1038/s41586-025-09676-7



This research, which sees the international oat research community come together to crack a particularly challenging genetic puzzle, transforms oats from a genetic 'black box' into a blueprint that will enable precision breeding for a healthier, more sustainable food future.



Prof Chengdao Li

Cold plasma treatment of wheat and canola for enhanced plant growth, vigour and yield

Murdoch project team:

A/Prof Kirsty Bayliss, Dr Tona Sanchez-Palacios, Dr Wendy Hunt, Onyemaechi Obiazikwor, Dr Odgerel Bumandalai, Dr Kay Howard

Collaborating Organisations:

WA Department of Primary Industries and Regional Development, South Australian Research and Development Institute, Eurofins Kalyx.

Acknowledgements:

This research is supported by the Grains Research and Development Corporation (Project code: UMU2503-004RTX)



Field trials of plasma-treated wheat have commenced in Beverley, WA

Project Overview:

Crop establishment is a critical phase in the production cycle as successful crop growth, development and yield are dependent on its success. Poor emergence and uneven establishment reduces crop growth and yield. During germination and emergence seeds may be subject to stresses such as soil water availability, and soil-borne pathogens.

Finding ways to mitigate these negative impacts and potentially increasing yields offers growers a means of reducing their reliance on chemical products and achieving greater profitability. The use of cold plasma (CP) technology in this regard offers such a solution.

CP is also known as low temperature (25°C – 100°C), atmospheric or non-thermal plasma, and is formed through the ionisation of a gas (including air) using an electric current, radio frequency or microwave energy. CP can also be fed through water to create plasma activated water, enabling liquid application.

CP is used in commercial applications ranging from microelectronic technology, biomedicine and food processing. The potential use of CP technology in crop production offers an environmentally friendly new path both for seed treatment and application during plant growth which could improve grain yield.

Relatively few field studies of CP technology in crop production have been conducted.

This project, which commenced in February 2025 will focus on the field evaluation of applying CP and plasma activated water to wheat and canola crops. Both seed treatment and CP application to developing plants will be evaluated over a range of agro-ecological production zones.

Glasshouse and small plot field trials were conducted comparing the use of cold plasma treated seed with untreated seed. Air as well as pure gases such as oxygen, nitrogen and argon were used for cold plasma generation in the glasshouse trials.

Only CP generated from air was used in the field experiments. Wheat and canola were tested in the glasshouse and wheat in the field. The impact of cold plasma on emergence, subsequent crop growth and yield and postharvest grain quality were measured.

Preliminary results suggest that crop emergence was increased in seeds treated with CP. However there was little difference in other parameters such as root or shoot biomass or yield, except for in furrow PAW.

In the glasshouse, air and nitrogen produced the best results.

Project Lead A/Prof Kirsty Bayliss and GRDC Manager of Sustainable Cropping Systems, Dr Uys Lourens at the launch of the project. The Cold plasma treatment of wheat and canola for enhanced plant growth, vigour and yield project will run until 2028.

Credit: GRDC



This investment will trial and evaluate the application of cold plasma and plasma activated water to both canola and wheat seeds and developing plants.

Through rigorous economic analysis, it aims to provide a definitive answer as to whether this technology should be implemented by growers. This includes a potential adoption pathway if implementation is economically sound.



GRDC Manager Sustainable Cropping Systems Dr Uys Lourens



Resolving the peanut mid-oleic mystery through population-specific pangenomics

Murdoch project team:

Prof Rajeev Varshney, Dr Vanika Garg.

Collaborating Organisations:

USA:

HudsonAlpha Institute for Biotechnology, University of Georgia, USDA-ARS.

Project Overview:

Peanut (*Arachis hypogaea* L.) is a globally important crop producing 54 million tonnes annually, valued for its oil and protein content.

A long-standing mystery in peanut breeding has been the existence of mid-oleic fatty acid phenotypes (55 to 75% oleic acid) that could not be explained by the known two-gene model involving *AhFAD2A* and *AhFAD2B*.

Understanding this phenomenon has been critical for the confectionery industry, which requires consistent oil quality in peanut products.

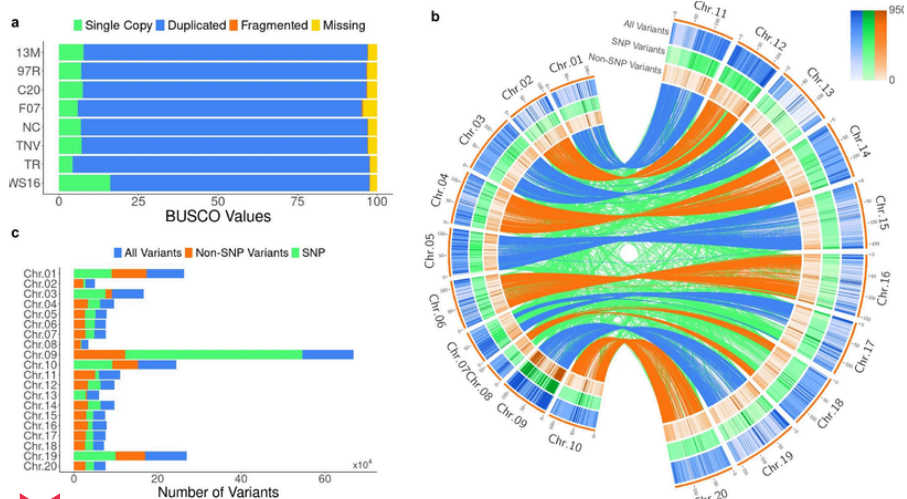
This project, led by the HudsonAlpha Institute for Biotechnology, constructed a population-specific, graph-based pangenome using the eight founder genomes of the PeanutMAGIC multiparental population.

Unlike a single reference genome or species-level pangenome, this population-specific pangenome captures all segregating haplotypes within the population, enabling precise genotyping and association analysis.

Using whole genome sequencing of 310 recombinant inbred lines, the team performed genome-wide association studies to map oleic acid content with unprecedented resolution.

This approach identified a novel third gene, *AhFAD2C*, located 1.3 Mb upstream of *AhFAD2B* on chromosome 19, which had been invisible to all previous single-reference approaches.

The study validated *AhFAD2C* using a biparental population, long-read RNA sequencing, and low-coverage long-read whole-genome sequencing, confirming its functional significance for oleic acid content.



a BUSCO values of the eight PeanutMAGIC founder assemblies. **b** Circos plot representing subgenomes of cultivated peanut with outer orange bars as scales in Mb. The distribution of all variant sites within the PeanutMAGIC pangenome is represented as a blue heatmap. **c** Number of PeanutMAGIC pangenome variants per chromosome. Blue bars represent all variants, orange bars represent non-SNP variants, and green bars represent SNP variants. Source: Nature Communications

Key Highlights:

- Constructed high-quality chromosome-level genome assemblies for all eight PeanutMAGIC founder genomes, generating a population-specific pangenome with 2,762,166 variant sites, nearly 20 times more markers than previously available for this population.
- Identified a novel third *FAD2* gene, *AhFAD2C*, located near *AhFAD2B* on chromosome 19, resolving the long-standing mystery of mid-oleic fatty acid phenotypes in peanut that the traditional two-gene model could not explain.
- Demonstrated that the population-specific pangenome detected the correct genomic location of *AhFAD2B* and the novel *AhFAD2C*, while single-reference genotyping produced a false-positive signal on chromosome 5 and mislocated the association signal on chromosome 19 by 1.1 Mb.
- Showed that six MAGIC Core lines genotyped as high-oleic using conventional *AhFAD2A* and *AhFAD2B* markers actually exhibited mid-oleic phenotypes due to recombination involving *AhFAD2C*, demonstrating the necessity of including this third gene in marker-assisted selection programs.
- Validated *AhFAD2C* as differentially expressed in developing seed tissue, with the C:ATTA haplotype showing higher transcript levels than low-oleic haplotypes, suggesting it may function as a negative regulator of other *AhFAD2* genes.

Impact and Applications:

This study fundamentally advances the understanding of peanut oil quality genetics, with direct implications for the global peanut industry.

By identifying *AhFAD2C* and the causal C/T SNP variant in its promoter region, the research provides breeders with a complete three-gene framework to accurately predict and select for high-oleic phenotypes through marker-assisted selection.

This is particularly significant for the confectionery industry, which relies on consistent oleic acid levels for product quality and shelf life.

Beyond the immediate peanut application, this work demonstrates that population-specific pangenomes provide superior accuracy over single-reference approaches for trait mapping in polyploid crops.

The methodology developed here is directly transferable to other multiparental and biparental breeding populations across crops, offering a new standard for genomic studies in complex plant genomes.

The freely available genomic resources, including the founder assemblies and pangenome, will accelerate peanut improvement globally and help address challenges of food security and nutritional quality in regions where peanut is a dietary staple.

This research was published in *Nature Communications*. DOI: 10.1038/s41467-025-67371-7

Peanut pangenome atlas uncovers structural variants driving seed size and weight

Murdoch project team:

Anu Chitikineni,
Prof Rajeev Varshney.

Collaborating Organisations:

China:

Henan Agricultural University,
Shanghai Jiao Tong University,
Shandong Academy of Agricultural
Sciences.

Acknowledgements:

This work was supported by grants from the Key Program of National Natural Science Foundation of China (NSFC)–Henan United Fund, Key Scientific and Technological Project of Henan Province, National Natural Science Foundation of China, Natural Science Foundation of Shanghai, Shanghai Key Program of Computational Biology and the National key R&D program.

Project Overview:

Peanut (*Arachis hypogaea* L.) is one of the world's most important oilseed and food legume crops.

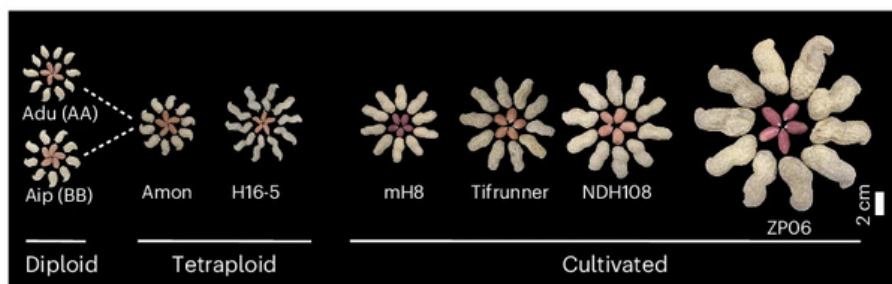
Seed size and weight are critical domestication and breeding traits that directly influence yield, yet the genomic rearrangements and structural variations (SVs) underpinning these traits had remained poorly understood due to the complexity of the allotetraploid peanut genome.

This project, led by Henan Agricultural University, generated a comprehensive peanut pangenome using eight high-quality genome assemblies spanning two diploid wild species, two tetraploid wild species and four tetraploid cultivated peanuts, supported by resequencing data from 269 accessions with diverse seed sizes.

Six of the eight genomes were newly assembled using Nanopore ultra-long, PacBio HiFi and Hi-C technologies, achieving scaffold N50 values of 134 to 148 Mb and BUSCO completeness of 98.6 to 99.4%.

The pangenome encompassed 50,097 gene families and 86,308 high-confidence SVs. Structural variant genome-wide association studies (SV-GWAS) identified 1,335 domestication-related SVs and 190 SVs linked to seed size or weight.

Functional characterisation of two key candidate genes, *AhCKX6* and *AhARF2-2*, revealed the molecular mechanisms by which SVs regulate seed expansion in peanut.



Comparison of pods from representative diploid, tetraploid and cultivated peanuts.

Source: *Nature Genetics*

Key Highlights:

- Generated six new chromosome-level peanut genome assemblies with exceptional quality metrics, enabling the most comprehensive peanut pangenome to date, encompassing 50,097 gene families across wild and cultivated accessions.
- Identified 86,308 high-confidence SVs across the peanut pangenome, revealing that subgenome A harbours significantly more SVs than subgenome B, reflecting asymmetric domestication pressures between the two subgenomes throughout peanut evolution.
- Discovered that insertions in the 3'-UTR of *AhCKX6* reduce its expression in developing seeds, leading to elevated cytokinin levels that promote early cell division and result in larger, heavier seeds in three-quarters of cultivated landrace and improved varieties.
- Showed that a 275-bp deletion in the 12th exon of *AhARF2-2* disrupts its interaction with *AhIAA13* and *TOPLLESS*, reducing suppression of *AhGRF5* and promoting seed expansion, validated through yeast two-hybrid assays, transgenic *Arabidopsis* and dual-luciferase experiments.
- Identified 1,335 domestication-related SVs and demonstrated that increasing pod size during domestication came at a cost to disease resistance, with the B subgenome showing stronger selection signals for yield-related traits during the transition from landraces to improved varieties.

Impact and Applications:

This study provides the most comprehensive genomic resource available for peanut improvement, offering breeders an unprecedented catalogue of structural variations associated with commercially important seed size and weight traits.

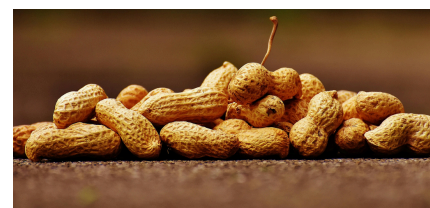
The identification of functional SVs in *AhCKX6* and *AhARF2-2*, together with the development of molecular markers for both genes, creates direct tools for marker-assisted selection to develop higher-yielding peanut varieties with larger seed sizes.

The pangenome resource is freely available to the global peanut research community and will accelerate genomic studies of other economically important traits including disease resistance, oil content and drought tolerance.

Beyond peanut, the methodological framework demonstrates the power of combining pangenomics with SV-GWAS for trait discovery in polyploid crops, offering a transferable approach for other complex legume and oilseed genomes.

Given that peanut is a dietary staple providing affordable protein and oil to hundreds of millions of people, improved yield from larger seeds has direct food security relevance at a global scale.

This research was published in *Nature Genetics*. DOI: [10.1038/s41588-025-02170-w](https://doi.org/10.1038/s41588-025-02170-w)







Nutrition and Food

Enhancing the nutritional quality of the narrow-leafed lupin by reducing anti-nutritional seed alkaloid levels

Murdoch project team:

Prof Chengdao Li (Project lead), Dr Gaofeng Zhou, Dr Bob Du, Dr Wienan Xu

Collaborating Organisations:

WA Department of Primary Industries and Regional Development, Australian Grain Technologies, CSIRO

Acknowledgements:

This research is supported by the Grains Research and Development Corporation (Project No: UMU2404-007RTX).

Project Overview:

Australian sweet lupin, more commonly known as narrow-leafed lupin, is a cost-effective protein source for animal feed, with Western Australia contributing to 80% of Australia's lupin production. Narrow-leafed lupin is effective at breaking cereal disease cycles and provides fixed nitrogen to cropping systems.

With the increase in population and growing demand for plant-based proteins, Australian pulse industry, including lupins, has a significant opportunity to expand its protein market.

However, human consumption of narrow-leafed lupin remains limited due to its antinutritional factors, such as quinolizidine alkaloids and inconsistencies in meeting alkaloid standards.

Genetic variability, environmental and management practices affect this alkaloid content, and this project addresses these issues by developing bittersweet lupin with low alkaloid in seeds but high alkaloid in vegetative tissues.

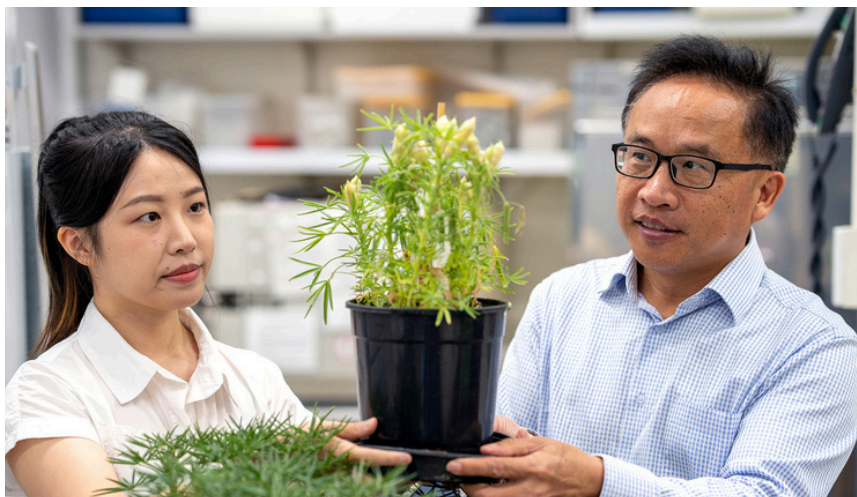
Key Highlights:

- Identification of QTLs: Two QTL (Chr.13 and 16) for lower alkaloid were identified from the KAT RIL population. And only the QTL on Chr.13 was associated with aphid tolerance.
- Candidate genes: Identified sweet gene RAP2.7, alkaloid transporter gene PUP1, normal synthesis gene LDC and CAO for alkaloid synthesis and transport in narrow-leafed lupin.
- VIGS: A transient gene silencing VIGS platform has been established for lupin gene study.
- T2T genome assembly: Completion of de novo genome assembly and annotation of the lupin variety, Rosemont.

Impact and applications:

The project provides growers with higher value lupin varieties with improved agronomic and quality traits to optimize Lupin utilisation in Australian farming systems and food production.

Its potential as a plant-based, high protein source could be a significant addition to Australia's wellness sector.



Murdoch University PhD student, Chunsheng Xiao and Professor Chengdao Li
Credit: Evan Collins/GRDC



Genetic variability, environmental factors and management practices contribute to alkaloid variations, posing a challenge for growers in producing consistent low-alkaloid lupins.

The anti-nutritional factors provide protection for plants from insects, such as aphids. The challenge is to have a lupin variety with constant low alkaloid, but good tolerance to these pests.

This project will address these challenges by developing lupin germplasm with stable, lower alkaloid seed levels and higher levels in vegetative tissue across diverse environmental conditions.



Project lead Prof Chengdao Li

Building an Advanced Genomics Platform for Australian horticulture

Murdoch project team:

Prof Rajeev Varshney (Project lead),
Dr Vanika Garg, Anu Chitkineni,
Dr Cassandra Tay Fernandez, Dr Rhys
Copeland.

Collaborating Organisations:

Queensland Alliance for Agriculture and
Food Innovation, The University of
Queensland, Queensland Department
of Primary Industries, Griffith University,
MGI Australia Pty Ltd.

Acknowledgements:

This project is supported by Hort
Innovation (AS21006).

Project Overview:

The horticultural industry is one of
Australia's largest agricultural sectors,
producing approximately 40% of the \$18
billion industry annually.

Despite its economic success,
improvements to crop productivity and
fruit quality are slow due to long
generation intervals, complex genetic
backgrounds, and limited knowledge of
complex trait architectures.

Genomic tools such as high-quality
genome assemblies have been used to
improve breeding programs and bypass
these issues by facilitating informed
decision-making and accelerating the
development of elite cultivars.

With the identification of key trait-
associated alleles, new genomic targets
for breeding are highlighted, and further
insights into domestication and
evolution can be gained.

However, there are few genomic
resources available for Australian
cultivars, and little information on the
yield and fruit quality.

This project aims to address these gaps
by developing comprehensive resources
for five fruit species: banana (*Musa* spp.),
custard apple (*Annona* spp.), papaya
(*Carica papaya*), passion fruit (*Passiflora*
spp.), and pineapple (*Ananas* spp.). So
far, a total of nine haplotype-resolved,
chromosome-length, reference-grade
assemblies and 30 reference-guided
assemblies have been developed and
annotated.

By developing this Advanced Genomics
Platform, we aim to deliver genetic
solutions and develop modern tools to
identify genetic variation for
improvement in these five horticultural
crops.



Attendees of the
Genome Data
Analysis and
Integration
workshop toured
CCFI and SABC to
see the sequencing
technology
enabling this
project

Key Highlights:

Genome assembly and annotation of horticultural crop genomes:

Chromosome-scale reference
assemblies were generated for 39
genotypes, comprising nine de novo
haplotype-resolved assemblies and
30 collapsed reference-guided
assemblies. Haplotype-resolved
assemblies were produced using
PacBio Hi-Fi long reads in
combination with high-throughput
chromosome conformation capture
(Hi-C) sequencing.

In total, approximately 443 gigabytes
(Gb) of PacBio data were generated,
with an average of 89 Gb per crop
type. Reference-guided assemblies
were produced using single-tube
long fragment reads (stLFR) and Hi-C
sequencing. A total of 1.89 terabytes
of stLFR data was generated, with an
average of 380 Gb per crop type.
Gene models were predicted using
an integrated approach combining
ab initio prediction, homology-based
inference, and transcriptome-based
approaches, yielding an average of
36,000 gene models per crop type.

Pangenomes for horticulture crops:

For each crop, a pangenome, or
super-pangenome, was constructed
using the reference genome
assemblies, identifying between
17,927–28,652 gene families per crop.
These were categorised as core
(present in all accessions), softcore
(present in all but one accession),
dispensable (missing in several
accessions), and accession-specific
gene families.

Across all pangenomes, the core
gene families were predominantly
enriched for fundamental biological
functions; while the dispensable
gene families were enriched for
more specialised roles including
stress response, transcriptional and
post-transcriptional regulation, and
metabolism.

Resequencing data for horticultural crops:

To capture broad genetic diversity,
whole-genome re-sequenced
(WGRS) and skim-seq data were
generated for diverse accession
panels and mapping populations
across all crop types.

In total, approximately four
terabytes of WGRS data were
produced. Additionally, skim-seq
data were generated for 214
pineapple and 242 custard apple
mapping population lines.

Phenotyping data:

Phenotyping data were collected or
compiled for a range of agronomic
traits across all crops in
collaboration with partner
organisations.

For papaya, 31 tree and fruit traits
were measured over two seasons, in
five locations.

For custard apple, leaf and flower
traits were measured in two
biparental populations of 132 and 110
lines, respectively.

For pineapple, phenotypic data
were collected for a range of leaf
anthocyanin and morphology
metrics, and fruit traits.

For banana, tree morphology and
yield traits were compiled for 28
accessions, and disease resistance
ratings for 267 accessions.



CCFI PhD
student Shri
Hari Prasad
collects
phenotyping
data for
custard apple

Building an Advanced Genomics Platform for Australian horticulture

HortCropBase

HortCropBase, a centralised genomics platform, was developed to host the newly generated assemblies and datasets, alongside publicly available data. Each crop has its own dedicated database, where users can download assemblies and perform basic bioinformatic analyses on said databases. Core analytical tools including BLAST, JBrowse and SNP search functionality, are already available on the platform.

Impact and Applications:

This project will deliver high-resolution genomic and phenotypic resources, including pangenome assemblies and genotyping platforms, that form the foundation for breeding innovation across five key Australian horticultural crops.

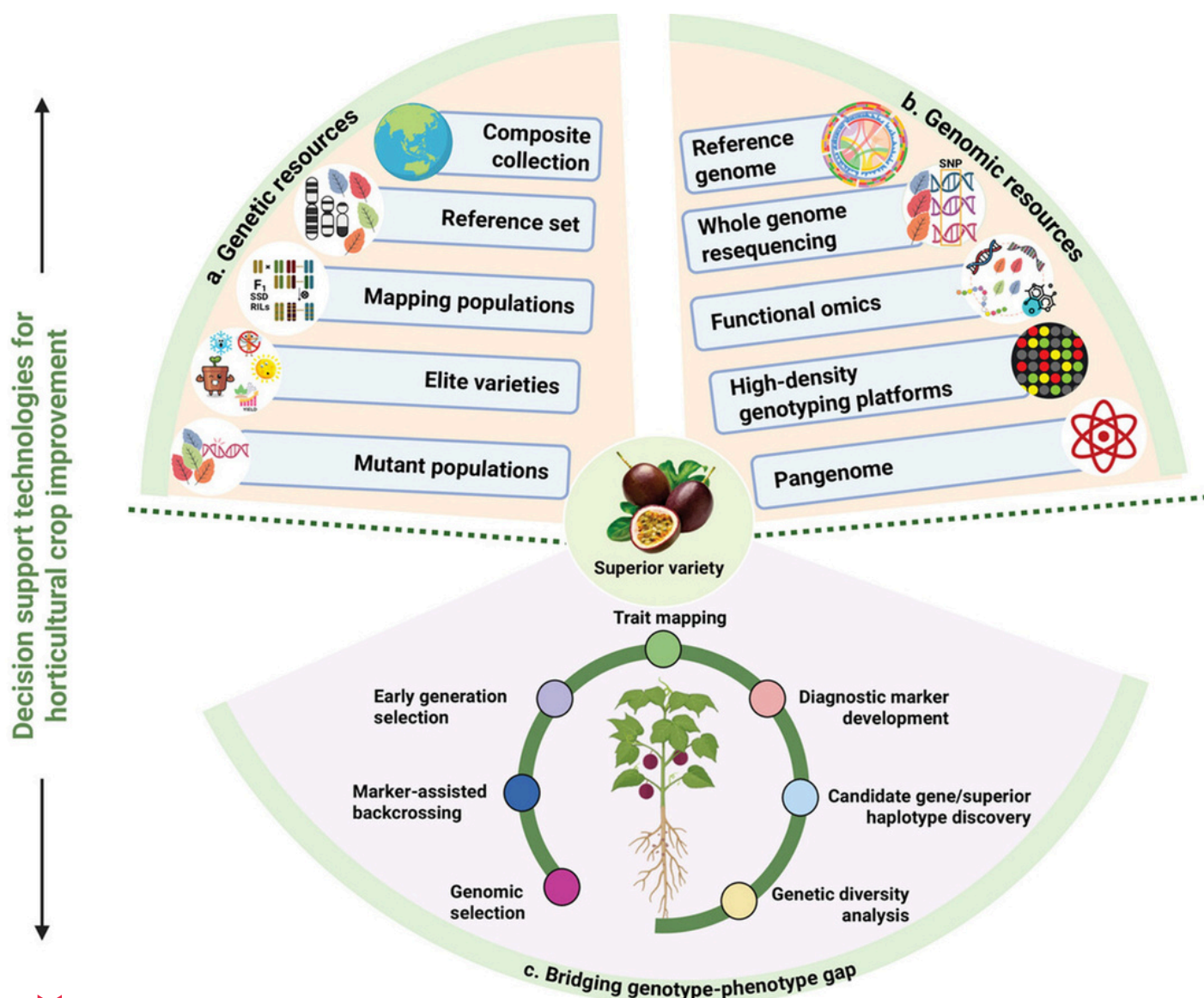
The pangenomes will provide a powerful resource for structural variant-based association studies, enabling the discovery of genetic signals underlying agronomically important traits such as yield, fruit quality, climate resilience, early flowering, and disease resistance.

By identifying molecular markers linked to these traits, the project will equip breeders with tools to accelerate genetic gains and streamline the selection of improved varieties. Customised, cost-efficient genotyping platforms will support both research and commercial breeding applications, including marker-assisted selection and genomic prediction. Given the importance of biosecurity to Australian horticulture, the genetic information generated will also support risk management for pests and diseases.

Outputs will be made accessible through a user-friendly database to ensure timely adoption by breeders and growers.

In the short term, the foundational genomic resources and biological knowledge generated will benefit translational research both nationally and internationally.

In the long term, the project will inform breeding and management strategies tailored to industry-specific needs, supporting the viability, sustainability, and global competitiveness of Australian horticultural industries.



Developing a rapid low-cost method for genotyping by sequencing

Murdoch project team:

Prof Rajeev Varshney,
Dr Vanika Garg, Anu Chitikeni.

Collaborating Organisations:

The University of Queensland, WA
Department of Primary Industries and
Regional Development, Diversity Array
Technologies.

Acknowledgements:

This project is supported by Hort
Innovation (AS22000).



CCFI PhD Student Kunal Kunal and Adj A/Prof Sultan Mia collect phenotyping data from apples grown in WA

Project Overview:

The RACE (Rapid, Accurate and Cost-Efficient) Genotyping Platform project is a newly launched collaborative initiative aimed at transforming DNA-based breeding tools for the Australian horticulture industry.

The project, led by UQ, brings together a multidisciplinary research team with direct links to breeding programs for four focus crops including macadamia, strawberry, apple and blueberry alongside Diversity Arrays Technology Pty Ltd (DARt) as the embedded commercial partner.

With over 23 years of experience delivering genotyping and sequencing services to clients across more than 80 countries, DARt provides a proven commercialisation pathway for the platform's outputs.

The project will develop an end-to-end platform integrating sample collection, genotyping-by-sequencing, target capture genotyping and skim-sequencing into a single modular and scalable workflow. A central ambition is to reduce genotyping costs to \$20 per sample in the near term, with a pathway to \$10 per sample as technologies and industry adoption mature.

This level of affordability represents a step change for horticultural breeding programs, many of which have been unable to fully leverage genomic tools due to cost constraints.

In the first year, the project will establish an operational RACE platform for targeted genotyping-by-sequencing across the four focus crops, supported by the development of an open-source field collection application and cross-genotyping method imputation software to streamline data integration.

The second phase will focus on optimising target capture genotyping and evaluating the cost-efficiency of emerging skim-sequencing approaches.

By project completion, a comprehensive suite of integrated genotyping methods will be delivered through DARt as a sustainable, industry-ready service for Australian and international horticultural clients.

Key Highlights:

- End-to-end RACE platform integrating sample collection, genotyping-by-sequencing, target capture genotyping and skim-sequencing, designed to be modular and scalable to emerging sequencing technologies.
- Target genotyping cost of \$20 per sample with a vision to reach \$10 per sample, representing a transformative reduction that will enable broader adoption of genomic tools across both large and small horticultural breeding programs.
- Open-source field collection app and cross-genotyping method imputation software will be developed to enhance data standardisation, simplify sample collection logistics and improve integration with existing breeding program datasets.
- Commercial delivery pathway secured through DARt, ensuring that project outputs translate directly into an industry-ready, sustainable genotyping service accessible to Australian and international horticultural clients.
- Four case-study crops spanning macadamia, strawberry, apple and blueberry, providing a diverse validation base that ensures the platform is applicable across a broad range of horticultural breeding systems and population sizes.

Impact and Applications:

The primary outcome of this project will be the establishment of a sustainable, low-cost RACE genotyping service for horticultural breeding and industry use.

Affordable access to DNA-based tools will transform breeding practices by enabling early-stage selection and culling of inferior material before costly field trials, resulting in reduced generation times, improved selection accuracy and accelerated delivery of superior cultivars to market. Low-cost identity verification will support accurate deployment of high-performing varieties, improving productivity and consistency across production systems.

The project aligns with Hort Frontiers Advanced Production Systems strategic priorities in plant genetics and advanced technologies, and will support broader industry goals including improved crop architecture, enhanced genetic materials and the development of new intensive production systems.

Smaller breeding programs will benefit significantly from the accessibility of the RACE platform, enabling them to integrate genomic tools and achieve meaningful genetic gains that were previously unaffordable.

The anticipated reduction in genotyping costs to as low as \$10 per sample could drive widespread adoption, positioning Australian horticulture at the forefront of genomics-enabled breeding innovation and supporting the development and deployment of superior plant varieties across domestic and international markets.

Flavour profiling of Australian oats and oat products

Murdoch project team:

Dr Bob Du, Prof Vicky Solah,
A/Prof Haelee Fenton, Dechen Tshering.

Collaborating Organisations:

Intergrain, the Grains Research and
Development Corporation

Acknowledgments:

This research is supported by the
Grains Research and Development
Project through the Oat Grain Quality
Consortium.



Project Overview:

The sensory attributes of oats — including appearance, colour, aroma, and flavour — are critical determinants of consumer acceptance and product marketability.

Although oats possess a characteristic nutty flavour, the biochemical and processing factors influencing aroma development remain incompletely understood, particularly within Australian oat products.

Industrial heat treatments used to stabilise oats generate Maillard reaction compounds and aldehydes, contributing desirable flavours, yet their quantitative relationship with volatile organic compounds (VOCs) and semi-volatile organic compounds (SVOCs) is not well defined.

This project addresses the gap between subjective sensory evaluation and objective chemical profiling.

The study aims to optimise analytical extraction methods for VOCs and SVOCs in oat flour, flakes, and oat milk alternatives. Headspace solid-phase microextraction (HS-SPME) coupled with gas chromatography-mass spectrometry (GC-MS) is used to characterise volatile compounds.

Semi-volatiles are analysed using high-performance liquid chromatography (HPLC). Industrial processing treatments are systematically documented to examine changes in aroma-active compounds across stages such as kilning, flaking, and thermal processing.

Sensory panels evaluate aroma and flavour attributes, and multivariate data fusion techniques correlate sensory perception with chemical composition.

Key Highlights:

The project is generating a comprehensive VOC and SVOC profile database for Australian oats and oat products. Early findings indicate that heat processing significantly alters aldehyde and Maillard-derived compound concentrations, intensifying nutty and roasted flavour notes. Variability between product types suggests processing conditions strongly influence aroma chemistry. Correlation analysis demonstrates measurable links between specific VOCs and sensory descriptors.

Impact and applications:

Outputs include an optimised analytical methodology for oat flavour profiling, a chemical-sensory correlation framework, and a volatile compound reference database for Australian oat products. Results are disseminated through peer-reviewed publications, industry workshops, and collaborative knowledge transfer activities. The findings support product optimisation and innovation within the Australian oat industry.

Reducing seed coat thickness and increasing protein content of narrow-leafed lupin

Murdoch project team:

Prof Chengdao Li (Project lead), Dr Gaofeng Zhou, Dr Viet Dang, Dr Weinan Xu

Collaborating Organisations:

Australian Grain Technologies, CSIRO

Acknowledgments:

This research is supported by Grains Research and Development Corporation (Project code: CSP2403-18RTX).

Project Overview:

Australian narrow-leafed lupin (NLL) is a vital pulse crop and a cost-effective protein source for animal feed.

With demand for plant-based diets rising, NLL's high protein, low starch, low fat, and low glycaemic index make it well placed for plant-based protein production, however, only 4% of Australian NLL is processed for human consumption, partly because of its thick seed coat.

This four-year investment aims to identify NLL germplasm and gene targets linked to thinner seed coats to give growers high-value varieties that meet consumer food standards and capitalise on expanding protein markets.

Key Highlights:

Three QTLs for seed coat thickness were found in a RIL population and can be used for genomic selection in breeding programs.

Mutant lines were also identified as potentially strong breeding germplasm; one reduced seed coat thickness by 20% versus current commercial varieties.

Impact and Applications:

The project gives growers higher-value lupin varieties with improved agronomic and quality traits, optimising lupin use in Australian farming and food production.



Crop Protection and Microbiome

Further discovery of new sources of septoria resistance for Australia's oat industry

Murdoch project team:

Prof. Chengdao Li (project co-lead),
Ethan Ryan, Dr Hieu Tran, Dr Manisha
Shankar (co-lead).

Collaborating Organisations:

WA Department of Primary Industries
and Regional Development, South
Australian Research and Development
Institute, The University of Adelaide,
Centre for Crop and Disease
Management (Curtin University).

Acknowledgements:

This research is supported by the
Grains Research & Development
Corporation (GRDC project code:
UMU2404-010RTX) and the WA State
Government Processed Oat
Partnership (POP).

Project Overview:

Septoria avenae leaf blotch (SLB) is a major threat to Australian oat crops, causing yield losses of up to 15%, and up to 50% in the most vulnerable varieties.

In response, the Oat Septoria Research Consortium (OSRC) was launched in mid-2025 with support from the GRDC to drive strategic disease resistance research.

Program 2 leads genetic discovery efforts in the consortium, building on the Processed Oat Partnership (POP) project's groundwork in pathogen mapping and germplasm screening. Its goal is to deliver validated, disease-resistant breeding material to the industry.

Program 2 is underpinned by achievements from the POP project, completed in mid-2025, which mapped pathogen virulence and developed resistant oat germplasm for breeding.

Genome-Wide Association Studies (GWAS) of 564 global oat lines identified key QTLs for Septoria resistance on chromosomes 1A, 1D, 2D, 4D, 6C, and 7D.

Key Highlights:

Since its official commencement in July 2025, the project has delivered a string of notable achievements that mark significant progress in the fight against Septoria avenae leaf blotch.



A primary scientific breakthrough has been the identification of novel genetic materials exhibiting high and stable resistance to Septoria.

These discoveries directly underpin the development of more resilient oat varieties, ensuring greater yield stability for growers nationwide.

A major milestone was the development of robust molecular markers linked to Septoria resistance. These markers serve as powerful tools for marker-assisted selection, enabling breeders to efficiently integrate durable resistance traits into commercial oat lines.

This advancement accelerates the breeding pipeline and boosts the precision of selecting superior germplasm.

On the methodological front, the team successfully optimised protocols for adult plant resistance screening.

Preliminary trials established an effective incubation system using detached oat leaves in humid chambers, resulting in consistent and reproducible development of pycnidia—the key indicator of Septoria infection.

This innovation ensures reliable and repeatable disease assessments under controlled conditions, laying the groundwork for future large-scale screening and virulence studies.

Impact and Applications:

The project provides invaluable insights to accelerate the development of disease-resistant and high-yielding oat varieties.

By delivering advanced germplasm to the National Oat Breeding Program, the project aims to:

- **Maximise Yield:** Eliminate the heavy yield penalties currently faced by growers, particularly in high-rainfall zones.
- **Environmental Stewardship:** Minimise the industry's reliance on chemical fungicides, leading to more sustainable farming systems.
- **Market Resilience:** Ensure a consistent supply of high-quality grain, securing Australia's reputation as a premium exporter of processed oats.

“If we can better understand the pathogen virulence mechanisms at the genomic level, it will enable improved identification of novel resistance mechanisms in the oat plant host.”

GRDC Genetic Technologies
Manager (barley, oats and
sorghum) Dr Michael
Groszmann

Source: GRDC Groundcover

Increasing stable lupin productivity through enhanced disease resistances

Murdoch project team:

Prof Chengdao Li (Project lead),
Dr Gaofeng Zhou, Prof Ferdous Sohel.

Collaborating Organisations:

Centre for Crop and Disease Management, Australian Grain Technologies, WA Department of Primary Industries and Regional Development, Australian Grain Technologies.

Acknowledgements:

This research is supported by the Grains Research and Development Corporation and the WA Agricultural Research Collaboration (Project code: DAW2305-006RTX).

Project Overview:

Narrow-leafed lupin (NLL) is valued for its nutritional content, nitrogen fixation and its role in sustainable agriculture practices. Seeds are used in both animal and human diets as a protein supplement. It forms symbiotic relationships with nitrogen-fixing bacteria in its root nodules and enriches the soil.

This species is becoming increasingly important in Australia as a fodder and green manure crop, accounting for more than 95% of all lupin grain production in Western Australia.

Western Australia is the only significant exporter of lupin grain and is responsible for about 80% of world production. However, it encounters issues such as disease susceptibility, with GRDC and WAARC jointly funding this project to address such issues, by bringing together lupin experts from DPIRD, AGT, Curtin and Murdoch Universities.



The lupin disease project team from DPIRD, MU, CCDM, AGT, GRDC, WAARC and AAGI attend the 2025 annual planning meeting

The aim of the project is to improve disease resistance of narrow leafed lupin to four prominent diseases anthracnose, stem and pod Phomopsis, sclerotinia and cucumber mosaic virus.

Key Highlights:

- Anthracnose: Identified a major QTL for anthracnose on LG_11 several other minor QTLs on LG_16 (contributes 5%). Combining both QTLs gives HR.
- Stem and pod Phomopsis: Identified a major QTL on LG_05 and a few minor QTLs from Unicrop x Tanjil RIL population. This major QTL was fine mapped to a ~200kb region 5 disease like candidate genes were identified.

- Novel sources of resistance: Phenotype screening of all four diseases has identified novel sources to resistance from a diversity set of narrow leafed lupin.
- Molecular markers: One KASP marker developed for Tanjil HR (anthracnose) and two KASP markers to target R haplotype for stem and pod Phomopsis.
- Imaging: a tool developed to facilitate variety identification and disease detection with high accuracy.

Impact and Applications:

The project will develop high throughput phenotyping methods, deploying traditional methodologies, artificial intelligence and molecular techniques to provide effective and robust disease screening tools for breeding companies and researchers.

MITC Soil Fumigation for Phytophthora disease

Murdoch project team:

Dr Bob Du, Dr Nik Radevski, Dechen Tshering.

Collaborating Organisations:

Dieback Working Group, Culford Agri Industry Precinct.

Acknowledgements:

This research is supported by the Dieback Working Group.

Project Overview:

Soil-borne pathogens like Phytophthora cinnamomi threaten agricultural productivity and biosecurity. Metham sodium is a widely used soil fumigant because it converts to methyl isothiocyanate (MITC), the active compound that controls pathogens.

However, efficacy varies with soil type, moisture, temperature, and sorption, and uneven MITC distribution can mean poor pathogen control, environmental risk, and economic loss.

This project investigates how MITC forms, diffuses, sorbs, and degrades across soil types.

The research covers (i) metham sodium-to-MITC conversion kinetics under controlled conditions, (ii) the effects of dilution, pH, temperature, and soil moisture, and (iii) MITC absorption and desorption in sand and clay.

Laboratory trials simulate field scenarios to map MITC concentration over time, supported by analytical monitoring and predictive modelling.

Key Highlights:

Soil composition strongly affects MITC retention and bioavailability. Clay-rich soils show higher sorption and slower release than sandy soils, altering exposure time and pathogen mortality. Temperature and moisture are the main drivers of diffusion rate. Together these explain much of the variability in fumigant performance.

Impact and Applications:

The project has produced validated protocols, predictive modelling tools, and industry guidance for better fumigation. Outputs include peer-reviewed papers, technical reports to industry partners, and conference presentations in plant pathology and biosecurity. The findings inform best-practice recommendations for soil treatment.

Horticultural crop microbiomes can improve growth, yield and stress tolerance.

Murdoch project team:

A/Prof Kirsty Bayliss (Project lead), Jennifer Goldberg, Dr Kay Howard, Prof Treena Burgess, Dr Penghao Wang, Prof Richard Bell, Emeritus Professor Giles Hardy, Henry Obiazikwor, Asad Zaman, Sumitra Saha.

Collaborating Organisations:

Hort Innovation, Future Food Systems CRC, Ecogrowth Australia, Melville Park, Neutrog.

Acknowledgements:

This research is supported by Hort Innovation (Project No. AS19004).

Project Overview:

The growth of crops is dependent on the microbiome, the myriad of microbes that exist within the soil and the plant itself. Microbes play a role in nutrient uptake, crop growth, and resilience to various stresses.

This project aims to select microbes that increase the yield of fruits and vegetables, as higher yields return greater profits to growers.

Our focus is tomatoes, avocados and potatoes. This year saw the completion of several field trials for this Hort Innovation-supported project.

The long-term goal is to develop new microbiome-based products that can be commercialised to increase profitability for Australian horticulture.

Key Highlights:

Across the three crops we identified:

- Core bacteria and fungi that are consistently associated with different varieties of each crop, when grown in different regions.
- The consistent presence of microbes suggests they are essential for the crop to grow, possibly having functions associated with nutrient uptake or crop growth.
- The researchers also identified microbes that appear to be associated with reduced nematode incidence in tomatoes, *Phytophthora* root rot tolerance in avocados, and heat tolerance in potatoes.

Impact and Applications:

One of the most exciting results from this project this year was the reduction in nematodes in tomatoes that were grown in soil preconditioned with biological products. The aim was to use these products to stimulate the microbiome and, in turn, increase crop yield.

The bonus was the significant impact this had on nematode infestation.

Also arising from this project was a recommendation for standardised sampling for field trials, particularly perennial fruit trees.

Research lead A/Prof Kirsty Bayliss and Dr Kay Howard have articulated this need in a review article published in the *Journal of Sustainable Agriculture and Environment* titled: *A Systematic Approach to Field Testing of Biological Products for Horticulture Is Required to Improve Food Security*.

In a statement on the project, Project Lead A/Prof Bayliss explained that the potential benefits of the team's findings could extend to key broadacre and cereal crops.

"To have a bank of microbiome data that can be easily accessed, analysed and visualised will accelerate both the discovery of microbes that can improve key crops and allow their commercialisation," she said.

"Beyond this phase, we hope to apply the technology we develop to a broader range of horticultural crops, including nuts and legumes, and focus on commercialising the most beneficial groups of microbes."



Ethyl Formate as an eradication fumigant for Khapra Beetle in shipping containers and silos

Murdoch project team:

Prof Rajeev Varshney (CI, Project reporting lead),
Dr Bob Du (PI, Technical Lead),
Prof Rob Emery (PI, Technical Guidance),
A/Prof Reyazul Rouf Mir (Liaison Officer)

Collaborating Organisations:

Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir.

Acknowledgements:

This research is supported by the Department of Agriculture, Fisheries and Forestry, Australia, and the Grains Research and Development Corporation.

Project Overview:

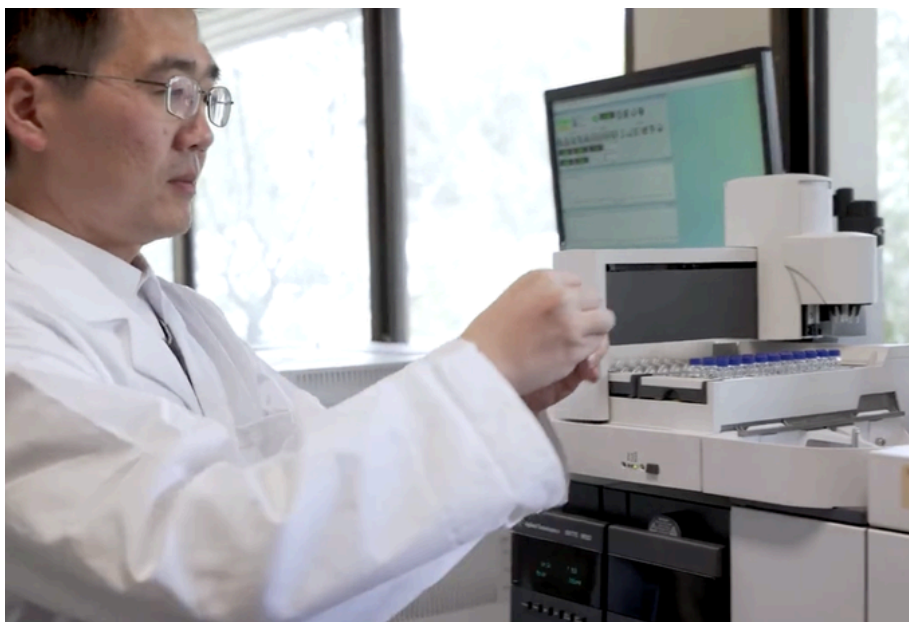
Khapra beetle (*Trogoderma granarium*) ranks among the most destructive pests of stored grain and dried plant products worldwide. It is regarded as one of Australia's highest-priority invertebrate pests for plant biosecurity and the leading priority pest for the grains industry. Capable of infesting well over 100 stored commodities, the beetle degrades grain to the point where it can no longer be used for human consumption or animal feed.

While Australia is currently Khapra Beetle free, concern over the likelihood of entry has grown.

In 2020, Australia's Department of Agriculture, Fisheries and Forestry (DAFF) reported an unprecedented rise in border interceptions, including detections in product types and from source countries not previously associated with the beetle.

Of these interceptions, at least 67 per cent were attributed to contaminated sea containers, within which the beetle can persist as a hitchhiker for years on little or no food.

Given that approximately 3 million containers reach Australian shores each year, screening every one is not practical, and establishment of this pest would carry serious economic consequences.



Dr Bob Du, whose expertise lies in post-harvest biosecurity research, is testing ethyl formate as a safer, non-ozone-depleting alternative to methyl bromide for eradicating Khapra beetles in sea containers. DAFF has stated that a widespread incursion could cost Australia \$15.5 billion over 20 years.

Addressing this threat requires not only stronger detection and border controls, but effective, field-ready treatment options that can meet international biosecurity standards.

This project is directed at that need.

Funded by DAFF and the Grains Research and Development Corporation (GRDC), this collaborative international research programme aims to develop and validate ethyl formate and nitrogen (EF + N₂)-based fumigation technology as a phytosanitary treatment for Khapra Beetle in grain storage facilities, silos, and shipping containers.

The central objective is to generate the scientific evidence and operational protocols required for national regulatory approval and international recognition under the FAO's International Plant Protection Convention (IPPC), positioning EF + N₂ as an effective and environmentally responsible alternative to conventional fumigants.

The programme is led by Prof Rajeev Varshney and Dr Bob Du at Murdoch University, who provide scientific leadership, technical oversight, project coordination, and stakeholder engagement.

Research is conducted in partnership with Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir (SKUAST-K), India, whose team is responsible for maintaining insect colonies, conducting laboratory bioassays, executing pilot and field trials, and developing treatment protocols.

Together, the team brings expertise across genetics, entomology, biosecurity, and stored-grain pest management.

The first stage of the project is complete, with a laboratory-based khapra beetle colony established at SKUAST-K for ethyl formate testing.

Subsequent stages will finalise fumigation protocols and deliver stakeholder demonstrations to support adoption and build the evidence base for future regulatory recognition both nationally and internationally.



Pic 1: Prof Barkat Hussain, from SKAUST-K's Division of Entomology, has established an insect colony for ethyl-formate and nitrogen testing.

Pic 2: Khapra Beetle larva under microscope.





Crop Adaptation to Climate Change & Soil Constraints

Determining the effects of climatic and soil properties on soil water repellency

Murdoch project team:

Prof Richard Harper, Prof David Henry, Maria Then, Naveeda Majid.

Collaborating Organisations:

The University of Newcastle, Cooperative Research Centre for High Performance Soils, Department of Agriculture, Fisheries and Forestry.

Acknowledgements:

This work was supported by the Cooperative Research Centre for High Performance Soils (CRC) and the Department of Agriculture, Fisheries and Forestry.

Project Overview:

Soil water repellency (SWR) poses a significant challenge in cropping systems, especially in regions with Mediterranean climates and sandy soils.

Soils resist wetting up following rain, leading to poor germination of both crops and weeds, as well as increased overland flow and erosion.

Various methods of tackling the problem are used, such as incorporating clay into topsoils, using wetting agents or inverting soil profile to bring easily wettable subsoils to the surface.

All are expensive, and two studentships funded by the CRC for High Performance Soils investigated the problem.



Maria Then examined the relationship between SWR and various soil and climatic factors across 355 locations in south-western Australia, in a project co-supervised by Profs Richard Harper and David Henry. SWR was strongly related to soil properties such as clay, silt and organic carbon (OC) contents.

Interestingly, SWR decreased as mean maximum temperature increased suggesting what may happen under future increased temperatures. Given the strong relationship between SWR and OC content, climate mitigation projects aimed at enhancing soil OC storage may inadvertently increase the expression and severity of SWR. Recognition of this should be included in soil carbon mitigation project protocols. This study has been published in *Catena*.

Naveeda Majid investigated the relationships of soil physical, chemical and microbiological attributes and SWR at 30 sites in South Australia in a project supervised by the University of Newcastle's Prof. Ravi Naidu and Dr Mezbaur Bahar and Prof. Richard Harper.

There were highly significant differences in soil clay and OC contents, dissolved iron and microbial activity between wettable and water repellent soils.

This study has been published in *Soil and Tillage Research*, and subsequent experiments have examined a range of microbial treatments for SWR. These will be published in 2026.

Establishing a new index to measure water stress in forests

Murdoch project team:

Thai Son Le, Prof Richard Harper, E/Prof Bernard Dell.

Collaborating Organisations:

Vietnam National University of Forestry, Vietnamese Academy of Forest Sciences.

Project Overview:

Thai Son Le, a Murdoch University PhD candidate who is a lecturer at the Vietnam National University of Forestry, has developed a new index for measuring water stress in natural forests in a study co-supervised by Profs Bernie Dell and Richard Harper.

The forests of south-western Australia span an area of 2 million hectares and are susceptible to recurring droughts and wildfires, and both may escalate with future climate change.

Controlled or prescribed burning is routinely used to reduce the intensity of wildfires, but the impact on forest water stress has not been examined.

This study found that water-stress was reduced for 7-8 years after prescribed burning and this may be a more cost-effective and strategic option to reduce water stress over broad areas compared to mechanical thinning.

The new index, namely the Infrared Canopy Dryness Index (ICDI), leverages the spectral reflectance properties of shortwave infrared channels in relation to tree canopy cover level.

Given that it uses freely available satellite data, it can be widely applied and offers remarkable potential for informed decision-making in forest resource management.



Increasing intrinsic heat tolerance of wheat through improved genetics in the source-sink relationship

Murdoch Project team:

Prof Rajeev Varshney, A/Prof Reyazul Mir, Dr Jingjuan Zhang, Zakaria Alam, Anu Chitikineni, Dr Vanika Garg, Prof Chengdao Li.

Collaborating organisations:

Western Sydney University, University of Tasmania, Australian Grain Technologies, Analytics for the Australian Grains Industry – Curtin University.

Acknowledgements:

This research is supported by Grains Research and Development Corporation (Project code: WSU2303-001RTX).



CCFI researchers Anu Chitikineni, Prof Rajeev Varshney and A/Prof Reyazul Mir assess heat-tolerance resilience in a late-sown field trial in WA

Project Overview:

Climate change-driven heat and drought stresses during reproductive stages pose a major threat to wheat productivity in Australia and globally.

This project, led by WSU, aims to identify the physiological traits, genetic loci and superior haplotypes that underpin wheat resilience to combined heat-drought (HD) stress and to deliver actionable genomic tools for breeding climate-ready wheat varieties.

To begin with, CCFI has established a diverse panel of 345 wheat genotypes that includes elite cultivars, landraces, and double-haploid lines.

These genotypes have been evaluated under controlled heat-drought stress, non-stress glasshouse conditions, and a late-sown field trial in Western Australia designed to expose plants to natural heat stress during flowering and grain filling.

Comprehensive phenotyping revealed that HD stress significantly reduced chlorophyll content, flag leaf area, biomass, grain number, seed-setting rate and thousand-grain weight.

However, a subset of genotypes consistently maintained higher chlorophyll retention, green leaf area, and grain weight, indicating that they are HD-tolerant.

Key Highlights:

Genome-wide association studies (GWAS), using a 40K SNP array, identified 124 candidate SNPs associated with 51 traits, including 78 loci specifically linked to heat and drought tolerance.

Importantly, 24 pleiotropic genomic regions were detected that controlled multiple traits across environments.

Strong genetic co-localisation was identified between stay-green traits such as chlorophyll content, leaf width and leaf area, as well as yield components that include grain number, seed-setting rate and grain weight.

Several superior haplotypes showing stable performance under stress were identified on chromosomes 1B, 3B, 5A, 5B and 5D, often colocating with key developmental genes such as *Vrn1* and *Rht*.

Physiological analyses demonstrated that the stability of chlorophyll content and flag leaf green area are reliable and early indicators of HD tolerance.

Additionally, heat-tolerant genotypes maintained photosynthetic function, experienced lower increases in leaf temperature, and incurred substantially smaller yield penalties compared with sensitive lines.

Impact and Applications:

Five genotypes, including LRPB Impala, Grenade CL Plus, LRPB Oryx, HG35 and x-262, emerged as high-confidence sources of combined heat-drought tolerance.

These lines, along with identified superior haplotypes and candidate genes, provide immediate value for marker-assisted selection and pre-breeding pipelines.

Overall, this project delivers an integrated *physiology × genomics* framework for improving wheat resilience under hot and dry environments.

Ultimately, the identified stay-green traits, validated genomic regions, and elite donor genotypes will accelerate the development of stable, high-yielding wheat varieties for Australian rainfed farming systems



Advancing genetic improvements in barley heat tolerance during flowering and grain fill

Murdoch project team:

Prof Chengdao Li (Project lead), Dr Penghao Wang, Dr Viet Dang, Dr Tianhua He, Dr Yanling Ma

Collaborating Organisations:

The University of Adelaide, WA Department of Primary Industries and Regional Development, The University of Melbourne, The University of Tasmania, InterGrain, Australian Grain Technologies, RAGT, Secobra Recherches.

Acknowledgements:

This research is supported by Grains Research & Development Corporation (GRDC Contract code: UMU2505-010RTX).

Overview:

Heat stress is a key constraint to Australia's barley production, reducing both grain yield and grain quality.

Exposure of barley crops to acute and chronic heat stresses ($> 30^{\circ}\text{C}$) during flowering and grain filling causes reduced grain plumpness, grain screenings ($< 2.2\text{mm}$), and grain loss.

It is estimated that heat stress reduces cereal yields by 13–15%, but in barley, this is expected to increase by a further 6–7% reduction with every 1°C rise in ambient temperature.

For Australia to remain a dominant global barley producer and exporter, developing new varieties that cope better with rising temperatures will be critical.

This project builds on genetic resources and foundational knowledge from previous research by six leading institutes.

The discovery phase focused on barley heat tolerance, generating significant genetic resources and insights. Now, these advances will be expanded, validated, integrated, and delivered to commercial barley breeders.

The objective is to transition existing IP from discovery to delivery, by identifying novel tolerance mechanisms, developing elite germplasm, diagnostic markers, genomic tools, and cost-effective phenotyping methods for heat stress.

The new outputs will help breeding companies develop heat-tolerant barley varieties, thereby safeguarding Australian barley production against future climate change.

Impact and Applications:

By 2030, Australian barley breeders will have access to elite germplasm and breeding tools that will enable the development of new barley varieties. These varieties are anticipated to offer at least a 5% yield increase under heat stress at either the flowering or grain-filling stage (or both).

In non-stressed conditions, these varieties will not incur any yield penalties when compared to the current highest-yielding barley cultivars.

By 2035, Australian barley growers and the industry will achieve higher productivity, sustainability, and resilience to climate change.



Project lead Prof Chengdao Li inspects the progress of barley heat trials at Murdoch University. The research team will build on the substantial genetic resources and foundational knowledge learned during the discovery phase of previous pre-breeding research efforts. In the next phase, these advances will be validated, integrated, and delivered to commercial barley breeders.

Fast tracking deployment of chickpea heat tolerance to develop chickpea varieties with improved high temperature tolerance

Murdoch Project team:

Prof Rajeev Varshney, Dr Rutwik Barmukh.

Collaborating organisations:

The University of Queensland; Flinders University; Queensland Department of Agriculture and Fisheries; NSW Department Primary Industries; The University of Sydney; Frontier Farming Systems

Acknowledgements:

This research is supported by Grains Research and Development Corporation (Project code: UOQ2402-010RTX).

Project Overview:

Chickpea is an important pulse crop in Australian farming systems, ranking highly in both production area and export value.

However, high temperature stress remains a major constraint to stable and profitable production, particularly affecting yield and seed quality.

Chickpea is especially sensitive during the reproductive stage, and late-sown crops are at greatest risk due to exposure to heat during flowering and pod set. As climate variability increases, developing varieties with improved heat tolerance has become a key priority to safeguard current production and enable future expansion.

Led by UQ, this national initiative brings together expertise in agronomy, crop physiology, plant breeding, and genetics from leading research organisations to accelerate genetic improvement in chickpea.

Multi-environment field trials are being conducted across major production zones and potential expansion areas using a diverse chickpea germplasm panel.

The project integrates advanced approaches such as crop modelling, high-throughput phenotyping, genomic prediction, and genetic simulations to identify key traits, develop improved selection tools, and generate pre-breeding material.

All phenotypic and sequencing data generated will be curated and made accessible through the "PulseBase" database.



CCFI researchers evaluate the efficacy of heat-tolerant chickpea lines at a field trial set up in WA

In close collaboration with industry partners, the project aims to accelerate the delivery of heat-resilient chickpea varieties with reduced yield losses under high temperature conditions.

Key Highlights:

During 2025, Murdoch University contributed by facilitating the sharing of whole-genome resequencing data for chickpea reference set lines included in the project's diversity panel.

This supported ongoing work in genomic prediction, chromosome segment-level haplotype analysis, and genetic simulation to inform the development of heat-tolerant breeding lines.

In addition, Murdoch University provided seed of selected reference set lines, through project partners at NSW DPIRD, to support multi-location field trials evaluating heat tolerance across environments.

Impact and Applications:

Australian chickpea growers are expected to benefit from more stable yields and improved grain quality, greater flexibility in sowing windows, and expanded production opportunities into warmer environments.

By 2027, breeders and researchers will have access to improved germplasm and enhanced genomic and phenomic tools to support the development of chickpea varieties capable of reducing yield losses by approximately 30% under high temperature conditions (day/night temperatures exceeding 32°C/20°C), including heat stress during flowering and heatwave events.

“The main output will take the form of a ‘base population’ that contains different configurations of desirable haplotypes for heat tolerance traits.

This will provide a big step towards next-generation chickpea varieties with heat tolerance and enable a deeper understanding of the benefits and trade-offs associated with different trait combinations.

Project lead Dr Millicent Smith, Senior Lecturer in Crop Physiology at The University of Queensland

Source: GRDC Groundcover

Developing high-value, acid-soil-tolerant chickpeas

Murdoch Project team:

Prof Chengdao Li (Project lead)
Prof Rajeev Varshney, Prof Richard Bell,
Dr Wendy Vance, Dr Yong Jia, Dr
Karthika Pradeep, Dr Rutwik Barmukh.

Collaborating organisations:

WA Department of Primary Industries
and Regional Development,
Department of Energy, Environment
and Climate Action of Victoria.

Acknowledgements:

This research is supported by the
Grains Research and Development
Corporation (Project code: UMU2303-
003RTX).

Project Overview:

Acid soils with aluminium toxicity are the largest constraint on Australian chickpea productivity after Ascochyta blight. Chickpea is the most acid-sensitive pulse crop, and current Australian varieties lack the genetic variation needed to breed for tolerance, limiting yield gains and expansion beyond traditional southern and northern growing regions.

Liming is the most effective remediation, but it is slow, and subsoil acidity often requires deep ripping to incorporate lime at depth.

Acid-tolerant varieties allow production to continue during amelioration. Summer heat, late-winter waterlogging, and periodic drought are likely to worsen Al^{3+}/Mn^{2+} toxicity, shrink root systems, reduce photosynthesis, and compound drought stress, even in well-managed soils.

Breeding for improved acid soils tolerance in chickpea would give Australian growers more pulse crop options, as well as facilitate the expansion of chickpea production onto soils where acid soils/ Al^{3+} toxicity currently preclude its cultivation.

Prior GRDC investment (UMU00044) identified acid-tolerant wild Cicer lines, developed recombinant inbred populations, and produced screening technologies.

By building on our previous research, this project aims to accelerate the move from discovery to deployment.

It uses genomics-assisted speed breeding to stack major and minor genes for acid soils, Al^{3+} , and Mn^{2+} tolerance into elite variety backgrounds, supported by controlled-environment screening, field validation across western, southern, and northern Australia, and diagnostic marker development to enable uptake by breeding programs.

The value of a chickpea QTL hotspot for abiotic stress tolerance will also be evaluated across these regions.



Screening early growth vigour germplasm to enhance the adaptive response to early drought in narrow-leafed lupin

Murdoch Project team:

Dr Gaofeng Zhou (Project lead),
Dr Weinan Xu, Prof Chengdao Li

Acknowledgements:

This research is supported by the
Council of Grain Growers Organisation
(Project code: 2025-2-(8))

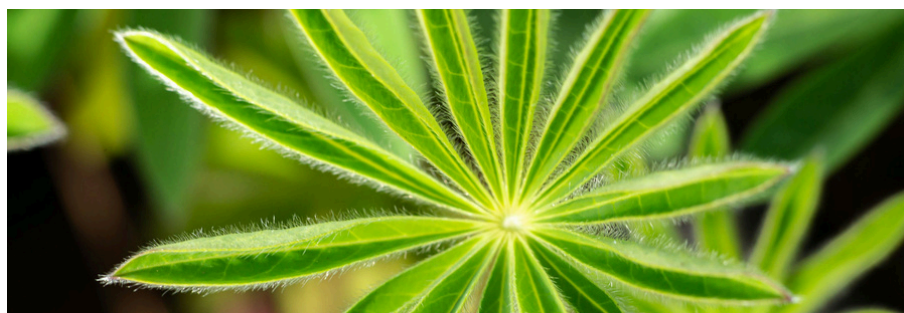
Project Overview:

Narrow-leafed lupin is generally more drought-susceptible than major cereals.

In Western Australia, lupin grain yield in 2023 declined by 62% compared to 2022, compared with ~40% reductions reported for wheat and barley. Drought-associated revenue losses in lupin are estimated at ~AUD 130 million per annum.

Early growth vigour is therefore a key target trait, underpinning improved early-season drought tolerance and enhancing weed suppression through rapid establishment.

This project aims to strengthen drought resilience in narrow-leafed lupin by developing early-vigour germplasm; validating tolerance to both early- and late-season drought; improving weed competitiveness; enabling deep sowing to better exploit soil moisture; and ultimately increasing grain yield under water-limited conditions.



Key Highlights:

A total of 36 candidate lines were identified to exhibit superior early vigour.

Early growth-vigour candidate lines were identified from our germplasm collection. Preliminary screening of 370 globally sourced narrow-leafed lupin accessions under drought conditions at Wongan Hills (May to June 2024).

Selection was based on plant height at 50 days after sowing (DAS). The candidate lines reached 15–24 cm at 50 DAS, compared with a mean of ~8 cm for the remaining 330 accessions.

These 36 lines represent material originating from 10 countries. The best 5–10 early-growth vigour lines under early drought stress conditions from glasshouse experiments.

We set up the glasshouse experiments to screen the early growth vigour to identify the top 10 lines under early drought stress.

Based on phenotypic data from 36 narrow-leafed lupin genotypes evaluated under glasshouse drought stress, we conducted an integrated assessment of drought tolerance, with particular emphasis on growth- and biomass-related traits, and ranked genotypes accordingly.

Impact and Applications:

The project provides growers with higher-value lupin varieties that exhibit improved early drought stress tolerance and early growth vigour.

The new lines may be used to improve grain yield in drought years.

Establishing the genetic blueprint of Australian chickpea to accelerate drought-tolerant breeding

Murdoch Project team:

Prof Rajeev K Varshney, Dr Vanika Garg, Dr Rutwik Barmukh, Dr Yan Huang, Annapurna Chitikineni, Dr Yong Jia, Dr Xin Liu, Prof Chengdao Li.

Collaborating organisations:

Chickpea Breeding Australia, NSW Department of Primary Industries and Regional Development, MGI Australia, Agriculture Victoria, Australian Grains Genebank, WA Department of Primary Industries and Regional Development, The University of Western Australia.

Acknowledgements:

This research is supported by the Grains Research and Development Corporation (Project codes: UMU2303-003RTX, UMU2403-009RTX).



Project Overview:

Chickpea (*Cicer arietinum* L.) is a globally important legume crop and a cornerstone of Australian agriculture.

Although Australia is the world's second-largest chickpea producer and a leading exporter, the genomic architecture of its cultivars remained largely unexplored, limiting breeding for stress adaptation and yield gains.

This project generated high-quality genome assemblies and annotations for 15 leading Australian cultivars (10 desi, 5 kabuli) using single-tube long-fragment read technology.

A pangenome was constructed to capture the complement of gene families across these cultivars, and comparative analysis identified millions of genetic variants, including many in key agronomic trait genes.

Haplotype analysis of the 'QTL-hotspot' region linked to drought tolerance and seed weight showed that superior haplotypes found in diverse global accessions are absent from current Australian cultivars.

KASP markers were developed and validated to accelerate the introduction of these haplotypes into Australian breeding programs.



CCFI Director Prof Rajeev Varshney and GRDC Senior Manager of Oilseeds and Pulses, Dr Francis Ogbonnaya, inspecting Australian chickpea field trial progress

Key Highlights:

The team generated 15 reference-grade genome assemblies for Australia's leading commercial cultivars in the first comprehensive genomic resource of its kind for the industry.

Pangenome analysis identified 34,345 gene families, including 13,986 dispensable families enriched for genes controlling disease resistance, flowering time, and seed weight.

The team catalogued ~2.5 million SNPs, ~200,000 insertions/deletions, and over 280,000 structural variants, delivering the most detailed map of genetic diversity in Australian chickpea to date.

Introducing the 'QTL-hotspot' region for drought tolerance could further improve Australian varieties, as its introgression into elite cultivars overseas has already delivered a 15–22% yield advantage.

Within the 'QTL-hotspot' region, the team identified four superior haplotypes (CaTSJT1-H2, CaTIFY4b-H2, CaLRX2-H4, and CaKIPI-H7) linked to improved seed weight and drought tolerance.

The team developed and validated KASP molecular markers that let breeders efficiently track and introduce these superior haplotypes into future Australian varieties.

Impact and Applications:

This study delivers a genomic toolkit that directly supports the GRDC's goal of improving yield stability and stress resilience. The pangenome and variant catalogue give breeders detailed insight into the genetic architecture of Australian cultivars, and the superior haplotypes identified offer a clear, actionable pathway to next-generation varieties with enhanced drought tolerance and yield.

As drought is the primary production constraint for Australian chickpea growers, these outcomes carry direct economic relevance for industry. The genomic resources have also been made freely available, supporting breeding in other regions facing similar climate challenges.

“It is fantastic to see the country's leading chickpea researchers unite to develop a significant genetic resource critical towards securing the future productivity and sustainability of chickpeas in increasingly challenging growing conditions.”

GRDC Senior Manager of Oilseeds and Pulses, Dr Francis Ogbonnaya

Genetic initiative to transform symbiotic nitrogen fixation in Australian pulse crops

Murdoch Project team:

Prof Rajeev Varshney, Dr Rutwik Barmukh, Dr Vanika Garg, Anu Chitकिनeni, Bhargava Kotte.

Collaborating organisations:

Australia:

The University of Queensland; La Trobe University; Australian National University; The University of Adelaide; New South Wales Department Primary Industries; CSIRO; Australian Grain Technologies.

International:

University of California Davis (USA).

Acknowledgements:

This research is supported by Grains Research and Development Corporation (Project code: UOQ2403-012RTX).



CCFI researchers evaluate the performance of chickpea lines under speed breeding conditions

Project Overview:

Australian pulse production is a cornerstone of the national agricultural economy, contributing more than \$1.99 billion annually and reinforcing Australia's position as a leading global exporter, with approximately 80% of production supplied to international markets.

Beyond their economic significance, pulses play a critical role in global food security by providing a sustainable, protein-rich source for human consumption and livestock feed.

Their value also extends into farming systems, where they support disease break cycles and improve weed management, while delivering one of their most important ecosystem services through Symbiotic Nitrogen Fixation (SNF).

Australia's six major pulse crops — chickpea, lentil, faba bean, lupin, field pea, and mungbean — can derive around 60% of their nitrogen requirements through biological nitrogen fixation, significantly reducing reliance on synthetic fertilisers. However, this contribution declines in nitrogen-rich soils, where plants increasingly depend on soil-derived nitrogen. In the context of rising fertiliser costs and increasing environmental concerns associated with greenhouse gas emissions, enhancing biological nitrogen fixation has become a national priority.

Strengthening this natural nitrogen system offers a more sustainable and regenerative pathway for Australian agriculture, particularly when pulses are integrated into cereal and oilseed rotations to improve soil fertility and system productivity.

Led by UQ, this \$14.69 million collaborative project brings together international expertise in nitrogen fixation research, predictive breeding, and Australian pulse breeding, genetics, and agronomy programs.

Key Highlights:

In 2025, the research team at Murdoch University achieved significant advances in pulse genomics aimed at improving nitrogen fixation efficiency.

High-quality whole-genome resequencing was completed for chickpea and faba bean diversity set lines, generating extensive genomic resources.

In chickpea, sequencing achieved approximately 89% genome coverage and identified 17.23 million variants, while faba bean analysis revealed over 1.99 billion variants.

These genetic variants provide a powerful foundation for identifying genomic regions associated with superior symbiotic nitrogen fixation performance.

To ensure these genomic resources are effectively translated into breeding outcomes, the project has developed PulseBase, a centralized and publicly accessible digital platform integrating sequence, phenotypic, and haplotype data across six major pulse crops. PulseBase provides advanced analytical and visualization tools to support genomics-assisted breeding, enabling efficient data integration and interpretation across datasets.

Impact and Applications:

By 2029, the project will deliver improved germplasm with enhanced nitrogen fixation capacity, alongside phenotyping tools and molecular selection approaches to Australian pulse breeding programs across chickpea, faba bean, field pea, lentil, lupin, and mungbean.

The long-term goal, expected by 2036, is the development of pulse varieties with at least a 10% improvement in nitrogen derived from fixation compared to current cultivars.

This will contribute to reduced reliance on nitrogen fertilisers, lowering greenhouse gas emissions and nitrogen pollution while improving system sustainability. Ultimately, the project is expected to enhance farm profitability, strengthen environmental outcomes, and improve the international competitiveness of Australian pulse production through more efficient and climate-resilient farming systems.

Deployment of QTL hotspot to develop high-value acid-soil-tolerant chickpea germplasm for Australian breeders

Murdoch project team:

Prof Rajeev Varshney, Dr Rutwik Barmukh, Anu Chitkineni, Dr Oluwaseun Akinlade, Prof Chengdao Li.

Collaborating Organisations:

Agriculture Victoria Research, WA Department of Primary Industries and Regional Development.

Acknowledgements:

This research is supported by Grains Research and Development Corporation (Project code: UMU2303-003RTX).

Project overview:

Acid soil and aluminium toxicity are significant constraints to improving pulse productivity in Australia. Chickpea is the most acid-sensitive of the major pulse crops, yet Australian varieties show very little genetic variation for tolerance, signifying a major gap that has directly limited breeding progress, especially outside the traditional growing regions in southern and northern Australia.

Liming remains the primary management tool for soil acidity, but its effectiveness is constrained by cost, slow action, and the difficulty of incorporating lime below the topsoil.

Subsoil acidity is particularly problematic, as surface applications rarely reach it and remediation typically requires deep ripping to improve lime penetration, drainage, and root access. Compounding this, drought, waterlogging, and heat stress can intensify Al^{3+} and Mn^{2+} toxicity by restricting root development, amplifying damage that management alone cannot reliably prevent.

Genetic tolerance, therefore, represents an important and enduring solution, as varieties adapted to acid soils would reduce dependence on costly interventions, enable production in more marginal areas, improve yield stability in existing regions, and serve as a buffer against stressors associated with increased climate variability.

Key Highlights:

In 2025, researchers from CCFI's Genomics, Pre-Breeding & Bioinformatics group developed a haplotype-based breeding strategy targeting the well-characterised genomic region in chickpea known as the "QTL-hotspot".

Superior alleles underlying this region were introgressed into the genetic backgrounds of eight Australian chickpea cultivars to develop improved lines with enhanced acid-soil tolerance.



Prof Rajeev Varshney showcases the project's progress to WA Chief Scientist Prof Sharath Sriram

Using marker-assisted backcrossing and speed breeding approaches, more than 100 BC2F4 lines across seven genetic backgrounds and over 50 BC3F3 lines across four genetic backgrounds were developed.

In addition, about 80 BC2F3 lines were evaluated under acidic soil conditions (pH ~4.5) at Merredin in 2025, providing an important field-based assessment of performance under stress.

Several lines showed improved performance compared with their parental lines and current commercial cultivars, particularly for grain yield, biomass, and other yield-related traits. These results highlight the value of the targeted "QTL-hotspot" region in improving adaptation to acid soils under Australian field conditions.

Impact and Applications:

Based on these outcomes, select high-performing lines will be advanced into grower demonstration trials in Western Australia in 2026, providing an important step toward on-farm validation.

This investment continues to integrate rapid germplasm improvement with genomic tools, combining major and minor genes for stress tolerance into elite Australian backgrounds. It also links controlled environment screening with multi-environment field validation across Australia, while developing molecular markers associated with tolerance to Al^{3+} and Mn^{2+} toxicity to support faster selection in breeding programs. In parallel, the broader value of chickpea "QTL-hotspot" regions for abiotic stress tolerance is being assessed across diverse Australian environments.

By 2027, Australian chickpea breeding programs are expected to have access to improved knowledge, validated tools, and pre-breeding germplasm with enhanced tolerance to acid soil constraints. This will enable more efficient incorporation of these traits into elite varieties.

Ultimately, by 2032, this work aims to expand Australia's chickpea production by 1.2 million additional hectares by delivering improved chickpea varieties that are higher yielding, disease resistant, and better adapted to acid soils across northern, southern, and western growing regions.

How wild crop relatives can unlock adaptive evolution and genetic potential

Murdoch project team:

Prof Chengdao Li (Project lead), Dr Yong Jia, Prof Rajeev Varshney, Dr Tianhua He, Dr Brett Chapman, Dr Vanika Garg.

Collaborating Organisations:

Australia

WA Department of Primary Industries and Regional Development.

International

Beijing Academy of Agriculture and Forestry Sciences, Chinese Academy of Agricultural Sciences.

Acknowledgements:

This project was supported by grants from the Natural Science Foundation of Beijing (Project code: 5222006), the Beijing Academy of Agriculture and Forestry Sciences (Project codes: JKZX202203, KJCX201907-2, KJCX20230117, KJCX20230404) and the National Natural Science Foundation of China (32101710, 31771769, 31801433).

Project Overview:

Australia's \$17.5 billion wheat and barley grain industry (ABS 2021-2022), particularly in regions like Western Australia and South Australia where dryland soil salinity affects over 2.5 million hectares, stands to benefit significantly from this research.

The lost agricultural productivity due to salinity damage is estimated at least \$519 million per year (DPIRD 2022 report, WA).

Crop wild relatives (CWRs) are invaluable for crop improvement. Among these, *Hordeum I*-genome species exhibit exceptional tolerance to alkali and salt stresses.

However, the lack of a reference genome for *Hordeum I* has significantly hindered breeders' efforts to tap the potential of this important wild species to improve salinity tolerance in current Australian wheat and barley production.

A groundbreaking study led by researchers from the Beijing Academy of Agriculture and Forestry Sciences (BAAFS) and Murdoch University in Australia has unveiled the first chromosome-scale genome of *Hordeum brevisubulatum*, a wild barley species renowned for its exceptional tolerance to alkaline and saline soils.

The study, published in *Nature Plants*, marks a significant leap forward in harnessing CWRs to combat soil degradation and climate change, with direct implications for improving barley and wheat production in Australia and globally.

Project Highlights:

The team assembled the high-quality genome of *H. brevisubulatum*, a perennial wild barley species native to saline-alkaline regions. By resequencing 38 accessions across seven related species, they identified critical genetic adaptations, including:



CCF and WCGA researchers have identified critical genetic adaptations, including the duplication of stress-response genes that enable efficient nutrient intake under alkaline stress.

Duplication of Stress-Response Genes:

Expansions in calcium-binding proteins (CaBPs) and nitrate transporters (NRT2) enable efficient nutrient uptake under alkaline stress.

Transgenic barley overexpressing these genes showed doubled biomass and improved yields in harsh conditions.

Horizontal Gene Transfer:

A fungal-derived gene, *Fhb7*, previously known for its role in disease resistance, was found to reduce oxidative stress in saline-alkaline environments.

Synthetic Crop Innovation:

The team developed *Tritordeum* (AABBII), a new hexaploid crop by replacing wheat's D subgenome with *H. brevisubulatum*'s I genome.

Tritordeum exhibited 47% higher nitrate uptake and 28% greater grain yield under stress compared to conventional wheat.

Impact and Applications:

The findings offer actionable insights for breeding programs to transform Australian Agriculture.

Not only does it offer a step toward food security and economic resilience by advancing global understanding of plant stress adaptation, it also positions Australia at the forefront of climate-smart crop innovation.

By accelerating the integration of wild barley's genetic traits into breeding programs, researchers aim to deliver new varieties within the next decade, ensuring timely support for farmers battling rising temperatures and soil degradation.

The team plans to expand field trials of *Tritordeum* across Australian saline-alkaline hotspots and explore additional CWRs for trait introgression.

This study has been published in *Nature Plants*. DOI: [10.1038/s41477-025-01942-w](https://doi.org/10.1038/s41477-025-01942-w)



Pathways to Impact



Promoting alignment or harmonisation of gene editing regulations in the Asia-Pacific region

Murdoch Project team:
Prof Michael Jones, Muhammad Adeel

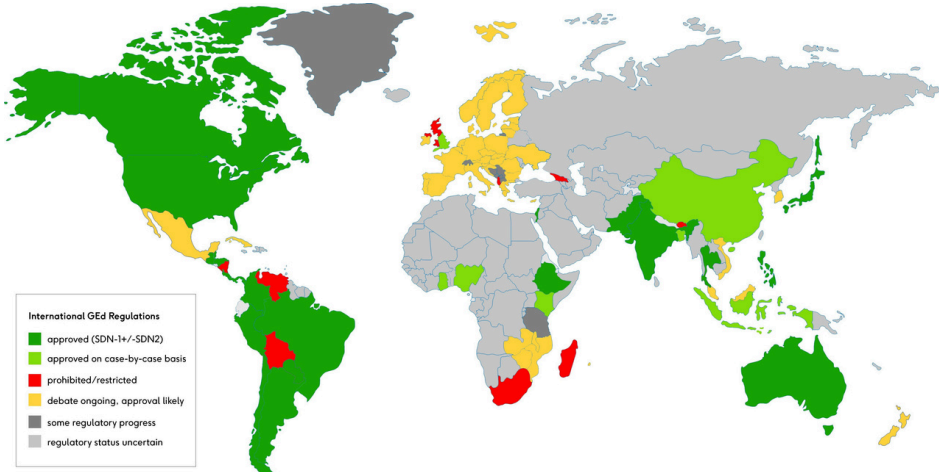
Collaborating organisations:
ISAAA, ASCA, Indian Academy of Agricultural Sciences, Industry Groups

Project Overview:

To realise the full potential of gene-editing technologies for grain and horticultural crop improvement, an exporting nation like Australia needs appropriate regulations in place in the countries that import its produce.

Over the past six years, this project has worked with scientists and regulators in importing countries to advance those regulations. Its aims are to:

- Provide scientific information on current and emerging gene-editing technologies
- Distinguish gene-edited (GE) produce from genetically modified (GM) produce
- Promote the alignment or harmonisation of gene-editing regulations across the Asia-Pacific region
- Engage with scientists, peak crop bodies, and regulators across the Asia-Pacific
- Deliver training courses regionally and nationally
- Provide Australian exporters with resources mapping the pathways to deregulation of GE produce in the Asia-Pacific
- Promote science diplomacy as a mechanism to support trade, domestically and internationally



Jurisdiction	SDN-1	SDN-2	SDN-3	Regulatory model
Australia	Exempt	GMO	GMO	Process-based
New Zealand	GMO (under review)	GMO	GMO	Process-based
Japan	Exempt	Usually exempt	GMO	Process-based
India	Exempt	Exempt	GMO	Process-based
China	Simplified	Simplified	GMO-like	Tier-risk system
South Korea	Case-by-case	Case-by-case	GMO	Process-based
Philippines	Exempt	Exempt/simplified	GMO	Process-based
Thailand	Exempt	Exempt	GMO	Process-based
Malaysia	GMO (under review)	GMO	GMO	Process-based, under review
Indonesia	Case-by-case	Case-by-case	GMO	Process-based
Latin America	Exempt	Usually exempt	GMO	Mainly product based
Canada	Trait-based	Trait-based	Case-by-case	Product-based
USA	Usually exempt	Usually exempt	Case-by-case	Product-based
EU	GMO, moving to SDN-1/NGT-1	GMO, under review	GMO	Process-based
England	Exempt	Exempt	GMO	Precision breeding
Nigeria/Kenya	Exempt/simplified	Case-by-case	GMO	Process-based
Israel	Exempt	Usually exempt	GMO	No foreign DNA criterion

Impact and Applications:

The project began with a grant from the Commonwealth Government's Department of Agriculture, Water and the Environment (DAWE, now DAFF) and included an international conference at the Shine Dome (Australian Academy of Science) in Canberra in 2023. Since then, the regional regulatory environment has moved quickly enough that the regulatory map developed under the project requires continual updating.

Prof Jones has been active on the international stage outlining the current status of GE. In 2024 he travelled to Bangkok and met with the Director-General of Thailand's Department of Agriculture, Mr Rapihat Chandarasrivongs, around the time Thailand signed its first regulation certifying genome-edited organisms for agricultural use.

A map detailing current international GE regulations. This resource is routinely updated.

In the Philippines, the Bureau of Plant Industry has issued a Certificate of Non-Coverage confirming Japan's gene-edited high-GABA tomato (Sanatech Seed's Sicilian Rouge) as non-GMO. These are among the clearest recent signs of a regional shift toward accepting gene-edited produce.

The potential of gene-editing technologies is now being recognised widely, with regulatory advances proceeding rapidly.

We maintain a map and a list of regulatory authorities to help ensure that gene-edited produce exported from Australia will be accepted. Notable advances have occurred in India, the Philippines, Japan and Thailand.

A remaining concern is that Australian regulation has, in some respects, fallen behind that of competitors and trading partners; future-proofing it will require a product-based rather than a process-based trigger for regulation.



Prof Jones travelled to Bilbao in 2025 to participate in an EU-funded workshop, in which he delivered a presentation on the current status of regulations in gene-edited (GE) plants in the Asia-Pacific region.

Building the foundations of hybrid crop development

Murdoch project team:

A/Prof Ryan Whitford (Project Lead),
Dr Thien Tran, Hitashi Aggarwal, Lien Do

Collaborating Organisations:

Australia:

CSIRO Agriculture and Food, Grains Research and Development Corporation (GRDC), University of Adelaide, The University of Western Australia, Australian National University, Agriculture Victoria Research

International:

BASF SE (Belgium)

Acknowledgements:

This research is supported by the Grains Research and Development Corporation (Project code: CSP2507-001RTX); the Australian Research Council (IM230100042); and industry partners in Australia and abroad.

Project Overview:

Achieving commercially viable hybrid crops remains one of the most powerful yet underexploited strategies to sustainably increase agricultural productivity under a changing climate.

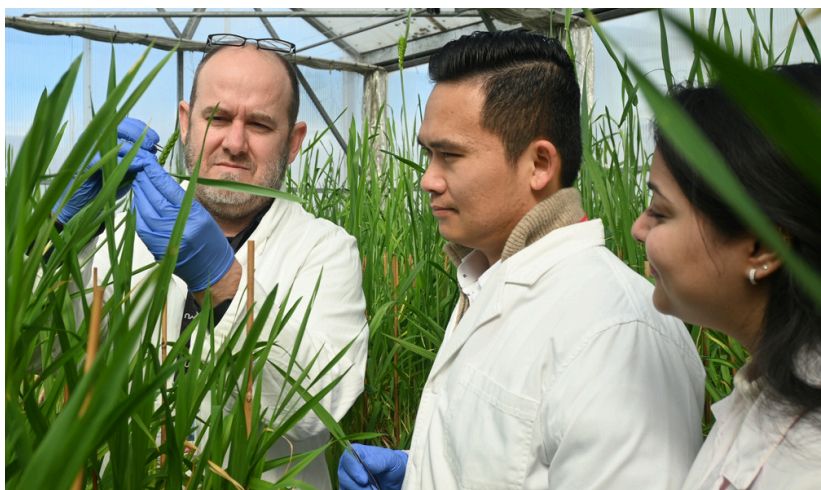
In self-pollinating species such as wheat, its floral biology presents a fundamental barrier to efficient hybrid seed production, including limited outcrossing, unstable fertility, and restricted access to genetic diversity from wild relatives.

The Crop Reproductive Biology Group, led by A/Prof Ryan Whitford, addresses these challenges by dissecting and manipulating the genetic, molecular, and developmental processes that underpin flowering, fertility, and recombination.

In 2025, the program focused on two interconnected research streams. First, it advanced understanding of **floral biology traits that control female receptivity, pollen release, and fertilisation efficiency**, with direct relevance to hybrid wheat development.

This work targets key traits, including stigma presentation, longevity, receptivity to airborne pollen, and anther extrusion dynamics, all of which are highly sensitive to environmental stresses such as heat, drought, and frost.

Second, the group developed genome editing-enabled approaches to overcome genetic barriers to crop improvement, particularly those that limit introgression breeding and recombination control in polyploids.



» A/Prof Ryan Whitford, Dr Thien Tran, Ms Hitashi Aggarwal examine wheat floral development in controlled environment glasshouse at Murdoch University

A major technical achievement has been the establishment of a transient transfection platform for CRISPR/Cas genome editing in both monocot and dicot crops, enabling rapid validation of candidate gene editing efficiency before undertaking stable transformation.

This platform accelerates trait discovery and provides a critical bridge between genomic insight and breeding application. Collectively, these activities aim to stabilise reproductive processes under climate variability and unlock new sources of genetic diversity for yield, quality, resilience, and disease resistance.

Project Highlights:

Genome editing capability established:

Developed a transient CRISPR/Cas transfection platform applicable to both monocot and dicot crops, enabling rapid editing efficiency determination before undertaking stable transformation.

International leadership in hybrid wheat:

Co-organised an international hybrid wheat alliance, culminating in a 2025 Plant Genome publication calling for global investment in floral biology traits for hybrid wheat. The initiative brings together multinational seed companies and academic leaders from Australia, Europe, the UK, and North America.

High-impact disease resistance discovery:

Contributed to a publication outlining the identification of a metacaspase-PEPR immune module conferring resistance to Fusarium head blight in wheat (The Plant Cell, 2025), linking reproductive and immune pathways to improve crop resilience.

Competitive grant success:

Secured a new GRDC-funded project (CSP2507001RTX) to unlock B-genome diversity in canola using CRISPR/Cas-mediated control of meiotic recombination, enabling precise introgression of beneficial traits from wild Brassica relatives.

Strategic international engagement:

Hosted senior delegations from the Institute of Hybrid Wheat (China) and industry leaders from global wheat breeding companies (GDM), strengthening partnerships in hybrid breeding, genomics, and pre-breeding.

Impact and Applications:

This research program delivers foundational knowledge and enabling technologies that directly address major bottlenecks in hybrid crop development and genetic gain.

By integrating reproductive biology, genome editing, and recombination control, the work supports the development of higher-yielding, climate-resilient wheat and canola varieties while reducing the cost and risk associated with hybrid seed production.

Outcomes from this program provide breeders with new molecular targets, validated traits, and practical tools to accelerate breeding pipelines and enhance long-term food security.



» Hosting Dr Eduardo Venske, the new territories wheat breeding manager for GDM (Brazil).

Improving frost resilience in wheat through targeted gene-editing (GEd)

Murdoch Project team:

Chandan Maharana,
A/Prof Ryan Whitford,
Prof Michael Jones

Collaborating organisations:

Indian Council of Agricultural Research,
Green Blueprint Pty Ltd.

Project Overview:

Reproductive frost damage is one of the most economically damaging constraints on autumn-sown wheat in Australia, with susceptibility at ear emergence, flowering and early grain set causing annual losses between A\$120–700 million.

A single event, such as the widespread frost across the WA grainbelt in September 2021, caused more than A\$100 million in damage. Another frost event in 2016 wiped about 2 million tonnes from WA's winter crop.

To survive freezing temperatures, plants undergo cold acclimation, a process in which exposure to low, non-freezing temperatures triggers physiological and molecular changes that build tolerance to subsequent frost.

This response is largely governed by the ICE-CBF-COR regulatory pathway: Inducer of CBF Expression (ICE) transcription factors act upstream to activate C-repeat Binding Factor (CBF) genes, which in turn switch on a suite of downstream Cold-Regulated (COR) genes that confer freezing tolerance.

This cascade is central to how wheat perceives cold and mounts a protective response, making it a key target for improving frost resilience.

The aim of this project is to develop a targeted genetic solution to frost susceptibility by using CRISPR/Cas9 gene-editing to manipulate the ICE-CBF-COR pathway, enhancing the expression of these key cold-response regulators so that wheat can better withstand temperatures of around -4 °C.

Because SDN-1 type edits are not regulated as GMOs in Australia and many grain-importing nations, the approach offers improved frost resilience while reducing regulatory and trade barriers.

Key Highlights:

The work is now well into its experimental phase.



In silico identification and characterisation of the ICE/CBF/COR gene network is underway, supported by two seasons of wheat cv. Fielder (2024 and 2025) grown and sampled under field-relevant cold stress for gene-expression analysis.

Spatial and temporal expression profiling of the target genes under cold treatment is being carried out by qRT-PCR, including analysis of homoeologue-specific transcript abundance across the wheat A, B and D genomes, to determine whether the pathway is active in the reproductive tissues where frost has its greatest effect.

A transient wheat protoplast transfection platform has been established to validate the cold-response pathway in vivo. Protoplasts have been successfully isolated, and fluorescent reporter control constructs (eGFP and dsRED) were created by Golden Gate assembly from a monocot transfection control and validated by restriction enzyme fingerprinting, with vector components sourced from the Addgene Modular Cloning kit.

Building on this, a dual-luciferase reporter system is being used to assess how the cold-responsive promoter activity of COR genes is regulated, testing whether COR expression is driven by CBF, and CBF in turn by ICE, in response to cold.

The system is also being used to examine the role of specific cis-regulatory elements in the COR promoter and the binding of transcription factors to these elements during cold activation.

A range of reporter and effector constructs has been generated, and initial co-transfection events have been carried out in wheat protoplasts to begin validating this regulatory cascade transiently.

In parallel, putative upstream open reading frames (uORFs) in the untranslated regions of ICE and CBF transcripts are being identified as targets for CRISPR/Cas knockout, a strategy designed to increase translation of downstream COR proteins and thereby boost cold tolerance.

Impact and Applications:

The next phases will validate the dual-luciferase reporter assay, finalise the expression analysis and gRNA designs, and progress to Agrobacterium-mediated transformation to generate heritable, stable wheat edits for evaluation under simulated and field frost stress. Improved frost-tolerant germplasm may be delivered to growers through Green Blueprint Pty Ltd, which is developing a path to market.

In the long term, the project aims to deliver elite wheat germplasm with superior frost tolerance, strengthening the resilience, productivity and competitiveness of the the grain sector.



Wheat plants undergoing cold stress treatments at Murdoch University.

Introducing, testing and breeding low saponin quinoa genotypes in Australia

Murdoch project team:

Dr Jon Clements, Jinwen Fan,
Prof Michael Jones.

Collaborating Organisations:

AgriFutures Australia

Quinoa (*Chenopodium quinoa*) is a dicotyledonous 'pseudo-cereal', meaning it is a dicotyledonous plant, but its edible seeds are consumed like cereal grains.

It is usually grown for its seeds, but its green leaves are also eaten as a vegetable. Its centre of origin, domestication, and diversity is in the Peruvian Andes, Lake Titicaca region, central and southern Peru, and the Bolivian highlands.

It was known as the 'mother grain' of the Incan Empire, and it contributed to staple diets together with crops such as maize, beans, potatoes, coca, sweet potatoes, and other species.

A major issue for quinoa is that most germplasm accessions contain saponins. These are bitter, soapy compounds that can constitute up to 4% of the dry seed mass, and must be removed before consumption.

Saponins are anti-nutritional, and can interfere with vitamin and mineral absorption, resulting in cytotoxicity if over consumed.

Saponins from *Chenopodium quinoa* are a complex mixture of triterpene glycosides. Traditionally, saponin levels have been reduced by washing or abrasion.

However, polished quinoa has about half the fibre of washed quinoa and lower protein, vitamin, and mineral levels.

Washing is often a three-step process that removes saponin without removing vital nutrients in the seed coat.

For genetically low saponin varieties, the pericarp and seed coat can remain largely intact to retain nutrients and may have a slightly coarser texture and altered flavour compared with washed and/or polished seed.



Australia's quinoa market is projected to reach approximately \$53 million to \$81 million by 2034

Key Highlights:

In the first part of this project, a quinoa germplasm collection was made, and lines were field-tested at different sites in Western Australia and assessed for yield and seed quality (seed colour, size, protein, saponin, and other quality factors) by site and season production combinations, with promising lines identified for growth in Australia.

In the second part of the project, Murdoch University provided funds to support a PhD studentship to develop gene-editing for quinoa, with the aim of targeting and editing gene(s) involved in saponin synthesis.

The full genome sequence of quinoa is now available, the target genes have been identified, and regeneration systems for quinoa from culture are now available.

The primary target gene identified for this work was *TSRL1*. This gene was isolated from quinoa DNA by PCR, sequenced and confirmed as the correct gene by comparison with the published genomic sequence.

Gene-editing constructs with multiple gRNAs were designed and constructed, with eight targeted regions in two different selectable plasmids, and introduced into *Agrobacterium tumefaciens* strain AGL1 for transformation work using kanamycin or paromomycin as selectable agents. This work is ongoing.

Impact and Applications:

The establishment of low or no saponin quinoa lines in Australia will reduce the substantial cost of removing saponins, and make quinoa a much more profitable alternative crop to grow in Australia.



PhD student Jinwen Fan presents her research on the desaponification of quinoa using CRISPR /Cas 9 Gene-editing techniques at the CCFI EMCR Seminar Series





Digital Agriculture

Digital agriculture update: Using technology to drive industry engagement and efficiency

Digital Agriculture offers significant opportunities for enhancing WA's ag sector. However, capitalising on these opportunities requires a trained future workforce that's eager to embrace, adopt, and deploy digital ag approaches.

Through its Digital Ag Research Theme, co-led by Dr David Berryman, CCFI has established a longstanding partnership with Curtin University and the WA Department of Primary Industries and Regional Development (DPIRD) that offers extracurricular activities for high school students focused primarily on agricultural automation and robotics career pathways.

In 2025, CCFI and its partners organised and hosted several events designed to attract interest in Digital Ag. These included delivering the WA Robotics Playoffs, a three-day competition featuring over 350 high school students.

30 high school teams participated in the DPIRD Agricultural Innovation Challenge, where they gave presentations to academic and industry experts outlining their solutions to industry-identified challenges, such as rethinking AI for weed management, bird deterrence in vineyards, and emission tracking.

Over the course of the competition, more than 700 members of the public and family attended, demonstrating the burgeoning interest in robotics that CCFI has helped cultivate.

CCFI and DPIRD also ran robotics displays and high-tech ag-career activations at the Dowerin Machinery Field Day and the Perth Royal Agricultural Show, including the fully autonomous Robotriks Traction Unit (RTU).



Showing the RTU Bot at the Dowerin Machinery Field Day.
Credit: Dr David Berryman



WARP gives WA students an avenue to foster a spirit of teamwork and develop a passion for robotics and technology.

Credit: WARP

On the research side, CCFI trialled RTU's autonomous navigation system in 2025 to positive results and began field testing of the high-precision RTK GPS system and the Open Weed Locator (OWL) precision spraying system at Murdoch University's Grains Research Precinct Field Trial Area (FTA).

Work is in progress to add precision seeding to the RTU, with the goal of fully autonomous seeding and weed management at the FTA.

Led by Adj. Assoc. Professor Graham Mann, testing of the FarmBot greenhouse phenotyping system continues, currently running plant-growth bioassays.

FarmBot greatly simplifies these assays by automatically watering plants at precise levels and imaging plants at specified times.

The images are automatically transferred to a remote server, where they are analysed by AI software to automatically determine plant growth under test conditions.

Spatial omics for accelerating plant research and crop improvement

Murdoch research team:

Prof Rajeev Varshney, Dr Rutwik Barmukh, Dr Vanika Garg, Anu Chitikineni, Adj. A/Prof Liu Xin.

Collaborating Organisations:

Australia:

The University of Queensland, Adelaide University.

China:

Guangdong Academy of Agricultural Sciences, BGI-Shenzhen

Acknowledgements:

This work was partially supported by the Grains Research and Development Corporation (Project codes: UMU2404-003RTX; WSU2303-001RTX; UMU2403-009RTX; UMU2303-003RTX) and Hort Innovation (Project codes: AS21006; AS23003).

Overview:

Modern agriculture faces increasing pressure to improve crop productivity and resilience under a changing climate while meeting the food demands of a growing global population.

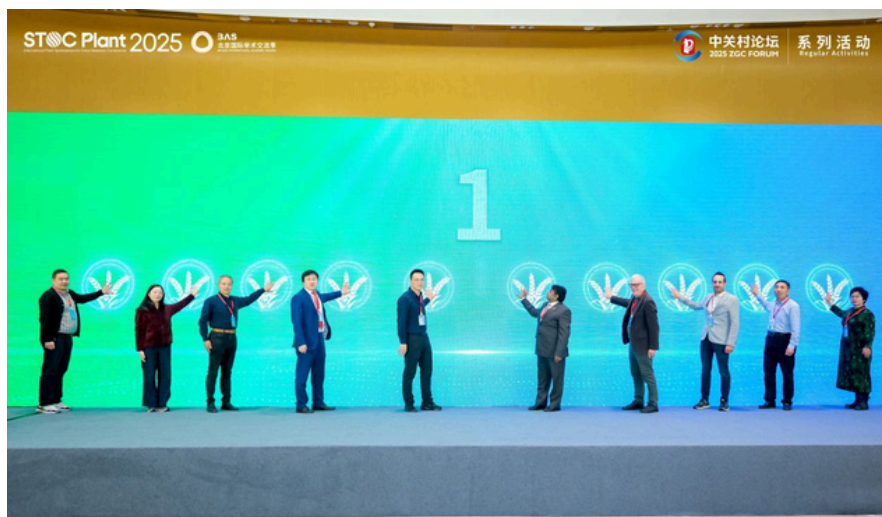
This requires understanding how different tissues and cell types coordinate growth, development, and stress responses at the cellular level.

Traditional molecular approaches analyse plant tissues in bulk, which obscures important differences between individual cells and removes information about their spatial organisation.

Spatial omics addresses this limitation by enabling scientists to measure molecular activity, such as gene expression, proteins, and metabolites, while preserving the spatial context of where these processes occur within intact plant tissues.

This represents a major advance for plant science, where spatial organisation is fundamental to processes such as root development, leaf function, flowering, and grain formation.

In crop research, spatial omics is particularly powerful because agronomic traits such as drought tolerance, disease resistance, and yield are often controlled by specific cell types and local tissue environments.



Prof Rajeev Varshney participates in the unveiling of STOC Plant 25's first flagship project: The Wheat Spatiotemporal Atlas Project

Credit: STOC Plant 2025

In our recent review article published in *Trends in Biotechnology*, we summarised the rapid development of spatial omics technologies and their applications in plant research, highlighting how advances in spatial transcriptomics, proteomics, and metabolomics are enabling researchers to build detailed maps of molecular activity within plant tissues.

We also discuss how combining multiple layers of spatially resolved data (known as spatial multi-omics) can provide a more complete picture of plant biology, linking genetic information to observable traits in crops, and outline current technical and analytical challenges including tissue complexity, computational tools, and large dataset integration.

Building on this momentum, the Wheat Spatial Omics Consortium (WSOC), co-led by researchers at Murdoch University, brings together more than 80 scientists across over 30 institutions worldwide to develop a comprehensive, high-resolution cellular atlas of wheat biology.

By systematically profiling how genes, proteins, and metabolites function across different wheat tissues and developmental stages, WSOC aims to enable more precise and efficient breeding strategies, supporting the development of wheat varieties that are more productive, resilient, and adapted to future climate challenges.

Together, our review and the WSOC initiative highlight spatial omics as a transformative platform for plant science—bridging molecular biology, advanced imaging, and data science to accelerate innovation in crop improvement.



A proud moment for CCFI researchers, with their review article on the potential impact of spatial omics on crop improvement research making the cover of *Trends in Biotechnology*.

Credit: Cell Press.

Genetics for next generation orchards

Murdoch project team:

Prof Rajeev Varshney, Dr Vanika Garg, Dr Penghao Wang, Anu Chitikineni.

Collaborating Organisations:

The Queensland University of Technology; Queensland Alliance for Agriculture and Food Innovation – The University of Queensland; Western Sydney University; WA Department of Primary Industries and Regional Development; Department of Primary Industries, Queensland; The University of Adelaide.

Acknowledgements:

This research is supported by Hort Innovation (AS23003)

Project Overview:

The Australian horticulture industry continues to grow, contributing over \$15 billion annually to the economy.

To remain globally competitive, Australian orchard production systems must transform, focusing on new varieties with enhanced resilience, better compatibility with automation, and earlier flowering and fruiting to expedite farmers' return on investment.

To address this, the *Genetics for Next Generation Orchards* program, a \$41m investment by Hort Innovation, aims to develop advanced tools for breeders, growers, and scientists to accelerate the development of new cultivars and sustainable orchard production systems.

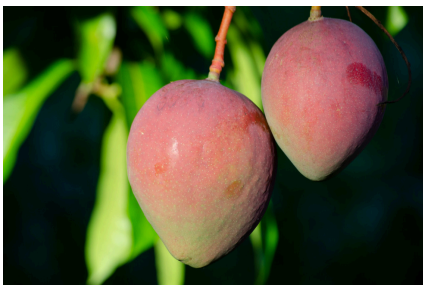
The project, led by QUT, focuses on enhancing productivity and profitability in Australian horticulture by integrating cutting-edge genomic technologies into breeding pipelines.

Within this program, Pillar 6 activities led by the Murdoch University team focus on the application of genomic prediction and advanced data-driven approaches to improve selection efficiency in orchard crops.

This includes identifying and characterising the genetic regulation of key productivity traits, integrating molecular markers, and developing genomic selection models that enable efficient selection of plants with desirable traits.

The program also explores improved orchard management strategies through targeted interventions, including the use of plant growth regulators.

By combining genomic insights with practical breeding and production approaches, this work will support the development of resilient, high-performing orchard systems suited to future challenges, including climate variability and evolving market demands.



Key Highlights:

Mango

Genomic prediction is being applied to accelerate breeding in mango, a perennial crop with long breeding cycles and complex trait architecture. Diverse global germplasm has been analysed to improve prediction of key traits including fruit weight, firmness, blush colour, and total soluble solids. Integration of datasets from Australia, the USA, and China increased the size and diversity of the reference population, revealing a highly admixed genetic structure and improving the detection of trait-associated genomic regions.

Prediction accuracy was primarily influenced by genetic relatedness and reference population composition, with limited gains from increasing model complexity.

Incorporating genotype-by-environment interactions and multi-trait approaches further improved prediction under specific conditions, while differences in phenotyping protocols remained a key limitation.

To complement these efforts, a mango pangenome is being developed by generating high-quality genome assemblies for nine cultivars that are unique or commercially important in Australia.

This work expands beyond the narrow Kensington Pride-derived lineage, capturing under-represented genetic diversity within Australian germplasm.

The resulting genomic resource will support molecular breeding, trait discovery, and more efficient selection strategies in mango improvement programs.



Apple

In Australia, apple breeding programs aim to improve fruit quality and stress resilience.

However, the genetic diversity within Australian cultivated and wild apples remains underrepresented, limiting the understanding of key traits related to domestication, adaptation, and breeding potential, thus preventing the development of superior apple cultivars.

In this study, a comprehensive Australian apple pangenome and an expanded apple super-pangenome will be constructed. The Australian apple pangenome will incorporate six newly assembled and annotated, haplotype-resolved genomes representing key Australian cultivated apple accessions.

These genomes will be primarily generated using PacBio high-fidelity (HiFi) sequencing and Chromatin Conformation Capture technology (Omni-C) and subsequently integrated with all publicly available apple genomes.

To further broaden the genetic landscape, an apple super-pangenome will be developed by incorporating two newly sequenced wild species along with existing genome assemblies of wild *Malus* species with the Australian apple pangenome.

The study will explore genome architecture with an emphasis on the diversity and evolution of chromosome-scale structural variations and their potential functional implications.

Genetics for next generation orchards

Additionally, the resulting pangenome and super-pangenome will be used as powerful resources to investigate evolutionary divergence of apple, identify candidate genomic regions associated with key agronomic traits and domestication, and enable downstream applications in trait discovery and genomics-assisted breeding.



Almond

This work will deliver advanced genomic resources to accelerate almond breeding and improve productivity in Australian orchard systems.

A primary outcome will be the development of chromosome-level genome assemblies for key Australian and internationally relevant almond cultivars, providing high-quality reference genomes for downstream genetic analysis.

Building on this, a comprehensive almond pangenome will be constructed to capture the full spectrum of genomic diversity, including large structural variations such as insertions, deletions, and gene presence/absence variation.

This will enable the identification of genomic regions associated with important traits including yield, kernel quality, drought tolerance, and disease resistance.

The project will also generate detailed catalogues of structural and functional genomic variation, supporting the development of robust molecular markers and enabling the implementation of genomic prediction models in almond breeding programs.

Impact and Applications:

This project delivers advanced genomic prediction tools and pangenome resources to enable faster and more precise breeding of orchard crops.

By integrating diverse genomic datasets and capturing previously under-represented genetic variation (e.g., in mango and apple), the project enhances the ability to identify key trait-associated regions and accelerates genetic gain.

The outcomes will support the development of high-yielding, high-quality, and climate-resilient cultivars, improving productivity and profitability in Australian horticulture. Genomic tools, markers, and prediction models will enable earlier and more accurate selection decisions, reduce reliance on extensive phenotyping, and lower breeding costs.

Integration with orchard management strategies will further translate genomic insights into practical on-farm benefits.

The approaches and resources developed are scalable and transferable across multiple horticultural crops.

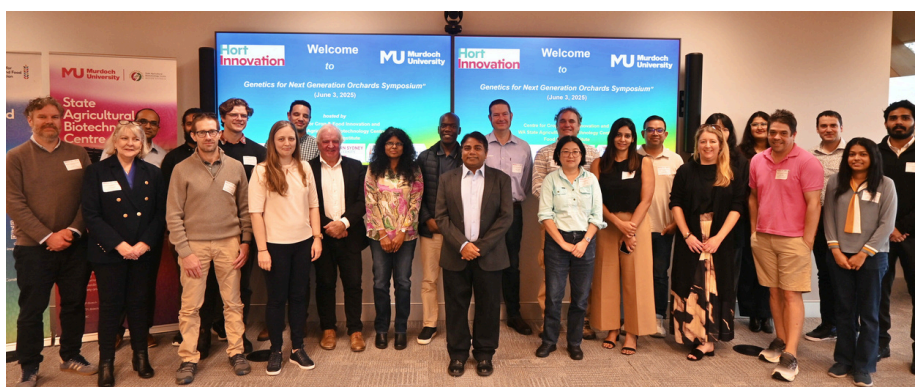
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We want to develop a mobile-based intelligent farm system that empowers breeders to make informed decisions, selecting new crop varieties that possess optimal trait combinations for future demands.

To remain globally competitive, Australian orchard production systems must undergo a transformation, producing new varieties and orchard practices that enable greater compatibility with automation, that improve resilience to climate and disease, and that flower and fruit more consistently at a younger age to expedite return on investment for farmers.

”

Prof Rajeev Varshney



CCFI hosted collaborators from Hort Innovation, The Queensland University of Technology, Western Sydney University, The University of Queensland, WA DPIRD, UWA, and Abacus Bio to Murdoch University for the Genetics for Next Generation Orchards (GNGO) Symposium.

The Symposium was a great opportunity for project partners to discuss progress, strategise, and explore ways to collaborate across project pillars. It was such a pleasure to host some of Australia's leading horticulturalists and to ensure that our respective outputs align with the needs of breeders, growers and consumers.







Capacity building, Networking, and Knowledge Dissemination



CCFI/SABC Events

Over the past year, CCFI and SABC have organised events ranging from internal meetings and seminars to stakeholder visits, strategy sessions and international conferences, sharing research with new audiences and deepening existing partnerships. A few highlights are below:

Genome Data Analysis and Integration Workshop

Date: 24-25 July 2025

Location: Murdoch University

Synopsis:

CCFI hosted leading genomics, genetics and bioinformatics experts from around the globe for a two-day workshop at Murdoch University. Presentations spanned reference genome development across diverse crop types, methods for analysing plant genomic complexity, pan-genome analysis, and emerging bioinformatics tools.

A key focus was the development and utilisation of pangenomics for plant productivity and stress resilience.

Number of Speakers: 14

Number of attendees: >50

Number of countries represented: 6



The GDAL workshop brought leading researchers from China, France, Germany and the USA to WA to discuss new research approaches designed to enhance crop productivity

4th Annual CCFI/SABC Strategy Meeting

Date: 21-22 August 2025

Location: Murdoch University

Synopsis:

This annual event provides a platform for agricultural scientists at Murdoch University to present their research and improve cross-departmental collaboration. This year, we hosted a panel session titled *"Innovation Through Integration: Enhancing Collaboration Across Research Frontiers"*, which featured leading researchers from across MU who discussed their research focus and gave practical advice to attendees on issues such as IP and Patent processes.

The meeting also gives industry and prominent Australian RDC attendees a comprehensive overview of our research focus and expertise..

Number of speakers: 41

Number of attendees: 80



L-R: HBI Executive Director Prof **Treena Burgess**; MU Dean of Graduate Research, Assoc. Prof **Belinda Brown**; MU Director, Research & Innovation, **Alasdair McDonald**; HBI Executive Director, Prof **Hamid Sohrobi**; FFI Pro-Vice Chancellor, Prof **Peter Davies**; Soilswest Director, A/Prof **Fran Hoyle**; SAGS Associate Dean - Research, Prof **Richard Harper**; CCFI Director, Prof **Rajeev Varshney**

Genome Assisted Breeding Workshop at PAG USA

Date: 14 January 2025

Location: San Diego

Synopsis:

This Workshop on genomics-assisted breeding (GAB), brought together genomics specialists from the public and private sectors to assess the current state of genomic resources and share practical strategies for applying genomics to crop improvement. As complete genome sequences and large-scale sequencing become available across crop species, the workshop focused on how breeders can use tools such as genome-wide association studies and genomic selection to translate genetic data into faster, more effective breeding.

Number of speakers: 8

Number of attendees: >400 from <25 nations



Virtual Workshop organised on behalf of the joint FAO/IAEA Centre

Date: 20–21 November 2025

Location: Online

Synopsis:

On behalf of the Joint FAO/IAEA Centre, CCFI led a virtual workshop on the application of advanced genomics tools to enhance crop breeding efforts and improve global food security. Attended by researchers, breeders, policymakers and stakeholders from across IAEA's 181 Member States, and led by CCFI Science Manager Anu Chitikineni, this workshop served as an important forum to share a replicable bioinformatics workflow for undertaking QTL-sequencing research.

Number of Speakers: 10 speakers

Number of attendees: >200

Number of countries represented: >60



CCFI Senior Science Manager Anu Chitikineni travelled meeting the Joint FAO/IAEA Centre senior leadership team



Researchers and senior stakeholders from ICRISAT, CAAS, Jiangsu Academy of Agricultural Sciences, ICARDA, China Jialing University, ICAR, University of Missouri and the Crop Trust visit Murdoch University

8th IFLRC & 5th APC 2025

Date: 15–19 September 2025

Location: Pan-Pacific Hotel, Perth

Synopsis:

This combined conference brought together scientists from multiple disciplines working on fundamental and applied aspects of the breeding, production, processing, consumption, nutrition, and environmental/health impacts of food legumes. During the conference, CCFI hosted a workshop on Pulse Genetic Gains for >50 attendees, before bringing an additional 40 key international researchers and policymakers to Murdoch University, where we showcased our facilities and detailed ongoing research aimed at enhancing pulse productivity.

Number of attendees: >90

Number of countries represented: 8

Advancing horticultural research in Brisbane

Date: 14–17 October 2025

Location: Brisbane, Australia

Synopsis:

CCFI researchers spent a week in Brisbane advancing two Hort Innovation-funded horticulture projects: the Advanced Genomics Platform for Australian Horticulture, whose 4th Annual Meeting CCFI hosted, and the Genetics for Next Generation Orchards project, marked by a two-day symposium. These projects are accelerating genetic improvement in fruits held back by complex genetics and a chronic underinvestment in genomics. During the trip, CCFI also participated in a workshop on the Genetics of Fruit Sensory Preferences. Across both projects, CCFI is driving the genomic resources and breeding strategies that underpin productivity and resilience in Australian horticulture.

Number of speakers: 20

Number of attendees: >30



Horticultural researchers and stakeholders from Hort Innovation, QUT, QAAFI, QLD DPI and Griffith University convened in Brisbane for a week of presentations and progress updates

Industry engagement, outreach and events

A selection of presentations, lectures, seminars and industry engagement efforts conducted by CCFI and SABC researchers in 2025 is listed below

Title: *Agricultural Research for the Development of Sustainable Food Futures*

Presenter: E/Prof Richard Bell

Type: Oral

Event Name: Sustainability Matters Forum, Australia

Summary:

At SMF, which was established to share ideas on Murdoch University's collective research contribution to the UN Sustainable Development Goals, E/Prof Bell presented a keynote lecture detailing his work on soils, land management, and mine rehabilitation, and his more recent work on conservation agriculture in Bangladesh.

Title: *Australian oat and barley pan genome*

Presenter: Prof Chengdao Li

Type: Oral

Event Name: Australian Crop Breeders Week, Australia

Summary:

Prof Li presented WCGA's contributions to the development of new oat and barley pangenome resources. Both efforts featured extensive collaboration between leading research institutes in Australia and abroad, and offer important insights for breeders of these commercially critical crops.

Title: *Deciphering Barley terminal heat tolerance*

Presenter: Prof Chengdao Li

Type: Oral

Event Name: Australian Crop Breeders Week, Australia

Summary:

In this presentation, Prof Li walked through GRDC-backed research into barley heat tolerance, and how his team have worked to identify the genes that protect barley yield and grain quality from heat-stress damage. He also detailed his progress in making heat-tolerant genetics more readily deployable

Title: *Decoding Crops, Delivering Impact*

Presenter: Prof Rajeev Varshney

Type: Oral

Event Name: Science at the Shine Dome, Australia

Summary: As part of his induction as an AAS Fellow, Prof Varshney presented a summary of his work to date, and how he and his colleagues have spent decades seeking to understand the genetics of different agronomic traits such as drought and disease resistance, and yield. He detailed his efforts to sequence 10,000 chickpea lines and how this research has helped develop high-yielding, climate-resilient and nutritious varieties of chickpea that have been released in India and across Africa.

Title: *Decoding Genomes, Driving Impact: Transforming Agriculture for Food and Nutrition Security*

Presenter: Prof Rajeev Varshney

Type: Oral

Event Name: M.S. Swaminathan Centenary International Conference, India

Summary:

In this Conference celebrating the life and legacy of Prof M.S. Swaminathan, Prof Varshney detailed how genomics and data-driven technologies offer transformative tools for sustainable crop improvement. His talk traced a journey from sequencing 15+ crops to breeding 20+ climate-resilient varieties now benefiting smallholder farmers across Asia and Africa. He highlighted pangenomics, haplotype-based breeding, AI prediction, and speed breeding, and advocated for global collaboration to establish resilient, nutritious food systems.

Title: *Decoding Genomes, Driving Impact: Translational Genomics for Climate-Resilient and Sustainable Agriculture*

Presenter: Prof Rajeev Varshney

Event Name: STOC Plant 2025, China

Summary:

As a Keynote Speaker, Prof Varshney articulated how genomics and genetics are key in future-proofing global food supplies. He added that nascent approaches, such as Spatiotemporal Omics can take Genomics-Assisted Breeding a step further by addressing the limitations of conventional omics approaches, as it can map molecular profiles to specific locations while tracking their dynamics across developmental stages, disease progression, or experimental conditions.

Title: *Decoding sex determination in papaya using chromosome-length genome assemblies*

Presenter: Dr Rhys Copeland

MU Collaborating Authors:

Liangwei Li, Dr Vanika Garg, Anu Chitikineni, Prof Rajeev Varshney

Type: Poster

Event Name: TropAg 25, Australia

Summary:

Papaya is a globally important crop and model for sex chromosome evolution, yet only 18% of Australian households buy it, citing inconsistent flavour. CCFI researchers are building haplotype-resolved genome assemblies to map sex determination and fruit colour genes, enabling genomic prediction of elite, consumer-appealing varieties.

Title: *Disease resistant genes in narrow-leaved lupin*

Presenter: Dr Gaofeng Zhou

MU Collaborating Authors:

Prof Chengdao Li

Type: Poster

Event Name: 8th International Food Legume Research Conference and 5th Australian Pulse Conference, Australia

Summary:

This poster presentation detailed progress on a GRDC-backed research project that is incorporating AI, genomics and molecular markers to accelerate breeding of higher-yielding and disease-resilient varieties of Narrow-leaved lupin.

Title: *Effects of novel soil amendments on nutrient leaching in a sandy soil*

Presenter: E/Prof Richard Bell

Type: Oral

Event Name: 2025 Global Sandy Soils Conference, Australia

Summary:

E/Prof Bell discussed research that tested compost, zeolite, spongolite and a water-absorbing polymer as amendments for water and nutrient retention in agricultural deep sand, using successive leaching-column experiments.

E/Prof Bell and his team found that Zeolite proved most effective, milled forms retained ammonium-N, P, and K better than rock, while compost added nutrients but leached readily. Spongolite and polymer showed little benefit.



Prof Rajeev Varshney presents at Science at the Shine Dome, an annual event established to celebrate science and honour outstanding achievements

Industry engagement, outreach and events

Title: Enhancing genetic gains in pulses through genomics and AI-guided breeding

Presenter: Prof Rajeev Varshney, Dr Rutwik Barmukh

Type: Workshop Presentation

Event Name: 8th International Food Legume Research Conference and 5th Australian Pulse Conference, Australia

Summary:

In this workshop, CCFI Director Prof Varshney and ECR, Dr Rutwik Barmukh detailed recent advances in genomics and AI-guided breeding strategies, and explained how CCFI is steadily incorporating these strategies across its various pulse and legume-related projects, including chickpea, lentil, faba bean and peanut.

Title: Field application of biological products preconditioned the soil and induced changes to the microbiome to reduce root-knot nematode infestation in tomato crops

Presenter: Dr Onyemaechi Henry Obiazikwor

MU Collaborating Authors:

Dr Anish Shah, E/Prof Giles Hardy, A/Prof Kirsty Bayliss

Type: Oral

Event Name: Australasian Plant Pathology Society Conference, Australia

Summary: Henry detailed the testing of three commercial biological products on field tomatoes across two Western Australian farms and a greenhouse nematode trial. The research team found that treated plots showed higher biomass and yield, and soil preconditioned with the products reduced root-knot nematode galling, though growth stage shaped microbial communities more than the products did.

Title: Gene Editing and its Regulation

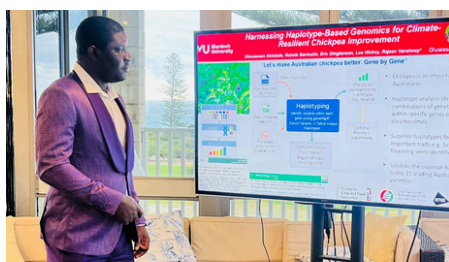
Presenter: Prof Michael Jones

Type: Oral

Event Name: XXXIII International Society of Sugar Cane Technologists Centennial Congress, Colombia

Summary:

In this plenary presentation, Prof Jones covered Omics technologies and GM applications with a focus on Gene Editing. He highlighted how Sugarcane would benefit from these technologies, as they enable targeting all copies of a gene of interest, which is something conventional breeding cannot accomplish.



Dr Akinlade presents his genomics research to ATSE Fellows

Title: Generational Transfer of Seed Potato Microbiome

Presenter: Sumitra Saha

MU Collaborating Authors:

Dr Anish Shah, Dr Penghao Wang, Prof Treena Burgess, A/Prof Kirsty Bayliss

Type: Oral

Event Name: For Food's Sake, Australia

Summary:

Sumitra detailed research that tracked bacterial transfer across three potato tuber generations in two cultivars. The researchers found that while environmental acquisition dominated, supplying over 98% of granddaughter-tuber bacteria, a small core set was reliably transmitted from one generation to the next.

Title: Genetic improvement for sustainable crop production

Presenter: Prof Rajeev Varshney

Type: Oral

Event Name: Food and Agriculture Organization Global Agrifood Biotechnologies Conference, Italy

Summary:

Presenting in the principal segment of the Conference, Prof Varshney discussed how next-generation genomics, molecular breeding, gene editing and the use of synthetic biology can deliver more sustainable crop production.

Title: Genetics and genes for low alkaloid content in narrow-leaved lupin

Presenter: Dr Gaofeng Zhou

MU Collaborating Authors:

Prof Chengdao Li, Chunsheng Xiao

Type: Oral

Event Name: 2025 Australian Crop Breeders Week, Australia

Summary:

Detailed efforts to develop "bittersweet" narrow-leaved lupins with low alkaloid (QA) content in seeds, in order to preserve nutritional value and food potential while retaining bitter compounds in vegetative tissues for natural pest defence.

Title: Genome Editing in the Era of the Dematerialization of Plant Genetic Resources – Regulatory Challenges in Comparative Perspective

Presenter: Prof Michael Jones

MU Collaborating Authors:

Muhammad Adeel

Type: Workshop Presentation

Event Name: EU Frames Research Group Workshop, Spain

Summary:

Prof Jones discussed the global agricultural biotechnology landscape, international trade, and the role of science diplomacy in enabling trade.

Title: Genome-wide association analyses identified candidate gene CaMYB114 controlling black seed coat in chickpea

Presenter: Dr Hao Lu

Type: Oral

Event Name: 8th International Food Legume Research Conference and 5th Australian Pulse Conference, Australia

Summary:

This presentation detailed research that identified a single major QTL and underlying candidate gene associated with the black seed coat trait in chickpea. This work unlocks the potential for breeding new chickpea varieties that meet market requirements.

Title: Genomic selection for environmental adaptation in barley

Presenter: Prof Chengdao Li

Type: Oral

Event Name: 2025 International Conference on Molecular Plant Sciences, China

Summary:

In a Session focused on Omics and Breeding, Prof Li detailed how the development of genomics resources can dramatically accelerate breeding timelines, reduce costs, and ensure that varieties can be developed to specific climatic conditions.

Title: Genomics and its Relevance to Food Secure Society

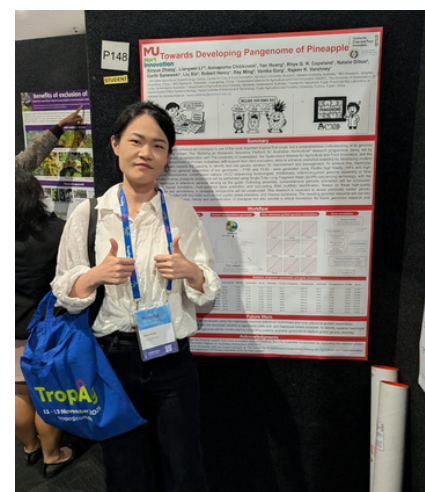
Presenter: Prof Rajeev Varshney

Type: Oral

Event: XVII Agricultural Science Congress, India

Summary:

In this keynote lecture, Prof Varshney highlighted the opportunities for enhancing global food security through the utilisation of genomics, genetics, and bioinformatics.



CCFI PhD student Xinyue (Luna) Zhang with her poster at TropAg 25

Industry engagement, outreach and events

Title: *Haplotype Dissection of Yield-related and Adaptation Traits in Chickpea*

Presenter: Dr Oluwaseun Akinlade

MU Collaborating Authors:

Dr Rutwik Barmukh, Prof Rajeev Varshney

Type: Poster

Event Name: 8th International Food Legume Research Conference and 5th Australian Pulse Conference, Australia

Summary:

CCFI researchers detailed how they combined GWAS with gene-based haplotype analysis to dissect six agronomic traits across 234 chickpea accessions in Ethiopia, Kenya, and India. The work identified 237 trait associations and superior haplotypes whose carriers outperformed others by 10–35%, producing a donor-allele catalogue for genomic selection.

Title: *Harnessing Haplotype-Based Genomics for Climate-Resilient Chickpea Improvement*

Presenter: Dr Oluwaseun Akinlade

Type: Oral

Event Name: Australian Academy of Technological Sciences and Engineering WA Division End of Year Event, Australia

Summary:

Dr Akinlade was invited by ATSE to detail his genomics research, and how it can drive chickpea improvement. His presentation covered ongoing research, and highlighted how genomic and haplotype-based approaches can drive sustainable breeding solutions for future climates.

Title: *Identification of anthracnose disease resistance gene in narrow-leaved lupin*

Presenter: Dr Gaofeng Zhou

MU Collaborating Authors:

Prof Chengdao Li

Type: Poster

Event Name: 8th International Food Legume Research Conference and 5th Australian Pulse Conference, Australia

Summary:

Presented an update on GRDC-backed research that uses AI, genomics and molecular markers to accelerate breeding of higher-yielding and disease-resilient varieties of Narrow-leaved lupin

Title: *Large scale genome-wide association analysis identified QTLs associated with aluminum tolerance in chickpea*

Presenter: Dr Yong Jia

MU Collaborating Authors:

Dr Kathika Pradeep, Dr Wendy Vance, Prof Richard Bell, Prof Chengdao Li

Type: Oral

Event Name: 8th International Food Legume Research Conference and 5th Australian Pulse Conference, Australia

Summary:

This poster detailed progress on the WCGA-led, GRDC-backed project that aims to develop genetics tools for breeders to develop and deploy high-value, acid soils-tolerant chickpea germplasm.

Title: *Managing Crop Nutrition for Food Security and Soil Quality*

Presenter: E/Prof Richard Bell

Type: Online presentation

Event Name: 2025 Annamalai University Conference, India

Summary:

In this presentation, E/Prof Bell examined Conservation Agriculture, specifically crop residue retention plus minimal soil disturbance, as a route to balanced nutrition in the Indo-Gangetic Plain's rice-based systems. He highlighted how these practices can reverse negative K, N and S balances, and cut greenhouse emissions by ~30%.

Title: *Panel Discussion: India-Africa Partnership in Agriculture*

Presenter: Prof Rajeev Varshney

Type: Oral

Event Name: XVII Agricultural Science Congress, India

Summary:

In this panel discussion, Prof Varshney discussed the many benefits of South-South agricultural partnerships, including capacity building, technology transfer, and leveraging shared experiences, such as exposure to the affects of a changing climate, to deliver solutions for a more sustainable and resilient agricultural food system.

Title: *Phytophthora cinnamomi influences the rhizosphere microbiome in orchard-grown Reed Avocado in Western Australia*

Presenter: MAU Zaman

MU Collaborating Authors:

Dr Anish Shah, Dr Penghao Wang, Prof Treena Burgess, A/Prof Kirsty Bayliss

Type: Oral

Event Name: Australasian Plant Pathology Society Conference, Australia

Summary:

Asad Zaman discussed work characterising the rhizosphere microbiome of Western Australian Reed avocado orchards using 16S and ITS sequencing, comparing thirteen orchards with and without *Phytophthora cinnamomi*. Indicator analysis identified distinct bacterial and fungal taxa enriched in disease-free soils, pointing toward microbial consortia that may suppress *Phytophthora* Root Rot and reduce phosphite dependence.

Title: *The Distinctive Features of Sands and their Management*

Presenter: E/Prof Richard Bell

Type: Oral

Event Name: 2025 GW Leeper Memorial Lecture, Soil Science Australia

Summary: E/Prof Bell delivered the renowned GW Leeper Lecture in 2025, in which he discussed the Distinctive Features of Sands and their Management and outlined how subtle differences in clay and organic matter content can transform water and nutrient dynamics across vast sandy landscapes.

Title: *Towards AI-guided haplotype stacking for enhancing seed yield in chickpea*

Presenter: Bhargava Kotte

MU Collaborating Authors:

Dr Rutwik Barmukh, Dr Oluwaseun Akinlade, Anu Chitkineeni, Prof Rajeev Varshney

Type: Poster

Event Name: 8th International Food Legume Research Conference and 5th Australian Pulse Conference, Australia

Summary:

Australia earns around AUD \$400 million annually from the chickpea, yet elite varieties have narrow genetic diversity. This poster describes how applying FastStack, an AI-guided haplotype-stacking method, to 200 diverse accessions, can identify superior yield-related haplotypes and optimise crossing design, accelerating high-yielding, climate-resilient cultivars for Australian growers.



Dr Akinlade, Ms Chitkineeni, Prof Varshney, Dr Barmukh, Mr Karkee, A/Prof Mir, and Mr Kotte all presented at IFIRC/APC 2025

Industry engagement, outreach and events

Title: Towards developing pangenome of pineapple.

Presenter: Xinyue (Luna) Zhang

MU Collaborating Authors:

Liangwei Li, Anu Chitikineni, Dr Rhys Copeland, Dr Vanika Garg, Prof Rajeev Varshney

Type: Poster

Event Name: TropAg 25, Australia

Summary:

Pineapple is a major tropical crop whose genomic diversity remains poorly understood. This project will assemble and annotate ten diverse Australian accessions using stLFR sequencing, guided by the F180 reference, then build a pangenome. The resource aims to reveal hidden variation in fruit quality, stress tolerance, and disease resistance, supporting future breeding.

Title: Trade in agricultural produce in the Asia Pacific region to feed the growing population – from new technologies to international regulations.

Presenter: Prof Michael Jones

Type: Oral

Event Name: Indo-Pacific Research Centre Seminar Series 2025, Australia

Summary:

Prof Jones highlighted that although only fourteen of the world's 369,000 flowering plants are widely grown for food, global food production must increase by roughly 70% to feed a growing population sustainably while preserving biodiversity. He highlighted that Gene-editing (GE) offers a precise, rapid tool for crop improvement that is already boosting yields and quality, yet it is often lumped together with the more heavily regulated GMOs.

He posits that many countries are now reassessing their rules on the principle that GE produce achieves the same result as conventional breeding, and therefore should not be regulated differently from conventionally bred varieties.

Title: WA Soils and Sustainable Agriculture – Past, Present and Future Challenges.

Presenter: E/Prof Richard Bell

Type: Oral

Event Name: Soil CRC Annual Conference, Australia

Summary:

E/Prof Bell delivered the keynote address in which he drew on his 40-year career to examine the historical, current, and projected challenges facing Western Australian soils and agriculture.



Media outreach

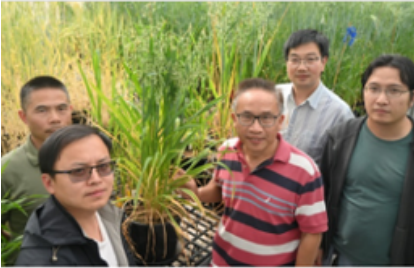
CCFI and SABC issued 8 press releases in 2025, achieving over 150 pieces of media coverage in international, national and trade publications. The Centres also established a monthly newsletter, *Lab & Land*, which is shared with our global network of stakeholders, collaborators, and key policymakers.

A selection of outreach from the two Centres is below:



NEWS 24 NOV 2025

Murdoch University researchers recognised as the best in their field in The Australian's Top 250 List



NEWS 30 OCT 2025

International research team deciphers key traits in oats in new pangenome project



NEWS 19 JUN 2025

New Australian Chickpea pan-genome poised to boost national Chickpea production



NEWS 28 APR 2025

New pangenome analysis uncovers genetic key to larger peanut yields



NEWS 22 MAY 2025

Australian Academy of Science honours Murdoch University agricultural researcher



NEWS 17 MAR 2025

Breakthrough in Wild Barley Genomics paves the way for climate-resilient crops

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NEWS FEATURE | 04 September 2025

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Chickpea pan-genome tailored by Australian researchers to strengthen specific agronomic traits

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2025 Publications

CCFI researchers have published over 150 papers in high-impact academic journals in 2025, with 7 in Nature-branded journals (including *Nature*, *Nature Genetics*, *Nature Communications*, *Nature Plants*), plus 4 in *Scientific Reports*. A selection of critical research in leading journals is highlighted below.

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Qiu L, Fang R, Jia Y, Xiong H, Xie Y, Zhao L, Gu J, Zhao S, Ding Y, Li C, Guo H, Liu L (2025). **The allelic mutation of NBS-LRR gene causes premature senescence in wheat.** Plant Science. DOI: 10.1016/j.plantsci.2025.112395

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PhD Research Students

Name	Title	Principal Supervisor
Hitashi Aggarwal	Unlocking the Potential of Nitrogen Use Efficiency Genes in Wheat Using CRISPR/ Cas9	A/Prof Ryan Whitford
Naznin Ahmed	Identification of Suitable Traits for Direct Seeded Rice	E/Prof Richard Bell
Zakaria Alam	Genetic Dissection of Heat Tolerance in Bread Wheat (<i>T. aestivum</i> L.)	Prof Rajeev Varshney
Adeeba Anis	Deep Learning based Lupin Disease Detection from Imagery	Prof Chengdao Li
Kunal Choudary	Unravelling the Genomic Diversity of Australian Apple Germplasm	Prof Rajeev Varshney
Nayani Dayarathna	Application of Parallel Comparative Functional Genomics to Identify Root-Lesion Nematode-Resistant Genes in Wheat	Dr John Fosu-Nyarko
Marcia Correa Queiroz de Lima	The Contribution of the Sub-Soil Potassium Supply to Wheat, Barley and Canola Plant Nutrition	Dr Wendy Vance
Thi Thuy Lien Do	Unlocking B-Genome Diversity in Canola Using CRISPR/Cas-Mediated Recombination	A/Prof Ryan Whitford
Jinwen Fan	De-saponification via Gene Editing. A Solution for Efficient Quinoa Seed Processing & Optimising Nutritional Value	Prof Michael Jones
Khushboo Fulara	Development of Genomic Resources in Passionfruit	Prof Rajeev Varshney
Rakshith Gowda	Unravelling the Genetic Basis of Heat Tolerance in Barley	Prof Chengdao Li
Saliah Gul Jabeen	Molecular Dissection of QTL Cluster 1_2B for Nitrogen Use Efficiency (NUE) and Associated Traits in Bread Wheat	Prof Rajeev Varshney

PhD Research Students

Name	Title	Principal Supervisor
Suprikesh Kadlag	Integrative Mechanisms of Aphid Resistance in Narrow-Leafed Lupin	Dr Gaofeng Zhou
Ajaya Karkee	Marker-Assisted Introgression of the “QTL-hotspot” Region in Leading Australian Chickpea Variety through Accelerated Backcrossing and Speed Breeding Approach	Prof Rajeev Varshney
Tarkjot Kaur	Artificial Intelligence-Assisted Genomic Prediction for Future Climate Change Breeding	Dr Penghao Wang
Amin Khan	Enhancing Septoria Resistance in Oats (<i>Avena sativa</i> L.) through Genomic Prediction and QTL Analysis	Prof Chengdao Li
Bhargava Kotte	AI-Guided Haplotype Stacking to Enhance Yield and Symbiotic Nitrogen Fixation in Chickpea	Prof Rajeev Varshney
Thai Son Le	Remote Sensing for Forest Water Stress Monitoring and Prediction	Prof Richard Harper
Albert Leen	Functional Characterisation of Cell Wall-Modifying Enzymes of Root-Lesion Nematodes Infecting Australian Cereals	Dr John Fosu-Nyarko
Wei Liu	Multi-Omics Dissection of Regulatory Mechanisms Underlying Reproductive Heat Tolerance in Australian Wheat Germplasm	Prof Rajeev Varshney
Lachlan Macphail	Integrating Artificial Intelligent Phenotyping into Systemic Genomic Prediction for Modern Agriculture	Dr Penghao Wang
Chandan Maharana	Improving Frost Resilience in Wheat through Targeted Gene Editing	Prof Michael Jones
Mohammed Abdullah Al Mahmud	Saline Land Restoration for Climate Mitigation in Dry Environments	Prof Richard Harper
Julie Meek	Effect of Composition and Processing on Bovine Milk Intolerance or Sensitivity	Prof Vicky Solah

PhD Research Students

Name	Title	Principal Supervisor
Trung Hieu Nguyen	To be confirmed	Prof Chengdao Li
Dorothy Nhepera	Molecular Characterization of Beta Glucan from Oat Varieties Grown in Western Australia and the Influence of Structure on Physiochemical Properties	Dr Wendy Hunt
Onyemaechi Henry Obiazikwor	Potential management of Fusarium wilt in tomatoes using the crop microbiome	A/Prof Kirsty Bayliss
Sumaiya Haque Omy	QTL Mapping and Gene Identification of Phomopsis Pod Blight Resistance in Narrow-Leafed Lupin (<i>Lupinus angustifolius</i> L.)	Prof Chengdao Li
Shri Hari Prasad	Developing Genomic Resources in Custard Apple	Prof Rajeev Varshney
Lewis James Price	Salinity and Plant Molecular Mechanisms Understood in Wheat and Barley	Prof Chengdao Li
Sultana Mahbuba Priti	Residual Activity of Herbicides in Rice-Based Cropping	Dr Wendy Vance
Christopher Reed	Hidden Heritability of Barley Grain Defects Using Pangenomes, Genomic Prediction, and Machine Learning	Prof Chengdao Li
Ashaduzzaman Sagar	Gene Editing to Improve Stress Resilience in Wheat	Prof Michael Jones
Sumitra Saha	Exploring the Potato Microbiome to Mitigate Heat Stress in Potato Production	A/Prof Kirsty Bayliss
Abhisek Sahu	Development of a Chromosome-level Almond Pangenome for Exploring Genomic Diversity and Genetic Improvement	Prof Rajeev Varshney
Ami Chand Sharma	Effect of Combined Application of Organic Manure and Synthetic Fertilizers on Taro Yield and Soil Properties	E/Prof Richard Bell
Sultana Sharmin	Gene Editing to Improve Frost Tolerance in Australian Wheat	Dr John Fosu-Nyarko

PhD Research Students

Name	Title	Principal Supervisor
Devshree Singh	Exploring Genetic and Molecular Pathways to Enhance Nitrogen Use Efficiency and Grain Yield in Wheat	Prof Rajeev Varshney
Brittany Clare Thornbury	Enhancing the Water-Use Efficiency of Barley (<i>Hordeum vulgare</i>) Through Genetic Technologies	Prof Chengdao Li
Jixiang Wang	Genetic Dissection of Branching Architecture in Narrow-leafed Lupin (<i>Lupinus angustifolius</i> L.) Using BSA-QTL-seq	Prof Chengdao Li
Zixun Wang	Molecular Mechanism of Cucumber Mosaic Virus Resistance in Narrow-Leafed Lupin	Prof Chengdao Li
Jack Weatherhead	Genetic Analysis of Grain Weight in Narrow-Leafed Lupin: Marker Development and Co-Analysis of Grain Quinolizidine Alkaloids	Prof Chengdao Li
Wangzhen Wu	Improving Oat Quality Through Genetic and Genomic Analyses of Lipid Content and Groat Yield	Prof Chengdao Li
Chunsheng Xiao	The Molecular Mechanism Regulating Quinolizidine Alkaloid Content in Vegetative Tissues and Seeds of Narrow-Leafed Lupin (<i>Lupinus angustifolius</i>)	Prof Chengdao Li
Ugyen Yangchen	Evaluation of Transition to Organic Agriculture in Bhutan: Farmers' Readiness, Consumer Preferences, and Institutional Support	E/Prof Richard Bell
Md Asad Uz Zaman	Investigating the Microbiome Associated with Rhizosphere Soil, Mulch and <i>Phytophthora</i> Infestation of Avocados	A/Prof Kirsty Bayliss
Haoze Zhang	To be confirmed	Prof Chengdao Li
Xinyue Zhang	Development of a Pangenome and Super-Pangenome for Exploring Genomic Variation and Evolution in Apple	Prof Rajeev Varshney
Ting Zhou	Consumer Perceptions and Sensory Evaluation of Oat-Based Foods	Dr Andrew Tilley

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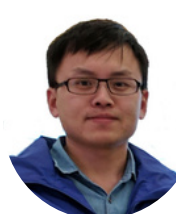
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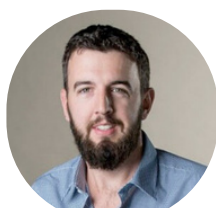


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