Murdoch University

Centre for Crop and Food Innovation

State Agricultural Biotechnology Centre
WESTERN AUSTRALIA

Annual Research Report

2024

Securing and sustaining the food bowls of the future

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 Prof Richard Bell)

Our expertise in soil, water and biodiversity management enables us 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 change 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
Director, CCFI

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, offering 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, increase tolerance to biological and environmental stresses.

Using cutting-edge genetic engineering methods, we transfer genes between related or unrelated species, employing recombinant DNA technology to develop genetically modified (GM) plants.

Our research also focuses on non-GM enhancements in yield, quality and 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.

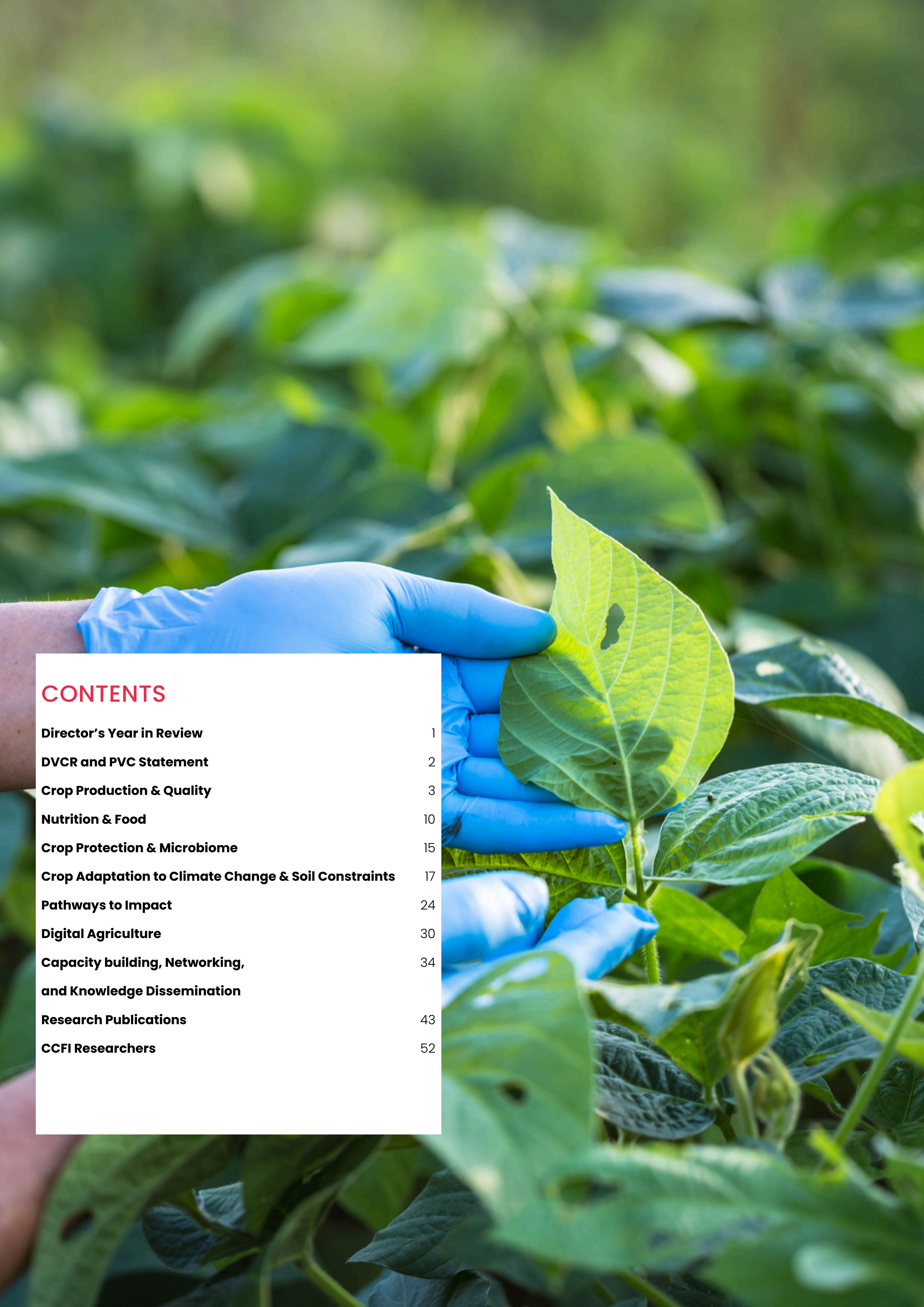
Inventive agri-tech and food technologies

Our teams of scientists, engineers and industry experts collaborate to unlock crop potential, employing advanced techniques including 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 contribute value to products through research on prolonging export shelf lives minimising anti-nutritional compounds and substituting plant proteins for animal proteins.



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Director’s overview

As the Director of the Centre for Crop and Food Innovation (CCFI) and the WA State Agricultural Biotechnology Centre (SABC), I am honoured to present our 2024 Annual Research Report and highlight key moments in an outstanding year of research excellence.

CCFI and SABC remains at the forefront of translational agricultural research in Australia, and through the efforts of our researchers, we are enhancing crop productivity and farmer profitability whilst striving for a more resilient and sustainable agricultural sector.

Together with our collaborators, we’ve made groundbreaking research contributions, particularly in genetics, genomics and molecular breeding.

A particular highlight has been our success in assembling pangenomes for key crops, including wheat, barley, peanut, and chickpea, while also developing improved genome assemblies for important horticultural species such as papaya, passionfruit, and pineapple.

These resources improve our understanding of genome evolution and provide actionable insights into traits that enhance productivity, nutrition, climate resilience, and resistance to pests and diseases.

I’m proud to share that collectively, CCFI researchers have contributed to +160 peer-reviewed papers, including 7 in Nature and Nature sister journals.

Importantly, our research outputs have not been bound to the hallowed halls of academia and I am immensely proud of our team’s effort to bring attention to their work through the various conferences, Centre tours, symposia and lectures that they have organised.

In total, CCFI and SABC have brought more than 1500 researchers, policymakers and industry representatives from +52 countries to Western Australia in 2024. We have also seen significant success in promoting our research to the public, achieving over 120 pieces of media coverage in key national and international publications to an audience of well over 80 million people.

We’ve also had fantastic success in promoting our research abroad, with CCFI researchers travelling to Argentina, China, India, the Philippines, Thailand, the UK, the USA, and more to present their research findings and add to the international research community’s efforts in enhancing crop productivity and achieving global food security.

A defining moment of the year was hosting the 3rd International Wheat Congress in September, which brought together over 950 members of the global wheat community to exchange knowledge, enhance productivity and advance wheat research.

The Congress had over 58 esteemed speakers, 35 panellists, 134 workshop speakers, and more than 380 poster presentations, covering a broad range of topics, including climate resilience, disease resistance, and the role of technology in transforming wheat farming practices. It also fostered important discussions on the most pressing challenges facing global wheat production, such as ensuring global food security whilst prioritising sustainability.

These events are important in demonstrating the quality of research being conducted across our two Centres and also play a key role in generating new research leads and collaborative opportunities with the international research community.

Speaking of collaboration, CCFI researchers have forged strong ties with industry in Australia and abroad. We have established excellent relationships with State and Federal government agencies, such as the Primary Industries in various states,; leading agricultural companies, such as Australian Grain Technologies, Chickpea Breeding Australia, and InterGrain; and international research organisations such as the Chinese Academy of Agricultural Sciences, Indian Council of Agricultural Research and the World Food Prize Foundation.

Through these collaborative endeavours, we can ensure that our research offers tangible and practical improvements for breeders, farmers and end-consumers in Australia and globally.

Another priority in 2024 has been capacity building and training the next generation of agricultural scientists.

Our early career researchers continue to go from strength to strength in terms of research outputs, and it has been fantastic to see them deliver presentations of their research at events such as the Plant and Animal Genome Conferences in Australia, China, USA, and the International Wheat Congress.

On the funding front, I am thrilled to share that in 2024 we secured over 10 new grants and investments for research and development for key cereal and horticultural crops.

I am sincerely grateful to our investors for their generous support, and we owe our success to their belief that we can contribute to research with impact. Special thanks go to the Grains Research and Development Corporation, Hort Innovation, the WA Agricultural Research Collaboration, International Atomic Energy Agency, and the Australian Centre for International Agricultural Research for their continued support of CCFI research; it’s sincerely appreciated.

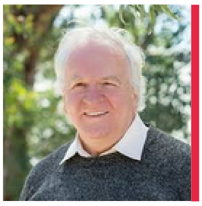
Finally, I’m delighted to note and celebrate the recognition of CCFI researchers for their outstanding research, including Prof Vicky Solah, who was awarded the Australian Institute of Food Science and Technology (AIFST) Keith Farrer Award for 2024, the Institute’s highest honour, and the CCFI researchers who received the 2024 Best Publication in STEMM Fields Award at Murdoch University’s 2024 Vice Chancellor’s Excellence Awards of Murdoch University.

In closing, I extend my deepest appreciation to our investors, collaborators, supporters, and of course, our exceptional team of researchers, whose passion, expertise, and dedication are the foundation of our success and the key to our future impact. I’d also like to thank Murdoch University’s research leaders, including the Vice Chancellor; Deputy Vice Chancellor, Research and Innovation; and Pro Vice-Chancellor, for their continued support of CCFI and SABC.

Professor Rajeev Varshney FRS

Director, CCFI, Murdoch University
Director, SABC, Murdoch University
International Chair - Agriculture and Food Security

PVC and DVCR Statement



Prof Peter Davies
Pro-Vice Chancellor,
Food Futures Institute

2024 has been a year of momentous achievements for CCFI and SABC. From world-class research to arranging industry-leading events, our researchers have continued to exemplify Murdoch University's commitment to research with impact.

While CCFI researchers have made their mark through pioneering research activity – as evidenced by the tremendous amount of papers published in prestigious academic journals – the most striking result from my perspective has been the two Centres' continued engagement with industry and the international research community.

We know that great research cannot be achieved in a vacuum – it requires inspiration, innovation, and a healthy dose of collaboration.

To that end, CCFI has maintained a phenomenal relationship with industry, the international research community and the general public through events, conferences, collaborative research initiatives and positive press coverage.

I'm pleased to note so many examples of ongoing collaboration. Internally, we've seen cross-disciplinary research between centres and a strengthening of ties with the School of Agricultural Science that ensures students are aware of the exciting career opportunities available to them.

Externally, we've seen new partnerships being made with prestigious research institutes around the world, support for exciting WA start-ups operating in SABC and fantastic knowledge-sharing and networking efforts through the myriad of conferences, guest lectures, strategy sessions and tours organised at Murdoch University.

Through continued engagement with industry, CCFI and SABC ensure that Murdoch University maintains its reputation as Western Australia's preeminent destination for agricultural research.

Prof Peter Eastwood
Deputy Vice Chancellor Research and Innovation, Murdoch University

Murdoch University is committed to undertaking interdisciplinary research of global significance, and we strive to align our research to three core strategic priorities, namely: Sustainability; First Nations Education; and Equity, Diversity and Inclusiveness.

It is with great pride that I note the ongoing success and achievements of CCFI and SABC researchers, who are at the forefront of internationally important research that paves the way for a more sustainable and inclusive world.

Throughout 2024, CCFI researchers have been involved in projects that deliver better results for Australian growers while reducing the environmental impact of commercial farming practices.

They have also lent their expertise and experience to neighbouring nations such as Bangladesh and India, spearheading important research projects that offer solutions to the growing challenges of climate change.

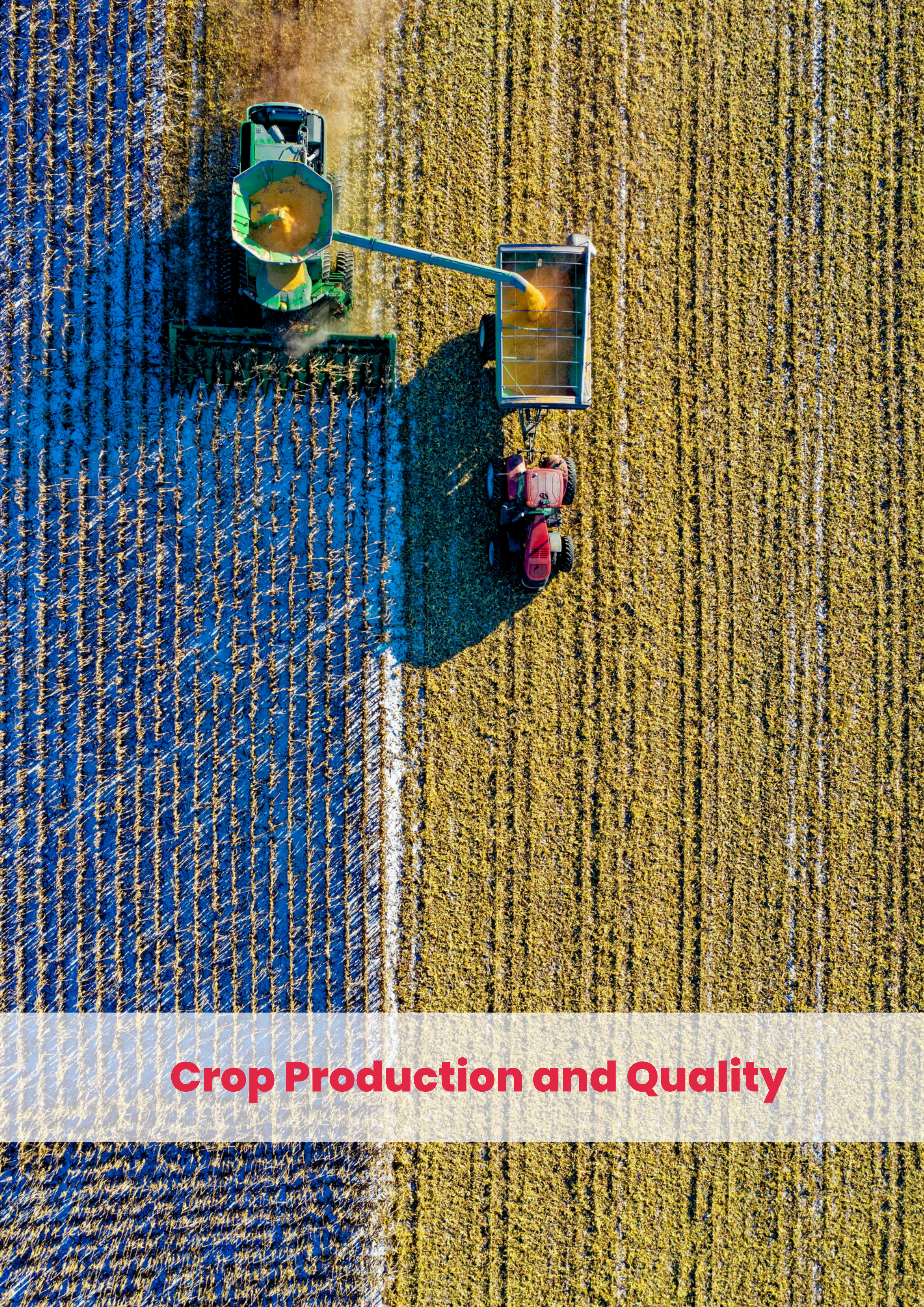
CCFI has a strong commitment to delivering agricultural research that improves the entirety of the food production process.

Under the CCFI umbrella, researchers are exploring soil health, water usage, seed quality, plant resilience, consumer health and much more.

This multi-pronged, cross-disciplinary approach is a powerful way to ensure that we have a future-proofed agricultural sector that can deliver better profits to farmers, reduce our carbon footprint, and improve food security and nutritional outcomes for all.

I am also excited to see Prof Varshney applying his expertise in genetics and biotechnology to the Health sector.

Given the links between food production, nutrition and overall health, his research in areas such as iron deficiency and anaemia adds great value to Murdoch University's capabilities as an outstanding provider of translational agricultural and health research.



Crop Production and Quality

Bridging structural variations with breeding and habitat adaptations in wheat

Murdoch project team:
Prof Rajeev Varshney (Project lead), Dr Vanika Garg, Anu Chitikineni.

Collaborating Organisations:
Australia:
Harry Perkins Institute of Medical Research, Fiona Stanley Hospital, La Trobe University.

International:
Chinese Academy of Agricultural Sciences, China; China Agricultural University, China; Smartgenomics Technology Institute, China; Nanjing Agricultural University, China.

Acknowledgments:
This research is supported by by Food Futures Institute, Murdoch University and Grains Research & Development Corporation (Project Nos. UMU2404-003RTX and WSU2303-001RTX).

Project overview:
Wheat is one of the three cornerstone crops that sustain human civilization, alongside rice and maize. It serves as a critical source of calories and nutrients for billions of people worldwide.

As climate change, evolving dietary preferences, and increasing population pressures reshape agricultural demands, a deeper understanding of wheat's genetic diversity and adaptability becomes essential.

The Wheat Pangenome Project is the most comprehensive study of wheat genomics to date, combining advanced long-read sequencing technologies to reveal structural variations, evolutionary dynamics, and breeding innovations spanning over seven decades.

This international effort, involving researchers from Australia and China, pushes the boundaries of wheat genomics and provides a vital resource for the next generation of breeding strategies.

Key highlights:

- Generated high-quality de novo assemblies of 17 wheat cultivars representing breeding stages from the 1950s to post-2000s, capturing the full breadth of genetic diversity.
- Identified 249,976 Structural Varioations, including 13,550 translocations and 1,049 inversions, providing insights into the genomic underpinnings of breeding history and crop evolution.
- Tracked mutations and duplications in the VRN-A1 gene, demonstrating how wheat adapted from spring to winter types in response to environmental changes.
- Found significant SVs in centromeric regions, which hinder chromosome recombination and are pivotal in sub-genome differentiation and cultivar evolution.
- Highlighted how genomic changes in wheat reflect dietary preferences, migration, and cultural integration in regions like Northwest China.

Impact and Applications

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

Key members of the international team of scientists from Australia and China attend IWC 2024

Adaptive diversification through structural variation in barley

Murdoch project team:
Prof Chengdao Li (Project lead), Dr Penghao Wang, Dr Brett Chapman, Dr Yong Jia, Dr Viet Dang.

Collaborating Organisations:
Australia:
Adelaide University, Agricultural Victoria, Department of Primary Industry and Regional Development (DPIRD).

International:
Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) Gatersleben, Germany; Carlsberg Research Laboratory, Denmark; The University of Montpellier, France; The James Hutton Institute, UK; Helmholtz Center Munich, Germany; The University of Zurich, Switzerland; Agriculture et Agri-Food Canada, Canada; The University of British Columbia, Canada; DSMZ-German Collection of Microorganisms and Cell Cultures GmbH, Germany; Lund University, Sweden; Guangdong Academy of Agricultural Sciences, China; Kazusa DNA Research Institute, Japan; King Abdullah University of Science and Technology, Saudi Arabia; Martin Luther University Halle-Wittenberg, Germany; Technical University Munich, Germany; The University of Minnesota, USA; Julius Kuehn-Institute, Germany; SECOBRA Recherches, France; University of Saskatchewan, Canada; Tottori University, Japan; Okayama University, Japan; University of Dundee, UK; German Centre for Integrative Biodiversity Research, Germany; Georg-August-University, Germany.

Acknowledgements:
This research is supported by the Grains Research & Development Corporation (Project No UMU1806-002RTX: Improved Genetic Gain through GRDC Participation in Barley Pan-genome Consortium), and the Department of Primary Industry and Regional Development.

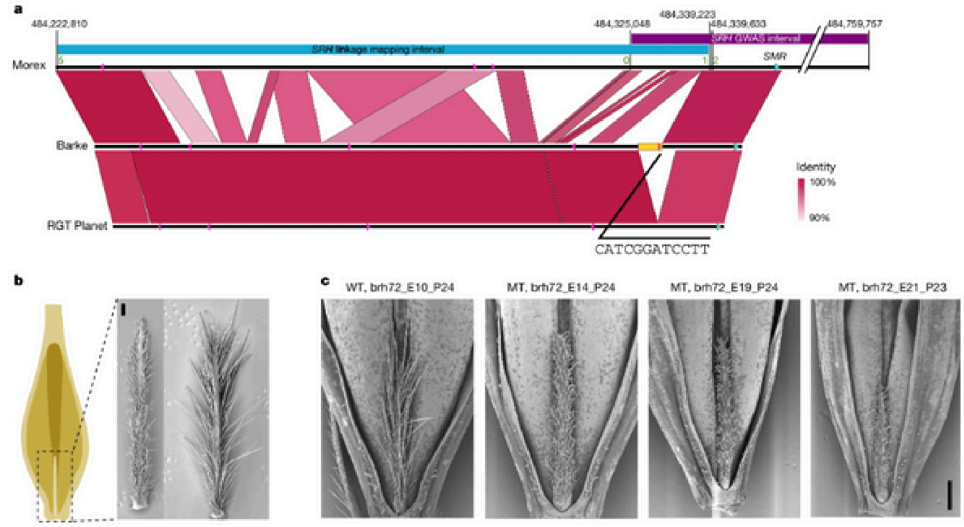


Fig A: Schematic representation of the high-resolution genetic linkage analysis at the Srh1 locus.
Fig B: Schematic drawing of a hulled and awned barley seed. On the right, scanning electron micrographs are shown of a short-haired and a long-haired rachilla of genotypes

Credit: Nature

Project overview:
Barley is among the top five crops globally and is the second largest crop in Australia. Its importance may increase in the future, because barley tolerates harsh and marginal environments and can adapt to dry climates.

Pangenomes are collections of annotated genome sequences of multiple individuals of a species.

The structural variants uncovered by these datasets are a major asset to genetic analysis in crop plants.

An international research team with 80 scientists from 12 countries completed a pangenome of barley comprising long-read sequence assemblies of 76 wild and domesticated genomes and short-read sequence data of 1,315 genotypes.

An expanded catalogue of sequence variation in the crop includes structurally complex loci that are rich in gene copy number variation.

Key project highlights:
Extensive genome assemblies:
We generated high-quality, long-read sequence de novo assemblies of 76 wild and domesticated genomes and short-read sequence data of 1,315 genotypes representing the worldwide barley germplasm diversity.

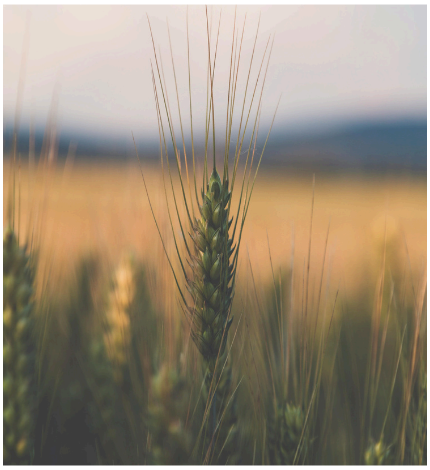
Exploring Australian Barley genomes:
The genomes for two popular barley varieties, *Maximus* and *RGT Planet*, were assembled and provided foundation for genomic-based barley breeding in Australia.

Dynamic barley genome:
Only one-third of the barley genes are conserved and two-third are variable, which provide new genetic variations for breeding.

Mechanism for better beer: Expansion of a family of starch-cleaving enzymes in elite malting barleys was linked to shifts in enzymatic activity in micro-malting trials.

Novel mechanism regulating gene function:
An enhancer motif is associated the developmental trajectory of the hairy appendages on barley grains.

Complex genetic loci for important traits:
Structurally complex loci have become hot spots of gene copy number variation in evolutionarily recent times and associated with disease resistance, plant architecture and nutrient release. Rapid evolution at structurally complex loci may have helped crop plants adapt to new selective regimes in agricultural ecosystems.



Adaptive diversification through structural variation in barley

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Impact and Applications:

The barley pangenome sheds light on crop evolution and breeding. For the first time, researchers were able to study the evolution of structurally complex loci of nearly identical tandem repeats, control disease resistance, plant architecture and malting quality. Phenotypic diversity has visibly increased in domesticated forms.

Malting created new selective pressures that only cultivated forms experienced. Novel allelic variation at disease resistance loci is both illustrative of the power of pangenomics, and is inline with our understanding of how disease resistance genes evolve.

A common concern among crop conservationists is dangerously reduced genetic diversity in cultivated plants.

But crop evolution does not need to be a unidirectional loss of diversity. This study has shown that valuable diversity can arise after domestication. Rapid evolution at structurally complex loci may endow domesticated plants with a means of adaptive diversification that aptly fulfills the needs of farmers and breeders.

More diverse crop pangenomes will help us understand how the counteracting forces of past domestication bottlenecks and newly arisen structural variants influence future crop improvement in changing climates.

From and Australian Perspective, gene copy number and structural variations provide new genetic resources for disease resistance, malting quality, and plant architecture improvement. The pangenome also provides a blueprint to bridge the genetic diversity gap between Australian barley and the worldwide barley germplasm.

> This knowledge will help us understand what other genetic resources are available but have not yet been used by barley breeders worldwide – opening the door to plant material from throughout the world from which to breed improved barley lines.
>
> *Prof Chengdao Li*

Project lead Prof Li and DPIRD Research Scientist Sharon Westcott undertake genetic sampling in the SABC lab.

Credit: DPIRD

Harnessing wild genes to revolutionise chickpea improvement

Murdoch project team:
Prof Rajeev Varshney, Dr Vanika Garg, Anu Chitikineni, Adj. Prof Abhishek Bohra, Adj. Prof Bharadwaj Chellapilla, A/Prof Reyazul Rouf Mir, Adj. Prof Kailash C. Bansal, Adj. Prof Xin Liu.

Collaborating Organisations:

Australia:
The University of Western Australia, Curtin University, MGI Australia.

International:
International Crops Research Institute for the Semi-Arid Tropics, India; The University of Missouri, USA; BGI Research, China; Baylor College of Medicine, USA; United Arab Emirates University, United Arab Emirates; The University of Georgia, USA; ICAR- Indian Agricultural Research Institute, India; SKUAST-Kashmir, India; NRGene Ltd, Israel; Washington State University, USA; National Academy of Agricultural Sciences, India.

Acknowledgements:
This research is supported by the Department of Agriculture and Farmers' Welfare, Ministry of Agriculture and Farmers' Welfare; Department of Biotechnology, Ministry of Science and Technology under the Indo-Australian Biotechnology Fund, Government of India; The Bill and Melinda Gates Foundation and Food Futures Institute of Murdoch University.

Project overview:

Food security stands as one of the most pressing global challenges today. The accelerating impacts of climate change are introducing a range of threats to agricultural systems.

Some regions are experiencing flash droughts, while others face severe flooding due to extreme rainfall. A warming planet is also creating favorable conditions for certain pests and diseases, further jeopardizing crop production

Compounding these challenges, access to food in many parts of the world has been steadily declining in recent years due to conflicts, inflation, and climate-induced extreme weather events.

To ensure farmers can continue producing food in the face of these uncertainties, developing resilient and versatile crop varieties is paramount.

Chickpea, a self-pollinating annual legume, is a vital crop cultivated primarily in arid and semi-arid regions. Its global production exceeds 17 million tons annually, underscoring its importance as a source of plant-based protein.

However, chickpea cultivation is constrained by several biotic (e.g., pests and diseases) and abiotic (e.g., drought, heat) stresses. While traditional and modern breeding techniques have enhanced chickpea productivity, further advancements are crucial to meet the increasing global demand for sustainable protein sources.

A significant challenge to chickpea improvement lies in its limited genetic diversity, a consequence of evolutionary bottlenecks, domestication, and selective breeding.

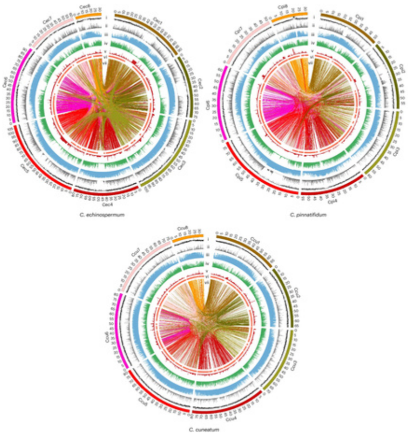
This low genetic diversity increases the crop's vulnerability to pests, diseases, and environmental stressors. To address this limitation, crop improvement programs are increasingly incorporating crop wild relatives (CWRs). CWRs are invaluable sources of genetic traits that confer resistance to pests and diseases and tolerance to harsh conditions such as extreme temperatures and drought.

The availability of a reference genome for chickpea (CDC Frontier genotype) has been a milestone in characterizing its genetic diversity. However, relying solely on a single linear reference genome captures only a fraction of the species' genetic variation, introducing biases and limiting the scope of breeding programs.

The concept of a pangenome, which encompasses the complete gene set of a species, has emerged as a solution to this limitation. To fully harness genetic diversity for crop improvement, a super-pangenome — including accessions from multiple species and wild relatives within the same genus— is critical.

This project highlights the development and analysis of reference-grade, de novo genome assemblies for eight annual wild species of the *Cicer* genus, which represent diverse gene pools: *C. reticulatum*, *C. echinospermum*, *C. bijugum*, *C. judaicum*, *C. pinnatifidum*, *C. yamashitae*, *C. chorassanicum*, and *C. cuneatum*.

These genomic resources will provide a foundation for unlocking the genetic potential of wild relatives, enabling the development of robust chickpea varieties capable of thriving under future environmental challenges.



Genomic features of C. echinospermum (top left), C. pinnatifidum (top right) and C. cuneatum (bottom) are shown as representative of three gene pools

Credit: Nature Genetics

Harnessing wild genes to revolutionise chickpea improvement

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Project highlights:

Genome assembly and annotation of wild *Cicer* genomes:
Chromosome-length assemblies for eight wild *Cicer* species were generated using high-throughput chromosome conformation capture sequencing (Hi-C), producing 1.14 terabytes of data, with an average of 143.03 Gb per species. Gene prediction, performed using ab initio, homology-based, and transcriptome evidence-based approaches, resulted in an average of 25,546 gene models per species.

Additionally, each genome contained an average of 94 microRNAs (miRNAs), 699 small nucleolar RNAs (snoRNAs), 704 transfer RNAs (tRNAs), and 11,590 ribosomal RNAs (rRNAs).

Genome organization and phylogeny:
Comparative analyses revealed significant genomic reorganisation between cultivated and wild *Cicer* species. Phylogenetic studies using single-copy orthologs classified the *Cicer* species into three main groups corresponding to primary (gene pool I), secondary (gene pool II), and tertiary (gene pool III) gene pools.

Cicer super-pangenome:
A total of 24,827 gene families were identified, categorized into core (14,748; present in all species), softcore (2,958; present in nine species), dispensable (6,212; present in two to eight species), and species-specific (909) gene families. Core genes, which were longer on average, were associated with essential biological functions like growth, DNA repair, and RNA processing. In contrast, dispensable genes were enriched for traits critical to cultivation, such as defense responses, auxin signaling, and ion homeostasis.

Furthermore, the graph-based super-pangenome spanned 626,731,090 nucleotides, comprising 20,044,138 nodes (sequence fragments) and 20,499,343 edges (connections between nodes).

Identification of SNPs and small InDels:
By aligning wild *Cicer* genomes and the desi type against the kabuli genome, 29.44 million nonredundant SNPs and 6.33 million small insertions and deletions (InDels, <50 bp) were identified. Variants linked to key traits, including LEO1 (vernalization), FCA (flowering time control), and EDR (enhanced disease resistance), were discovered.

.Identification of structural variations:
A total of 491,937 structural variations (SVs) were identified, comprising 260,421 deletions, 199,890 insertions, 25,215 translocations, 5,224 inversions, and 1,187 duplications. Notably, analysis of SVs in the drought-responsive 'QTL-hotspot' region on chromosome 4 revealed variations affecting *ERL1* and *TIFY 4A* genes.

Variations in flowering-time and resistance genes:
A total of 678 SVs overlapped with 200 flowering-related genes, with 88.11% (200 of 227) of these genes showing variations across the genus. For instance, the flowering-related gene Ca_v2.0_16385, encoding lysine-specific demethylase JMJ14, was impacted by SV events.

Additionally, 13 dispensable flowering-related gene families were identified. Population-wide SV analysis revealed 1,667 SVs affecting 556 resistance (R) genes, indicating that 67.07% (556 of 829) of R genes exhibited variations. The *Ca_v2.0_04252.1* gene, encoding the disease resistance protein *RGA1*, was notably affected.

Impact and applications:

The identification of candidate genes associated with adaptation to diverse abiotic and biotic stresses presents significant opportunities to enhance the resilience of cultivated chickpea to climate variability.

The graph pangenome offers a powerful genotyping platform for SV-based association studies, enabling the discovery of genetic signals underlying agronomically important traits.

These genomic resources, encompassing genome assemblies, genetic variations, and the graph pangenome, provide a foundation for accelerating chickpea improvement and will greatly benefit the global chickpea breeding and research community.

> The genomic resources and unique genes presented in distant relatives of modern-day chickpeas in this new study will greatly benefit chickpea breeding and the advancement of the research community in this area in Australia and globally
>
> The *Cicer* super-pangenome offers a powerful way to study chickpea genes to perform association analyses and determine the most important traits for our farming industry.
>
> Our study found that the wild species have more genetic diversity and variations that could be useful for improving chickpea traits such as disease resistance, flowering time, and stress tolerance.
>
> *Prof Rajeev Varshney*

There is significant scope to enhance Australian chickpea production, which would contribute to both environmental sustainability and growers' profitability.

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.

Collaborating Organisations:

Australia:
The University of Queensland; Agriculture Victoria; New South Wales Department of Primary Industries and Regional Development; Chickpea Breeding Australia; The University of Adelaide; The University of Sydney; Analytics for the Australian Grains Industry - Curtin University.

International:
International Center for Agricultural Research in the Dry Areas, India.

Acknowledgements:
This research is supported by Grains Research & Development Corporation (GRDC Contract code: UMU2403-009RTX).

Dr Rutwik Barmukh and Prof Rajeev Varshney review chickpeas growing in SABC's glass house.

Credit: CCFI

Project Overview:

Australia's current pulse-based production systems face challenges related to low profitability, which can be improved by enhancing crop productivity alongside market development.

A key factor contributing to the limited genetic gains in pulse breeding programs is the narrow genetic base of cultivated varieties, coupled with the insufficient integration of modern genomic resources and technologies.

This genetic bottleneck limits the adaptability of pulse crops to climate change, highlighting the urgent need to exploit the untapped potential of genetic diversity and advanced genomic tools.

By incorporating genetic diversity from wild relatives and leveraging cutting-edge technologies such as speed breeding, genomic selection, and AI-driven breeding, it is possible to achieve an unprecedented 1.5% increase in genetic yield gain for pulse crops.

As part of this project, select diverse germplasm for three pulse crops will be imported from ICARDA to Australia. Concurrently, a core set of 200–300 germplasm accessions for these pulses will be identified and thoroughly characterized through genome sequencing/genotyping, alongside multi-location field evaluations for yield and agronomic traits across 3–5 sites in 3–4 states over a two-year period.

The resulting comprehensive datasets will be analysed to establish haplotype catalogues at both chromosome and gene levels.

Subsequently, artificial intelligence (AI), genomic prediction, and speed breeding will be employed to stack novel and superior haplotypes for yield and yield-related traits.

Finally, the project aims to establish "PulseBase", a centralised platform to host the newly generated datasets along with other relevant existing data.

This comprehensive approach is expected to support various breeding programs in delivering high-yielding pulse varieties, meeting the evolving demands of agriculture in Australia and beyond.

Close up of a Chickpea flower growing in the SABC glass house

Credit: CCFI

> By incorporating genetic diversity from other landraces and employing the aforementioned advanced breeding techniques and AI, we believe we can achieve a 1.5 per cent increase in genetic gain, which would be unprecedented.
>
> Pulses are such important crops for Australian growers because of their benefits to soil fertility and environmental sustainability
>
> We believe the research and breeding activities could lead to increased uptake of the three crops in non-traditional growing areas, particularly across Western Australia.
>
> *Prof Rajeev Varshney*

Nutrition and Food

Discovery of desirable aroma, flavour and texture compounds for oat food and beverage applications

Murdoch project team:
Dr Bob Du, Prof Vicky Solah, Andrew Tilley, Dr Wendy Hunt.

Collaborating Organisations:
InterGrain; Curtin University; Edith Cowan University; Agriculture Victoria; Fancy Plants; Oatly; Sanitarium; Uncle Toby's, Blue Lake Milling; Quker; Noumi; Seamild; Australian Export Grains Innovation Centre; Shaanxi Normal University, China.

Project overview:

The Oat Grain Quality Consortium (OGQC) is a collaborative Grains Research and Development Corporation (GRDC) investment aimed at addressing the crucial need for innovation in oat quality research, informing oat quality classification and market positioning.

This research initiative will see more than $12.5 million invested in oats over 5 years – $5.75 million from GRDC complemented by $6.7 million from research and industry partners.

Led by InterGrain and the South Australian Research and Development Institute (SARDI: the research division of the Department of Primary Industries and Regions SA), the consortium will bring together a diverse group of organisations spanning the research, production, processing, and food and beverage manufacturing sectors.

Key Highlights:

·Program 2: Discovery of desirable aroma, flavour and texture compounds for oat food/beverage applications, aims to help differentiate Australian oats in the market by providing breeders with actionable information on the genetic variation of 'taste' compounds, and support breeding efforts to enhance the sensory appeal of Australian oats for existing and new oat products.

It will also provide industry and researchers with insights into desirable aroma, flavour and texture compounds for oats.

Impact and Applications:

The project will provide crucial information to improve the value and quality of Australian oats.

L-R, Dr. Janine Croser, SARDI program leader for crop and pasture improvement; Nigel Hart, Managing Director, GRDC; Dr. Dini Ganesalingam, Research and Business Development Manager, InterGrain; Dr. Haelee Fenton, Cereal Chemist, InterGrain.
Credit: GRDC

> We know that the global demand for diverse and nutritious oat-based products is on the rise and there is a clear opportunity for Australian agriculture to lead the way in quality and sustainability. This is why GRDC has initiated and invested in this consortium on behalf of Australian growers.
>
> This research will benefit the entire Australian oat supply chain by providing breeders with new traits that align with market demands, improving efficiency and reducing costs for processors, and expanding the range of oat-based products that manufacturers can offer consumers globally.
>
> Ultimately this work aims to position Australian oats as the go-to-product for consumers, both domestically and overseas, which will have significant flow-on benefits for our growers.
>
> *GRDC Managing Director Mr Nigel Hart*
> Source: GRDC Groundcover

Building an Advanced Genomics Platform for Australian horticulture

Murdoch project team:
Prof Rajeev Varshney (Project lead), Dr Vanika Garg, Anu Chitikineni.

Collaborating Organisations:
Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, Queensland Department of Primary Industries, Griffith University.

Acknowledgments:
This research is supported by Hort Innovation (AS21006).

Project overview:

The horticulture industry, encompassing fruits and vegetables, is one of Australia's most vital agricultural sectors, with an annual production value exceeding $15 billion.

However, improving fruit crops remains challenging due to long generation intervals, heterozygous and heterogeneous genetic backgrounds, and limited knowledge of complex trait architectures. For instance, breeding a single commercial variety of custard apple, 'Maroochy Gold,' took 25 years.

To address these challenges, cutting-edge genomic tools, enabled by advanced sequencing technologies, are revolutionising breeding programs by facilitating informed decision-making and accelerating the development of elite cultivars.

Major fruit crops such as apple, mango, and melon have already benefited from high-quality genome assemblies and the identification of key trait-associated alleles. Genomic analyses in these crops have provided critical insights into domestication and evolution, highlighting genomic targets for future breeding.

However, genetic information related to yield and fruit quality remains limited for many other fruit crops.

To bridge this gap, this project aims to develop comprehensive genomic resources for five economically significant fruit species: banana (Musa spp.), custard apple (*Annona muricata*), papaya (*Carica papaya*), passionfruit (*Passiflora edulis*), and pineapple (*Ananas comosus*).

As part of this $13 million investment, launched in 2022, we have made significant progress in generating high-quality genomic resources.

We have selected five banana accessions, two pineapple accessions, three papaya accessions, one custard apple accession, and three passionfruit accessions for the development of haplotype-resolved, chromosome-length, reference-grade genome assemblies. These selections include commercial cultivars, breeding program parent lines, and wild relatives with key traits for crop improvement.

For these accessions, we have successfully generated high-throughput long-read sequencing data and long-range genomic information. Reference-grade assemblies have been completed for ten accessions average two from each crop providing a strong foundation for ongoing research and breeding efforts. Beyond these chromosome-length reference assemblies, we have selected 58 additional accessions across the five target crops (24 banana, 10 pineapple, 8 papaya, 8 custard apple, and 8 passionfruit) for the development of reference-guided genome assemblies.

Sequencing data have already been generated for 55 of these accessions using our in-house high-throughput DNBSeq-T7 platform. Additionally, transcriptome sequencing data have been generated for all five crops, further supporting gene function prediction and annotation efforts.

As part of our capacity-building and knowledge dissemination efforts, two PhD students and two research associates have been recruited and are actively being trained in advanced genomic techniques.

Furthermore, multiple workshops and conference presentations have been conducted to promote the project and engage with the broader scientific and industry communities.

These activities not only contribute to workforce development but also facilitate knowledge exchange, ensuring the project's long-term impact on horticultural research and breeding.

Impact and applications:

This project lays the groundwork for sustainable crop production and breeding programs by providing high-resolution genomic resources.

These datasets will empower breeders and researchers to develop resilient, high-yielding varieties tailored for Australian agriculture, ensuring long-term productivity and sustainability in the horticulture sector.

> Australian growers not only face customer demand issues, but they are dealing with climate change, food security and agricultural issues.
>
> Our state-of-the-art platform will deliver genetic solutions and the development of modern tools to identify genetic variation for improvement in these five important horticultural crops.
>
> *Prof Rajeev Varshney*

Globe artichoke: Characterisation from farm to plate

Murdoch project team:
Prof Vicky Solah, A/Prof Kirsty Bayliss, Dr Julia Anwar-McHenry, Dr Mark McHenry, Andrew Tilley.

Collaborating Organisations:
Future Food Systems CRC, Mt Lindesay farm, Murdoch University Food Futures Institute, Australian National Phenome Centre.

Acknowledgements:
This research is supported by Future Food System Co-operative Research Centre (Project No. P3-006). Andrew Tilley is supported by an Australian Government Research Training Program scholarship.

Overview:

There is growing interest in expanding the Australian globe artichoke industry by pursuing export opportunities. However, distance from international markets and short shelf-life of fresh artichokes presents a barrier.

Value-add processing into ready-to-eat products with longer shelf life is a viable way to overcome these challenges. However, the high phenolic concentrations in artichoke that appeal to consumers for their health benefits also cause rapid and extensive enzymatic browning during processing.

Previous efforts have focussed on selecting varieties with low phenolic concentrations as a way of reducing browning susceptibility.

Development of new artichoke varieties with high phenolic concentrations and low browning susceptibility can provide Australian growers with a point of differentiation in the competitive international markets.

This project utilised the crop grown at Mt Lindesay to identify artichoke lines with high phenolic concentrations and low browning susceptibility. How environmental factors influence phenolic accumulation was investigated.

Mechanisms of browning were explored and the relative contribution of specific phenolics analysed.

Plasma-activated water (PAW) was evaluated for its anti-browning potential during artichoke processing.

Key Highlights

- Environmental factors: Identified solar radiation as important factor influencing phenolic accumulation in artichokes
- High phenolic, low browning artichoke lines: Identified artichoke lines with desired attributes for subsequent vegetative propagation.
- Phenolic contribution to browning: Demonstrated that some phenolics contribute relatively more to development of browning.
- PAW as an effective anti-browning treatment: Demonstrated its efficacy as an additive free anti-browning treatment during artichoke processing.

Impact and Applications
Browning affects many fruit and vegetable crops, understanding how specific phenolics contribute to browning opens new opportunities for developing low browning varieties while maintaining nutritional quality.

The project provided new evidence to support the progression of PAW as a new processing technology for the food industry.

> “Looking forward beyond just artichokes, this applies to a wide range of horticultural products.
>
> Can we apply this same approach of identifying specific phenolics to create apple lines that don't go brown but have a high phenolic content?
>
> There's a lot of potential to explore this sort of approach in creating processing friendly cultural lines that are still really good for us.”
>
> *Andrew Tilley*

L-R: Andrew Tilley, Dr Doan Nguyen, Dr Nima Gunness, Dr Mark McHenry in artichoke fields at Mt Lindesay, WA

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; the Department of Primary Industries and Regional Development; Department of Primary Industries, Queensland; The University of Adelaide; The Northern Territory Department of Industry, Tourism and Trade.

Acknowledgments:
This research is supported by Hort Innovation (AS23003)

Project overview:
The Australian horticulture industry continues to grow, contributing over $15 billion annually to the national economy.

Among its key sectors, fruit tree orchard industries including almond, apple, citrus, macadamia, and mango generate over $3 billion in revenue annually, underscoring their critical importance.

However, this sector faces evolving challenges and opportunities, such as the rise of automation, labor shortages, emerging diseases, and climate change.

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.

Addressing these priorities, this $41 million investment will deliver tools for breeders, growers, and scientists to accelerate the development of new cultivars and sustainable growing systems, enhancing production and profitability in next-generation orchard systems.

Specifically, this project aims to identify/characterise the genetic regulation of key productive traits, integrate molecular markers, develop genomic selection models for current breeding programs that efficiently select plants with desirable traits, and enhance orchard production systems through better interventions with plant growth regulators.

To maximise space and resources in next generation orchards, this project will focus on the development of smaller, less vigorous tree varieties planted at higher densities.

These smaller, high-density orchards will maximise yield per unit area and support the implementation of automated management tools that will help growers improve their productivity at reduced costs.

Increased knowledge of the genes and molecular signals that regulate important traits, such as flowering and reproductive bud dormancy, tree architecture and vigour, fruit quality (blush/degreening), retention and nut drop, disease resistance can enable precision breeding for traits of interest and improve orchard management through the application of molecular breeding, the application of specific plant growth regulators and automated management.

This project focusses on mango, macadamia, citrus, apple, and almond as core tree crops fundamental to horticulture innovation in Australia.

Impact and applications:

This program builds on the previous work of the National Tree Genomics Program (AS17000), which delivered essential genomic resources and genetic knowledge around key traits for five important Australian tree crop species: almond, citrus, macadamia, apple and mango.

These genomic resources paved the first steps towards enabling breeders with new genetic knowledge that assists in delivering new varieties with beneficial traits and new tools for growers to enhance productivity in next-generation orchard systems.

This phase of research focuses on further integrating genomics and molecular markers into breeding programs.

It aims to equip breeders with advanced tools to inform decision-making and optimize the selection of new varieties with desired trait combinations. These efforts align with Hort Frontiers' strategic priorities, which include increasing labor-use efficiency, enabling automation, and improving resilience to climate change and diseases.

In the long term, this program will support the development of high-value new varieties, significantly enhancing industries currently worth $3 billion annually.

By doing so, the program will ensure the long-term viability, sustainability, and global competitiveness of these critical sectors.

Australia's horticulture industry contributes over $15 billion annually to the national economy

Led by:

Crop Protection and Microbiome

Determining the microbes associated with avocados, tomatoes and potatoes

Murdoch project team:
A/Prof Kirsty Bayliss (Project lead), Prof Treena Burgess, Dr Penghao Wang, Prof Richard Bell, Dr Giles Hardy, Dr Anish Shah, Jennifer Goldberg, Dr Kay Howard, Henry Obiazikwor, Asad Zaman, Sumitra Saha.

Collaborating Organisations:
Hort Innovation, Future Food Systems CRC, Ecogrowth, Melville Park.

Acknowledgements:
This research is supported by Hort Innovation (Project No. AS19004), Future Food Systems CRC (Project P2-021), Ecogrowth and Melville Park.

Project Overview:

Increasing the yield of fruits and vegetables, particularly those that are popular with consumers, means greater profits for Australian growers and for our horticulture sector.

Hypothesising that healthier crop microbiomes mean more productive plants, the project team is looking for the microbes most strongly associated with higher-yielding plants in popular Australian horticultural crops.

The goal is to identify a range of microbes associated with increased production and yield, especially in the face of abiotic and biotic stresses. Our focus is potatoes, tomatoes, and avocados, and we have selected stresses ranging from nematodes and root rots to high temperatures.

The project is now in Year 3, and has generated some interesting results.

Key project highlights:

Tomatoes
Application of biological products increased the yield of field-grown tomatoes by at least 20 % compared with untreated controls.

Similarly, treated plots had at least a 15 % increase in dry root biomass compared with the untreated control.

However, plant growth stage may substantially impact the microbiome structure more than the biological product applied, and the impact of treatment on the microbiome may be independent of the plant growth stage.

Potatoes
Bacterial communities associated with the peel and flesh of two potato varieties had different responses when grown in the same field. For both varieties, the peel microbiomes of the seed and daughter tubers changed significantly, becoming very uniform in the daughter tubers. This suggests the peel microbiome is strongly influenced by the surrounding environment.

For the flesh however, while the seed and daughter tuber microbiomes did change, they were not as uniform in the daughter tubers as the peel.

Four bacterial families were consistently associated with all potato samples, across both varieties, suggesting these are members of a core potato microbiome.

One bacterial species was identified that is known to be heat tolerant, and this will be investigated in forthcoming trials.

Avocados
Analysis of the microbiome data from avocados in three biogeographical regions in Western Australia suggests a core microbiome is found across the regions, but there are unique core taxa specific to each region.

Core taxa may be associated with avocado growth regardless of farm management practices, climate or soil type.

Sampling Challenges
Three different sampling strategies were tested, to confirm if the method used to collect microbiome samples in the field has any impact on the microbial community.

Comparing the strategies in two different avocado orchards, it was found that the relationship between bacteria and soil physicochemical properties changes depending on the sampling used.

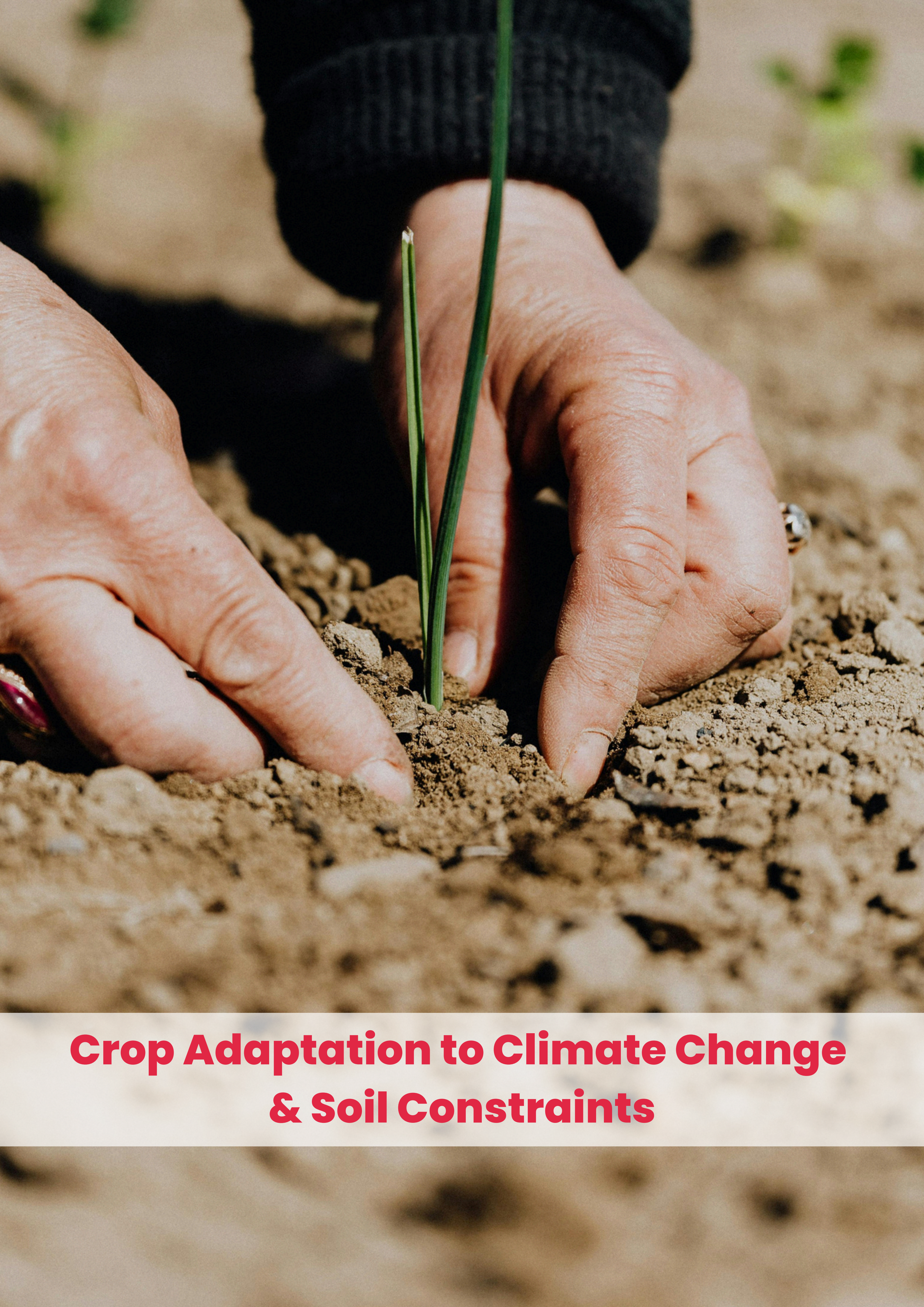
For example, soil pH was a driver in the grid-based sampling, but sulphur, nitrate and ammonium were the drivers in a longitudinal transect.

However, for the fungal community, there was no significant soil property identified as driving that community, in any of the three designs.

Impact and Applications

Our goal is to discover consortia of beneficial microbes based on a sequence data-driven approach.

We aim to select microorganisms associated with crops that exhibit higher tolerance to our selected stresses and develop these into new products that increase crop yield.



Crop Adaptation to Climate Change & Soil Constraints

Increasing wheat nitrogen use efficiency through improved genetics

Murdoch project team:
Prof Rajeev Varshney (Project lead), A/Prof Reyaz Rouf Mir, Dr Vanika Garg, Anu Chitikineni.

Collaborating Organisations:
Department of Primary Industries and Regional Development, The University of Western Australia, Australian Grain Technologies, Analytics for the Australian Grains Industry - Curtin University.

Acknowledgements:
This research is supported by Grains Research & Development Corporation (GRDC Contract code: UMU 2404-003RTX).

Overview:

Nitrogenous fertilizers are vital to agriculture. However, wheat crop uses less than 40% of applied nitrogen and only 33% is recovered in the grain.

Improving Nitrogen Use Efficiency (NUE) will maximise wheat yield and grain protein - and thereby profitability - to wheat growers.

Our previous research identified large effect QTLs (genes) in wheat that have a positive impact on NUE and/or grain protein content (GPC) without detrimental effects on grain yield (GY).

In 2023, Prof Rajeev Varshney, in collaboration with partners succeeded in securing a grant from the Grains Research and Development Corporation (GRDC) for a total investment of $7.2 M to develop wheat lines with higher NUE, grain protein content and grain yield.

This project, led by Murdoch University, in collaboration with The University of Western Australia, DPIRD-WA, and Australian Grain Technology breeding company under the framework of Western Australian Agricultural Research Collaboration, plans to elucidate the molecular mechanism and function of alleles/haplotypes of the target QTLs and develop robust genetic selection tools for breeders.

The project team will also introgress target QTLs into Australian wheat varieties and will select improved introgression lines following multi-location evaluations in Western Australia, South Australia and New South Wales.

In summary, the project will expand the understanding of genetic regulation of NUE related traits and will deliver robust genetic selection tools, phenotyping protocols and pre-breeding material for enhancing grain growers' profitability and to improve sustainability of wheat production in Australia.

L-R, Prof Rajeev Varshney (CCFI), Dr Dion Bennett (AGT Breeding) and Dr Darshan Sharma (DPIRD) inspect NUE wheat project progress in Northam
Credit: CCFI

> Enhancing nitrogen use efficiency is pivotal for maximising wheat yield, grain protein content and, ultimately, the profitability of wheat growers.
>
> While nitrogenous fertilisers play a crucial role in agriculture, wheat crops currently use less than 40 per cent of applied nitrogen, with only 33 per cent being recovered in the grain.
>
> By collaborating with leading institutions and industry partners we are not only expanding our understanding of genetic regulation in wheat but also providing practical solutions and tools for breeders to develop improved wheat varieties.
>
> *CCFI Director and Project Lead Prof Rajeev Varshney*

Novel foliar fertilisers and nutritional trait diversity of grains

Murdoch Project team:
Prof Richard Bell (Project lead), Dr Tona Sanchez-Palacios, Prof David Henry, Prof Gerard Poinern, Dr Beth Penrose

Collaborating Organisations:
Grains Research and Development Corporation, Australian Nuclear Science and Technology Organisation, Australian Synchrotron, Wongan Hills Research Station, Department of Primary Industries and Regional Development, Australian Export Grains Innovation Centre.

Acknowledgements:
The 'Synchrotron Postdoctoral Fellow no. 4: Plants' project is funded by Grains Research and Development Corporation (UMU2001-001RTX). Access to Synchrotron-based technology and Nuclear Facilities at Lucas Heights in NSW was provided based on ANSTO's merit-based grant application scheme (M17443 & M18953)

Project Overview:

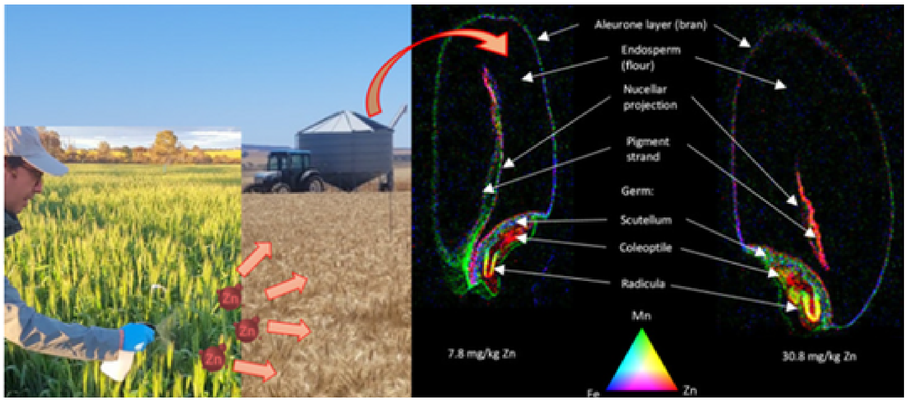
Benchmarks of micronutrients in modern high-yielding wheat cultivars that are relevant for human health have remained largely uncharacterised in Australian-producing regions.

The scope of this study is to investigate the nutritional profile of wheat grains cultivated over the past five years across different environments and soil types from field sites of the National Variety Trial (NVT) program established in Australia's South-Eastern and Western agroecological regions.

This project specifically investigates key agronomic and environmental variables that play a role in the concentration of micronutrients in the grain including zinc, iron, iodine and potent human antinutrients such as phytate.

Zinc in grain is of particular interest for this project as the soil zinc bioavailability is below sufficient (<0.2 mg Zn/kg as Zn-DTPA) in Australian subsoils.

Outcomes:
We determined low levels of dietary Zn in wheat cv. Scepter. Consequently, we developed and tested new liquid foliar fertiliser mixtures to be sprayed on mature wheat plants during flowering and grain-filling stages.



Dr Tona Sanchez-Palacios spraying Zn-foliar formulations on mature wheat plants at the field trial of Wongan Hills Research Station, WA. Zinc applied foliarly is then translocated to grain parts during the grain filling stage. Synchrotron-based X-ray fluorescence microscopy techniques can be used to resolve the spatial distribution and accumulation patterns of micronutrients in grains that are of interest to human nutrition - published in Advances in Agronomy, 2024.

This approach resulted in Zn-enriched wheat grain with concentrations matching and surpassing the recommended target for wheat Zn at 45 mg Zn/kg of grain, established by the World Health Organisation (WHO).

We further analysed the derived zinc-enriched grains for flour production and bread quality-baking analysis in collaboration with the Australian Export Grains Innovation Centre (AEGIC).

We employed state-of-the-art technology developed at the Australian Nuclear Science and Technology Organisation (ANSTO) to confirm the efficiency of zinc foliar penetration and mobility to wheat edible parts – the grains. ANSTO-based studies revealed the presence of Zn in parts of the grain that form the white flour during milling.

Two conference papers were presented at the biofortification workshop that took place at the 3rd International Wheat Conference (IWC) in Perth, Australia. This workshop brought together experts in the enrichment of wheat with micronutrients i.e. biofortification.

Discussion of different biofortification methodologies during the workshop ensures that the most appropriate and relevant approaches are provided to the Australian Grain Industry.

Participants of the International Wheat Biofortification Workshop in Perth, 2024. From left to right, Dr Velu Govindan (CIMMYT), Dr Roopali Bhoite (DPIRD, WA), Prof Richard Bell (Murdoch University), Dr Tona Sanchez-Palacios (Murdoch University) and Prof Alex Johnson (Melbourne University).

Key highlights

- Coordinating the wheat biofortification workshop as part of the 3rd International Wheat Congress.
- Presenting two conference papers at the biofortification workshop that highlighted the main findings of our project – the development and testing of new foliar fertilizers that increased the zinc (Zn) concentrations in wheat grain beyond the recommended dietary intake level of 45 mg Zn/kg, and the nutritional implications of high grain Zn levels in baked bread and cooked noodle products.
- Dr Tona Sanchez-Palacios and Dr Velu Govindan meeting in Mexico; Murdoch University is strengthening ties with CIMMYT in the area of wheat biofortification.
- Co-authoring an integrative literature review published in Advances in Agronomy on 'Zinc in soil-crop-animal-human health continuum'.

Impact and applications:

This project was developed to provide quality information on the nutrient profile of Australian wheat grains and the benefits of foliar fertiliser for producing wheat grain with a higher mineral nutrient profile.

This project investigated the application of Zn foliar fertilisers on wheat to achieve improvements in grain zinc concentrations for Australian grain producers to remain competitive in global export markets in the event of commercialisation of zinc-enriched wheat grains.

Understanding crop development and yield responses to mitigate high soil strength in Australian soils

Murdoch project team:
Prof Richard Bell, Dr Wendy Vance.

Collaborating Organisations:
The University of Queensland, AgCommunicators, La Trobe University, South Australian Research and Development Institute (SARDI), The University of Adelaide, Agriculture Victoria (AgVic), Western Australia No-Till Farmers Association.

Acknowledgements:
This two-year project is funded by Grains Research and Development Corporation (UOQ2308-006RTX).

Project overview:

High soil strength (HSS) is a widespread problem which restricts root growth and crop access to soil nutrients and water.

While deep tillage can increase yields in HSS, these effects are inconsistent and can be short-lived. Problems associated with tillage, such as efforts to implement and concerns about erosion, persist.

Despite considerable research on crop responses to deep tillage, several important questions thus remain:
How can growers assess whether they need to loosen the soil?

Will all crop species benefit equally from ripping?

Can the benefits of deep tillage be enhanced by growing crops with greater tolerance to HSS, or can tolerant crops overcome the need to rip?

Can primer crops penetrate HSS better and improve subsequent crops' rooting environment?

Murdoch University (MU) is collaborating with the Western Australia No-Till Farmers Association (WANTFA) for the Western Australian component of Objective 4.

Field experiments were set up in Western Australia (WANTFA and MU), Victoria (AgVic) and South Australia (SARDI) to identify:

- Crop production in relation to root growth limiting factors associated with high soil strength and water availability,
- Confirm the relevance of penetrometer benchmarks developed in the glasshouse for root growth for key grain crops and potential 'primer crops' in key soil types,
- Examine the potential for primer crops to improve root penetration in HSS to improve productivity of subsequent crops.

Murdoch University Crop and Pasture Science students in discussion with Farmers Trevor Symes and Dustin Michael in front of a tillage radish plot

Key project highlights:

Timely rainfall in both WA and SA led to good crop establishment, whereas below-average rainfall in Victoria resulted in poor establishment.

Early field trial results showed variable responses to ripping: positive in SA, neutral in WA, and negative in Victoria.
·Deep ripping in the WA site removed the soil strength barrier at 20 cm to 60cm depth in the soil profile.

Murdoch University Crop and Pasture Science students visited the site in the Bolgart to get an insight into soil constraints to crop production and the farming systems and management of the region.

Impact and applications
This project aims to provide knowledge to growers to improve profitability of high strength and compacted soils through crop selection, soil amelioration, and/or a combination of both.

> A major outcome of the project is to provide growers with some fundamental information on abilities for crop species to penetrate a high strength soil and provide a ranking scale that will aid grower decision making.
>
> *GRDC Sustainable Cropping Solutions Manager – West, Dr Rowan Maddern*
>
> *Source: GRDC Groundcover*

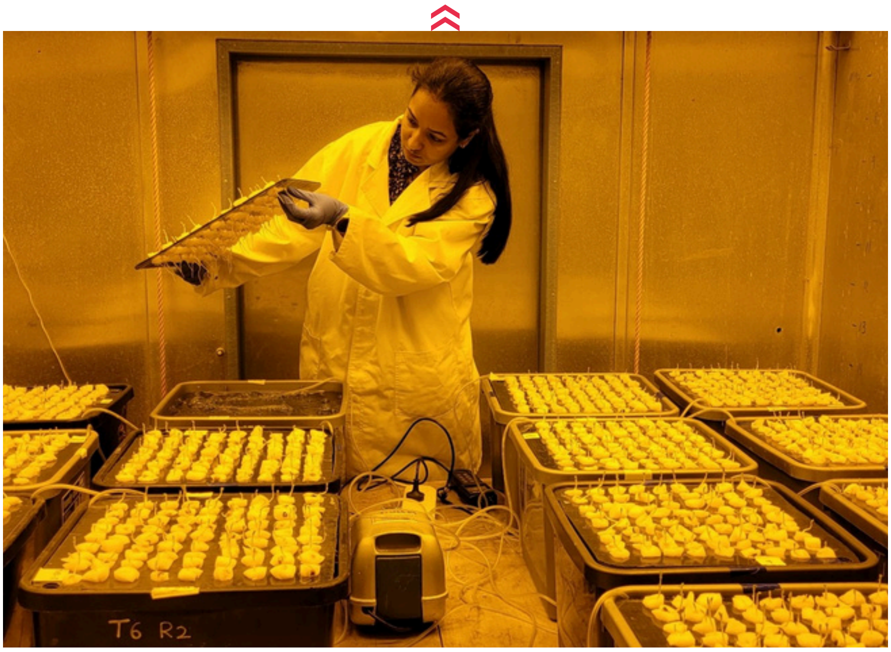
Identification of manganese toxicity tolerance in chickpea germplasm

Murdoch project team:
Prof Chengdao Li (Project lead),
Prof Richard Bell, Dr. Wendy Vance,
Dr Karthika Pradeep, Dr Yong Jia.

Collaborating Organisations:
Department of Primary Industries and Regional Development, Agriculture Victoria, Analytics for the Australian Grain Industry - Curtin University.

Acknowledgements:
This project is funded by Grains Research and Development Corporation (UMU2303-003RTX).

Dr Karthika Pradeep checking the transplanted chickpea seedlings in the growth cabinet at Murdoch University.



Project Overview:
Chickpea (*Cicer arietinum L.*) is an important pulse crop grown worldwide, with annual production exceeding 17 million tons worldwide.

The global chickpea market has increased considerably over the past decade, with an estimated 7.4% annual growth predicted between 2024 to 2032.

The soil current pH (CaCl2) recommendation for chickpea cultivation is > 5.5 and in acid soils, toxic levels of aluminium (Al) and manganese (Mn) are the limiting factors for plant growth.

Despite being an economically important crop, to date there has not been an acid tolerant cultivar developed.

Identification of acid tolerance could increase the productivity and expand the chickpea cultivation area into moderately acidic soils of Australia.

While excess Al is most common in severely acid soils, Mn is likely in moderately-to-strongly acidic soils, however, under waterlogging the toxicity is exacerbated and Mn toxicity can be seen even in recently limed or neutral soil if the parent material contains sufficient Mn.

High Mn concentrations in soil are widespread problem in south-eastern Australia, in north-eastern Victoria, and in waterlogging prone areas of Western Australian wheat-belt.

Identifying acid tolerance only based on Al toxicity will be incomplete without ensuring tolerance to Mn toxicity in chickpea germplasm.

With the advancements in sequencing and bioinformatics, markers from genome-wide association study (GWAS) could be used for genomic selection to predict superior lines based on genomic estimated breeding values (GEBVs). For a complex trait like Mn toxicity, GWAS is not widely reported in legumes and there is no study available on chickpeas.

Key project highlights
High throughput, reliable solution screening methodology for Mn toxicity tolerance in chickpeas was developed and 540 chickpea accessions were screened in solution culture based on relative shoot growth, root length and root growth parameters, and scoring of leaves for Mn toxicity symptoms.

A selection of 150 tolerant lines for Mn were identified from solution screening based on GEBVs and phenotyping analysis for further validation in soil screening.

GWAS results identified seven quantitative trait loci (QTLs) associated with Mn toxicity tolerance in chickpeas. Further allelic and haplotype analysis were performed based on QTLs and the superior haplotypes were identified.

Mn toxicity tolerance mechanism in chickpeas will be investigated in a selection of tolerant and sensitive lines.

Impact and applications:

This project aims to deliver the acid-tolerant (both Al and Mn) chickpea lines by 2027 through a comprehensive effort using the combination of controlled environment screening in solution and soil, genomic assisted breeding (genomic selection) and field validation.

This project aims to transfer the superior tolerance into key elite variety backgrounds for rapid adoption and integration within chickpea breeding programs.

Dr. Yong Jia collects flowering time data of the chickpea accessions sown in Merredin, WA.

Genetic solution for acid soil tolerance of chickpea

Murdoch project team:
Prof Chengdao Li (Project co-lead), Prof Rajeev Varshney (Project co-lead), Prof Richard Bell, Dr Yong Jia, Dr Wendy Vance, Dr Karthika Pradeep

Collaborating Organisations:
Department of Primary Industry and Regional Development, Agricultural Victoria, Pulse Breeding Australia.

Project overview:
Acid soils with aluminium toxicity is the single largest constraint after Ascochyta blight (AB) limiting chickpea productivity in Australia.

Among the pulse crops, chickpea is the most sensitive to acid soil conditions.

Current Australian chickpea varieties do not possess sufficient genetic variation for acid soils tolerance, which has hampered breeding progress for improved yield and local adaptation beyond the traditional areas of cultivation in southern and northern Australia.

While liming is the most effective management practice for reversing soil acidification, the use of crops tolerant of acid soils enables production to continue while the often-long process of soil amelioration proceeds.

Lime is also difficult to incorporate into the subsoil. While shallow incorporation of lime is sufficient to ameliorate surface soil acidity, serious subsoil acidity sometimes requires deep ripping to incorporate the lime to depth.

Extreme environmental conditions such as high temperature in summer, waterlogging at the end of winter and periodic drought, are likely to increase the incidence of Al3+/Mn2+ toxicities, which result in smaller plant root systems and compromised photosynthetic capacity. Al3+ toxicity can accentuate the problem with drought 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/Al3+ toxicity currently preclude its cultivation.

GRDC investment to screen wild Cicer lines for acid soil tolerance and Al^{3+} and Mn^{2+} toxicity tolerance has led to the identification of genetic variation for these traits and the development of segregating populations and a variety of screening technologies.

Key Highlights:
A large-scale genotyping and hydroponic-based Al tolerance screening of ~ 1500 diverse chickpea germplasm including natural accessions, wild Cicer lines, crossing populations, Australian chickpea cultivars have been completed.

Significant QTLs associated with Al tolerance have been identified on chromosomes 1, 4, and 7.

The corresponding SNP markers and putative candidate genes underlying these quantitative loci have been identified and assessed with gene expression analyses in selected parental lines.

A first-round selection and crossing of 10 Al-tolerant chickpea genotypes with selected cultivars have been performed to introduce the tolerant allele to Australian chickpea cultivars.

Genome sequencing and assemblies for 10 Australian chickpea cultivars have been completed. Candidate genes associated with Al3+ tolerance near the QTL from GWAS analyses have been identified and are being validated based on gene sequencing and RT-qPCR analyses.

Second year trial sites (2 in WA, one at NSW, VIC, and SA) have been selected and trial design finished. Third round of crossing from 26 complex cross combinations (designated as F1i-2) has been completed, yielding 312 F1 seeds, which has also been genotyped using the Pulse 30K SNP array.

Application and impact:
Acidic soils are a significant limitation towards improving chickpea productivity in Australia.

In growing regions such as Western Australia, over 75 per cent of cropping areas have acidic soils in the top or sub soils. With the exception of lupins, legumes do not usually adapt well to these soils. We estimate that the research outputs from this project could help expand Australian chickpea production into an additional 1.2 million hectares.

We are working very closely with chickpea breeders, almost in parallel, so the acid-tolerant germplasm and genetic markers that are being identified are delivered to the breeding program as soon as possible.

Acknowledgements:
This research is supported by Grains Research & Development Corporation (Project No UMU2303-003RTX: Developing genetic tools to facilitate breeder use and deployment of high value acid soils tolerant chickpea germplasm) and DPIRD.

WCGA Director Prof Chengdao Li, DPIRD Development Officer Greg Shea, GRDC Senior Manager - Genetic Technologies, Dr Francis Ogbonnaya and CCFI Director/Project Co-lead Prof Rajeev Varshney review progress of Cicer lines grown in acidic soil.

Credit: DPIRDWA

Genetic initiative to transform symbiotic nitrogen fixation in Australian pulse crops

Murdoch Project team:
Prof Rajeev Varshney (Project lead), Dr Rutwik Barmukh, Dr Vanika Garg, Anu Chitikineni.

Collaborating Organisations:

Australia:
The University of Queensland; La Trobe University; Australian National University; The University of Adelaide; New South Wales Department of Primary Industries and Regional Development; CSIRO; Australian Grain Technologies

International:
The University of California, Davis, USA.

Acknowledgments:
This research is supported by Grains Research & Development Corporation (GRDC Contract code: UOQ2403-012RTX).

Project overview:
The intensification and advancement of pulse cropping system present significant and multifaceted opportunities for Australia.

Pulse crops offer a unique array of benefits, serving as a rich protein source for both human consumption and animal feed, thereby supporting global food security and enhancing Australia's capability to meet national nutritional demands.

Additionally, their ability to fix and contribute nitrogen (N) to the soil provides environmentally sustainable strategies for agricultural production while aiding in achieving carbon-reduction targets.

Currently, pulse crops contribute \$1.99 billion to the national export economy and present a lucrative opportunity for producers, driven by the rapidly increasing global demand for plant-based protein.

Australia cultivates six primary pulses for both export and domestic consumption—chickpea, lentil, faba bean, lupin, field pea, and mungbean. These crops typically obtain around 60% of their nitrogen requirements from the atmosphere through symbiotic nitrogen fixation (SNF) with rhizobia bacteria. However, the proportion of nitrogen derived from the atmosphere (Ndfa) declines as soil mineral and organic nitrogen levels increase, leading plants to rely more on soil nitrogen. This gradual depletion of soil nitrogen necessitates the use of costly inorganic fertilizers in subsequent growing seasons. A deeper understanding of the SNF process at the genetic level, combined with the recognition of natural genetic variation in SNF efficiency within pulse species, presents significant opportunities to enhance nitrogen fixation through both phenotypic and genotypic selection in breeding programs.

Chickpea crops thriving in the SABC greenhouse

Highlights:

This \$14.69-million collaborative investment, including \$1.19 million allocated to Murdoch University, unites global leaders in nitrogen fixation research and predictive breeding with key pulse breeders and agronomists from Australia's diverse pulse-growing regions.

Building on two decades of legume research, the project leverages genetic insights from model legume species and cutting-edge technologies—such as artificial intelligence and advancements in molecular genetics and genomics—to enhance nitrogen fixation in Australia's major pulse crops, including chickpea, faba bean, field pea, lentil, lupin, and mung bean.

As part of this initiative, the project will establish a publicly accessible database, 'PulseBase', which will serve as a comprehensive repository of genotypic and phenotypic data for all six pulse crops included in the study.

Impact and applications:

By 2029, the project will provide Australian breeders of chickpea, faba bean, field pea, lentil, lupin, and mungbean with access to germplasm exhibiting improved N-fixing capacity, alongside reliable phenotyping tools and molecular selection techniques.

This will empower breeding programs to develop pulse varieties with enhanced nitrogen fixation potential.

The long-term vision, projected for realization by 2036, is to deliver new pulse varieties to Australian growers that achieve at least a 10% increase in nitrogen derived from fixation compared to current varieties.

Ultimately, this initiative will contribute to reducing the dependence on nitrogenous fertilizers in Australian farming systems, leading to lower greenhouse gas emissions (N_2O and CO_2) and reduced nitrogen pollution.

In addition to environmental benefits, growers will experience increased profitability and enhanced international competitiveness in terms of price, sustainability, and climate resilience.

Pulse crops contribute \$1.99 billion to Australia's export economy

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; New South Wales Department of Primary Industries; The University of Sydney; Frontier Farming Systems

Acknowledgements:
This research is supported by Grains Research & Development Corporation (GRDC Contract code: UOQ2402-010RTX).

Project Overview:

Chickpea is an important pulse crop in Australian farming systems, ranking among the largest in terms of production, cultivated area, and export value.

However, high temperatures pose a significant threat to current and future chickpea production, adversely affecting both yield and seed quality.

Chickpea is particularly sensitive to heat stress during the reproductive phase, with late-sown crops being especially vulnerable.

To help Australian growers maintain their competitive advantage and support future expansion, the development of new chickpea varieties with enhanced genetic heat tolerance is urgently needed.

This national initiative unites a multidisciplinary team of experts in agronomy, crop physiology, plant breeding, and genetics from leading research institutions to drive chickpea production advancements.

Field trials utilising a diverse range of chickpea germplasm will be conducted across key production regions and potential expansion areas.

State-of-the-art approaches, including crop modelling, high-throughput phenotyping, genomic prediction, and genetic simulations, will be employed to generate valuable insights, develop phenomic and genomic selection tools, and create pre-breeding germplasm.

CCFI Researchers review chickpeas growing in SABC's glass house.

Credit: CCFI

All phenotypic and sequencing data generated through this project will be made available in the 'PulseBase' database.

By working closely with industry partners, the project aims to accelerate the development of chickpea varieties with improved resilience to high temperatures, ensuring lower yield losses.

Australian chickpea growers are expected to benefit from sustained productivity and quality in existing growing regions, increased flexibility in sowing schedules, and opportunities to expand production into new areas.

By 2027, chickpea breeders and researchers in Australia will have access to improved germplasm and advanced genetic selection tools to support the development of chickpea varieties with 30% lower yield losses under day and night temperatures exceeding 32°C/20°C and during heat wave events at flowering.

> We know that when it comes to heat tolerance, we are dealing with complex genetics due to an interacting suite of physiological traits.
>
> That means many genes and gene interactions are at play.
>
> Deploying heat tolerance genetics will, therefore, entail learning which gene combinations to bundle together for different environments.
>
> Genomic prediction technology is ideally suited to performing these highly complex calculations and data integrations.

Dr Millicent Smith,
University of Queensland
Crop physiologist and
Project lead

Source: GRDC Groundcover

Led by:

Pathways to Impact

Towards improving tolerance to environmental stresses in wheat using gene-editing (GEd)

Murdoch project team:
Prof Michael Jones (Project Lead) Dr John Fosu-Nyarko, Dr Diem Ly, Ashaduzzaman Sagar, Upama Mondal, Chandan Maharana, Sandali Fernandes.

Collaborating Organisations:
Council of Grain Growers Organisations, Indian Council of Agricultural Research, Bioceres Crop Solutions, GreenBlueprint Pty Ltd.

Project overview:
Drought, frost, heat and salt stresses are major factors that limit wheat yield in Australia, and their incidence is predicted to increase.

The overall aim of this work is to improve tolerance to frost, drought and heat stress in wheat using GEd technology, which can result in produce that is not regulated as GMOs, and to enable GM wheat to be grown in Australia.

Project highlights, impact and applications:

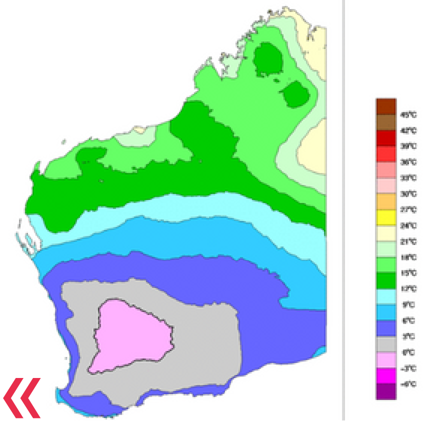
For frost tolerance, the approach is to increase the expression of endogenous antifrost proteins at critical stages of early seed set using GEd (COGGO, GB, MU). Similarly, GEd is being used to increase the diversity of wheat germplasm available for drought and salt stress.

In contrast, through a collaboration with Bloceres Crop Solutions (based in Argentina) and GB, we now have the HB4 wheat (from sunflower) in Australian germplasm.

This gene is reported to increase yields under water stress by 20%, with no yield penalty when water in not limiting.

HB4 wheat has been grown in more than 50,000 Ha in Argentina: HB4 soybean has also been grown commercially.

Flour from HB4 wheat has been passed by FSANZ for human consumption in Australia, and OGTR has recently passed HB4 wheat for field trials in Australia.



Widespread frost in the WA grainbelt, Sept '21

Credit: Australia Bureau of Meteorology

An international approach to harmonisation/alignment of gene-editing regulations in the Asia–Pacific region to enable trade in gene-edited produce

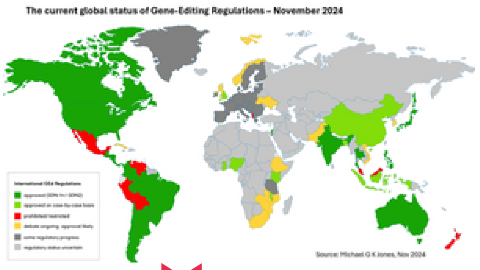
Murdoch project team:
Prof Michael Jones (Project Lead) Dr John Fosu-Nyarko, , Dr Sadia Iqbal, Mr Muhammad Adeel

Collaborating Organisations:
Department of Agriculture, Fisheries and Forestry; International Service for the Acquisition of Agri-biotech Applications; Malaysian Biotechnology Information Centre; FuturaGene; Corteva; Agriculture and Food Systems, PrBIO, U.S. Soybean Export Council; U.S Grains Council; Crop-Life Australia, U.S. Department of Agriculture; Thailand National Center for Genetic Engineering and Biotechnology; Thai Seed Trade Association, APSA; CropLife Asia.

Project overview:

There is considerable excitement amongst crop scientists about the opportunities for crop improvement using gene-editing (GEd) technologies, which can benefit both producers and consumers.

This must be tempered by the understanding that Australia is a food-exporting nation, and GEd crops/produce are subjected to the internal policies and regulations of countries which import Australian produce.



The current status of global Gene-Editing Regulations

Credit: Prof Michael Jones

Project highlights:

In this project, which has been running for about 5 years, we have been engaging with the countries which import Australian crop produce with the aims of:

- Providing scientific information on current and developing gene-editing technologies
- Differentiating GM and GEd produce, and promoting updating and alignment of GEd regulations
- Engaging with scientists, peak crop bodies and regulators in the Asia Pacific region
- Running training courses across the region and nationally
- Providing resources for Australian exporters in terms of outlining the pathways to de-regulation of GEd produce in the Asia-Pacific region
- Promoting Science Diplomacy as a mechanism to aid trade both nationally and internationally.

Impact and applictations:

Since this project started with the support of a major grant from the Commonwealth Government DAWE (now DAFF), and running a major international Conference in the Shine Dome (Australian Academy of Sciences) in Canberra in 2023, we have seen a dramatic and encouraging shift in the global regulatory environment, such that the world regulatory map developed in this project needs constant updating.

For example, Prof Jones was invited to meetings in Bangkok, including with the Director General of the Department of Agriculture, Thailand, at which the de-regulation of two forms of gene-editing (SDN-1, and SDN-2) was announced, accompanied by an MOU to import GEd produce (high GABA tomato) into Thailand from Japan.
A similar MOU is on place for the Philippines, providing the first examples of trade in GEd produce in the region.

Developing the Quinoa crop for Australia

Murdoch project team:
Prof Michael Jones (Project lead), Dr Jon Clements, Ms Jojo (Jinwen) Fan.

Collaborating Organisations:
Agrifutures Australia; GB; Coorow Seeds

Project overview:

Quinoa is an ancient seed grain crop from South America. The main plant product, the seed, is highly nutritious and has a higher protein and fibre content than cereals: protein content averages 14%, but can be up to 22%.

The seed has an excellent amino acid profile and a low glycaemic index, it is gluten-free, has low allergenicity, and can be cultivated over a wide range of environments.

Genotypes are tolerant to salinity, drought and low temperatures. However, wild type quinoa contains saponins in the seed coat, which are bitter and soapy, and these must be removed before consumption. Quinoa is a high value crop valued at ~AUD5,000/tonne, although the cost of subsequent desaponification, if required, is considerable.

The aims of this work include:

- Accessing global germplasm of quinoa
- Field testing a range of quinoa genotypes (~120) for their potential growth in different environments and years to identify genotypes best suited to Australian conditions
- Developing agronomic packages to improve yields
- Identifying low saponin lines
- Using gene-editing (GEd) to reduce the saponin content of high-yielding adapted genotypes.

Project highlights, impact and applications:

Lines yielding more than 3 tonne/Ha in WA have been identified, especially suitable for growth in the Geraldton region, with the latest field data under analysis.

For GEd, Undertaken by PhD student Jojo (Jinwen) Fan, a target gene for GEd has been identified, which, if mutated, significantly reduces saponin levels in the seed coat.

This is backed by good-quality genomic data, and a recent publication on the regeneration of plants from inflorescence tissues means that all components or GEd to reduce saponins are in place.

Australian Quinoa Industry RD&E Plan 2024-2029

Following interviews with all participants in the Quinoa industry and value chain - including seed suppliers, growers, manufacturers, retailers and customers - with Mr Doug Hall, we have developed the '*Australian Quinoa Industry RD&E Plan 2024-2029*' for AgriFuture Australia.

As outlined in the report, the key priorities for this RD&E proposal are to:

- Develop new quinoa varieties for Australian conditions with improved seed quality and yield.
- Increase consumer demand through understanding customer, retailer and manufacturer awareness and knowledge of the health benefits, nutritional benefits and culinary uses of quinoa and quinoa based products, and address identified gaps through extension activities.
- Establish a quinoa industry network that will take ownership of and facilitate strategies to grow the Australian industry.
- Develop agronomic information packages for existing and new varieties to improve yield and increase seed quality and profit.
- Undertake an economic analysis of quinoa supply chains to better understand the benefit-cost ratio of priorities and strategies in this RD&E Plan and those that may evolve from the proposed quinoa industry network.

This resource is available at: https://agrifutures.com.au/product/australian-quinoa-industry-rde-plan-2024-2029/

Australian
Quinoa Industry
RD&E Plan
2024-2029

by J. C. Clements, D. J. Hall and M. G. K. Jones
December 2023

AgriFutures
Emerging
Industries

Foreword

Quinoa (*Chenopodium quinoa*) is an 'ancient grain' that was domesticated about 8,000 years ago in South America, where it became an important part of Andean indigenous diets.

The main plant product, the seed, is highly nutritious and generally has a higher protein and fibre content than cereals; protein content averages 14%, with a range of 7.5 to 22%. Quinoa seed also has an excellent amino acid profile and a low glycaemic index, is gluten-free, and has low allergenicity. Additionally, the flour can be used as a gluten-free substitute in wheat-based baking.

Quinoa can be cultivated over a wide range of latitudes and altitudes, and is tolerant to adverse environments, including high salinity, drought and low temperatures. With global annual production of about 147,000 tonnes, mainly from Peru and Bolivia, there is good scope for quinoa to become more important in other countries, including Australia, especially on marginal soils in a range of environments.

The Australian industry consists of a diverse but small set of quinoa growers and producers, several quinoa seed and processed product importers, and a limited number of product manufacturers (who use mainly imported quinoa but also some Australian-produced quinoa).

To further develop the Australian quinoa industry, AgriFutures Australia commissioned this RD&E Plan. The Plan is based on a combination of desktop research and consultations with stakeholders across Australian quinoa supply chains. It summarises the status of the industry and outlines five RD&E priorities, each with associated strategies and activities, to support its long-term growth.

The priorities are:

① **Develop new quinoa varieties** for Australian conditions with improved seed quality and yield.

② **Increase consumer demand** through understanding customer, retailer and manufacturer awareness and knowledge of the health benefits, nutritional benefits and culinary uses of quinoa and quinoa-based products, and address identified gaps through extension activities.

③ **Establish a quinoa industry network** that will take ownership of and facilitate strategies to grow the Australian industry.

④ **Develop agronomic information packages** for existing and new varieties to improve yield and increase seed quality and profit.

⑤ **Undertake an economic analysis** of quinoa supply chains to better understand the benefit-cost ratio of priorities and strategies in this RD&E Plan and those that may evolve from the proposed quinoa industry network.

This RD&E Plan has been produced as part of AgriFutures Australia's Emerging Industries Program, which focuses on new and emerging industries with high growth potential. Emerging animal and plant industries play an important part in the Australian agricultural landscape. They contribute to the national economy and are key to meeting changing global food and fibre demands. Most of AgriFutures Australia's publications are available for viewing, free download or purchase online at www.agrifutures.com.au.

John Smith
General Manager, Levied and Emerging Industries
AgriFutures Australia

Authors of the Australian Quinoa Industry R,D&E Plan 2024-2029 – Dr Jon Clements, Mr Doug Hall and Prof Michael Jones

Lowering the cost of seed production for hybrid wheat

Murdoch project team:
A/Prof Ryan Whitford.

Collaborating Organisations:
BASF SE, Belgium;
The University of Adelaide, Australia

Acknowledgments:
This research is supported by Food Futures Institute, Murdoch University, The Australian Research Council and BASF SE (Project No. IM230100042).

Project overview:

The commercial realisation of hybrid wheat represents one of the last technological challenges to sustainably increase food production for our growing population in a changing climate.

Despite recent advances in pollination control systems, the inefficient out-crossing of wheat's self-pollinating florets remains a barrier to hybrid seed production.

There is a pressing need to investigate wheat floral biology and enhance the likelihood of ovaries being fertilised by airborne pollen so breeders can select and utilise male and female parental lines that will produce hybrids cost-effectively.

An improved understanding of the underlying biology of floral organ development and fertility will help stabilise pollination and fertilisation under a changing climate.

Specifically, this program works on priority areas of research which include:

- Structural aspects of wheat florets that affect female presentation, longevity and receptivity to airborne pollen;
- Pollen release dynamics (eg. anther extrusion and dehiscence), and how environmental cues such as heat, drought, irradiation and humidity each affect these reproductive processes.

High-throughput field relevant approaches are being developed to robustly measure these key floral characteristics for trait selection ensuring wheat's diverse germplasm pool can be fully exploited for the yield improvements derived from hybrid vigour.

A/Prof Ryan Whitford inspecting experimental wheat trials in Adelaide, SA

Project highlights:

Comprehensive Transcriptome Assembly:

Generated a high-quality transcriptome of the male-sterile wheat cultivar Chris, representing critical developmental stages in female reproductive development.

Key gene targets identified:
Identified 904 genes, including 60 transcription factors that correlate with the peak of cross-pollination seed set. It reveals an important role for gibberellic acid and reactive oxygen species homoeostasis in female receptivity to air-borne pollen.

Key germplasm identified:
27 durum and 116 bread wheat genotypes were assessed for stigma presentation traits.

Quantitative trait loci (QTL) analysis on contrasting durum genotypes revealed the Rht14 containing locus improves total stigma length by between 19.2 and 25.2%, which also improves total stigma length when introduced into bread wheat.

International hybrid wheat workshop:
An alliance of multinational seed genetics companies is calling on the international wheat community and its funding agencies for more research into "Floral Biology Traits for Hybrid Wheat".

This was the culmination of a workshop organized by A/Prof Ryan Whitford (MU) and Antje Rohde (BASF, Belgium) at the 3rd International Wheat Congress.

This industry-academic alliance involves researchers from Australia, UK, USA, Switzerland, Germany and Belgium.

It aims to push the boundaries of wheat improvement using next generation sequencing, functional genomics using CRISPR/Cas gene editing systems and the latest high throughput phenotyping technologies.

Impact and applications:
This project provides deeper insights into wheat's floral biology needed to accelerate the deployment of high-yielding wheat hybrids and line varieties that are resilient for a future climate.

The knowledge generated will equip both researchers and breeders with the necessary tools to select optimal parental line combinations that will be cost-effective in producing hybrid seed.

A/Prof Ryan Whitford and Dr Antje Rohde (BASF, Belgium) host a workshop at the 3rd International Wheat Congress on "Floral Biology Traits for Hybrid Wheat".

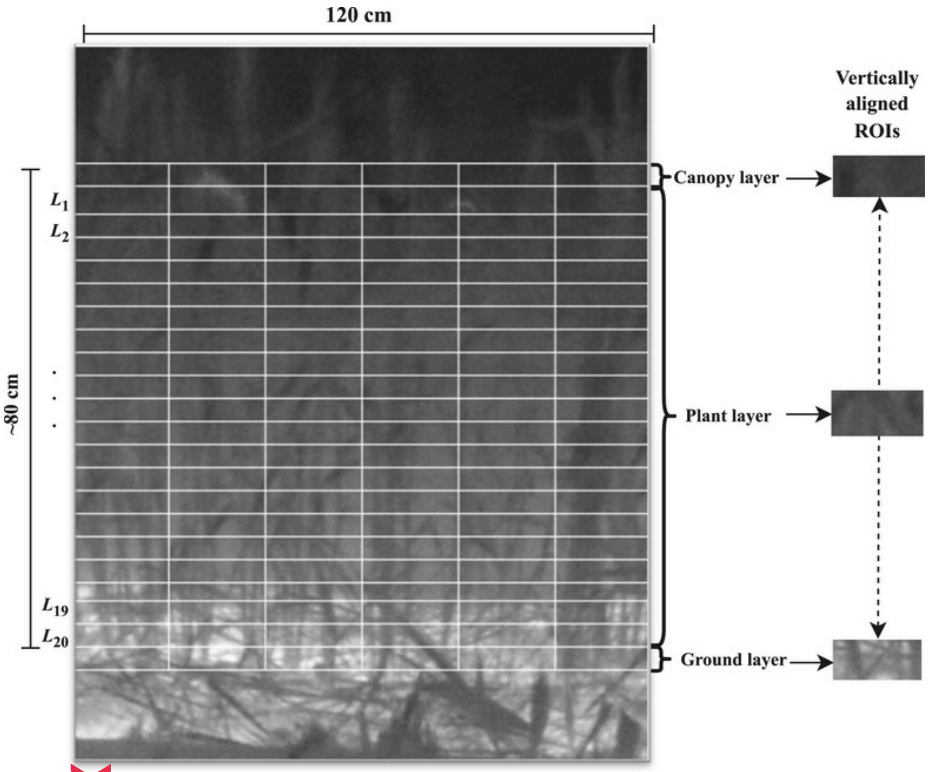
Digital Agriculture

Early frost detection in wheat using machine learning from vertical temperature distributions

Murdoch Project team:
Prof Ferdous Sohel, Dr Sayma Shammi, Prof Dean Diepeveen, Dr Sebastian Zander, Prof Michael Jones.

Collaborating Organisations:
Department of Primary Industries and Regional Development.

Acknowledgements:
This work was partially supported by a Murdoch University Strategic PhD scholarship to Sayma Shammi



A schematic diagram of the three-layer data structure.

Credit: Computers and Electronics in Agriculture

Project Overview:

Frost damage significantly reduces global wheat production. The development of vertical temperature gradients within wheat crops during frost events plays a critical role in understanding and managing frost risks.

This study explores the relationship between canopy, plant, and ground temperatures to detect frost early.

The patterns in temperature distribution between these layers were translated into an ML problem to detect frost early.

This study shows infrared thermal (IRT) images (from field-grown wheat crops) integrated with machine learning (ML) models early detect the coldness scales leading to frost nights with different degrees of severity.

This study presents a strong foundation for developing early frost detection systems.

Key Highlights:

Early indicator of frost:
Temperature data was extracted from IRT images of field-grown wheat crops across three distinct layers: canopy, plant, and ground. Our study shows that in these temperatures there is a relationship that can be used to determine frost early.

Pattern in canopy, plant and ground temperature:
The patterns of these three temperatures on a frost night differ from a cold no-frost winter night. On a no-frost night, we observed that the canopy is the coldest, the plant is warm, and the soil is warmest, and these three temperatures did not converge.

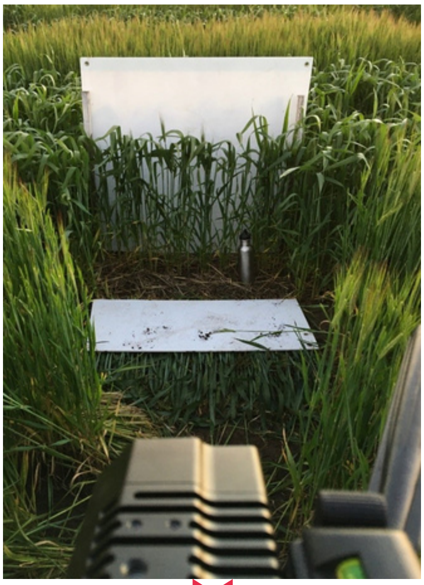
On the other hand, on a frost night, before the frost event, the canopy and plant temperatures converged as the cold air penetrated through the canopy.

IRT-based Machine learning (ML) model:
The study applied four machine learning (ML) models: gated recurrent unit (GRU), convolutional neural network (CNN), random forest (RF), and support vector machines (SVM) to classify coldness scales leading to frost events of varying severity levels based on the temperatures conducive to frost formation of a certain severity degree.

Highly accurate results:
Results show that the ML models can determine the coldness scales automatically with 93%–98% accuracy across the four models.

Impact and Applications

This research provides the groundwork for early frost detection systems to help farmers mitigate frost-related yield losses. It also supports sustainable agriculture by reducing crop losses, optimising resource use, and improving food security through data-driven decision-making in wheat production.



The plot and thermal camera setup at the trial site in West Dale, Western Australia

Credit: CCFI

Barley net blotches detection in a data scarcity context

Murdoch Project team:
Prof Ferdous Sohel, Dr Masoud Rezaei, Prof Dean Diepeveen, A/Prof Hamid Laga, Prof Michael Jones, A/Prof Sanjiv Gupta.

Collaborating Organisations:
Department of Primary Industries and Regional Development.

Acknowledgements: This work was partially supported by a Murdoch University Strategic PhD scholarship to Masoud Rezaei.

Project Overview:

Automatic plant disease detection is vital in agriculture since numerous diseases adversely affect and disrupt food production.

However, traditional disease detection methods are costly, laborious, and inefficient. Recent developments show that artificial intelligence (AI) can detect anomalies in visual samples, which can be used to detect disease symptoms effectively.

This project uses deep learning (DL) networks to offer an automatic monitoring system for plant disease identification. Well-known DL methods were used for plant disease detection, especially for barley – Australia's primary product.

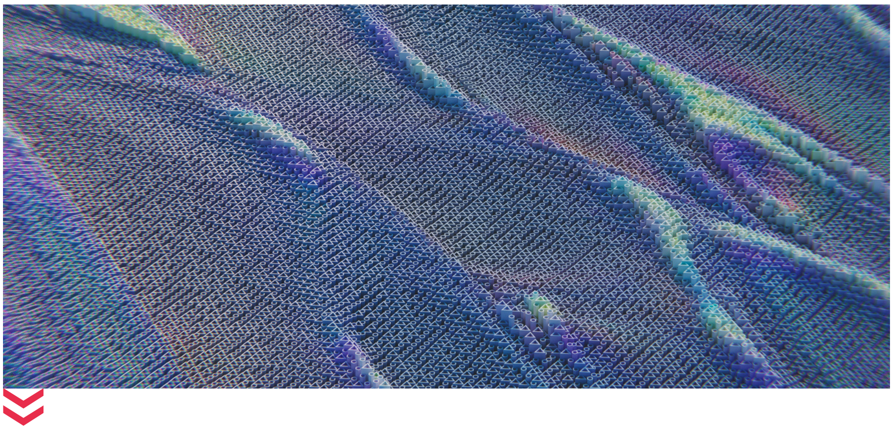
As a result, we captured barley disease samples from test-bed trials and applied the generated barley dataset to pre-trained DL networks, including MobileNet and ResNet.

As DL methods need a large training dataset, we further addressed the challenge and proposed a few-shot learning (FSL) pipeline to resolve the data scarcity issue.

The FSL method needs as few as five samples in each class for training, which mitigates the hurdle caused by data collection and annotation, especially for rare diseases.

In addition, the method is equipped with a feature attention module to reduce the adverse effects of complex backgrounds and unwanted objects in the samples.

The achieved performance indicates that techniques can be applied to disease detection in smart agriculture.



An artist's illustration of artificial intelligence (AI).

Credit: Google DeepMind

Key Highlights:

High performance with limited training samples:
The classic method achieved high detection accuracy using the small training dataset. The few-shot learning (FSL) method achieved high detection accuracy and throughput, given only five training samples per class.

Investigating data curation methods:
Transfer learning and data augmentation attenuate the impact of limited data.

Working with in-field complex data:
A barley disease dataset, which includes visual samples of barley diseases, such as net blotches and scald, was captured in the barley field. In the real-case scenario, samples include complex backgrounds and other unwanted objects. In the FSL task, the attention module decreases the negative impact of complex backgrounds.

Evaluating DL abilities in disease detection:
We proposed a deep learning pipeline for disease detection in different scenarios, including classical classification and few-shot learning. Methods' capabilities were investigated when they faced limited training data.

Assessing the performance of vision transformers in FSL:
Vision transformers can enhance the classification results, especially for complicated samples, in the few-shot setting.

Impact and Applications:
The project provides digital systems for plant disease detection, which can reduce potential losses and enable smart management.

This automatic and intelligent monitoring system can diagnose plant diseases using a non-invasive and non-destructive method, an effective substitution for inefficient methods, to improve the quantity and quality of crops in large-scale farms.

In addition to being cost-effective, rapid, and automatic, this project can alleviate labour requirements and workload, reduce costs, and promote economic yields.

Moreover, rapid disease detection can reduce the potential pollution caused by chemical run-off. The project can be further expanded to facilitate other applications, including weed and pest detection.

The achieved high performance and throughput highlight the methods' potential in smart agriculture.

Barley net blotch is a fungal disease that can cause yield reductions of 20-30% and affect overall grain quality.

Credit: DPIRD

Agricultural insect pest detection and size measurement with uncertainty estimates

Murdoch Project team:
Prof Ferdous Sohel, Dr Abderraouf Amrani, Prof Dean Diepeveen, Prof Michael Jones.

Collaborating Organisations:
Department of Primary Industries and Regional Development.

Acknowledgements:
This work was partially supported by a Murdoch University Strategic PhD scholarship to Abderraouf Amrani.

Project Overview:

Aphids are insect pests that severely impact agricultural productivity. Detection of aphid infestations is critical for mitigating their effects.

In addition, the size of the aphids is an important indicator of infestation severity. We present an AI approach to detect aphids and estimate their size in crop images captured by consumer-grade RGB imaging cameras.

Notably, DL models are known to suffer from uncertainty, which is primarily due to the randomness in the data and lack of knowledge about the true parameters of the model.

Uncertainty measurement in AI decisions, especially in pest detection and size estimation, represents a crucial yet often overlooked concern.
We propose a Bayesian multi-task learning model to detect the presence of aphids and estimate their size simultaneously.

Our model employs a joint loss function, combining detection loss that is associated with identifying images containing aphids and a size loss that accounts for the size of the aphids.

Integrating Bayesian frameworks within deep learning models offers a promising solution, enabling the quantification of uncertainty in predictions and enhancing decision-making in object detection and classification.

The model utilises a ResNet18 backbone, ensuring robustness and adaptability across various conditions.

Key Highlights:

- The proposed model simultaneously detects the presence of aphids, estimates their size, and qualifies the uncertainty in the inference.
- This enhances the reliability and robustness of the detection system, supporting more well-informed decisions in pest management.

Impact and Applications:

This work presents a new Bayesian multi-task learning model for the detection and size estimation of aphids in agricultural crops, using a ResNet18 backbone and a custom joint loss function.

A key aspect of the proposed model's design is the ability to provide uncertainty estimates associated with its predictions, which enhances the reliability and robustness of the detection system, supporting more well-informed decisions in pest management.

This work paves the way for developing more automatic, robust, and effective pest management systems.

Future research could focus on overcoming the model's limitations, including data dependency and computational needs while extending its applicability to a wider range of pests and agricultural scenarios.

Further optimisation of architecture and training could also be explored to enhance performance and efficiency.

In tests, the model achieved aphid presence detection accuracies of 75.77%, 66.39%, 70.01%, and 59% for corn, rape, rice, and wheat images, respectively.

Credit: Kelly Lacy

Digital agriculture update: Engaging with industry and inspiring the next generation of farmers

The Centre for Crop and Food Innovation (CCFI) is in the third year of a 5 year partnership with DPIRD and Curtin University aimed at youth and community engagement, with a particular focus on agricultural automation and robotics career development.

This partnership supported the 2024 WA Robotics Playoffs (WARP) event for 25 regional and metropolitan high school robotics teams, with over 250 students, as well as teachers and academic and industry mentors.

Over 500 members of the public and family attended WARP 2024. Awards for the robotics competition and associated Agricultural Innovation Challenge were presented by the Hon. Shelley Payne, Member for the Agricultural Region, and DPIRD DG Heather Brayford.

Robotics displays and high tech agricultural career opportunities were also promoted at the Wagin "Woolrama", Dowerin Machinery Field Day, Perth Royal Agricultural Show, Nannup South West Food Bowl, and Brunswick Agricultural Show.

DPIRD Director General **Heather Brayford** and The Hon. **Shelley Payne** present the Innovation Challenge Awards to the winning students at WARP 2024

2024 marked the conclusion of our $77,500 "Maker Projects – Community STEM Engagement Grants 2022" grant. This project supported the 2023/24 WARP and field day events and funded the purchase of a Robotriks Robotic Traction Unit (RTU).

The fully autonomous RTU platform was shown as a static display at several regional field day events as well as at WARP 2024.

CCFI researchers are currently in the process of adding precision spraying via the Open Weed Locator (OWL) system and multi-spectral computer imaging/data analytics capability to the RTU, using Unispectral's Monarch II camera.

This will enable the RTU platform to be trialled in a range of different field environments across several different CCFI research projects

The RTU Bot with the OWL attached was showcased at the Murdoch University Open Day. Credit: Dr David Berryman

Farmbot, an open-source precision farming model, demonstrated exceptional accuracy in determining key growth stages whilst minimising the need for manual labor for menial tasks.

CCFI researchers Dr David Berryman and A/Prof Graham Mann have continued trailing a low cost robotic phenotyping platform – the Farmbot Genesis – in greenhouse studies. In these studies, the Farmbot genesis was programmed to autonomously plant lupin seeds in pots, water the plants daily, and capture daily individual plant images over several weeks as the plants grew.

These images were automatically sent to a remote server and analysed by AI software for select growth milestones such as emergence and 2 leaf stage.

The results showed 98% accuracy in determining these growth stages, and the initial results demonstrate the significant potential for the FarmBot Genesis to automate many of the routine plant maintenance and measurement tasks currently carried out by hand .

Capacity building, Networking, and Knowledge Dissemination

CCFI/SABC Events

From meetings and mini symposiums to Senate visits and international conferences, the teams at CCFI and SABC have had a busy year organising events that showcase cutting edge research and strengthen connections with colleagues and collaborators.

3rd International Wheat Congress

Date: 22-27 September 2024
Location: Perth Convention and Exhibition Centre, Australia
Synopsis:

The International Wheat Congress (IWC) is a prestigious biennial event that began in July 2019 in Saskatoon, Canada.

It serves as an important gathering for the global wheat community, providing a platform for leading experts, researchers, policymakers, and industry professionals to discuss advancements in the field of wheat breeding, genetics, genomics, and agronomy.

Number of Speakers: 58 speakers, 35 panellists, 134 workshop speakers and >380 poster presentations
Number of attendees: >950
Number of countries represented: >52

More details of the event, topics discussed and early outcomes can be viewed here.

*L-R: CCFI Director and Chair of the IWC National Organising Committee, **Prof Rajeev Varshney**; CEO of ACIAR, **Prof Wendy Umberger**; Managing Director of GRDC, **Mr Nigel Hart**; Director General of DPIRD, **Ms Heather Brayford**, Chair of the Scientific Board at the Wheat Initiative, **Prof Peter Langridge**, President and Vice-Chancellor at Murdoch University, **Prof Andrew Deeks**; Director General of CIMMYT, **Dr Bram Govaerts**.*

2nd International Symposium of SABC/CCFI on Legumes Research and Applications

Date: 7 October 2024
Location: Murdoch University, Australia
Synopsis:

This symposium brings together outstanding contributors in the field of legume research to discuss current research strategies designed to develop climate-resilient and more nutritious legume crops that enhance farmer profitability, enable food and nutrition security, and deliver positive environmental sustainability outcomes.

Number of speakers: 22
Number of attendees: >60
Number of countries represented: 6

3rd Annual CCFI/SABC Strategy Meeting

Date: 4 July 2024
Location: Murdoch University
Synopsis:

This annual event provides a platform for agricultural scientists working at Murdoch University to present their research and develop cross-department collaboration and synergy. The meeting also gives industry and prominent Australian RDC attendees a comprehensive overview of our pioneering research, as well as open up potential collaborative opportunities.

Number of speakers: 37
Number of attendees: 75

The CCFI/SABC Annual Strategy Meeting brought together researchers, primary industry and RDCs to share and discuss agricultural research priorities

CCFI/SABC Events

International Plant and Animal Genome Conference (PAG) Australia

Date: 18 - 20 September 2024
Location: Perth, Australia
Synopsis:

In response to the expanding global population, worldwide climate changes, and dramatic plant and animal genome research occurring in Australia and the Asia Pacific Region, the organisers of the Plant and Animal Genome Conference implemented a 'mini' version of PAG in Perth, Western Australia.

Number of Speakers: 150 speakers
Number of attendees: >350
Number of countries represented: 26

PAG Australia 2024 offered delegates a deep into the fascinating world of agri-genomics

Prof Rajeev Varshney poses with longterm collaborators from the international research community at his PAG USA workshop on Genomes Assisted Breeding ,

Genome Assisted Breeding Workshop at PAG USA

Date: 16 January 2024
Location: San Diego, USA
Synopsis:

This workshop provided a critical assessment of the status and availability of genomic resources and genomics research in crop plant species.. Genomics specialists with extensive experience in applying genomics in breeding from both public and private sectors shared their experience and proposed novel ideas in this workshop to use GAB more effectively.

Number of speakers: 8
Number of attendees: >400
Number of countries represented: >25

National Academy of Agricultural Sciences expert consultation on Digital Sequence Information in Agriculture

Date: 26 March 2024
Location: Hybrid - Online and in New Delhi, India
Synopsis:

Digital Sequence Information (DSI) is pivotal for sustainable agriculture and climate resilience, as leveraging DSI innovation in crop productivity and climate adaptation. However, equitable access and benefit-sharing pose challenges, highlighting the need for international guidelines to ensure fair sharing of DSI benefits and foster collaborative research. This meeting served as a platform for DSI experts to discuss the establishment of a regulatory framework that balances access with equitable benefit distribution.

Number of speakers: 10
Number of attendees: >100
Number of countries represented: >19

DSI Experts discuss the establishment of a new regulatory frameworks

Credit: Prof Rajeev Varshney.

CCFI/SABC Events

China-Australia Symposium on Scientific Innovation and Development for Barley Industry

Date: 12 - 15 January 2024
Location: Hangzhou, China
Synopsis:

Scientists and industry partners from Australia and China presented progress on recent research and development. They discussed the industry challenge for both countries and the development of collaborative networks and proposals.

Number of Speakers: 24 speakers, 15 panellists
Number of attendees: >400
Number of countries represented: >2

Prof Li and delegates attend the China-Australia Symposium on Scientific Innovation and Development for Barley Industry

CGIAR-ICAR-MU Mini Symposium on Crop Genomics, Biotechnology and Pre-breeding

Date: 16 September 2024
Location: Murdoch University, Australia
Synopsis:

At the CGIAR-ICAR-MU Mini-Symposium on Crop Genomics, Biotechnology, and Pre-Breeding, CCFI brought leading researchers from three CGIAR institutes, namely the International Maize and Wheat Improvement Center (CIMMYT), the International Rice Research Institute (IRRI), and the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), as well as other premier Indian research institutes including the Indian Council of Agricultural Research - National Bureau of Plant Genetic Resources (ICAR-NBPGR) to Murdoch University to discuss ongoing research and potential collaborative opportunities.

Number of speakers: 23
Number of attendees: +50
Number of countries represented: 2

L-R, Dr Rutwik Barmukh (CCFI); Dr Dr Manish Vishwakarma (CGIAR - BISA/CIMMYT); Dr Pallavi Sinha (CGIAR -IRRI); Dr Sundeep Kumar (ICAR-NBPGR); Prof Rajeev Varshney (CCFI); Dr Manish Pandey (ICRISAT); Anu Chitikineni (CCFI) pose for a pre-symposium photo.

Digital Image Computing: Techniques and Applications (DICTA) Perth

Date: 27-29 November 2024
Location: Novetel Perth, Western Australia
Synopsis:

DICTA is the premier conference organised in Australia on computer vision, image processing, pattern recognition, and related areas. The conference offers ample opportunities to connect with the brightest minds from academia and industry in the field of digital image processing speakers.

Number of speakers: 38
Number of attendees: >100
Number of countries represented: >10

Prof Sohel takes part in the Oral Session on 3D Vision, LiDAR, Shape and Texture Analysis.

Credit: DICTA

Industry engagement, outreach and events

A selection of presentations, lectures, seminars and industry engagement efforts conducted by CCFI and SABC researchers in 2024 is listed below

Title: *A journey towards biotech control of plant- invertebrate pests (nematodes, aphids).*
Presenter: Prof Michael Jones
Type: Oral
Event Name: International Plant Molecular Biology Conference 2024, Australia
Summary:
This presentation described the work done at Murdoch University using RNAi to control plant parasitic nematodes (root-knot, cyst and root lesion nematodes), and the green peach aphid. It also outlined how gene-editing can be developed to control plant pests, emphasising that this strategy involves targeting genes for susceptibility in plants, and that this approach can result in plants which are not regulated as GMOs.

Title: *Accelerating genetic gain for yield in pulses: Integrating genomics, phenomics, and AI for breeding improved varieties*
Presenter: Prof Rajeev Varshney
Type: Oral
Event Name: Australian Crop Breeders Week, Australia
Summary:
This presentation covers research using nascent technologies to accelerate genetic gain for yield in pulses and overcome traditional breeding limitations by enabling the identification and selection of superior pulse varieties which offer faster and more effective crop improvement results.

Title: *Access to Information, Research, and Resources in the Global South*
Presenter: Prof Rajeev Varshney
Type: Panel discussion presentation
Event Name: Voices from the Global South, Australia
Summary:
This panel discussion discusses how limited access to resources, inadequate funding, and fewer publication opportunities impact the work of researchers in the Global South. Panellists discussed collaborations which are bridging these gaps and fostering high-quality research, explored the vital role that institutions in the Global North can play in promoting equitable research opportunities, and shared actionable steps that research communities can take to address research inequalities and foster global collaboration.

Dr Wendy Hunt at IWC 2024

Title: *Advanced Genomics Platform for Horticulture in Australia.*
Presenter: Ms Anu Chitikineni
MU Collaborating Authors:
Prof Rajeev Varshney
Type: Oral
Event Name: PAG Asia, China
Summary: Part of a series of presentations in the CCFI organised '*Genomic Interventions for Trait Improvement*' Workshop, this presentation discussed the development of an advanced genomics platform designed to help producers overcome industry challenges and improve the performance and profitability of popular Australian horticultural crops.

Title: *Amylose content of wheat flour noodles effects postprandial satiety and glycaemic response in healthy adults.*
Presenter: Dr Wendy Hunt
MU Collaborating authors:
A/Prof Haelee Fenton, A/Prof Dean Diepeveen, A/Prof Vicky Solah
Type: Plenary presentation
Event Name: 3rd International Wheat Congress (IWC), Australia
Summary:
This presentation outlined research into the effect of consumption of high amylose noodles on satiety and postprandial glycaemic response. Satiety was mean fullness over 2-hour periods measured by monitoring changes in feelings of fullness and calculating the total area under the curve. The study found that noodles made from high amylose wheat flour increase satiety and attenuate postprandial glycaemia in healthy young adults, as characterised by the significantly lower blood glucose concentration and reduction in glycaemic response.

Title: *Balancing wheat-based product quality and nutritional quality requirements*
Presenter: Prof Vicky Solah, A/Prof Haelee Fenton, David Doepel, Dr Suwimol Chockchaisawasdee, Prof Wujun Ma
Type: Workshop presentation
Event Name: 3rd International Wheat Conference (IWC), Australia
Summary:
In this workshop, Murdoch University researchers presented research on wheat product quality and nutrition. Presentations included balancing nutrition and quality, new collaborative approaches to sourdough bread, upcycling spent grains for food applications, and the impact of sulphur deficiency on modern wheat.

Title: *Breeding crop for climate adaptation.*
Presenter: Prof Chengdao Li
MU Collaborating Authors:
Dr Tianhua He, Dr Yong Jia, Dr Brett Chapman, Dr Penghao Wang
Type: Oral
Event Name: The 3rd Sanya International Conference of Seed Industry Scientists and International Seed Industry Science and Technology Expo, China
Summary:
For the first time, we provide evidence that the effects of climate change on crop production might be less severe than what is currently believed because the advancement of technologies and development of climate-resilient crop varieties may mitigate the adverse effect of climate change to some extent.

The greater use of genetic techniques in crop breeding will play a vital role in sustainable global food production in the era of climate change.

Title: *Challenges and prospects in the regulation of CRISPR-edited crops*
Presenter: Prof Michael Jones
Type: University lecture
Event Name: Chandigarh University, India, International Faculty Development Program
Summary:
A detailed description of gene-editing technologies was provided, GM and GEd technologies differentiated, the importance of nomenclature was discussed, examples of gene-editing crops were provided, and implications for international trade in gene-edited produce were discussed.

This visit involved discussions with staff and students on biotechnology and its applications, their curriculum and course content, and the signing of an outline collaboration document.

Prof Michael Jones and Chandigarh University Vice-Chancellor Dr Manpreet Singh Manna

Industry engagement, outreach and events

Title: *Developing genomic resources in custard apple for accelerating crop breeding efforts.*
Presenter: Shri Hari Prasad
MU Collaborating Authors: Prof Rajeev Varshney
Type: Oral
Event Name: PAG Australia
Summary:
This presentation discussed the lack of genomic resources for the Australian custard apple and how researchers are addressing this gap via modern sequencing technologies and analytical tools. By developing genomic resources for custard apple, researchers will be able to uncover desirable traits that can enhance crop productivity and generate new market opportunities.

Title: *Developing genomic resources for papaya to accelerate the progress of crop improvement.*
Presenter: Dr Rhys Copeland
MU Collaborating Authors: Prof Rajeev Varshney
Type: Oral
Event Name: International Conference on Tropical Plants
Summary: To increase retail demand and become competitive in international markets, Australian papaya breeding needs a significant boost in the current rate of genetic improvement. This presentation outlines research into the development of genetic resources that contribute to genomic prediction approaches for the development of elite papaya varieties that appeal to consumers and boost industry growth.

Title: *Enhancing Crop Productivity and Quality through Mutation by Speed Breeding*
Presenter: Prof Chengdao Li
MU Collaborating Authors: Prof Michael Jones
Type: Oral
Event Name: Workshop on mutation breeding, Austria
Summary:
This presentation discussed developing and refining the strategy for plant mutation breeding, including vision, mission, strategy, operating framework, and work plans for Asia, the Pacific and globally.

Technologies and capacities utilising nuclear science and technologies were discussed, including seed system modalities to identify or refine successful models contributing to food security and sustainable agriculture.

Title: *Exploring Chickpea's Genetic Landscape with Insights from the Cicer Super-Pangenome*
Presenter: Dr Vanika Garg
MU Collaborating Authors:
Prof Rajeev Varshney, Anu Chitikineni
Type: Oral
Event Name: PAG Asia, China
Summary:
Part of a series of presentations in the CCFI organised *Genomic Interventions for Trait Improvement* Workshop, this presentation discussed how the development of a Cicer Super-pangenome has unlocked the ability to identify valuable traits that will benefit breeders and farmers.

Title: *Food Innovations: Product Development in WA*
Presenter: Andrew Tilley
Type: Oral
Event Name: Home Economics Institute of Australia (Western Australia) Annual Conference
Summary:
This presentation explores WA's strengths, weaknesses, challenges, and opportunities for developing its export food industry. We look at how the new Sustainable Innovative Food Technologies centre is helping WA businesses grow by reducing risk and how we are integrating it into teaching at Murdoch University.

Title: *Future directions for Green Biotechnology in Mauritius*
Presenter: Prof Michael Jones
Type: Oral
Event Name: The future of Green Biotechnology in Mauritius
Summary:
Prof Jones was invited by the Government of Mauritius to discuss the future of food security in Mauritius. His trip involved a range of meetings and discussions with research organisations, industry and growers, and the development of a concept roadmap to reduce food imports over the short, medium and long term.

Title: *Gene-editing Technology and Plant Variety Improvement*
Presenter: Prof Michael Jones
Type: Oral
Event Name: Workshop on plant breeding innovations for sustainable agriculture and agricultural development, Thailand
Summary:
In this presentation, the evolution of plant breeding technologies was outlined, with the development of new varieties using a range of plant breeding technologies, including marker-assisted and genomic breeding, RNAi, transgenics and gene-editing technology.

Title: Genes and genomes to drive barley breeding success in Australia
Presenter: Prof Chengdao Li
MU Collaborating Authors:
Dr Tianhua He, Dr Yong Jia, Dr Brett Chapman, Dr Penghao Wang
Type: Oral
Event Name: China-Australia Symposium on Scientific innovation and development for barley industry, China
Summary:
With complete genomes and high coverage re-sequencing data of modern barley varieties from Europe, Australia and North America, and field characterisation on their phenology, we showed that directional breeding selection in Australia has fundamentally transformed the genomic architecture and landscape of adaptive genes in Australian and North American barley varieties.

Title: *Genetic improvement of nitrogen use efficiency in barley via gene editing.*
Presenter: Dr Sakura Thennakoon Mudiyanselage
MU Collaborating Authors:
Dr Xiao-Qi Zhang, Prof Chengdao Li
Type: Oral
Event Name: Australian Barley Technical Symposium
Summary:
Nitrogen (N) is a main determinant of grain yield and quality. Its excessive application leads to environmental pollution and high production costs. Improving nitrogen use efficiency (NUE) is therefore imperative in sustainable agriculture.

The presentation discussed our study that investigates barley tolerance to low N, retrieving candidate genes and developing barley materials with high NUE.

Title: *Genomics for food and nutrition security: striving to realise the vision of Bharat Ratna Prof MS Swaminathan*
Presenter: Prof Rajeev Varshney
Type: Oral
Event: MS Swaminathan Centenary Lecture Series, India
Summary:
The current pace of genetic enhancement in crops falls short of meeting the global food demand expected by 2050. To address this growing need for sustenance, a fundamental transformation in conventional breeding approaches is imperative. This presentation outlines recent advancements in genomics research which have introduced innovative ideas and tools with significant potential to elevate the precision and effectiveness of plant breeding techniques.

Industry engagement, outreach and events

Title: *Genomics of tropical crops for enhancing crop productivity and growers' profitability.*
Presenter: Prof Rajeev Varshney
Type: Oral
Event Name: International Conference on Tropical Plants, Australia
Summary:
ICTP serves as an important platform for the world's leading experts in tropical plants to discuss novel research approaches in crop biology, emerging technologies and the establishment of frameworks that can advance research on tropical plants. This presentation outlined the role genomics, genetics and pre-breeding can play in enhancing crop productivity and farmer profitability, using ongoing CCFI research as examples of the efficacy of this field of research.

Title: *GMOs and Gene Editing (GEd) for crop improvement: enabling trade in GEd produce*
Presenter: Prof Michael Jones
Type: Seminar and Laboratory Visits
Event Name: Guest lecture at Zheijiang University, China
Summary:
A comprehensive survey of GM technologies, including transgenic crops, RNAi, and their application at Murdoch, was followed by a presentation of work at the University on gene-editing of potato and wheat, international regulations and trade, and pathways for their commercial development.

Title: *GWAS analyses identified QTLs associated with aluminium tolerance and other traits in chickpea*
Presenter: Dr Yong Jia
MU Collaborating Authors:
Sharon Westcott, Dr Karthika Pradeep, Dr Wendy Vance, Prof Richard Bell, Prof Chengdao Li
Type: Oral
Event Name: 2024 GRDC Grains Update, Australia
Summary:
The presentation was based on two recently completed GRDC-backed projects, where we used genomics-assisted speed breeding to rapidly stack major and minor genes for acid soils tolerance and Al3+. The project aims to accelerate the transition from discovery to deployment of chickpea germplasm with improved acid soil tolerance in genetic backgrounds based on elite chickpea varieties.

Title: *Harnessing genetic variation for improving heat tolerance in wheat.*
Presenter: *Prof Rajeev Varshney*
Type: *Oral*
Event Name: *Presentation to ICAR-Indian Institute of Wheat and Barley Research, India*
Summary:
This presentation discussed genomic technologies and breeding strategies that enable the identification of beneficial genes for climate resilience, as well as the steps being taken to develop improved varieties.

Title: *Identification of anthracnose disease resistance gene in narrow-leafed lupin*
Presenter: Dr Gaofeng Zhou
MU Collaborating Authors:
Prof Chengdao Li
Type: Oral
Event Name: PAG Australia
Summary:
This presentation discussed ongoing research into identifying genes responsible for resistance to lupin anthracnose disease in narrow-leafed lupin.

Title: *Identification of sweet alkaloid genes in narrow-leafed lupin*
Presenter: Dr Gaofeng Zhou
MU Collaborating Authors:
Prof Chengdao Li
Type: Oral
Event Name: 11th International Conference on Legume Genetics and Genomics, Australia
Summary:
In wild narrow-leafed lupin (Lupinus angustifolius) seeds, the quinolizidine alkaloid (QA) content was around 2%. In contrast, the QA content in sweet lupin cultivars decreased 100 times to ~0.02% to meet the industrial limit. By investigating >300 lupin re-sequencing data and their phenotypes, one SNP within the gene region was identified to be associated with alkaloid content. In this presentation, we summarised our research in determining which gene is responsible for controlling the sweetness in narrow-leafed lupin cultivars.

Dr Gaofeng Zhou presents research into disease resistance genes in Narrow-leafed Lupin

Title: *Identifying tolerant wheat varieties under heat and drought stresses at anthesis*
Presenter: *Dr Jingjuan Zhang*
MU Collaborating Authors:
Dr Weinan Xu, Raksith Gowda, Dr Vanika Garg, Anu Chitikineni, Prof Chengdao Li, Prof Rajeev Varshney
Type: *Oral*
Event Name: 3rd International Wheat Congress, Australia
Summary:
Terminal heat and drought stresses have greatly affected wheat production since the high temperature and dry weather are in company with the stages of wheat flowering and grain filling. In this presentation, we outline efforts to quantify the impact of heat and drought stresses and improve our understanding of the genetic basis of tolerant genotypes.

Title: *Integration of mutation with fast breeding technologies in Australia*
Presenter: Prof Chengdao Li
MU Collaborating Authors:
Prof Michael Jones
Type: Oral
Event Name: Final Review Meeting on Enhancing Crop Productivity and Quality through Mutation by Speed Breeding, Laos,
Summary:
Both mutation and speed breeding techniques are advanced and matured in Australia. A major gap is to integrate the technologies for enhancement of mutation breeding efficiency and provide technical support for capacity building in member countries. In this presentation, we outlined key project activities and gave an update on research findings.

Title: *International and Australia Barley Pan Genome*
Presenter: Dr Tianhua He
MU Collaborating Authors:
Prof Chengdao Li
Type: Oral
Event Name: PAG Australia
Summary:
In this presentation, we summarised research into the international barley pan-genome, which revealed allelic diversity at structurally complex loci, providing a genetic foundation to adapt to new selective regimes in agricultural ecosystems

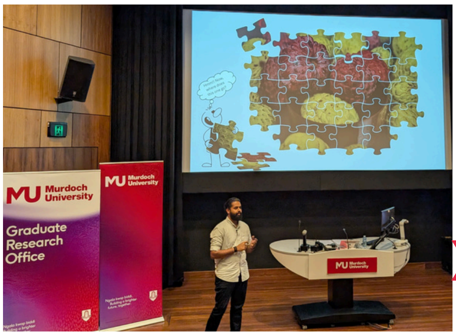
Industry engagement, outreach and events

Title: *Molecular markers, sequencing, GM and GEd.*
Presenter: Prof Michael Jones
Type: University Lecture
Event Name: Chandigarh University, India, International Faculty Development Program
Summary:
A history of plant breeding (Agriculture 01; Agriculture 02, Agriculture 03, Agriculture04), was provided, leading to the development and application of new genetic technologies, molecular markers, genome sequencing, transgenics and gene editing of plants.

Title: *Next-generation genomics technologies for crop improvement in context of climate change.*
Presenter: Prof Rajeev Varshney
Type: Oral
Event Name: Joint Session of the Consultancy Meetings of the International Atomic Energy Agency on 'Ensuring Food Security and Safety by Future-Proofing Dryland Crops under Climate Change', Austria.
Summary:
Part of a series of three consultancy meetings under the PUI project *Ensuring Food Security and Safety by Future-Proofing Dryland Crops under Climate Change*, this presentation outlined advancements in genomics, genetics and pre-breeding approaches that can improve crop productivity and resilience to abiotic stresses.

Title: *Pre-breeding on lupin disease*
Presenter: Prof Prof Chengdao Li
MU Collaborating Authors:
Dr Gaofeng Zhou, Sharon Westcott
Type: Oral
Event Name: Australian Breeder Assembly, Australia
Summary:
Several known fungal and viral diseases constantly threaten lupin production across Australia, particularly in WA, where over 85% of the world's lupin crop is produced. Reliance on disease resistance of new lupin cultivars in the farming system has been critical to controlling these diseases and minimising their related impacts.

In this presentation, we report on the identification of disease resistance genetic resources and molecular mapping of disease resistance genes.



Shri Hari Prasad presents at the Three Minute Thesis University Challenge.

Title: *Sweet Science: Decoding the custard apple genome.*
Presenter: Shri Hari Prasad
MU Collaborating Authors:
Prof Rajeev Varshney
Type: Oral
Event Name: Three Minute Thesis, Australia
Summary:
The annual Three Minute Thesis competition is held in more than 200 universities worldwide and challenges participants to present their research in just 180 seconds. This presentation summarised the development of genomics resources for custard apple that can enable the identification of desirable traits, boost productivity, and deliver new export opportunities. Mr Prasad secured a third place finish in his heat.

Title: *The barley pangenome graphs*
Presenter: Dr Viet Dang
MU Collaborating Authors:
Dr Brett Chapman, Prof Chengdao Li
Type: Oral
Event Name: PAG Australia
Summary:
Single reference genomes are being replaced by pan-genomic references as they represent more genetic diversity, provide better variant call accuracy and reduce reference bias. By utilizing the high-quality genome assembly of 76 barley accessions from the barley pangenome project, we constructed the barley pangenome graphs using two graph construction methods.

Title: *The current status of international regulations in gene-edited (GEd) crop produce: enabling trade*
Presenter: Prof Michael Jones
Type: Oral
Event Name: The 22nd Conference on International Exchange of Professionals, Shanghai, China: Gathering of Global Talents and Pursuing Win-Win Cooperation.
Summary:
In this presentation the global food trade system was discussed and the current status of international regulations relating to gene-editing (GEd) of crop plants was presented. Lack of international harmonisation or alignment of regulations will present a barrier to world trade, prevent implementation of GEd produce and prevent the delivery of the benefits of GEd technologies for food production and consumers.

Title: *The impact of gene duplication and functional divergence on barley grain colours.*
Presenter: Dr Yong Jia
MU Collaborating Authors:
Dr Brett Chapman, A/Prof Ryan Whitford, Prof Chengdao Li
Type: Oral
Event Name: 2024 Greater Bay Area (Guangdong) Agricultural, China
Summary:
Grain colour of cereal crops is one of the most important agronomic traits subjected to both human and natural selections, which have been shown to significantly influence grain quality, yield and also environmental adaptability. We presented our research that explores the genetic mechanisms controlling barley grain colours.

Title: The status of gene-edited (GEd) crops: regulation in Asia and Australasia
Presenter: Prof Michael Jones
Type: Oral
Event Name: 7th Asian Short Course on Agrobiotechnology, Biosafety Regulation and Communication, Thailand
Summary:
In this presentation, the status of gene-editing crop regulations in the Asia-Pacific region and Australasia was presented, together with the different forms of gene-editing, what needs to be done to accept GEd produce as non-GM, and related issues.

Title: *Towards developing Australian wheat pangenome*
Presenter: Dr Vanika Garg
MU Collaborating Authors:
Anu Chitikineni, Prof Chengdao Li, Prof Rajeev Varshney
Type: Oral
Event Name: 3rd International Wheat Congress, Australia
Summary:
Bread wheat is one of the most widely cultivated and consumed crops worldwide, however wheat production must increase significantly to meet the food demands of the rapidly growing global population.

In this presentation, we discuss modern genomics approaches, our work in developing the wheat pangenome which provides an exhaustive overview of genetic variation within the species. These genetic insights will enable the effective mining and utilisation of functional genetic diversity, facilitating the development of improved wheat varieties tailored to specific market needs and environmental conditions.

Industry engagement, outreach and events

Title: *Towards developing genomic resources for passionfruit.*
Presenter: Khushboo Fulara
MU Collaborating Authors:
Prof Rajeev Varshney
Type: Oral
Event Name: PAG Australia
Summary:
Increased climatic changes and consumer challenges have highlighted a need to develop passionfruit cultivars which can withstand climate change impacts and deliver better returns to farmers working in unfavourable environmental conditions. This presentation covers research on the development of modern genomic resources in passionfruit, which enable the identification of desirable traits that can enhance crop yield and offer consistent fruit quality.

Title: *Transcriptional signatures associated with female receptivity and presentation in a genetically male-sterile wheat cultivar Chris (Triticum aestivum L.)*
Presenter: A/Prof Ryan Whitford
Type: Oral
Event Name: 3rd International Wheat Congress, Australia
Summary:
Wheat hybrids have the potential to capture yield benefits arising from heterosis, but their commercial deployment is restricted due to high seed production costs, itself a result of wheat's floral architecture and poor outcrossing characteristics.

This presentation discussed the research and development of a comprehensive transcriptome dataset spanning the pistil and stigma life cycle of emasculated wild-type and genetically male-sterile wheat cv. 'Chris'.

Title: Unravelling the genetic basis of heat tolerance in wheat
Presenter: Rakshith Gowda
MU Collaborating Authors: Dr Weinan Xu, Dr Jingjuan Zhang, Prof Chengdao Li
Type: Oral
Event Name: 3rd International Wheat Congress, Australia
Summary:
Heat stress affects a plethora of physiological mechanisms in plants, ,leading to a deterioration in grain quality and quantity. It is therefore critical to adapt to the climate scenarios of the future to meet global food security needs.

This presentation discusses our work to identify the candidate genes and superior haplotypes associated with heat tolerance-component traits in a panel of 345 diverse wheat genotypes, which include cultivars and landraces.

Title: *Utilising artificial intelligence techniques like deep neural networks for barley disease detection.*
Presenter: A/Prof Sanjiv Gupta
MU Collaborating Authors:
Adj. Prof Dean Diepeveen, A/Prof Hamid Laga, Prof Michael Jones, Prof Ferdous Sohel
Type: Oral and poster
Event Name: International Barley Genetics Symposium, Argentina
Summary:
At this event we presented our research into artificial intelligence deep learning (DL) techniques for barley disease detection and recognition from images captured at trial sites by consumer-grade cameras. Our findings demonstrated that DL networks can be deployed for disease identification and screening in a timely manner for resistant varietal development.

Title: *Western Crop Genetics Alliance-WCGA update.*
Presenter: Dr Sakura Thennakoon Mudiyanselage
Type: Oral
Event Name: China-Australia Agriculture and Life Health Academic Forum
Summary:
The presentation was about the research progress of the Western Crop Genetics Alliance. It covered all the ongoing projects within the team by all researchers. Mainly includes lupin disease, alkaloid and seed coat projects, chickpea acid soil tolerance projects, pan-genome projects, and other projects on barley and oat.

Title: When will it be possible to trade gene-edited wheat?
Presenter: Prof Michael Jones
Type: Oral
Event Name: 3rd International Wheat Congress, Australia
Summary:
The complex pathways involved in the international trade of food products, focusing on wheat, was presented. Prof Jones highlighted the transnational nature and the current regulatory issues that govern the international trade of plant produce, as well as the need for alignment or harmonsiation before the products of new breeding technologies enter the world trade pathways.

The latest world map summarising the current status of these regulations was also presented.

Media statements

CCFI and SABC issued 19 press releases in 2024, achieving over 120 pieces of media coverage in key international, national and trade publications that collectively reached an audience of well over 80 million people.

A selection of press releases issued from the two Centres is below:

NEWS 28 NOV 2024

Unravelling wheat's genetic past to transform its future

NEWS 19 NOV 2024

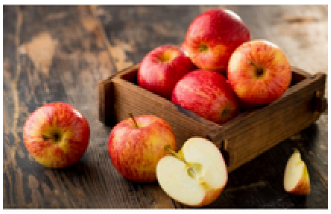
Murdoch health and agricultural scientists recognised as Highly Cited Researchers in 2024 Clarivate List

NEWS 14 OCT 2024

Climate in focus at global gathering of wheat experts

NEWS 24 SEP 2024

Future of wheat in focus at global congress



NEWS 26 AUG 2024

$41 million investment to boost fruits, nuts and crops

OPINION 14 AUG 2024

Wild genes in domestic species: how we can supercharge our crops using their distant relatives

NEWS 25 JUL 2024

Genomics breakthrough opens door to new crop varieties

NEWS 26 JUN 2024

Genetics and AI approaches to power-up pulses

NEWS 18 JUN 2024

Mapping a plant's 'superfamily tree' can build resilient crops amid climate crises

NEWS 11 JUN 2024

Soil knowledge website sharing science and management insights for agriculture

NEWS 23 MAY 2024

Better chickpeas possible, harnessing genetic traits of wild cousins

NEWS 22 MAY 2024

High-tech food centre offers innovation edge to WA food industry

NEWS 01 MAY 2024

Murdoch University Professor awarded prestigious fellowship to India

NEWS 23 FEB 2024

Future foods centre to super-charge new product development in WA

NEWS 22 FEB 2024

AI and robotics in farming on the agenda at 2024 For Food's Sake Summit

NEWS 21 FEB 2024

A better peanut for your plate?

2024 Publications

CCFI researchers have demonstrated exceptional research output in 2024, with over 160 papers published in high-impact academic journals, including 2 papers in *Nature*, 3 in *Nature Genetics*, 1 in *Nature Communications* and 1 in *Nature Plants.* A selection of critical research in leading journals is highlighted below.

Ahmad A, Hoffman NE, Jones MGK, Zhang B. (2024). **Editorial: Frontiers in global regulatory landscape of CRISPR-edited plants** Frontiers in Plant Science 15: 1367698

Akhtar K, Ain NU, Prasad PVV, Naz M, Aslam MM, Djalovic I, Riaz M, Ahmad S, Varshney RK, He B, Wen R. (2024). **Physiological, molecular, and environmental insights into plant nitrogen uptake, and metabolism under abiotic stresses**. The Plant Genome 17: e20461

Ali S, Tyagi A, Park S, Varshney RK, Bae H. (2024). **A molecular perspective on the role of FERONIA in root growth, nutrient uptake, stress sensing and microbiome assembly**. Journal of Advanced Research https://doi.org/10.1016/j.jare.2024.11.002

Amrani A, Diepeveen D, Murray D, Jones MGK, Sohel F. (2024). **Multi-task learning model for agricultural pest detection from crop-plant imagery: a Bayesian approach**. Computers and Electronics in Agriculture 218: 108719.

Aravind B, Shreeraksha RJ, Poornima R, Ravichandran D, Krishnaraj PU, Chimmad VP, Mirajkar KK, Bagewadi B, Janila P, Pandey MK, Varshney RK, Nayak SN (2024). **Impact of heat stress on physiological characteristics and expression of heat shock proteins (HSPs) in groundnut (*Arachis hypogea* L.)**. Physiology and Molecular Biology of Plants 30: 1691-1706.

Bharathi A, Upadhyaya HD, Varshney RK, Selvaraj K.S, Gowda CLL. (2024). **Association of phenotypic characters with genetic markers by using simple sequence repeats in finger millet (*Eleusine coracana L. Gaertn*)**. Plant Archives 24(2): 2679-2684.

Bhoite R, Han Y, Chaitanya AK, Varshney RK, Sharma DL (2024). **Genomic approaches to enhance adaptive plasticity to cope with soil constraints amidst climate change in wheat**. The Plant Genome 17: e20358.

Bohra A, Choudhary M, Bennett D, Joshi R, Mir RR, Varshney RK (2024). **Drought-tolerant wheat for enhancing global food security**. Functional & Integrative Genomics. 24: 212

Bolan N, Srinivasarao Ch, Rocco C, Bolan S, Mansoor S, Wani O, Ahmad P, Weiss D, Northover G, Sánchez-Palacios JT, Cheng M, Bell R, Kumar GR, Naidu GM, Hou D, Jia X, Xie, Y, Wang H, Antoniadis V, Melo TM, Shaheen SM, Rinklebe J, Kirkham MB, Siddique KHM. (2024). **Zinc in soil-crop-animal-human health continuum**. Advances in Agronomy 189: 1-61 .

Bowichean R, Bell RW, Cheng M, Thanachit S, Anusontpornperm S. (2024). **Release kinetics of boron in acidic soils as affected by calcium from different sources**. Applied and Environmental Soil Science, Article ID: 6418954.

Cao Y, Feng X, Ding B, Huo H, Abdullah M, Hong J, Jiang L, Wang H, Li R, Cai Y, Li X, Xia Z, Varshney RK, Hu H, Lin M, Shen F (2024). **The gap-free genome assemblies of two Pyrus bretschneideri cultivars and GWAS analyses identify a CCCH-type zinc finger protein as a key regulator of lignin biosynthesis and stone cell formation in pear fruit**. Plant Communications 6: 101238.

Chang HW, Wu TT, Shalmani A, Xu L, Li CD, Pan R, Zhang WY. (2024) **Heat shock protein HvHSP16.9 from wild barley enhances tolerance to salt stress**. Physiology and Molecular Biology of Plants 30: 687-704.

Chaturvedi P, Pierides I, López-Hidalgo C, Garg V, Zhang S, Barmukh R, Bellaire A, Li J, Bachmann G, Valledor L, Varshney RK, Ghatak A, Weckwerth W (2024). **Natural variation in the chickpea metabolome under drought stress**. Plant Biotechnology Journal 22: 3278-3294.

Cheng J, Jia Y, Hill C, He T, Wang K, Guo G, Shabala S, Zhou M, Han Y, Li C. (2024) **Diversity of Gibberellin 2-oxidase genes in the barley genome offers opportunities for genetic improvement**. Journal of Advanced Research 66: 105-118.

Chu L, Yang K, Chen C, Zhao B, Hou Y, Wang W, Zhao P, Wang K, Wang B, Xiao Y, Li Y, Li Y, Song Q, Liu B, Fan R, Bohra A, Yu J, Sonnenschein EC, Varshney RK, Tian Z, Jian J, Wan P. (2024). **Chromosome-level reference genome and resequencing of 322 accessions reveal evolution, genomic imprint and key agronomic traits in adzuki bean**. Plant Biotechnology Journal 22: 2173-2185.

Danakumara T, Kumar N, Patil BS, Kumar T, Bharadwaj C, Jain PK, Nimmy MS, Joshi N, Parida SK, Bindra S, Kole C, Varshney RK (2024). **Unraveling the genetics of heat tolerance in chickpea landraces (*Cicer Arietinum L.*) using genome-wide association studies**. Frontiers in Plant Science 15: 1376381.

Deng Q, Du P, Gangurde SS, Hong Y, Xiao Y, Hu D, Li H, Lu Q, Li S, Liu H, Wang R, Huang L, Wang W, Garg V, Liang X, Varshney RK, Chen X, Liu H (2024). **ScRNA-seq reveals dark- and light-induced differentially expressed gene atlases of seedling leaves in Arachis hypogaea L**. Plant Biotechnology Journal 22: 1848-1866.

Ding B, Hu H, Cao Y, Xu R, Lin Y, Song Y, He G, Han Y, Guo H, Qiao J, Zhao J, Feng X, Yang S, Guo X, Varshney RK, Li L (2024). **Pear genomes display significant genetic diversity and provide novel insights into the fruit quality traits differentiation**. Horticultural Plant Journal 10: 1274-1290.

Djalovic I, Kundu S, Bahuguna RN, Pareek A, Raza A, Singla-Pareek SL, Prasad PVV, Varshney RK (2024). **Maize (*Zea mays L.*) and heat stress: Physiological, genetic and molecular insights**. The Plant Genome 17: e20378.

Feng D, Han Q, Xu L, Sohel F, Hassan SG, Liu S. (2024). **An ensembled method for predicting dissolved oxygen level in aquatic environment for efficient production**. Ecological Informatics, vol. 80: 102501.

Feng X, Chen X, Meng Q, Song Z, Zeng J, He X, Wu F, Ma W, Liu W. (2024). **Comparative Long Non-Coding Transcriptome Analysis of Three Contrasting Barley Varieties in Response to Aluminum Stress**. International Journal of Molecular Sciences, 25: 9181.

Fosu-Nyarko J, Adams IP, Jones MGK, Fox A, Jones RAC. (2024). **Comparisons between sequenced and re-sequenced genomes of historical subterranean clover mottle virus isolates**. Journal of Plant Pathology 106: 395–401.

2024 Publications

Gangurde SS, Korani W, Bajaj P, Wang H, Fountain JC, Agarwal G, Pandey MK, Abbas HK, Chang P-K, Holbrook CC, Kemerait RC, Varshney RK, Dutta B, Clevenger JP, Guo B (2024). **Aspergillus flavus pangenome (AflaPan) uncovers novel aflatoxin and secondary metabolite associated gene clusters**. BMC Plant Biology 4: 354.

Garg V, Bohra A, Mascher M, Spannagl M, Xu X, Bevan MW, BennetzenJL, Varshney RK (2024). **Unlocking plant genetics with telomere-to-telomere genome assemblies**. Nature Genetics 56: 1788-1799.

Ghatak A, Pierides I, Singh RK, Srivastava RK, Varshney RK, Prasad M, Chaturvedi P, Weckwerth W (2024). **Millets for a sustainable future**. Journal of Experimental Botany. https://doi.org/10.1093/jxb/erae507.

Guerra-García A, Trněný O, Brus J, Renzi JP, Kumar S, Bariotakis M, Coyne CJ, Chitikineni A, Bett KE, Varshney RK, Pirintsos S, Berger J, von Wettberg EJB, Smýkal P (2024). **Genetic structure and ecological niche space of lentil's closest wild relative, Lens Orientalis (Boiss.) Schmalh**. Plant Biology 26: 232-244.

Halder U, Biswas R, Shaw R, Chitikineni A, Varshney RK, Bandopadhyay R (2024). **Genome-based characterization of the deep-sea psychrotolerant bacterium Bacillus altitudinis SORB11 isolated from the Indian Sector of the Southern Ocean**. Polar Biology 47: 115-133.

Han Y, Abair A, van der Zanden J, Nageswara-Rao M, Vasan S, Bhoite R, Castello M, Bailey D, Revell C, Li C. (2024). **Transcriptome-Wide Genetic Variations in the Legume Genus Leucaena for Fingerprinting and Breeding**. Agronomy 14 (7): 1519.

Harish D, Reddy SPP, Kumar N, Bharadwaj C, Kumar T, Parida S, Patil BS, Kumar S, Jain PK, Kumar Y, Varshney RK (2024). **Integrating multilocus genome-wide association studies in chickpea landraces to discern the genetics of drought tolerance**. Frontiers in Sustainable Food Systems 8: 1389970.

Hasan ASM M, Diepeveen D, Laga H, Jones MGK, Sohel F. (2024). **Object-level benchmark for deep learning-based detection and classification of weed species**. Crop Protection 177: 106561.

He X, He Y, Dong Y, Gao Y, Sun X, Chen W, Xu X, Su C, Lv Y, Ren B, Yin H, Zeng J, Ma W, Mu P. (2024). **Genome-wide analysis of FRF gene family and functional identification of HvFRF9 under drought stress in barley**. Frontiers in Plant Science 15: 1347842.

He X, Yang L, Zhou L, Gunness P, Hunt W, Solah V, Sun Q. (2024). **Effect of lecithin on the complexation between different botanically sourced starches and lauric acid**. International Journal of Biological Macromolecules 268 (2): 131996.

He Y, Yang X, Xia X, Wang Y, Dong Y, Wu L, Jiang P, Zhang X, Jiang C, Ma H, Ma W, Liu C, Whitford R, Tucker MR, Zhang Z, Li G. (2024). **A phase-separated protein hub modulates resistance to Fusarium head blight in wheat**. Cell Host & Microbe 32: 710-726.

Hill CB, Angessa TT, Westcott S, McFawn L, Shirdelmoghanloo H, Han Y, Li C. (2024). **Evaluation of the impact of heat stress at flowering on spikelet fertility and grain quality in barley**. Agriculture Communications. 2 (4): 100066.

Hou Y, Gan J, Fan Z, Sun L, Garg V, Wang Y, Li S, Bao P, Cao B, Varshney RK, Zhao H (2024). **Haplotype-based pangenomes reveal genetic variations and climate adaptations in moso bamboo populations**. Nature Communications 15: 8085.

Hu H, Scheben A, Wang J. et al. (2024). **Unravelling inversions: Technological advances, challenges, and potential impact on crop breeding**. Plant Biotechnology Journal 22: 544-554.

Huai D, Xue X, Wu J, Pandey MK, Liu N, Huang L, Yan L, Chen Y, Wang X, Wang Q, Kang Y, Wang Z, Jiang H, Varshney RK, Liao B, Lei Y (2024). Enhancing peanut nutritional quality by editing AhKCS genes lacking natural variation. Plant Biotechnology Journal 22: 3015-3017.

Huang, L, Umer M.J, Liu H, Li H, Wang R, Qianxia Y, Li S, Varshney RK, Pandey MK, Hong Y, Lu Q, Chen X. (2024). **Transcriptome based weighted gene coexpression network analysis reveals synergistic effects of darkness and mechanical stimulation on pod development in peanut (Arachis hypogea L.)**. BMC Plant Biology. https://doi.org/10.21203/rs.3.rs-5400642/v1.

Isha I, Singh S, Jha U, Laxuman C, Kudapa H, Varshney RK, Thudi M (2024). **Meta-QTL analysis enabled identification of candidate genes and haplotypes for enhancing biotic stress resistance in chickpea**. Journal of Plant Biochemistry and Biotechnology. https://doi.org/10.1007/s13562-024-00873-5

Islam KZ, Murray D, Diepeveen D, Jones MGK, Sohel F. (2024). **LoRa localisation using single mobile gateway**. Computer Communications, vol. 219, pp. 182-193.

Islam KZ, Murray D, Diepeveen D,Jones MGK, Sohel F. (2024). **LoRa-based outdoor localization and tracking using unsupervised symbolization**. Internet of Things, vol. 25, no. 101016.

Islam MJ, Kumar U, Cheng M, Maniruzzaman M, Nasreen SS, Haque ME, Jahiruddin M, Bell RW, Jahangir MMR. (2024). **Conservation Agriculture improves yield and potassium balance in intensive rice-based cropping systems.** Nutrient Cycling in Agro-ecosystems 128: 238-250.

Islam MS, Bell RW, Miah MAM, Alam MJ. (2024). **Determinants of farmers' fertilizer use gaps under rice-based cropping systems: Empirical evidence from Eastern Gangetic Plain**. Journal of Agriculture and Food Research 17: 101228

Islam MS, Bell RW, Miah MAM, Alam MJ. (2024). **Effects of unbalanced fertilizer use on system productivity and profitability under rice-based cropping systems: Evidence from Eastern Gangetic Plain**. Soil Use and Management 40 (3): e13107.

Itam MO, Iohannes SD, Albertsen M, Andrade M, Bor GA, Atta-Krah K, Bertram R, Danquah, E, Horvath DM, Jones T, Mugehu E, Okwuonu I, Ooko-Ombaka A, Roberts RJ, Slamet-Loedin I, Tripathi L, Ubi BE, Varshney RK, Venturi V, Wagaba H, Zeigler R, Creasey Krainer KM. (2024) **Demonstrating the benefit of agricultural biotechnology in developing countries by bridging the public and private sectors**. Nature Plants 10: 2-5.

Jamedar HVR, Gandham P, Bajaj P, Thati S, Rao VS, Varshney RK, Saxena RK (2024). **Identification of superior haplotypes for seed protein content in pigeonpea (Cajanus cajan L.)**. Journal of Plant Biochemistry and Biotechnology 33: 178-188.

Jan S, Rustgi S, Barmukh R, Shikari AB, Leske B, Bekuma A, Sharma D, Ma W, Kumar U, Kumar U, Bohra A, Varshney RK, Mir RR (2024). **Advances and opportunities in unraveling cold-tolerance mechanisms in the world's primary staple food crops**. The Plant Genome 17: e20402.

Jellen EN, Wight CP, Spannagl M, Blake VC, Chong J, Herrmann MH, Howarth CJ, Huang Y-F, Juqing J., Katsiotis A., Langdo**n T, Li C, Park R, Tinker NA, Sen TZ. (2024). A uniform gene and chromosome nomenclature system for oat (*Avena spp.*)**. Crop & Pasture Science 75, CP23247.

2024 Publications

Jayakodi M, Lu Q, Pidon H, Rabanus-Wallace MT, Bayer M, Lux T, Guo Y, Jaegle B, Badea A, Bekele W, Brar GS, Braune K, Bunk B, Chalmers KJ, Chapman B, Jørgensen ME, Feng JW, Feser M, Fiebig A, Gundlach H, Guo W, Haberer G, Hansson M, Himmelbach A, Hoffie I, Hoffie RE, Hu H, Isobe S, König P, Kale SM, Kamal N, Keeble-Gagnère, Keller B, Knauft M, Koppolu R, Krattinger SG, Kumlehn J, Langridge P, Li C, Marone MP, Maurer A, Mayer KFX, Melzer M, Muehlbauer GJ, Murozuka E, Padmarasu S, Perovic D, Pillen K, Pin PA, Pozniak CJ, Ramsay L, Pedas PR, Rutten T, Sakuma S, Simpson C, Skadhauge B, Spannagl M, Steffenson BJ, Thomsen HC, Tibbits JF, Nielsen MTS, Tratewig C, Vequaud D, Voss C, Wang P, Waugh R, Westcott S, Rasmussen MW, Zhang R, Zhang XQ, Wicker T, Dockter C, Mascher M, Stein N. (2024) **Structural variation in the pangenome of wild and domesticated barley**. Nature 636: 654–662.

Jia Y, Barrero J, Wang J, Considine M, Nakamura S, Li C. (2024). **Seed Dormancy, Germination, and Pre-Harvest Sprouting, Volume II. Front**. Plant Sci https://doi.org/10.3389/fpls.2024.1399510.

Jiang CC, Kan JH, Gao GQ, Dockter C, Li CD, Wu WX, Yang P, Stein N. (2024). **Barley2035: A decade vision on barley research and breeding.** Molecular Plant 18(2): 195-218.

Jiao C, Wen M, Jing X, Garg V, Zhou C, Chen L, Xu F, Hao C, Xiao J, Wang H, Varshney RK, Zhang X, Wang X. (2024). **Accumulation of beneficial haplotypes in Huang-Huai Hai wheat region and its application in molecular breeding**. Journal of Integrative Agriculture https://doi.org/10.1016/j.jia.2024.12.003.

Jiao C, Xie X, Hao C, Chen L, Xie Y, Garg V, Zhao L, Wang Z, Zhang Y, Li T, Fu J, Chitikineni A, Hou J, Liu H, Dwivedi G, Liu X, Jia J, Mao L, Wang X, Appels R, Varshney RK, Guo W, Zhang X. (2024). **Pan-genome bridges wheat structural variations with habitat and breeding**. Nature 637: 384-393.

Joshi P, Soni P, Sharma V, Manohar SS, Kumar S, Sharma S, Pasupuleti J, Vadez V, Varshney RK, Pandey MK, Puppala N. (2024). **Genome-wide mapping of Quantitative Trait Loci for yield-attributing traits of peanut**. Genes 15: 140.

Kabiraj A, Halder U, Chitikineni A, Varshney RK, Bandopadhyay R (2024). **Insight into the genome of an arsenic loving and plant growth-promoting strain of Micrococcus luteus isolated from arsenic contaminated groundwater**. Environmental Science and Pollution Research 31: 39063-39076.

Khan AW, Garg V, Sun S, Gupta S, Dudchenko O, Roorkiwal M, Chitikineni A, Bayer PE, Shi C, Upadhyaya HD, Bohra A, Bharadwaj C, Mir RR, Baruch K, Yang B, Coyne CJ, Bansal KC, Nguyen HT, Ronen G, Aiden EL, Veneklaas E, Siddique KHM, Liu X, Edwards D, Varshney RK. (2024). **Cicer super-pangenome provides insights into species evolution and agronomic trait loci for crop improvement in chickpea**. Nature Genetics 56: 1225-1234.

Kohinoor H, Mahfuza SN, Bell RW, Chowdhury AK. (2024). **Assessment of genetic divergence in linseed (*Linum usitatissimum L.*) using germination related traits under normal and salt stress condition**. European Journal of Ecology, Biology and Agriculture 1(4), 35-47.

Kudapa H, Ghatak A, Barmukh R, Chaturvedi P, Khan A, Kale S, Fragner L, Chitikineni A, Weckwerth W, Varshney RK (2024). **Integrated multi-omics analysis reveals drought stress response mechanism in chickpea (Cicer arietinum L.)**. The Plant Genome 17: e20337.

Kumar A, Naik YD, Gautam V, Sahu S, Valluri V, Channale S, Bhatt J, Sharma S, Ramakrishnan RS, Sharma R, Kudapa H, Zwart RS, Punnuri SM, Varshney RK, Thudi M (2024). **Genome-wide association mapping reveals genes and genomic regions controlling root-lesion nematode resistance in chickpea mini core collection**. The Plant Genome 18:e20508.

Kumar U, Cheng M, Islam MJ, Maniruzzaman M, Nasreen SS, Haque ME, Jahiruddin M, Bell RW,Jahangir MMR. (2024). **Retention of crop residue increases crop productivity and maintains positive sulfur balance in intensive rice-based cropping systems**. Journal of Soil Science and Plant Nutrition 24: 6856-6867.

Lambani Y, Lokesha R, Thudi M, Roorkiwal M, Palakurthi R, Rachappa V, Muniswamy S, Kenganal M, Varshney RK. (2024). **Screening and validation of drought tolerance and Fusarium wilt resistance in advance breeding lines of chickpea (*Cicer arietnum L.*)**. Legume Research 47: 1599-1605.

Lawal KG, Aslam R, Nazir A, Sundarakani B, Stathopoulos C, Maqsood S. (2024). **Carboxymethyl cellulose – Polyvinyl alcohol bioactive films loaded with green extracted date seed polyphenols for active packaging of Shiitake mushrooms**. Food Bioscience, 62: 105330.

Lawal KG, Nazir A, Sundrakani B, Stathopoulos C, Maqsood S. (2024). **Unveiling the effect of natural deep eutectic solvents-based date seed polyphenolic extract on the properties of chitosan-PVA films and its application in shrimp packaging**. International Journal of Biological Macromolecules 280(1): 135593.

Laxuman C, Naik YD, Desai BK, Kenganal M, Patil B, Reddy BS, Patil DH, Chakurte S, Kuchanur PH, Shiva Kumar K, Gaddi AK, Yogesh LN, Nidagundi J, Dodamani BM, Sunkad G, Thudi M, Varshney RK. (2024). **Development and evaluation of Fusarium wilt-resistant and high-yielding chickpea advanced breeding line, KCD 11**. The Plant Genome 17: e20460.

Le TS, Dell B, Harper R. (2024). A New **Remote Sensing Index for Forest Dryness Monitoring Using Multi-Spectral Satellite Imagery**. Forests 15: 915.

Li B, Jia Y, Xu L, Zhang S, Long Z, Wang R, Guo Y, Zhang W, Jiao C, Li C, Xu Y. (2024). **Transcriptional convergence after repeated duplication of an amino acid transporter gene leads to the independent emergence of the black husk/pericarp trait in barley and rice**. Plant Biotechnology Journal 22: 1282-1298.

Liu H, Guo Z, Gangurde SS, Garg V, Deng Q, Du P, Lu Q, Chitikineni A, Xiao Y, Wang W, Hong Y, Varshney RK, Chen X. (2024). **A single-nucleus resolution atlas of transcriptome and chromatin accessibility for peanut (*Arachis hypogaea L.*) leaves**. Advanced Biology 8: e2300410.

Lu Q, Huang L, Liu H, Garg V, Gangurde SS, Li H, Chitikineni A, Guo D, Pandey MK, Li S, Liu H, Wang R, Deng Q, Du P, Varshney RK, Liang X, Hong Y, Chen X. (2024). **A genomic variation map provides insights into peanut diversity in China and associations with 28 agronomic traits**. Nature Genetics 56: 530–540.

Malik AI, Bell R, Zang H, Boitt G, Whalley R. (2024). Editorial. **Exploring the plant and soil mechanisms by which crop rotations benefit farming systems**. Plant Soil 507: 1-9.

Maniruzzaman M, Cheng M, Islam A, Kumar U, Islam J, Nasreen SS, Haque E, Akhter S, Jahiruddin M, Bell R, Jahangir MMR. (2024). **Conservation Agriculture increases phosphorus pools and stock in the top 30 cm of soil: A three-year study on a subtropical legume-rice rotation**. Soil Use and Management 40: e13153.

2024 Publications

Maniruzzaman M, Sarangi SK, Mainuddin M, Biswas JC, Bell RW, Hossain MB, Paul PLC, Kabir MJ, Digar S, Mandal S, Maji B, Burman D, Mandal UK, Mahanta KK. (2024). **A novel system for boosting land productivity and income of smallholder farmers by intercropping vegetables in waterlogged paddy fields in the coastal zone of the Ganges Delta**. Land Use Policy 139: 107066

Maniruzzaman Md, Mainuddin M, Bell RW, Biswas JC, Hossain Md B, Yesmin MS, Kundu PK, Mostafizur ABM, Paul PLC, Sarker KK, Yu Y. (2024). **Dry season rainfall variability is a major risk factor for cropping intensification in coastal Bangladesh**. Farming Systems 139: 107066.

Naik YD, Sharma VK, Aski MS, Rangari SK, Kumar R, Dikshit HK, Sahani S, Kant R, Mishra G, Mir RR, Kudapa H, Elango D, Zwar RSt, Varshney RK, Thudi M. (2024). **Phenotypic profiling of lentil (*Lens culinaris Medikus*) accessions enabled identification of promising lines for use in breeding for high yield, early flowering and desirable traits**. Plant Genetic Resources 22: 69-77

Nguyen DD, Solah V, Daubney S, Jani S. (2024). **Determination of Ca, P, K, Na and Mg in Australian Retail Pasteurised Milk Using Inductively Coupled Plasma Atomic Emission Spectroscopy (ICP OES)**. Journal of Analytical Methods in Chemistry. Article ID 4417607.

Nguyen DD, Solah V, Hunt W, Daubney S, Meek J, Gray N, Du X. (2024). **Fatty acid profiling of Western Australian pasteurised milk using gas chromatography-mass spectrometry**. Food Research International 180: 114050.

Obiero CO, Milroy SP, Bell RW. (2024). **Influence of auxin on growth, physiology, and yield of potato exposed to high temperature episode**. Australian Journal of Crop Science 18, 905-915.

Pallotta M, Okada T, Roy S, Pearson A, Baumann U, Whitford R. (2024). **Diversity in bread and durum wheat stigma morphology and linkage of increased stigma length to dwarfing gene Rht14**. Theoretical and Applied Genetics 137: 160.

Pandey MK, Gangurde SS, Shasidhar Y, Sharma V, Kale SM, Khan AW, Shah P, Joshi P, Bhat RS, Janila P, Bera SK, Varshney RK (2024). **High-throughput diagnostic markers for foliar fungal disease resistance and high oleic acid content in groundnut**. BMC Plant Biology 24: 262.

Panigrahi S, Kumar U, Swami S, Singh Y, Balyan P, Singh KP, Dhankher OP, Varshney RK, Roorkiwal M, Amiri KM, Mir RR. (2024). **Meta QTL analysis for dissecting abiotic stress tolerance in chickpea**. BMC Genomics 25: 439

Parthiban M, Jan F, Mantoo MA, Kaur S, Rustgi S, Wani FJ, Varshney RK, Mir RR (2024). **Antioxidant and secondary metabolite responses in wheat under cereal leaf beetle (*Oulema melanopus L.*) infestation**. Physiologia Plantarum 176: e14158

Paul PLC, Jahan A, Kundu PK, Roy D, Bell, RW, Hossain B, Sultana R, Pranto MRBH, Islam T, Benes SE Islam MR. (2024). **Rice growth and yield responses to saline water irrigation are related to Na+/K+ ratio in plants**. PLoS One 19(11): e0312372.

Peng Y, Lyu X, Xu D, Wang Z, Xia X, Hao Y, Wu H, Ma W. (2024). **Genome-wide atlas of loci involved in chromosomal recombination in common wheat**. BMC Plant Biology 24: 1124.

Penrose B, Magor E, Wilson M, Wong H, Cresswell T, Sanchez-Palacios JT, Kaestli M, Bell RW (2024). **Investigating environmental and geographical factors affecting iodine concentrations in Australian wheat (*Triticum aestivum L.*) grain**. Science of the Total Environment 956: 177160.

Pyone WW, Bell RW, Rose MT, McGrath G. (2024). **Phytotoxicity risk assessment of diuron residues in sands on wheat, chickpea, and canola**. PLoS ONE 19(12): e0306865.

Ranasinghe M, Stathopoulos C, Sundarakani B, Maqsood S. (2024). **Changes in the rheological, textural, microstructural and in vitro antioxidant properties of biscuit dough by incorporation of the extract and fiber-rich residue obtained through green extraction of defatted date seeds**. Food Structure 42: 100395.

Ranasinghe M, Stathopoulos C, Sundarakani B, Maqsood S. (2024). **Valorizing date seeds through ultrasonication to enhance quality attributes of dough and biscuit, Part-1: Effects on dough rheology and physical properties of biscuits**. Ultrasonics Sonochemistry 109: 107015.

Raza A, Bashir S, Khare T, Karikari B, Copeland RGR, Jamla M, Abbas S, Charagh S, Nayak SN, Djalovic I, Rivero RM, Siddique KHM, Varshney RK. (2024). **Temperature-smart plants: a new horizon with omics-driven plant breeding**. Physiologia Plantarum 176: e14188.

Raza A, Bhardwaj S, Rahman MA, García-Caparrós P, Copeland RGR, Charagh S, Rivero RM, Gopalakrishnan S, Corpas FJ, Siddique KH, Hu, Z. (2024). **Fighting to thrive via plant growth regulators: Green chemical strategies for drought stress tolerance**. Physiologia Plantarum 176: e14605.

Raza A, Bhardwaj S, Rahman MA, García-Caparrós P, Habib M, Saeed F, Charagh S, Foyer CH, Siddique KHM, Varshney RK. (2024). **Trehalose: a sugar molecule involved in temperature stress management in plants**. The Crop Journal 12: 1-16.

Raza A, Chen H, Zhang C, Zhuang Y, Sharif Y, Cai T, Yang Q, Soni P, Pandey MK, Varshney RK, Zhuang W. (2024). **Designing future peanut: the power of genomics-assisted breeding**. Theoretical and Applied Genetics 137: 1-30.

Raza A, Salehi H, Bashir S, Tabassum J, Jamla M, Charagh S, Barmukh R, Mir RA, Bhat BA, Javed MA, Guan D-X, Mir RR, Siddique KHM, Varshney RK. (2024). **Transcriptomics, protemoics and metabolomics interventions prompt crop improvement against metal (loid) toxicity**. Plant Cell Reports 43: 1-34.

Rehman SA, Gul S, Parthiban M, Isha I, Reddy MSS, Chitikineni A, Thudi M, Penmetsa RV, Varshney RK, Mir RR. (2024). **Genetic resources and genes/QTLs for gram pod borer (*Helicoverpa armigera Hübner*) resistance in chickpea from the Western Himalayas**. The Plant Genome 17: e20483.

Rezaei M, Diepeveen D, Laga H, Jones MGK, Sohel F. (2024). **Plant disease recognition in a low data scenario using few-shot learning**. Computers and Electronics in Agriculture 219: 108812.

Rezaei M, Gupta S, Diepeveen D, Laga H, Jones MGK, Sohel F. (2024). **Barley disease recognition using deep neural networks**. European Journal of Agronomy 161: 127359.

Sarker KK, Mainuddin M, Bell RW, Kamar SKSA, Akanda MAR, Sarker BC, Paul PLC, Glover M, Shahadat MK, Khan MSI, Rashid Md H, Barrett-Lennard EG. (2024). **Response of sunflower yield and water productivity to saline water irrigation in the Coastal zones of the Ganges Delta**. Soil Systems 8(1): 20.

Shammi S, Diepeveen D, Zander S, Jones MGK, Sohel F. (2024). **Early frost detection in wheat using machine learning from vertical temperature distributions**. Computers and Electronics in Agriculture 221: 108950.

2024 Publications

Scanlan CA, Bell RW, Cheng M, Boyes T. (2024). **Subsoil testing required to detect the rundown of soil potassium to deficient levels for wheat production on loam-textured soils**. Crop and Pasture Science 75(11) 1-12.

Shafi S, Tahir M, Bawa V, Jan F, Choudhary N, Khan MA, Singh Y, Kumar U, Bhat BA, Dar WA, Sofi PA, Bhat MA, Padder BA, Shikari AB, Paliwal R, Varshney RK, Mir RR (2024). **Biochemical defense arsenal, Genes/QTLs and transcripts for imparting anthracnose resistance in Common bean (*Phaseolus vulgaris L.*)**. Plant Stress 14: 100609.

Sharma V, Mahadevaiah SS, Latha P, Gowda SA, Manohar SS, Jadhav K, Bajaj P, Joshi P, Anitha T, Jadhav MP, Sharma S, Janila P, Bhat RS, Varshney RK, Pandey MK (2024). **Dissecting genomic regions and underlying candidate genes in groundnut MAGIC population for drought tolerance**. BMC Plant Biology 24: 1-21.

Shivaprasad KM, Dikshit HK, Mishra GP, Sinha SK, Aski M, Kohli M, Mishra DC, Singh AK, Gupta S, Singh A, Tripathi K, Kumar RR, Kumar A, Jha GK, Kumar S, Varshney RK (2024). **Delineation of loci governing an extra-earliness trait in lentil (*Lens culinaris Medik.*) using the QTL-Seq approach**. Plant Biotechnology Journal 22: 2932-2949.

Sihag P, Kumar U, Sagwal V, Kapoor P, Singh Y, Mehla S, Balyan P, Mir RR, Varshney RK, Singh KP, Dhankher OP (2024). **Effect of terminal heat stress on osmolyte accumulation and gene expression during grain filling in bread wheat (Triticum aestivum L.)**. The Plant Genome 17: e20307.

Singla A, Nehra A, Joshi K, Kumar A, Tuteja N, Varshney RK, Gill SS, Gill R (2024). **Exploration of machine learning approaches for automated crop disease detection**. Current Plant Biology 40: 100382.

Tang Y, Huang Z, Xu S, Zhou W, Ren J, Yu F, Wang J, Ma W, Qiao L. (2024). **Candidate genes conferring ethylene-response in cultivated peanuts determined by BSA-seq and fine-mapping**. The Crop Journal 12: 856-865.

Thudi M, Samineni S, Li W, Boer MP, Roorkiwal M, Yang Z, Ladejobi F, Zheng C, Chitikineni A, Nayak S, He Z, Valluri V, Bajaj P, Khan AW, Gaur PM, van Eeuwijk F, Mott R, Xin L, Varshney RK. (2024). **Whole genome resequencing and phenotyping of MAGIC population for high resolution mapping of drought tolerance in chickpea**. The Plant Genome 17: e20333.

Umer MJ, Lu Q, Huang L, Batool R, Liu H, Li H, Wang R, Qianxia Y, Varshney RK, Pandey MK, Hong Y, Chen X. (2024). **Genome-wide association study reveals the genetic basis of amino acids contents variations in Peanut *(Arachis hypogaea L.)***. Physiologia Plantarum 176: e14542.

Varshney RK, Barmukh R, Bentley A, Nguyen HT (2024). **Exploring the genomics of abiotic stress tolerance and crop resilience to climate change**. The Plant Genome 17: e20445.

Vu TH, Johnson SK, Fenton H, Nguyen, DD, Bhattarai RR. (2024). **Submerged fermentation of empty carob pods to enhanced-pinitol, total phenolic and dietary fibre contents and associated bioactivity**. International Journal of Food Science and Technology 59: 6388-6397.

Wang J,Yao L, Hao J, Li C, Li B, Meng Y, Ma X, Si E, Yang K, Zhang H. (2024). **Growth Properties and Metabolomic Analysis Provide Insight into Drought Tolerance in Barley (*Hordeum vulgare L.*)**. International Journal of Molecular Sciences, 25(13): 7224.

Wang L, Chen H, Zhuang Y, Chen K, Zhang C, Cai T, Yang Q, Fu H, Chen X, Chitkineni A, Wang X, Varshney RK, Zhuang W. (2024). **Multiple strategies, including 6mA methylation, affecting plant alternative splicing in allopolyploid peanut**. Plant Biotechnology Journal 22: 1681-1702

Wang Y, Wang B, Chen J, SunL, Hou Y, Wang Y, Wang J, Gan J, Barmukh R, Li S, Fan Z, Bao P, Cao B, Cai C, Jing X, Singh BK, Varshney RK, Zhao H. (2024). **Dynamics of rhizosphere microbial structure and function associated with the biennial bearing of moso bamboo**. Journal of Environmental Management 351: 119977.

Xu L, Wang P, Zhang X, Zhang Q, Wang P, Xu Y, Li C, Zhang W. (2024). **Natural variations in a barley aldehyde oxidase 1 gene affect seed germination and malting quality**. The Crop Journal 13(1): 299-303

Xue H, Zhao K, Zhao K, Han S, Chitikineni A, Zhang L, Qiu D, Ren R, Gong F, Li Z, Ma X, Zhang X, Varshney RK, Zhang X, Wei C, Yin D. (2024). **A near complete genome of *Arachis monticola*, an allotetraploid wild peanut**. Plant Biotechnology Journal 22: 2110-2112.

Yang F, Sun X, Wu G, He X, Liu W, Wang Y, Sun Q, Zhao Y, Xu D, Dai X, Ma W, Zeng J. (2024). **Genome-Wide Identification and Expression Profiling of the ABF Transcription Factor Family in Wheat (*Triticum aestivum L.*)**. International Journal of Molecular Sciences 25: 3783.

Yang T, Zhang W, Cui Y, Wang Y, Qin H, Lv X, Xie X, Yang F, Ren K, Ni J, Dai X, Zeng J, Liu W, Ma W, Zhang H, Xu D. (2024). **Genome-Wide Association Studies for Wheat Height Under Different Nitrogen Conditions**. Agriculture 14: 1998.

Yu B, Liu N, Huang L, Luo H, Zhou X, Lei Y, Yan L, Wang X, Chen W, Kang Y, Ding Y, Jin G, Pandey MK, Janila P, Sudini HK, Varshney RK, Jiang H, Liu S, Liao B. (2024). **Identification and application of a candidate gene AhAftr1 for aflatoxin production resistance in peanut seed (*Arachis hypogaea L.*)**. Journal of Advanced Research 62: 15-26.

Zaman QU, Garg V, Raza A, Nazir MF, Hui L, Khan D, Khokhar AA, Hussain MA, Wang H-F, Varshney RK (2024). **Unique regulatory network of dragon fruit simultaneously mitigates the effect of vanadium pollutant and environmental factors**. Physiologia Plantarum 176: e14416.

Zaman QU, Raza A, Lozano-Juste J, Chao L, Jones MGK, Wang H-F, Varshney RK. (2024). **Engineering plants using diverse CRIPR-associated proteins and deregulation of genome-edited crops**. Trends in Biotechnology 42: 560-574.

Zeng J, Wang Y, Wu G, Sun Q, He X, Zhang X, Sun X, Zhao Y, Liu W, Xu D, Dai X, Ma W. (2024). **Comparative Transcriptome Analysis Reveals the Genes and Pathways Related to Wheat Root Hair Length**. International Journal of Molecular Sciences 25: 2069.

Zhang S, Ghatak A, Bazargani MM, Krammml H, Zang F, Gao S, Ramšak Z, Gruden K, Varshney RK, Jiang D, Chaturvedi P, Weckwerth W. (2024). **Cell-type proteomic and metabolimic resolution of early and late grain filling stages of wheat (*Triticum aestivum L.*) endosperm**. Plant Biotechnology Journal 22: 555-571

Zhao C, Siddique AB, Guo C, Shabala S, Li C,Chen Z, Varshney RK, Zhou M. (2024). **A high-throughput protocol for testing heat-stress tolerance in pollen**. aBIOTECH 6: 63-71.

Zhou C, Xiong H, Jia Y, Guo H, Fu M, Xie Y, Zhao L, Gu J, Li H, Li Y, Xin P, Chu J, Li C, Liu L. (2024). **Identification of a von Willebrand Factor Type A Protein Affecting Both Grain and Flag Leaf Morphologies in Wheat**. Science China Life Sciences 67: 2283-2286

Zhou G, McFawn L-A, Zhang X, Angessa TT, Westcott S, Li C. (2024) **Genome-wide association study on seed dormancy in barley**. Seed Science Research 34: 113-119.

2024 Book Chapters

Barmukh, R., Varshney, R.K. (2023). **Genomic Innovations for Improving Crops: The CRISPR Way.** In: Bansal KC, Lakra WS, Pathak H. (eds) Transformation of Agri-Food Systems. Springer, Singapore. https://doi.org/10.1007/978-981-99-8014-7_20

Bohar R, Dreisigacker S, Lindqvist-Kreuze H, Kante M, Pandey MK, Sharma, V, Chaudhari, S, Varshney RK. (2024). **Forward breeding for efficient selection**. In: Pandey MK, Bentley A, Desmae H, Roorkiwal M, Varshney RK. (eds) Frontier Technologies for Crop Improvement. Sustainability Sciences in Asia and Africa. Springer, Singapore. https://doi.org/10.1007/978-981-99-4673-0_8

Bohra A, Parihar AK, Lamichaney A, Mishra RK, Varshney RK. (2024). **Breeding Grain Legumes for Biotic Stress Resistance: Status, Challenges, and Opportunities for Genomics-Assisted Approaches**. In: Parihar AK, Bohra A, Lamichaney A, Mishra R, Varshney RK. (eds) Genomics-aided Breeding Strategies for Biotic Stress in Grain Legumes. Springer, Singapore. https://doi.org/10.1007/978-981-97-3917-2_1

Bollam S, Deva PA, Sai Bindu KC, Varshney RK, Srivastava RK. (2024). **Pearl Millet Genome Sequencing: Utilization of Sequencing Information for Pearl Millet Improvement**. In: Srivastava RK, Satyavathi CT, Varshney RK. (eds) The Pearl Millet Genome. Compendium of Plant Genomes. Springer, Cham. https://doi.org/10.1007/978-3-031-56976-0_4.

Dao MTT, Dell B, Henry DJ, Harper RJ. (2023). **Soil Water Repellency in Sandy Soils: A Review**. In: Hartemink AE, Huang J. (eds) Sandy Soils. Progress in Soil Science. Springer, Cham. https://doi.org/10.1007/978-3-031-50285-9_24

Jones MGK. (2023). **Trade in Gene-Edited Crops; International Perspectives**. In: Bansal KC, Lakra WS, Pathak H. (eds) Transformation of Agri-Food Systems. Springer, Singapore. https://doi.org/10.1007/978-981-99-8014-7_23

Jones MGK. (2024). **An international perspective on trade in gene-edited crops: issues and current status**. In: Bansal KC. (ed) National Academy of Sciences India Chapter Transformation of Agri-Food Systems for Achieving Sustainable Development Goals. Springer-Nature.

Jones MGK, Iqbal S, Fosu-Nyarko J. (2024). **Regulation of CRISPR-edited plants in Australia and New Zealand**. In: Kamel A, Elsalam A, Ahmad A. (eds) Genome Modified Plants and Microbes in Food and Agriculture, Global Regulatory Outlook for CRISPRized Plants. Academic Press.https://doi.org/10.1016/B978-0-443-18444-4.00008-9.

Pandey MK, Bentley A, Desmae H, Roorkiwal M, Varshney RK. (2024). **Introduction: Frontier Technologies for Crop Improvement**. In: Pandey MK, Bentley A., Desmae H, Roorkiwal M, Varshney RK. (eds) Frontier Technologies for Crop Improvement. Sustainability Sciences in Asia and Africa. Springer, Singapore. https://doi.org/10.1007/978-981-99-4673-0_1 .

Then M, Lobsey C, Henry D, Sochacki S, Harper R. (2023). **Proximal Sensing in Soil Water Repellency Management: A Review**. In: Hartemink AE, Huang J. (eds) Sandy Soils. Progress in Soil Science. Springer, Cham. https://doi.org/10.1007/978-3-031-50285-9_7.

Veerendrakumar HV, Barmukh R, Shah P, Bomireddy D, Jamedar HVR, Roorkiwal M, Vasanthi RP, Varshney RK, Pandey MK, Bomireddy D. (2024). **Genomic Selection in Crop Improvement**. In: Pandey MK, Bentley A, Desmae H, Roorkiwal M, Varshney RK. (eds) Frontier Technologies for Crop Improvement. Sustainability Sciences in Asia and Africa. Springer, Singapore. https://doi.org/10.1007/978-981-99-4673-0_9.

PhD Research Students

Name	Title	Principal Supervisor
Naznin Ahmed	Identification of Suitable traits for Direct Seeded Rice	Prof Richard Bell
Mahjuba Akter	Effects of Exogenous Application of Kaolin on Physiology, Growth and Yield of Potato Plants under High Temperature	Prof Richard Bell
Abderraouf Amrani	Advances in deep learning techniques with uncertainty quantification for image-based detection of agricultural pests	Prof Ferdous Sohel
Masood Anwar	Mapping for QTLs related to Nitrogen Use Efficiency in Hexaploid Wheat under Australian Conditions	Prof Wujun Ma
Rhys Copeland	A study of Pratylenchus spp. in the southwest of Western Australia, and how P. neglectus finds host roots	Dr John Fosu-Nyarko
Thi Thanh Mai Dao	Understanding the contribution of different Australian plant species to soil water repellency	Prof Richard Harper
Lucas de Castro Moreira da Silva	Modeling and assessing hydraulic properties of selected Brazilian and Australian soils	Prof Richard Bell
Jinwen Fan	De-saponification via Gene Editing. A Solution for Efficient Quinoa Seed Processing & Optimising Nutritional Value	Prof Michael Jones
Hennadige Fernando	Functional characterisation of orthologues of an anti-frost gene of wheat	Prof Michael Jones
Khushboo Fulara	Development of genomic resources in passionfruit	Prof Rajeev Varshney
ASM Mahmudul Hasan	Deep learning techniques for green-on-green weed detection from imagery	Prof Ferdous Sohel
Jian He	Transposable Elements (TEs) and Species Radiations, Organismal Fitness and Genomic Plasticity: A bioinformatic evaluation of vertebrate, bacteria and plant genomes	Dr Penghao Wang

PhD Research Students

Name	Title	Principal Supervisor
Khondoker Ziaul Islam	Localization, tracking, and data transmission using LoRa	Prof Ferdous Sohel
Saiful Islam	Root lesion nematodes on potato in Western Australia, and assessing candidate genes of Pratylenchus penetrans for control using RNAi	Prof Michael Jones
Yanan Jiang	Investigation of polyploid wheat genetic variation through whole genome sequencing	Prof Wujun Ma
Maninder Kaur	Cold plasma inhibits Fusarium graminearum growth in vitro but does not translate to field-contaminated grain	A/Prof Kirsty Bayliss
Keshala Karunarathna	Application of biotechnology to improve frost tolerance of wheat	Prof Michael Jones
Thai Son Le	Remote sensing for forest water stress monitoring and prediction	Prof Richard Harper
Qing Li	Development of dominant genic male sterility lines in potato	Prof Michael Jones
Qier Liu	Cloning and Characterizing Candidate Genes Underlying Major QTLs for Wheat Stem Pith Thickness and Stem Diameter	Prof Wujun Ma
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
Md Resad Malik	Characterising genetic recombination associated with the integration of two novel HMW-Gs (1Slx2.3+1Sly16) from Aegilops longissima to Australian wheat cultivars	Prof Wujun Ma
Maria Maqsood	Towards understanding common mechanisms of nematode and aphid effectors in plant parasitism	Prof Michael Jones

PhD Research Students

Name	Title	Principal Supervisor
Farhana Momtaz	Cold plasma treatment of fungal communities to reduce postharvest strawberry spoilage	A/Prof Kirsty Bayliss
Upama Mondal	Molecular characterisation of wheat germplasm with improved tolerance to abiotic stresses	Prof Michael Jones
Onyemaechi Henry Obiazikwor	Potential management of Fusarium wilt in tomatoes using the crop microbiome	A/Prof Kirsty Bayliss
Sumaiya Haque Omy	To be announced	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
Nimali Rathnayake	Genetic Mapping and Molecular Characterization of Candidate Genes for Al toxicity tolerance in Chickpea	Prof Chengdao Li
Masoud Rezaei	Advanced Deep Neural Networks for Plant Disease Recognition	Prof Ferdous Sohel
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
Md Atik Us Saieed	Identification and Characterization of Novel Genes Contributing to Wheat Grain Yield	Prof Wujun Ma
Hassan Sardar	Response of potato varieties to an episode of high temperature	Prof Richard Bell
Ami Chand Sharma	To be announced	Prof Richard Bell

PhD Research Students

Name	Title	Principal Supervisor
Sayma Shammi	Machine learning-based frost detection in plants from infrared thermography	Prof Ferdous Sohel
Devshree Singh	Exploring Genetic and Molecular Pathways to Enhance Nitrogen Use Efficiency and Grain Yield in Wheat	Prof Rajeev Varshney
Nasrin Sultana	Identification of Salt Tolerance Genes in Australian Wheat Breeding	Prof Rajeev Varshney
Brittany Clare Thornbury	Enhancing the water-use efficiency of barley (Hordeum vulgare) through genetic technologies	Prof Chengdao Li
Cen Tong	Genetic mapping and molecular characterisation of the candidate gene responsible for root aerenchyma formation under waterlogging stress in barley	Prof Chengdao Li
Chunsheng Xiao	The molecular mechanism regulating quinolizidine alkaloid content in vegetative tissues and seeds of narrow-leafed lupin (Lupinus angustifolius).	Prof Chengdao Li
Zhichao Yang	Deep data mining approaches to unravel genetic loci for Australian wheat NUE enhancement.	Dr Penghao Wang
Md Asad Uz Zaman	Investigating the microbiome associated with rhizosphere soil, mulch and Phytophthora infestation of avocados	A/Prof Kirsty Bayliss
Wenjuan Zhang	Manipulating WRKY Transcription Factors for Genetic Improvement in Barley	Dr Penghao Wang
Shunlin Zhang	Evaluation of the impact of sulfuryl fluoride (SF) fumigation on metabolites of wheat and its finished products	Prof Chengdao Li
Ruihua Zhao	Genome-wide characterization of the metacaspase gene family in wheat and exploration of TaMC4 heat stress mechanism	Prof Wujun Ma

CCFI Researchers

Genomics, Pre-breeding and Bioinformatics


Prof Rajeev Varshney
Centre Director


Anu Chitikineni
Senior Science Manager


A/Prof Reyaz Rouf Mir
Associate Professor


Dr Vanika Garg
Senior Research Fellow


Dr Jingjuan Zhang
Research Fellow


Dr Rutwik Barmukh
Research Fellow


Dr Rhys Copeland
Research Fellow


Dr Cassandria Tay Fernandez
Research Associate


Dr Weinan Xu
Research Associate


Dr Oluwaseun Akinlade
Research Associate


Nicholas Ingram
Administrative Officer


Sudhakar Gorantla
Administrative Officer

Western Crops Genetics Alliance (WCGA)


Prof Chengdao Li
WCGA Director


Dr Xiao-Qi Zhang
Laboratory Manager


Dr Tianhua He
Leader: Crop Genomics


Dr Tianhua He
Leader: Crop Genomics


Dr Yong Jia
Research Fellow


Dr Sakura Karunarathne
Postdoctoral Researcher

Agricultural Biotechnology


Prof Michael Jones
Professor: Ag Biotech


Dr John Fosu-Nyarko
Postdoctoral Research Fellow

CCFI Researchers

Grain Chemistry and Quality

Prof Wujun Ma
Professor: Grain Chemistry and Quality

Crop Protection & Microbiome

A/Prof Kirsty Bayliss
Academic Chair: Biosecurity & Food Security

Dr Anish Shah
Postdoctoral Research Fellow

Crop Adaption to Climate Change & Soil Constraints

Prof Richard Harper
Professor

Prof Richard Bell
Professor: Sustainable Land Management

Dr Wendy Vance
Lecturer/Researcher

Dr Tona Sanchez-Palacios
Postdoctoral Research Fellow

Dr Karthika Pradeep
Research Associate

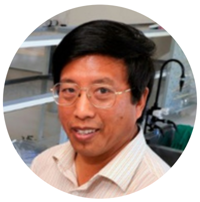
Nutrition and Food Science

Dr Wendy Hunt
Senior Lecturer: Research & Teaching

Prof Vicky Solah
Associate Professor: Food Science

Andrew Tilley
Researcher

Post-Harvest Plant Biosecurity



Prof Yonglin Ren
Professor: Plant Biology

Dr Bob Du
Senior Lecturer

Digital Agriculture

Prof Ferdous Sohel
Professor: School of IT

Robotics

Dr David Berryman
Senior Laboratory Manager: SABC

Hybrid Wheat

A/Prof Ryan Whitford
Inaugural ARC Industry Fellow

Biostatistics

Dr Penghao Wang
Senior Lecturer: Biostatistics

Honorary/Adjunct Researchers

Emeritus/Honorary Professors

Prof Rudi Appels
Honorary Professor:,
UoM, Australia

Prof PK Gupta
Emeritus Professor,
CCSU, India

Prof Peter Langridge
Chair, Scientific Board
Wheat Initiative, Germany

Adjunct Professors

Prof Ramesh Aggarwal
CSIR, India

Dr Vivienne Anthony
SFSA, Switzerland

Prof Kailash Bansal
NAAS, India

Dr Alison Bentley
ANU, Australia

Dr Jose Crossa
CIMMYT, Mexico

Dr Eric Danquah
WACCI, Ghana

Prof Andreas Graner
IPK, Germany

Dr Chike Mba
FAO, Italy

Ms Cathy Reade
Crawford Fund, Australia

Prof Matthew Reynolds
CIMMYT, Mexico

Prof Xu Xun
BGI Group, China

Associate Adjunct Professors

Dr Dion Bennett
AGT, Australia

Dr Nalishebo Meebelo
ReNAPRI, Zambia

Dr Liu Xin
BGI Group, China

Dr Manuel Spannagl
Helmholtz Munich, Germany

Dr Martin Mascher
IPK, Germany

Dr Abhishek Bohra
ICAR-IIPR, India

Dr Bharadwaj Chellapilla
IARI, India

Contact us:

Phone: (+61)08 9360 1726

Email: rajeev.varshney@murdoch.edu.au

Web:
www.murdoch.edu.au/research/ccfi
www.murdoch.edu.au/research/sabc

Connect with us:

- 𝕏 @MU_CCFI_Biotech
- in CCFI | SABC
- f MU.CCFI.Biotech
- ▶ @rajeevvarshney6803

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