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Techno-economic Analysis of Astaxanthin from *Haematococcus pluvialis* for Edible Cosmetics and Thalassotherapy

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Edible cosmetics with vegan food-grade ingredients are a natural, safe and sustainable alternative to the many chemical-based cosmetics in the market. Incorporation of edible cosmetics in a Thalassotherapy Centre, which focuses on a therapeutic use of seawater and its marine elements such as algae for beauty and health is a promising business idea for Australia. The aim of this study was to carry out a techno-economic analysis (TEA) of astaxanthin extracted from an Australian strain of freshwater microalgae, *Haematococcus pluvialis*, using a low-cost sustainable process so that the red astaxanthin carotenoid would be used as a key ingredient in edible cosmetic formulations along with Australian native botanicals and marine-based elements. The astaxanthin was extracted into ten different plant-based oils, including Australian macadamia virgin oil, Australian sandalwood nut virgin oil, Australian jojoba virgin oil and other oils sourced from different countries prior to cosmetic formulation. A discounted cash flow analysis approach was used to study the economic feasibility of this process. The cost indicators utilised a defined value of internal rate of return (IRR) and a net positive value (NPV). An investigation on the sensitivity of the minimum astaxanthin-in-oil selling price (MAOSP) to some variations of selected parameters illustrated that astaxanthin concentration yield, type of oil used as a biosolvent, and extraction efficiencies are vital parameters that significantly affect the feasibility of the process. The most important parameter is astaxanthin concentration; as it varies from 0.5 mg to 1 mg the MAOSP decreases from AU\$3.13 to AU\$1.50 per mg/ml of astaxanthin.

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Information Communication Technology (ICT) Impact on Citrus Value Chain Efficiency

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In developing countries like Pakistan, farmers and other agricultural value chain stakeholders with many other problems are also unable to access the desired information with the existing public sector resources and inefficiencies. Poor information base impacts value chain actors' poor planning and decision-making, resulting in low gains of their efforts. Recent penetration of mobile, computer, internet, etc., allows curing inefficiencies across the citrus value chain. Research results show that farming community, a key actor in citrus value chain, is improving information access with conversant information sources other than mainly relying on fellow farmers. Farmers, including the smallholders, have increased their bargaining power in input and output markets to enhance gains with lesser exploitation by the concerned value chain actors. All other citrus value chain stakeholders, including input suppliers, laborers, transporters, pre-harvest contractors, exporters commission agents, wholesalers, retailers, and consumers, benefit from the innovative information availability with the use of modern ICT, especially mobile technology using the internet. ICT considerably contributes to lowering the risk across the value chain, access to new domestic and international markets, and improving fair gains among the value chain actors. Smallholder farmers, laborers, and retailers are concerned about the lack of awareness, knowledge of the technology, and ICT usage expense. The encouraging adoption of modern ICT at the household level provides a promising opportunity for the youth, especially the women, to make possible contribution to citrus value chain and improve household livelihood under the prevalent cultural norms.

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Role of Policy in Pulses Industry Value Chains: A Systematic Literature Review

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The global demand for pulses is continuously increasing because of the changes in people's food habits and the positive role of pulses in nutritional, ecological and sustainable outcomes. Despite the importance of the industry and significant market opportunities, evidence suggests that in developing countries pulse industry is considered not receiving the required attention in the public policies, and the pulses producers are not benefiting from the market growth and opportunities. Using a systematic literature review and applying a value chain framework to analyse, this paper explores pulses-related policy measures in both developed and developing countries and their pathways of impact. The results show that overall policy responses in the pulses industry are more production-oriented than holistic and systematic. In developed countries such as Canada, USA and EU, the policies focus on self-sufficiency and export, particularly enhancing the export capacity by creating enabling environment. In contrast, in developing countries such as India, Pakistan, Bangladesh, and China, the focus is on bridging the gap between domestic demand and production. The analysis revealed that public policies on pulses lack a whole chain perspective. The inability of the pulses producers in developing countries to leverage the advantage of market opportunities and their growing sense of lack of policy priorities for the pulses industry could be attributed to this lack of a whole chain perspective. This is because any support and resulting production efficiency would not be translated into incentives due to the unsupported and weak domestic intermediaries that link production with markets.

Keywords: Performance, pulses industry, review, policy, value chain

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Effectiveness of the mall for youth entrepreneurship development in Kenya

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Fast population growth is leading to a large youth bulge, which is an ongoing concern for Kenya whose 2019 census revealed out of the 13.7m youth, 5.3m (38.9%) are jobless. The ILO report on Global Employment trends for youth 2020 (International Labour Organization, 2021), indicates, with only a minority continuing to tertiary education which includes university or tertiary-level technical or vocational training, even so, those who are ready to transition to work face extreme hardships finding meaningful employment. In sub-Saharan Africa, women (Ben-Ari, 2014) operate the majority (60%) of agribusinesses. Comparatively, the 2020 KNBS reported that there were 65.3% males in the labor force compared to (48%) females and that COVID 19 had rendered more women jobless compared to men as they work in jobs vulnerable to disruption, especially small businesses, agriculture, service and manufacturing. In addition, Kenya's urban population is soon approaching the level that makes it difficult to feed the massive urban populations in a sustainable way. Since the urban consumer values are widely diverse and selective, there is need for an innovative approach for Agri-Food entrepreneurs to develop a modern Agri-Food system that is sustainable, meets the needs of the diversified urban consumers and spurs business innovation that can address food security and curb unemployment. So where will these Agri-Food entrepreneurs be trained for these new skills and best practices? Alternatively, where can they find support for these processes?

The Global Agribusiness Management and Entrepreneurship (GAME) Center at the United States International University-Africa (USIU-Africa's) Metro Agri-Food Living Lab (MALL) model applies a field based action research approach where the entrepreneur's site serves as the lab for testing interventions. The model involves a rigorous survey and experimental (RCT) research that aims to co-create knowledge among researchers, mentors, entrepreneurs and other stakeholders to determine what works. The current MALL project was conceptualized to address the triplet problem of youth unemployment, food security and gender inclusivity.

The research objective of the project was to evaluate effectiveness of the Metro Agri-Food Living Lab for gender inclusive entrepreneurship development among the youth. This project involved three phases – experiential learning, mentorship and access to finance – with a view to improving the entrepreneurial business profitability, productivity and job creation among other indicators. The interventions involved technical business skills along with mentorship by experienced entrepreneurs, coupled with linkages to credit financing sources. The interventions were expected to improve business knowledge, skills and attitudes to increase their sales, profits, diversification, quality, employment opportunities and commercial prowess of young men and women Agri-preneurs. The first intervention was capacity building through a decentralized rural training. The second phase consisting of mentorship sought to enhance implementation of skills obtained during the training phase and to finalize the business plan. However, due to COVID-19 pandemic, the team adopted a virtual mentorship approach for three months involved electronic individualized interaction sessions, group sessions, and online discussions through WhatsApp, emails, phone calls and/or SMS and GAME Center organized webinars. The final phase linked up entrepreneurs with a financier for potential loans. This research strived to not only assess the envisaged business growth, creation of job opportunities, and sustainable Agri-Food Systems, but in light of the COVID 19 pandemic, to assess the resilience of agribusiness entrepreneurs.

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Market Analysis of Calamansi in Homonhon Island, Eastern Samar: Value Chain Approach

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Calamansi (*Citrofortunella macrocarpa*) is the top crop in the small island communities in Homonhon Island, Guiuan, Eastern Samar, Philippines. By virtue of the smallness and remoteness of the island, Homonhon's calamansi growers face unique constraints to the gains that could be optimized from the mainland markets, which in turn limits their economic welfare. Agribusiness development strategies hence need to incorporate the small-island context to appropriately address peculiar challenges in these types of local commodity sectors. Unfortunately, there is scant knowledge about this area of study.

In this paper, we investigate the calamansi farming communities and value chains in the small island of Homonhon. Data collection was by semi-structured interviews of participants from within calamansi distribution channels. Value chain mapping showed that fresh calamansi produce was traded to consolidators, trader-assemblers, wholesalers, processors, and retailers in the mainland market. Also, chain performance analysis revealed that island-based upstream players are alarmingly facing declining output per unit effort in their farming activity, while medium traders and processors gain the most along the chain due to high economies of scale and value-added.

On the surface, the problem seems to root in poor post-harvest and logistic practices. However, upon further analysis, strengthening extension support through training and capability development and provisions of common service facilities appropriate to small island environments are necessary to develop the local processing activity into products with higher value-adding and longer shelf life. Therefore, these are recommended as the optimal upgrading strategies to enhance the entire value chain's competitiveness and profitability.

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Business Model and Oil Palm Smallholders' income

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Many assume oil palm smallholders are a group with similar characteristics, yet they vary in terms of competencies, productivity, and income. This heterogeneity arose from differing institutional conditions and business models, which led to various challenges and support models for each group. This study was conducted to determine the best business model for smallholder support. The data was collected from 1080 smallholder respondents in Indonesia and Malaysia, covering six states, and was analysed using the compare means test. The business model was estimated using nine components, namely resources, revenue stream, value proposition, cost structure, partnership, activities, marketing channel, customer segment, and customer relationship. The findings show that smallholders also receive income from certificate sales. However, although some groups have received sustainable certificates, their FFB value proposition is still based on the physical quality. Therefore, they have not sold their certified FFB. The compare means tests show that income is significantly higher for smallholders in organized, partnered, or certified groups than in non-organized, non-partnered, or non-certified groups. Such differences are mainly due to the economies of scale, direct marketing channel, and physical FFB quality improvement of the former groups that decrease average costs and increase productivity and selling prices. The organized, partnered scheme group showed the highest average income, while the non-organized, non-partnered non-certified groups showed the lowest. Therefore, good organization management and partnerships are crucial in improving smallholder income. The government needs to collaborate with palm oil companies and NGOs to support the smallholders' capacity and facilitate partnerships.

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Motivation for adoption and non-adoption of organic vegetable farming in Vietnam

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Organic farming plays a crucial role in improving farmers' livelihoods and environmental sustainability and is widely considered to promote a healthy dietary system. Socio-demographic and economic factors have been identified as the influencing factor in the adoption of organic farming. However, the influence of the relationship between actors in a value chain on the adoption of organic farming has not been widely studied. This paper investigates the relationships between actors in an urban fresh food system and farmers in peri-urban agricultural systems near Hanoi, Vietnam. We investigate the impact of these relationships on the adoption of organic farming. A semi-structured interview involving 32 participants was used to explore the relationships in conventional and organic vegetable value chains, which connect urban consumers with peri-urban farmers. The results identified that transactional relationship is dominant in conventional vegetable value chains, while collaborative and hybrid relationship in organic vegetable value chains. Farmers in transactional relationships are opportunistic and driven by flexibility in price and quality requirements which discourages them from adopting organic farming. In contrast, farmers in collaborative relationships adopt organic farming systems to obtain a guaranteed market at fixed and premium prices underwritten by contracts with retailers, indicating an economic motivation. We determine that farmers in hybrid relationships adopt organic farming for the perceived health benefits for themselves and the consumers, indicating a moral motivation. The findings have implications for policymakers in designing interventions to improve the rate of organic farming adoption in peri-urban and urban fresh food systems.

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Empowering women in contract farming in Bangladesh's vegetable seed value chains

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The empowerment of women smallholder farmers is widely associated with increasing productivity, economic growth, and income equality and, thus, is fundamental to accomplishing the 2030 Agenda for Sustainable Development. As women's participation in contract farming in developing countries rises, investigating whether and how women obtain empowerment within contract farming activities is needed. Specifically, this research explores how contractual arrangements in vegetable seed value chains in Bangladesh contribute to empowering women who participate in them. Empirical qualitative data is drawn from ten female farmers, eighteen value-adding female actors and six company personnel, with findings analysed thematically according to key elements of women's empowerment identified in the development literature. Our analytical framework emphasises how increasing or decreasing "power" accelerates or hinders women's empowerment. It sees empowerment as a multidimensional process incorporating the "power to" recognise one's goals, the ability to exercise "power with" others, the capacity to find and nourish "power within" the self, and "power over" someone or something. While these dimensions of power were observed for women in contract farming in this research, we find that women exercise more "power to" bargain and control income at the individual level than at the household and farm level. Furthermore, both women farmers and women involved in value-adding possess more power in the community (i.e. power with) due to participation in contract farming, which indicates collective empowerment. By contrast, seed companies retain significant 'power over' female farmers regarding price-fixing and product selection, inhibiting women's empowerment with implications at both individual and collective levels.

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Focus Farm Extension Approach: An experience from dairy smallholders' development project

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Farmers' individual goals and priorities are essential in developing a successful extension approach to drive farm practice changes. This paper details on how IndoDairy Project, dairy smallholders' development project in Indonesia, trialled Focus Farm as farmer-led extension approach using a real case study farmer. In 2019, two Focus Farms were established in Bogor, a dairy producing district in West Java Province. They were selected on the competitive basis, consisting of interviews on the motivation statement, verification through farm visits, assessment by comparing the strengths and weaknesses among all candidates, and confirmation as a chosen focus farmer. After agreed, farmers selected their own Support Farmers' group with 3-5 members, where the Focus Farmers and Support Farmers would learn together. The Project Team recommended experts for the Advisory Group, who were selected adjustably based on their expertise to support the technology implementation. Each Focus Farm had monthly meetings over six-month period to monitor and update the farm condition, discuss progress, and develop a plan for the next meeting. The project facilitated farmers to trial planting high-quality forages and make silage from these forages. Moreover, the project facilitated laboratory analyses for samples of soil, forages, concentrates, and composts they used when planting the forages, where farmers had the opportunity to learn about nutrition balance from local feed resources. Results of the evaluation present that 81% of farmers gained new knowledge, and 19% partially gained new knowledge. Lastly, Open Day was conducted by inviting more farmers and stakeholders as in farmer-to-farmer learning.

Keywords: focus farm, farmer-led, extension approach, dairy smallholder

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Improving knowledge of dairy farming practices using women centred training

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Delivering a series of Women's Discussion Groups in West Java as part of a smallholder dairy development project (IndoDairy) showed an increased knowledge of technology and practices, enabling increased adoption. This paper examines the change in knowledge of women farmers after participating in a three-day training program. From November 2021 to April 2022, 17 groups (each 30 people) participated reaching a total of 470 women farmers across three regencies in West Java, Indonesia. The training aimed to increase the participation of women in dairy farming, empower them to apply the learnings, and adopt better farming practices. The training covered both knowledge and practical aspects in various topics particularly nutrition, calf management, animal health, reproduction, milk quality, farm business management and digital literacy. Practical components were integrated into the training, including a farm visit to collect information and to use some technologies, such as paddle tray to detect subclinical mastitis. To assess the change in knowledge, pre- and post-evaluations were carried out with each group. Data were analysed using a t-test (paired two sample for means). Results showed a significant improvement (p value $3.02E-162$, $p < 0.05$) in knowledge after the training and aspired to apply knowledge and skills on their farms. Online discussion platforms were set up for each group showing that most women were eager to apply the knowledge gained immediately after the training. Facilitating intensive training whilst maintaining support advisory services was an effective way to develop knowledge on dairy farming practices and encourage farm practice change for better performance.

Keywords: women participation, women farmers, dairy smallholder, dairy training

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Participatory extension approach to enhance the adoption of best dairy farming practices

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A top-down extension approach tends to be commonly applied in developing countries, including Indonesia, which is found to be ineffective, especially in increasing the adoption of agricultural technologies. One promising participatory extension approach called Discussion Group (DG) was trialled among smallholder dairy farmers in Indonesia under the IndoDairy Project. DG was carried out in four main dairy-producing districts in West Java Province for 10 months in 2019 involving 189 farmers. There were 13 DGs, including one group that consisted of only women farmers as the members. The activities included: a series of meetings to discuss topics on technologies chosen by the members of DG and ongoing advisory by Village Level Researchers (VLRs), regular on-farm visits, providing simple technologies, and monitoring. To assess the effectiveness of the DG, information on knowledge, attitude, and practices (KAP) were collected before and after the delivery of the DG. A year after the program concluded, a follow-up group discussion was conducted in a small number of groups using social medium (WhatsApp) during the COVID-19 pandemic in 2021 to understand the uptake of technologies and practices. The overall results show that the participatory extension programs through DG have improved farmers' knowledge about best dairy-farming practices leading to farm practice changes. Some examples include the adoption of teat dipping after milking, feeding colostrum to calves, record-keeping practice, and feeding high protein concentrates. Understanding farmers' aspirations and needs through the DGs was an important element of this extension approach to ensure the topics discussed were addressing farmers' needs.

Key words: extension, participatory, discussion group, adoption, dairy smallholders

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A review of export supply chains for Australian horticulture: Exploring efficiency dimensions

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Horticulture is a key economic sector in Australia but is currently experiencing limited access to export markets due to inefficiencies in export supply chains (ESC). Australia's horticultural export sector has the potential to contribute roughly \$15 billion to the national economy by 2026-2027, but inefficient supply chains could stymie this growth. To help unlock the full potential of horticultural exports, this study aimed to identify the key dimensions of an efficient horticulture ESC of Australia, and how each of these dimensions influences the different stages of the ESC. A scoping review was conducted to identify key efficiency dimensions, using Electronic databases such as ScienceDirect, Scopus and Google Scholar. A total of 17 studies met the inclusion criteria. After reviewing the selected literature, five key efficiency dimensions of an ESC were identified: economic efficiency, time efficiency, management efficiency, network efficiency and innovation efficiency. Assuring these efficiency dimensions in the ESC is expected to facilitate both efficiency and competitiveness in the long run. It was demonstrated that management, time, and network efficiencies should be applied at every stage of the ESC and the other two efficiency dimensions are only required at certain stages. This research contributes to our understanding of the various dimension of horticulture ESC in Australia and globally and will be of interest to relevant stakeholders such as researchers, industry bodies, growers, distributors, processors, exporters, retailers and policymakers.

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COVID-19 Impacts and livelihood strategy based on agriculture during pandemic in Indonesia

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COVID-19 has impacted agricultural sector in Indonesia in various aspects including increasing risk and uncertainty, disturbing food supply chain, and decreasing income. This paper aims to analyze impacts of COVID-19 for small holder farmers in an integrated crop-livestock system and livelihood strategies to cope with pandemic conditions in West Nusa Tenggara (WNT), Indonesia. A mixed-methods study was held in three districts of WNT from August 2020 to April 2021 by collecting quantitative and qualitative data using survey, FGD, observation and key informant interview methods. Respondents were selected purposively covering 103 small holder farmers. Decreased income up to 20% and increased household expenditure to 10% were reported by majority of respondent. Travel restriction between April to July 2020 that coincided with harvest period subsequently led to labour shortage, abandoned harvest, deteriorating product quality and lack of on farm and off farm works were among contributing factors for decreased income. Meanwhile, home schooling and increased goods prices contributed to increased household expenditure. Small holder farmers implemented strategies to cope with these pandemic situations by utilizing home grown vegetables or those planted in the rice bund, sharing food with neighbours and collecting food from nature like fishing. Most respondent reported no changes in food availability, only more difficult to access it because of decreased income. This study proves resilience of livelihood strategies based on agriculture to cope with COVID-19 pandemic situation.

Key words: crop-livestock system, income, expenditure, travel restriction

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Assessment of biochar production potential from biomass residues in plantations in Vietnam

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Vietnam has about 4.4 million hectares of planted forests (MARD, 2020), across eight regions. The Central Highlands has been planted with around 0.46 million hectares owned by smallholders. The main species planted in this region is the *Acacia* hybrid (*A. auriculiformis* × *A. mangium*) for production of pulpwood and sawlogs. Harvesting these trees results in a timber residue is currently not used. There is however, no data on this harvest residue, even though biomass residues could be used for biochar production or energy product. This study aimed to estimate biomass of aboveground tree components from a small-scale harvesting operation of young *Acacia* plantations at 6.5 years old (stocking was 2500 – 3000 tree ha⁻¹) in Dak Lak province, Central Highlands of Vietnam. To accomplish this objective, destructive sampling methods were used to sample tree components, including stem, bark, large branches, and small branches and leaves to estimate the biomass waste. Dry weight biomass was then converted to potential biochar production. Total accumulated aboveground biomass was 327.7 ± 273.1 Mg ha⁻¹. The biomass components were stems (75.1%) > small branches and leaves (10.7%) > bark (8.2%) > large branches (6.0%). Biomass residues (excluding commercial stems) were 78.7 ± 65.6 Mg ha⁻¹ equivalent to a 33.0 ± 27.5 Mg ha⁻¹ biochar yield. The findings indicate that collecting forest residues left on the ground of small-scale plantations, following harvesting could provide biomass for biochar production, bringing income diversification for smallholders and carbon sequestration benefits.

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Impact of Donor Investment in Agriculture Research and development sector of Pakistan

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Agriculture sector is indispensable to the country's economic growth, food security, employment generation and poverty alleviation particularly, at the rural level. Due to tight financial challenges, the developing countries, need international support in agriculture research and development so to increased agricultural production, enhanced income opportunities along with new employment opportunities. This paper attempts to cover the donor investment on agriculture R&D in Pakistan. We will cover initiatives by the international community with explicit focus on Australian initiatives. One of the strategic objectives of Australia's development partnership with Pakistan is to accelerate sustainable growth and employment by supporting agricultural industry. The role played by the Australian agriculture scientists has been very critical and their strength of Australian program has been in developing person to person linkages for the promotion of agriculture research and development cooperation. For this Australia, draw teams from its world-class expertise to work along with Pakistan scientists. Queensland Agriculture Department and University experts have been more engaged as the fresh fruits have bene the initial focus. The study is review based, secondary data is used focusing the Australian research and development investment in last ten years. Data suggest that donor investment has positive impact on agriculture sector specially in horticulture crops, livestock and water. Donor initiatives has improved the livelihood of farmers through adoption of new technologies and developing their capacity beside the farmer these investments has contributed to capacity development of researcher as well. Which ultimately contributed to poverty reduction and sustainable development in rural areas.

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A Regional Information Sharing Network for Breadfruit Production in the Pacific

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With increased climate-related threats to food security in the Pacific, sustainable food systems and value chains have never been more critical. Breadfruit, a well-known and produced crop in the Pacific, is a hardy, climate-resilient, fruit that has a wide variety of uses as a food source. Breadfruit links Pacific countries through its cultural heritage as well as the emerging new products, including the export of processed breadfruit flour and frozen and fresh breadfruit. In an effort to support the growth of breadfruit and create new breadfruit value chains, the creation of a regional information sharing network, the “Breadfruit People” has allowed research, innovation, and developments to be shared and promoted among breadfruit growers. The online community includes growers, consumers, traders, processors, researchers, and lovers of breadfruit, with the aim to encourage more people to grow, buy, eat and use breadfruit and to also connect with those already working with the crop. The Breadfruit People amplifies the work of the network through communication and education and serves as a hub for all things related to breadfruit. The documentation and sharing of innovation accomplished through webinars, community sharing events, technical trainings, and social media have led to the regional advancement of the crop and broken barriers into markets and products that would not have been possible without the support of the regional network.

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Integrating carbon offsets into northern Australia's land use systems

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Australia's carbon offsets market is entering a period of substantial change, with overall demand increasing as companies set themselves ambitious corporate decarbonisation targets; with the decarbonisation credentials of traditional offsets projects being challenged; and with a growing recognition that the offsets market should primarily deliver projects that remove and sequester carbon dioxide (CDR) from the atmosphere (rather than support emissions mitigation by existing sectors). With all those drivers in play, expectations are that the growth in demand for 'good quality' offsets will rapidly outstrip supply, putting considerable upward pressure on price.

While that is stimulating renewed interest in carbon farming initiatives based on managed planting of timber species, question marks remain over how quickly and to what extent that opportunity would likely grow. The history of technical and commercial plantation failures is widely known, compounding a major reluctance by Australia's landholders to integrate managed timber plantations into their operations. In the context of CDR offsets, the idea of developing a domestic oil production industry from *Pongamia pinnata* offers an intriguing prospect. While investigations into a pongamia-biofuel industry have yielded little action, recent innovation that opens up the human food market could substantially change the value proposition for pongamia plantings.

Innovative new options will be needed for Australia to deliver high quality CDR offsets at sufficient scale, relying heavily on the integration of CDR into existing landuse systems. In that context, we review how different options might stack up for the agricultural and land use systems of northern Australia.

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Leveraging Gender Relations in Cocoa Agricultural Value Chain of Davao City, Philippines

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The Philippine Republic Act 115471 recognized Davao City as the “Chocolate Capital” of the Philippines, where 80-90% volume of dried cocoa beans are produced. A gender lens is integral in any development, yet to be explicitly embedded in the design of agricultural high-value commodity chain development initiatives. This paper aims to fill the gap by utilizing a gender lens in the development of a co-design approach in the cocoa industry of Davao City consisting of 8,558 smallholder farmers in over 5,000 hectares (ha) of land, and production of 0.87 metric tons/ha of yield. A household survey of 239 cocoa farmers (58% male and 42% female) indicated that 55% with intercropped (coconut, fruit trees) cacao farms as their main source of income. Family labor is done by men and women in cocoa production, while additional paid labor is contracted during the harvesting season. Focus Group Discussions (FGD) reveal that heavy works (hauling, spraying) and bringing wet and dried beans to market are usually done by men but decisions are shared by partners. Farmers sell wet cocoa beans to local consolidators acting as intermediaries to processors and consolidators. Beans of a lower quality are sundried, processed into “tablea” or sold as unfermented beans to local traders, including a leading supplier of dried beans to the international market. Hence, a co-design approach is undertaken to leverage existing gender relations in value-adding opportunities in Davao cocoa value chain development because even well-intentioned VCs can also miss out on gender and development gains and opportunities.

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Influence of livelihood assets on livelihood strategy of the smallholder rice farmers

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Rice is the most important commodity in Indonesia as the staple food of most of its 270 million population and a critical part of the rural economy. Thus, supporting smallholder farmers' sustainable livelihoods in rice production pockets is a priority for national governments to ensure sustainable production and national food security. The livelihood strategies of smallholder farmer households depend on the conditions of their assets, and farm households cope with risks and shocks. Thus, examining the relationship between the livelihood assets and the livelihood strategies of smallholder farmer households helps understand their livelihood conditions and formulate programs and policies for poverty reduction. The first stage of this study is to establish the mechanism of the influence of smallholder farmer livelihood assets on livelihood strategies, followed by evaluating different farm household livelihood assets by establishing an evaluation index system. Lastly, we conduct an empirical analysis of the influence of farm household livelihood assets on livelihood strategies using a multinomial logit model. The results of the different types of livelihood assets and their impact on livelihood strategies are discussed. Lessons are drawn that could be useful in applications of public policy aimed at the betterment of smallholder farmer livelihood strategies, which involve thousands of families in the region of West Java, one of Indonesia's central rice producers.

Keywords: rice, smallholders, livelihood, Indonesia

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Enhancing market channel for vegetable purchase as a COVID-19 response in Indonesia

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Vegetable purchases are usually done in traditional markets by most Indonesians. COVID-19's arrival, and associated restrictions on activities, reduced the movement of customers to buy vegetables at traditional markets.

This study sets out to estimate the extent to which Indonesian vegetable purchase behaviour was affected by movement restrictions due the COVID-19 . This information is then used to project future demand and to identify mechanisms for supporting consumption. Surveys were conducted in 14 provinces and included purchase behaviour both at household level (n=1219) and in hotel, restaurant and retail businesses (n=285).

Results identify some behaviour change for vegetable purchases due to movement restrictions. This included an increase in online purchases. Although the change in behaviour is not statistically significant, it was notable amongst consumers with higher incomes. Vegetable purchases at groceries also increased, relative to central markets.

Groceries are the commodities sold by a grocer or in a grocery store. Customer buy these goods in a stores not necessarily close to their neighbourhood. Online shopping is shown to be essentially a premium niche market specially in Java. Preferences for purchase location and channel amongst hospitality venues remain largely unchanged, mostly from the market (69.94%), contract with wholesaler 20,52%, contract with farmer 5.78% and retail 3.76%.

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Agri- businesses digitalization in Covid-19 time in Lam Dong province, Viet Nam

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Background: Digital innovation in agriculture has delivered benefits to farmers in optimizing resource use, improving sustainability, and better targeting high value markets. These benefits have taken various forms. In the time of COVID-19, agricultural businesses suffered substantially and hi-tech applications played a role in their survival and success. Lam Dong province, in the Central – Highland of Viet Nam, is a powerhouse vegetable and flower production powerhouse. The pandemic and associated public health responses restricted transport, personal contacts, and flows of inputs, product and payments both to other provinces and to export markets. Almost 90% of flower orders were cancelled by 16 April 2020, and flower prices had declined 70-80%.

Materials and methods: This study presents the experience of 4 agribusiness enterprises, in information transfer and the utilization of digital technologies. The benefits generated from these tools during the Covid-19 period are examined. In-person managers’ interviews are supplemented by secondary data on these enterprises.

Results and discussions: Results include the accounts of actions taken to identify and exploit online opportunities for distributing the products, and adjustments made at all stages of the production and marketing system to apply digital technologies and enhanced information flow. Companies utilized digital technology in a 10-20% increase in production, with greatly reduced energy use, after the pandemic. Growers saved 10-50% water for irrigation and reduced up 30% fertilizers. The findings provide lessons for other agribusinesses in Lam Dong province, and Viet Nam.



Fig 1: Using machine to spray natural enemies at the Da Lat Hasfarm Company (L) and fertilizer controlled machine (R).

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Inconsistent interpretations of Entrepreneurial Orientation by SMEs & Sri-Lankan government officials: Misalignment

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The Sri Lankan government set out to promote export competitiveness and build a prosperous country by implementing a five-year Innovation and Entrepreneurship (I&E) strategy. However, the inability of government agencies and officials to plan, finance, execute and oversee I&E policies and programmes has been stressed by practitioners and business organisations. This study looks at how two constituencies, SMEs and government officials, interpret Entrepreneurial Orientation (EO) to determine the alignment of understanding and what dimensions of entrepreneurship development should be emphasised in execution. Based on the semi-structured interviews with 18 exporter SMEs, this study shows that, consistent with the literature, SMEs associate innovativeness, proactiveness, risk-taking, competitive aggressiveness and autonomy with EO. SMEs also emphasised perseverance as an important EO dimension. We also interviewed eight government officials, who design, execute and evaluate, I&E development policies and programs for SMEs, to explore their perception of EO dimensions. Surprisingly, government officials primarily associate EO with innovation only. Such a discrepancy in EO interpretations could lead to misalignment of actual development needs and government support provided. This study identified major problems in the execution of I&E policy support; Emphasising innovation without developing entrepreneurial SMEs as vehicles for commercialisation are problematic. The findings also contribute to EO as a multi-dimensional construct by identifying perseverance as a potential extension.

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Analysis of Tomato Value Chain of Smallholder Farmers in district Muzaffargarh, Pakistan

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Pakistan is still in the early phases of implementing vegetables value chain and specifically the tomato value chain with main focus. Tomato production in South Punjab districts particularly Muzaffargarh has played a critical impact on the livelihood of smallholder tomato growers. These growers faced numerous challenges from variety selection to product delivery to targeted market. As a result, tomato growers experienced low product prices, a lack of market information and market ineptitudes. Therefore, this study was aimed to determine about existing tomato value chain, and to identify the major tomato market opportunities through participatory action research, capacity building and whole family extension model with focusing to consumer context. Results showed that foundation farmers' group had reduced their average production costs by 26%, while increasing their average crop yields by 38%, their saleable produce by 22% and their prices by 63%. Per acre, their total revenue was 125% higher than before the project started. Overall, they increased gross profits by 133%. While, qualitative data showed the impact of whole family extension approach was also evident in the involvement of family members in the decision-making process and physical and financial benefits are directly correlated with knowledge and skills required to successfully plan and implement best practice. Results of this study recommended that value chain strengthening activities indicate that their focus, process, content and execution have the potential to build the capacity of the smallholder farmers to identify, evaluate and capture market opportunities that have the potential to increase their household incomes.

Key Words: Tomato value chain; Smallholder farmers; whole family; market research

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Challenges faced by farmers in production technology of loquat value chain in Pakistan

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The research project aims to unravel various barriers to the adoption of various production strategies by the Loquat (*Eriobotrya japonica*) growers in Pakistan. The research captures the difficulty faced by the small farm holders in generating value of their products coupled with the adoption of technology to improve productivity. The study captures the primary data collected from 144 growers and was analysed using SPSS (statistical package for Social Sciences) methodology. The current state of research will further be analysed using current literature for growers in the region and southeast Asia to improve their knowledge on agronomical aspects ensuring effective management of the farm.

The study indicated that growers are facing some serious issues in using current production technology and lack of training exacerbates the problem. The objective of engaging the growers was successful as it will further evaluate the issues and opportunities faced by various agribusinesses and their contribution to the loquat value chain with a focus to improve its social and economic outcome. One promising research approach was to contextualize the research questionnaire after doing a pre-test on a group of growers who were not included in the actual sample to improve the genuinity of the answers. Descriptive as well as inferential statistics were used to explain the result of the study.

Keywords: Agricultural technology, Value chain, Smallholder farmers, SPSS analysis

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Understanding, Integrating and Mainstreaming Gender into Vegetable Value Chains in Pakistan

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The significance of gender mainstreaming in agricultural value chains and its inherent challenges in doing so is well documented in literature. But research highlighting successful understanding, integration and mainstreaming of gender in vegetable value chains is lean. This research, therefore, presents a collection of success stories where agricultural advisory services under the Australian Centre for International Agricultural Research, ACIAR-Pakistan collaborative project “Strengthening vegetable value chains in Pakistan for greater community livelihood benefits (SVVCP)” were able to successfully understand, integrate and mainstream gender research and development into vegetable value chains, and categorised in terms of best-fit practices. Despite higher involvement of women in agriculture labour, their contribution remains unrecognized and undervalued leading to exclusion from the agricultural advisory services. The SVVCP project recognised that mainstreaming gender throughout this initiative would be essential to its success. Thus, women and small farmer families were chosen as a target group adopting whole family approach striving to address gender throughout all programme activities. The project successfully understood the cultural context of three diverse communities involved in tomato, potato and onion value chains, identified the opportunities for gender integrations and mainstreamed the gender research and development in target communities. The whole family approach allowed gender mainstreaming activities, included identification of their roles in value chain and improving their skills and facilitating to negotiate their position in their family and value chain.

Key Words: value chain, gender, mainstreaming, whole family approach

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A Rapid Market Assessment for GAP Certified Vegetables in Northern Mindanao, Philippines

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Smallholder vegetable farmers in the country are now applying for Good Agricultural Practice (GAP) certification. Unfortunately, only less than ten percent opted to renew as various constraints along the value chain still hamper its adoption.

To provide evidence on the market environment of GAP certification, we conducted a rapid assessment in Cagayan de Oro City in Northern Mindanao, one of the largest vegetable trading centers in the country. Data collection was by focus group discussions (FGDs) with farmer groups and government officials, and interviews with key market players. Data were then analyzed using the value chain framework to characterize and assess the vegetable value chains.

Chain mapping revealed that GAP certified vegetables that enter the commercial level are largely absorbed by the traditional markets where concern for certified food products is non-existent. Moreover, information flows showed that the GAP credential does not flow down the chain as most downstream players prioritize availability and price over quality. In addition, business models display exiguous concern towards the certificate and vegetable safety.

These chain characteristics revealed that certified products are not valuable yet. Further analysis shows that the certificate cannot provide a competitive advantage for smallholder farmers due to the underlying issue of product image. Intensive promotional programs on the importance of the certificate are recommended to improve its competitiveness in the market and to establish a customer base that would ultimately translate to profit for smallholder farmers.

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Exploring young agricultural entrepreneurs' perceptions of institutions and support functions in Laos

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Combining agricultural value chains, technology and entrepreneurship is well-established as a strategy for supporting agrarian transition. The participation of youth in this transition is essential for its sustainability and requires a better understanding of the constraints and opportunities they face. In Laos, a country with a young and highly rural population, the government has prioritised shifting from subsistence farming into more commercialized and entrepreneurial models of agriculture, however institutional, policy and social challenges that hinder transformation remain. Accordingly, we interviewed 74 young Laotian agricultural entrepreneurs (agripreneurs) to explore their perceptions related to the role of institutions and support functions as the potential enabling or hindering environment. They reported that the enabling environment in Laos has generally improved to make agripreneurship easier than before, with infrastructure, and new, digitalised, online-offline platforms for information sharing, banking, marketing, delivery, and logistics identified as specific areas of improvement. Commercial agriculture policy has resulted in increased food production, income generation and opportunities for technical advice, financial access, market linkages, product development, and farmers' group/organisation establishment from public, private and (I)NGOs. However, young agripreneurs identified seven areas in which institutions impeded the growth and sustainability of agripreneurship. They are services obstacles, quality of extension staff, coordination, effectiveness of policies implementing and monitoring, unclear administrative/tax fees, research mismatch, and schools' values, curriculum design and learning-teaching method. Our investigation demonstrates that institutions have a vital function in enabling agripreneurship by young farmers, however administrative obstacles and poor implementation of policies carry the risk of having the opposite effect.

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Comparing the domestic market of virgin coconut oil in Rabi and Cicia

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The value chain of Virgin Coconut Oil (VCO) study was conducted for the domestic market, comparing the islands of Rabi and Cicia in Fiji. The VCO in both sites was initiated by and for the women's association, providing a back-up source of income for households. The villagers have contributed through the supply of raw materials and labour. There are three main categories of VCO involvement for the villagers – nut supply, actual VCO production and a combination of both activities. Females constitute 61% of total participants in Cicia and 23% in Rabi. Government and culture and traditions also influences the decision-making in the two sites. Division of labour and specialization may help minimize issues related to labour costs exceeding revenue received. Support services such as infrastructure, financing (and savings), internet and telecommunication contribute to the success of the value chain. This also highlights the middlemen's role as a link between customers and producers – especially when the production site is geographically far from the market. It is with the hope that this study will help interested parties and readers, in general, better understand the nature of business operations in rural areas – taking advantage of its strengths and opportunities, avoiding risks and improving on the weaknesses.

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Communicating the value of native food products in Australian retail markets

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Australian native foods have long been associated with oversimplified narratives of primitive ‘bush tucker’ and witchetty grubs. British colonisation and the subsequent effects of globalisation have had devastating effects on the prevalence (i.e. abundance and supply), overall familiarity, and preference for native foods amongst urban Australian consumers – Indigenous and non-Indigenous alike.

There have been major shifts in consumer perceptions over the last 10-15 years, however a continued narrative exists for the value of ‘*wild harvest*’ native foods, grown in remote and highly variable landscapes. Whilst key native plant species are permitted by regulatory authorities as ‘traditional’ foods and ingredients, there are no benchmark requirements regarding the safety of *wild harvest* product. Furthermore, there are no defined standards or industry best practices relating to labelling of such foods at retail level, for naïve consumers.

A 2008 industry report offered a series of recommendations relating to *Food safety standards and labelling for native plant foods* in Australia. Many years on, in the context of new food labelling standards, consumer trends and expectations, the current study serves as a review of brand and product communication across a range of native food products in the Australian retail market, particularly as they relate to aspects of product origin, food safety, quality, and authenticity.

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Designing an Enabling Environment for Nutmeg Agribusiness Development in Indonesia

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Nutmeg (*myristica fragrans*) agribusiness development is challenged by increasing risks and uncertainties of climate change, market volatility, shifting consumer preferences, and growing competition. Smallholder dominates nutmeg agribusiness with low productivity and added value. At the same time, rural agroindustry has not been supported by appropriate technology and is characterized by raw materials that are usually perishable, vary in quality, and irregularly available throughout the year. Smallholders cannot accommodate the challenges and develop sustainable production systems simply by only improving technical farming. Agribusiness system sustainability can only be secured by a sizeable increase in productivity and added value. On the other side, single interventions in programs and policies cannot address such a wide range of environmental, economic, and social challenges. Consequently, in the context of Indonesia, where nutmeg plays a significant role in generating income and the national economy, designing an enabling environment is very important. This study aims to analyse the constraints faced by smallholders and develop an Enabling Environment framework for nutmeg agribusiness development. The analysis used descriptive statistics and pairwise comparison analysis. The findings indicate that the constraints faced by smallholders are related to technical production aspects and managerial or institutional issues. There are 16 elements from 3 categories of enabling environments for the nutmeg agribusiness: Essential Enablers, Important Enablers, and Useful Enablers. The priority ranking of these elements differs, reflecting each region's development level and the critical constraints faced by commodities. Agricultural infrastructure, agribusiness financing, and investment support services are important elements for nutmeg agribusiness development.

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Nutritional and bioactive properties of Kakadu plum derived products

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In this project, Kakadu plum is used as a functional ingredient to develop value added products with other edible plant material to enhance nutritional and commercial value. The role of functional food ingredients is to add specific quality attributes to the final product. With the improvement of people's quality of life, consumer awareness of the purchase of functional foods continues to increase. As a result, underutilized crops such as Kakadu plum has a great potential to contribute to the growing functional ingredient market. So, we compare the nutritional value of Kakadu plums and foods containing Kakadu plum extract additives, and compare their antioxidant capacity, antimicrobial capacity, mineral content, etc. data, in order to look forward to products containing Kakadu plum additives. Has better nutritional value.

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Prospects and challenges of demand-led plant breeding

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A business approach to plant breeding could be the answer to developing, disseminating and enhancing the adoption of demand-led crop varieties for food and nutrition security and local, regional and international markets. Demand-led plant breeding (DLB) is a market-driven approach with imputes in plant breeding education, variety design and product profiles based on farmer and market preferences. This paper shares the prospects and challenges of demand-led plant breeding in Africa. It outlines lessons gained from the international team of DLB, and pinpoints the enablers for the new generation of demand-led breeders in Africa. The paper describes the critical enablers for demand-led breeders, including integrating academic and business intelligence, championing plant breeding projects and stakeholders along the value chains, attracting investment and creating entrepreneurship and enterprises. A significant and continued investment support is required in plant breeding projects and training centres to serve farmers and their value chains and transform regional or global economies. Business-led and new generation plant breeders are the drivers of transforming Africa's public and private sector plant breeding and seed systems.

Africa, Demand-led plant breeding, Investment cases, Value chains

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Mungbean Prominence in farmer cropping systems for nutrition and livelihood in Kenya

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Knowledge of recurrent challenges in crop production systems and benefits accrued from farming are central to choices that smallholder farmers make on crop varieties they grow. A study was conducted to assess farmers' views on selection of crop varieties and cropping systems in semi-arid Kenya. Individual farmer interview using structured and open-ended questionnaire method was used. The study revealed that farmers grow diverse crops as a cushion to environmental shocks. In Tharaka Nithi and Kitui in eastern Kenya where farmers rely on rain-fed agriculture, mungbean was the predominant crop among 28% and 26 % of the farmers, respectively. Intercropping systems or crop rotations of mungbean with climate resilient cereals or legumes is commonly practiced. Farmers in Baringo in Rift Valley region have access to irrigation and hence prioritize horticultural crops. However, mungbean was viewed as the second most important legume, after common bean. Mungbean, cowpea, pearl millet and sorghum were the valued crops for their adaptability, diverse food uses and income. Maize featured prominent among 16-38% of respondents as it is the main staple food crop in Kenya. We asked farmers about major constraints and if they influence their decisions on crops they cultivate. Drought, diseases, insect pests, inaccessibility to certified seed and market were the major problems considered in decision making. Farmers' carefully choose crop varieties that fit in their production systems, besides meeting their needs. Understanding farmers' perceptions and disseminating suitable technologies has a potential of empowering vulnerable communities.

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New developments in protoplast technology for Australia's top-secret narcotic

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Global pharmaceutical industry worth 1.78 trillion AU dollars. Australia's share in this domain is strong, though there is a massive potential considering the genetic resources of the country, especially in native flora. The *Duboisia* is an Australian native shrub, the only commercial source available for scopolamine, an alkaloid used as an antimuscarinic. It is a million-dollar industry that hold 70% global market share for Australia. The demand for scopolamine and other alkaloids such as hyoscyamine is increasing, pressing the need for advancements.

Ploidy manipulation through protoplast fusion is a well utilised method in in vitro plant breeding for a variety of agricultural plants. Application of this technology to *Duboisia* to produce new breeds with large/thicker leaves, bigger and fast-growing plants can ensure more production per cultivated square meter. The important alkaloid scopolamine is stored in the leaves of *Duboisia*, and polyploid is expected to yield more scopolamine, bringing a higher commercial value.

The current study aimed at establishing a suspension culture system leading to protoplast isolation and fusion with an end goal to produce new genotypes with higher ploidy levels. Optimisations were carried out for two different *Duboisia* hybrids to initially induce leaf callus then to produce rapidly multiplying suspension culture. This study will present the first successful protoplast isolation and fusion platform optimised for the high scopolamine containing *Duboisia* hybrids; *D.myoporoides* × *D.leichhardtii* and *D.myoporoides* × *D.hopwoodii*, using a suspension culture system, paving the way to produce superior cultivars for the benefit of this invaluable Australian industry.

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Integrating co-design approach for farm diversification in the Gilbert Catchment, Northern Queensland

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Participatory System Approaches (PSA) have been increasingly integrated in the Australian agriculture sector. The gaps in the theory and practice in farming systems seen in the developing world in 1960s paved a pathway for reframing the nature of agricultural research in Australia. PSA is proposed to present scientific research more relevant to the farmer. It eases the process of learning and conflict resolution with its assumptions of differentiated goals, power, and access to resources and catalyses local learning, analysis, and action. The approach is used to co-design a case study farm in the Gilbert catchment in Northern Queensland. Historically, farmers in the catchment have been mostly dependent on extensive dryland beef-cattle farming and are unfamiliar with cropping. With rising fluctuations in cattle prices and increasing drought events, farmers are exploring opportunities to diversify their production systems. In this study, the Agricultural Production Systems Simulator (APSIM) was used to analyse the potential of developing a cotton-mungbean- soybean system in 3000 ha of a cattle property. The model used publicly available climate & soil data along with farmer inputs to compare production scenarios. It was found that rainfall variability and water accessibility formed the biggest constraints on the proposed systems. In the absence of irrigation, some of the proposed systems would incur significant loss to the farmer. Less risky scenarios include the expansion of existing forage system or alternative, robust crops.

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Haplotype-based GWAS and genomic prediction: path to increase genetic gain in chickpea

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Chickpea (*Cicer arietinum* L.) is the second most important legume crop consumed worldwide and an important pulse crop for agronomic systems. Future production will need to increase to ensure consistency of supply and reliability for the growing plant-based protein market. To accelerate genetic gain efficient breeding methodologies are required. Haplotype-based genome-wide association and genomic prediction are becoming mainstream tools in modern crop improvement programs. However, the utilisation of these approaches in chickpea has not been widely explored. In this study, we used a chickpea multi-parent advanced generation intercross (MAGIC) population derived from eight elite founders to investigate the ability to dissect region modulating important traits including days-to-flowering, digital biomass, leaf area, and water use efficiency. In collaboration with International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), field trials were conducted across two years (2013 and 2014) and the population was evaluated for canopy development traits under a high throughput phenotyping LeasyScan platform in India (2021). A genome-wide association study (GWAS) revealed haplo-blocks influencing canopy traits and genetic relationships that underpinned days to flowering in these environments. Results demonstrate moderate to high prediction accuracies for these traits. These results highlight the opportunity for breeders to integrate haplotype-based genomic approaches and genomic prediction to improve genetic gain in chickpea breeding.

Keywords: *Cicer arietinum*, Haplotype-based GWAS, genomic prediction, MAGIC population, genetic relationship

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Digitising mango trees to understand physiology, growth and development using plant modelling

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Horticultural crops are usually trialled in the field with specific production systems, and if unsuccessful, a change in methods takes place until an acceptable level of yield is achieved. Monitoring the growth and development of mango (*Mangifera indica*) crop is vital for understanding the effects of tree architecture and intensification of orchards. Digitising tools including a magnetic digitiser were used in this research to record the growth and development of mango trees in Queensland, Australia with the aim to overcome the risks of traditional (trial and error) horticultural production systems. The digitiser allows to precisely locate points in the tree by using a magnetic field. The length and breadth of the leaves, inter/nodes, branches, and flowers were measured, and these measurements will be repeated at different stages of plant growth. The data was recorded and then visualised with a purpose-built software (*Floradig*) to create a digital virtual plant in the computer. Later, the digital plant datasets will be utilised to develop a plant model. The initial outcome of this research activity will provide insights for making decisions to manage mango trees with simulated inputs, for example- light interception, training pruning of branches, by better understanding how the tree architecture could be managed to maximise the overall productivity of mango crop in high-density orchards.

Keywords: Digitiser, productivity, intensification, high-density orchards, tree architecture

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Machine learning for performance prediction in species with polyploid and hybrid genomes

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The sugarcane genome is extremely complex, high polyploid and with multi-species ancestry. Simple additive models for genomic prediction of clonal performance might not capture interactions between genes from different ploidies and ancestral species. Here we use investigate machine learning (ML) approaches for genomic prediction in complex genomes such as sugarcane. By performing convolutional network (CNN), random forest models to the dense clonal sugarcane genotyping data (3k clones 26K high-quality SNPs), we received average accuracy (in cross-validation) as 35% for total cane harvested (TCH) prediction, 35% for commercial cane sugar (CCS) prediction and 45% for Fibre content prediction. The capacity of ML to predict TCH and Fibre content was competitive with, and in some cases slightly better than BLUP approaches that included dominance and epistasis. The study also tested a series of ML hyper-parameter sets, observed the special increase of TCH prediction accuracy with the increase of the neural units in full connected layers. Meanwhile, for random forest, the capacity of TCH prediction was obviously enhanced by larger decision trees which contain more features. This study also performed a series of downstream analysis aimed to unpack the ML black box when applied to prediction, finding hidden relationship patterns and more abstract features that relate to the difficulty of sugarcane prediction.

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Developing flexible models for genetic evaluations in smallholder crossbred dairy farms

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The productivity of smallholder dairy farms is very low in India and other developing countries. Important genetic gains could be realized using genomic selection but genetic evaluations need to be tailored for lack of pedigree information and small farm sizes. To accommodate this situation, we propose a flexible Bayesian model that model allows us to simultaneously account for non-genetic random effects for farms and varying genetic additive variances for marker effects.

We use simulations based on real genotyped data to demonstrate the proposed model can separate the true genetic and non-genetic parameters even for small farm sizes (average=2) although with great uncertainty in scenarios with low heritability. We also apply the model to real data from 4,655 crossbred animals with 106,109 monthly test day milk records and 689,750 autosomal SNPs. We estimated a heritability of 0.16 (0.04) for milk yield and using cross-validation a genomic estimated breeding values (GEBV) accuracy of 0.18 and bias (regression of phenotype on GEBV) of 1.04 (0.26). Candidate genes nearby the top variants, *IMMP2L* and *ARHGEF2*, have been previously associated with milk protein composition, mastitis resistance and milk cholesterol content.

The estimated heritability and GEBV accuracy for milk yield are much lower than those from intensive or pasture-based systems which suggest that the sample size is still modest for an accurate genetic evaluation in the presence of large environmental effects and crossbreeding. Further increases in the number of phenotype and genotyped animals in farms with at least two animals are needed in smallholder dairy farms.

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Application of irrigation decision system in mango orchard in changing climate

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Current challenges in this changing climate include sustaining agricultural production. In the Philippines, irrigation management is becoming important in mango production. We argue that irrigation is done efficiently and effectively by determining and applying the right amount of water that will not only sustain yield but also ensure that the water resources are judiciously used. Water use of mango in a mango orchard in Bataan Philippines was determined with sap flow meters.

The study site was located N 14° 65.988' and E 120° 46.527' at Barangay Dangcol, City of Balanga, Balanga, Bataan, Philippines. A total of nine (9) sample mango trees were selected and characterized. For the irrigation trial, we considered three (3) mango trees per treatment (Treatment – 1 no irrigation; rainfed, Treatment – 2 50% irrigation water, Treatment – 3 100% irrigation water). Before the experimental irrigation application, the installed devices were tested, observed, and analyzed the generated data and computed the average consumption of around 92.6 liters per day per mango tree which was applied in the identified experimental mango tree.

Initial results showed that Treatment – 3 is more advantageous than the other treatments in terms of higher harvested fruits, bigger sizes, heavier weight per fruit, and produced less reject and deform fruits. This experiment proves that applying the exact amount of irrigation water requirements for mango trees will provide 85.69% additional mango fruit produced as compared with no irrigation application while around \$104.71 per mango tree will be added as a benefit in favor of the farmer.

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Deployment of IoT Sensors for Water Use Estimation in Philippine Mango Orchard

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The Philippine mango industry is trading fresh and processed products contributing to the country's agricultural exports and employing 2.5M farmers. Mango is considered a high value and an important commodity. The yield of mango production is targeted to increase from 5.82 tons/ha to 15 tons/ha and there is a nationwide push to improve irrigation to increase the yield. Studies showed optimal irrigation resulted in better yield by improved fruit retention and water use efficiency (WUE). In this study, the researchers adopted *smart farming precision agricultural* technology in an established mango orchard. The study site is located in Balanga City, Balanga, Bataan, Philippines. The aim was to deploy IoT-enabled sensors in the plant, soil, and environment; determine the water use of mango trees; and provide baseline data on soil moisture and key environmental parameters. We also described the sensors, wireless nodes integration deployed in the mango orchard and online dashboard platform.

Preliminary water use estimation indicates that mango takes up about 92.6L of water per day. Water use also varies, expectedly, depending on ambient environmental conditions. For instance, sap velocities increased to 10 cm-hr⁻¹~20 cm-hr⁻¹ on average from cool to warm months. Hourly water use peaked in the middle of the day from 4L in the cooler month (December~January) to 8L in the warmer month (April). This information is crucial for irrigation decisions that are appreciated by mango farmers.

As an offshoot, a subsequent study is underway to determine the optimal irrigation regime and water use of mango under Philippine conditions.

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ConstraintID: web-based tool to identify soil variability and select sampling locations

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It is widely understood that crop yield across Australia is limited by a variety of soil constraints (e.g., sodicity, salinity, acidity, compaction). These constraints often vary spatially across paddocks, resulting in yield variability that increases the challenges associated with crop management. Identifying the location and type of soil constraint/s present is an essential first step to optimising paddock management. However, farmers are often reluctant to attempt spatial diagnosis of constraints due to insufficient knowledge of how to identify spatial zones and select soil sampling locations. We have developed a free, web-based tool called “ConstraintID” that uses Landsat data to monitor crop growth over a 20-year period (using an Enhanced Vegetation Index) and map consistently higher, consistently lower, and inconsistently performing paddock zones. Zones that consistently perform worse than the rest of the paddock often indicate the presence of a soil constraint. This identification of yield variability can be used to guide the selection of soil sampling locations to diagnose soil constraints and identify site appropriate management. The ConstraintID program uses an algorithm to automatically identify soil sampling locations within each zone that together are representative of the zone and provide good spatial coverage and generates latitude and longitude coordinates for the user. This tool significantly increases the ease with which users can identify soil sampling locations that will provide the most useful data to identify soil constraints and improve management decisions.

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Partial replacement of maize with cassava root-moringa leaf and vegetable oil blends for finisher broilers

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The partial replacement of maize with cassava root meal-moringa leaf meal and vegetable oil combinations (CMOC) was investigated in finisher broilers. One hundred and sixty male broilers aged 30 days were diets containing 0, 15, 30 and 45 % CMOC as replacement for maize. Each diet was given to five pens in a completely randomized design. Birds given the 30% CMOC replacement diets ate more feed and grew faster than the control birds. There were no dietary effects ($P > 0.05$) on dressing percentage or the yield of breast and thighs but drumstick proportion was significantly ($P < 0.05$) higher on the 30% CMOC diet than on the control, 15 and 45% CMOC diets. There were no statistical differences ($P > 0.05$) in the weight of digestive organs (gizzard, liver, proventriculus, intestine and its length) among the four diets. Gizzard pH was higher ($P < 0.05$) in the control birds compared to the test groups. Feed cost per kg carcass was significantly ($P < 0.05$) reduced on the CMOC test diets compared to the control. It was concluded that replacing up to 30% of the maize with CMOC is beneficial and that replacement up to 45% is not detrimental. The economic benefits of maize replacement with CMOC, however, need to be re-evaluated with a range of more normal ingredient prices, less affected by the present COVID-19 pandemic.

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Implementation of electronic data capture in the Ethiopian bread wheat breeding program

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Ethiopia is the largest wheat producer in sub-Saharan Africa yet remains a net importer. Currently wheat is grown on about 1.8 million ha, with an estimated 5 million farming household's dependant on it. Increasing domestic wheat production is a national priority, with only 75% of national demand met by domestic production. Wheat production in Ethiopia is behind its potential productivities. The use of old traditional wheat varieties is an important contributing factor to yield stagnation. In order to develop high yielding varieties, the national wheat breeding program in Ethiopia has been redesigned and new technologies and mechanisation introduced to accelerate the rate of genetic gain. Here we describe the implementation of electronic data capture and management systems into the national program. This has not only sped up the collection of field trial data, including visual and measured traits, and allowed the direct capture of plot weight from scales, but also has reduced the need for manual data entry further reducing errors and speeding up the analysis of trial data enabling larger trials to be grown for minimal extra resources. Electronic data capture also facilitates the implementation of advanced statistical methods resulting in improved selection accuracy and breeding efficiency. Overall the efficiencies generated by electronic data capture, additional technological mechanisation and new statistical methods, has enabled the wheat breeding program to increase population sizes and data collected more than 10-fold. It is anticipated that these changes should result in large increases in genetic gain and better wheat varieties for Ethiopian farmers.

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Prioritizing candidate genes and genetic variants for fertility improvement in Beef cattle

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Profitability in the beef herd is closely related to reproductive performance. The discovery of quantitative trait loci (QTL) is an important step to identify and understand genetic variants associated with fertility traits, and genome-wide association study (GWAS) has become a widely used approach to identify associations of single-nucleotide polymorphisms (SNPs) with complex traits such as fertility. However, GWAS only identifies those SNPs strongly associated with the trait of interest and does not reveal the underlying biological mechanism involved. In this study, a stepwise conditional multi-trait GWAS analysis was performed to identify significant variants and genes associated with four fertility traits, including a binary trait (heifer pregnancy status) and three continuously distributed traits (fetal age in weeks, measured via manual palpation at pregnancy diagnosis; heifer age at first calving, defined as the number of days between the birthdate and calving date; and days to calving, defined as the number of days between the date of bull turn out at the beginning of the breeding season and calving date). We also investigated mutations affecting gene expression QTL (eQTL) for more than 10k genes expressed in whole blood across 500 cows. Moreover, we identified genes whose expression levels were associated with fertility due to pleiotropy or causality by integrating GWAS results with the eQTL data. The eQTLs explained only a small fraction of QTLs. Our results showed multiple genomic regions affecting fertility traits, some previously reported and some novel. Key findings included mutations in or close to the genes *RNF150*, *EPHA6* and *HELB*.

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Statistical methods to Accurately Predict Grain Yield in Hybrid Maize Multi-Environment Trials

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Genetic studies in crop improvement programs rely on the phenotyping of important agronomic traits in multi-environment trials to estimate genetic effects. The accuracy of the estimates of these genetic effects impact the genetic gain per breeding cycle in any crop breeding program. Here we present a statistical model for grain yield in multi-environment hybrid maize trials in Ethiopia, using a linear mixed model framework. We first jointly modelled spatial field heterogeneity and inter-plot competition, including genetic effects due to neighbours and a constrained autoregressive process for inter-plot interference. Secondly, we explored the impact of shelling percentage on grain yield per plot and demonstrated the magnitude of the bias of the grain yield estimation using a bivariate analysis to partition weight of grain and weight of cob. Lastly, we extended the statistical model to incorporate the genetic relationship of the parental inbred lines to predict the additive and dominance genetic effects. These genetic effects were used to classify inbred lines into different heterotic pools that can be used for future hybrid breeding in Ethiopia. The statistical methods outlined here will be used in future variety evaluation trials to accurately predict the genetic merit of the genotypes under evaluation in maize and other crop breeding programs in Ethiopia.

Keywords: Linear mixed model, Bivariate model, Genetic relationship

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Spatial analysis using proximal soil sensing to improve cropping trial analytics

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The spatial variability of edaphic soil properties has confounded cropping trial data interpretation since early field experiments were conducted at Rothamsted England in the 1830's. Statistically robust trial plot designs and their subsequent analytics have been the subject of much agronomic debate since that time. Conducting cropping trials where the edaphic effects of soil properties significantly limit yield metrics in the salinity affected coastal zone of Bangladesh and West Bengal is a considerable technical challenge to local agronomists (Rawson *et al* 2013). Here we apply electromagnetic induction (EM) proximal soil sensing techniques in combination with Geographic Information System (GIS) spatial analytics and covariance statistics to improve and validate the significance of yield responses where soil edaphic factors affect cropping trial results. We introduce how and when to apply this methodology within this new method sequence. The premise of the method employed has much potential for adaptation to other proximally sensed soil measurement techniques, where the associated edaphic soil properties, impact the statistical significance of crop yield response to the trial treatments.

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Environment Specific Varietal Recommendation Based on Genotype-Environment Interaction and Yield Stability

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It is often challenging to assess the potential of promising rice genotypes in multi-environment trials (MET). Critical components of the accurate assessment are the analysis of yield stability in the environments and the genotype-environment (GE) interactions. In Bangladesh, during the 2018 Aman (wet) cropping season, eighteen promising rice genotypes were evaluated for their adaptability and yield stability in three different agro-ecological environments. The study was performed through an RCBD-based trial with three sets of replications. Additive Main Effects and Multiplicative Interaction (AMMI) model and Genotype plus Genotype by Environment (GGE) biplot were used to assess yield stability and adaptability. The observed GE interactions were significant, and it was evident that the genotypes responded differently to the dissimilar environments. The highest average grain yield was observed in BRR1 dhan71 followed by BRR1 dhan79, 66 and BR11 and the lowest in DRR42. The Interaction Principal Component Axes (IPCA) score was close to zero with a marginal interaction effect as some genotypes performed better in Rajshahi and Bogura. The analysis indicated that Rajshahi was the most discriminating environment and BRR1 dhan71, 79, 66 and BR11 were the most environment responsive genotypes. The results of the AMMI analysis were further supported by the GGE biplot. It is evident from the results that the AMMI model is significantly helpful in MET. The information coupled with visual comparisons enables the separation of genotypic responses, thereby making the model ideal for the assessment of stability and adaptability. Such information can assist plant breeders in decision-making regarding new varieties.

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Genomic relationship between heifer pregnancy and stayability in Brahman cows

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Stayability is a complex cow reproduction and productivity trait that represents her ability to consistently produce a calf year after year. While economically important, cow stayability is difficult to measure and lowly heritable, making genetic improvement challenging. Therefore, it would be advantageous if an alternative, highly correlated phenotype may be used to indirectly select for stayability, earlier in the animal's life. In this study we aimed to determine the genetic relationship between heifer fertility traits and cow stayability. For this analysis, lifetime productivity records from an industry Brahman herd were utilized ($n = 7,453$). Here, stayability was defined as a cow's ability to give birth to two consecutive calves, following successful heifer pregnancy (i.e. 3 calves by 5 years of age; 1 = success, 0 = failure). Two measures of heifer fertility were modelled: heifer days to calving, measured as the number of days between first bull exposure and first calving, and heifer weeks pregnant, recorded as the foetal age of a heifer's first pregnancy, estimated via manual palpation. Using a multivariate linear model and fitting an H relationship matrix, the genomic correlations between these four traits were estimated. Stayability was found to be highly genetically correlated with both heifer fertility phenotypes ($r > 0.70$), while only moderately correlated with 600-day weight ($r = 0.36$). This suggests that measures of heifer fertility, which may be determined as early as ~2 years of age, may be a suitable proxy trait when selecting for improved cow stayability.

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Characterising the function of key flowering genes in tree crops

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Flowering is a complex process regulated by many different environmental signals and endogenous signaling pathways. Much of what we understand about the genetic pathways controlling flowering has come from studies in model species such as *Arabidopsis thaliana*. Although studies in non-model species indicate that many of the genetic pathways regulating flowering are highly conserved within angiosperms. Tree crops are highly valuable to Australia, accounting for half of the horticulture industry value. However, little is known about the genetic pathways that control flowering in these tree crops. We performed phylogenetic analyses to identify homologs of key flowering genes in the tree crops: almond, avocado, citrus, mango, and macadamia. RNA-seq analyses from almond, macadamia and mango leaf and bud samples collected over a time-course highlighted genes likely to be involved in floral induction in these species. Furthermore, we are using transformation techniques to functionally characterise these key flowering orthologs. Here, I will present our latest work in understanding the role of key flowering genes in regulating flowering in these important horticultural tree species.

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Establishment of the National Plant Phenomic Center in Taiwan

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Taiwan is located in the subtropics and tropics, and the varieties of crops are various. Since climate change has made the environment more harsh and unpredictable, making crop breeding challenges. Several strategies, i.e., GxExM modeling and genomic selection, have been advocated to solve the above troubles. However, the high-quality and large-scale phenotyping is still the bottleneck for the breeding program. For these purposes, Taiwan Agricultural Research Institute (TARI) is establishing a national plant phenomic center to meet the requirements of future crop phenomics. The facilities can be divided into a greenhouse auto-conveyor phenotyping system and a field auto-gantry one. The previous one extracts each plant's image characteristics to survey the hard-to-measure traits and then understand the correlation and regulatory relationship in these complex traits. High-precision field phenotypic data can be obtained from the field gentry one, which can be used as a benchmark for field trials to develop robust field phenotypic analysis methods for various test sites. The center is expected to be completed in 2023. Currently, TARI also performs the core collection programs of essential crops, including vegetable soybean, tomato, pepper, and eggplant. In the future, we will also advocate the integration of digital breeding databases and provide facility services for large-scale phenomic research in East Asia and Southeast Asia.

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Establishment of the pepper core collection in Taiwan

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Pepper (*Capsicum* spp.) is one of vital vegetables in Taiwan, but the extreme climate has seriously threatened its production in recent years. Therefore, the rapid breeding of pepper to meet extreme climate change and various global market demands has become an essential subject for seedling industries. The germplasm is a crucial source of genetic diversity and the basis for developing new varieties with desirable agronomic traits. Therefore, we created a core collection of pepper with a less germplasm population but kept the most incredible genetic diversity according to their genotypes. This result can improve the consistency and availability of germplasm evaluation and further breeding efficiency. Finally, a genomic database containing 6,437 SNPs was established. Five core collections with 250, 200, 150, 100, and 50 germplasm were obtained using CoreHunter3. Their allele coverages range from 0.92 to 0.88. These results provide the breeders to select the appropriate core collection according to the scale of the breeding program. The results also demonstrated that the core collections of pepper have a high diversity in the configuration, suggesting these materials can be applied for future research on the configuration of *Solanaceae* crops.

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Smart dryland agroecosystem in tropical agriculture makes a difference for smallholder farmers

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Smallholder farmers on tropical dryland agriculture face the most difficult management challenges. Climate change and geosocioeconomy circumstances in East Nusa Tenggara–Indonesia have made the tropical dryland's long-term viability uncertain. Soil erosion is increasing, soil fertility is dropping, and soil moisture is decreasing, all of which are limiting land capabilities. As a result, predictive agriculture is critical for enhancing the efficiency and effectiveness of local farmers' land management. For the local farmer, applied research has resulted in the development of a "Smart dryland agroecosystem-SDA" app. This unique mobile application will assist the farmer in identifying acceptable plants for their area, as well as tillage, irrigation, and fertilizer recommendations. Using QR codes, all cultivation procedures will be recorded and sent to the cloud-based app. The field was validated for three treatments using two replications and four rows per plot. The treatments were 20% over calculation, 20% under calculation, and 100% the same as the SDA application's computation. Even though plant growth and biomass achieved equivalent results (plant height, fresh & dried biomass) across treatments, the nutrients remaining after harvest will be significant for the sustainability system's subsequent crops. This app must be updated on a regular basis and incorporated into the sensor and automatic digital system before it can be used by farmers, based on its performance and analysis. On the other side, this app has saved some money and can help dryland agriculture remain sustainable by maintaining land productivity.

Keywords: predictive, agroecosystem, dryland

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Exploring intravarietal variation in grapevine

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The concept of single vine selection, or “clonal selection” within major varieties of grapevine (*Vitis vinifera*) has a long history and was initially started as a means to improve reduced yields due to virus infections. Its huge success laid the foundation for clonal selection activities in many public and commercial programs. It has been shown clonal propagation of major varieties for hundreds or thousands of years has resulted in substantial intravarietal trait variation.

Therefore, the Department of Grapevine Breeding at Geisenheim University has established large collections of major grapevine varieties. This includes almost 1,200 clones of the variety Riesling and almost 400 clones of Pinot. Clones were selected from single vines planted at the Department trial site in an unreplicated design. Over more than ten years, key traits have been measured to assess the level of clonal variation within and across varieties.

The objective of this study is to quantify and assign sources of intravarietal variation using extensive data. A mixed model-based approach to decompose the phenotypic variance revealed substantial between-clone variation. Around 50% of the variation observed for yield within Riesling can be attributed to clonal differences. While it is established that mutations and epigenetics are the most likely underlying drivers, the relative importance of genetic vs. epigenetic variation in grapevine remains unclear. To shed light on this, we are applying new genomics and epigenetics approaches. This will help to improve our understanding of the genetic architecture of important traits.

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Utilising drone analytics in commercial agave farming for improved yield management

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There is an exciting potential for drones in tropical agriculture, not only to support agronomic decision making, but also harvest scheduling, market forecasting and client/community engagement. We spoke at Tropag 2019 about the barriers to adoption of drone technology and why drones were not being used in decision making in agriculture. This is still evidenced by the irregular use of drones on farms, poor understanding of the data needed, and how to integrate this information with farm practises.

Over the last couple of years AirBorn Insight has partnered with Top Shelf International who have seen the capabilities afforded by drone data turn into a practical reality for on ground decision making on their agave farm in North Queensland.

Key value adds we have been working toward include:

1. Developing 'vegetation health maps' to inform scouting and integrating this with farm management practices so this data is used day to day.
2. Individual plant counting and sizing for development of size distribution maps for whole paddocks. This data better informs yield management, harvest timing and location, product application and market forecasting.

The processes undertaken by TSI and AirBorn Insight to get the project to its current state will be discussed. We will also share examples and the practical application of feeding the data into day-to-day decisions on the farm and how we are now accessing health at individual plant level across whole paddocks.

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A Route to Improving Feedlot Performance through the Automation of Bunk Management.

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Feedlot bunk management (BM) drives cattle performance, however, traditional BM is highly subjective, and poor decisions can decrease health and performance. The objectives of this experiment were to determine the feasibility of automating BM on performance, health, and carcass outcomes.

Bos indicus cross steers (n=5509) (average initial weight 420.48 Kg) were inducted into a commercial feedlot and randomly assigned to one of three treatments, traditional BM (TBM), semi-automated BM (SBM), fully automated BM (FBM), based on a randomised complete block design (7 blocks, 21 pens, n=265 hd). Cattle were fed on average for 109 days on feed (DOF), during which daily feed deliveries, morbidity, mortality, re-implant weight and pen exit weights were recorded. Treatments were slaughtered at equivalent days of feed endpoint and carcass data were collected by a MSA grader.

Performance results showed no difference ($P \geq 0.05$) between the three treatments for key outcomes of final body weight, average daily gain, dry matter intake and feed:gain across the feeding period. Moreover, automation (SBM and FBM) did not negatively impact ($P \geq 0.05$) any animal health parameters, mortality, or relevant carcass values. Dry matter intake (DMI) ($P=0.027$) and net energy for maintenance (NE_m) ($P=0.032$) intakes were greater for TBM and SBM treatments from 1-43 DOF. However, from 44-107 DOF, DMI ($P=0.001$) and NE_m ($P=0.001$) intakes were greater for the TBM and FBM treatments. These differences did not significantly impact overall weight gain and feed intake.

In conclusion, BM can be automated to reach equivalent performance and health outcomes as a highly-skilled bunk caller.

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On-animal proximity loggers to assess behavioral associations in extensively grazed prepubertal heifers

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Reproductive performance is a major factor contributing to production and profitability of northern beef enterprises. The extensive nature of conventional northern operations restricts opportunities for producers to collect relevant phenotypic data to establish genetic selection preferences for increased fertility. However, capturing continuous measurements of behavioural associations in heifers during social events, such as oestrus, can be achieved using on-animal proximity loggers. The objective of this study was to quantitatively measure associations between prepubertal heifers to generate understandings of social behaviour. Proximity loggers programmed to record data at 1.5 second intervals for 2 minutes every 10 minutes were fitted to ten *Bos indicus* heifers with mean (\pm s.d.) weight and age of 276.4(\pm 31.1) kg and 11(\pm 0.82) months. Ultrasound scanning occurred weekly to examine ovarian development and to classify pubertal status based on the presence or lack of a corpus luteum. The overall mean daily contacts per device was 5430.2(\pm 1220.1), demonstrating relatively consistent grouping behaviours. On average per hour, loggers recorded 243.1(\pm 139.9) interaction events, however a large range between 12 and 1087 contacts was observed. These results demonstrate that female behavioural associations can be quantitatively measured in growing cattle in paddock environments through using on-animal sensors. The significant peak in hourly contacts occurred during a grouping event, therefore proximity generated data demonstrates potential at detecting substantial behavioural variations to infer the formation of sexually active groups. Further development and validation of proximity loggers to measure variations in behavioural metrics to detect first oestrus may provide an accurate method to quantitatively assess reproductive merit.

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Uncovering Genetic and Epigenetic Factors as Sources of Trait Variation in Grapevine

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The Department of Grapevine Breeding at Geisenheim University (Germany) has a collection of almost 1200 clones of the grapevine variety of Riesling alone that encompass a broad range of trait characteristics, e.g. growth types or leaf structure. While the phenotypic variation in this collection is well described the underlying genetic and epigenetic mechanisms remain largely unknown. Therefore, we are applying state-of-the-art sequencing technologies like sequencing of unmethylated regions and Oxford Nanopore Sequencing to generate long DNA sequences that enable simultaneous scoring of genome-wide methylation patterns. This type of data is especially suited to detect differences between the two haplotypes of the diploid grapevine genome so that a reference assembly can be generated that contains both haplotypes of all 19 chromosomes. The new grapevine reference genome for the Riesling variety will enable to study the variation between the two haplotypes within clones while also being able to assess the degree of differential mutation and methylation between clones. This information is then analysed with comprehensive phenotypic data collected from over more than a decade to unravel underlying causal polymorphisms and determine the relative importance of genetics vs. epigenetic for trait variation in Riesling. This information can then be used to facilitate the identification and selection of clones that are better adapted to certain vineyards, which is especially important in the light of rapidly changing environments due to climate change.

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Effect of anthropogenic aerosols on wheat production in the eastern Indo-Gangetic Plain

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The Indo Gangetic Plain (IGP) is a food basket of South Asia and is considered a hot spot of air pollution due to persistent and high emissions of anthropogenic aerosols. High levels of aerosols in the IGP not only affect the health of people but also the health of the natural system and climate of the region. Aerosol effects on crop production in the IGP is an emerging area of interest of policymakers and the scientific community due to their possible effect on food security and livelihood of millions of people in the region. To investigate the effect of anthropogenic aerosols on wheat production in the eastern IGP, we used a calibrated Agricultural Production System Simulator (APSIM) model at the Sustainable Resilient Farming Systems Intensifications (SRFSI) project nodes in the Bangladesh, India and Nepal components of the eastern IGP during 2015-2017. The effects of anthropogenic aerosols on wheat production were examined by running the APSIM model in three conditions: firstly, in the condition with anthropogenic aerosols by using the observed meteorological data; secondly, in the condition without anthropogenic aerosols by considering only the radiative effect of anthropogenic aerosols; and thirdly, in the condition without anthropogenic aerosols by considering the radiation as well as temperature effects of anthropogenic aerosols. The study revealed that on average anthropogenic aerosols have reduced the wheat grain yield, biomass yield, and crop evapotranspiration by 11.2-13.5%, 21.2-22%, and 13.5-15% respectively during 2015-2017 at the SRSFI nodes of the eastern IGP. The study also showed a reduction of more than 3.2 kg per capita per annum of wheat production in the eastern IGP due to anthropogenic aerosols, which represents a substantial effect on food security in the region. Moreover, the loss of wheat grain yield due to anthropogenic aerosols in the eastern IGP is estimated to be more than 300 million USD per annum during the study period, which indicates a significant effect of anthropogenic aerosols on wheat production in the eastern IGP.

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Modelling Spatial Distribution of *Canarium indicum* (Galip) in Papua New Guinea

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“Galip” (*Canarium indicum*) is an indigenous tree that grows naturally in lowland landscapes of PNG. It has a very high social, traditional and customary importance for some societies in the coastal areas. Galip trees produce highly nutritious nuts known as “Galip Nuts”. In rural villages, mature nuts are collected, cracked and the kernels are prepared as a food source for immediate consumption or preserved for future consumption. This indigenous nut tree has the potential to improve the livelihoods of local population in terms of generating income but also in providing food security.

In PNG, COVID-19 has had an impact on food security as the selling and buying of locally produced fresh food was disrupted. Addressing food security became paramount and research into Galip nut resource availability was necessary for understanding how this non-timber forest product could improve local food security and livelihoods. Currently, knowledge on distribution of Galip is limited, thus this project was conducted to provide crucial information on the distribution of Galip in the country.

Presence/absence point data were collated from the National Forest Inventory (NFI) database, Permanent Sample Plot (PSP) database, and PNG National Herbarium and bioassay sample collections and integrated with climate and topographic data to develop a species distribution model for Galip. Momase and New Guinea Island regions of PNG were found to be highly suitable for Galip. The output of this project supports other national and international organisation’s efforts to domesticate and commercialize Galip nut in PNG.

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A software application for estimating trends in irrigated crop water use efficiency

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Water use efficiency of irrigated crops can be difficult to measure in-situ across time and space. Remote sensing offers a cheap and scalable alternative to assessing spatiotemporal trends in water use efficiency. Irrigated crop water use efficiency can be defined as the ratio of gross primary productivity to evapotranspiration. A generalised additive model (GAM) framework can be applied to these measures to estimate trends. Furthermore, confounding variables, such as rainfall, can be accounted for so that the model estimates trends in applied water use efficiency. The web application, IrriGAM, enables users to select a bounded area on a world map, for which a water use efficiency dashboard is produced. This enables inferences to be drawn, such as whether there have been changes in crop production, water use, and their ratio over a given period. Applying this web application to an example smallholder irrigation scheme in Zimbabwe, which received technological and social interventions from 2013 to 2017, indicates that increases in water use efficiency can be attributed to gains in crop productivity rather than water savings. The web application therefore offers a scalable means to assess medium to long-term trends in irrigated water use efficiency at a range of scales.

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Prior Knowledge-driven Branching Phenotype Prediction for Shoot Architecture Improvement

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Axillary bud outgrowth is a determinant of shoot architecture and is dependent on environmental factors. Bud outgrowth and branching are inhibited by apical dominance mediated via hormonal and sugar signalling. The shoot tip has dual functions as a source of auxin that indirectly inhibits bud outgrowth and a sugar sink that inhibits bud outgrowth by reducing sucrose availability to axillary buds. Further auxin indirectly regulates bud outgrowth via controlling cytokinins and strigolactone. Using prior biological (i.e., genetic, molecular physiology, phenotypic) knowledge from *Arabidopsis* and pea and hypothesis-driven mechanistic modelling — we aim to understand how plants regulate bud outgrowth and discover new network components that will be useful breeding targets.

First, prior knowledge will enable the development of a logical sequence of intermediate traits between genotype and phenotype. Later a model will enable — Formalize knowledge of plant bud outgrowth morphogenesis traits linkages; Identify the component for genetic studies; Understanding connections between genome, phenome, and G X E landscape; and generate new testable hypotheses to study bud outgrowth in plant populations. Notably, the workflow we are developing will enable understanding other phenotypic traits — physiological mechanisms and gene networks underpinning plant success across plant lineages in nature and agriculture.

In addition, critical regulators at any of these signaling networks are potential targets for novel gene-editing and breeding technologies. Further, validating these mechanistic predictions in the laboratory and populations will enhance the power of predictive phenotype models, enhance the rate of genetic gain in crops, and understand interconnectivity across scales from genome to phenome.

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The pattern and distribution of deleterious mutations in the Australian mango gene-pool

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Most new mutations in a population are deleterious with only few being beneficial. Natural selection is expected to keep strongly deleterious mutations at low frequencies. However, in cases of rapid domestication, genetic diversity can be lost through a narrow selection of breeding families making purging of deleterious mutations less likely. When deleterious alleles are closely linked to key traits that have been targeted for breeding, they can rise in frequency instead of being purged from the population. This is particularly problematic for selection on highly polygenic traits where allelic effects are numerous and spread across the genome. Here, we explore the extent of putative deleterious mutations across the genome of 242 mango accessions from the gene-pool of the Australian Mango Breeding Program. To identify putative deleterious mutations, we use a sequence homology approach to detect non-synonymous amino-acid substitutions in conserved genomic regions. The identification of these putative deleterious alleles in breeding programs will facilitate the purging of deleterious effects on crop improvement.

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Use of continuous genotype in the genomic prediction of complex sugarcane

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Polyploidy is common among plant species and significantly impacts agriculture and food production. Sugarcane, a complex polyploid species that account for 80% of global sugar production, can potentially be the primary crop for bioenergy production. Despite their importance, polyploid crops have been slower than diploid species to adopt genomics-assisted breeding. This delay is primarily due to a lack of genetic resources and genotyping software. SNP detection in autopolyploids, particularly sugarcane, has been difficult due to polysomic inheritance caused by high ploidy levels. Because of the complexity of the sugarcane genome, genetic studies have traditionally relied on single dosage markers. The main limitation of single dosage markers is that all heterozygotes are classified into a single class. As a result, the majority of genotype classification information is effectively lost. While genotype classification is a well-established noise reduction step in diploids, it becomes more complex as ploidy levels increase. Alternatively, continuous genotype values can be used for association analysis and genomic prediction studies. This study's data set includes 1318 elite sugarcane clones and 58,363 probes. The phenotypes of tonnes of cane per hectare, commercial cane sugar, and fibre content were predicted using linear mixed and Bayesian mixture models. Genotyping calling does not improve the prediction accuracy of traits studied. Using continuous genotype expedites computation, simplifies analysis, and results in more potential markers. This approach could be very useful for species with higher ploidy levels or for emerging crops where ploidy is unknown.

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Use of timelapse photography to determine flower opening time in banana

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Sterility and low seed set in bananas is the main challenge to their conventional genetic improvement. The first step to seed set in a banana breeding program depends on pollination at the right time to ensure effective fertilization. This study aimed at determining bract opening time (BOT) to enhance efficient pollination and seed set in bananas. A Nikon D810 digital camera was set-up to take pictures of growing banana inflorescences at five-minute intervals and time-lapse movies were developed at a speed of 30 frames per second to allow real-time monitoring of BOT. Genomic groups studied included wild banana, Mchare, Matooke, and plantain. Events of bract opening initiated by bract lift for female flowers ($P < 0.01$) started at 16:32 h and at 18:54 h for male flowers. Start of bract rolling was at 18:51 h among female flowers ($P < 0.001$) and 20:48 h for male flowers. Bracts ended rolling at 02:33 h and 01:16 h for female and flowers respectively ($P < 0.05$). Total time of bract opening (from lift to end of rolling) for female flowers was significantly longer than that of male flowers ($P < 0.001$). Bract rolling increased from partial to complete rolling from proximal to the distal end of the inflorescence among female flower. On the other hand, bracts subtending male flowers completely rolled. Differences in BOT of genotypes with the same reference time of assessment may be partly responsible for variable fertility. Hand pollination time between 07:00 – 10:00 h is slightly late thus an early feasible time should be tried.

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Effects of dense cultivation on the yield performance of cultigen rice: meta-analysis

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The growth and yield of cultigen rice are known to be affected quantitatively and qualitatively by plant spacing and density level. There have been some contradictions regarding the adequate spacing or density for rice crops. For example, it was reported that wider spacing produced significantly higher rice grain yield and tillers than planting at closer spacing. Other studies indicated that closer spacing for rice was superior to wider spacing as the plant canopy can capture more solar radiation, water, and nutrients. Meta-analysis provides formal statistical techniques for summarizing the results of independent experiments to quantitatively estimate the effect of some adopted agronomic practices such as dense planting (i.e. narrow spacing) versus sparse planting (i.e. wide spacing) on the rice yield. We also identified the management and environmental factors that contribute to the yield differences between dense and sparse cultivation. The results showed that dense planting /closer spacing significantly increased rice yield under transplanted rice system, ranging from (+3.4% to 8.9%). Similarly, applying a high seed rate enhanced the yield by (+9%) under direct-seeded rice. Rice type and N application rate had the largest impact on the yield performance. With respect to soil properties, the yield was significantly increased by planting in areas that are clayey in texture and acidic soils. Thus, optimizing management practices is necessary for increasing yield in rice paddies. Overall, this meta-analysis demonstrates that; closely-spaced plants are a promising practice for increasing yield in rice paddies when combined with appropriate management practices and suitable soil prosperities.

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Genomic and phenotypic studies of *Curtobacterium flaccumfaciens* pv. *flaccumfaciens* on mungbean

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Tan spot of mungbean (*Vigna radiata*), caused by *Curtobacterium flaccumfaciens* pv. *flaccumfaciens* (*Cff*), is an economically important disease impacting profitability of the mungbean industry in Australia. In the absence of effective chemical control, tan spot management heavily relies on the use of clean seed and varietal resistance. However, no resistant mungbean varieties are available to Australian growers, and varieties considered to be moderately resistant at the time of their commercial release are currently rated as moderately susceptible. The reason underlying this decline is that the resistance of mungbean varieties is not well understood. The recent development of genomic resources for *Cff* strains isolated from mungbean and soybean in Australia has enabled temporal and spatial population genomic analyses of pathogen populations using whole genome sequencing of historical and contemporary pathogen populations. Moreover, an optimised phenotyping protocol was developed and deployed to study the aggressiveness and host range of *Cff* strains on mungbean and other fabaceous crops. Results from this study shed light on the evolution and host range of the *Cff* population in Australia and assist the National Mungbean Improvement Program in development of new mungbean varieties with improved resistance to tan spot by providing highly aggressive bacterial strains and improved phenotyping methodologies.

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Identification of Mungbeans using Multivariate Technique and Multi-Trait Index Approach

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Mungbean genotypes (166) were evaluated during September to November in 2019 and 2020 in randomized complete block design with three replications. Among qualitative traits, hypocotyl color was 66.27% green-purple followed by green (26.51%) and purple (7.23 %). The majority of genotypes were sparsely pubescent (50.60%) followed by intermediate (37.35%) and highly glabrous (11.45%). Dark green leaf was present in 39.16% genotypes followed by light green type (22.89%). The corolla was primarily (49.40%) greenish yellow colored followed by yellowish green (39.76%) and yellow (10.84%) colors. Round pod beaks was 64.46% followed by with pointed pod beaks (35.54%). Eigenvalues contributed 76.50% of the variability. The first PC accounted for 29.90% of the variances, followed by 15.70%, 11.20%, and 7.90%, indicated an increasing proportion of variable information represented by PC2, PC3, and PC4, respectively. Seed weight/pod, yield/plant, 100 seed weight, pod length, harvest index and days to maturity contributed to PC1, while yield/plant, pods /plant, biological yield/plant, and pod/cluster contributed to PC2, and days to flowering, and plant height contributed to PC3. The genotypes were grouped into seven clusters and maximum genotypes were in cluster II (34) and the minimum in cluster VII (10). The largest inter cluster distance was between clusters II and VI (9.53), followed by clusters IV and VI (8.77) and clusters III and VI (7.41). Based on multivariate technique and a multiple trait stability index, genotypes; G45, G5, G22, G55, G143, G144, G87, G138, and G120 were selected as high-yielding and tolerant to yellow mosaic disease.

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Climate change adaptation strategies; a victim knowledge and scientist field trial

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The effect of coastal saltwater on agricultural production and food security are significant. Farmers' salinity adaption tactics may be influenced by how they perceive the problem and the technology developed by scientist. The farmer perception of salinity effect on rice production, adaptation strategies and policy implications in coastal sites was analysed by interviewing 200 rice growers. Based on farmers adaptation strategy and scientific knowledge we conducted field trials to identify the best practice for avoiding salinity impact on staple food production in most climate susceptible areas of Bangladesh. Awareness of salinity and its increase over the past 20 years was widespread among rice farmers. A high proportion of farmers (90%) perceived the reproductive stages of the rice plant is the most sensitive to salinity stress. Most of the farmers (67%) were undertaking early transplanting and applying irrigation in order to adapt to salinity problems which occur later in rice crop growth during Boro season. Similar results we got in our 60 experimental plots. Early transplanting rice increased the grain yield by 47 – 89% over mid and late transplanting date. Thus, farmers' actions demonstrated that their perceptions of salinity and adaptation responses were pre-emptive of when salinity was most likely to have an impact on the rice crop. Farmers' perceptions of salinization and measures to manage salinity need to be considered in research prioritization and policy formulation by the government. This action could potentially secure rice production and thus contribute to the achievement of Sustainable Development Goals (SDG-1, 2 and 3).

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Integrated technologies to improve genetic gain in Ethiopian common bean breeding program

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Common bean (*Phaseolus vulgaris* L.) contributes to food and nutrition security, and income generation for smallholder farmers and enhances foreign exchange earnings in Ethiopia. The crop is one of the major pulses that serve as a rotational crop in cereal based cropping systems in the lowland areas. However, the gap between the potential and national average productivity remains high due to a range of genetic, environmental and management factors. The national common bean breeding program at EIAR has recently undergone a strategic redesign to increase the rate of genetic gain for targeted products. We describe the implementation of demand led breeding strategies including the development of product profiles and redesigned advanced stage testing trials.

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Interaction of *Lactobacillus buchneri* and molasses on physicochemical properties of cassava-leaf silage

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Fiji does not have a strong agriculture base and thus relies on imports for conventional feed ingredients. For sustainable livestock production, cassava leaves can be used to replace the conventional feed ingredients. Cassava leaves can be prepared in various ways to make them palatable for livestock. The objective of the study was to determine the effects of using *Lactobacillus buchneri* (LAB) and molasses on the physicochemical properties of cassava silage. Adding molasses and LAB speeds up the fermentation process and improves the quality of the silage as a feed source for livestock. *Lactobacillus buchneri* was inoculated in the cassava leaves at different concentrations of 0, 3.1×10^6 , 3.1×10^8 and 3.1×10^{10} cfu/g, whereas 0, 3, 5, and 7g/kg were the levels included for molasses. Silage physical properties, pH, proximate composition and mineral content were determined. The inclusion level of LAB and molasses improved physical properties of cassava-leaf silage ($P < 0.05$). The pH decreased with an increase in inclusion level of LAB and molasses ($P < 0.05$). While molasses inclusion level had no effect on crude protein content, LAB inclusion level generally increased crude protein content ($P < 0.05$). Mineral content in cassava silage fermented with different levels of LAB and molasses did not differ ($P > 0.05$). To ascertain whether the fermented leaves are suitable for feeding animals, animal feeding trials are necessary.

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Comparative genomics reveals key effector and avirulence genes in *Ascochyta rabiei*

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Ascochyta blight of chickpea is a foliar disease which is caused by the necrotrophic ascomycete fungus *Ascochyta rabiei*, causing lesions on leaves, stem and pods of chickpea and subsequently, leading to significant yield and profit losses. In recent years, efforts were made to develop genomic resources for *A. rabiei*, including the assembly of a near chromosome-level reference genome and a transcriptome assembly that focused on the repertoire of transcription factors expressed by the pathogen. Recent studies by our group revealed that despite a limited genetic diversity of the clonally propagated Australian population in the absence of a second mating type, *A. rabiei* isolates rapidly adapt and overcome the resistant cultivars developed and used by the industry. To better understand what features in the *A. rabiei* genome drive this adaptation and pathogenicity potential, we performed an in-depth comparative genomics investigation using whole-genome resequencing data of 230 Australian *A. rabiei* isolates, which were phenotyped and assessed for their aggressiveness against a differential chickpea host set. We identified single nucleotide polymorphism (SNP) variants and loci with variable copy-number that are associated with high-aggressive isolates and annotated them and the genes they impact. We combined the results with transcriptomic data produced by our group to provide further evidence of the function of these variants and how they control the aggressiveness of *A. rabiei*. These results shed new light on the molecular interactions on *A. rabiei* and chickpea and will allow us to develop targeted genomic and molecular assays to rapidly identify high-risk isolates.

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Agronomic research supporting cultivation of Australian native rices

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Australian native rices (*Oryza australiensis*, *O. meridionalis* and *O. rufipogon*) have potential as high value ancient grains for Australian tourist and gourmet markets, especially due to their Australian Aboriginal cultural identification. However, harvesting commercial quantities from wild populations is hazardous due to the presence of estuarine crocodiles and difficult due to variable water levels that affect access when the grain is mature on the plant. Cultivation by some Aboriginal enterprises and communities is desired, and would overcome these supply issues, but basic agronomic information for the cultivation of the species is lacking. Research in greenhouses has started investigating these issues. Yield responses of *Oryza meridionalis* and *O. rufipogon* to the effects of pot size and fertiliser application were investigated. We found that both species showed greater tiller production and greater yield when grown in pots of up to 300 mm diameter compared to smaller pots. Additional fertiliser greatly increased growth and yield. We also found great plasticity in growth of plants within the same accession. However, harvesting the grain was challenging due to mature grains being shed over a several month period. Further experimental work has investigated methods of collecting the mature grains, and has provided more information on morphological and yield variation between plants. We can grow these plants and produce grain under trial conditions. Research is continuing to develop protocols for optimising yield under commercial scale cultivation.

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Molecular identification and secondary-endosymbionts distribution in *Bemisia tabaci* population of Andhra Pradesh-India

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The whitefly (*Bemisia tabaci* Gennadius) (Hemiptera: Aleurodidae) is a cryptic species complex composed of 44 morphologically indistinguishable species. A new study was initiated to identify cryptic species of *Bemisia tabaci* population associated with yellow mosaic disease of blackgram in Andhra Pradesh, India and screening of *B. tabaci* population, collected from mungbean yellow mosaic virus infected black gram fields as well as from healthy blackgram fields for detecting infection by six secondary endosymbionts, *Arsenophonus*, *Cardinium*, *Hamiltonella*, *Firtschea*, *Rickettsia* and *Wolbachia*. The results revealed that Asia II-1 and Asia I cryptic species of *B. tabaci* population in Andhra Pradesh and seventy eight per cent of *B. tabaci* population were infected with *Arsenophonus* followed by *Cardinium* (57.5%), *Rickettsia* (41.3%), *Wolbachia* (26.3%), *Firtschea* (20%), and *Hamiltonella* (6.3%). The infection of *Arsenophonus*, *Cardinium*, *Rickettsia* and *Wolbachia* endosymbionts varies significantly in virus infected and virus free *B. tabaci* samples of Andhra Pradesh ($p= 0.02, 0.029, 0.003$ and 0.015 respectively). In our study two cryptic species (Asia I and Asia II-1) of *B. tabaci* were reported from Andhra Pradesh, India. As per the earlier reports, the infection of *Hamiltonella* and *Firtschea* was detected only in Mediterranean (MED)/Q biotype, Middle East Asia Minor (MEAM)/B biotype of *B. tabaci* but not in Asian population. For the first time in few *B. tabaci* samples of Andhra Pradesh, the infection of *Hamiltonella* and *Firtschea* was reported. Hence, there is a possibility for the presence of invasive MED and MEAM biotypes in Andhra Pradesh.

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Impact of weed management on weed community composition and yield of DWSR

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Direct wet seeding rice (DWSR) with alternate wetting and drying (AWD) systems of water management has become a proven resource-conservation (RC) technology for rice production. This study aimed to investigate different weed dynamics and integrated weed management strategies in DWSR under the AWD irrigation system. Two field experiments using seven weed control strategies were undertaken in the experimental field at the Bangladesh Rice Research Institute, Gazipur, during two consecutive years in 2009-10 and 2010-11. The treatments included pendimethalin 33 EC @ 2.5Lha⁻¹+1HW(at 55 DAS), oxadiargyl 400 SC @ 187.5 ml ha⁻¹+1HW(55 DAS), mefenacet+bensulfuran methyl 53% WP @ 1111g ha⁻¹+ 1HW(55DAS), pyrazosulfuron-ethyl 10 WP @ 150g ha⁻¹ +1 HW(at 55 DAS), hand weeding (at 30, 55 and 80 DAS), BRRRI weeder (at 30 DAS)+1 HW at 55 DAS and weedy check as control. The weed species *Scirpus juncooides*, *Echinochloa crus-galli* and *Cynodon dactylon* appeared as the most important weeds, whereas *Fimbristylis miliaceae*, *Cyperus iria*, and *Lindernia floribunda* seemed to be the least important group in Boro season. Weed indices were computed, which indicated that all chemical weed control treatments considerably decreased weed infestation compared to the weedy control. The application of pyrazosulfuron ethyl or a mixture of mefenacet and bensulfuran methyl with one hand weeding at 55 DAS reduced the weed persistence index (WPI), weed management index (WMI), agronomic management index (AMI) and increased crop resistance index (CRI) correspondingly. These two weed control strategies may be used to minimize the cost of weed management in Bangladesh.

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Single node grafting: A novel efficient clonal propagation method for macadamia

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Macadamia is the only Australian native food crop that is cultivated and highly valued worldwide. The Australian industry exports 75% of production that has a farm-gate value of \$293M. Due to the lengthy and inefficient clonal propagation system, plant supply for new orchards is restricted. This project aimed to develop a rapid and cost-effective grafting method for the macadamia industry. An elite cultivar, 'L64', was selected as the scion to graft onto a standard rootstock ('Beaumont') at an age of 7 months after germination and a stem diameter of 4-8mm. Using single node scions from cinctured and non-cinctured branches, two grafting methods (whip and cleft) were compared over three seasons: summer, autumn, and winter. A randomised row-column design with ten replicates was used in each season. At eight weeks post-grafting, the growth of the scions was measured and variations due to the effect of cincturing, grafting types and seasons were compared. The amount of carbohydrate and photochemical reflectance index of the scion wood were measured to explore the possible reasons of variability in graft success due to the treatment effects. Results from this study will provide a scientific evidence-based method of clonal propagation that will enable year-round plant production and ensure continuous development of the industry, supporting future expansion.

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Seasonal and yield-scaled emissions of rice produced under SAWAH technology in Ghana

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The per capita rice consumption in sub-Saharan Africa continues to rise and for Ghana it currently stands at 63kg per annum. With an average rice grain yield of 2.8tha⁻¹, local rice production in Ghana, which is predominantly smallholder, has not been able to meet growing rice demand over the years. Potentially, the yield from Ghanaian rice farms can reach 6.5 tha⁻¹ but constraints including poor land management, inappropriate water management, ineffective fertilizer management, post-harvest losses and rainfall variability has hindered increased productivity. Developed by the Soil Research Institute of Ghana, the SAWAH technology for rice production has shown potential in significantly increasing rice yield to an average of 6 tha⁻¹ across various rice growing regions in the country. The SAWAH technology refines indigenous farmer knowledge in the management of land, water and fertilizer for increased rice production. The technology has proven effective in water and soil conservation, weed control and uniform fertilizer distribution on the rice fields which has maximized and sustained rice yield. However, with rice production being an important driver of Greenhouse Gas emissions, the emission footprint of the SAWAH technology has not been determined. Employing the static chamber method, this work will quantify the seasonal flux of methane and nitrous oxide from rice produced under the SAWAH technology. The Global warming potential of the target gases and the yield-scaled emission of rice produced using the technology will then be determined. The data generated will provide the basis for an assessment of the environmental sustainability of the SAWAH technology.

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SIGS as a tool to fight plant diseases in Mediterranean regions.

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Plant diseases seriously compromise our life quality and global food security. In the Mediterranean region some agricultural and forestry species are seriously threatened by pathogenic fungi and oomycetes that have been treated for a long time with chemicals, which have a high ecological impact on nature. Moreover, these methods are not entirely effective in controlling the diseases and some pathogens are developing resistance. Even in forestry, the use of such products is not allowed in forests. Thus, other sustainable alternatives are in the spotlight of plant pathology at the moment. One of these alternatives is spray-induced gene silencing (SIGS), which is a plant protection method based on the ability of eukaryotic organisms to uptake small RNAs from the environment that induce silencing of genes through RNA interference (RNAi). This strategy is environmentally friendly and could be a sustainable alternative to chemical disease control methods. We are studying the potential of SIGS in the treatment of crop diseases such as those caused by *Fusarium graminearum* and *Phytophthora capsici*, and in forest diseases such as those caused by *Fusarium circinatum* and *Phytophthora cinnamomi*. Environmental RNAi approach is being used to silence genes involved in critical pathways of the pathogens, such as vesicle trafficking, signaling and the RNAi machinery. Silencing these genes would reduce growth and infectivity of the pathogens, offering a sustainable alternative for the treatment of these diseases. The results of this research will help to explore the use of this technology especially in forestry where it is not widely developed.

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Cambodian smallholder farmers' soils knowledge and practices: implications for land management capacity

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Land degradation poses considerable challenges to the sustainable development of Least Developed Countries (LDCs), like Cambodia. Smallholder farmers in the upland regions of Cambodia are particularly vulnerable to land degradation, due to recent land clearing, traditional farming practices and erosion, and there are significant yield gaps between farmers' practice and improved agronomic practice. In order to develop smallholders land management capacity, the Cambodian Upland Soils Project (CUSP) sought to understand smallholder farmers' knowledge, attitudes and practices relating to soils and soil fertility management. Smallholders from Kampong Speu and Tboung Khmum Provinces participated in a community soils activity and interviews. Smallholders involved in the community soils activity demonstrated that they had good knowledge of local soil types and a detailed language for describing their soils. However, follow up interviews highlighted that there was limited understanding of soil fertility processes and the connection between crop symptoms and nutrient deficiencies. More than 70% of the smallholders considered that crop yields and soil fertility were declining in their upland fields; however, inorganic and organic fertiliser use was limited. Three main reasons were provided for not using fertiliser: a perceived lack of need to fertilise newly cleared upland soils; a lack of funds to purchase fertiliser; and, concerns that fertiliser, particularly inorganic fertiliser, was bad for their soil, crops and health. These findings highlight the need for extension activities that demonstrate effective ways to manage Cambodian upland soils that build on local understanding of soils while addressing knowledge and awareness gaps.

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Bovine lung organoids to model engineered viral resistance

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Livestock susceptibility to disease and productivity are intrinsically linked; in Australia, pests and diseases account for approximately \$3 billion in annual losses for cattle producers alone. The sustainability of the red meat industry in the face of increasing global food demand requires breeding robust, disease-resistant animals. Recent advances in genetic technologies show the potential to establish breeding lines of cattle resistant to infection by endemic viral pathogens, like bovine viral diarrhoea virus (BVDV). Herein lies an opportunity; to accelerate the improvement of the Australian beef herd through gene editing technology, by driving superior phenotypes into production systems much quicker than conventional breeding. However, assessing the effectiveness of specific gene edits is costly, time consuming and arguably unethical. Organoids are three-dimensional tissue structures, grown in the lab from induced pluripotent stem cells (iPSCs) or other stem cells, that can be used to model complex cellular phenotypes and biological interactions *in vivo*. Therefore, the purpose of this study is to develop and investigate the use of lung organoids to model the effects of genetically editing bovine cells to be resistant to infection with BVDV. To demonstrate the feasibility of organoids to model disease resistance, this study will; (i) streamline the generation of iPSCs from primary fibroblast cultures; (ii) differentiate iPSCs to lung tissue which mimic native cellular functions; and (iii) evaluate the impact of gene editing iPSCs to produce BVDV-resistant lung tissue. This study will be the first to develop and test bovine organoids for modelling genotype-phenotype interactions.

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Intact dsRNA is mobile and triggers RNAi against viral and fungal pathogens

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Topical application of double-stranded RNA (dsRNA) as RNA interference (RNAi) based biopesticides represents a sustainable alternative to traditional transgenic, breeding-based or chemical crop protection strategies. A key feature of RNAi is its ability to act non-cell autonomously, a process that plays a critical role in plant protection. However, the uptake of dsRNA upon topical application, and its ability to move and act non-cell autonomously remains debated and largely unexplored. Here we show that when applied to a leaf, unprocessed full-length dsRNA enters the vasculature and rapidly moves to multiple distal below ground, vegetative and reproductive tissue types in several model plant and crop hosts. Intact unprocessed dsRNA was detected in the apoplast of leaves, roots and flowers after leaf application and maintained in subsequent new growth. Furthermore, we show mobile dsRNA is functional against root infecting fungal and foliar viral pathogens. Our demonstration of the uptake and maintained movement of intact and functional dsRNA stands to add significant benefit to the emerging field of RNAi-based plant protection.

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Diagnosics of Moko disease on banana

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Moko is a new encounter bacterial wilt of banana originating in Latin America which has spread to the Philippines and Malaysia. It causes major diseases losses in banana plantations wherever it occurs and its management is costly. Causal agents are strains of *Ralstonia solanacearum* which cluster into seven sequence variants (sequevars). Existing diagnostic methods consist of two assays, one includes a multiplex PCR targeting four variants, and the other includes a duplex PCR claiming to target all described Moko sequevars. However, these assays have not been comprehensively validated for analytical specificity (inclusivity and exclusivity), limit of detection, accuracy, and ruggedness. To assess their efficacy, we tested DNA extracted from 87 Moko-associated isolates, 110 *Ralstonia* species and 32 bacteria isolates (non-*Ralstonia*). These tests include a subset of samples collected in Brazil where three endemic sequevars causing Moko occur. We found that the two existing protocols could not detect isolates from these three sequevars. Validation results showed that only four out of seven sequevars can be reliably detected using the multiplex PCR, and 36 isolates out of 82 were detected using the existing duplex PCR.

Using comparative genomics, we designed new PCR based detection methods that target *R. solanacearum* from the three sequevars found in Brazil. Our PCR assays amplified all three sequevars. Reliable and early detection of pathogens is vital to safeguard plantations from the introduction of Moko in Australia and allows our banana industry and consumers to benefit from its exclusion.

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Can the agronomic management recommendations for wheat in Bangladesh be improved?

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Conservation agriculture practices, such as zero tillage (ZT) and partial residue retention, have the potential to produce higher grain yield due to better utilization of water and nutrient compared to conventional tillage (CT) practices. Currently, agronomic recommendations to produce wheat are uniform across Bangladesh. We hypothesised that the agronomic recommendations should vary for different deep water access environments, soil types, and tillage practices. Grain yield, water input, irrigation water productivity (WP_i), and nitrogen use efficiency (NUE) were evaluated for two seasons at each of two diverse EGP sites under CT vs ZT, five irrigation treatments, and at three nitrogen (N) rates. Wheat responded to N at both sites, but to irrigation only when the water table was much lower than the root zone. In the presence of shallow fresh groundwater, wheat could access water directly from the water table as well as from capillary rise, achieving maximum yield without irrigation. Where the water table was deeper, the grain WP_i was increased with reduced irrigation, with maximum productivity in rainfed treatment but at the cost of reduced grain yield. At the deeper water table site, ZT produced greater wheat yields than CT following current recommended irrigation (3 post-sowing irrigation at critical growth stages) and N (120 kg N ha^{-1}) management. Therefore, this work suggests that agronomic recommendations should incorporate different irrigation guidelines for different water table situations, soil types and tillage practices and, potentially different N and irrigation applications should be recommended for ZT and CT wheat systems.

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Conservation agriculture enhances profitability, energetics, and emissions of the rice-wheat system

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Evolution of rice-wheat (RW) cropping toward lower resource inputs (water, labour, nutrient, and energy) and production costs, reduced environmental footprint, and higher system productivity and profitability are essential for the sustainability of this system in the Eastern Gangetic Plains (EGP). We hypothesised that intensification of the traditional RW system (conventional puddled transplanted rice–conventional-till wheat, CS₁) through the inclusion of mungbean (CS₂) would increase productivity and profitability, while additions of conservation agriculture (CA) elements (unpuddled transplanted rice–zero-till wheat–zero-till mungbean, CS₃) would enhance these benefits while saving energy and reducing emissions. We tested the performance of two interventions (CS₂ and CS₃) along with the current recommended system (CS₁) at two diverse sites (differing in soil type, hydrology, and agro-climatic conditions) in Bangladesh. In silt loam soil, the CA-based intensification (CS₃) increased the average system profit (57%), reduced energy use (6%), increased energy use efficiency (39%), and produced less CO₂-equivalent emission (14%) over CS₁. In sandy loam soil, the benefits of shifting from CS₁ to CS₃ followed a similar trend to the silt loam site in the first year, however, there was a gain in gross margin in CS₃ over CS₁ only in the second year. Before recommending CA-based technological interventions on a wider scale, we suggest that identification of the benefits and problems of CA should be explored locally considering soil types, climate, and hydrology. Thereafter, a refined CA technology (full CA or partial CA) that best fits the local environment should be recommended for large scale extension.

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Long-term variability of maize yield as influenced by growing seasons: APSIM analysis

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Maize is an important cereal grown in the sub-tropical environment of the Eastern Gangetic Plains (EGP). Farmers of Bangladesh grow maize both in *Rabi* (winter) and *Kharif* (summer) seasons. However, limited research reports are available on the performance of maize grown in different seasons and there is also a deficit of long-term data sets which are required to have a greater insight into the evaluation of the long-term variability of maize yield as influenced by growing seasons. A robustly calibrated and validated model, when used from inputs of short-term experiments and long-term climate data, can help understand the risk of the crops grown and explore opportunities for agronomic interventions. We, therefore, aim to do a comprehensive evaluation of the capacity of APSIM in simulating the performance of maize grown in two different growing seasons. We then used the tested model for analysing the long-term variability (40 crop seasons, 1981-2021) of maize yield. We found that APSIM-Maize satisfactorily simulates crop phenology, above-ground biomass, and grain yield across the seasons. APSIM simulations during 40 years across two growing seasons showed longer crop duration and higher grain yield of maize in the *Rabi* season compared to the *Kharif* season. The *Rabi* maize benefitted from comparatively cooler temperatures and higher solar radiation than *Kharif* maize. The inter-annual variability of grain yield in the *Rabi* season was minimum compared to the *Kharif* season. Our results explain the variability of maize yield across seasons and could help increase maize production by taking appropriate agronomic interventions.

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Sustainable rice production in the Mekong Delta, Vietnam

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Vietnam is the world's third largest exporter of rice of which 53.4% is produced in the Mekong Delta (MD) with 90% exported. Achieved via the intensification to 2-3 crops per year by ~1.5 million smallholder farmers who rely on rice production for their livelihood, rice is the most important agricultural sector in MD. However, with intensification, several issues have arisen including: reduced returns to farmers; increased soil degradation and environmental pollution; decline in seed purity and quality; and relatively low paddy quality, restricting export market opportunities. Furthermore, the typical rice supply chain in MD is long and complex, with at least 5-6 actors between farmgate and consumer.

The establishment of a highly productive, sustainable, traceable, quality-assured inclusive value chain, benefiting rice-farming households and meeting high-valued markets is required for MD. This is the aim of this first of its kind, public-private partnership project between Australian Centre for International Agricultural Research and SunRice Limited, an Australian company who operates the Lap Vo rice mill in Vietnam.

Working with rice cooperatives, the project will utilise a participatory approach to encourage the adoption of sustainable practices with indicators measured within the Sustainable Rice Platform (SRP) framework. SRP promotes resource-use efficiency and climate change resilience throughout the value chain. The project will quantify production and quality advantages and resulting economic value from the implementation of SRP. The scientific understanding of the agronomic and post-harvest practices across multiple actors in the value chain required to optimise grain yield and quality for MD will be improved.

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Innovative RNAi biopesticides for management of sugarcane root feeding pests

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Greyback canegrub (*Dermolepida albohirtum*) is a major pest throughout Australian sugarcane growing regions. This root feeding pest causes up to 40-80% of a total loss to sugarcane production in Australia and its control relies on the chemical pesticide imidacloprid. Toxicity both in human health and the environment, lack of specificity, and the development of resistance are major issues with the use of chemical pesticides. The increasing use of imidacloprid in Queensland agriculture, particular in sugarcane - the major crop grown within the Great Barrier Reef's catchments, has led to its run-off detected in inshore areas, which poses additional threats to the Reef itself. In this project, we explored the potential of using RNA-based biopesticides as a sustainable alternative to chemical-based control measures. For the first time, a RNAi approach is investigated for controlling greyback canegrubs. To target canegrubs with accuracy and specificity, we sequenced the genome of this pest and selected genes that are specifically targeting canegrubs. To establish stable RNAi effect, we developed clay particle-based delivery systems for topical application of RNAi based biopesticides without transgenes. To define practical delivery options and feasibility of the approach, the movement and uptake of the biological active (dsRNA) in sugarcane was investigated, with novel insights brought into the movement and processing of dsRNA in sugarcane as a host plant. Furthermore, a canegrub laboratory colony and its artificial diet was developed to screen the constructs that efficiently target canegrubs, and to establish proof of concept for this novel and sustainable RNA-based biopesticide.

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Alternative dwarfing genes scope in Indian wheat establishment traits for water-use efficiency

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Climate change threatens the yield across the wheat growing regions for all countries. By 2050, the demand of cereal's production will become challenge due to recurrent drought and yield-limiting factors. Currently breeders are more inclined towards the new physiological parameters for new adapted cultivars for future warming so that they can minimise the yield gap in the abiotic strained environment. Generally >70% of all wheat cultivars retains the GA₃-insensitive gene majorly that responsible for green revolution in celling crop yield. Although in water deficit zones where water lies at deeper soil zone fails to emerge out ought to a negative effect of these genes on coleoptile length too. Alternate option to use novel genotypes using GA₃-sensitive gene (*Rht4*, *Rht5*, *Rht8*, *Rht13* etc) to facilitate emergence at deep sowing to extract the stored water with no effect on coleoptile length but still reduce plant height. The Indo-Australian collaborative project provides 62 wheat line having different GA₃-insensitive; sensitive *Rht* gene and commercial checks. The presence of genes trade in from CSIRO was validated by external application of GA₃ in controlled and field trial. The genetic variation for emergence were validated at three different zones of India at two sowing (early and timely) and depths (10cm and 15cm) for two years. The phenological & morpho-physiological data recorded at seedling stage depicts that's the lines containing GA₃-sensitive gene perform good at both depth and sowing than the rest of the lines. The best identified lines were used extensively in Indian wheat breeding programme and four lines are national coordinated rainfed yield trial. Hence, the study provides new perspective to inculcate the new GA₃-sensitive genes in upcoming wheat cultivar for greater water use efficiency and drought tolerance.

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Prepartum supplementation increases colostrum quality and passive immunity transfer

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Improper colostrum formation in the last weeks before calving and poor passive immunity transfer are associated with calf morbidity and survival. We hypothesized that lack of dietary protein during late pregnancy with its effects on hormonal and metabolic profiles are important modulators of colostrum quality and delivery. Thirty-six late pregnant Brahman cows (live weight = 519 ± 45.43 kg) were blocked and randomly assigned to 12 feedlot pens. The pens were randomly allocated to 3 nutritional treatments: *Control*, ad libitum low-quality hay; *Protein*, control plus 1 kg/day of a protein supplement; and *Yeast*, the addition of 14 g/d of a *Saccharomyces cerevisiae* fermentation product (NaturSafe, Diamond V, USA) to the protein treatment. For cows, plasma was collected three times in the last week before calving and two times in the days after calving and analysed for metabolites and progesterone. Colostrum was collected *circa* 6 to 8 h after calving for immunoglobulin G1 (IgG1) determination. For calves, blood was collected twice during the first 5 days of life and growth was monitored by weighing six times during the first 14 days. Data were analysed using the linear mixed-effects model in RStudio. Protein supplementation improved prepartum cows' live weight gain, increased plasma urea, decreased fat mobilization metabolites, increased colostrum IgG1, and improved calves' growth. *Yeast* further decreased cows' plasma progesterone and increased calves' plasma IgG1. In conclusion, protein supplementation and yeast fermentation products in the supplement improved colostrum quality, the transfer of passive immunity, and increased calves' growth.

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Association of scion stomatal traits with vigour: study on diverse macadamia rootstocks

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Stomatal control of transpiration is one of the major strategies by which plants tolerate water-stress. Rootstocks contribute to affect plant's response to water stress through their influence on stomatal behaviour of the scion. However, mechanisms underlying the contribution of macadamia rootstocks to the control of scion stomatal traits and the effect of this rootstock-scion interaction on transpiration, photosynthesis, and carbon accumulation, are still unknown. In this study, we used 24 diverse seedling and cutting rootstocks to determine the genetic variability of rootstock effects on scion stomatal size, density, leaf stomatal area and its association with plant vigour. Stomatal traits were characterised by applying transparent nail polish to the abaxial leaf surface and imaging peel prints under a light microscope. Images were analysed using Fiji, an image analysis software, to measure stomatal size and density. Leaf area was measured to calculate total leaf stomatal area. The variability in stomatal size, density and area as affected by rootstock genotypes and propagation types will be evaluated. The heritability of stomatal traits, and their relationship with plant growth traits, will be explored. Results from this study will provide insights on rootstock-scion interaction for stomatal traits which have possible implications in climate change adaptation through the regulation of transpiration, photosynthesis, and water-use-efficiency. Highly heritable stomatal traits, if any, could be effectively utilized for early rootstock selection to achieve production and sustainability goals for future macadamia orchards.

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Exploring mungbean flowering behaviour to guide crop improvement for variable environments

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Mungbean (*Vigna radiata L.*) is a high protein, high value pulse crop cultivated in the subtropics and is a main summer rotation option in northern Australia. Due to the asynchronous flowering window, mungbean is vulnerable to abiotic stress including drought and heat, which can lead to yield penalties. Diverse flowering behaviour has been identified in mungbean germplasm including varying flowering duration and photoperiod responses. Despite these records, the underlying physiological and molecular basis of flowering behaviour in mungbean is poorly understood. A diverse panel of 31 mungbean lines including wild germplasm, breeding lines and commercial cultivars were evaluated in 2022 in the field at Gatton, QLD and in a controlled environment facility in short-day conditions (8 h light) to characterise flowering behaviour. Key traits were measured including days to flowering, flowering duration, plant height, node number and internode length. Variation in flowering behaviour was identified amongst the panel which will be further studied to understand signalling pathways underpinning flowering time. Understanding the physiological basis of flowering behaviour across varied environments in mungbean lays a foundation to allow further understanding of the molecular and genetic controls of flowering. Findings from this research will guide the development of improved mungbean cultivars with optimised flowering behaviour to improve yield stability of mungbean in the subtropics.

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Breeding for PVY tolerance in tobacco using CRISPR-Cas9 gene editing

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Tobacco is a commercially important crop contributing to the GDP of most developing countries. The cultivation of tobacco is challenged by a plethora of diseases with the potato virus Y (PVY) being a threat to many tobacco growers. PVY is a virus belonging to potyviridae family and it causes a total destruction in all affected plants. To date, there is no chemical produced that is able to prevent PVY viral infection and thus the solution is to develop PVY tolerant varieties. Virgin A mutant (VAM) is one such variety that is tolerant to PVY. VAM has been produced by mutating the eukaryotic initiation factor (eIF4E) gene. Thus the aim of the study was to produce a PVY tolerant tobacco variety by mutating the eIF4e gene utilizing CRISPR-Cas9 gene editing technology. The study commenced by growing a Zimbabwean local tobacco variety (ONC) in tissue culture. The sequence for designing the sgRNA targeting the eIF4E gene was obtained on NCBI and the sgRNA was synthesized. Thereafter successive cloning of the sgRNA into pChimera plasmid and pCas9 was conducted. Following, the gene construct harboring the sgRNA scaffold and the pCas9 enzyme was transformed into *Agrobacterium tumefaciens* and using the leaf disc method the tobacco leaflets were cultured in tissue culture and were left to root. The rooted plants were transferred into the greenhouse for subsequent growth. RNA from the wildtype and the transformed ONC were extracted, converted to cDNA and were sequenced, Sequencing results showed significant differences between the wild-type and the transformed ONC varieties indicating successful gene editing. The study unraveled the use and importance of CRISPR-Cas 9 in tobacco transformation and going forward the transformed ONC will be used in breeding programs in order to produce PVY tolerant varieties.

Keywords: Transformed, Wild-type, tobacco, CRISPR-Cas9

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The Effects of different rates of Paclobutrazol and pruning on breadfruit yield.

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There are documentary records referring to paclobutrazol (PBZ) as a growth bioregulator and its application increases yields in fruit and vegetable crop productions. Its agronomic management includes it as an emerging technology to reduce vigour, promote flower induction and flower development in fruit trees with increased economic returns. Therefore, the aim of this article was to collect, analyse and summarise relevant information on the use of PBZ in breadfruit production and possible rates of application used for maximum production in breadfruit. The results obtained indicated that the application of PBZ can be effective in solving some problems related to flowering if it is applied in the right amount and at the right time. However, it is necessary to elucidate the physiological processes with which it is associated and its response to be considered to increase yield. PBZ is currently used in fruit trees such as mango, lime, apple, and guava, increasing their productivity and this trial would be the first for breadfruit. More research is needed in promoting this study in the future for breadfruit production and PBZ.

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Improving irrigation water management through water monitoring, learning and governance.

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There was lack of information for connecting the interests of irrigation scheme clients (farmers, scheme managers, researchers, investors and governments) and also lack of accountability system for tracking the productive use and governance of water for irrigation within irrigation schemes in Malawi. The ACIAR funded project, Virtual Irrigation Academy II is improving the system from its current function to a water learning and governance platform to support the needs of smallholder farmers and address the information deficits at scheme to national level. Soil moisture monitoring, learning and water governance were implemented in sixty five irrigation schemes across the country with an average of 20 farmers per scheme. Series of activities were implemented and produced positive impacts and outcomes. For instance, 1936 farmers and 129 district agricultural personnel were sensitized on water governance, 1126 farmers, 68 extension workers and 6 scheme managers were formally trained on the use of 1,067 Chameleon Sensors, 108 Chameleon Readers, 54 Chameleon Card, 89 Chameleon Card sensor arrays, 673 Wetting Front Detectors, 60 Nitrate strip, and 42 Chameleon Ec meter that was distributed to farmers. At least 42,356 data was uploaded on the VIA platform. Field days were conducted at three irrigation schemes in Rumphi, Chitipa and Ntcheu districts. Video shootings were carried out at two irrigation schemes in Salima and Rumphi. Within these phase, scientific explanation of the soil moisture and nutrient monitoring tools has been extended to farmers across the whole Malawi. The farmers are now able to manage water, salts, and nutrients in their fields. Through the use of the monitoring tools, farmers are now able to understand the relationship between the different colours of the Chameleon reader and the soil moisture status in the soil. In this way, the farmers are able to manage their water resource within their irrigation schemes. They are able to use the chameleon reader and interpret the colours into a decision as whether to irrigate or not. Furthermore, through the use of the Fullstop Wetting Front Detectors, farmers are able to determine the right amounts of water to irrigate their crops and also know the levels of nitrates and salts hence make rightful decisions on their cropping systems for their specific irrigation schemes. Likewise, the improvements made on the VIA platform on data products has enabled irrigation and drainage scientists and engineers to easily understand current situation in smallholder irrigation schemes. As such, the VIA project has laid out an innovative foundation of irrigation water management research in Malawi. This understanding, has influenced high level discussions and interaction among irrigation experts in the country. It can be concluded that VIA II has improved information access for connecting the interests of farmers, scheme managers, researchers, investors and governments as well as ensuring accountability system for tracking the productive use and governance of water for irrigation in Malawi.

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The potential of genetic resources in wild sorghums in crop improvement

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Sorghum bicolor (L.) Moench is a versatile food crop with diverse genetic resources residing in its wild relatives. Australia is the home to the majority of these unexploited wild sorghum species. In this study, we used a total of 15 Australian sorghum accessions from the wild gene pool of the Sorghum genus, representing the five subgenera, to determine the phylogenetic relationships in the genus using next generation sequencing of the whole chloroplast genome and 99 single copy nuclear genes, to study the variation in the grain size related genes of the genus and to investigate the differential gene expression of cyanogenesis-related genes in response to water stress in the leaf tissue of the domesticated species Sorghum bicolor and the Australian native wild species Sorghum macrospermum. Phylogenetic analysis of both the chloroplast and nuclear genes revealed a similar topology with two distinct clades including Eusorghum, Chaetosorghum, and Heterosorghum in one clade and Parasorghum and Stiposorghum clustered in a second clade. The variant analysis showed that sorghum grains contain polymorphism in the coding sequence regions of six selected grain size-related genes, Sobic.001G335800 (qGW7/GL7), Sobic.001G341700 (GS3), Sobic.002G257900 (GW8), Sobic.003G035400 (GW5/qSW5), Sobic.004G107300 (GW2), and Sobic.009G053600 (GS5). Transcriptome analysis identified differential expression of the cyanogenesis-related genes CYP79A1, CYP71E1, UGT85B1, DHR, and HNL between the domesticated and wild species with the wild having a negligible hydrogen cyanide content in the leaves. This study provides an improved understanding of the potential traits in wild sorghum species which can be beneficial in future breeding programs.

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Trait-based design of multifunctional cover crops for improved agronomic and environmental outcomes

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Functional trait diversity in crop mixtures has been utilized to promote multifunctionality of ecosystem services from cover crops. However, mixture expression of crops with divergent functional traits is influenced by arrays of agronomic and environmental filters that differently influence cover crop performance. We utilized a trait-based approach to assess the potential of three cover crop types (Grass vs. Legume vs. Brassica) that differ in N acquisition, phenology, water use and pest-suppressiveness traits, to enhance agroecosystem multifunctionality. Specific functions investigated included cash crop productivity, cover crop biomass production, soil water conservation, soil N retention and supply, pest suppression, and soil health improvements. The cover crops were established as a mixture experiment in a simplex centroid design yielding 10 treatment combinations ranging from monocultures to three-way mixtures; a conventional fallow treatment was implemented as a control. The grass-legume mixture yielded the highest multifunctionality (>0.5) due to high N supply and retention, moderate water use, biomass accumulation, and greater cash crop yields. The conventional fallow had the least multifunctionality (<0.3). Overall, we found greater multifunctionality in cover crop mixtures compared to monocultures, likely due to trait combinations that maximized ecosystem multifunctionality. However, the most diverse cover crop mixtures did not necessarily have the greatest multifunctionality. This study demonstrates that careful selection of cover crops with specific trait combinations can maximize agroecosystem multifunctionality. Therefore, for cover crop integration into dryland cropping systems, grower management should focus on suites of traits that are most likely to deliver specific desirable agronomic and environmental outcomes.

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Source-sink dynamics in mungbean

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Yield advance in current commercial Australian mungbean remains a challenge due to high yield instability. Grain yield is determined by the balance between supply of photoassimilate from leaves (source) and reserves from other storage organs, and the capacity of the plant to fill its grains with these assimilates. Hence, understanding the physiology underpinning source-sink dynamics is vital for improvements in productivity. The aim of this study was to determine whether source or sink limitation had a greater effect on grain yield in mungbean. Two experiments were conducted at Gatton in southeast Queensland, Australia, to examine the effects of shading (source manipulation) and sink manipulation through late clipping of non-photosynthesizing vegetative apices on yield, biomass, and photosynthetic rates in mungbean. Data for yield and yield components, growth rates, biomass and photosynthetic rates were recorded. Shade treatments significantly impacted rates of photosynthesis, resulting in reduction in growth rate, biomass, and grain yield. Reductions in grain yield was associated with grain number. While, reductions in grain number in shade treatments was a consequence of decreases in pod length and seed number (pod⁻¹). Contrastingly, late clipping of non-photosynthesizing vegetative apices enhanced assimilate supply during reproductive phase to flowering, podding and roots. There were genotype-specific responses. Harvest index of mungbean increased in response to vegetative sink removal via clipping. This study established that increased partitioning to reproductive structures by reducing vegetative growth can be an approach to increase HI and yield in mungbean.

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Genotypic variation of physiological traits contributing to grain yield in aerobic rice

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Water limitation is a major industry concern for Australian rice production. It has been suggested that aerobic rice production may provide a saving in water requirement. Historically, the target production environment has been permanent water conditions and hence the value of physiological traits contributing to grain yield (GY) under reduced water availability is under explored. Therefore, forty genotypes selected for high and low canopy to air temperature differential (CTD) were evaluated in three aerobic field experiments with different water availability. The objectives were to explore the ability of genotypes to maintain GY and to determine physiological traits contributing to maintenance of GY.

On average the well-watered experiment (WW) achieved high GY at 8.99 t ha⁻¹. There was a 41% and 12% reduction in GY under intermittent water deficit (IWD) and mild water deficit (MWD) experiments, respectively. There was genotypic consistency in stomatal conductance (g_s), CTD and photosynthesis rate (Pn) across three experiments. In MWD and IWD, 26-29% of variation in GY was explained by variation in g_s , with this declining to only 15% under WW indicating g_s was more likely to contribute to GY under unfavourable conditions. Compared to the high CTD group, the low CTD group had 20% to 42% higher g_s , 37% to 78% higher Pn and 18% to 35% higher GY in the three experiments. Therefore, low CTD and high g_s may contribute to the maintenance of Pn and GY under varying degrees of reduced water availability in aerobic rice production.

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Evaluation of bulb onion varieties under protective structure in Leyte, Philippines

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Onion is regarded as “Queen of the Kitchen” because of its vital importance in many regional cuisines. Philippines, however is importing it from other countries due to low production as they are mainly grown in Central Luzon and Ilocos Region having a distinct dry season from November to April during which onions are planted. Eastern Visayas region where Leyte is a province under it has a year-round even distribution of rainfall making production difficult. So far, no trial has been done yet in Leyte on their adaptability. Hence, this study was conducted under protective structure to determine which of the four available varieties is adaptable to Leyte condition. Results revealed that of the four varieties trialed, namely: Red Colorado, Red Horse, Red Winner and Yellow Granex (YG), the three red varieties were late maturing with 80% top-down after 74-88 days while YG was early maturing that exhibited 80% top-down after 66 days from transplanting. Moreover, red varieties had the greatest number of undersized and small bulbs while YG had the most number of medium, large and oversize bulbs. Considering desirable growth and yield parameters, all the four varieties are suitable for planting under Leyte condition provided they are grown under protective structure with YG being the most promising. It produced a yield of 18 tons/ha compared to only 12 tons from the red varieties. Furthermore, being a high valued vegetable, YG generated a net return of P31,000.00 per 200m² relative to the average of the three varieties of only P20,000.00.

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Measurement of Greenhouse Gas Emissions of different Irrigated climate resilient varieties

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Rice fields are one of the vital sources of global greenhouse gas (GHG) emissions, especially methane (CH₄). A study was conducted at the research farm of Bangladesh Agricultural University, Mymensingh from January to May, 2019 to estimate methane gas emissions of climate-resilient rice varieties under two irrigation methods i.e., alternate wetting and drying (AWD) and continuous flooding (CF). The experiment was carried out in a split-plot design with three replications with six rice varieties. Emissions of CH₄ were measured using the closed chamber technique and their concentrations were determined using a gas chromatograph. The methane emissions in AWD were observed lower (32.82 to 95.33 mg m⁻² day⁻¹) compared to CF method (62.41 to 161.41 mg m⁻² day⁻¹) with six rice varieties. In AWD, variety wise emission response was Binadhan-10> BRRI dhan29> Binadhan-8> Binadhan-17> BRRI dhan47> BRRI dhan69 and in CF BRRI dhan69> BRRI dhan47> Binadhan-10> BRRI dhan29> Binadhan-8> Binadhan-17. In the AWD method, water depth was kept at a range of -14 to 9 cm while in the CF method water depth was kept at a range of 2 to 4 cm at different days after transplanting (DAT) of different rice varieties. However, the yield ranging 5.11 to 5.82 t/ha in the AWD was a little higher than in the CF method ranging 4.88 to 5.76 t/ha. In the AWD method, different varieties showed different responses in methane emissions, without any yield penalty, therefore it could be considered a promising strategy in rice fields to mitigate GHG emissions.

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Participatory on-farm evaluation based on genotype-environment interaction and traits preference

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Farmers adopt varieties that provide benefits such as better productivity, yield stability, insect and disease resistance, and grain size/shape/color. Therefore the present study identified efficient rice varieties in an agro-meteorological region by involving stakeholders in the rice value chain (male & female farmers, extension workers, scientists, agro-input dealers/millers). "Crop cafeteria" was conducted to evaluate twenty varieties in four different agro-climatic regions of Bangladesh in the 2019 monsoon season. The study was performed based on a randomized complete block design using three replications. Stability performance and genotype-environment interaction led us to a non-bias assessment. Based on measured traits and different stakeholders' preference rankings (on a 5-point rating scale), suitable varieties were identified for promotion to farming communities. Total scores of each variety obtained from stakeholders were added to get the total comparative weightages. Based on these weightages, BRRi dhan52 and BRRi dhan71 were ranked "highly desirable" by the evaluators. Multiple environment trials data analysis was the use of genotype and genotype by environment biplot model. To assess the stability and adaptability of yield performance the genotype (G), the environment (E), as well as the relationship between the genotype and the environment (GE), were observed, and it was evident that genotypes reacted differently to the various environments. Compared with the genotypes, Binadhan-17 and BRRi dhan52 were viewed as more adaptive to a series of environments. Participation of different stakeholders in the "crop cafeteria" could be an effective approach to identifying the best varieties for a specific location.

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Targeted Subsidies for Water Conservation in Smallholder Agriculture

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Groundwater depletion threatens long-term food security in developing countries. Moreover, groundwater pumping contributes to climate change. We evaluate the effect of targeted subsidies for technology to use groundwater more efficiently in agriculture. Using a randomized controlled trial across 360 villages in Bangladesh, we show that subsidies reduce electricity used for pumping by 38 percent, but only when targeted to water sellers. Subsidizing technology to individual farmers has smaller effects. Features of the groundwater market can explain this result. Natural monopolist water sellers charge fixed fees to farmers, but maintain a role in irrigation planning, incentivizing them to adopt conservation practices.

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Strategies for non-race specific resistance to safeguard small-scale wheat farmers in Ethiopian

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Fast population growth in Africa raises serious concerns about the continent ability to build secure and resilient food systems by increasing crop yields and reducing crop losses due to disease. Wheat is one of the strategic crops in Africa. But the production is very lag behind the demand and most of the countries dependent on wheat import. Biotic factors are one of the major production's bottlenecks especially in the Eastern Africa countries like Ethiopia and Kenya. Stem rust caused by *Puccinia graminis* f. sp. *tritici* (*Pgt*) is one of economically important wheat rust disease of bread wheat (*Triticum aestivum* L.) in Ethiopia. The frequent emergence of new *Pgt* races with increased virulence remains a major constraint for wheat production. Assessing source of non-host specific resistance is one of the most economical and viable strategy to mitigate the prevailing stem rust disease in Ethiopia. The objectives of this study were to evaluate and identify the ideal genotypes (n~250) holding non-race specific resistance for both seedling and adult plant stage evaluation using the predominant Ethiopian wheat stem rust races; *TTKSK*, *TKTTF*, *TRTTF*, and *JRCQC*. Both seedling and adult plant stage evaluation showed a high phenotypic variability for infection types and level of severity for wheat genotypes across the four races. This result showed the necessity of a strategic rust resistance evaluation to safeguard the wheat production by the small-scale farmers. This non-host specific resistance will give long-lasting protection of the wheat cultivars in rust hotspot areas such as Ethiopia.

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Artificial Nanovesicles for dsRNA Delivery in Spray-Induced Gene Silencing for Crop Protection

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Plants are constantly under attack by pathogens, pests, and parasites. Of the various classes of plant pathogens, fungi are among the most devastating. Alarmingly, drug resistance has been reported in in each major class of fungicides used in agriculture. Due to this, development of novel crop protection strategies is critical for global food security. Recent discoveries found that fungi can take up environmental RNAs, which can then target and silence fungal genes. This finding has inspired the development of spray-induced gene silencing (SIGS) to control fungal pathogens, through application of virulence-gene-targeting dsRNAs or sRNAs onto pre- and post-harvest crops. This method has been shown to be effective in combatting viruses and fungal pathogens. In contrast to traditional fungicides, which can leave toxic residues in soil, dsRNA degrades after application. In fact, this instability of RNA, which can be rapidly broken down by RNAses or when exposed to rainfall, high humidity, and UV light, is a major drawback to current SIGS approaches. Here, we utilize three AV formulations to shield dsRNA from degradation and deliver dsRNA to the fungal pathogen, *Botrytis cinerea*. These AVs lengthen stability of dsRNA on plant tissue, even after rinsing plant tissue with water. All three formulations are effective in both dsRNA delivery and protection, and, greatly extend the length of dsRNA mediated plant protection. Overall, these findings provide an organic antifungal dsRNA delivery platform, improving the utility of SIGS applications

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Intra- and Inter-sample Variation in Wool Cortisol Concentrations of Australian Merino Lambs

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Stress in pregnant Merino ewes can lead to a reduced wool productivity in the offspring. In this study we investigated the intra- and inter- sample variation in wool cortisol levels of weaner lambs whose mothers had higher or lower stress levels during late gestation. We conducted two experiments, the first was to determine the intra- and inter- sample variation in wool samples taken from the topknot of 10 weaned lambs, which resulted in 40 subsamples. The other aim was to determine any difference between maternal stress during late gestation on absolute wool cortisol levels of weaned lambs, so 23 lambs with known mothers were used. The samples were then extracted and analysed using a cortisol enzyme-immunoassay in order to determine the concentration of cortisol in each of the samples. Statistical analysis for the first experiment showed that there was no significant difference between the subsamples of each topknot wool sample taken from each lamb ($p = 0.39$), but there was a statistical difference between samples ($p < 0.001$), which was to be expected. In the second experiment, there was a significant difference between the lambs born to mothers with different stress levels ($p = 0.033$), with the lambs of the ewes with lower cortisol having higher average wool cortisol levels. This study confirms that the topknot wool sampling can be a reliable method adapted by researchers for wool hormonal studies in lambs. Second, low-stress ewes gave birth to lambs with higher cortisol concentrations than high-stress ewes, which warrants further investigation.

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Conservation Agriculture for Intensive Rice-based Systems: Lessons from a Decade On-farm Practice

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Worldwide, Conservation Agriculture (CA) has proven sustainability benefits for dryland crop production. However, continuous refinement is necessary for farm-level practice of CA especially for rice-based cropping systems. The outcomes of long-term CA in cropping systems are particularly influential in this regard. Research and development (R&D) on CA were carried-out in diverse and intensive rice-based systems in the Indo-Gangetic region since 2010. The R&D on CA were focused on machinery development and commercialization through the private sector and farmers' networks, establishment of diverse crops, soil health, nutrient and water management, weed dynamics and control, systems productivity, profitability, carbon footprint and greenhouse gas implications. A wide range of farmers, extensionists, private sector entities, and a diverse range of scientists from National and International Agricultural Research and Educational Systems were involved in these investigations and packaging the outcomes of the R&D. Practicing long-term CA confirmed multiple benefits including increasing crop yield and profitability; increase water productivity for dryland crops; improved soil health and soil organic carbon sequestration; decreased crop production cost and weed pressure; and reduced greenhouse gas emission. To acquire the full potential of CA, the practitioner should allocate substantial time for learning since it is a complex set of innovations. In this paper we will unpack the learning from the long-term CA in diverse rice and upland crops in smallholders' resource-limited farms. These lessons may be useful for new practitioners of CA in diverse cropping systems to enhance food security, soil health, family livelihoods and to mitigate global warming potential.

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Foliar Uptake of Topically Applied dsRNAs

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Over the last two decades RNA interference (RNAi) has been in the spotlight as a promising tool for sustainable crop protection strategy against viruses, fungal pathogens, and insect pests. Expanding this to a foliar application whereby external double-stranded RNA (dsRNA) is sprayed onto plant surfaces to induce RNAi via a non-transgenic mechanism represents a significant advance in the plant biotechnology field and stands as a sustainable alternative to either genetically modification (GM) or chemical-based pesticide mediated control measures. However, RNAi efficiency depends on the delivery of sufficient dsRNA or dsRNA-derived small interfering (siRNA) molecules to target pests/pathogens. In many crop protection scenarios, topically applied intact dsRNA needs to be internalized into the plant's vasculature and systematically transported to distal plant tissues. This means that sprayed dsRNA needs to overcome various anatomical and physiochemical barriers of the plant leaf to enter the plant system. Using Cy3-labelled dsRNA we detected signal inside the leaves of diverse plant species, indicating foliar uptake of dsRNA molecules applied on the leaf surfaces. The fluorescent signals showed entry into plant vasculature and was maintained in the apoplast around the plant cells. Additionally, we also tested potential additives to enhance dsRNA uptake, which can be incorporated for application targeting the morphological diversity of different plant species. Finally, we demonstrated that dsRNA once taken into the vasculature of the leaf can move from application site to distal tissues.

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Growth, yield and phytochemical content of organic and inorganic cultivated *Centella asiatica*

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Centella asiatica L. is a traditional medicinal plant popular in several Asian countries. The cultivation of this herb is facing the problem of overuse of chemical fertilizers and quality deterioration. The aim of this study was to evaluate the effect of organic and non-organic fertilizer on growth, yield and phytochemical content of centella. The set-up was performed in the field from February to November 2021. The treatments were: (T1) no fertilizer (control); (T2) inorganic fertilizer (the farmer's recommended rate; 200 kg N ha⁻¹:50 kg P ha⁻¹: 50 kg K ha⁻¹); (T3) organic compost (10 tones ha⁻¹); (T4) inorganic fertilizer (a half of recommendation rate; 100 kg N ha⁻¹:25 kg P ha⁻¹: 25 kg K ha⁻¹); (T5) organic compost (5 tones ha⁻¹) plus inorganic fertilizer (a half of recommendation rate; 100 kg N ha⁻¹:25 kg P ha⁻¹: 25 kg K ha⁻¹). The application of organic compost and/or inorganic fertilizer increased the leaf number, leaf area, rosette diameter, total chlorophyll content and biomass production of centella. The use of organic compost enhanced total phenolic content and antioxidant activity of the herb. Nonetheless, the high amount of inorganic fertilizer led to a reduction in the phytochemical content and antioxidant activity in centella leaf. The combination of organic compost and inorganic fertilizer at a half of recommendation rate produced maximum growth and increased the total phenolic content and antioxidant activity. This treatment should be considered as the optimal amount for reconciling limited yield loss and maintaining the quality of centella.

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Digital remote monitoring to improve horticultures environmental performance

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There is increasing pressure on the Australian horticulture industry to improve its environmental performance. This has occurred particularly in Queensland, where fertiliser inputs have become more heavily regulated. The basis for increased regulation is the widespread environmental impact of nitrogen and phosphorus loads on the Great Barrier Reef.

Landcare Australia and Hort Innovation are co-funding the development of a farm management tool to present on-farm sensor and modelled data. Called 'Control Tower', it aims to improve environmental compliance and productivity by facilitating best management practice. Control Tower is being developed by Hitachi Vantara with input from Applied Horticultural Research.

Four pilot sites have been established for the vegetable, banana, nursery, and avocado industries. These pilot sites are being monitored using a range of sensors to measure environmental impacts and key productivity parameters. The sensor data are being used to inform water balance, nutrient load, and growth models under development by Applied Horticultural Research. These models will be integrated into the Control Tower dashboard by Hitachi Vantara, along with weather forecasts and intelligent productivity monitoring.

The project is also being supported by AUSVEG, Greenlife Industry Australia, Freshcare, Growcom and Australian Banana Growers' Council who are facilitating the development of the Control Tower into a system to automatically provide evidence for certification audits, including EcoHort and Freshcare Environmental. The aim of this collaboration is to reduce barriers to the Australian horticulture industry for environmental compliance.

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Integrated plant nutrient systems with different irrigation regimes on rice yield

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Combined application of organic and inorganic fertilizer could increase rice yield. However, the effects of integrated plant nutrient systems (IPNS), which combines organic (poultry litter; PL and vermicompost; VC) and inorganic fertilizer (prilled urea; PU and UDP) at 1:1 ratio under alternate wetting and drying (AWD) irrigation, and their interaction on rice yield and nitrogen use efficiency (NUE) remain unknown. We conducted field experiments during the dry and wet seasons of 2018, 2019, and 2020 to compare the effects of fertilizer treatments including control (no N), urea deep placement (UDP), PU, and IPNS (PU +VC, PU+PL and UDP+PL) under two irrigation regimes, i.e., AWD and continuous flooding (CF) on rice yield and NUE. UDP significantly increased rice yield, total dry matter (TDM) and NUE compared to broadcast PU. Similarly, IPNS treatments either PU with PL or UDP with PL significantly increased rice yield, TDM and NUE compared to broadcast PU. However, UDP alone and combined application of PU with PL as IPNS showed higher rice yield under AWD irrigation compared to CF during dry season. Across the year and fertilizer treatments, AWD irrigation significantly increased rice yield, TDM and AE_N compared to CF condition during dry season, while AWD irrigation showed similar rice yield and NUE with CF during wet seasons. This study suggest that combined application of organic and inorganic fertilizer as IPNS basis might be considered as an efficient technology for improving crop productivity as well as maintaining soil fertility.

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Mitigation strategies of greenhouse gas emissions from lowland rice cultivation in Bangladesh

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Efficient fertilizer management, particularly urea deep placement (UDP) and water saving irrigation alternate wetting and drying (AWD) could mitigate greenhouse gas (GHG) emissions. However, studies on the impacts of UDP and integrated plant nutrient system (IPNS) that combines poultry litter (PL) and prilled urea (PU) with different irrigation regimes on GHG emissions and yield in rice cultivation are limited. We conducted multiyear field experiments during the dry seasons to compare the effects of four fertilizer treatments including control (no N), PU, UDP and IPNS with two irrigation regimes (AWD and continuous flooding, CF) on GHG emissions and rice yield. CH₄ and N₂O emissions were measured using the closed chamber technique and their concentrations were determined using a gas chromatograph. CH₄ and N₂O emissions varied across fertilizer treatments and irrigation regimes. Across irrigation regimes, UDP significantly ($p < 0.05$) reduced cumulative CH₄ emissions by 11% and 17% compared to PU and IPNS treatments, respectively. Across the year and fertilizer treatments, AWD irrigation significantly ($p < 0.05$) reduced cumulative CH₄ emissions, and GHG intensity by 31% and 33%, respectively without any yield penalty compared to CF condition. Although AWD irrigation increased cumulative N₂O emissions by 68%, it reduced the total global warming potential by 30% compared to CF irrigation. The CH₄ emission factor was lower in AWD compared to CF irrigation. Across the irrigation regimes, UDP significantly increases rice yield compared to PU under both irrigation regimes. These results suggest that both UDP and AWD irrigation might be considered as an eco-friendly technology.

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Understanding farmers' perspectives: Potential research area to increase drought resiliency in Australia

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Drought is a recurrent and inevitable feature of the Australian agriculture and projected climate change scenarios indicate Australian agricultural industries are likely to become more vulnerable to drought. A wide range of uncertainties exist in drought management decision making due to variations in understanding of drought perspectives among scientists, policy makers and primary producers, making adapting to and mitigating drought impacts difficult. A multi-stage systematic review of existing research activities in Australia was carried out to explore potential drought management research areas. Popular databases in the field of agricultural research, and relevant websites, were used to investigate research activities using pre-defined search terms related to drought. After applying inclusion/exclusion criteria a total 64 research projects were selected. A thematic content analysis was conducted using Nvivo 12 plus software to explore the project outcomes, and key focus area of these research projects undertaken. Findings of this study demonstrated that drought related research activities followed a highly top-down approach and were predominantly influenced by the scientists' perspectives. Results also indicated that grazing industries attracted top-most priority in terms of drought related research, and the vegetable crops got the least attention. Among the research projects conducted, only 24% of these projects considered the necessity of farmers' involvement in improving drought management planning research, and building social and natural capitals did not get much pace in these research activities at all. Our study thus emphasises the necessity of producer-oriented research programs to improve drought resilience across the agricultural sector.

Keywords: Drought resilience, drought preparedness, agriculture, farmers' perspectives

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A genomics approach to improve breeding time in Australian tropical tree crops

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Economically important woody crops, such as fruit trees, present unique challenges for commercial breeders in Australia. Compared with herbaceous crops, trees can spend a significant time (3-20yrs) in a juvenile state during which the tree cannot flower or produce fruit. This lengthy juvenile period is a less desirable trait. It significantly delays the production of a fruit crop and has greatly limited the speed of tree domestication and genetic improvement of elite varieties. The juvenile to adult reproductive phase change in trees is likely to be under firm genetic control. My research characterises two genes from the PEBP family, FLOWERING LOCUS T (FT) and TERMINAL FLOWER 1 (TFL1), that can influence the transition to a reproductive state. The genes that belong to the PEBP family are known to have gone through multiple duplication events. Consequently, it has led to a diversification of functions, making the functional characterisation of PEBP genes interesting and challenging. Over time, the PEBP family has evolved both activators and repressors of flowering; FT is a promoter of the plant's transition to a reproductive phase, while TFL1 inhibits this transition. This study will thoroughly investigate the roles and protein interactions that FT and TFL genes have in three significant Australian tropical fruit trees, macadamia, mango, and avocado. This research aims to provide genetic resources that could be used to shorten the juvenile phase of fruit trees and enable a shorter breeding cycle to select traits for genetic improvements, including disease resistance and abiotic stress resistance.

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Minimally invasive biomarkers for assessment of heat stress in grazing sheep

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Non-blood glucocorticoid measurements are gaining popularity as a measure of stress, being less invasive than blood sampling. Thus, cortisol levels in feces and wool are potential biomarkers of heat stress (HS) adrenal status. Prolactin levels also rise during HS and prolactin receptors (PRLR) have been demonstrated in ovine apocrine glands (Choy et al. 1997). Merino lambs (n=30/group) were randomly allocated to pastures either with shade (trees) or without shade for one month (February) during summer and standard farm practice was applied with *ad libitum* access to water. Blood and fresh fecal samples were collected manually on the initial and final days. Wool samples were collected by shearing 10x10cm² area of the shoulder region and skin biopsies were taken from the neck region at the end of the study. Plasma prolactin concentration was measured by radioimmunoassay (Clarke et al. 1982), fecal and wool cortisol were estimated using enzyme-immunoassay (Narayan et al. 2018 and Sawyer et al. 2019) and PRLR expression was quantified by real-time PCR. Exposure to HS increased plasma prolactin concentrations (P<0.01), irrespective of group, but the incremental rise was greater (P<0.05) in the non-shaded group than in the shaded group. HS also increased fecal (P<0.05) and wool (P<0.01) cortisol concentrations, with the greater values being observed in non-shaded group. The shaded group had lower PRLR mRNA expression (P<0.05) than the non-shaded group. Thus, estimation of fecal, wool cortisol, plasma prolactin concentration and gene expression of the PRLR in skin could be used as biomarkers to assess HS in sheep.

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Quinoa and cowpea provide alternative crop options for the Vietnamese Mekong Delta

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Dry-season soil salinisation is a prominent production and food security issue for farmers in the Vietnamese Mekong River Delta (MRD). Rice crop failure due to salinity exposure occurring at critical reproductive phases is forcing the need to identify and implement alternative dry season crops to rice that can withstand low rainfall and salinity concentrations above 4 g L⁻¹. A glasshouse trial compared the growth of soybean (*Glycine max*), cowpea (*Vigna unguiculata*) and quinoa (*Chenopodium quinoa*) in saline conditions using Chameleon soil moisture sensors to control irrigation frequency. All three plant species had significantly lower yields when irrigated with saline water however soybean was most affected by salinity with a termination of growth once irrigation concentrations reached 4 g NaCl L⁻¹. Consequently, soybean is not suitable for growth in the high saline conditions found in the Vietnamese Mekong River Delta. Cowpea and quinoa tolerated the higher salinity concentrations through reproductive phases despite soil solute potentials below -1 MPa. Cowpea used significantly more saline water throughout the growth period than quinoa and recorded the highest yields when constantly and not intermittently watered with saline water. No significant yield difference existed between quinoa plants that were constantly or intermittently watered with saline water. Cowpea is recommended as an alternative dry season crop to rice when an abundance of saline irrigation water is available, and quinoa is suitable when water irrigation sources are limited or saline. These alternative option crops could help contribute to Vietnam's food security and provide financial returns to farmers households.

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Five Capitals Food System Resilience Score Analysis Tool

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The food system is a complex web of actors/agents and interactions that spans production to the consumption of food. The global food system has been severely disrupted by the COVID-19 pandemic putting millions of people at risk of hunger and malnutrition. In a post-COVID-19 era, a stock-take will be required to see how our food system changed in response to current drivers/pressures and what lessons we learnt regarding the actions required to improve its resilience. The ability to understand, interpret, evaluate, and monitor key aspects of the food system is pivotal in building resilient food systems, as it is through this collection and analysis of information that we can improve resource allocation and effective decision-making. Thus, we present a diagnostic tool that can identify and monitor food stress using a food system resilience score. This score is derived from several indicators that describe natural, human, social, financial, and manufactured dimensions of the food system. The tool incorporates three major functionalities - situational awareness, scenario analysis, and intervention analysis. The situational awareness component helps derive a clear understanding of the strengths and weaknesses of food systems, while the scenario analysis component enables the anticipation of how various aspects within food systems may change when exposed to food shocks. The intervention analysis component points out the most effective and realistic interventions against anticipated food shocks. We have constructed the tool so that it can be deployed at various levels to enable better-informed decision-making toward building resilient food systems in the long term.

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Evaluation of pearl millet landraces for conservation, adaption and promotion in India

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Pearl millet landraces conserved by farmers have wide range of diversity and adaptability to unfavourable conditions, constituting an important source of stress tolerant local seeds for pearl millet therefore contributes a lot to millet production in India. Hence, characterizing the genetic diversity of pearl millet could contribute to a sustainable pearl millet productivity through better breeding programs. To achieve this goal, mainstreaming of available pearlmillet landraces at farmers field was planned as crowd sourcing trials which included mother and baby trials at research stations and farmers' fields during 2019, 2020 and 2021. The seeds of the different landraces were collected across the Rajasthan state. Firstly, the selected landraces were assigned codes and feed in CLIMMOB APP for recording of crop parameters. The coded packets were given to the farmers for sowing at 'Farmers Field'. Simultaneously, 'Mother Trials' were conducted at research farm of AICRP on Pearl Millet, Agriculture University Jodhpur and CAZRI, Jodhpur. The well performed landraces based on farmer's preference showing high yield and tolerance to different stresses were taken in the record and listed for conservation, multiplication and promotion under seed chain programmes at community level seed bank. Out of 102, 7 landraces viz., *Moochwali Bajri*, *Pili Bajri*, *Sulkhaniya Bajri*, *Sundaram Verma Local*, *DR-1*, *DR-2* and *Chanana Bajri* were found promising in yield as well as nutritional parameters which were submitted to NBPGR for conservation and allocation of IC numbers. *Sulkhaniya Bajri* yielded maximum grain yield (12 q/ha) whereas *Moochwali Bajri* had maximum fat content (5.2%).

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Responding scarcity of agricultural labour by out-migration: understanding coping strategies in Myanmar

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This paper examines the farmers coping' strategies in Mandalay and Sagaing Regions of Myanmar that have been used to mitigate the negative impacts of agricultural labour shortages caused by rural out-migration, and investigates respondents' recommendations for national government in order to promote the effective coping mechanisms. 70% of selected farmers adopted various strategies to combat labour scarcity at the micro level, which involved five measures management of labour, time, crop, land, and farm mechanisation. The farmers interviewed still preferred using human labour rather than farm machines, even though they faced agricultural labour shortage. The labour management strategies cited by farmers, they commonly used to offer higher wages, extensive use of family labour, and searching for labour from other places. Interestingly, a cooperative working system was a strategy specifically set up a counter labour shortage in high migrant sending areas such as Depeyin and Meiktila townships through establishing social community cohesion during the period of peak labour demand. However, community leaders and public officials stated that agricultural mechanisation is the best potential coping strategy for farmers. Some coping mechanisms (time, land, crop management) were used by farmers when they were facing serious labour shortage problems. Labour shortage caused negative side effects such as abandoned agricultural land, postponement of agricultural activities, and changing agricultural practice. This research highlights key adaptive coping strategies that farmers can utilise and policy interventions should improve coping mechanisms to mitigate the impact of labour scarcity in Myanmar agriculture.

Keyword: Migration, Labour scarcity, Coping strategies, Recommendations

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Divergent Technology Adoption in a Philippine Native Chicken R&D Utilization Program

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In Western Visayas, Philippines, the most dominant breed of native chicken is called Darag. Efforts to promote the Darag-raising sector can be traced back to the 1980s though the Philippine government initiated large scale projects for the improvement, utilization, and conservation of Darag native chicken in the region by the 1990s. From 2005 to 2007, the R&D utilization program for productivity and product quality improvement of Darag was implemented by several institutions. As with most public investments, the Darag program needs to be assessed for its contribution to the development of livelihoods in the rural sector. Such concern is important for accountability and for informing future investment decisions.

In this paper, we present the application of the integrated approach to impact assessment, co-developed with researchers from two Philippine universities and CSIRO, to generate rich insights and explore diverse values surrounding the implementation and results of the Darag R&D utilization program in Western Visayas. In doing so, we highlight pragmatic concerns of complexity in development programs and the application of an integrated approach to the assessment of “research for development” (R4D) interventions’ impacts.

Applying the sequential exploratory mixed-method design, we conducted KIIs, FGDs, and document review, which was later followed by a farmers’ survey. Results show divergent technology adoption practices arising from unintended modifications or mixing of technologies. With technological modifications beyond the program cycle, the extent of intended economic impacts would naturally be limited. Additionally, stakeholder engagement evolves to continually influence future of farmers’ practices.

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Intraspecific Variation of *Cocos nucifera* Populations on Viti Levu and Taveuni

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Coconuts are pantropical terrestrial species which play an essential role agriculturally, economically, culturally and represent as a symbol of tropical Pacific Islands. This iconic palm, popularly known as the 'Tree of Life' is an important food security crop and source of livelihood for many farmers, of whom many are smallholders that cultivate coconut palms. Intraspecific variation of *Cocos nucifera* and population genetics of *C. nucifera* is currently being assessed for effective coconut resource management in Fiji. This study is significant as the available information is sparse with regards to the distribution of genetic diversity within and between coconuts populations; therefore, it is crucial to capture coconut genetic diversity and conserve unique cultivars found in the Pacific region. A sample of 121 randomly selected coconut palms representing both dwarf and Tall varieties were characterized morphologically from Viti Levu and Taveuni Island in Fiji. Potential population variation will be assessed using potential Single Nucleotide Polymorphism (SNP) markers determined from Next Generation Sequencing (NGS) within varieties; possible hybrids are also currently being analyzed and preliminary results of these studies will be presented. Genomic analyses will allow an assessment of outcrossing or introgression in 'natural' populations of coconuts around Viti Levu and selectively bred individuals at Taveuni. Further investigations on natural and human-driven hybridization between coconut varieties are useful for the management of natural stands and improved utilization of coconut diversity, given predicted climate change scenarios.

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Effect of nitrogen application rate on structure, and properties of starch in japonica rice

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The quality and starch properties of rice are closely affected by nitrogen. Two *japonica* cultivars Bengal and Shendao 505 were used in this study over two years to investigate the effect of nitrogen application rate (0, 180, and 230 kg/ha) on texture of cooked rice, hierarchical structure and physicochemical properties of starch. The results show that cooked rice in nitrogen treatments performed a harder and not sticky character than N0, thus reduced the texture quality. Amylose content, mean diameter of starch granule, and pasting properties decreased significantly, while the region of lamellar crystallinity increased with the increasing nitrogen rates, and the starch granules became smaller with an increase in uneven and pit surfaces. The proportion of short-chain amylopectin rose and long-chain amylopectin declined, which increased external short-range order, 1045/1022 cm⁻¹, 995/1022 cm⁻¹, and relative crystallinity. These changes in hierarchical structure and grain size, which was regulated by nitrogen rates, synergistically increased the setback viscosity, gelatinization enthalpy and temperature and reduced the overall viscosity and breakdown viscosity indicating that gelatinization and pasting properties was the result of the joint action of several factors. All the results showed that increasing nitrogen affects the structure and properties of starch, eventually deteriorating eating quality and starch functional properties. Moderate reduction of nitrogen application improve the texture and starch quality of rice.

Keywords, fine amylopectin structure, texture quality, thermal properties, hierarchical structure of starch, nitrogen application

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The Australian Oaten Hay Use for Sustainable Dairy Production

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The export fodder industry is one of the important agricultural sectors in Australia, with an annual export of more than \$500 million to the global market. Australian oaten hay is one of the major fodders exported overseas (e.g., Japan, China and the United Arab Emirates). However, there is a lack of scientific data suggesting the best use of Australian oaten hay (e.g., quality level, inclusion rate and complementary forage) in these countries with a total mixed ration (TMR) to support sustainable dairy production development. This study explored international literature and documented the facts and identified the research gaps. The literature reviewed 39 studies based on keywords “oaten hay”, “oat hay”, “dairy”, and “cattle” searching on the google scholar, ScienceDirect, Web of Science, Scopus and China National Knowledge Infrastructure (CNKI), and 22 studies were selected for the review as oaten hay been compared with other roughages as a treatment in dairy cattle diets. The summarised results indicate that adding oaten hay in TMR for lactating and dry cows can potentially increase the dry matter intake (DMI) with no more than a 15% inclusion rate. The milk yield and quality change were found to be inconsistent, likely due to the differences in oaten hay qualities among the studies and interaction between oaten hay and basal TMR diet. Therefore, further studies are needed to find out the combinations of oaten hay and other roughages with a clear inclusion rate and the quality level.

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Spray application of dsRNA targeting ZYMV reduces infection incidence in *Cucurbita pepo*

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Zucchini Yellow Mosaic Virus (ZYMV) is an aggressive plant virus causing disease in cucurbits, leading to significant production and economic losses in tropical and sub-tropical cucurbit cropping regions in Australia. Current approaches to the management of virus diseases in crops are by chemical application to kill insect vectors or genetic modification to engineer resistance. Either approach can lead to negative environmental or ecological impacts with the latter suffering from adoption and acceptance issues. Therefore, the need for new crop disease management approaches is constantly growing. Topical application of cognate dsRNA to plant viruses has been shown to induce protective effects through the induction of the RNA interference (RNAi) pathway. Here we adopted a cutting-edge dsRNA-clay-particle platform, BioClay, to establish the protection efficacy of RNAi by applying dsRNA to zucchini (*Cucurbita pepo*) plants targeting the Coat Protein (CP) genes of ZYMV. We also demonstrate RNAi against two putative virus receptors in the insect vector *Myzus persicae* with orally delivered dsRNA. Together, this research aims to control ZYMV infection and transmission by targeting both the virus and insect factors to lay the foundation for a non-chemical, non-transgenic, safe and effective alternative in crop protection against viral disease.

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Effect of biochar and phosphorus on the yield of five crops, Timor-Leste

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Rice hulls are waste product that has a potential to be used as a biochar which can overcome soil constraints, especially on acid tropical soils. This researchers aims to determine the effect of the application rice-hull biochar, the farmers method of applying cow manure and phosphate fertilizers on yield of tomato, long bean, chili, soya bean and maize in an acid soil in Timor-Leste. The Ph of the soil was 5.2 and Olsen P level of less than 5ppm. The experimental design used was a two way factorial consisting of five crops and five soil additives. The soil amendments were Nil, Buffalo manure (1.2 t/ha), rice-hull biochar(20t/ha), SP36 (80kg P /ha) and a combination of 20 t/ha rice-hull biochar and 80 kgP/ha.

Maize yield was zero in all treatments due to the acid soil with low available P levels. Across the other four species, the application of 20 t/ha biochar increased yield by 298%, much more than the traditional method of applying 1.2 t/ha of cow manure (47%). Applying 80kgP/ha increased yield by 113 % over the five species. The impact of biochar and phosphatic fertilisers were additive so that when both applied, with increased by 442%.

This data shows that although rice-hull biochar can increase yields in acid low P soils, greater yields can be increase with the addition of rice-hull biochar as phosphatic fertilisers.

Keywords: introduce new innovation to farmers to increase production.

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Root Meristem Growth Factor (RGF) Peptides in Soybean Root Development and Nodulation

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Legumes represent a valuable commodity by producing protein rich foods and oils as well as helping to protect the environment. Most legumes interact with specific soil bacteria called rhizobia which enables biological nitrogen fixation (BNF). As such, legumes have a reduced the reliance on industrial nitrogen fertiliser inputs which mitigates the detrimental greenhouse gases during fertiliser decomposition that usually occurs in farming systems. During the symbiosis, BNF occurs by the bacteria in nodule root organs on the host plant, with the bacteria also receiving a photosynthesis-derived carbon (Ferguson et al., 2019). However, nodulation requires complex signalling networks to develop the novel root nodules while optimising energy use given inputs from the external environments. During these process, small signalling peptides act as vital regulators for signal transduction (Hastwell et al., 2015; Reid et al., 2011; Roy et al., 2022). We aim to characterise a novel peptide family, Root Meristem Growth Factors (RGF) in root development and nodulation in soybean (*Glycine Max*), the most produced legume worldwide. This has been done using multidisciplinary and cutting-edge molecular biology methods include bioinformatic, histochemical, loss and gain-of-function analysis and biochemical synthetic peptide application. Specifically, we have identified specific RGF peptides critical for proper nodule development and root growth. The findings will indeed benefit future crop development programs to enhance biological nitrogen fixation and advance legumes crop development to work towards agriculture sustainability.

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Role of Agricultural Institutions in Sustainable Rural Development in South Pacific

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The purpose of this paper is to investigate agricultural training in tertiary colleges, their relevance to rural communities in Fiji and other South Pacific Island countries, and how best they can contribute to alleviating rural poverty. These institutions train farmers (vocational and adult education) and/or provide agricultural extension officers and researchers. Therefore, we provide insights on the correlation between agricultural institutions and sustainable rural agricultural development. It is necessary that agricultural institutions adjust their programs to accommodate the emerging fields, as well as establishing new partnerships with the private sector and providing new learning and teaching frameworks. Furthermore, they should also engage in constant dialogue with policy makers in addition to expanding their representation in governance. These institutions can potentially present local customs and knowledge, generating opportunities for sharing the regional culture, ethical customs, and global movements of Pacific Island communities.

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Sustainable livestock development in Pacific Island countries

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Agriculture contributes for around 10.4% of Fiji's GDP, supports the livelihoods of 27% of the people, and is the primary source of employment for more than 83 percent of the country's rural population. However, the estimated contribution of livestock is low and not well known. Livestock production has decreased in the recent decade, yet it remains a vital industry for Pacific Islanders' livelihoods, income, and food security. To meet future demand and lessen reliance on imports of livestock products, livestock sector must develop at a faster rate than the present less than 4% per year. For long-term growth, government assistance and private investment are critical. Small livestock, such as chickens, sheep, and goats, can be incorporated into the farming system to provide additional revenue and food security in the face of climate change.

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Dynamics of radiation interception and radiation use-efficiency of three pigeonpea (*Cajanus cajan* (L.) Millsp.) genotypes at different sowing dates

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Understanding of dynamics of yield development in pigeonpea is critical in identifying genotypes suitable for sustainable production. To examine the physiological determinants of grain yield of pigeonpea genotypes, field trials were established at the Gatton Campus, The University of Queensland, Australia in 2017/2018 and 2018/2019 summer seasons. The field trials were laid out in split-plot design, with sowing date as main plot and genotypes as subplots.

The results revealed that sowing date had significant impact on crop growth rate and reproductive development. The grain yield ranged between 2.8 and 4.1 t ha⁻¹ and total dry matter (TDM) between 4.2 and 13.3 t ha⁻¹ due to the variation in cumulative thermal time from sowing to maturity (1413 – 2225 °Cd). The seasonal radiation use-efficiency (RUE) and RUE during reproductive phase ranged from 0.81 - 1.11 gMJ⁻¹ and 0.22 – 0.71 gMJ⁻¹, respectively. The duration to reach maximum leaf area index showed a positive linear relationship with radiation use efficiency ($r^2 = 0.44$) and grain yield ($r^2 = 0.76$). Grain yield was positively associated with the radiation use efficiency ($r^2 = 0.62$), and the relationship was stronger ($r^2 = 0.83$) during the pod filling period. Positive association between grain yield and radiation use efficiency during the pod filling period, suggesting that maintaining optimum leaf area during the pod filling period is instrumental for high grain yield in pigeonpea genotypes. A positive and significant correlation ($r = 0.79$, $P < 0.001$) between the shoot dry matter before flowering and grain yield suggest that higher TDM before flowering is critical for high yields. Mean maximum temperatures above 33.3 °C during the reproductive phase resulted in decreased grain yield likely due to the impacts on flower drop, pollen viability and pod abortion leading to reduction in pod number.

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Cropping System Intensification Options in the Coastal Zone of Bangladesh

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Coastal areas in Bangladesh cover about 2.85 million ha (Mha) of which about 1.0 Mha affected by varying degrees of salinity in dry season. Rainfall variability, waterlogging, lack of fresh water during dry season, heavy textured soils and frequently occurred natural hazards are the major obstacles for crop intensification in coastal Bangladesh. Fresh water resource development is the first and foremost option for increasing cropping intensification in the coastal zones. As river water salinity starts to rise after December/January, fresh water (< 4 dS/m) can be trapped in the existing canal system within the polder for use during dry season crop production. There are other avenues as well. Advancement of *T. Aman* harvesting season by about 15-30 days through introduction of short duration high yielding (4.0-5.0 t ha⁻¹) rice varieties open up opportunities for establishment of low water demanding crops like watermelon, mask melon, cucumber, pumpkin and zero tillage potatoes in the dry season. However, untimely heavy rainfall in dry season creates waterlogging and sometimes damage non-rice crops- a risk considered by the most farmers in coastal areas. Under such conditions, growing dry season salt tolerant rice varieties paved the ways of harvesting 5.0-6.0 t ha⁻¹ rice successfully and consistently. Besides, pre-monsoon rice can also be grown with an additional harvest of 4.0-4.5 t ha⁻¹ rice in the coastal areas. These technologies, developed through ACIAR-BRRI ventures, can be utilized for adapting unpredictable heavy rainfall distribution and for using saline river water management across coastal zone of Bangladesh.

Key words: *Crop establishment, Time of sowing, Waterlogging, non-rice crops, Boro rice, Aus rice*

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Assessing climate risk to agriculture and potential mitigation options in Ganges delta

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The Ganges delta includes a unique coastal ecosystem, highly vulnerable to climate change because of immediate proximity to sea, low elevation, excessive population pressure on limited natural resources and relatively weak coping mechanisms. Agriculture of the region is risk prone with low productivity. This paper presents preliminary results from a study on climate risk to agriculture in the deltaic region of Bangladesh and West Bengal, India. The study is being conducted using recent climate data from the IPCC's 6th assessment report. We have considered Upazila and Block; the third level administrative unit in Bangladesh and India, respectively as a functional unit for risk assessment. The risk is estimated as a product of climate hazard (e.g. extreme temperature and rainfall events) and vulnerability of element (e.g. crop area, cropping intensity, irrigated area) at risk to prioritize the adaptation and mitigation measures. A total of 7 climate indicators (e.g. extreme temperature, extreme rainfall, seasonal rainfall, number of rainy days) relevant to crop growth is used to quantify risk for each functional unit. Researchers and NGOs from Australia, Bangladesh and India have been working together in Ganges delta since 2015 under ACIAR funded project and has developed a risk mitigation strategy by engaging farmers to strengthen their confidence through judicious management of harvested rainwater, introducing suitable salt tolerant plant type/ varieties, careful planning of the crop calendar and efficient agronomic practices. The strategy would be upscale in the region with the help of remote sensing and geo-special techniques via machine learning.

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Sustainable Intensification of Eastern India Rice-fallows through Tillage, Mulching and Cropping Systems

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The eastern Indian states (Assam, Bihar, Chhattisgarh, Jharkhand and Odisha) are highest in the multidimensional poverty index score. In these states, about 8.5 million hectares of cultivable land remain fallow due to soil moisture depletion and irrigation water scarcity during the *Rabi* season after harvest of the *Kharif* rice (area 19 million ha). Sustainable cropping intensification options have been developed during 2015-2022 to address these challenges. Intercropping of climbing-type vegetables by strategically placing nylon bag reinforced soil columns in *Kharif* rice fields, rice-raised bed maize, rice-potato zero tillage planting with mulching (ZTM), and cropping patterns such as rice-potato ZTM-green gram, rice-garlic ZTM, rice-mustard ZTM-green gram, and solar power drip irrigated vegetable, homestead gardening, and fodder crop-based livestock farming were promising. Green manuring/azolla, rock phosphate/lime for amelioration of acid saline soils (pH 4.6 to 4.8), solar drip irrigation with paddy straw mulching increased the mean yields of crops by 20-101% and saved 40-60% of irrigation water over flood irrigation. System rice equivalent yield increased from 4.2 tha^{-1} in rice-fallow to 26.3 tha^{-1} in rice-potato ZTM-green gram (R-PZTM-GM). The soil salinity (ECe) diminished to 2.8 dSm^{-1} from 7 dSm^{-1} under conventional practice. There is scope to sustainably intensify the rice-fallow lands at least to 200% from the current 150% with higher returns (US\$ 1341 ha^{-1}) from existing US\$ 540 ha^{-1} . The R-PZTM-GM system has less irrigation water (0.31 $\text{m}^3 \text{kg}^{-1}$ rice-eq) and carbon (10.08 $\text{t CO}_2\text{-eq ha}^{-1}$) foot prints than rice-rice system (1.19 $\text{m}^3 \text{kg}^{-1}$ rice and 30.51 $\text{t CO}_2\text{-eq ha}^{-1}$).

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Optimizing mill mud application for *Amaranthus viridis* production

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Amaranthus viridis, an annual and cosmopolitan herb, is a naturally gluten-free plant with potential to provide high nutritional quality (protein, vitamins, fatty acids, minerals) and medicinally active compounds (squalene, tocopherols, antioxidant compounds, phytates). Since the human consumption of gluten-free products has been medically recognized, there is vested research interest in the different aspects of *Amaranthus* cultivation practices. Hence, this study investigated the effect of mill mud – a by-product that remains after sugarcane juice filtration – on the growth and yield of this potential super food. The experiment was conducted in a randomized complete block design (RCBD) with four replicates in a field trial. Five different treatments (T) of mill mud mixtures with soil were tested: T₁= 0t/ha (control), T₂=10 t/ha, T₃=20 t/ha, T₄=30 t/ha, T₅= 40 t/ha. The treatments were applied to a week prior to planting and re-applied 2 and 4 weeks after planting. The phenological parameters measured were plant height, leaf length, leaf width and plant weight and yield parameters included harvest duration, average number of leaves per plant and maturity date. All measured parameters showed higher values in treated plants compared to control, however no linear correlation between increased mill mud application and yield was found. The highest yield was evident in T₃ and T₄ (5.7 and 6.3 t/ha) which was significantly different from 2.7 t/ha found for the control T₁ (p<0.05). Therefore, it is concluded that mill mud is a high nutrient additive which increases the yield of *Amaranthus viridis* and may become a cost-effective way to increase production for farmers in the future.

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Advancing the *Duboisia* industry for sustainable alkaloids

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Duboisia is a high value Australian native, utilised in the global alkaloid industry. The key alkaloid produced by *Duboisia* is called scopolamine which is used to synthesise anti-spasmodics. Commercial production of scopolamine is centered on the production of *Duboisia* leaves (97% of worldwide production) in the South Burnett region of South-East Queensland. Today this industry is worth \$100 million per annum for Australia, however the potential for expansion is yet to be realised.

Commercial production of *Duboisia* hybrids is generally limited to the red vertosol soils found in the South Burnett Region. Commercial breeds are a hybrid of the local wild species *D. leichardtii* and a species typically found in the periphery of rainforests *D. myoporoides*. There are two other *Duboisia* species found in Australia: *D. hopwoodii* which is found primarily in central Australia and *D. arenitensis* which has only been found in West Arnhem land, in the Northern Territory, Australia. The private nature of the *Duboisia* industry, has limited the creation of publicly available information pertaining to the agronomy, growth habit, seasonality, genetics, breeding for commercial traits, and clonal propagation.

Queensland Alliance for Agriculture and Food innovation at the University of Queensland has taken the initiative to develop technologies for a progressive *Duboisia* industry. The project encompasses the areas of *Duboisia* improvement through conventional breeding and biotechnology approach, tissue culture based high throughput propagation and long-term field evaluation of parent species and new breeding lines. Through these resource and technological advancements, better economical returns are expected for a broader community within and beyond Australia.

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Determination of mutation rates derived from chemical mutagenesis in Sorghum using next generation sequencing

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Mutagenesis is a natural process that has been harnessed by plant breeders, via the use of chemical, biological, and physical mutagens, to create new diversity within crop species. In this experiment, sorghum (*Sorghum bicolor*) seed was treated with the chemical mutagen ethyl methanesulphonate (EMS) which generates genomic point mutations. Previous studies in sorghum have utilised a mutagen solution of 0.1-0.3%, however, whole genome sequencing has not yet been used to ascertain the number of mutations that are derived from different EMS treatments in Sorghum. Here, the sorghum seed was subjected to four different concentrations of EMS (control, 0.05, 0.15 and 0.25%) to ascertain how the level of EMS effects the viability of treated plants and derived M2 seed via field observations and seed germination testing. Whole genome Illumina sequencing of M2 plants derived from the EMS treatments, was used in variant analysis to determine the type and number of mutations at each treatment level. In total, 40 Illumina libraries were generated, with an average coverage of 15x. The primary outcomes of this study included: 1. Defining the optimal EMS rate that produces many mutations without causing sterility or unviable seed 2. Where in the genome the mutations are taking place 3. Based on the rate of mutations, estimating the number of sorghum mutants that would be needed to find a mutation in any specific gene of interest. This study will better inform future users of EMS in the generation of large-scale mutant libraries in crop species.

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Generating a large-scale mutant-library, providing new sources of genetic variation in Sorghum

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Mutagenesis is a key factor in the evolution of species and is generally a spontaneous event generated via normal cellular processes or via erroneous DNA repair or replication. As instances of mutagenesis create new diversity within genomes, this process has been harnessed by plant breeders to create novel traits, utilising chemical, biological and physical mutagens. In this project, we generated 150,000 mutant lines of an inbred sorghum (*Sorghum bicolor*) variety BTx623, using the chemical mutagen ethyl methanesulphonate. Seed was collected and bagged in bulks containing the seed from 100 mutant lines. DNA will then be extracted from bulk subsamples, followed by digital PCR screening (FIND-IT). The newly developed FIND-IT protocol has previously been utilised to isolate variants of interest in a large M1 mutant library of barley (x500,000) and in a small sorghum M1 library (x 7,000). The use of this protocol will reduce or even eliminate the need for backcrossing. Since sorghum is utilised for food, animal feed, ethanol and biofuels, the production of this large sorghum mutant library will provide a new source of genetic diversity in this species. This will contribute to breeding efforts focussing on enhancing disease resistance, drought tolerance, plant microbial interactions, and biofuel production traits in sorghum.

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Are there alternative hosts for the ginger pathogen *Fusarium oxysporum* sp *zingiberi*

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Ginger has been grown for hundreds of years for its medicinal and its culinary uses. As a crop, it is susceptible to a range of factors that can limit its growth, including devastating diseases caused by *Fusarium oxysporum* f. sp. *zingiberi* (Foz) and *Pythium myriotylum*; nematodes; weeds; and poor soil. Successful management of these factors requires an integrated approach to reduce dependency on pesticides and chemical fertilisers and to make pest and weed management more environmentally sustainable. For example, in ginger production systems, the use of rotational crops like oats, forage sorghum and brassicas can help reduce pathogenic nematode populations, weed pressure, and improve the soil structure while improving the environmental sustainability of the crop. However, it is not known if these rotational crops have an impact on the populations of pathogens like *Fusarium* and *Pythium*. Our previous research has found that Foz can exist in the soil for several years between ginger crop cycles. Our results so far show that common weeds of ginger, taken from Foz infected ginger crops, did not host Foz. So the question remains, does Foz use the rotational crops as an alternative host when the ginger crop is absent? To answer this question, we will sample rotational crops, such as oats, forage sorghum and brassicas to see if they host Foz in the absence of a ginger crop. This will provide a valuable insight into the host specificity of Foz and how it remains as a viable pathogenic population in the absence of its principal host.

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Nutrient management for growing cabbage in foodcubes with fresh and composted mulch

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Limited arable land in the urban areas and poor soil conditions in atolls are major constraints for growing crops in some Pacific Island countries. Modular structures of specially designed boxes, known as foodcubes (FC), was developed by Biofilta, Australia, and commissioned by the Australian Department of Foreign Affairs and Trade, to address poor soil conditions in urban areas and atolls. Here, three organic treatments namely White popinac (*Leucaena leucocephala*) fresh and composted mulch and seaweed fresh mulch were applied to soils and compared against the control for growing Chinese cabbages in the foodcubes under the South Pacific islands' agro-ecological conditions. Weeds were reduced by 78.3 %, 65.0 % and 72.2 % in fresh mulch, composted legumes and seaweed treated FCs respectively compared to the control treatment. Moreover, the average soil temperature in the FCs were significantly reduced by 3.1 %, 2.1 % and 2.0 % in fresh mulch, composted legumes and fresh seaweed treatments, respectively. There was a significant increase in N mineralization, cabbage leaf area index and fresh yield in legume mulched treatments. The maximum dry weight was harvested from leguminous fresh mulch treated soils, followed by composted legumes and fresh seaweed which was 218 %, 114 % and 39 % higher than the control treatment, respectively. Organic amended also improved the nutrient content of the harvested crops.

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Robust markers for young microspore stage low temperature tolerance in rice.

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Low temperature tolerance (LTT) at the young microspore stage (YMS) is an important trait for Australian rice production in both temperate or tropical environments. LTT at YMS is difficult to routinely and accurately phenotype in a breeding program. Hence, marker assisted selection using markers linked to moderate to large effect quantitative trait loci (QTL) has been proposed. However, QTL first need to be identified, and subsequently robust markers linked to the QTL need to be developed and their utilitarian value determined. These have been one of the primary goals for the pre-breeding projects that have been based at the University of Queensland. To date, 22 QTL for LTT have been identified. One QTL, *qYMCT10*, has been implemented into the breeding program with tightly linked marker assays developed and its benefit has been demonstrated in multiple backgrounds. Two additional QTL, *qYMCT6.1* and *9.1*, are going through preliminary validation in the breeding program, however, results indicated that more robust markers are needed. Improved markers will be developed in conjunction with whole genome resequencing of the parents, and other lines. The utilitarian value of *qYMCT5* and *8* have been demonstrated, however, additional markers are necessary before their implementation which will be achieved through fine-mapping. Genic based markers have been developed for another QTL, *qYMCT3*, but its utilitarian value has yet to be determined. The development of robust markers linked to QTL that are not background specific will increase the genetic gains in the Australian breeding program in relation to LTT at YMS.

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Na, K and Cl distributions constitute salt tolerance traits in sweet potato**Mr Shimul Mondal**¹, Mrs Julia Asch², Mr Ebna Habib Md Shofiur Rahaman³, Mr Folkard Asch⁴

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Two sweet potato (*Ipomoea batatas* L.) genotypes, CIP 189151.8 (salt sensitive) and CIP 420001 (salt tolerant) were grown hydroponically at two air humidity levels (~40% , ~80% rH) and were subjected to 0 mM and 100 mM NaCl root zone salinity for two weeks in greenhouse at the University of Hohenheim, Germany. Na, K and Cl concentrations were measured in roots and stems, leaf blades, and petioles of four sections of the vines differing in age, namely old (basal), middle (mid), young (distal) and very young (tip). Air humidity did not significantly affect Na, K and Cl uptake in salt stress conditions. Na and Cl uptake in the sensitive genotype was significantly higher ($p < 0.05$) than in tolerant genotype independent of rH (Relative humidity). Genotypes differed in the distribution of Na and Cl across the length of the vine. In the tolerant genotype Na and Cl concentrations were highest in the older parts of the vine while the younger parts showed lower concentrations, whereas in the sensitive genotype the pattern was inverted. In the tolerant genotype Na and Cl concentration of stems and petioles were higher than those of the leaf blade. No genotypic difference in the distribution of potassium along the vine was found. We conclude that relative air humidity does not affect Na, K and Cl uptake and sequestration of large shares of Na and Cl in stems and petioles serve as a tolerance trait protecting leaf blades in sweet potato.

Key Words: Salinity, Ion distributions, and Sweet potato

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Effect of Elevated CO₂ on *Macrophomina phaseolina*-Mungbean Interaction and Associated Defence Responses

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Increasing carbon dioxide concentrations globally lead to climate change, which is of emerging concern, affecting the plant's physiological, agronomic, and genetic performance in terms of yield, quality and nutritive value along with the advancement of disease progressions. This global concern may lead to the outbreak of several diseases like dry root rot (*Macrophomina Phaseolina*), which is favoured by elevating CO₂ and temperature. In this context, an experiment was carried out in open-top chambers during the *Kharif* (July and August)-2021. To study the expression of the disease under elevated CO₂, six mungbean mini-core accessions (VI001400 AG, IPM99-125, EC693369, VI001244 AG, VC 3960-88, EC693361) from the World Vegetable Center were sown in the pathogen inoculated pots. Data on germination percentage, disease score, shoot length, root length, chlorophyll content and yield parameters were recorded for all the accessions during different growth stages under ambient (380 ppm) and two elevated CO₂ concentrations (550 and 700 ppm). The elevated CO₂ concentrations with the disease pressure of *Macrophomina phaseolina* altered the germination percentage, shoot and root length, total chlorophyll content, and yield parameters. Molecular analysis of all the samples of the six accessions under ambient and elevated CO₂ levels, would identify the differentially expressed genes conferring the resistance to the pathogen. The experimental findings regulating differential genes and qRT-PCR derived expression dynamics of stress-responses will be studied with implications that would decipher the resistance mechanisms and growth dynamics operating behind the responses of mungbean to elevated CO₂ for addressing the challenges in future breeding programmes.

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A simple bioassay method for diagnosing copper toxicity on vegetable species

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In developing countries, farmers often overuse crop protectant products to control pests and diseases on vegetable crops to satisfy increasing quality demand of domestic and export markets. Copper (Cu) based fungicides and bactericides have been widely applied to control vegetable diseases, leading to Cu accumulation in agricultural soils and potentially Cu toxicity to crops, particularly in acidic soils (pH<6) where rhizo-toxic Cu²⁺ is favoured. Diethylenetriaminepentaacetic acid (DTPA) is a routine extractant for Cu but is effective in identifying Cu sufficiency but not necessarily Cu toxicity. In developing countries there is often limited analytical capacity so the development of a bioassay for diagnosing plant Cu toxicity would provide a practical diagnostic tool. In this research, nine vegetable species, viz. capsicum, lettuce, sweet corn, eggplant, tomato, cabbage, broccoli, cucumber, and green bean, were grown to evaluate effects of Cu toxicity on seedling root length. The soil was collected from a long-term field experiment on Cu toxicity that included 11 Cu treatment. The results showed that root length of vegetable seedlings decreased with increasing Cu concentrations. Seedling root length of all nine species started to decrease at a critical threshold Cu concentration in extracted soil solution of 0.45 µM. At this Cu concentration, root length of sweet corn decreased 20% compared with the control treatment, while broccoli decreased 63%, and the other vegetables decreased from 21% to 48%. There was considerable genotypic variability in response to Cu concentration with sweet corn being the most tolerant and broccoli was the least tolerant.

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Genetic variation for high temperature tolerance in rice genotypes at reproductive stages

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High-temperature events are becoming more frequent and severe globally due to climate change. High temperature poses a risk to rice production in Australia, particularly during the young microspore (YMS) and flowering stages, which induces spikelet sterility (SS) and reduces grain yield. The objective of this study was to examine the consistency of genotype performance after high-temperature exposure across the YMS and flowering stages and identify potential donors for high temperature tolerance. Two glasshouse experiments were conducted under controlled temperature conditions to determine genetic variation for high temperature among 300 diverse rice genotypes of relevance to the Australian breeding program. The plants in both experiments were grown in control temperatures (28°C/22°C, day/night), except for the 14 days of exposure to high temperatures at 38 ± 2°C for six hours per day during the YMS and flowering stage, and SS was quantified. The YMS experiment (25%) had significantly lower SS than the flowering stress experiment (44%). This finding indicated that the heat stress at the flowering stage caused greater loss than at the YMS. A significant number of lines appeared to be consistently susceptible or tolerant in both. A number of genotypes sourced from various countries such as M7 (USA), YRL118 (Australia), Bartle Frere (Laos), Lafitte (USA), Gavina (Spain) and Amaroo (Australia) were identified as tolerant at both reproductive stages and are considered suitable donor varieties for thermotolerance for the Australian breeding program. These tolerant genotypes have been crossed into elite Australian backgrounds for further evaluation.

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Clearing bottlenecks to quality fingerling production for satellite tilapia hatcheries in PNG

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Inland fish-farming is Papua New Guinea's fastest growing food producing sector and has the potential to resolve protein deficiency issues, particularly in rural areas. Around half of the children in Papua New Guinea experience stunting due to under nutrition and a low protein diet. Inland fish farming is undertaken in earthen ponds, often integrated into vegetable gardens. Reliable access to fish feed, well managed broodstock, and quality fingerlings are the main bottlenecks to growth of the industry and farm-level productivity. Satellite hatcheries are currently being established by the National Fisheries Authority to increase access to fingerlings for remote farmers across 22 provinces. This research builds on past ACIAR - funded research on fish nutrition and improving fingerling production, which was mainly based on methods suited to large hatcheries. However, satellite hatcheries often face different challenges, such as reduced access to utilities, more difficult growing environments, a lower farmer asset base, and poorly maintained brooders. This study is investigating cost-efficient technologies for satellite hatcheries to produce monosex (all male) tilapia, and to optimise feed and feeding strategies to improve the quality and growth performance of fingerlings. The research project will compare low-cost technologies in partnership with hatchery operators. The goal of the project is to empower satellite hatchery operators in rural areas to supply quality fingerlings to farmers, reduce the cost of production, and reduce pressure on government-run hatcheries. The satellite hatcheries will eventually be developed as farming nuclei providing fingerlings, fish feed and training to support grow-out farmers.

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Enhanced yield and reduced pests of sweet pepper treated with wood vinegar

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Sweet pepper (*Capsicum annuum* L.) is one of the most important vegetable crops grown extensively throughout the world. The use of wood vinegar has been reported as one of the natural and organic way of increasing yield of sweet pepper as well as controlling pests and disease incidence. Thus, this study was conducted to evaluate the growth and yield of sweet pepper as affected by methods of application and the dilution rates of bamboo wood vinegar applied; determine the most effective method of application and dilution rate; and assess the effects of wood vinegar application on the pest incidence and fruit disorders. The experiment was laid out in split-plot design arranged in Randomized Completed Block Design with three replications. The methods of wood vinegar application through drenching and foliar served as the main plot and the different dilution rates as the sub-plot factor which include D₁-tap water, D₂-750x, D₃-500x and D₄-250x. Results showed that the lowest dilution rate of wood vinegar of 250x applied through drenching significantly produced the heaviest yield and reduced blossom-end rot disorder on fruits. On the other hand, foliar application of diluted wood vinegar significantly reduced fruit fly and broad mite infestation compared to those applied through drenching. Among the eight treatment combinations, application of 250x diluted wood vinegar through drenching generated the highest net return which was almost three times higher than the control. This opens positive avenue for farmers to consider applying wood vinegar in increasing yield and minimizing pest damage.

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Major and trace elemental analysis for determining fibre quality traits in sugarcane

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Worldwide, sugarcane (*Saccharum spp.* Hybrids) is a valuable commodity for sugar, bioethanol, molasses, feedstock, and an evolving list of renewable bio-products. With this green revolution, there is considerable research into the second-generation biofuel production of lignocellulosic biomass, known as sugarcane bagasse and fibre. Whilst the fibre quantity is well documented, there is less established knowledge on the qualities of the fibre. In Australia, the local breeding program develops new varieties to advance agricultural and sugar yield properties. Occasionally, there are varieties with undesirable fibre quality released due to other commercially desirable traits. In this research project, two varieties with extremes in fibre quality measurements, are compared to ascertain phenotypical traits associated with fibre quality of the sugarcane stalks. Here in this experiment, we used inductively coupled plasma optical emission spectroscopy and mass spectroscopy to measure the mass fraction of seventeen major and thirty-five trace elements. Sugarcane alcohol-insoluble fibre was isolated from the soft and hard fibre varieties, which were randomly sampled from three replicated plots, all grown under the same trial field conditions. This poster presents the significant interactions between fibre quality trait, stalk tissue sections and internodal development stage on the mass fractions of major and trace elements digested from sugarcane fibre.

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Weed management in lowland rice cropping systems in Cambodia and Lao PDR.

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The development of sound weed management for the evolving lowland rice cropping systems of Cambodia and Lao PDR is vital to address the new challenges and opportunities that mechanized and direct seeded rice (DSR) systems brings. This is the aim of a five-year ACIAR project, “Weed management techniques for mechanised and broadcast lowland crop production systems in Cambodia and Lao PDR”. Using a participatory approach, focused on engaging with farmer groups, the project targets smallholder farmer practicing DSR in lowland rainfed and flood prone rice ecosystems in six and eight target villages in Cambodia and Laos, respectively. In these target villages the project will determine the most effective and labour efficient current weed management methods, and the obstacles and constraints to changing these practices; identify novel weed management options for smallholder farmers; and determine how different weed control options can be integrated for positive systemic (multi-criteria) outcomes with criteria covering income, wellbeing, gender, and sustainability. Research activities include the baseline survey of the current weed management, socio economic and gender, determination of weed seedbank and field infestation, demonstration of promising methods, capacity building and training, grain quality analysis, gender analysis, experiments for current and new practices and economic analysis of various alternative strategies. On completion, the project outcomes are expected to include effective weed management identified in specific lowland conditions; gender sensitive integrated weed management package development; and availability of high quality and weed competitive varieties. Initial results of the baseline survey and experiments will be presented during the conference.

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Production efficiency benefits of intensive mango planting

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Tropical food needs are projected to grow considerably to match population growth. Production of mango, a major tropical fruit, is projected to grow by 3.3 % per annum until 2030 and likely beyond. To avoid further land clearing it is essential that production increases are driven by greater land use efficiency rather than increased production area.

The Queensland Department of Agriculture and Fisheries and collaborators are driving production increases in mango through improvements in orchard systems, management and understanding of plant physiology, in the Hort Innovation National tree crop intensification program. One of the primary research activities in this project is a long-term orchard planting systems trial, designed to explore the effect of planting density, training system and variety on orchard productivity per hectare. The trial has been cropping for 6 years and has recently reached an important transition point.

The 2021 / 2022 production season was the first where the medium planting density has equalled or surpassed production per hectare of the high planting density as the medium density trees are close to filling their allocated space in the orchard. However, the high-density trees have achieved a cumulative production per hectare 176 % greater than the medium density and 316 % greater than the industry standard low planting density (averaged across 3 varieties) while maintaining fruit quality.

These findings, and the understanding of light and plant physiology that underpin them, offer an important route to sustainably increasing food production in the tropics without increasing the mango production area.

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Partial mixed ration modifies volatile fatty acids concentrations and calculated methane yield.

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Partial mixed ration (PMR) feeding systems involves feeding silages and concentrates in conjunction with grazing pastures. This system can increase milk production and limit methane production (O'Neill *et al.* 2012). Two experiments were performed to evaluate 1) five Lucerne post-grazing heights (10%, 25%, 40%, 55% and 70% of pre-grazing height) combined with high (14 kg/h/d) or low (7 kg/h/d) PMR level, and 2) three PMR compositions (white-sorghum, corn and forage-sorghum). Both experiments were performed at The University of Queensland, Gatton campus, comprising 30 multiparous Holstein cows (610 ± 49 kg BW) equally divided into 10 treatments for Experiment 1, while Experiment 2 used 36 multiparous Holstein cows (685.3 ± 52 kg BW) divided into 3 treatments. Rumen fluid samples were collected, and subsampled (1.5 mL rumen fluid + 0.3 mL 25% w/w Metaphosphoric acid) to estimate volatile fatty acids (VFA) as described in Forwood *et al.* (2021). Methane yield (CH₄Y) was calculated based on total (TVFA) and individual VFA concentrations (Williams *et al.* 2019). In Experiment 1, TVFA was high with increasing Lucerne post-grazing heights (P < 0.001), whilst acetate (P = 0.014) decreased. High PMR level (Experiment 1) and white-sorghum composition (Experiment 2) presented promising outcomes, where high PMR level promoted TVFA (P = 0.031), propionate increased with both PMR features (P = 0.02, P < 0.01, respectively), whilst acetate (P < 0.001), leading to low estimated CH₄Y (P < 0.001). Increasing Lucerne post-grazing height accompanied with 14 kg/h/d of white-sorghum PMR, might improve milk production and decrease calculated CH₄Y.

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Investigating CLE peptides in the soybean pangenome

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CLAVATA3/ESR-related (CLE) peptide hormones are critical regulators of plant development (Corcilius et al., 2017; Ferguson et al., 2019; Mens et al., 2021). Previous investigations identified 84 unique CLE peptide encoding genes in the genome of the economically significant legume crop, soybean (*Glycine max*; Hastwell et al., 2015). This was achieved using the single reference genome available at the time. We now aim to extend this search to the soybean pangenome constructed from 28 different lines, including wildtypes, landraces and improved cultivars procured from around the world (Liu et al., 2020). A thorough homology search followed by alignment, trimming and manual validation will be used to identify CLE peptide encoding genes across the soybean pangenome, which will establish Presence Absence Variants (PAR), as well as unique polymorphisms existing amongst the CLE genes of the lines investigated. A bioinformatics pipeline is being developed to achieve this objective. Findings are anticipated to provide valuable insight into determining core and dispensable CLE peptide encoding genes of soybean, as well as establishing those that are unique to geographical regions, and those that have been lost or gained during domestication. Outcomes could help establish important CLE peptide encoding gene targets in future legume breeding efforts.

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Short-term heat stress doesn't alter rumen microbial diversity indices of second-cross lambs

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The effects of climate change are forecast to increase the frequency and severity of summer heatwaves, increasing the prevalence of heat stress (HS) in animal production systems. Therefore, there is a need to understand how HS impacts livestock to aid in the development of mitigation strategies. Due to the importance of the rumen microbiota in efficient production, the aim of this experiment was to quantify the impact of short-duration heatwaves on rumen microbiota diversity in lambs. Twenty 2nd cross [Poll Dorset×(Merino×Border Leicester)] female lambs (8-12 months old) were divided into four equal groups with differences in HS durations. The treatments were, thermoneutral, 1-day HS, 3-day HS, and 5-day HS. Animals were slaughtered at the end of the study to obtain the solid and liquid phases of rumen fluid for 16s rRNA (V3-V4 region) sequencing. The different durations of HS and different rumen fluid phases had no significant ($p>0.05$) effects on the alpha diversity metrics such as Shannon entropy, Pielou's evenness or Chao's species-richness of the lambs. The beta diversity analysis of the ruminal microbiota was performed using the principal coordinate analysis on unweighted-unifrac distance method. Different durations of thermal exposure did not influence population dissimilarity between groups ($p>0.05$). Significant dissimilarity was identified between the solid and liquid phases of rumen fluid beta-diversity ($p=0.001$). In conclusion, short-term HS did not influence the rumen microbial diversity indices of second cross lambs. However, further research is required to determine the impacts of ongoing or prolonged HS on the rumen microbial diversity of lambs.

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Evaluating the nitrogen nutrition dynamics of sugarcane genotypes

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Nitrogen (N) is the most limiting nutrient to achieving yield goals in Australian sugarcane production and optimizing N use efficiency with reduced polluting N losses is an industry priority. Understanding biomass production and N status over the crop cycle across a range of sugarcane genotypes will provide insights into the potential for cultivar improvement and refined fertilizer management. A field experiment was conducted to evaluate biomass accumulation and Nitrogen Nutrition Index (NNI), determined from the critical N dilution curve concept, during plant and first ratoon crops. Ten sugarcane genotypes were grown under three mineral N fertilizer treatments (0, 80, and 200 kg N ha⁻¹) and sampled at three growth stages (3 months, 6 months, and harvesting). A significant genotypic and N treatment effect existed for biomass and N accumulation in the growth cycle. However, there was no genotype by N interaction effect for the measured traits throughout the cropping cycles. The biomass accumulation in the ratoon crop was faster than the plant crop during the first 3 months under three N supply. N accumulation was significantly reduced in ratoon crops compared to plant crops after 6 months. The NNI calculated with 200 N kg/ha supply at 3 and 6 months were >1, indicating that N did not limit the growth in both plant and ratoon crop. Genotypic variation and N treatment effect were not consistent throughout the sugarcane growing cycle and the information generated can be utilized for breeding purposes, enabling the development of improved varieties in Australia.

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Evaluating salinity tolerance in diverse taro wild relatives to improve food security

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Pacific Island nations are among the most vulnerable to our changing climate, with rising sea levels and an increase in cyclone activity leading to increasing frequencies of coastal inundations by salt water. The future success of Pacific Island Countries and Territories (PICTs) is dependent upon the ability to grow their own food and maintain self-sufficiency, as salt contaminated soil and ground water can impact the cultivation of staple food crops such as taro.

Wild relatives of taro that are native or naturalised to Australia may hold the key to developing salinity tolerant taro for the Pacific region. Often found growing in areas with regular tidal intrusion, the wild relatives' adaption to natural environments without human intervention means they are likely to be significant sources of abiotic and biotic stress tolerance traits.

In collaboration with the leading scientific organisation of the Pacific Islands (The Pacific Community, SPC), this project will identify - with the help of community science app iNaturalist - collect, and conserve taro wild relatives growing in saline habitats in and around South East Queensland. The germplasm will be screened through our high throughput phenotyping platform for salinity tolerance, and promising accessions will be genotyped to identify molecular markers (Quantitative trait locus) that are associated with salinity tolerance. This will improve the capacity for Pacific led organisations to utilise this germplasm to develop salinity tolerant taro varieties for the region.

Not only will this project lead to enhanced food and nutrition security of PICTs but will also grow and strengthen institutional links between the Australian tertiary sector and the Pacific region.

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Controlled environment agriculture: Philippines case study hydroponically grown of leafy vegetables

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Controlled environment agriculture (CEA) has been established by several countries through both greenhouse and indoor vertical systems for several high value crops. In the Philippines, as in every tropical country where varying climate has become a major challenge to produce consistent and best quality crops, indoor vertical farming is being considered one of the best alternatives. We designed a vertical grow rack system and evaluated its efficiency in producing consistent leafy green vegetables under soilless indoor (hydroponic) system. With all environment conditions optimized, our results showed a consistent yield across several planting cycle, from published 50g/plant grown on soil to at least 80g grown in CEA using hydroponics for loose leaf lettuce, proving that the grow rack system works in a CEA. Based on our cost analysis, one of the highest contributors of production cost is electricity. In order for an indoor vertical growing system to be sustainable and profitable, this cost due to electricity should be reduced to at least 50%. We therefore recommend further research using alternative sources of electricity such as solar, turbine or hydrological sources which are all available in the Philippines.

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RNA interference against the Green Peach Aphid, *Myzus persicae* (Hemiptera).

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Aphids are sap-sucking agricultural crop pests that cause significant fruit and fibre damage by infestation and transmission of plant viruses. Current means of aphid control rely on chemical pesticides, however a potential control method using double-stranded RNA (dsRNA) as a spray on technology to induce RNA interference (RNAi) is gaining traction. For spray-on RNAi to be effective against sap sucking insects, critical genes need to be identified that when targeted, disrupt homeostatic function, induce mortality, or significantly reduce insect fitness. Here, we show the ingestion of dsRNA via artificial diet (AD) assay, targeting several genes of the Green peach aphid, *Myzus persicae*, encompassing neuronal functioning; osmoregulation, probing/feeding behaviours or nucleic acid and protein metabolism either individually, in combination, or as a stacked construct induced mortalities ranging from 14 – 72%, 78 – 85% and 54%, respectively. Transcript level knockdown of the respective target genes ranged from 6.3% to ~54%, with inconsistent correlation observed when compared to mortality. Here we have identified several genes that may be targeted in a potential spray on RNAi based crop protection product against *M. persicae* infestation.

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The effect of biochar, Superphosphate and Zinc on mung beans in Timor-Leste.

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The effect of rice-hull biochar, Superphosphate and Zinc application on the production of mung beans (*Vigna radiata* L.) In three different soil of North coast Timor-Leste.

Jose da Costa Ronal Freygen, Robert L William, Luis Pereira

The addition of rice-hull biochar increases crop yield in many of the poor soils in Timor-Leste. This pot experiment was to determine if the yield response to biochar was in addition to the response to added phosphate and Zinc fertiliser on three different soils.

This pot trail was completed at Loes Research Station, on the north coast of Timor-Leste from May to September 2021. The test species was mung bean.

The experiment was a three way factorial of three rates of rice-hull biochar (0,5 and 20 t/ha), two rates of SP36 (0 and 80kg P/ha) and two rates of Zinc fertilizer application (0 and 5 kg/ha).

The three soils differed in color and pH. The three soils were colored brown (pH 8.4), grey (pH 6.8) and red (pH 7.5).

With no soil additives, the mung bean yield was 3.8, 5.7 and 4.6 g/pot for the brown, grey and red soil respectively. Large and significant increases in yield were observed with the addition of rice-hull biochar across all three soils. The application of 20 t/ha biochar increased yield to 7.9, 8.2 and 7.7g/pot for the three soil types. However even higher yields were obtained with the addition of rice-hull biochar, Phosphate and Zinc addition for all three soils (12.8, 13.5 and 13.1 g/pot, for the brown, grey and red soil respectively).

This data shows the low fertility level of these three soils. The addition of biochar was able to relieve some of the chemical deficiencies, but the maximum rate (20 t/ha) was unable to eliminate all deficiencies of phosphate and Zinc in these three soils. Further chemical analysis of the soils will be able to determine the nature of soil fertility status with and without added biochar.

Keyword: Biochar, Sp36, Zinc fertilizers, soil nutrition.

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Post-anthesis water stress can accentuate genotypic differences in late wheat root development

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The root system plays an important role in crop performance particularly under rainfed conditions. Limited crop production under water deficit conditions would highly benefit from a genetic improvement as irrigation and other management practices are often not a viable option in many cropping areas. Narrow and deep roots can help wheat to extract more water at depth late in the season and improve yield and yield stability, where crops heavily rely on deep soil moisture. We examined shallow and deep root growth of two wheat cultivars, Mace and Scout, under well-watered and terminal water-stress conditions up to maturity. Plants were grown in 1.5m poly vinyl chloride (PVC) tubes under (i) well-watered conditions, (ii) mild water stress, withholding water between early anthesis to early grain filling or (iii) severe water stress, withholding water from heading to maturity. There was little difference in dry root biomass, root diameter and root length density between genotypes under well-watered conditions either at anthesis or at maturity ($p \geq 0.05$). When water was withheld between early anthesis and early grain filling Scout had higher dry root biomass at maturity than Mace for both shallow (30-40cm) and deep roots (110-120cm). In these conditions, Scout also had higher root diameter and root length density for shallow roots (30-40cm). Under severe water stress, both genotypes were similarly severely affected leading to decreased dry root biomass, root diameter and root length density. These results suggest that mild water stress, can be used to highlight and identify wheat genotypes whose root architecture is better adapted to terminal drought.

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Investing better in agrifood innovation for sustainable impact

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Recent analyses identify that only 7% of the current \$60B of investment in innovation in the agrifood systems of developing economies have specific environmental objectives (Dalberg Asia, 2021). In addition, less than half of these investments have any entrenched social objectives (Dalberg Asia, 2021). As investment grows to fill the identified \$15B gap (Rosegrant et al, 2021) and to ensure a reduction of the climate finance gap (IPCC, 2022), it is critical that the investment portfolios developed and managed by national governments, private sector, development partners and private equity consider formal ways to measure and improve sustainable innovation impact. As the investment portfolio become balanced to ensure economic, environmental and social outcomes, both “green innovations” and the role of the private sector integrated into a multi-stakeholder partnership approach will be a key part of producing sustainable agrifood systems. This approach will enable future agrifood systems to deliver productivity growth, improved livelihoods for those involved, contribute to global food and nutritional security and most importantly reduce Greenhouse Gas Emissions (GHG). A number of key success factors, including the role of leadership through the innovation process, have been identified to improve the sustainable impact of innovation. These success factors in innovation pathways across technology, finance, policy and capacity building will be discussed to support investors and implementers achieve more sustainable impact at scale.

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Physiological and anatomical bases of transpiration efficiency in sorghum

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Maintaining sustainable crop production systems in current and future climate scenarios will require high yielding crop varieties with improved water use efficiency. Better understanding the physiological and anatomical traits associated with transpiration efficiency (TE, biomass produced per unit of water transpired) will likely contribute to crop improvement under water-limiting conditions. To explore the avenues of improving TE_{shoot} (shoot dry mass to total transpiration) in sorghum, individual plants of various genotypes were grown in 4L lysimeters under well-watered conditions. The lysimetry facility is designed to screen 560 plants per run. Detailed physiological and anatomical measurements were undertaken on a sub-set of 20 sorghum genotypes based on their racial background plus some elite lines. Differences in stomatal density, stomatal pore length, leaf mesophyll cells, root xylem number and diameter were observed. These leaf and root anatomical traits, either directly or indirectly, contribute to the regulation of water extraction and transpiration. This understanding should provide opportunities to develop sorghum germplasm with enhanced TE for water-limited environments.

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Scaling Conservation Agriculture in South Asia

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Natural resource (soil, water and environment) degradation is a serious challenge for sustainable farming in South Asia. Climate change causing melting of Himalayan glaciers, rising sea level in Bay of Bengal, contracted flash-floods, frequent draught and terminal heat are some real concerns. Therefore, there is an urgency to adopt practices around regenerative agriculture. Conservation agriculture (CA), also known as no-till agriculture, is an alternate system being successfully adopted in drylands worldwide to improve soil, mitigate climate change, sustain crop yields and reduce input cost by the farmers in South and North America as well as in Australia. Somehow, scaling of CA in South Asia is constrained due to prevailing cultivation practices, lack of policy support, unavailability of zero tillage drills, and poor farm advisory services. On the contrary, adoption of CA for sustainable intensification (CASI) is critical for future food, nutrition and environmental security of the region. Thus, a comprehensive regional strategy to scale CASI is warranted through an inter-institutional and inter-country partnership to promote both climate smart and regenerative agriculture. Earlier, a regional rice-wheat consortium involving Bangladesh, India, Nepal and Pakistan had been successful to promote CA in Indo-Gangetic region covering around 3.5 mha. This area can easily be doubled through increased investment and enabling policies that help carbon sequestration and conservation natural resources. The paper highlights an obvious need to initiate a mission mode program for promoting regenerative agriculture around CA in the region by involving all stakeholders (communities, farmers, researchers, extension workers, government-officials, public and private players).

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Sustainable Alternatives to Fertilizers-Vermicomposting technology as a value add to Agrifood systems

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Vermicomposting is a sustainable alternative to chemical fertilizer. A study was undertaken to utilise farm organic waste and convert them into financially viable value-added resources to be used on farms as manure. The research study compared and contrasted the degradation of farm organic waste in 3 conditions- aerobic, earthworm-assisted decomposition, and anaerobic. The degradation of organic waste was monitored and analyzed by incorporating various parameters like C:N ratio, pH, temperature, moisture content, etc. The variation of physio-chemical parameters for the three conditions was studied and this approach captured the variation in the nutrient property of the soil during the vermicomposting period.

Vermicomposting, which is the biodegradation of organic wastes using earthworms, has been reported as an effective and sustainable farm management strategy. The technology is also considered a bioecologically sustainable process in which renewable biological resources with an added value are produced.

The objective of the study was to compare different waste decomposition methodologies and determine sustainable options for farmers between manures and fertilizer. Clearly, the preliminary results demonstrated that vermicompost manure has good potential to conserve nutrients, soil added with vermicompost, and vermijuce tends to attain neutral pH. NPK content in soil added with vermicompost was higher by 15% as compared to chemical fertilizer. Earthworm action enhances natural biodegradation and decomposition of wastes (between 60 to 80 percent under optimum conditions), thus significantly reducing the composting time by several weeks. Within 5 to 6 weeks, 95-100 % degradation of all cellulosic materials was achieved.

Keywords: Organic wastes; biodegradation; vermicomposting

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Sweetpotato production and plant-available phosphorus in crop rotations in the PNG Highlands.

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Strongly weathered acidic soils are common in the PNG highlands. These soils may be high in total phosphorus (P) but have inadequate plant-available phosphorus (PAP) supply. The low PAP can result in low root tuber yield in sweetpotato (*Ipomoea batatas*) which is the dominant staple crop. Crop rotations using specific crops may be an economical means of mobilizing PAP for following crop species. To improve PAP in sweetpotato based cropping systems, 7 different crop/ fallow rotation systems were studied over 2 rotational seasons using a randomized complete block design with 3 replicates. The study was conducted at the NARI Highlands Regional Centre – Aiyura. The indicator crop was virus-free *Waghi best minj 2* sweetpotato. Treatments assessed included *natural fallow-sweetpotato* (NF-SP), *Tithonia-sweetpotato* (T-SP), *pigeon pea-sweetpotato* (PP-SP), *carrot-sweetpotato* (CR-SP), *cassava-sweetpotato* (CA-SP), *wheat-sweetpotato* (W-SP) and *sweetpotato-sweetpotato* (SP-SP) as the control. An ANOVA analysis did not detect any significant differences between treatments for marketable root tuber yield ($p = 0.694$) and top biomass production ($p = 0.526$). Treatment means of marketable root tuber yields ranged between 25.8 t ha^{-1} to 30.2 t ha^{-1} ; SP-SP and NF-SP being the least and highest yielding cropping sequences respectively. Nonetheless, effect sizes were predominant in the fallow rotations – NF-SP and T-SP (Cohen's $d = \sim 0.7-0.8$) - relative to the crop rotations (Cohen's $d = \sim 0.3-0.6$). Analysis for P content in soil and plant tissue was omitted as it was concluded that differences in soil and plant P would be negligible considering that yield differences were non-significant.

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Negotiating Gender Inclusion in Irrigation Water Management in Pakistan

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Existing studies on socio-economic differentiation in Pakistan mainly focus on the inequality between men's and women's access to and control over the resources and neglect the disparities among gender towards access to knowledge and skills to utilize the available resources. This research presents empirical evidence in which agricultural advisory services under an Australian Centre for Agricultural Research, ACIAR-Pakistan collaborative project "Developing approaches to enhance farmer water management skills in Baluchistan, Punjab and Sindh in Pakistan" successfully mainstreamed gender research and development into irrigation water management to improve household food security. Farmers Integrated Learning Model (FILM) was found best fit for the adult learning in the rural settings and helped farmers especially women's inclusion identify and resolve their challenges collectively at household and community levels. Furthermore, diverse ways were identified for women inclusion and their roles were successfully transformed and maintained to improve their food security and livelihoods in rural Pakistan. Elucidating these processes of inequalities helped to promote livelihood opportunities that support the diverse development pathways of different ethnic and gender groups, thus increasing the relevance of development interventions.

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Sustainable farming systems as an economical viable enterprise

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An unsustainable cropping practice is one that initially yields sufficient production at a lower enough cost to provide a worthwhile income considering the effort put in. However, over time, because of the farming practices adopted, production falls and costs increase. This means less income for the farmer, which eventually is insufficient to justify the effort involved and the costs incurred. The damage done to the soil and the environment often means that the land can no longer be used for farming (becomes obsolete for agriculture). This is illustrated by a number of examples from important agricultural industries in Fiji (sugar, taro, kava, ginger and pineapples). These unsustainable practices can often provide the farmer with a higher income for the first few years before income falls away. The primary reason for the decline in crop yields to non-viable levels is due to soil loss (both quantity and quality).

A sustainable cropping practice is one that yields sufficient production, at a lower enough cost, to continue to provide a reasonable income for the farming household over time. By working with nature rather than against it, farmers can manage their farms in ways that avoid damaging the environment and at the same time improve the income they can earn. Farmers in the Pacific can have an advantage in working with nature because of traditional knowledge and the inherent resilience of most traditional Pacific Island food crops to climate change.

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Growing Capsicum and Tomato with Drip Fertigation System under Tropical Island Situation

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In Pacific Island countries like Samoa where environmental conditions limit the growing of high-value vegetables such as Capsicum and Tomato year-round, thereby dependent on imports. Protected cultivation (PC) with drip fertigation system could potentially tackle these challenges by minimizing the problem related to harsh climate, soil fertility, space availability, and pest and disease pressures. This study aims to determine the feasibility of growing tomato and capsicum under PC compared to the open field (OF) cultivation in Sunshine Farm (2020). PC grown capsicum recorded more number of fruits and highest average yield (1.47 kg/plant) compared to OF (0.35 kg/plant). The same trend in tomato grown under PC (2.68 kg/plant) compared to OF (0.65 kg/plant). The Average Return (AR) of capsicum and tomato were estimated as WST750187 and WST678222 ha⁻¹, respectively considering the respective realized yield levels for the remaining duration of six years. Corresponding to the respective estimated AR, the Net Present Value (NPV) with discount factor at the rate of 11% is registered as WST1372262 and WST1155596. The B:C ratio for capsicum and tomato were 1.74 and 1.62. The Payback Period (PP) estimated as 2.48 and 3.70 years for capsicum and tomato crops, respectively against the project establishment cost of WST1859752. Internal Rate of Return (IRR) analysis indicated the financial feasibility at higher interest rate of 11.80% and 11.86% for capsicum and tomato, respectively. Thus, it is feasible and profitable to cultivate both crops under PC with drip fertigation in Samoa, however, capsicum observed to be more profitable than tomato.

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Importance of fertilisers and seasonal response for peanut production in Cambodian uplands

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Recently cleared upland soils in Cambodia become degraded in their nutrient content due to current practice of continuous cropping cycles, inadequate nutrient additions, and inappropriate agronomic management. Significant yield gaps develop for upland crops (e.g., maize, peanut, soybean, cassava, mungbean) that can be narrowed with the addition of organic manures, chemical fertiliser (N and K highly recommended) and lime. Smallholder farmers in Kampong Speu Province participated in on-farm trials (2019 to 2021) that compared the effects N (recommended rate) plus P and K fertilizer rates (recommended rate or 2 x recommended rate) with farmer practices (no fertilizer) on peanut yield on various soil groups. Differences in soil type, rainfall and other limiting conditions meant there was considerable variability in yields among sites, seasons, and years. However, compared to farmer practice, additions of P and K fertiliser improved peanut yields by up to 47 % in the early wet season (EWS) and 25 % in the main wet season (MWS). Profits were estimated to increase by 60 % and 30 % respectively in the EWS and MWS. Whilst farmers voted maximum NPK rates as best for plant growth and yield, farmers indicated that when the economic analysis and other risk factors were considered preference would be for the lower recommend rate. A key part of the study was farmers participation in field days to discuss specific issues of farmer concern. Further on-farm activities will combine organic and inorganic inputs with agronomic management techniques that improve soil health and maintain crop nutrient supplies.

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Characterising groundwater resources in Laos to enhance climate resilience and agricultural productivity

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Climate change is increasingly resulting in unreliable rainfall patterns and droughts in the Greater Mekong Region. In Laos, where 69% of the population relies on subsistence farming, rural livelihoods and food security depend on reliable water supplies. Away from perennial rivers groundwater is commonly the only source of water for communities during drought. Groundwater systems in much of Laos have not been studied and there is limited capacity to sustainably develop and manage groundwater resources.

Xayabouly Province is affected by drought when the rainy season starts late and groundwater extraction rates are increasing. We aimed to characterise groundwater resources in Ban Namphou, Xayabouly Province, to inform sustainable groundwater management and to enhance drought resilience locally. Groundwater is currently being used for domestic and horticultural purposes in Ban Namphou, and, relative to other parts of Xayabouly Province, there is high groundwater potential, plentiful arable land, poor access to perennial rivers, and good access to markets.

We collected groundwater and surface water level and quality data, socioeconomic data, and rainfall samples in the Ban Namphou area in 2021-22. Results show that the groundwater table mimics the land surface topography, with shallower depths to groundwater at lower elevations. Groundwater in the area comes from one unconfined aquifer. Groundwater recharge is estimated at 39% of annual rainfall, and roughly 1% of this groundwater recharge volume is currently used by people. If managed well, groundwater use can be sustainably increased in the Ban Namphou area to support a climate-resilient community and increased agricultural productivity.

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Building resilience in smallholder crop-livestock systems with responsive food & forage management

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Mixed crop–livestock systems remain hugely important in the developing world and potentially support more equitable, resilient, nutritious and sustainable agriculture than other food systems. According to FAO 2010, two-thirds of the global population live in these systems generate almost 50% of the world’s cereals and most of the staples consumed by poor people. Such systems also produce the bulk of livestock products: 75% of the milk, 60% of the meat and employ many millions of people on farms and connected industries and value chains. The integration of animals and crops is central to the objectives of sustainable intensification, therefore enhancing the possibilities to better utilize biomass as food and forage needs further RD&E in 3 main areas:

1. Development of varieties of cereals, especially maize, millet and sorghum, that possess superior traits for fodder quality (yield and digestibility) as well as desirable grain traits.
2. Development of the tools and knowledge to target the farming systems where such germplasm can be deployed and scaled most effectively.
 - a. Whole farm models applied to food-feed enterprise planning
 - b. Risk profiles of farm types and agroecologies for farming systems design and policy support for targeting resilience and food security.
3. Using a climate risk lens, develop the concept and tools for growing crops for both food and forage in crop-livestock systems to better manage the outcomes of cropping seasons tactically.
 - a. Pre- and in-season prediction tools that empower farmers to respond to prevailing weather and utilise in-season prediction to target the objectives of resilience and income.
 - b. Create risk profiles for smallholder farmers across agroecologies that encourage farm enterprise planning for resilience and food security.
4. Development of feed conservation methods that utilise available farm forage resources for the animal production target.

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Decision-Making Actors and Strategy to Minimize Fusarium Wilt Disease in Banana

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Most people in the village grow bananas in their backyard due to the economic benefits. However, not all farmers apply organic practice to solve a fusarium wilt disease in bananas so that it is necessary to understand the process of how farmers finally make decisions. Therefore, this research aimed at: (1) understanding the decision-making actors in banana farming, (2) the process of how farmers make a final decision in banana farming, and (3) the strategy of local wisdom practice to minimize the fusarium wilt disease attacks. This research was conducted in the Special Region of Yogyakarta where many farmers grow bananas from small to large-scale farming. Seventy farmers were randomly chosen as samples and the data were analyzed descriptively. The findings show that the dominant actors involved in long-term and complex farming practice are non-farmer friends, agricultural extension workers, and banana buyers or traders. Although most farmers usually make their own decision based on the actors' suggestion, some farmers depend on public extension workers and only few of them trust their colleague and family member for the final decision. There are several basic considerations to deal with fusarium wilt disease: understanding the resistant varieties, finding plants that can be rotated with banana plants, and understanding the biological controllers; but not many farmers understand the microbiome of their banana plants. It is also found that an innovative farmer tends to apply and share his findings in making biocontrol from traditional herbs to diminish the fusarium wilt disease attacks.

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Farmer hybridising previous knowledge and new techniques to develop novel innovations: Timor-Leste

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Agriculture production in Timor-Leste is dominated by 120,000 farming households on the edge of the cash economy. These family farms produce food for the household, and often a small surplus to sell. Government and international partners have worked with farming families to test, pilot and demonstrate a wide range of new techniques that can improve their production and food security.

This paper will follow the testing and adoption of three technologies that have been widely adopted by Timorese farming households. The three include variety selection, broadcasting mung beans and new varieties of sweet potato. In all three cases the external technologies were introduced into the community for testing and extension combined with local knowledge and then developed into new innovations. Reflecting on the process after successful adoption, we realised that on farm testing (and demonstrating), both the researcher with the farmers are co-developers of the novel innovations. The new innovation or technology can change/modified/adapted by the family to best suit the family's needs.

Recognising that farmers often add their knowledge to new techniques to produce novel innovations we have four recommendations for researchers working with farmers. These are 1) expect the farmers to adapt and change introduced techniques 2) allow farmers extra inputs and time to do their own experiments 3) visit the co-operating farmers after the testing/demonstration is finished to discuss and understand their response and changes and 4) recognise and promote the novel innovations as co-created.

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Hunger and thirst: a challenge for designer root systems

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Nutrients with low mobility (e.g., P) are increasingly stratified in topsoils, causing them to become spatially disjunct with water in all but the wettest years. Crop root system responses to this spatial separation will determine productivity and may be modified through selection of root traits via plant breeding. Using a lysimeter facility, we planted two wheat lines with contrasting seminal root angles (Narrow vs. Wide) but similar phenology into P-stratified topsoil with starter-P. Plants received one of three water regimes: Wet (profile maintained at ~80% soil water holding capacity [WHC]), Dry (topsoil allowed to dry after mid-tillering) or Rewet (same as Dry but topsoil returned to ~80% WHC). These regimes were crossed with one of four P treatments: Control (no additional P), P-Band (at ~25 cm depth), P-Layer (P dispersed through 10 cm soil layer centred at ~25 cm depth), or Mixed P (P dispersed throughout soil profile; only in Wet regime). Plant P uptake was greatest in Wet regime with Mixed P and lowest in Dry + Control. Dry and Rewet regimes limited access to stratified P, though rewetting improved responses to P-Band and P-Layer treatments. In Wet regime, P-Band and P-Layer had lower P uptake than Mixed P, showing that concentrated application of P cannot fully compensate for low soil P fertility. No major differences were observed between the wheat lines. Results indicate that agronomic factors that maximise soil water and P availability are critical for crop productivity, with variety selection based on root traits of lesser importance.

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Novel Propagation Technologies for Australian Macadamia

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Australia's macadamia industry is worth around A\$855M in 2021, with both global demand and production set to increase in the future. However, the expansion of the industry faces several hurdles, such as slow tree growth, resources and environmental costs of increasing tree supply, and the preservation of cultivar and germplasm resources in the face of climate change. While current industry-wide initiatives have enabled productivity improvements to meet increasing global demand, novel technologies that could help push production barriers would still be required to meet future demand and address climate uncertainties. This project is developing a novel high-throughput tissue culture-based propagation system for macadamia, and is critical for addressing limitations in macadamia tree production, aiming to minimize resources and the carbon footprint for propagation. This system requires innovative plant tissue culture techniques, optimized culture conditions, and novel media composition to enable high shoot multiplication capacity and large-scale propagation of multiple healthy plants from minimal plant material. It will address existing issues such as loss of shoot vigor, poor survivability, and rooting difficulty reported in previous attempts of macadamia tissue culture, while facilitating the study of underlying molecular mechanisms regulating root induction in woody plant species. This system is also being leveraged for cryopreservation of macadamia germplasm, for long-term preservation. At present two cultivars; Beaumont and MCT1, have been initiated into tissue culture, with shoot production and multiplication optimisation ongoing. Successful development and employment of this system in the industry will enhance the productivity and sustainability of the macadamia industry in Australia.

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Improving disease resistance of Australian tropical long grain rice

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One of the largest limitations to sustainable rice production in the tropics is disease. The currently available commercial varieties have largely been developed in and for the temperate south, and hence have produced variable results in the tropics, particularly in relation to disease susceptibility. In addition, international germplasm that may have tolerance to the disease do not meet the quality specifications that are necessary to meet the Australian domestic and international markets. However, robust quantitative trait loci and markers for the most common diseases, and their donors, are available. The focus of the pre-breeding program is to introgress and pyramid multiple sources of disease resistance into a soft-cooking long grain to incorporate into the tropical breeding program. The University of Queensland is an established pre-breeding hub for the Australian rice industry and will utilise marker-assisted selection for its initial assessment. Preliminary analysis of historical data sets has demonstrated a large amount of genotype by environment interaction within northern Australia, and with Gatton, presumably due to differences in disease pressures and seasons. In addition to the pre-breeding work to develop elite material, global germplasm will be utilised for incorporating biotic (and abiotic) stress resistance to future proof the Australian rice industry for pests that are not yet present in the country.

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Nutrient Management under Conservation Agriculture (CA) in Double Rice Cropping System

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Conservation Agriculture (CA) systems are based on enhancing soil health and productive capacity to sustainable production intensification. Nutrient management in CA must be endorsed within this framework. The experiment was initiated at Paba, Rajshahi, in Boro 2018-19 seasons with the objectives to determine the nutrient requirement of rice in Boro-Fallow-T. Aman cropping pattern, and to improved soil health under CA practices. Three cycle of the cropping pattern Boro-Fallow-T. Aman has been completed. Two crop establishment methods, Unpuddled (UPd) and Puddled (Pd) in main plot, two residue management practices, Rice Straw incorporation (RSi) and Rice Straw removed (RSr) in sub plot and four fertilizer doses as recommended fertilizer (RD) 100%, 125% of RD, 75% of RD, and 50% of RD in sub sub plot were assigned in split-split plot design with three replications. UPd cultivation of Boro rice required 25% additional fertilizer compared to recommended dose. But in T. Aman season, UPd rice cultivation required 100% recommended fertilizer for optimum yield while Pd rice required 75% of recommended fertilizer for optimum yield. RSi significantly increased the rice yield in both season. After harvest of the six season rice, soil samples were collected from the 0–30 cm soil depth. Among the crop establishment method, UPd had lower bulk density than Pd up to the 20 cm soil depth. The decrement was 1.4-2.1% over the Pd condition. The lower bulk density associated with better soil aggregation and porosity due to straw incorporation. The UPd condition had a greater soil organic carbon than the Pd condition up to 0-20cm soil depth. This study indicates the UPd sustained yields along with enhance soil health.

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Isolation and selection of indigenous bacteria capable of antagonizing *Erwinia* sp.

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Indigenous microorganisms (IMO) have great potential in agricultural uses since they have high ability in biodegradation, nitrogen fixation, phosphate solubilization, plant growth hormone production as well as bio-control. However, deeply scientific knowledge about IMO has been limited and should be elucidated. The aim of this study was to isolate and select bacteria in IMO having functions in biological giants *Erwinia* sp. causing soft rot disease on green onions. Biocontrol bacteria were isolated on the TSA agar for 2 days and biocontrol activity of isolates were evaluated on King's B agar after 6 day of incubation. The results illustrated that from 4 different indigenous microbial communities 13 isolates in total were able to against plant pathogenic *Erwinia* sp.. Quantitative tests showed that 4 selected isolates antagonized very strongly against pathogenic bacteria on onion plant *Erwinia* sp. at a density of 10^7 CFU/mL with Radius of sterile halo zone ranged from 17.8-20.8 mm and statistically significantly higher than those of pesticides which only 14.8-15.3 mm. In which two strains of selected bacteria labeled *Bacillus amyloliquefaciens* M6 and *Bacillus velezensis* M14 showed their most pronounced activity in biological control of two plant pathogenic bacteria *Erwinia* sp. The present work demonstrated that the indigenous microorganism communities have a great potential in biological control of phytopathogenic bacteria in soil and can be exploited in plant protection.

Keywords: *Antagonism, Bacillus, Biocontrol bacteria, Erwinia* sp., *Indigenous microorganisms*

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Potassium solubilizing bacteria improved the growth, yield of spinach and soil properties

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The aim of this study was to evaluate the efficacy of two potassium solubilizing bacteria (PSB) on the growth and yield of spinach (*Spinacia oleracea* L.) as well as some soil properties under greenhouse conditions. Spinach seeds were soaked in bacterial solution with a density of 10^8 cfu/mL for 24 h and grown for 45 days under the conditions of the soil applied 1 ton of rice straw/ha and 50% of the recommended potassium fertilizer. The results showed that inoculation of PSB strains helped to increase the growth and yield of spinach by 45.3-80.0%, also increased the total K content in spinach biomass as well as exchangeable K content in the soil, and simultaneously reduced up to 50% of the amount of inorganic potassium fertilizer. Thus, the two PSB strains, *Burkholderia vietnamiensis* L1.1 and *Staphylococcus hominis* T7.3, had a great potential to develop as microbial fertilizers to help increase growth and yield of crops, reduce chemical fertilizers, and implement friendly and sustainable agricultural production.

Keywords: *Burkholderia vietnamiensis*, spinach, potassium solubilizing bacteria, potassium, soil microorganisms, *Staphylococcus hominis*

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Silicate solubilizing bacteria enhanced salt tolerance capacity and rice yield

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Rice grain yield loss due to salinity intrusion impact has become more severe. Silicon can increase rice salt tolerance ability when cultivated in soil-affected soil. The study aimed to evaluate the efficacy of silicate solubilizing bacteria (SSB) on growth, and yield of MTL480 rice cultivar cultivated in salt-affected soil under the greenhouse condition in two consecutive crops. *Ochrobactrum ciceri* TCM_39 (TCM_39), *Microbacterium neimengense* MCM_15 (MCM_15), *Klebsiella aerogenes* LCT_01 (LCT_01), *Citrobacter freundii* RTTV_12 (RTTV_12), and *Olivibacter jilunii* PTST_30 (PTST_30) were isolated from various sources from bamboo, sugarcane, rice planted soils, earthworm intestine, and earthworm feces as bacterial sources in this study. Silicon concentration was measured by Molybdenum Blue Colorimetric method. The result showed that the treatments inoculated with SSB helped to enhance the salt tolerance capability and yield of rice plant considerably as compared to the non-inoculation treatments. Especially, the treatment inoculated a mixture of five SSBs, or TCM_39, or RTTV_12 had significantly higher levels of number of silicate solubilizing bacteria in soil, soluble silicate concentration in soil, silicate content in rice stem, K^+/Na^+ ratio in rice stem, and fill grain weight in pot as compared to other treatments including the positive control (100% NPK recommended). Moreover, soluble silicon concentration in soil had an excellent correlation with other soil parameters. Therefore, these five bacteria showed a high potential for bio-product production to protect rice when grown in the salt-affected soils.

Keywords: rice cultivation, salt-affected soil, salt tolerance ability, silicate, silicate solubilizing bacteria

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Early Withering of Enlarged Ovules in Pollinated Fruits of Bananas Suggest Abortion

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Sterility in edible bananas is as a result of a long history of anthropogenic-driven selection for sterile genotypes, since seed is not desirable in fruit pulp for human consumption. However, this poses a challenge to conventional genetic improvement by slowing breeding pipelines. In this study, we investigated whether pollen tubes reach all parts of the ovary, the position of fertilized ovule development in fruits, and potential seed set in selected banana genotypes. We selected four cultivars of East African Highland Cooking bananas (EAHBs), a Matooke hybrid '222K-1', improved diploid '2905', and wild bananas 'Zebrina (G.F.)' and 'Calcutta 4'. There was evidence of pollen tubes in the distal, mid and proximal sections of the fruit, irrespective of hand position and genotype. Fertilization, as indicated by an increase in ovule size, happened along the entire length of the fruit but complete development was biased at the distal end in some genotypes. There were some differences in ovule fertilization rates between hands, with distal hands having more ovules and higher ovule fertilization rates. Ovule fertilization happens in bananas but the vast majority aborts, especially at the proximal end of the ovary. Ovule fertilization rates are generally much lower than available ovules.

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Glucose performs best for germination of banana pollen

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Poor stigma receptivity is one of the limitations to seed set in East African Highland Bananas (EAHBs) that constrains their improvement through conventional breeding. This study aimed at identifying a suitable pollen germination media (PGM) for faster germination of banana pollen both *in vitro* and *in vivo*. PGM was prepared by dissolving 0.01 g H₃BO₃, 0.25 g MgSO₄·7H₂O, 0.25 g KNO₃ and 0.4 g Ca(NO₃)₂ in 1 L along with different sugars. Sucrose, glucose, fructose, glucose + fructose, and glucose + fructose + sucrose at six concentration levels of 10, 30, 50, 100, 150 and 200 g L⁻¹ were tested. Pollen from Calcutta 4 and TMB2x8075-7 diploid bananas was dusted on a cover slip and slowly lowered over four drops of PGM on a glass slide. The set up was incubated in a humid chamber for 3 h and germinated pollen counted using a light microscope at X40 magnification. Results revealed that glucose at 10 and 30 g L⁻¹ concentration performed best with the latter having the higher pollen germination percentage. Results from comparison of 30 g L⁻¹ glucose PGM with diluted banana nectar from Tereza and TMB2x8075-7 showed that 30 g L⁻¹ glucose PGM generated highest pollen germination. It is suggested that glucose being a monosaccharide is a more readily available energy source for pollen. When 30 g L⁻¹ glucose PGM was applied on stigmas after pollination, stigma receptivity was enhanced.

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Seed set in bananas depends on weather before, during, and after pollination

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Seed set in banana is influenced by weather yet the key weather attributes and the critical period of influence are unknown. We therefore investigated influence of weather during floral development for a better perspective of seed set increase. Three East African Highland Cooking bananas (EAHBs) were pollinated with pollen fertile wild banana 'Calcutta 4'. At full maturity, bunches were harvested, ripened, and seeds extracted from fruit pulp. Pearson's correlation analysis was then conducted between seed set per 100 fruits per bunch and weather attributes at 15 day intervals from 105 days before pollination (DBP) to 120 days after pollination (DAP). Seed set was positively correlated with average temperature ($P < 0.05 - P < 0.001$, $r = 0.196 - 0.487$), and negatively correlated relative humidity (RH) ($P < 0.05 - P < 0.001$, $r = -0.158 - -0.438$) between 75 DBP and the time of pollination. After pollination, average temperature was negatively correlated with seed set in 'Mshale' and 'Nshonowa' from 45 - 120 DAP ($P < 0.05 - P < 0.001$, $r = -0.213 - -0.340$). Correlation coefficients were highest at 15 DBP for 'Mshale' and 'Nshonowa' whereas for 'Enzirabahima', the highest were at the time of pollination. Maximum temperature as revealed by principle component analysis at the time of pollination should be the main focus for seed set increase.

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Seed set patterns in bananas show asymmetric distribution in bunches and fruits

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Low female fertility in bananas is the biggest hurdle for banana breeding. The aim of this study was to determine seed set patterns in East African Highland Cooking bananas (EAHBs) to inform future decisions on a more targeted approach of increasing seed set and subsequently banana breeding efficiency. Matooke (AAA) and Mchare (AA) bananas are genetically distinct but belong to the same genetic complex, referred to as EAHBs. Seed set patterns in “Enzirabahima” (AAA), “Mshale” (AA), and “Nshonowa” (AA), all with residual fertility, were examined after hand pollination with a highly male fertile wild banana “Calcutta 4” (AA). Seed set in “Enzirabahima” is predominant in distal hands. There is a gradual increase in seed set from proximal to distal hands with a slight drop in the last hand. There is also a drop in seed set per 100 fruits per hand from small to larger bunches. However, larger bunches have a higher pollination success compared to smaller bunches. They therefore set more seed on 100 fruits per hand and per bunch basis, if bunches without seed are accounted for. Pollination success rate increases from smaller to larger bunches of EAHBs. Seed set is biased toward the distal third part of fruits. Seed set bias in the distal hands and distal end of fruits suggests a systematic mechanism rather than a random occurrence. It is expected that this information will provide a foundation for increased crossbreeding efficiency in bananas.

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Integrated Pest Management in Australian Native Rice Trial.

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In Australian native rice (*Oryza* spp.) nursery trials pests can cause poor growth of plants, unhealthy inflorescences, and empty seeds. Pests found in native rice plants in Darwin, Australia included melon aphids, white flies, grasshoppers, and ginger ants. Pests increased at the beginning of the wet season when rainfall commenced, and temperatures were rising. Aphids resulted in empty seeds in many inflorescences and whiteflies caused damage. Our aim was to manage these pests without causing harm to the plants or environment. Whiteflies were found under the leaves of rice plants and aphids were found all over the inflorescences. Integrated pest management included physical, chemical, and biological control. Physical removal to control whiteflies included wiping leaves with paper towel moistened with 70% ethanol. Chemical control used twice weekly spraying of pyrethrum. However, two to three days after spraying with pyrethrum was stopped, aphids were found all over the inflorescences again. For biological control, lacewing larva and lady beetle adults and larva were released in trial areas. Replacing overhead sprinklers with drippers also helped reduce aphids. Pests, diseases, and disorders found in rice plants were recorded and we found lady beetles were effective at clearing all the aphids within a very short time without causing damage to the plants. This integrated pest management approach (chemical, physical and biological control) managed these pests in the nursery trial. Biological control was found most sustainable and effective.

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Acacia seed positively impacted the structural and technological properties of beef emulsions

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Acacia seed (AS), commonly known as wattle seed, is a native Australian legume rich in protein and dietary fiber, with distinctive oil absorption and emulsifying properties. This study investigated the structural and technological properties of beef emulsion systems prepared with different amounts (2, 4 and 6%) of two processed AS flours (roasted and protein concentrates) and 6% soy protein isolates (SPI). Flour types and amounts significantly affected the protein contents of cooked beef emulsions, with the highest contents found in emulsions prepared with 2 and 4% AS flours and 6% SPI. Emulsion stability, hardness and chewiness were only affected by flour types with beef emulsions prepared with AS roasted flour (ASRo) having the lowest values, while AS protein concentrates (ASPC) and SPI were comparable with the control (no added plant proteins). Addition of ASPC at 2, 4 and 6% did not affect the cooking loss of the beef emulsions as compared with the control and SPI, which was in contrast to the ASRo beef emulsions showing a greater cooking loss. Redness values of cooked beef emulsions prepared with ASRo decreased as flour levels increased. However, the redness values were not affected by addition of ASPC, irrespective of the flour levels and SPI. Furthermore, similar microstructures were observed in cooked beef emulsions prepared with ASPC and the control. In conclusion, ASPC may be used as functional ingredient to prepare beef emulsions with favorable structural and technological properties.

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Orange capsicums: can nutritional benefits be gauged by skin colour?

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Orange capsicums are known for their high concentration of zeaxanthin. Zeaxanthin, a carotenoid, is also found in the macular region of the eye and plays a vital role in reducing the incidence of age-related macular degeneration. Although orange capsicums have been identified as an excellent dietary source of zeaxanthin, very little is known about the distribution of zeaxanthin within the pericarp. To understand the difference in concentration of zeaxanthin within the different layers of the pericarp, seven orange capsicum varieties were analysed. Fruit pericarps were manually cut into a 70:30 ratio of inner to the outer pericarp. Carotenoids were extracted from these tissues using dichloromethane (DCM): hexane (30:70) extraction solvent. The extracted carotenoid concentration was analysed using absorbance spectroscopy at 450 nm, using zeaxanthin as a standard. It was observed that for all varieties, the outer pericarp accounted for most of the carotenoids in pericarp tissue. Moreover, it was also observed that varieties that had higher concentrations of zeaxanthin in outer pericarps were observed to have higher concentrations of zeaxanthin in their inner pericarps. However, there was an exception to this observation in one variety, where a high concentration of carotenoid in the outer pericarp was not linked to a high concentration of carotenoid in the inner pericarp. Thus, it can be concluded that skin colour can be an indicator of zeaxanthin concentration in orange capsicums, as the outer pericarp is where most carotenoids are located.

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Assessing The Safety of Native Australian Infusions: Lemon Myrtle and Jilungin

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Lemon Myrtle (LM) (*Backhousia citriodora*) and Jilungin (JG) (*Terminalia canescens*) are important native Australian Bush food plants. Both plants have been widely consumed by the Aboriginal community as traditional infusions and their use is emerging in the wider community. The current study was carried out to evaluate the safety of LM and JG infusions in the *in vitro* intestinal (Caco2 and HT29-MTX-E12) and hepatic (Hep G2) cell lines using Cyquant™ NF Cell proliferation and CellTiter-Glo® Luminescent Cell Viability Assays. In addition, the cell viability observed in the infusion samples were compared with that in the plant extracts (70% ethanol and 80% methanol for LM and JG, respectively). The results showed that the cell viability was decreased in a concentration-dependent manner. The extracts of both LM and JG were more active than the corresponding infusions in reducing cell viability observed in both assays. The IC₅₀ (half maximal inhibitory concentration) values of JG infusion were higher than that of LM infusion, indicating that more JG infusion is required to pronounce the same effect on the studied cell lines compared to LM infusion. HT29-MTX-E12 cell line was the most affected cell line among the three tested cell lines observed in both assays. Whereas Caco2 and Hep G2 cell lines were found to be the least affected cell lines in CellTiter-Glo® Luminescent Cell Viability Assay and Cyquant™ NF Cell proliferation assay, respectively. The findings from this study suggest that JG and LM have immense potentials to be used as alternatives to commercial herbal infusions with promising safety profile.

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Peat based bioformulation of *Pseudomonas* spp. for management of rice sheath blight

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This study was conducted to formulate phylloplane *Pseudomonas* bacterial strain *P. fluorescens* and *P. asplenii* and to determine their efficacy on sheath blight suppression as well as on yield components of rice. These strains when preserved in peat at 4°C was found to be more suitable and retained high viable cells of individuals and consortiums as well. Evaluation of these strains alone or in consortium for suppression of sheath blight disease revealed that the consortium and *P. fluorescens* alone significantly reduced the area under disease progress curve (AUDPC) compare to untreated control. Percent reduction of AUDPC was 32.79, 32.58 and 21.19 for consortium *P. fluorescens* and *P. asplenii*, respectively. Strain mixture also significantly reduced disease progress rate (0.011unit/day). In addition to disease suppression, strain mixture enhanced plant height, percentage of effective tiller, percentage of fertile grain per plant. Effects of all the treatments on mean flag leaf area, total number of tiller and number of effective tiller were insignificant. However, the weight of 100-grain was significantly (1.65g) highest in strain mixture applied plants. This study suggested that indigenous *Pseudomonas* bacteria isolated from rice plant can be preserved in peat at 4°C until 6 months in storage and used as efficient biocontrol agents for sheath blight management.

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Generation of CRISPR/Cas9 mediated rice lines targeted pest resistance and aroma traits

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Clustered regularly interspaced short palindromic repeats (CRISPR)-associated protein (Cas) (CRISPR/Cas) is a breakthrough tool allowing precise and specific genome editing that are stably inherited across the following generations. Since the CRISPR/Cas genome editing was first implemented in 2013, has become the most common and cost-effective breeding tool for crop improvement, economic traits such as scent, color, medicinal, nutritional and economic value, as well resilience toward challenging and unpredictable abiotic and biotic stresses. In this study, first time in Bangladesh, we have employed CRISPR/Cas9 tool to create novel alleles of *CYP71A1* and *BADH2* in elite rice varieties BRRI dhan87, BRRI dhan89 and BRRI dhan92. The recombinant vectors VK005-01 having Cas9/*CYP71A1* or *BADH2* sgRNA were transformed into *Agrobacterium tumefaciens* LBA4404 strain by freeze-thaw method. PCR analysis of putative transformants using primers targeting the flanking regions of sgRNA identified 24.55% potential multi-allelic mutations in T₀ generation. Sequence analysis of these T₀ lines identified 6 different types of mutations located within sgRNA regions. Stable transmission of CRISPR/Cas9-mediated *CYP71A1* and *BADH2* genes editing without the transferred DNA was confirmed by segregation in the T₁ generation. With respect to many investigated agronomic traits including pollen development, there was no significant difference between homozygous mutants and non-transgenic control plants under greenhouse growth conditions. This study demonstrated the use of CRISPR/Cas9 in creating novel alleles of *CYP71A1* and *OsBADH2* to insert insect resistance and aroma trait into any non-aromatic high yielding rice varieties. It also indicates that the CRISPR/Cas9-mediated mutation can be successfully employed for non-transgenic crop improvements.

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Landscape heterogeneity influences natural pest control at multiple spatial scales in agroecosystems

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Agricultural landscapes are constantly changing as farmers adopt new production practices and respond to changing environmental conditions. Some of these changes alter landscape heterogeneity with potential effects on biodiversity and ecosystem services. Impact of landscape change on natural enemies (NE) of pests and pest suppression in rice agroecosystems is poorly understood. Here, we investigated the effect of landscape composition and configuration on NE, herbivore suppression and rice yield at multiple spatial scales in two rice producing regions of Bangladesh. Excluding predators significantly increased brown planthopper abundance in caged plots and reduced rice yield in both regions. Landscape heterogeneity effects on pest abundance were observed at all scales and were most pronounced at the 1000 m scale for all NE combined and at smaller spatial scales for ladybird beetles (500 m), and spiders (200 m) individually. Ladybird beetles were positively influenced by rainfall, roads, and fallow land, while spiders were strongly influenced by rice phenology. The proportion of water-bodies and specially of natural habitat had low weight in statistical models but, high proportion of natural habitat together with fallow land was associated with increased abundances of NE. Natural enemies also responded to landscape configuration and declined with increasing patch cohesion and aggregation, while increasing with increasing edge density suggesting that finer grained rice landscapes are better suited to pest suppression. These results suggest that promoting fallow lands and edges between growing rice patches along with decreasing the prophylactic use of insecticides can lead to more sustainable insect pest management in rice.

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A rapid crush-side test to confirm vaccination and detect BRD-associated pathogens.

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The Australian red meat industry contributes \$28.5 billion to the annual economy, supports 80,000 businesses, and employs 405,000 people throughout the supply chain. Global competition, consumer expectations, climate change, geopolitics, and bovine diseases pose significant challenges to the profitability and sustainability of the industry. Bovine Respiratory Disease (BRD) is a multifactorial disease and the most significant disease affecting feedlot cattle. Bovine herpesvirus 1.2b (BoHV-1.2b) plays a significant role in the development of BRD. The virus can cause Infectious Bovine Rhinotracheitis (a highly contagious respiratory disease) and establish latency in the sensory neural ganglia, presenting a significant barrier to eradication. Sporadic viral reactivation may occur as a result of reduced immune function due to stress. BRD risk reduction strategies include cattle management, feed supplements, and vaccination with Rhinogard at feedlot induction. Rhinogard is an attenuated strain of BoHV-1.2b with a non-functional thymidine kinase gene. The vaccine has been extensively used in Australia's feedlot cattle. Currently, there are no methods to enable rapid differentiation of field and vaccine strains of BoHV-1. Our novel crush-side test, based on the CRISPR system, will be easy to use, rapid, cost-effective, and sensitive enough to differentiate between Rhinogard and wild-type BoHV strains. In addition, the future development of our test will enable it to be multiplexed to detect other BRD-associated pathogens. The test will help feedlot operators manage BRD outbreaks more efficiently, confirm vaccination status, and monitor circulating pathogens. Together, they will help improve the profitability and sustainability of the feedlot industry through more effective BRD management.

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Formulation and characterization of milk gel-polyol food simulant for 3D printing

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Increased flexibility and agility are needed to meet the rising demand for customized food alternatives, particularly in light of the expanding market for personalized food options. Traditional mass manufacturing techniques are unable to provide this level of specificity; however, the developing technology of 3D food printing (3DFP) may provide the solution. This study investigates the applicability of low fat heat acid coagulated milk (HACM) gels enriched with functional protein and low calorie polyol composition as a potential bioink in 3DFP. The bioink was prepared by incorporating different concentration of whey protein isolate (WPI) and maltitol (MT) in HACM semisolid and then its rheological, microstructural, and textural properties were analyzed. The results illustrated that at the same level of total solids of the formulations, an increase in the concentration of MT above 2% (w/w) decreased the yield stress (σ) from 1309 ± 0.40 to 938 ± 0.45 Pa, and the recovery index from 95.4 to 77.17% while the increased concentration of WPI above 2% enhanced the recovery index and storage (G') and loss (G'') moduli of the formulations significantly ($p < 0.05$). The concentration of WPI:MT=4:2 in the gel resulted in the best dimensional stability and shape retention of the printed constructs. The formulation and characterization methodology provided in this paper establishes a framework for quantifying and forecasting printability for 3DFP of complex food compositions.

Keywords: Heat acid coagulated milk semisolids; Additive manufacturing; Bio-polymeric ink; Rheology; Food customization

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PBRcowpeaXTRA, a long-term solution against the cowpea pod borer in West Africa

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Cowpea (*Vigna unguiculata*) is a vital staple crop in West Africa where it represents the principal source of protein. Nigeria, the largest producer, still needs to import around 500,000 tonnes per year to meet domestic demand, and this is because insects can reduce yields by up to 90%. Because of that, a genetically engineered pod borer resistant (PBR) cowpea carrying the *cry1Ab* gene was developed against the major pre-harvest pest, the lepidopteran *Maruca vitrata*. This Bt cowpea variety provides full protection against the pod borer and has been successfully deployed to farmers in Nigeria, where it is currently being grown. Our team is now working on the development of a second generation of PBR cowpea carrying the *cry1Ab* and the *cry2Ab* genes. This new variety, that will be known as PBRcowpeaXTRA, will help guarantee long-lasting protection against the pod borer. An elite *cry2Ab* transgenic line has been already selected and successfully tested in Nigeria, Ghana and Burkina Faso. This transgenic line is currently going through regulatory approval and breeders from the partner organizations in Africa are already crossing this new line with the original PBR cowpea. Simultaneously we are also attempting the combination of both cry genes in a molecular stack to facilitate breeding operations. This biotech solution against one of the major cowpea pests will bring large economic and health benefits to farmers and consumers.

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Kakadu plum bioactivity against microorganisms and oxidative reactions in raw beef patties.

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This study explored the effects of dried Kakadu plum powder (KPP) as natural preservative in raw beef hamburger patties. The hamburger patties were treated with 0 additive (negative control), 450 ppm of Sodium metabisulphite, and KPP (0.2%, 0.4%, 0.6%, 0.8%) and stored at $4 \pm 1^\circ\text{C}$ for 20 days under modified atmosphere packaging (80% O₂, 20% CO₂). Results show that the Thiobarbituric acid reactive substances (TBARS) were significantly lower throughout the storage period for KPP treated samples compared to both the negative control and Sodium metabisulphite treated samples. The incorporation of KPP in hamburger patties at level of 0.2% and 0.4% was efficient in delaying the growth of food spoilage microorganisms compared to the negative control, however, Sodium metabisulphite had higher antimicrobial activities. At the end of the storage period on day 20, no difference was observed between the samples in terms of L*, a*, b*, Hue angle and Chroma colour ordinates. A correlation ($r = -0.66$) was noted between the addition of KPP in the mix (treatments) and TBARS, but there was no correlation ($r = -0.006$) between the treatments and microbial growths. This study demonstrated that Kakadu plum could be used as natural food preservative for shelf-life extension of raw hamburger patties

Key words: Natural antioxidant, antimicrobial, Beef patties, Kakadu plum, bioactive compounds

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Exogenous application of modified forms of dsRNA enhances gene silencing in plants

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Exogenous application of double-stranded RNA (dsRNA) is a promising strategy for crop protection against pathogens, and consequently for securing global food production. This strategy is based on RNA interference (RNAi), which is a natural defence mechanism in plants, animals and fungi. Previous research has shown that ~10% of plant messenger RNAs (mRNAs) harbour sequences in their 3' region that fold to adopt transfer RNA-like structures (TLSs), a folding structure that confers graft-transmissibility to such mRNAs. Similarly, the methylation of cytosine residues in mRNAs has also been shown to facilitate graft-transmissibility in plants. Here, we show that fusion of a TLS to the 3' termini, or the incorporation of methylated cytosine residues into long dsRNAs significantly increased the capacity of the topically applied dsRNAs to induce the silencing of the targeted reporter genes in *Arabidopsis*. We have also compared small interfering RNA (siRNA), long dsRNAs, and artificial microRNA precursors (pre-amRNAs) with and without a TLS fused to their 3' ends for their ability to induce silencing of reporter genes in *Arabidopsis*. This analysis revealed that post topical application, siRNA or the pre-amRNA with a 3' TLS fusion induced the highest levels of reporter gene silencing. Our results will be discussed in the context of using these RNA sequence and structural modifications when designing topically applied dsRNAs that offer the most effective protection against plant pathogens.

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Impact of growing region on the sugar content of *Terminalia ferdinandiana* fruit

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Natural sugars in fruits and vegetables can have a significant impact on the quality, sensory attributes and consumer perception. However, the sugar content and composition (number and ratio of individual sugars) in fruits and vegetables can vary considerably, especially when wild-harvested. Region, climate, soil quality, bushfires and other environmental factors can have a significant impact on the sugar content and composition. Wild-harvested *Terminalia ferdinandiana*, commonly known as Kakadu Plum (KP), an important native Australian fruit, was investigated in the present study. KP fruit samples from Western Australia (WA) and the Northern Territory (NT) were analysed for individual sugars by UHPLC-MS/MS and antioxidant capacity (total phenolic content (TPC) and DPPH radical scavenging capacity assay). KP fruit collected in WA contained significantly ($p < 0.05$) more fructose, glucose and sucrose than the samples collected in NT (7.3 g/100g DW vs. 3.0 g/100 g DW for fructose, 7.0 g/100 g DW vs. 2.0 g/100 g DW for glucose, and 2.8 g/100g DW vs. 0.2 g/100 g DW for sucrose). However, TPC and DPPH radical scavenging capacity were lower in the WA KP fruits compared to the NT samples (136.5 mg gallic acid equivalents/g DW vs. 196 mg gallic acid equivalents/g DW for TPC and 1219.0 μmol Trolox equivalents/g DW vs. 2253 μmol Trolox equivalents/g DW for DPPH). Further studies are warranted to determine the impact of the higher sugar content in the WA KP samples on fruit quality, shelf-life, sensory attributes and food applications.

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Avian influenza A/H5 environmental contamination at live bird markets in Dhaka, Bangladesh

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Background: Avian influenza virus (AIV) A/H5 persistence in the environment of live bird markets (LBMs) is primarily related to poor market-level biosecurity practices in Bangladesh.

Objective: This study aimed to characterize the differences in the proportion of AI(H5) environmental contamination in LBMs of two local government areas of the Dhaka metropolitan. We further quantified factors associated with the probability of market-level AIV A/H5 environmental contamination risk and work-zone specific (i.e., arrival, slaughtering and processing, and sales areas) contamination patterns.

Materials and Methods: This study investigated 104 LBMs of Dhaka from January-March 2016 by univariable Fisher's exact test to identify the significance differences by location of Dhaka markets. We performed Bernoulli generalized linear models and multinomial logistic regression models to quantify factors associated with the probability of market-level AI(H5) environmental contamination and work-zone specific environmental contamination patterns, respectively.

Results: LBMs located in Dhaka North City Corporation are more vulnerable to AIV A/H5 environmental contamination than Dhaka South City Corporation markets. The probability of AIV A/H5 environmental contamination is equally likely in all market work zones investigated. Results showed higher environmental contamination in LBMs that have both wholesalers and retailers compared with retailer-only markets and in March compared with January.

Conclusion: The findings provide policy-relevant insights into AIV A/H5 environmental contamination risk areas in the Dhaka metropolitan, which would be appropriate in designing a market-level biosecurity intervention to minimize the human AIV A/H5 infection risk linked with LBMs.

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Effects of variety, early harvest and germination on texture of brown rice

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Brown rice is superior to white rice in nutritional value and in prevention of chronic diseases. However, it is not the preference of consumers, and the relative consumption of brown rice is limited due to several factors including chewiness and perceived hard texture after cooking. While both early harvested brown rice and germinated brown rice have been shown to contain superior nutritional components, there is limited knowledge on textural properties of these types of brown rice relative to standard brown rice, and how varieties may affect such properties. Thus, the present study examined the effect of variety, early harvest and germination on those properties of 8 rice varieties with contrasting amylose content and known texture in terms of milled rice. Early harvest and germination decreased pasting viscosities and cooked grain hardness. However, their effect on the characteristics of flour and whole grains differed, in which germination had greater effect on pasting properties, while early harvest on texture of cooked grains. Softer texture of brown rice, about 32% lower could be achieved by germination, and 46% by harvesting early. There was a good relationship between pasting characteristics particularly setback and hardness among different varieties in brown rice, germinated brown rice and also in early harvest brown rice. This is the first time the comparison of texture between the 3 brown rice types has been reported. The results also provide new options for selection of desired characteristics for food processing and brown rice consumption. Future study should include sensory test of different brown rice types and white rice.

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Identification of plant host resistance to *Fusarium* wilt in wild banana relatives.

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The global banana production is currently being threatened by the tropical race 4 (TR4) strain of the soil-borne pathogen *Fusarium oxysporum* f. sp. *ubense* (*Foc*). Since the early 1990s, *Foc*-TR4 has rapidly spread to most regions in South East Asia, including the Northern Territory of Australia, where it decimated the entire banana production. More recently it has been found in northern regions of Queensland, on a few farms within the primary site for banana production in Australia. Host genetic resistance may provide a durable solution to the TR4 problem. To this end, UQ, and its collaborative partners, are using genetic resources and tools to characterise *Musa accuminata* subsp. *malaccensis*, a fertile (seed setting) wild relative of the commercial varieties, with the aim to identify gene(s) conferring resistance to *Foc*-TR4. Resistance genes identified from this project can be introduced into susceptible varieties by breeding or transformation. Molecular markers linked to the resistance locus can also be used to facilitate marker-assisted-selection in breeding programs. By adopting these methodologies and tools, we hope to accelerate the efforts to identify and introgress durable *Foc* TR4 resistance genes into commercial cultivars. This will in turn allow the deployment of resistance cultivars into *Foc* TR4 affected regions in Australia and other countries around the world.

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Quality changes of Burdekin plums during storage

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Pleiogynium timoriense, best known as Burdekin plum, is one of Australia's native fruits. Within Australia, it is mainly distributed from Cape York peninsular to southeast Queensland. It belongs to the family of Anacardiaceae, which includes several economically important fruits and seeds such as mango, cashew and pistachio. The fruits were found to exert strong antioxidant capacity as well as other biological activities such as anticancer and anti-inflammatory.

The fruits are dark purple, shaped like plums with a thin layer of flesh and large stone. Fruits are hard and astringent when just harvested. Indigenous Australians used to bury them in the ground for a few days to make them more palatable. However, only limited data are available on the nutritional and sensory quality of Burdekin plum grown in Australia as well as its changes during storage. Therefore, in this study, the variation in quality of Burdekin plums including titratable acidity, total soluble solids, weight, color, firmness, vitamin C, major phenolic compounds and antioxidant capacity was evaluated during one week storage at ambient condition as well as its sensory quality at the end of storage.

The results showed that fruits varied in their physicochemical and sensory properties regardless of the locations harvested. Fruits turned softer, sweeter, less astringent after storage while its vitamin C content, total phenolic content and ferric reducing capacity was reduced by day seven. Therefore, room temperature storage for a week can improve the palatability of Burdekin plums while compromise some of the nutritional benefits.

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OneWelfare: a skeleton key to new, more productive narratives about animal agriculture?

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Stakeholdership in discussions of production animal welfare rightfully belongs to all members of society. The topic is a foundational element within ongoing debate of sustained social licence to farm, but how might a richer understanding of interrelated human, animal and environmental wellness influence perspectives which inform this debate? OneWelfare, seeded by the OneHealth discipline, redirects the lens of scientific inquiry from the human-animal-environment physiological health nexus to explore and characterise interdependent wellness. For example, where OneHealth measures vitality statistics, OneWelfare has typically inquired about antagonistic effects to human, animal and environmental wellness in association with interactions between. At its origin in Canada in 2010, the OneWelfare initiative sought to address poor animal and environmental outcomes identified to be in association with poor farmer wellbeing. However, herein we report early findings from a social research pilot study performed at The University of Queensland, which employed a semi-structured, interview protocol to evaluate how relationships and interactions between humans, animals and nature was reported to influence the health and wellbeing of each. Characterizable, sustained, reciprocal, protective and enhancing effects for human, animal and environmental wellness were reported, and emerged as a common theme within the interview data. These findings may support new initiatives to explore positive wellness effects more purposefully, and across the living landscape of agriculture. The emerging narrative is one not common within social licence to farm debates, but perhaps should be.

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Understanding women's role managing mango fruit-flies and banana fusarium wilt in SEA

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Women play an essential role in implementing plant pest and disease management; however, their roles are often not well-recognised in agricultural research and development projects. Consequently, their needs are often not reflected in the design and implementation of Integrated Pest Management (IPM) and Area Wide Management (AWM) programmes. Yet, the long-term success of such projects maybe heavily dependent on the support of women. Additionally, their involvement as key leaders and decision-makers in pest management may help improve agricultural output and productivity.

Thus, the Women as IPM leaders programme (cross-cutting component of the ASEAN Action Plan on Fall Armyworm Control) seeks to empower women as leaders in IPM across Southeast Asia (SEA). As a part of this programme, two gender projects will be undertaken in the coming months as part of a variation of the ACIAR projects, "*Development of AWM approaches for fruit-flies in mango for Indonesia, Philippines, Australia and Asia-Pacific*" and "*An IPM response to the spread of Fusarium-Wilt of banana in SEA*".

Both gender projects aim to understand the role of women in managing plant pest and disease and assess the impact of any proposed management and biosecurity strategies for improved biosecurity. Both projects will be achieved through focus group discussions (FGDs) and interviews with farming communities and value chain actors to help describe current gendered roles and implications for awareness and uptake of fruit-fly and Panama disease IPM and AWM practices respectively across households. Implications for women in the establishment of IPM and AWM programmes will be described.

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Colletotrichum cross-infection studies for anthracnose

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The aim of this study was to determine the potential of *C. asianum* from mango to infect other fruit and vegetables commonly grown in Fiji, specifically chilli, papaya and banana. And different species of *Colletotrichum* obtained from these three hosts were assessed for their ability to cause anthracnose in mango.

To reduce levels of natural infection, mature colour-break papaya fruits cultivar 'Fiji Red' were hot water treated at 54°C for 4 minutes before air drying overnight. Cavendish banana fruits that not received any fungicide application were harvested with ¼ of skin still green and kept for 2 days at room temperature. Green mature mangoes were hot water treated at 55°C for 5 minutes and left to air-dry before inoculation while 'Bird's eye' mature green were surface sterilized in 1% (a.i.) sodium hypochlorite solution for 5 min then thoroughly washed air-dried before inoculation. Inoculation of fruits were based on both the "wound/drop" and "non-wound/drop" methods; Inoculated fruits were incubated at high humidity before being transferred to cardboard ripening boxes.

Cross infection studies showed that a representative isolate of *C. asianum* isolate from mango was highly pathogenic on unwounded, detached mango fruits, but was only able to infect hosts other than mango (i.e. banana and papaya) when the skin of fruit was wounded prior to inoculation, suggesting a degree of host specificity.

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Folate vitamers of the native Australian green plum (*Buchanania obovata*)

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The native Australian green plum grows on the tree *Buchanania obovata* in the Northern Territory and Western Australia. This small green fruit has been discovered as a promising dietary source of folate. The purpose of this study was to confirm the high level of folate in green plums by analysing a larger number of ripe fruit samples from multiple locations and harvests. This study analysed green plums for the folate vitamers tetrahydrofolate (H₄folate), 5-methyltetrahydrofolate (5-CH₃-H₄folate), 5-formyltetrahydrofolate (5-CHO-H₄folate), 10-formylfolic acid (10-CHO-PteGlu) and pteroylmonoglutamic acid/folic acid (PteGlu) using a stable isotope dilution assay on a liquid chromatograph mass spectrometer (LC-MS). There is some variation in vitamer amounts between fruit from different locations and sets of trees, however, all ripe green plums tested are considered good dietary folate sources, containing between 82.4 ± 5.5 and 149.4 ± 10.7 µg/100g FW as pteroylmonoglutamic acid equivalents. The red-coloured green plums are discovered as being even higher in folate than the green-coloured fruit. This study confirms green plums are a good dietary source of folate and especially of 5-CH₃-H₄folate and that the ripe fruit is high in folate from a number of locations.

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Effect-of-dietary-supplementation with live microalgae (*Chlorella vulgaris*) on performance and carcass-characteristics of white-dorper-lambs

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Omega-3 long chain polyunsaturated fatty acids (n-3 LC PUFA), eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA) have been shown to reduce coronary heart disease (CHD) in humans. Unlike fish, humans do not have the ability to synthesize these health claimable PUFA due to lack of specialize enzymes (delta 12 and delta 15 desaturase) and therefore, must obtain these essential fatty acids (EFA) in the diet. Dietary supplementation with dried microalgae had been shown to enhance the levels of n-3 LC PUFA in ruminant meat; however, there is lack of research on the supplementation with live microalgae (genus: *Chlorella*) in lamb diets. This study evaluated the effect of dietary supplementation with live *Chlorella vulgaris* (CHV; Genesis Co. Pty Ltd.) on the performance and carcass characteristics of lambs over 100 days. Forty-five, 4 month old white dorper lambs with an average live weight of 31.46 kg were randomly allocated into three groups (n-15) in a completely randomized design (CRD). The basal diet comprised barley hay and feedlot pellets (49:61%, respectively) fed at 3.5% body weight. Treatments were: 1) control, no CHV supplementation; 2) 0.5% DM CHV supplementation; and 3) 1% DM CHV supplementation. All lambs had unlimited access to fresh and clean drinking water. We hypothesize that supplementation of lamb feedlot diets with live CHV would enhance the growth performance and carcass characteristics compared to the control diet.

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Digestibility and nitrogen retention in supplemented crossbred pre-parturient Boer does

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Dry tropical grass pastures typically have a low crude protein (CP) concentration that can limit diet digestibility and microbial protein supply to the small intestine resulting in low rates of milk production in does and low rates of liveweight gain in their progeny. We measured whole tract apparent dry matter digestibility (DMD) and nitrogen retention (NR) in pre-parturient Boer does fed Rhodes grass hay offered *ad libitum* (Cont.) or supplemented with urea (Urea), cotton seed meal (CSM) or both urea and cotton seed meal (Urea+CSM). Treatments (Urea, Urea+CSM and CSM) were formulated to be iso-nitrogenous and to provide sufficient CP to meet requirements but varied in the relative amounts rumen degradable protein (RDP) as non-protein nitrogen (NPN) and true protein (TP), and undegraded dietary protein (UDP). All diets also contained a mineral supplement (Rumevite^o Fermafos). Dietary CP concentration for the Cont. was 107 g/kg DM and 143 g/kg DM for the supplemented groups. Relative amounts of RDP to UDP (g/kg DM) were 70 and 37 for Cont., 105 and 37 for Urea, 100 and 43 for CSM+Urea and 94 and 49 for CSM. The CSM+Urea treatment significantly ($P < 0.05$) increased DMD (612, 584, 576 and 579 g/kg DM; CSM+Urea, CSM, Urea, Cont., respectively) and NR (6.05, 1.61, 1.74, -3.12 g/day; CSM+Urea, CSM, Urea, Cont., respectively) when compared with other treatments. Average daily gain of suckling kids in two week after birth followed the similar order of treatments 233, 189, 186 and 138 g/d, respectively. We concluded that a supplement that increased the concentration of RDP in the diet using a combination of true protein and NPN was most effective at optimizing NR and DMD.

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Establishment of Progardes® Desmanthus

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Progardes® Desmanthus is a pasture legume blend of selected JCU cultivars for neutral to alkaline clay soils in semiarid subtropical/tropical regions. Project CRC P 58599 investigated blade ploughing and herbicide methodologies for establishing this legume on a broadacre scale.

Method 1: In 2017 a 420 ha Gidgee land type paddock near Hughenden, Northwest Queensland was blade ploughed and stick raked and aerial seeded to Progardes® at 3kg/ha.

A Botanal survey in March 2021 found that the Desmanthus established at 1 plant/m² with a composition (by weight) of 28% and a frequency of 21% with 0.27 seedlings/m².

Method 2: In 2019 a 500ha buffel grass pasture on a Brigalow land type near Springsure in Central Queensland was aeriually sprayed with Glyphosate followed by aerial seeding of Progardes® at 3kg/ha.

Botanal surveys in July 2021 found 1.05 Progardes plants/m² with a 28% (by weight) composition and a frequency of 48% with 0.52 seedlings/m².

Blade ploughing and aerial seeding of Progardes® has proved successful in establishing the legume on a Gidgee land type despite below average rainfall. In the Brigalow region the aerial application of Glyphosate and aerial seeding of Progardes® has also produced successful establishment. Further calibration of herbicide rates is recommended to refine the most desirable application rate for the initial suppression and later regeneration of the grass species. The successful establishment of Progardes® at both sites is attributed to reduced grass competition, stored soil moisture, the presence of dead or suppressed ground cover, and the good agronomic traits of Progardes.

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Contrasting metabolic effects of severe and moderate heat stress in Angus steers

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Heat stress is an ongoing issue in the agriculture industry and animal production. In mammals, extreme heat stress causes catastrophic failures, including heat stroke, severe dehydration, and acute renal failure. Thus, efficient body thermoregulatory mechanisms are necessary to combat heat load. Black Angus steers (*Bos taurus*) are important for beef production, but they are more susceptible to heat stress due to their acclimation to temperate regions. It is important to understand the metabolic changes in *Bos taurus* due to heat stress to develop methods of offsetting its impact.

We subjected grain-fed Black Angus steers to two different heat load levels: **severe** (maximum T_a 40°C, stepping down to 36°C over seven days) and **moderate** (maximum T_a 35°C over seven days). For a detailed biological analysis via a systems-wide overview, we combined NMR-based metabolomics and clinical biochemistry. Multivariate statistical analysis identified metabolites and clinical parameters that change significantly depending on the treatment level. During a severe heat load, steers drastically reduce their metabolic rate to decrease endogenous heat. Metabolic changes include alterations in electrolyte balance and buffering, reduced gluconeogenesis, and using ketone bodies for fuel. This extreme survival mechanism contrasts with a moderate heat load, where steers experience slight metabolic perturbations, including negative energy balance and nutrient partitioning. When recovering from either level of heat stress, steers' metabolic states do not fully return to baseline days after the heat load event, suggesting they are in a homeorhetic state and that steers, regardless of treatment, require prolonged recovery periods from heat load events.

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RNAi as a control measure for sea lice infestation on salmon fishes

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Sea lice (*Lepeophtheirus salmonis*), a marine ectoparasite copepod on salmon fishes is a major challenge to the salmon aquaculture industry that imposes huge economic losses annually (~50 B). Current methods of sea lice control such as chemical controls and vaccinations, in turn, develop resistance to parasites and affect the environment including salmon health. RNA interference (RNAi) is a natural pathway that encourages researchers to develop a novel, non-toxic, eco-friendly control measure for this problem. Biopolymers are used as a transporter to deliver the double-stranded RNA (dsRNA) to initiate the RNAi pathway. In our studies, we considered three biopolymers to stabilise the dsRNA on the surface of fish. Sections of fish skin were treated with fluorescein labelled (Flu) dsRNA only, polymer PEI encapsulating Flu-dsRNA, polymer et-PEI encapsulating Flu-dsRNA and polymer PDMAEMA encapsulating Flu-dsRNA. Following application, the Flu-dsRNA was imaged using fluorescent microscopy. After imaging, the fish skin samples were washed, re-imaged, and stored at 4°C. After 24 hours the samples were re-imaged to find the evaluate the persistence of the Flu-dsRNA. Biopolymers encapsulated dsRNA were stable and visible after washing the three fish samples. Flu-dsRNA alone, et-PEI encapsulating Flu-dsRNA and PDMAEMA encapsulating Flu-dsRNA were detected after 24 hours, while the PEI encapsulating Flu-dsRNA was not. The stability of dsRNA incorporated with two of the three degradable biopolymers provides evidence for a solution to effectively deliver dsRNA to salmon. The application of RNAi can improve salmon fish health which will underpin the future profitability of the salmon aquaculture industry.

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The effect of maturity on the concentration of fatty acids in macadamia

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The fatty acid profile of macadamia nuts has gained increased attention over the past few years, due to their high concentration of monounsaturated fats, including palmitoleic acid (C16:1) and oleic acid (C18:1), which, on average, constitute 19% and 63% of the fatty acid profile, respectively. Both of these fatty acids are known to exhibit multiple beneficial physiological and biological functions, as well as different protective effects against various chronic diseases, including obesity, diabetes, and cardiovascular diseases. During kernel development, C16:1, as well as the main saturated fat in macadamia, palmitic acid (C16:0), tend to decrease, while C18:1 tends to increase. The extent of this change varies significantly between cultivars. A possible explanation to this phenomenon is that, for different cultivars, the elongation pathway from C16:0 to C18:0 fully upregulates at differing stages of the kernel maturation process. This variation in timing of fatty acid elongation for different macadamia accessions, may account to some degree for the difference in percentage of C16 versus C18 fatty acids. These results also suggest that rather than there being a divergent C16:0 desaturase (Cahoon et al. 1998), the desaturation of both C16:0 and C18:0 is controlled by a single C18:0 desaturase, rather than a C16:0 desaturase and C18:0 desaturase. By understanding how the concentration of principal fatty acids change during kernel development, it is possible to gain a better understanding of relevant biosynthetic pathways of these fatty acids, provide insight into future plant breeding, and assist in developing food products with increased nutritional value.

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Determination of phenolic compounds and organic acids of stingless bee honey from Malaysia and Australia

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Phenolic acids, flavonoids, and organic acids are well-known bioactive compounds in stingless bee honey which can be used as a geographical origin indicator. Therefore, in this study, stingless bee honey from the species *Heterotrigona itama*, *Geniotrigona thoracica*, *Tetragonula carbonaria* and *Tetragonula hockingsi* were evaluated for their phenolic acid, flavonoid, and organic acid content. These profiles in honey (n=8) were determined using UPLC MS QTRAP. Separations were performed using Thermo Scientific C18 column on an UltiMate 3000 UHPLC system (Dionex). High resolution mass spectrometry was carried out using a MicroTOF QIII Bruker Daltonic using an ESI negative ionization. Accurate mass data of the molecular ions were processed by Compass Data Analysis software 4.1. Mass spectral fragmentation patterns of identified phenolic acid, flavonoid and organic acid were compared with the literature. Rutin and apigenin are flavonoid phenolic compounds that were found to be present only in the Australian honey while *p*-Coumaric acid was only identified in the Malaysian honey. In addition, pinocembrin-5-methyl ether was a flavonoid solely detected in *T. carbonaria* honey. Gluconic, cinnamic, citric and phenyllactic acids were organic acids detected in all samples. These results suggest that flavonoids rutin and apigenin could possibly be used to differentiate Australian from Malaysian stingless bee honeys and that pinocembrin-5-methyl ether is unique to *T. carbonaria* honey. However, further studies involving additional honey samples and direct comparisons with standards will further examine these results, with compounds present in honey likely dependent on the predominant floral nectars in the vicinity of stingless bee honey production.

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Quantification of rare earth elements in rice samples using ICP-MS

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Rare earth elements (REE) are recognized as lanthanides and are composed of seventeen elements including lanthanum to lutetium in the periodic table. Despite their rising concern and utilization, little attention is given to them as emerging environmental contaminants and their associated health risks. The concentration of these elements in urban and agronomic soil are critical and may trigger bioaccumulation in plants and may enter the food chain. Also, the consumption of fertilizers in agricultural practices on a larger scale is a significant challenge. The REE enriched fertilizers are a risk factor for contamination in soil and food. However, there is very limited data in literature regarding the occurrence of these elements in rice. Thus, this study is aimed at investigating a suitable method for rice sample preparation as well as validating and applying the method for quantifying REE concentration in rice by using Inductively Coupled Plasma Mass Spectrometry (ICP-MS). The analytical method was validated by using two certified reference materials (CRMs) to get the precision and accuracy of the developed method. The method was applied for analysing 200 rice samples (including polished, brown, and parboiled) from different regions of the world and consumed by the Australian population. Validation parameters showed that the method was validated and optimized for the quantification of REEs. The outcome of this study includes filling the subsequent knowledge gaps in analysing REEs in rice. This study also indicated the need to establish monitoring programs for this type of cereals, aiming at promoting public health.

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Inside out and upside down: Looking closer at Australian native wattleseeds

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Recent archaeological findings indicate that over 200 plant seeds from different species have been utilised by Australian aboriginal communities. The largest known group of seeds that were consumed were from the Acacia family. Also known as wattleseeds in Australia, over forty of these are known to be edible. Dietary patterns have since changed, and the usage of wattleseeds has declined over the past decades.

To better understand and utilize them, we will report compositional, microscopic (CLSM, XRF, micro-CT), spectroscopic (NMR) and sensory (aroma profiles) characterization of selected wattleseed varieties. These will be discussed both before and after subjecting them to different models for food processing.

The results from this study provide guidance for unique mechanisms to design wattleseed - containing food with nutritional benefits. Ethically combining the traditional knowledge and cultural heritage surrounding wattleseeds with instrumental analyses and smarter food design could reinvigorate wattleseed use while fostering a shared experience of health and wellbeing.

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Quantitative proteomics to identify biomarker(s) for Bovine Genital Campylobacteriosis immunity in cattle

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Bovine Genital Campylobacteriosis (BGC) is a contagious venereal disease of cattle caused by *Campylobacter fetus* subspecies *venerealis* (CFV). This reproductive disease of cattle causes infertility and is categorized as a “List B” notifiable disease by the World Organization for Animal Health. BGC is of particular concern for cattle herds in Northern Australia and causes approximately \$13 million in economic loss per annum due to reduced breeding efficiency and increased culling rates.

Diagnosis of the disease is challenging in field conditions and available tests could not be able to identify the organism. So, immune biomarkers could be a potential tool to determine immunity in cattle associated with BGC. A total of 12 normal cycling heifers, where 6 were vaccinated with the commercial vaccine VibroVax® (Zoetis) were challenged intravaginal with an inoculum of live CFV bacteria. Serum samples were collected before challenge, after challenge and after recovery from infection (based on qPCR analysis). Sequential window acquisition of all theoretical fragment ion spectra coupled to tandem mass spectrometry (SWATH-MS) was used to measure the relative abundance of proteins in both groups at three timepoints. A total of 130 unique proteins were identified during search. The number of differentially abundant proteins was significantly higher in the group after recovery from infection ($p < 10^{-5}$ and $\text{Log}_2\text{FC} > 0.2$). The abundance of Immunoglobulin G, Serotransferrin, and Kininogen increased in nonvaccinated group ($p < 10^{-5}$) after challenge and in vaccinated group after recovery from infection. Changes in abundance of proteins associated with vaccine-challenge could be investigated as potential biomarkers for BGC immunity.

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Prevalence and identity of pathogens affecting macadamia nurseries in Australia

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Continuing expansion of the macadamia industry in existing and new growing regions has resulted in an ongoing demand for young trees. Establishment of new orchard is best done with healthy trees to ensure long term productivity. However, the current rapid expansion has given rise to a high demand for young trees which may not be always of a high health status. Depending on the cultivar, geographic distribution and production system, young trees in a nursery may be colonised by fungi. To test the hypothesis that different fungal pathogens infect and inhabit macadamia plants at various growth stages and seasons in nurseries in Australia, we surveyed 3 macadamia nurseries in Australia and characterize the culturable fungal communities. A total of 23 fungal genera belonging to four classes Dothidiomycetes, Sordariomycetes, Eurotiomycetes and Mortierellomycetes were isolated from macadamia nursery plants at different growth stages. The most diverse fungal community was in leaf tissue compared to the fungal communities in stem and the root tissues. The fungal community composition also varied significantly between growth stages and seasons. The three most dominant genera included *Diaporthe* (~23%), followed by *Pestalotiopsis* (~19%), and *Neopestalotiopsis* (~17%). To determine the impact of the presence of these fungi in macadamia trees, pathogenicity, and aggressiveness trials of the isolates in the three most common fungal genera are underway.

Keywords: Microbial diversity, Endophyte, Ascomycota, Tree nut

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Does storage affect the in vitro bioaccessibility of anthocyanins in 'Rubycot' plumcot?

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Diet plays an important role in maintaining human health and including the recommended servings of fruits and vegetables high in fiber, essential micronutrients and bioactive phytochemicals helps maintain a healthy body. Anthocyanins are a group of phytochemicals found in red, blue, and purple pigmented plants that have potential health benefits. Plumcot is a novel stone fruit and hybrid between plum and apricot developed in Australia. 'Rubycot' is a dark red coloured plumcot with a relatively high anthocyanin content (76.3 mg/100g of FW). Storage at ambient temperature significantly affects the physicochemical and phytochemical composition of stone fruits. In this study, Rubycots were harvested at commercial maturity and stored at 23°C for 7 days. After storage, the anthocyanin content increased significantly ($p < 0.05$) by 95% compared to fresh Rubycots. Storage can also affect plant matrix integrity impacting nutrient and phytochemical bioaccessibility. To determine if storage impacts Rubycot anthocyanin bioaccessibility and intestinal uptake, anthocyanins were measured in digesta prepared from fresh and stored Rubycots using the INFOGEST 2.0 static oral-gastrointestinal digestion method. Results from this study will provide crucial information about the effects of storage on postharvest anthocyanin biosynthesis and anthocyanin release and stability within the gastrointestinal tract.

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Nutritional Qualities of Landraces of Pearl Millet in Rajasthan State of India

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Millet (nutri-cereals) are world widely known for their nutritional quality parameters hence the UN declared 2023 as the International Year of Millets. They are not only nutritionally but also environmentally good and adaptable to local conditions. In the present study, phenotypically varied different pearl millet landraces collected across the Rajasthan State were grown as crowd sourcing trials at research stations as well as farmers' fields during rainy season of 2019, 2020 and 2021. Based on farmer's preference showing higher yield but most importantly good for consumption purpose on the basis of nutritional profiling, out of 102 landraces of pearl millet, 7 landraces viz. *Sulkhaniya Bajri*, *Chadi Bajri*, *Moochwali Bajri*, *DR-1*, *DR-2*, *Pili Bajri* and *Chanana Bajri* were found superior in quality parameters. The nutritional composition of these landraces were found ranging carbohydrates from 56.26 to 62.45%, amylose from 21.02 to 26.25%, total soluble sugars (TSS) from 1.84 to 2.65%, protein from 9.91 to 15.90%, total dietary fibre (TDF) from 8.87 to 13.23% and phytic acid from 0.62 to 0.94%. The maximum TSS (2.65%) was found in *Sulkhaniya Bajri* whereas, maximum starch (62.45%) was recorded by *Pili Bajri*. The protein was maximum (15.90%) with DR-2 whereas, DR-1 had maximum amylose content (26.25%). The maximum total dietary fibre (TDF) (13.23%) and Phytic acid (0.94%) was found in *Chanana Bajri*. The seeds of these landraces have been conserved at gene bank of ICAR-NBPGR, New Delhi and further multiplication for promotion at community level in selected sites of Rajasthan state.

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Rheology and composition of Jelly Bush honey

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The rheology of Australian Jelly bush honey is known to be thixotropic and non-compatible with upcoming hive designs. However, the cause of its thixotropy has yet to be determined. The purpose of this project was to relate the chemical composition of 6 Jelly Bush honeys across varying methylglyoxal (MGO) and leptosperin (LSP) concentrations with their rheological behaviour. Ion chromatography was used to quantify glucose and fructose content. Ultra-high-performance liquid chromatography with ultraviolet–visible spectroscopy (UHPLC-UV/Vis) was used to quantify MGO and LSP content. Brix refractometry was used to determine Total Soluble Solids content. Rheological measurements consisted of amplitude, frequency, temperature and flow sweeps. Multivariate analysis was used to relate the different rheological properties and the chemical composition. LSP content was found to be inversely related to $\tan \delta$ and glucose and fructose contents had little relation to the rheological variables. LSP content may be a possible indicator for rheological behaviour in Jelly Bush Honey, but a larger sample sizing would be recommended in future studies. Understanding the physical behaviour and flow properties of jelly bush honey may allow future hive design to incorporate the unique properties of high value honey and ensure compatibility.

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An analytical chemistry approach to unlocking wider health benefits of pomegranate fruit

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Pomegranate is one of the most powerful foods for overall good health with most of the beneficial health effects due to the polyphenolic compounds contained in the fruit. Besides its traditional food industry applications, pomegranate has great potential for nutraceuticals, cosmetics and dyes. Pomegranate is an emerging industry in Australia with great export potential. The bioactive content varies between the different parts of the fruit and is also influenced by cultivar, growing region, maturity and cultivation practice. The objective of this project was to monitor a range of bioactive compounds present in pomegranate and the fruit processing waste streams. Australian and the USA grown fruit and commercial processed products were analysed. On dry weight basis, husks of fresh fruit had higher antioxidant capacity (AOX) and total ellagic acid (TEA) than its juice or aril residues. The total phenolic content (TPC) of husks was higher than the juice followed by its aril residues. The commercial pomegranate extract product had the highest AOX, TEA and TPC among tested samples. Anthocyanins were higher in fresh fruit juice than in commercial juice and freeze-dried samples, but not detectable in oven-dried samples. Pomegranate seed oil samples ranged between 79.5- 90.2% poly-unsaturated fatty acid content. The study details will be discussed at the conference. The outcomes from this project funded by Agri-Science Queensland Innovation Opportunity of the Department of Agriculture and Fisheries will provide much needed data on the levels of bioactives in Australian grown pomegranate, enabling the Australian pomegranate industry to make informed choices regarding breeding programs, consumer/market research and product development.

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Escherichia coli persistence in manure amended soils under two types of cultivation

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The incorporation of biological soil amendments of animal origin, such as manures, is deemed important in promoting the growth and yield of crops and general soil health. However, it is also a recognized source of zoonotic pathogens. In the Philippines, few studies have been done on the analysis of microbial contaminants on leafy produce applied with different manures. Hence, this study investigated the persistence of *Escherichia coli* as an indicator for faecal contaminants in manure amended soils planted with lettuce under protective structure and open field. Treatments employed were without manure, carabao manure, fresh chicken dung, dried chicken dung, vermicast and goat manure. *E. coli* populations in soil and leafy type lettuce at weekly interval and at harvesting were examined, respectively. Initially, soils incorporated with fresh chicken dung obtained the highest *E. coli* counts of 5.82 and 6.11 log CFU/g in protective structure and open field, respectively. Over the trial, *E. coli* decline was evident among all treatments ranging from 1 to 4 log reduction. Moreover, it was found out that at 35 days, all treatments in protective structure and open field were below the critical limit of <2 log CFU/g. At harvest, only 2% of the total harvested lettuces were above *E. coli* detection limits of 1 log CFU/g and the rest were at lower counts. Results of this research may benefit farmers, policy makers or individuals in terms of manure quality and application to harvest interval in fresh produce specifically lettuce as an essential vegetable and salad ingredient.

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Cowpea Aphid (*Aphis craccivora* Koch.) Resistant Resources in Mungbean Mini-core

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Mungbean (*Vigna radiata* (L.) R. Wilczek) is one of the very important legume crops grown in sub-tropics and tropics. The crop production is limited by several biotic and abiotic stresses. Among the insects, cowpea aphid, *Aphis craccivora* Koch. (Homoptera: Aphididae) is an important cosmopolitan pest affecting more than 50 host plants including mungbean and other *Vigna* species. The adults and nymphs of cowpea aphids suck the sap from tender plant parts such as leaves, growing tips, flower stalks, and young pods. Heavy infestations also result in distortion of leaves and stunted plants with small, poorly nodulated root systems; ultimately leading to yield reduction. In this context, this study aimed to identify the resistant resources to the cowpea aphid among the mini-core accessions at World Vegetable Center, Hyderabad during 2017-2021. During screening, all the mini-core accessions were visually scored based on the cowpea aphid population density and the consequent symptoms developed on the plant parts at 30 and 60 days after sowing using a scale of 1–5 (1=highly resistant, 2=moderately resistant/tolerant, 3=moderately susceptible, 4=susceptible, 5=highly susceptible). Among 296 accessions, 96 genotypes showed resistance to cowpea aphids conducted during 2017-18. This sub-set of resistant genotypes were screened in rainy (June-August) and post-rainy (September-December) seasons during 2020-2021. Among them, 10 genotypes viz; VI000736 AG, VI001124 AG, VI001221 AG, VI001244 AG, VI001535 BG, VI002647 AG, VI003534 BG, VI003925 B-BLM, VI003954 BG, VI004954 BG consistently showed resistance to cowpea aphid attack.

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Evaluation of Stepped Training Approach to the Philippine Good Agricultural Practices Adoption

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Good Agricultural Practices (GAP) are methods that protect the safety and quality of food and non-food agricultural products by addressing the sustainability of on-farm activities. Along with neighboring countries and the world, the Philippines has created Philippine Good Agricultural Practices (PhilGAP) to promote the marketability of Philippine agricultural products. Nonetheless, the Philippines lags behind its Southeast Asian neighbors in terms of the implementation of GAP. The adoption constraints are classified as knowledge, cost, process, and reward/incentive constraints on behalf of the farmers' situation. The stepped training approach is a strategy to intensify awareness among farmers. This constitutes four levels: Level 1 – Foundation, Level 2 – Intermediate, Level 3 – Advanced, and Level 4 – PhilGAP, and the key aspects of GAP are included that farmers could readily implement in a step-by-step process. The gradual adoption of good agricultural practices facilitates ease of compliance for farmers with the recommended protocols. There are seven farmer groups with 103 farmers in total who are participating in the delivery of stepped training on GAP. Currently, there are two farms that have passed the PhilGAP inspection and were issued with the certification using the stepped training approach, namely, Mazo's Farm and Uy's Integrated Farm of Baybay City, Leyte. This strategy of intensification of awareness through a stepped training approach to farmers and leveraging the collaborative potential of the local and national government offices is found to be essentially recommended to work hand-in-hand to encourage GAP adoption in the country.

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Prevalence of Botryosphaeriaceae fungi in Australian macadamia orchards

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Botryosphaeria fungi are known pathogens of several tree crops. In macadamia, species of Botryosphaeriaceae causing Botryosphaeria branch dieback have not been truly characterised. Therefore, this study examined the prevalence of Botryosphaeriaceae in commercial macadamia orchards and nurseries in Australia. We determined the ability of each species of Botryosphaeriaceae to cause Botryosphaeria branch dieback. Based on phylogenetic analysis of four gene regions (internal transcribed spacer - ITS, translation elongation factor 1-alpha - *tef1α*, beta-tubulin - *tub2* and DNA-directed RNA polymerase II second largest subunit - *rpb2*), 10 species of Botryosphaeriaceae in two major genera (*Lasiodiplodia* and *Neofusicoccum*) were identified from macadamia in Australia. Four putative novel *Lasiodiplodia* clades, with three other *Lasiodiplodia* spp. (*L. iraniensis*, *L. pseudotheobromae* and *L. theobromae*) and three *Neofusicoccum* spp. (*N. luteum*, *N. mangroviorum* and *N. parvum*) were characterised. The most frequently isolated species were *L. pseudotheobromae*, that constituted 40% of the isolates from diseased tissues of mature trees, whereas *Neofusicoccum* spp. were mostly obtained from the young diseased nursery tissues and symptomless tissues. Both the *in vivo* and *in planta* pathogenicity assays revealed that all Botryosphaeriaceae fungi obtained from macadamia, except *N. mangroviorum*, caused Botryosphaeria branch dieback in macadamia.

There was significant difference in the aggressiveness among the species, which showed that *L. theobromae*, *N. luteum* and *L. iraniensis* were the most aggressive of all 10 species. This study has improved our understanding on the pathogen biology and ecology that would aid disease management system of macadamia in Australia.

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Pyrolysis of oil palm wastes offers opportunities for disease management.

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Oil palm (*Elaeis guineensis* Jacq.) is a long-term perennial crop of great economic importance to many countries in tropical Asia/Oceania, providing export revenue and much needed income to both large plantations and smallholders. Unfortunately, basal stem rot (BSR), caused by the fungus *Ganoderma boninense* Pat., poses a major threat to the oil palm industry and hence to farmers' livelihoods. A potential long-term control measure for this disease would be through improved cultural practices. In a related project we have confirmed that oil palm residues from previous planting (windrowed logs and stumps) are a source of inoculum for new planting thus continuing the disease cycle. Therefore, a disease management measure would be to remove old logs and stumps from the field. This is costly and time consuming, especially to the smallholder. Thus, we investigated pyrolysis of oil palm residues (logs, fronds and empty fruit bunches) using two technologies (low and medium cost) as a way to convert oil palm residue into biochar, a charcoal like material. We demonstrated that biochar made with both technologies promoted growth of vegetable seedlings in a commercial nursery, indicating that oil palm residue is a good clean feedstock for pyrolysis. Biochar from oil palm residues has the potential to close the circular economy by converting waste into a higher value product.

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Broad mites and other Arthropods on Capsicum Under Protective Structures in Fiji

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Capsicum annum L. is grown in Viti Levu, Fiji under protected structures to meet market demands during the off-season (November-April). Protected structures provide the ideal temperature and relative humidity (RH) conditions for temperate crops like capsicum to grow in a tropical climate like that of Fiji. These conditions are also favourable to pests such as broad mites. To determine the abundance and damage severity (DS) of broad mites on capsicum inside the protected structures, as well as the presence of other arthropods associated with capsicum grown in protected structures, plants were sampled weekly from January to July 2022. A significantly higher number of broad mite eggs (9.91/cm² of the leaf) and immatures (6.32 /cm² of the leaf) were recorded in June wherein the average minimum and maximum temperature, and RH were at 22.4 °C, 32.5 °C and 74.7%, respectively. While the highest number of adults (2.60 /cm² of the leaf) was recorded in March wherein average temperatures were at 26.7 °C (min.), 37.3°C (max.) and 70.3% RH. High numbers of broad mite eggs (11.25/cm² of the leaf) and immatures (5.74/cm² of the leaf) were recorded on plants showing a slight discolouration of leaves (DS1) while adult densities of 2.45 adults/cm² of the leaf were recorded on plants showing slight curling of apical leaves (DS3). Aphids were recorded on plants in all sampling periods along with white footed ants, thrips and whitefly. Rust mites, predatory mites, lady beetle, and mealy bug were only occasionally observed.

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MLVA-19 scheme suitably explores genetic diversity of *Xanthomonas vasicola* pv *musacearum* populations

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We describe the development of a new genotyping method on *Xanthomonas vasicola* pv. *musacearum* (Xvm), based on Multi Locus variable number of tandem repeats Analysis (MLVA), to understand Xvm population structure and diversity. Mining nine publicly available Xvm genomes, the POLLOC-V pipeline (L.-M. Rodriguez-R, R. Koebnik) detected 36 microsatellite loci, among which 21 were selected for primer design. Based on typeability, reproducibility, and polymorphism, 19 markers were retained and multiplexed into 5 mixes. Most loci were highly typeable, with 18 of the 19 loci amplified in more than 97% of strains. Specificity was clear to Xvm and *X. vasicola*: seven loci were amplified within the two other pathovars of *X. vasicola*, but gave Xvm-specific allele sizes. The Genotype Accumulation Curve indicated that the number of markers used is sufficient for further diversity analyses. This MLVA-19 scheme was applied on a 335 Xvm strain collection from seven countries collected over several years. The microsatellite markers grouped the Xvm collection into three clusters; with two of the clusters similar to the SNP-based clusters sublineage I and II and cluster three revealing an unknown diversity in Ethiopia. Genetic differentiation among countries was evaluated with Wright's fixation index (FST) and Slatkin's FST analogue (RST), which were calculated by computing distance matrices for haplotypic data. All country populations were highly significantly differentiated from each other (P<0.001), except DRC and Rwanda. This MLVA scheme is a tool of choice for molecular epidemiology of the Xvm populations affecting banana- and enset.

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Benchmarking mineral concentration, bulb yield and quality across garlic genotypes

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Garlic (*Allium sativum* L.) is an important culinary and medicinal (allicin) crop for which about 300 genotypes are broadly adapted to tropical and temperate climates. Genotypic differences in allicin and yield are well documented. However, there is very limited information that relates these traits to mineral nutrition despite mineral elements being directly involved in the biosynthetic and metabolic pathways of allicin.

A benchmarking of foliage and bulb mineral concentration for 32 genotypes was conducted. Youngest fully expanded leaf (YFEL) samples at the 6-7 leaf stage and cured bulb samples were collected.

Mineral concentrations in YFEL and bulbs varied significantly ($P < 0.05$) across the 32 garlic genotypes. The YFEL concentrations of macronutrients (g/kg) for nitrogen (41-57), phosphorus (3.6-5.6), magnesium (4.3-6.0), and calcium (6.9-8.9) fell within an adequate range for garlic (Reuter and Robinson, 1997). Concentrations of sulfur (3.8-10.3 g/kg) and micronutrients (mg/kg) including B (21-31), molybdenum (1.0-5.5), iron (59-125) and copper (3.1-8.0) are the first time documented. Principal component analysis (PCA) divided 32 genotypes into 3 phenotypic groups and showed a strong relationship between YFEL mineral status, yield, and allicin concentration. Bulb mineral concentrations were positively correlated with bulb allicin concentration, but negatively correlated with bulb weight (with the exception of calcium and boron). Group II genotypes showed significantly higher phosphorus, sulfur, molybdenum, copper and allicin concentration than Groups I and III.

This is the first documentation of the mineral status of garlic and its relationship with bulb weight and allicin concentration.

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Development of a molecular diagnostic tool for detection of phytoplasmas infecting banana

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In the Madang province in Papua New Guinea (PNG), a phytoplasma-associated disease is causing devastating losses in banana and coconut palms. The diseases are caused by Banana Wilt Associated Phytoplasma (BWAP) and phytoplasmas associated with the Borgia Coconut Syndrome (BCS). Banana germplasm imported to Australia must be indexed for banana phytoplasmas as part of the post-entry quarantine screening to ensure Australia remains free of these emerging diseases. Phytoplasmas cannot be cultivated in standard laboratory growth media, which poses major challenges to the study of these pathogens. PCR-based methods used for the detection of banana phytoplasmas mostly rely on universal primers that typically target conserved regions of the phytoplasma genomes. However, one common problem with this approach is that phylogenetically related endophytic bacteria share these conserved regions, such as bacteria belonging to the genus *Bacillus*, leading to false positive results. The only way to confirm if the visualised amplification product derives from a Phytoplasma is by Sanger sequencing, which adds more time and cost to the final diagnosis. To develop a more reliable molecular diagnostic tool for detection of BWAP we used draft phytoplasma and *Bacillus* genomes to identify regions that were unique to phytoplasmas and absent in *Bacillus* to prevent false positive results. Molecular detection methods were designed using this approach and results from testing and validations of these assays will be presented.

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Exogenous RNAi as a sustainable control against soilborne pathogens

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Soilborne plant pathogens are one of the leading causes of plant diseases and significantly contribute to annual crop production losses worldwide. Fungicides are the main control for disease management, but can lack specificity, run-off into the environment, may be toxic to humans and non-target organisms, and can lead to the development of pathogen resistance. Hence, a new innovative strategy is key to environmentally friendly disease management of soilborne pathogens for greener and sustainable agriculture. An emerging non-genetically modified (GM), environmentally sustainable and target-specific crop protection platform is spray-induced gene silencing (SIGS), which uses exogenously applied double-stranded RNA as bio-fungicides. Here, the requirements for effective exogenous RNAi against soilborne plant pathogenic fungi and oomycetes including *Verticillium dahliae* and *Phytophthora cinnamomi* were examined. Different target genes, RNA application methods and doses were assessed. dsRNA targeting essential fungal genes significantly reduced pathogen growth *in vitro* and bioassays were developed to determine whether this translated to protection *in planta*. The dose of dsRNA and timing of delivery were found to be important factors for effective SIGS. Interestingly, dsRNA applied to shoots could be detected in root tissue and dsRNA applied to roots was found in leaves of some model host crops. These findings will inform the development of sustainable RNAi-based crop protection approaches against soilborne plant pathogens.

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Maturity effect on selected quality parameters in wild-harvested *Terminalia ferdinandiana* (Exell) fruit

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Terminalia ferdinandiana Exell., also known as Kakadu plum, is a wild-harvested native Australian fruit with very limited information on how maturity is affecting the nutritional quality of the fruit. Therefore, the present study investigated the following parameters and compounds in Kakadu plum related to fruit quality and their changes during maturity: hydrolysable tannins, phenolic acids, sugar profile, standard physico-chemical parameters and antioxidant capacity at four different maturity stages (immature to fully mature). The hydrolysable tannins (chebulagic acid, geraniin, chebulinic acid, castalagin, and punicalagin) and gallic acid showed a continuing decrease during fruit maturity; whereas elaeocarpusin, helioscopin B, corilagin, 3,4,6-tri-*O*-galloyl-*S*-glucose and ellagic acid increased at the beginning of fruit growth (immature stage), but decreased when the fruits reached their full maturity. Overall, the total content of hydrolysable tannins and phenolic acids was significantly ($p \leq 0.05$) lower in the fully mature fruit samples compared to the immature samples. Total phenolic content (TPC) and DPPH radical scavenging capacity did not vary ($p > 0.05$) between different maturity stages. Pearson's correlation coefficient test indicated that TPC and DPPH positively ($p \leq 0.05$) correlate with most of the studied tannin compounds. Sugars (glucose, fructose, and sucrose), total soluble solids and titratable acidity increased during fruit development. Furthermore, principal component analysis (PCA) was used to differentiate between immature and mature fruit samples, based on their nutritional profile and antioxidant capacity. The PCA results also suggested a high variability between individual trees, highlighting the challenges of wild harvest practice.

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Topical application of RNAi to improve crop health against fungal pathogens

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Fusarium Head Blight (FHB) is a fungal disease affecting grain crops caused by *Fusarium graminearum*. It can lead to 20% - 100% of grain yield loss and produce mycotoxins during infection which are harmful to humans and animals. Chemicals such as Demethylation Inhibitors (DMI) are commonly used for reducing incidence and impact of FHB however the overuse of these fungicides can cause potential harm to soil-beneficial microorganisms, affect soil structure and fertility, and lead to fungicide resistance. Biological controls have since been an alternate source of control, with RNA interference (RNAi) technology showing immense potential as a tool in agriculture to overcome pests and diseases. RNAi is a post-transcriptional gene silencing mechanism, and we are investigating its potential as an exogenous application for the treatment of FHB for wheat and barley. Initially, uptake of exogenous dsRNA by *Fusarium graminearum* was confirmed using the confocal microscopy. Additionally, an *in vitro* method for screening potential target genes using target-specific dsRNA was developed as a tool to investigate fungal inhibition. *In plantae* seedling assays using the *Fusarium graminearum* – wheat/barley pathosystems were also tested, using both spraying and point inoculation of dsRNA and spores. Uptake studies showed that *F. graminearum* successfully takes up dsRNA from its environment. Results from the *in vitro* assays also showed some inhibition of the fungi, indicating the potential to upscale and experiment in the glasshouse and eventually in the field. There is unprecedented potential in using target-specific dsRNA as a biocontrol against FHB, as well as other fungal diseases.

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Quality plant proteins with minimal processing: Developing healthy and tasty plant-based burgers

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Plant-based foods require less water, land and have less impact on animal welfare than animal-based foods leading to economic and environmental benefits. Shifting from a diet largely dependent on animal products to a diet based on plant and plant-based material offers many scientific challenges and opportunities for innovation. A range of plant-based meats, including burgers, have been developed in recent years, however, these products typically rely on formulation with synthetic ingredients to maintain sensory and textural quality. These added-ingredients conflict with a parallel consumer demand for clean labelling and minimally processed foods. Thus, one of the major challenges for plant-based 'meat analogues' is obtaining a meat-like texture and flavour from natural formulations of plant materials with minimal processing.

The objective of this research is to obtain plant protein ingredients that are consumer acceptable in terms of texture and flavour properties using more 'natural' preparation techniques requiring minimal processing. Various sources of plant protein were evaluated to better understand how plant protein ingredients are impacted by processing in terms of functionality and sensory outcomes. Importantly, the effect of manufacturing on the microstructure and the macrostructure of plant-based burgers was explored. The next steps will be to develop and apply new and existing food manufacturing methods (such as fermentation) with view to create superior plant protein ingredients, with high functionality, that reduce the need for complex formulation while delivering a meat-like eating experience.

With a future protein shortage predicted it's essential to provide high quality plant-based protein foods. This research supports the development of premium plant-based meats with improved health and consumer credentials.

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Diagnostic assay development for Bovine Genital Campylobacteriosis

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Bovine Genital Campylobacteriosis (BGC) is a venereal disease of cattle that is caused by *Campylobacter fetus* subspecies *venerealis*, a gram-negative bacteria that inhabits the microaerophilic environment of the bull preputial crypts and transmitted to females during mating. Bulls are asymptomatic carriers but infection in females is associated with reduced fertility and late-stage abortions. BGC outbreaks are notifiable diseases and accompanied by trade restrictions of infected cattle. Since Australia is the second largest beef exporter in the world and exports half of the milk it produces, BGC can significantly hamper the economic exports which was observed as 66% reduction in profits. Infection remains undetected due to generic symptoms that overlap other diseases and inability to culture the slow-growing, fastidious bacteria, thereby making diagnosis essential. Although many diagnostic tools are available, they cannot distinguish *C. fetus venerealis* from its genetically and phenotypically similar subspecies *Campylobacter fetus fetus* leading to false-positives. Following genomic sequencing of 14 *C. fetus fetus* and *C. fetus venerealis* genomes which were compared with an additional 9 published genomes, diagnostic Single Nucleotide Polymorphisms (SNPs) were identified in candidate gene RS04330 (hypothetical protein). This study exploited a novel TaqMan SNP qPCR detection assay based on RS04330 to distinguish the two subspecies. The assay was optimised for temperature, checked for specificity by testing against other bacteria that inhabit the bovine genital tract, and finding limit of detection. Results were favourable with specific detection of *C. fetus venerealis* and indicates that the assay could be adopted by veterinary diagnostic laboratories upon further optimization.

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In vitro bioaccessibility of anthocyanins and folates in strawberries treated with photosensitization

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In conventional agriculture, synthetic fungicides are possibly the most commonly used method to control postharvest decay, but these are expensive, lead to pathogenic resistance and also has a detrimental impact on human health and the environment. Therefore, there is a need to develop environmentally friendly and sustainable technologies, to extend postharvest storage life and retain the nutritional quality of fresh produce. Photosensitization, a non-thermal and eco-friendly preservation technology, was used to preserve the commercial strawberry cultivar 'Red Rhapsody'. Strawberries were sprayed with 50 μM curcumin before being exposed to 433 nm light-emitting diodes (LED) at a dose of 15 J/cm^2 . *In vitro* bioaccessibility of anthocyanins and folates was explored in treated and untreated strawberries by measuring the release of these compounds in strawberry digesta prepared using the 'INFOGEST' static *in vitro* oral-gastrointestinal digestion model. No differences ($p>0.05$) were observed in bioaccessibility of total anthocyanins and total folates between treated and untreated strawberry samples. Furthermore, bioaccessibility of pelargonidin-3-glucoside, the major anthocyanin in strawberry, and 5-methyl-tetrahydrofolate, the major folate vitamer in strawberry, was unaffected by photosensitization. These promising results support photosensitization as a novel, green, sustainable, and effective preservation technique for the strawberry industry. However, further studies, such as sensory evaluation of photosensitized strawberries and *in vivo* human intervention trials to determine pharmacokinetic profiles of polyphenols, are suggested to investigate the efficiency of photosensitization technique.

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Juice treatment Using Nanosecond Pulsed Electric Field Technology

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Pulsed electric field (PEF) technology is a promising physical method for application in food processing and preservation as an alternative 'cold' treatment method. It involves the use of high-voltage pulses to generate an electric field strength at sufficient levels ($\text{kV}\cdot\text{cm}^{-1}$) to inactivate microorganisms through electroporation and electroporeabilisation mechanisms. This study aimed to investigate bacterial inactivation using nanosecond-PEF (nsPEF) treatment in batch-mode in sterile apple (Pink lady) and navel orange (Sunkist) juices inoculated with gram-negative (*Escherichia coli*) or gram-positive (*Lactopantibacillus plantarum* or *Leuconostoc mesenteroides*) microorganisms. Sterile juice samples were inoculated at an initial concentration of $7 \log \text{CFU}\cdot\text{mL}^{-1}$. $1000\mu\text{l}$ of the juice was placed in a PEF treatment chamber (aluminium electrodes with 4-mm inter-electrode distance) where high-voltage pulses were applied. After applying several different nsPEF treatment protocols, the most effective PEF condition in our study was to deliver 800 unipolar pulses (in four fractions) with 290 ns pulse width with a pulse repetition rate of 1 Hz. The calculated electric field strength ranged between 42 to $46 \text{kV}\cdot\text{cm}^{-1}$ across the chamber. This condition achieved 4 log reduction in *Escherichia coli* and 3 log reduction in both *Lactopantibacillus plantarum* and *Leuconostoc mesenteroides*. The peak temperature recorded during treatment was monitored using a fibre-optic sensor and reached 34.6°C from an initial temperature of approximately 24.0°C , which is not sufficient to impact bacterial inactivation through thermal means. These results suggest that nsPEF method has the potential to be an alternative of conventional thermal method in juice processing.

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Agronomic performance of introduced bananas with high provitamin A content in Tanzania

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Malnutrition is a major public health problem in developing countries including Tanzania, contributing up to 50 % of under-five mortality. Vitamin A deficiency (VAD) significantly affects children and women of reproductive age with the prevalence of 42%. To address this, a number of approaches have been implemented for example, supplementation; bio-fortification; dietary diversification, and disease control measures. Food-based approaches that promote production and consumption of vitamin A-rich foods are noted to be sustainable, and particularly suited to the rural poor communities. Besides, it promotes self-sufficiency food and nutrient security because the promoted foods provide more than vitamin A. In regards to this, a study was conducted in Kagera and Arusha regions, Tanzania. The study evaluates agronomic performance of nine banana cultivars of different subgroups with higher-than-average fruit pro-vitamin A content level originated from different countries, and two local check varieties. Different growth and yield parameters were collected for the first, second and third crop cycles. The results revealed that the growth and yield parameters were significantly affected by the interaction between sites and cultivars ($P < 0.05$). Banana cultivars yield was much influenced by the combined effect of genotypes and crop cycle duration. The most promising cultivars in terms of yield were Apantu, Biira, PisangPapan, and Lahi over sites and crop cycles. This indicates that although ecological factors could have influenced their performances over sites, the type of genotype could be the most important influencing factor. The official release and dissemination of these cultivars to banana farmers in Tanzania is highly recommended.

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Invitro bioaccessibility and intestinal absorption of minerals and phytochemicals from Australian halophytes

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Halophytes are unique plants that grow and thrive in high saline environments. These plants are considered as emerging functional foods due to their unique composition. Saltbush and samphire are Australian indigenous edible halophytes belonging to the Amaranthaceae family. Previous compositional analyses have revealed saltbush and samphire to be valuable sources of minerals and protein. Furthermore, celosianin II and isocelosianin II were identified as the main betalains (bioactive phytochemicals) in samphire with reported *in vitro* anti-inflammatory and anti-hyperglycemic activity. However, studies investigating bioaccessibility and intestinal absorption of samphire and saltbush nutrients, like minerals and phytochemicals, are very limited. Therefore, the aim of the present study was to investigate the *in vitro* bioaccessibility and intestinal absorption of iron and betalains in saltbush and samphire using simulated *in vitro* digestion and cell-based assays. The INFOGEST 2.0 static oral-gastrointestinal digestion method was used to prepare digesta from saltbush and samphire to determine bioaccessibility. Intestinal absorption of the target compounds was investigated using a Caco-2-HT29-MTX-E12-cell transwell membrane model following treatment with digesta. The present study provided crucial information about the bioaccessibility and digestive fate of iron and betalains in saltbush and samphire. This information can be used for the development of saltbush and samphire as ingredients in new products for the food and functional food industry.

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X-ray fluorescence (XRF) spectrometry for micronutrient determination in rice (*Oryza sativa* L.)

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Micronutrient deficiency is considered one of the emerging challenges to ensuring food security, particularly in developing countries. To ameliorate this deficiency, researchers are working to enhance grain rich in Iron (Fe) and Zinc (Zn) through different breeding strategies. The determination of micronutrient concentrations in rice grain samples is thus very important for analyzing their nutritional content. Most micronutrient analysis techniques depend on inductively coupled plasma (ICP) spectrometry techniques, which are often expensive, laborious, time-consuming, and complicated. Recently, handheld X-ray fluorescence (XRF) spectroscopy is randomly applied in earth sciences however it is rarely practiced in quantifying mineral content in rice samples. To establish the association between the two technologies, the paired-t-test/ANOVA/ Pearson correlation coefficient was computed using data from three replications. The statistical findings confirmed that the Zn and Fe data of rice varieties acquired by XRF is highly significant compared to ICP-OES. This study demonstrated the promise of XRF as a reliable and low-cost alternative to ICP-OES techniques for evaluating Zn and Fe content in rice samples since it permits the analysis of a larger number of samples in a shorter period of time and with a significantly lower cost.

Keywords: X-ray fluorescence spectroscopy, ICP-OES, Micronutrient, Rice, Zinc, Elements.

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Phenotypic and genotypic antimicrobial resistance of *Glaesserella australis* from Australian pigs

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Glaesserella australis is a newly identified bacterial species occurring in the lungs of Australian pigs with respiratory disease. As a newly identified species, no data is available on antimicrobial resistance (AMR). This study aimed at investigating the AMR patterns of 41 isolates of *G. australis* obtained from 15 farms. *G. australis* did not grow on the media stipulated by CSLI for fastidious bacteria. We developed a new media for performing the disc diffusion assay. As there are no agreed criteria for interpretation of disc diffusion results, no allocation to sensitive or resistant is possible based on clinical treatment criteria. As well, due to small sample size, no distinction could be made between the resistant and sensitive population using epidemiological cut-off values. However, some isolates showed obviously smaller inhibition zone than other isolates, which may suggest potential resistance. For further description of AMR, we used whole genome sequencing (WGS). The presence of AMR genes was tested using three existing databases, ResFinder, CARD, ARG-ANNOT and an in-house built database from published works of AMR genes in the *Pasteurellaceae* family from Australian livestock. Preliminary data shows that *G. australis* possesses *tet(B)* and *tet(R)* genes which may be driving phenotypic resistance to tetracycline. One isolate showed apparent possible phenotypic resistance to ampicillin and penicillin (much small inhibition zones) with this being presumably driven by the presence of *bla_{ROB-1}* in this isolate. Further analyses of the WGS data are on-going to characterise the genetic features of virulence genes as well as strain relatedness.

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Extraction of juice and bioactive compounds from blueberries using pulsed electric fields

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Blueberries are an excellent source of antioxidants, vitamins, minerals, and other bioactive compounds. These compounds benefit human health as polyphenols and anthocyanins have the ability to scavenge radicals, which has anticancer, antioxidant, and anti-inflammatory effects. The phenolic compounds and anthocyanins mainly exist in the vacuoles of fruit skin, which through conventional processing methods are commonly wasted due to inefficient extraction processes. Pulsed electric field technology (PEF) is a physical method of interest that may be utilised as a pretreatment process to enhance extraction of valuable nutritional and bioactive compounds from fruits. The extraction mechanism of the PEF treatment is through electroporation and electropermeabilisation phenomena. The aim of this research is to improve polyphenol and anthocyanins extraction, total juice yield, and antioxidative capacity from blueberry fruits. Whole blueberry fruits were placed between two stainless steel electrodes (SS316) with a gap distance of 2.0cm where bipolar square wave pulses were applied to the blueberries with an electric field strength ranging between 8-10kV.cm⁻¹, with a specific energy input of 5-60kJ.kg⁻¹, and a pulse repetition rate of 1-2Hz. Each polarity of the bipolar pulse had a pulse width of approximately 5μs with an interphase delay time of approximately 4μs. The texture and firmness of the blueberry fruits were also examined pre- and post-PEF treatment and compared with a negative control (no treatment).

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Food Diversity and Consumption Pattern of Smallholder Farm Families in Punjab, Pakistan

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Diverse and healthy food contributes significantly both at micro and macro levels and central part to develop high quality of human resource. Diet quality comprises four key aspects: variety/ diversity, adequacy, moderation and overall balance and is vital to build food security. Access to and consumption of diversified foods depends on the households' income however, families modify their food choice according to income and gender choices in rural households. This research aims to explore the consumption of healthy and diverse food at smallholder farm families in District Okara, Punjab using mixed methods research. The results indicate food dietary diversification is extremely low and consumption of key food items such as vegetables and fruits are limited in rural smallholder farm families. The food expenditure was mainly on cereals, dairy, sweeteners, and fats. Wheat/roti (bread) is the major source of calories, providing about half of the total daily calories in rural households. Furthermore, the research also explored that there is lack of awareness and knowledge among the rural farm families. Furthermore, inadequate knowledge/awareness, affordability, gender-based liking/disliking were found some of the key factors of limited food dietary diversification in small holder farm families in Punjab Pakistan. Therefore, awareness through participatory approach involving whole family regarding the diversified and healthy food choices is vital to small holder farmer family's health and well-being.

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Flesh colour in mangoes as an indicator for provitamin A, beta-carotene levels

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Vitamin A (retinol) deficiency is a widespread nutritional disorder in developing countries, commonly associated with symptoms such as night blindness, and, in severe cases, stunting of growth. Beta-carotene is the most common dietary plant-based source of provitamin A, and orange-fleshed fruits such as mangoes (*Mangifera indica* L.) are potentially an excellent source of pro-vitamin A. Hundreds of mango varieties exist, ranging in flesh colour from pale-yellow to dark orange. It is likely that flesh colour is also an indicator of the beta carotene level, as (all-trans)-beta-carotene is an orange pigmented carotenoid and the principal carotenoid in mangoes. It is also the most efficient provitamin A carotenoid, able to produce two retinol molecules compared to only one by other provitamin A carotenoids.

Currently, the relationship between beta-carotene concentration and mango flesh colour has not been fully established. The present study reports the impact of beta-carotene concentration, as well as the impact of other carotenoid compounds present in the flesh of 27 representative mango varieties, on the flesh colour of mango fruit. This data clarifies if flesh colour can be accurately used as a predictive tool to determine the beta-carotene concentration within existing mango cultivars, and if orange cultivars are actually better sources of beta-carotene.

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Evaluation of Mycotoxins and Microbiological levels in cassava products consumed in Zambia

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Cassava (*Manihot esculenta*) is a staple crop after maize in Zambia and requires post-harvest processing before consumption. Microbiological and mycotoxin contaminations of cassava-based products occur mainly during processing and storage. Cassava product samples were collected from households, processors, open markets, and closed markets (supermarkets) across seven districts of Zambia. One hundred samples of cassava products were analyzed for microbial contamination using ISO 21527-2 (2008) method, and fifty samples were analyzed for mycotoxins contaminations, using AccuScan GOLD reader, Reveal Q+ quantitative method. The yeast and mould count were above East African Standard 739:2010, and the most prevalent fungal species were *Aspergillus sp.* (40%), *Fusarium sp.* (12%), and *Rhizopus sp.* (20%). At the same time, *Penicillium spp.* was negative in all the samples. The bacteria isolated from the various samples resulted in a *Total aerobic plate count* above ISO 4833:2010 limit of 1×10^4 cfu/g, *Staphylococcus aureus* (85%), *Total coliform count* (48%) samples recorded 1 to 3×10^4 cfu/g, *Escherichia coli* (16%), and *Bacillus cereus* (8%). Mycotoxins levels were found to be within 10 ppb recommended by the CODEX STAN 193-1995. Therefore, the study concluded that exposure to mycotoxins through the consumption of cassava products in Zambia was minimal. However, consumers are exposed to microbiological poisoning. Thus, the study recommends that farmers and household processors be trained on good hygienic practices, adopting best practices in processing, soaking and washing raw cassava tubers after chipping and before drying, good storage techniques, and the government of Zambia create standards for cassava products.

Keywords: Cassava products; Mycotoxins; Microbial analysis; Contamination, Post-harvest processing

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Positive human interaction prior to weaning improves meat quality in pigs

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Early life experiences are known to shape how an individual reacts to situations later in life. Early experience during this period can affect stress resilience later in life. Since stress can negatively influence pork quality and increase sensory quality failure rates of pork, improving stress resilience may also improve pork quality. It was hypothesised that pigs that received maternal contact or positive human contact early in life will have improved carcass and pork quality.

Seventy-nine Large White x Landrace mixed sex pigs, selected from 72 litters in a 2 x 2 factorial design for treatments available/restricted maternal contact (MC+/MC-) and positive/standard human contact (HC+/HC-), were followed to slaughter for carcass and objective pork quality assessment. Modified farrowing crates were used to restrict maternal contact (MC-) and litters in the HC+ treatment received five minutes of daily positive human interaction (patting) if piglets approached the experimenter during lactation. Treatments ceased at weaning. Results were analysed using REML models that incorporated design features of the study. The *m. longissimus thoracis et lumborum* ultimate pH was higher in HC+ than HC- pigs (5.50 vs 5.56, $sed=0.019$, $P=0.009$), but no MC effect or interaction was found. No treatment effects ($P>0.05$) were observed for a range of other quality measurements, including hot carcass weight, P2 backfat fat depth, colour measurements, drip loss and shear force.

The higher ultimate pH in HC+ pigs not only indicates improved pork quality, but also suggests an reduced stress response in the live animal prior to slaughter.

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Does legume introduction to intensify cropping systems improve farmer health and well-being?

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Effective and sustainable agricultural intensification requires positive outcomes for both humans and the environment. Although studies indicate that introducing legumes to traditionally mono-cropped systems can sustainably intensify agriculture, legume diversification is routinely ignored in socio-ecological assessments of agricultural intensification. Research and policy also typically focus only on environmental outcomes, ignoring the full suite of human well-being outcomes. To identify the social, ecological and economic contexts under which win-win outcomes are achieved for people and the environment, we perform a global systematic review of 243 studies that simultaneously evaluate ecosystem-service and human well-being outcomes of grain legume intercropping and rotational cropping. Our results support findings of positive outcomes across a wide range of ecosystem services, with the greatest benefits for food provisioning, nutrient cycling, soil organic carbon sequestration, and disease, weed and water regulation. More importantly, more than 90% of cases demonstrate co-joint increases in ecosystem services and well-being. This contrasts with global reporting that non-leguminous agricultural intensification rarely leads to positive outcomes for both people and the environment. The most frequently reported well-being outcomes of legume diversification are increased income, natural capital, food security, health and nutrition. Well-being outcomes are more likely to be mixed (negative and positive) than environmental outcomes, due to negative impacts on employment, property rights and physical capital. However, most non-economic well-being indicators remain poorly studied. Farmers are likely to benefit from improved environmental health and livelihoods when introducing legumes to food-cropping systems, but well-being trade-offs must be considered when designing policy instruments to encourage adoption.

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Processing of green seaweed (*Ulva* sp.) protein biomass to enhance consumer acceptance

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Seaweed is an emerging crop in Western cuisine, despite being well established in Asian countries mainly as human food. In Western countries the acceptance of novel seaweed ingredients by food manufacturers introduces challenges, such as aroma and taste. Although seaweed has various health benefits and its production is more environmentally friendly compared to legumes, its use in western foods is limited due to sensorial characteristics. One promising method to modify sensorial properties and sometimes change the nutritional quality of food, is fermentation. To date, limited studies investigate the effect of seaweed fermentation on sensorial properties and its effect on consumer acceptance. This is the first study using fermentation as a tool to modulate the aroma of protein rich biomass from seaweed. Preliminary investigations, involving various common lactic acid bacterial (LAB) and fungal strains, demonstrated successful fermentation of seaweed protein biomass (SPB), through sensorial modification and reduction in the 'green' note. Paired comparisons revealed significant differences in the seaweed aroma between the fermented and raw SPB for both LAB ($p \leq 0.05$) and fungal ($p \leq 0.01$) strains. Additionally, a trained sensory panel developed a lexicon to describe qualitatively aroma differences. Using a multi-disciplinary approach, the effects of fermentation with a range of microbial species for effects on aroma and taste will be investigated. Further, fermented SPB will be incorporated into a previously developed food matrix for sensory profiling. The goal is to develop a versatile SPB that maintains or improves its nutritional quality and sensorial characteristics for commercial food applications.

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Nanosecond pulsed electric field for non-thermal milk pasteurization: safety and quality aspects

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Non-thermal food processing technologies effectively inactivate bacteria while limiting the negative impact on food quality and extending shelf life. Instead of conventional pulsed electric field (PEF) systems ranging from milli- to micro-second pulse widths, nanosecond PEF (nsPEF) that delivers a peak power of up to 18MW was investigated in this study. Ultra-high-temperature (UHT) milk inoculated with a fixed number of bacterial colonies and raw bovine milk were used and analysed for both safety and quality aspects. UHT milk (50, 65, and 100mL) were inoculated with 10^7 colony forming units (CFU)/mL of *Escherichia coli* (JM109) and treated with 10,000 to 20,000 unipolar pulses with 290 ns duration (50 Hz) in a rod-to-rod batch-type setup with an electric field of 20 to 30 kV/cm using a high-power pulse generator. The delivered energy was 5.2 J per pulse. More than 5 log reduction was achieved in all sample volumes, with a peak temperature below 25°C. Similar treatment conditions were applied to raw milk (50mL), and the results after applying 8000 pulses were comparable to conventional pasteurization method; approximately 2 log reduction was achieved in total plate count with an initial bacterial count of 10^3 CFU/mL. Raw milk, low temperature long time (LTLT) pasteurized milk, and nsPEF processed milk were all tested for quality. Free fatty acid levels were significantly decreased in both nsPEF and LTLT treated samples, whereas viscosity was slightly increased in the nsPEF treated samples. Particle size was reduced after nsPEF treatment, but no protein denaturation was observed in the samples.

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Breakdown of sweetpotato bedding roots: investigating plant pathogens in Australia and PNG

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Sweetpotato (*Ipomoea batatas*) storage root breakdown in plant beds is regularly seen in commercial sweetpotato production and leads to decreased productivity of shoots for field planting. Cultivar differences and abiotic factors such as soil temperature, soil moisture, and poor drainage may drive physiological changes in storage roots. Biotic factors such as soilborne pathogens and endophytic bacteria and fungi may also play a role in premature breakdown of bedding roots. Previous research has shown that *Erwinia* spp., *Fusarium* spp. and *Sclerotium rolfsii* have been implicated in root rots and wilting of the shoots. In Australia and Papua New Guinea, it is unclear which of these microorganisms are associated with or cause breakdown of sweetpotato storage roots. In Bundaberg, QLD, we collected sweetpotato storage roots and shoots from healthy and diseased plants across three farms, representing a total of seven cultivars (Beauregard, Bellevue, Bonita, Eclipse, Orleans, Murasaki and Northern Star). Plant specimens were sub-sampled, sectioned, and plated onto growth media. Pure cultures were obtained and have been frozen for future DNA extraction, PCR, and sequencing, to identify cultures to species level. Representative fungi and bacteria will be examined for their role in storage root breakdown, by confirming Koch's postulates in the glasshouse. Understanding what microorganisms are present in the storage roots has implications for both plant disease management and biosecurity. This study aims to create a better understanding of plant pathogens that may impact sweetpotato production both in Australia and PNG to minimize yield losses associated with plant disease in plant beds.

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Decolonising food regulatory frameworks: Rethinking the dietary risk assessment of First Foods

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As interest in Australian native products continues to grow world-wide, Aboriginal and Torres Strait Islander peoples (First Peoples) are striving to be industry leaders in the production of “First Foods” that are being developed for commercial markets. To successfully gain market approval both within Australia and globally, food regulatory authorities require at least a documented history of safe use to indicate dietary safety. Moreover, many countries also require compositional analysis and safety data to further support their safe human consumption. However, safety data is lacking for many of these traditional food items and the history that surrounds their safe use has rarely been recorded in written form, but rather passed on through cultural practices and language.

This project evaluates the suitability of current regulatory frameworks and highlights the food safety regulatory hurdles that are felt by First Peoples and their businesses attempting to enter the Australian native foods industry. These issues also extend to the requirements of food regulatory authorities around the world, when assessing food safety and the market eligibility of traditional food items.

Through consultation with policy makers and Community, a novel framework approach has been developed to help address these problems, including the incorporation into current food regulatory frameworks of evidence-based dietary risk assessments of traditional food products in a manner that better accommodates the stories, traditional knowledge, and interests of First Peoples, whilst also meeting the safety data requirements set out by regulatory bodies both within Australia and around the world.

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Topical RNAi for Sustainable Animal Health in Australian Sheep Flystrike

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Sheep flystrike is one of the most economically important diseases affecting the Australian sheep and wool industry (>356M/annually). Currently, control of *Lucillia cuprina* relies almost exclusively on chemical controls and have developed resistance to nearly all control chemicals used in the past, it is critical to develop an alternative solution to control and manage flystrike. RNA interference (RNAi) technologies have been successfully explored in multiple animal industries for developing parasite controls. This research project aims to a RNAi based biological control for sheep blowfly. Double-stranded RNA (dsRNA) has already proven successful against viruses, fungi and insects. However, the instability of dsRNA is a major bottleneck with a protection window only lasting 5-7 days. Bentonite polymer (BenPol) technology can overcome this problem, as it can be tuned for controlled release of the dsRNA in the blowfly larvae gut challenging pH environment, prolonging its exposure time to and uptake by target cells. We have investigated four different BenPol carriers for their dsRNA loading capabilities of which three of them were able to afford dsRNA stability under multiple temperatures (4°C, 22°C, 40°C, 55°C) in the sheep serum. Our results, establish that the dsRNA when loaded on BenPol particles is stable unlike dsRNA alone which degraded rapidly in serum. A stable nanoparticles delivery system that can protect and increase the inherent stability of the dsRNA molecules at higher temperatures in a complex biological fluid like serum, offers a great deal of promise for the future use of this approach for enhancing animal protection.

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Amoxicillin susceptibility of avian *Pasteurella multocida*; setting the epidemiologic cutoff value

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Poultry is the most consumed meat in many countries as it is a low-cost, high-quality protein. Fowl cholera, a contagious bacterial disease of chicken caused by *Pasteurella multocida*, causes significant economic losses in many countries, particularly in layer chickens in free range production systems. In Australia, prevention is achieved by routine vaccination but once a disease outbreak happens, the flocks need to be treated with antimicrobials. Up to 2019, only 15 antimicrobials (Apramycin, Neomycin, Spectinomycin, Trimethoprim/sulfadiazine, Sulfadimidine, Flavophospholipol, Lincomycin, Erythromycin, Tylosin, Avilamycin, Tiamulin, Zinc bacitracin, Virginiamycin, Chlortetracycline, Oxytetracycline) were registered to be used in the Australian poultry industry. Amoxicillin is the newest antimicrobial registered to be used for poultry in Australia. Susceptibility testing is an important tool for monitoring the development of resistance, with its utility based on the availability of breakpoints or epidemiological cut-off values (ECOFF). However, there are no interpretation criteria for amoxicillin against *P. multocida* from poultry in the major standard methodologies such as CLSI or EUCAST. In this study, 80 *P. multocida* isolates from chickens that had not been exposed to amoxicillin were subjected to disc diffusion assay to determine inhibition zone diameters (IZD) for amoxicillin using the CLSI methodology. Based on the normal distribution of IZD values in our work, wild type bacteria that are sensitive to amoxicillin will show a diameter of ≥ 28 mm, a cut-off which categorized 95% of the isolates as wild type. This work will help support amoxicillin stewardship in the chicken industry in Australia.

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Understanding the nutritional quality and functionality of *Persoonia* species

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Persoonia genus from the *Proteaceae* family is endemic to Australia and comprises of 99 species, which are mainly distributed in western and eastern Australia. Fire-prone habitat and unique seed dormancy of the *Persoonia* genus contribute to poor propagation and transplantation. Thus, some *Persoonia* spp. are listed as threatened species. Moreover, *Persoonia* spp. have been traditionally used by Indigenous Australians for food and the treatment of eye disorders, skin infection and diarrhea. In the present study, we are investigating the morphology, physicochemical properties, proximate, mineral and trace element composition, main phytochemicals as well as antioxidant and antimicrobial activity of *Persoonia stadbrokensis* and *Persoonia linearis* to get a better understanding and to find the potential market access of their nutritional quality and functional properties. Results will be presented at the conference.

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Gel properties of almond yoghurts with varying protein, fat and sugar contents

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Almond-based dairy yoghurt substitutes are more sustainable and environmentally friendly than dairy yoghurts. It is suitable for consumers who suffer from lactose intolerance, minerals deficiency and dairy protein allergy issues. Studies on almond yoghurts have mainly focused on sensory attributes and nutritional benefits. However, most commercial almond-based yoghurts still have protein inadequacy problems. The balanced nutritional panel of almond yoghurt also need to be considered as reducing the calorie intake from sugar and fat has become the main concern for public health. This research evaluated how the major components influence the gel properties of almond yoghurt by determining their physicochemical and microstructural characteristics. The protein, fat and sugar in the almond yoghurts varied from 2% to 6%, 0.8% to 7% and 0.6% to 7%, respectively. The results revealed that an increase in proteins from 2% to 6% enhances the water holding capacity, firmness, cohesiveness, lightness, the flow and gelation behaviour of almond yoghurt. Increased fat contents in the range of 0.8% to 5% played a similar role in the gelling properties of almond yoghurt, similar to increased protein contents. However, the increased fat content of up to 7% may have an adverse effect. There was no significant difference observed in the flow behaviour of almond yoghurt with sugar concentration variation. The physicochemical characterisation results of almond yoghurts with composition variance will provide valuable knowledge on the production of reduced-fat and sugar contents of almond yoghurt with considerable protein content comparable to dairy yoghurts.

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Transcriptome analysis of *Musa balbisiana* cultivar Kepok Against Blood Disease of Banana

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Blood Disease of Banana caused by *Ralstonia syzygii* subsp. *celebesensis* (Rsc) which originated from Selayar Island, South Sulawesi, Indonesia. The disease symptoms of banana infected by Rsc were red-brown vascular staining, discoloration of young fruit, vascular rottenness, and leaves becoming chlorotic and rotten. A control method of the disease is urgently needed to suppress the loss caused by the disease however the information about Rsc, diversity, and molecular character is still limited compared with *Ralstonia solanacearum*. The first draft genome of Rsc originated from Indonesia was published and can be used for references genome to develop research-based on transcript both on host-infected and the virulent pathogen to know the pathogenesis on the molecular aspect. The research was conducted to know the transcript profile on *Musa balbisiana* cultivar Kepok infected by Rsc and Rsc cultured on host extract medium using Next-Generation Sequencing. Overall the number of differentially expressed genes (DEGs) was higher in Rsc infection than in RS and Mock, furthermore, 5296 genes were up-regulated and 2769 genes were down-regulated in Rsc and 2759 genes were up-regulated and 1929 genes were down-regulated. In the transcript of Rsc growth on host extract medium, only 166 genes were identified to have DEGs including 155 genes were up-regulated and 11 genes were down-regulated. The transcriptomics revealed some resistance-related genes, pathogenesis-related genes, and volatile organic compound (VOC) –related genes caused by host-pathogen interaction. This revealed gene can be a starting point to develop the research on molecular aspect to design a control method of the disease.

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Facilitating adoption of multiscale monitoring tools for managing Australian mango crops

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Key advances in the development of multi-scale monitoring tools including in-field machine vision and satellite yield mapping promise to greatly improve the accuracy and efficiency of on-farm and regional yield forecasting for the Australian mango industry. These technologies will have benefits on-farm, through enhanced harvest planning, logistics and transport coordination. Accurate and timely volume forecasts also enables wholesalers and retailers to accurately prepare market plans to ensure fruit is moved quickly in peak periods, minimising lower prices to the farmer and maintaining good quality fruit for the consumer.

A collaborative project “Multi-scale monitoring tools for Australian Tree Crops – Phase 2” funded by the Australian Governments Rural R&D for Profit Program and Hort Innovation has worked closely with Australian mango growers for the past 4 years to ground-truth and develop these new multi-scale technologies. Key partners include the University of New England, Central Queensland University, QDAF, NTDITT and the Australian Mango Industry Association.

The two main techniques developed for mango orchard yield mapping were the use of satellite imagery and vehicle mounted machine vision equipment. The satellite imagery methodology developed by UNE uses high and medium resolution satellite imagery, with 18 representative trees selected and then manually counted in-field. The machine vision technology developed by CQU involves identification and the counting of individual fruit on the tree using vehicle mounted cameras with advanced “fruit recognition” software. Analysis of both these methods have achieved yield accuracies of around 90% when compared with actual final harvest counts.

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Goldfinger bananas - a variety that is tasty and TR4 resistant

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In 2015 Fusarium wilt tropical race 4 (TR4) was detected for the first time in north Queensland, and is now located on six farms. This disease has the potential to destroy whole crops of the commercial variety, Cavendish, which accounts for 95% of Australian production, valued in excess of \$500 million. The variety Goldfinger has TR4 resistance but its relatively soft fruit texture and lacklustre flavour has greatly curtailed commercial potential. Queensland DAF have used mutation breeding to seek improvement of its eating characteristics. Variants were firstly generated by the Maroochy team. Agronomic assessment and in-house taste testing then took place at South Johnstone. Five selections were identified and advanced to the next stage of more detailed sensory analysis and larger scale consumer panelling by the consumer intelligence team at Coopers Plains. Cavendish, Lady Finger and the original unmutated Goldfinger were included as controls in the comparison tests. The large-scale taste panelling has indicated that consumer acceptance of four of the Goldfinger variants was equivalent to the existing commercial varieties of Cavendish and Lady Finger. All five variants had better consumer acceptance than the original Goldfinger. The next stage will involve on-farm trials and detailed postharvest ripening and handling studies. This research represents an important step forward in the development of a banana variety that is both tasty and TR4 resistant, having demonstrated that mutagenesis was successful in improving the eating characteristics of Goldfinger bananas.

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Satellite remote sensing ‘time series’ model for monitoring tea tree crop phenology

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Remote monitoring of tea tree crop phenology is crucial for optimizing the farm management activities, improving crop productivity, yield estimation and evaluating the crop resilience to extreme weather conditions. In this study, high resolution Sentinel-2 data from 2015 to 2021 have been explored to monitor tea tree crop phenology. All available cloud free images (less than 30%) were acquired, and cloud and cloud shadow masked using Google Earth Engine (GEE). The images were clipped according to the tea tree crop boundaries and the vegetation index (VI) was derived using multiple band combinations and plotted against the time to visualize the tree growth pattern. This information showed the trends of crop vigour at different key phenological stages and the effect of different constraints such as droughts, floods and management. This also indicates when optimal harvest timing should occur and how the timing can vary over different farms. The average of all VI values during 7 years period were plotted against the time of season and the resultant quadratic model ($R^2 = 0.78$) was fitted to represent the generic progression of crop growth. The evolution of VI profile shows a distinct growth phases of tea tree crops such as vegetative development and the senescence of the crop. The model indicates that the VI value or the crop vigour reaches its peak on first week of March. It also allows growers to bench mark tree performance to better respond to constraints such as soil moisture, fertilizer, pests, diseases and any extreme weather events.

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BenPol nanoparticles as a ds-RNA delivery system in crustaceans

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Diseases are major drawback in aquaculture industry, especially viral diseases which markedly cause lower production and economic losses. Different treatments have been applied to control and solve the disease, but the main challenge in aquaculture is to establish an effective system to deliver treatment doses or medicine to the target the pathogen of interest in the most practical way. RNA interference (RNAi) is a mechanism that can manipulate expression of gene by using double-stranded RNA (dsRNA) as triggers for target RNA degradation through enzymatic processes inside eukaryotic cells. RNAi technology has been used as a potential tool in aquaculture to overcome aquatic diseases. To deliver RNAi to aquatic organisms, various nanoparticles have been developed to enable efficient delivery. In this study, **Bentonite** complexed with Poly[2-(Dimethylamino) ethyl Methacrylate] (PDMAEMA) **Polymer** (BenPol) were used. BenPol is positively charged which can condense with negatively charged materials such as DNA, RNA or dsRNA. The BenPol complexes are cell permeability and can protect dsRNA from environmental and enzymatic degradation making them ideal for use in biological systems. Thus, this study aimed to investigate BenPol for dsRNA delivery to prawns. DsRNA-beta actin was used and complexed with BenPol before administration to the model crustacean, *Macrobrachium australiensis*, by injection and oral administration. Suppression of the beta-actin gene was higher in both BenPol-dsRNA complex injection and feeding groups compared to ds-RNA only. Moreover, the reduction of protein expressions was higher in BenPol-dsRNA complex feeding compared to other treatments. Therefore, BenPol is promising material to deliver dsRNA into prawn.

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Constant water table rainproof pot system: An outdoor method to measure WUE

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Outdoor screening of plants in pots provides a more field-like environment, avoids the 25% loss in sunlight commonly occurring in a glasshouse, and can be beneficial when indoor space is limited. However, this system needs to be rainproofed for any water use efficiency (WUE) study. Therefore, a cost-effective modification was applied to Hunter's (1981) constant water table ANOVApot[®] to rainproof the system. These modifications are described, tested and reported on two mungbean genotypes both in inside and outside environments during extremely wet weather conditions.

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Innovating cryopreservation for conservation of the endangered Australian native plant *Gossia fragrantissima*

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Myrtaceae is a well-established family in Australia and contributes significantly to the diversity of Australian flora and ecosystems. *Gossia fragrantissima* is an Australian native rainforest species from the Myrtaceae family, characterized as having the rare trait of hyperaccumulating metal elements, a process that has potential application in phytomining and phytoremediation. The species is now threatened by human activities and Climate change. Moreover, it is also susceptible to 'Myrtle rust', a threatening fungal disease first identified in Australia in 2010. Common conservation methods (e.g. seed banking) are not very suited to the species because the seeds are sensitive to long-term -20 °C conditions. Cryopreservation, which refers to store regenerable tissues in liquid nitrogen (LN) at -196 °C, may provide an alternative method to preserve the species *in vitro* at a low cost and space requirement.

In the study, two types of cryoprotectants, Plant Vitrification Solution 2 (PVS2) and Vitrification Solution L (VSL), were trialed to develop a cryopreservation protocol for *G. fragrantissima* shoot tips. Survival and regrowth of shoot tips treated with PVS2 were 76.7% and 23.3% respectively, while those treated with VSL were 63.3% and 20.0%. The results indicated that PVS2 supported better pre-cryopreservation viability of shoot tips than VSL. Cold pretreatment (10 °C, 13 days) of donor plants was found to improve the survival of shoot tips subjected to LN by 16.67%. This study is the first attempt to preserve *G. fragrantissima* using cryotechnology, providing opportunity for future translation to other endangered *Gossia* species and wider Myrtaceae under threat.

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Sequencing of Australian wild AA genome rice species

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Rice is grown all over the world and eaten by about 3 billion people, or about half of the world's population. The genus *Oryza* comprises two cultivated (AA-genome) and 24 wild rice species (AA-HHJJ genome), encompassing a total of 11 genomes. Wild rice belonging to the AA genome group and closely linked to domesticated rice, can be found across the tropical world. There are two species of wild rice native to Australia: *Oryza rufipogon* type (Taxa-A) and *Oryza meridionalis* (Taxa-B) belong to AA genome. Australian AA genome wild rice populations are distinct from Asian domesticated rice populations and provide a foundation for studying the rice genome before domestication and represent a potential source of unique traits for rice breeding. *O. meridionalis* (Taxa-B) is the most distant species in the AA genome group, according to phylogenetic relationship based on chloroplast and nuclear genome sequences, making it a valuable resource for enhancing rice and studying rice evolution. The two Australian AA genome species were sequenced (PacBio HiFi) and assembled to allow comparative of these wild rice genomes with those of domesticated rice and wild rice from Asia. Significant structural rearrangements of the genomes that may be associated with domestication were characterized. The development of high-quality genome sequences for Australian wild rice species has provided new insights into the history of rice domestication. In addition, desirable genes from Australian wild rice species will be transferred to domesticated rice to enhance rice production.

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Mungbean-compatible wild bradyrhizobia from north Queensland: A valuable untapped resource

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Bradyrhizobia are bacteria required by mungbean for nitrogen fixation. Currently only one commercial strain of bradyrhizobia, CB1015, is used by Australian growers to inoculate mungbean crops. Australia is a centre of diversity for mungbean, hosting several native species, mostly in the tropics. We collected wild bradyrhizobia strains from a range of sites in the dry tropics of Queensland and compared them with the commercial strain, CB1015, for performance of inoculated mungbeans in a glasshouse experiment. We found that most of the collected strains promoted growth at least as well as the commercial strain under both acid and neutral conditions, with some significantly outperforming the commercial strain under neutral conditions. This study suggests that gains could be made in mungbean performance through use of better-adapted bradyrhizobia. Further, there is significant untapped genetic diversity of wild bradyrhizobia that could be exploited to improve performance of legume crops in northern Australia.

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Comparison of short/long read sequence data in generating a chloroplast genome sequence

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Independent evolution of the nuclear and chloroplast genomes of plants has been used in phylogenetic analysis providing inference of the evolutionary relationship even at the species level. Phylogenetic analysis makes use of sequence differences to define relationships. A number of phylogenetic studies carried out using the entire chloroplast genome sequence have relied on using Next generation sequence data which is now affordable for this application. Depending on the plant species, up to 2,500 chloroplasts can be present in a single plant cell. Hence, chloroplast genome sequence can be easily assembled using short read illumina data sets even at low genome sequence coverage. Long read data sets using the PacBio sequencing platform are an attractive option for the assembly of a complete and accurate chloroplast sequence. Use of the PacBio continuous long reads (LCR) reads, with a read length of tens of kilobases, maybe an option to generate the entire chloroplast genome sequence in one or a few reads. Alternately, use of the PacBio HiFi option which generates shorter (15 to 25 Kb) but more accurate reads is another attractive option in assembling an accurate chloroplast genome sequence. We have compared the utility of these sequence data sets generated from a number of species to generate/assemble a chloroplast genome sequence.

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Transcriptomes of wild and domesticated rice

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Transcriptome profiling is useful in providing information regarding the function and expression patterns of the genes controlling important traits. The transcriptome of domesticated rice (*Oryza sativa* ssp. *japonica* var Nipponbare) and two Australian wild rice (*Oryza rufipogon* type taxa and *Oryza meridionalis*) showed a complex diversity. The long reads (Iso-seq) derived from leaves, roots, seeds, inflorescences, and panicles of domesticated rice produced 346,190 non-redundant full-length non-chimeric reads resulting in 33,504 high-quality transcripts. The transcriptome included 33,456 isoforms from 12,772 genes (11,803 annotated and 969 novel genes) of which 18,582 (55.5%) of the splicing isoforms were known and 14,874 (44.46%) were novel. 12,755 (17%) of the total splicing junctions (73,659) represented novel splice junctions with canonical and non-canonical intron boundaries. Gene expression analysis using RNA-seq revealed that genes were significantly differentially expressed from early to late stages of seed development in both wild rice and domesticated rice. Genes related to domestication traits (seed shattering, grain size, hull colour and pericarp and seed coat), starch and sucrose metabolism, and seed storage proteins were differentially expressed, declining from early (5 DPA (days post anthesis)) to the middle stage (15 DPA) while expression of a hull colour gene (*Bh4*) continued from early to the later stage of seed development. A total of 38 novel transcripts with coding potential corresponding to domestication loci, starch and sucrose metabolism, and seed storage proteins were identified. This information might help to improve the current reference genome for rice and explain differences in rice grain quality and nutritional value.

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Progress towards accelerating genetic gain in the Ethiopian durum wheat breeding program

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We describe a recent project which aims to address food security issues in sub-Saharan Africa by seeking an enduring increase and stability in productivity of durum wheat through the development of more effective local durum wheat crop improvement programs in Ethiopia. The project involved improving the strategic focus of the program, through defining product concepts targeted to specific agro-ecologies in Ethiopia, changing strategies and re-designing the breeding pipelines in addition to introducing new technologies and methods, to enable the program to manage large numbers of genotypes. This will be achieved by the phased introduction of new technologies and mechanization to allocate and use resources more efficiently at relatively low extra cost. Such technologies include electronic data capture, improved seed tracking and barcoding systems, data storage and data sharing systems and enhanced statistical analyses of trials.

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Scanning the wild for fitness in macadamias against *Phytophthora* diseases

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The wild population of the four *Macadamia* species (*M. integrifolia*, *M. tetraphylla*, *M. ternifolia* and *M. jansenii*) are vulnerable to new and emerging pathogens, including those belonging to the genus *Phytophthora*. Wild germplasm is often regarded as sources of genetic materials in breeding programs. In Australia, *P. cinnamomi* and *P. multivora* are the major species causing stem cankers and root rot in macadamia orchards. There is no information on their interaction with the *Macadamia* species, therefore, this study utilised wild *Macadamia* accessions to examine host-pathogen interaction and to identify resistant accessions to the two *Phytophthora* species. Disease severity was generally high in *M. ternifolia* compared with the other three *Macadamia* species, in field conditions. Approximately 60% of the wild *M. tetraphylla* and 40% wild *M. integrifolia* genotypes were tolerant to *Phytophthora* disease symptoms (slow decline and stem canker), in the field. Results from *in vivo* assays identified 4 *M. tetraphylla* and two *M. integrifolia* genotypes as resistant to both *P. cinnamomi* and *P. multivora*. *M. tetraphylla* and *M. jansenii* were the most resistant to *P. cinnamomi*, whereas *M. ternifolia* and *M. jansenii* showed the least disease severity levels to *P. multivora*. This study revealed that quantitative variations exist among the wild *Macadamia* genotypes that strongly partitioned the wild genotypes into three resistance groups, thus, are potential candidates for use in macadamia breeding programs.

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Haplotype-resolved genome assembly of jojoba revealed genes associated with drought tolerance

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Jojoba (*Simmondsia chinensis*) is a dioecious plant (the male and female reproductive organs are found in different individuals) native to North America. It is a common desert perennial shrub known for its high water-stress tolerance and economic importance due to producing highly valued ester-wax oil which is being widely used in cosmetic industry. In this study, first we sequenced the female and female plants using PacBio HiFi reads. The genomes were assembled using an Improved Phased Assembler (IPA) and HiFiasm. They were scaffolded further into a chromosome-level assembly using a Dovetail Omni-C pipeline. The results clearly indicated a 10 MB difference between the male and female assembly sizes. Further analyses identified an additional 10 MB region (including two insertions) in Chromosome 9 defining the male plants. These two insertions (Y1 and Y2) only exist in the male and are absent in the female. To understand the novel genes responsible for the exceptional drought tolerance of this species, we created a long read IsoSeq reference transcriptome of jojoba leaves. This study identified 426,380 isoforms with a total length of 1,110 Mb and an N50 of 2,993 bp. To further investigate the drought-associated genes, a differential expression analysis was conducted between plants grown under contrasting drought conditions (well-watered to sever drought). The results also revealed a significant number (10,936) of differentially expressed genes under normal and drought condition including antioxidant activity-related genes (SODs and PR4), water and molecular bio-channels such as AQPs, cell membrane protectants such as LEAs, and growth regulators such as ACCs. A total of 880 novel transcripts representing novel genes that were associated with jojoba water stress tolerance were also identified.

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Innovative cryopreservation technology for Australia macadamia

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Macadamia is a high-value nut crop that is endemic to Australia and valued at over AU\$3 billion globally. The genetic base of the commercial cultivars is narrow as most of the commercial trees originated from Mooloo in regional Queensland, Australia. The wild germplasm of macadamia remains unexplored for breeding and some of the diversity in the wild is suffering from loss due to the destruction of the macadamia habitat. Traditional conservation methods such as seed banking are unfavourable for macadamia as it belongs to exceptional species and cannot be stored at -20 for the long term. Thus, cryopreservation of macadamia is a potentially significant tool to supplement macadamia conservation efforts and effectively maintain germplasm collections in the long term.

The objective of this study is to establish the first cryopreservation technology for macadamia cultivars using true-to-type shoot tips. A tissue culture regeneration system will also be developed to regrow the preserved plant tissues after Liquid N₂ treatment. Shoot tips were dissected in the size of 1 x 2 mm under the microscope by using untreated *in vitro* macadamia cv. 'Beaumont' plants. Preliminary results of shoot tip dissection achieved an 80.0% of survival and 76.6% of regrowth. Trials of cryoprotectants to prevent the formation of ice crystals during the cryopreservation process are underway. The droplet vitrification method to cryopreserve the shoot tips in Liquid N₂ will then be tested. This study aimed to provide a foundation for the preservation of diverse macadamia germplasm to ensure the macadamia industry of the future.

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Discovery and curation of global cereals held by the Australian Grains Genebank

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Over the past 100 years, there has been several amalgamations of Australian genetic resource centres in an effort to consolidate, evaluate and appropriately store unique germplasm. Grain crop seed banks originally established by Australian Universities and Agricultural Research Institutions are now located in one national centre, The Australian Grains Genebank (AGG).

As the AGG Cereals Curator, I have had the pleasure of transposing the phenotypic and historical information stored within past curators preserved journals and fieldbooks in an effort to describe and make visible, on a modern digital online space, the story of these seeds that was once only told by pen and paper.

With a consolidated digital platform pre-breeders and breeders have an easily accessible opportunity to target accessions that are more likely to perform as expected. This also allows them to gain a greater appreciation of the diversity and potential of accessions previously hidden behind only a name and a number. The AGG cereals collection has a large amount of material donated by the USDA, which is the most diverse and informative cereals collection on the planet. Amongst these USDA donations are 1500 accessions of wheat, barley and oat species that were originally collected in the Asia Minor, Europe and Northern Africa by Jack Harlan and his father Harry.

In this presentation, I will illustrate the origins, diversity and importance of the AGG cereals collection while at the same time reveal the regions of the world that are unexplored amongst a collection of 100,000 cereal accessions.

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Sequencing Diversity of Macadamia Species

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Macadamia is an evergreen perennial rainforest tree of the family Proteaceae, indigenous to Australia. Two of the four species, *Macadamia integrifolia* and *Macadamia tetraphylla*, have been commercialized for their edible nuts, valued for their delicate flavour and being a good source of nutrients. Macadamia is a mostly outcrossing plant and understanding of genetic diversity at the species level would be beneficial for plant breeders in developing superior cultivars with desirable characteristics. Diversity analyses in macadamia has been reported using morphology, biochemical and molecular markers. However, to date, the genetic diversity has been poorly characterized although it was domesticated one and half centuries ago. The advent of high throughput sequencing techniques allows more complete analysis of diversity. We have compared phylogenetic relationships in the genus *Macadamia* by means of chloroplast and nuclear genome sequencing. Accurate chloroplast genome assemblies were generated for all four macadamia species. Phylogenies were investigated using both chloroplast genome and nuclear genome sequences. This study has supported the identification of the species status of cultivars of unknown origin and defined the geographical distribution of diversity of wild material. It will also allow whole genome analysis of associations between sequence variation and traits of value in breeding. This research will inform our understanding of the evolution of macadamia species.

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Oryza australiensis*; a potential source of diversity for rice improvement*Ms Sabrina Morrison^{1,2}**, Dr Agnelo Furtado^{1,2}, Dr Pauline Okemo^{1,2}, Professor Robert Henry^{1,2}¹University Of Queensland, St Lucia, Australia, ²Queensland Alliance for Agriculture and Food Innovation, St Lucia, Australia

Crops require ongoing advancements in order to address the increasing nutritional needs of populations and withstand fluctuations in climate extremes. Wild relatives of domesticated species are potential sources of novel genes that can be used to enhance existing crops and subsequently better meet global demands. The perennial wild rice species endemic to Australia, *Oryza australiensis*, is a promising potential source of genes for improving domesticated rice. *O. australiensis* is more highly diverged from commercial rice than other Australian wild *Oryza* species and possesses a range of unique characteristics that allows it to survive in northern Australian climates. *O. australiensis* exhibits heightened thermotolerance properties and an enhanced carboxylation capacity compared with the cultivated *O. sativa*. Salinity tolerance, disease resistance, and grain nutritional properties are also areas of interest that are currently being explored. The species' capacity to tolerate drought by existing as a rhizome in dry seasons is also a trait that warrants further investigation. This study aims to isolate genes that confer desirable or advantageous traits in *O. australiensis* and deploy them into the domesticated rice species, *O. sativa*. Sequencing and assembly of the *O. australiensis* whole genome has already been completed. Functional annotation of the genome will identify these candidate genes, and then CRISPR gene-editing approaches will be used for rapid and targeted integration of these genes into the *O. sativa* genome to assess the phenotypes in domesticated rice. Consequently, this study will provide insight into how traits in *O. australiensis* may be transferred into and thereby advance commercial rice cultivars.

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Characterising sorghum's crop wild relatives

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Sorghum (*Sorghum bicolor* [L.] Moench) is a promising crop for improving food security in the face of climate change. However, issues regarding sorghum's genetic diversity and ability to produce dangerous cyanogenic glucosides must be overcome if dependence on this crop is to continue increasing. Sorghum's diverse crop wild relatives could be used to introduce new traits to sorghum, increasing the crop's resilience and mitigating safety issues. However, the agronomically advantageous traits of wild sorghums are understudied, and crop wild relatives are generally poorly conserved. In order to tackle these issues, we used species distribution modelling to predict the environmental optima and tolerances of the wild sorghums, and screened a variety of taxa under various conditions and stressors to determine whether they too can produce dangerous levels of cyanogenic glucosides. Our results suggest that sorghum's wild relatives are relatively well conserved, cover a wide range of environmental niches, and generally do not store high concentrations of cyanogenic glucosides, highlighting their great potential for use in crop improvement.

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Phylogenetic relationships between Australian native citrus and commercial varieties

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Citrus is widely consumed across the world as a fruit crop. Despite many citrus species being extensively studied around the world, phylogenetic relationships among Australian native species and commercially important varieties in Australia remain unresolved. Here we present phylogenetic relationships among five Australian native species, four commercially important varieties and a previously unknown species found in Cape York Peninsula based on chloroplast genomes. Complete chloroplast genomes were de novo assembled using GetOrganelle toolkit and annotated by Geseq tool. Phylogenetic trees were constructed using PAUP*v 4.0 software with Maximum Likelihood (ML) method and MrBayes v. 3.2 in Geneious. The trees displayed two major clades. The first major clade contains the unknown citrus species and all the Australian native citrus species excluding *Citrus inodora*, which shows a close genetic relationship with *Citrus aurantium* and *Citrus limon*. *Citrus glauca* and *Citrus australis* formed one cluster revealing their close genetic relationship. Three seedlings of the unknown species and *Citrus garrawayi* were grouped into one subclade within the 1st clade. 198/192 SNP/INDEL variations between the unknown species and *C. garrawayi* also indicate that the unknown species could be a new distinct species closely related to *C. garrawayi*. The commercial species used in this study (mandarins) are within one sub cluster in the 2nd major clade indicating their close genetic relatedness. The results will further be verified by a nuclear gene phylogeny using 107 single copy genes. The present study will provide insights into a better understanding of phylogenetic relationships among Australian citrus species.

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Time gain compensation: The genetics of grain filling duration in sorghum

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Yield increases in sorghum, like other cereals has been attained in part through manipulation of grain number and size using genetics and management. Understanding the genetic control of a nexus of grain traits that contribute to a yield advantage in sorghum, especially with projected changes to the production environments promise to future proof sorghum yields. In this study we used a sorghum diversity panel of 904 individuals, genotyped with medium to high density genome wide SNPs and tested in three environments across two years to study variation in the grain filling duration (GFD).

A greater correlation across the test sites was observed when GFD was expressed in thermal time (0.57) than when expressed in diurnal days (0.30). Additionally, GFD ranged from 400 to 750 thermal units across the sites, with clear racial differentiation having Asian durra and Guinea sorghums predominantly on the upper range of GFD and Kafirs and Caudatums on the lower range of GFD. Further, GFD was correlated with kernel weight (0.32) across the test environments. A genome wide association analysis revealed 12 QTLs, six of which collocated with previously reported grain size QTLs in sorghum. A Chi-square test revealed substantial enrichment with a P-value of 0.014.

This study reports a potential common genetic control of GFD and grain size in sorghum, and racial differences in GFD. These findings are important in selection for longer grain filling genotypes in breeding programmes where grain size traits may be employed as proxy traits for GFD. Additionally, racial differences in GFD is instrumental in understanding selection and adaptation signatures of sorghum races.

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Genetic Diversity and Association Studies for Agronomic Traits in *Vigna* Species

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The genus *Vigna* is agronomically important taxa with many of its species under cultivation while others offering useful genes for improving cultivated types. 119 *Vigna* accessions from 19 species including 2 of *Phaseolus* were evaluated for yield and related traits and genotyped using 102 cross-genera and cross-species simple sequence repeat markers to study their genetic diversity, population genetic structure, and marker-trait associations (MTAs). The genotypes were grouped into four major clusters and 9 sub-clusters. All cultivated species shared a single cluster while the wild accessions were distributed in different sub-clusters. The model-based population structure analysis categorized 114 accessions into 6 genetically distinct sub-populations (K=6) following admixture-model based simulation. 91 accessions resembled their hierarchy and 23 were observed as the admixture forms. Subsequently, the panel was shortened to 98 accessions (13 species) and genotyped using 92 SSRs to study MTAs. Population genetic structure analysis grouped these 98 acc. in three genetically distinct sub-populations. MLM (Q+K) analysis revealed 13 MTAs namely, VR018, VR039, VR022, CEDG033, GMES0337, MBSSR008, CEDG220, VM27, CP1225, CP08695, CEDG100, CEDG008, and CEDG096A with 9 traits. 7 markers viz., VR018 for plant height (PH) and terminal leaflet length (TLL), VR022 for 100-seed weight (HSW) and pod length (PL), CEDG033 and MBSSR008 for days to 50% flowering (DFF) and days to maturity (DM), CP1225 for chlorophyll content at 30 days (CC30), DFF and DM, CEDG100 for PH and TLL, and CEDG096A for CC30 and CC45 were associated with multiple traits. The marker CEDG100 associated with HSW, PH and TLL is co-localized in gene encoding histone-lysine N-methyltransferase *ATX5*. Similarly, VR22 associated with PL and HSW is co-located in gene encoding *SHOOT GRAVITROPISM 5* in mungbean. These associations may be highly useful for marker-assisted improvement of *Vigna* species.

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Identification of New Sources of Resistance to Yellow Mosaic Disease in Mungbean

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Yellow mosaic disease (YMD) caused by any or a combination of the three Begomoviruses viz., *Mungbean yellow mosaic India virus* (MYMIV), *Mungbean yellow mosaic virus* (MYMV) and *Horsegram yellow mosaic virus* (HgYMV) is a major disease of mungbean and other *Vigna* species. The disease-causing viruses are transmitted by whiteflies (*Bemisia tabaci*) to healthy plants which spread quickly in the presence of susceptible host, congenial environment and viruliferous vector. While chemical control of the vector and the disease are not absolute and environment friendly, host plant resistance (HPR) is the most effective approach for management of this disease. Considering this, efforts were made during 2017 to 2021 for identification of new sources of resistance to YMD in mungbean. Over 450 genotypes comprising of advanced breeding lines and germplasm resources available at Indian Institute of Pulses Research (IIPR) and 296 mini-core accessions received from World Vegetable Centre (WorldVeg) were screened under natural field conditions using infector-row technique in wet-summer and spring seasons. Three advanced breeding lines (IPM 526-11, IPM 08-1 and IPM 312-17) developed at IIPR and seven accessions (VI001692 AG, VI003658 BG, VI000815 BG, VI004145 B-BLM, VI004069 BG, VI004789 BG, and VI003337 BG) from the WorldVeg mungbean minicore collection were observed as highly resistant and the disease incidence ranged between 0 to 3.1% as compared to 61.1 to 100% in the susceptible check (DGGV 2). Also, the disease severity was significantly lower (<1%) in resistant genotypes compared to DGGV 2 (>70%). The identified new sources of YMD resistance could be deployed for broadening the genetic base for resistance to YMD and for development of mapping populations to map genomic regions conferring resistance to this disease.

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An overview of Nepalese rice landraces: fine, coarse and aromatic

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The high demand of fine and aromatic rice in Nepal is fulfilled either from imports of open borders or super polished grain by local traders. In either case, the consumers are compelled to pay higher cost for low quality grains. With the recent issue of Geographical Indication (GI) tag claim by India on Basmati rice, the situation would be even worse. Nepalese need the past evidences on fine aromatic rice landraces to claim their originality which are popularized by their local dialect names as Basmati Anadi, Basmati Anpjhutte, Choti Basmati, Gola Basmati, Danda Basmati, Joroyal Basmati, Kalo Tunde Basmati, Jorpal Basmati, Lalka Basmati, Pahade Basmati, Rato Basmati, Rato Tunde Basmati, Rato Basmati Sano, Ujarka Basmati, etc. cultivated in diverse environment by local farmers but utilization in national rice improvement program is insufficient. There are just handful of landraces used as parental lines to develop improved varieties viz. Jarneli in Khumal-2, Pokhrela masino in Khumal 4, Khumal -5 and Palung- 2, Jumli marsi in Khumal-8 and Manjushree 2, pureline of Jethobudho as Pokhrela Jethobudho, pureline of Lalkabasmati as Lalkabasmati. The prevailing trend of fast-track registration of the exotic improved lines has overshadowed our grassroots level efforts. However, some landraces (Jarneli, Kalo marshi, Kalo nuniya, Mansara, Mutmur, Pakhe jhinuwa, Sali dhan, Samudraphij, Sotwa, Sukirato) were analysed for the traits: nutritious, medicinal, abiotic stress tolerance, resilience to low fertility soil. These Landraces need to be molecularly characterized to identify genes of valuable traits and understand phylogenetic diversity rewarding the future rice breeding program.

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Genomes of the four Macadamia species

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Macadamia is one of the few Australian native species grown for international export. The *M. jansonii* genome has been used as a model plant for testing sequencing methods using a wide range of long read sequencing techniques. Advanced long read sequencing technology and assembly methods enabled the assembly of a high-quality reference genome of four species of *Macadamia*, often with a single contig covering the complete chromosome, telomere to telomere. An initial, *M. jansonii* reference genome was generated using CLR contigs and Hi-C technology. Later, the CCS/ HiFi contigs of the four species, were scaffolded using the *M. jansonii* reference assembly. The *M. jansonii* genome showed about 20% genome duplication about 20 million years ago. The small populations of this rare species also explains the low heterozygosity of 0.98%. The assembly statistics showed 99% genome completeness with N50 > 53 Mb size. The genome size varied from 775 Mb to 796 Mb, where *M. tetraphylla* had the largest and *M. ternifolia* had the smallest assembly size. The genome comparison of the four species showed structural and functional variations. Understanding the genomic variations among four species will help in converting the large amount of genomic data into usable knowledge for the macadamia breeding programs.

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Studying the evolutionary significance of genome size diversity in the Proteaceae family

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A small genome has an advantage in terms of reduced cost of development and reproduction. However, the extent of interspecific and intraspecific variation in genome size content elevates inquisitiveness about its evolutionary and ecological significance. The Proteaceae family includes plants with genomes varying 300 folds from the smallest to the largest. Genome size may increase by expansion of repetitive DNA segments such as transposable elements (TE) and increases in ploidy whereas reductions may result from unequal recombination and loss of DNA during repair. This study will use the diversity of genome sizes in the Proteaceae to characterize how genome structure and composition varies with size. Flow cytometry will be used to measure DNA content of diverse members of the Proteaceae. Genome sequencing and assembly will allow chromosome level comparison of genome structure and organization in genomes of differing sizes. The gene content, extent of gene and genome duplication and repeat content (quantity, type and organization) will be related to genome size. Insights into the mechanisms of genome size variation in the Proteaceae will be used infer potential adaptive significance of genome size in the environments in which the species are found.

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Disease resistance breeding: a critical step towards future-proofing wheat in Sub-Saharan Africa

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Africa is faced with an impending food insecurity crisis. In less than four decades, one in every four persons on the planet will be from Africa. This population expansion raises a serious concern to build secure and resilient food systems in Africa by improving crop yields and nutritional quality and preventing crop losses to diseases. Wheat is one of the strategic crops for food self-sufficiency in Africa. The demand for wheat in Africa has increased more than for any other crop, yet it produces less than half of the wheat it consumes. Ethiopia is one of the leading wheat-producing countries in Sub-Saharan-Africa and it is grown by small-scale farmers. However, the local production satisfies two-thirds of the demand, and the remaining is imported from external markets. Several biotic and abiotic factors contribute to wheat yield losses in Ethiopia. Wheat stem and stripe rusts are the most predominant biotic factors limiting wheat production in the country. Genetic resistance is one of the sustainable and environmentally friendly management strategies for rust control, especially for resource-poor farmers. Therefore, the ultimate objective of this study is to understand the genetic structure of bread wheat breeding population and identify new source of rust resistance genes for the predominant stem and yellow rust pathotype using the old wheat collection "Vavilov Diversity Panel". The results of this study will directly contribute to the Ethiopian wheat breeding program's effort to improve rust resistance breeding in order to meet the country's goals of increasing wheat production and self-sufficiency.

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The INGB Lentil Core: a resource for accelerating lentil improvement

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Increasing demand for lentils as a staple pulse has led to the unlocking of diverse germplasm collections conserved in the genebanks to develop its superior varieties. Incorporation of new sources of genetic diversity into plant breeding programs is crucial for improving yield and quality, as well as tolerance to abiotic and biotic stresses. The Indian National Genebank (INGB) currently has 2,324 accessions comprising 1,796 indigenous and 528 exotic collections. The INGB core, composed of 170 worldwide accessions of cultivated lentils, has been assembled, having been derived based on the characterization data from the entire INGB lentil collection and geographical origin using a heuristic method and PowerCore software. The geo-referenced map showed that the INGB core set represented all agro-ecological zones where lentils are grown globally. This core set was sufficiently diverse and representative of the entire collection based on the comparison made using Shannon–Weaver diversity indices and the χ^2 test. This core set can be used in the genetic enhancement of lentils because of its composition of a potential set of germplasm identified for earliness, erect type, seed size, high yielding, multiple-podding, fast water uptake, high protein content and other vital traits. In summary, this diverse yet compact lentil collection constitutes a relevant resource to open the avenues for germplasm utilization in the selection, mapping, genomics, and trait discovery to attain sustainable lentil production under climate changing regime.

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Utilising gene editing to improve citrus flowering

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The Australian citrus industry is a large industry with exports amounting to 450 million Australian dollars in 2019 alone. With climate change potentially changing growing conditions for citrus trees in the future, understanding how fruit production is affected by these conditions becomes even more important. Flowering in citrus is highly correlated with fruit production and is also controlled by environmental factors like temperature and water availability. Climate change is likely to have a big impact on temperature and water availability, potentially affecting fruit production in the future. Currently, much of what is understood about flowering was learned from the model organism *Arabidopsis thaliana*, but the exact nature of flowering in *Citrus* trees is less known. This project aims to uncover what genes, gene regulatory processes and protein interactions are controlling flowering in citrus. RNA-seq is being used to uncover genes whose expression is correlated with floral induction. ChIP-seq is being used to uncover genes with expression silencing marks that are correlated with floral induction. CRISPR-Cas9 gene editing will be used to then edit flowering genes in the citrus model *Fortunella hindsii* to determine how flowering phenotypes may change based on loss of gene function. It is hoped that work from the project can also be transferred to industry to breed better citrus varieties by utilising gene editing to target specific genes of interest in commercial citrus species.

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Amaranthus Diversity in Papua New Guinea

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Amaranth is an important traditional vegetable that grows throughout the year in Papua New Guinea (PNG). Different species of *Amaranthus* occur in most parts of the country; however, there is very little knowledge of the genetic diversity that exists. The objectives of this study were to morphologically characterize amaranths based on their morphological traits; identify species; and molecularly characterize to confirm diversity and variations between accessions. From a working collection of landraces collected from farmer's fields in three provinces in PNG, nineteen accessions were morphologically characterised in an open field condition in Laloki, PNG from January to April 2017 and in a greenhouse condition in Gatton, Australia from August to November, 2018. Flower parts and inflorescence were examined to identify species and DArT fingerprinting was conducted to molecularly assess variation and confirm species identification. Pattern analysis of morphological traits indicated traits mostly performed consistently in both sites. Principle component analysis of quantitative traits showed a difference in accessions from both growing conditions. Flowering traits drove differences amongst accessions in PNG while in Gatton, differences were driven by vegetative traits. Six species were identified from the working collection to be; 1. *A. caudatus*; 2. *A. dubius*; 3. *A. blitium*; 4. *A. hypochondriacus*; 5. *A. cruentus* and 6. *A. tricolour*. DArT fingerprinting results confirm that there are six distinguished clusters from the nineteen accessions. The molecular and morphological data will provide a better understanding of the genetic diversity amongst Amaranth species in PNG.

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Analysis of phylogenetic relationships in genus *Mangifera* using chloroplast and nuclear phylogeny

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Mango (*Mangifera indica*), an evergreen dicotyledonous angiosperm belongs to the genus *Mangifera* of the family Anacardiaceae and is considered one of the most economically successful fresh fruit grown in tropical and subtropical regions of the world. To date, most accepted classifications of the genus *Mangifera* describe 69 species mainly based on morphological features of their reproductive tissues but the classification is not always supported by molecular studies where species categorized under different subgenera and sections have shown close phylogenetic relationships and some species defined as distinct species are recognized to be hybrids. Except for domesticated mango, 26 species have been identified that produce edible fruits and, wild species have been identified with desirable characteristics useful in trait-specific breeding programs to develop improved cultivars. Gaining benefit from these wild *Mangifera* species requires germplasm characterization but so far, molecular markers of chloroplast and nuclear genomic regions have been used to assess genetic diversity and relationships among species, and very few studies have used assembled whole chloroplast genomes and none of the studies have used multiple nuclear genes. Therefore, in this study, we conduct whole chloroplast genome assembly and nuclear gene phylogeny for a set of 11 *Mangifera* species to resolve taxonomical ambiguities and to analyze phylogenetic relationships in the genus, 43 commercial cultivars to assess genetic diversity among domesticated mango, and for 21 mango accessions to confirm their species identity. The results will provide a significant step towards using and selecting species and cultivars with agronomically important traits in future breeding programs.

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Traditional use of Australian native rice by Aboriginal people, Northern Territory, Australia

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We review information from across the Northern Territory about the use of Australian native rice by Aboriginal people, in order to capture the story of cultural affiliation with native rice.

There is growing interest among Aboriginal communities and organisations in commercialising native rice. Cultural identification and provenance are likely to be a source of pride for producers. Grain that has demonstrated cultural affiliations is likely to attract a premium price in some discerning and ethical consumer markets.

Monsoonal Australia supports expansive stands of three species of Australian native rice, that have been a widely consumed, and in some cases important, food in Aboriginal diets in the Northern Territory. Using ethno-botanical sources, we have found over twenty Aboriginal language names for native rice. Primary sources of traditional knowledge provide information on the culture around grain harvesting, processing and food preparation. We describe the challenges of the floodplain habitat of native rice in order to understand the task of harvesting. We reviewed studies of the geomorphology of northern monsoonal floodplains, and studies of floodplain archeology, to understand the likely use of native rice through time.

We discuss findings in the context of the model of grain-use proposed by Tindale, whereby the importance of grains in the traditional economy of Aboriginal people varied according to the availability of other resources. The study also discusses the limitations of ethnobotanical approaches that omit the context for plant use and overlook the important matters of the language and culture associated with harvesting and processing food.