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Recent trends in drought, heat and frost-induced yield losses across the Australian wheatbelt

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While global food demand is projected to grow by 50-80% by 2050, Australia is expected to continue its significant contribution to global food security. We quantified how recent climatic changes have affected wheat crops in Australia over the last 38 years. Changes in drought, heat and frost stresses affecting a mid-maturing cultivar sown on May 15 were quantified over 1981-2018 using an improved version of the Agricultural Production Systems sIMulator (APSIM). National drought-induced yield loss exceeded 40%, significantly increasing by 3.6% per decade ($P \downarrow 0.1$). Locally, decreasing trends, though statistically insignificant, were recorded in most sites from the South. The national average impact of hot days ($T_{max} \uparrow 26^\circ\text{C}$) on grain number, individual grain weight and total grain yield have increased by 0.3% ($P=0.21$), 1.3% ($P=0.05$) and 2.8% ($P \downarrow 0.05$) per decade, respectively. Frost damage has significantly increased by 6.4% per decade ($P \downarrow 0.001$). On average since 1981, heat and frost have been responsible for 15 and 14% wheat yield loss, respectively. On another hand, the rising atmospheric CO₂ concentration compensated for 2.4% of long-term average yield loss, with an increasing benefit of 1.8% per decade ($P \downarrow 0.001$). Overall, wheat yield has decreased at a significant rate of 180 kg ha⁻¹ per decade ($P \downarrow 0.01$) with the largest decreasing rate in the South-East (390 kg ha⁻¹ decade⁻¹) and East (220 kg ha⁻¹ decade⁻¹). As heat and drought are expected to remain predominant yield-limiting factors in the future, adaptation of wheat germplasm to warmer and drier environments appears to be a priority to enhance grain yield in Australia.

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Fall armyworm invasion and impact in Africa

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Maize is a major staple food crop grown in diverse ecological zones and consumed by many people in Sub-Saharan Africa (SSA). An estimated 208 million people in Africa depend on maize as a food security crop and a major source of calories. Similarly, a vast majority of smallholder farmers cultivate maize for its economic returns. However, in recent years, maize yields from various fields across Africa have declined due to the invasion of Fall Armyworm (FAW) *Spodoptera frugiperda*. The study presents a literature review on the widespread distribution and impact of FAW on maize yields in Africa. The study identifies that maize yield loss in most countries continues to increase, which poses a present and future food security threat to farmers and their families. While most farmers have adopted various chemicals to control FAW, the majority of these chemicals are associated with health and environmental problems. The study, therefore, recommends extensive education of farmers on the early identification of FAW and appropriate management and control methods. It also stresses the need for various governments, as part of the national policy, to focus on environmentally safe and sustainable control methods to reduce the impact of FAW and increase maize yields.

Key Words: Fall Armyworm (FAW); Maize yield; Food security; Control methods.

Transcriptomics analysis for the detection of novel drought tolerance genes in Jojoba (*Simmondsia chinensis*)

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Jojoba (*Simmondsia Chinensis*) is a perennial stress tolerant desert shrub that has oil containing seeds and inhabits the Sonoran desert in the southwest of the United States and northwest Mexico. It has attracted a growing worldwide interest for multi-purpose uses. However, the most attractive characteristics of Jojoba are the richness of the oil content of the seed and the superior stress tolerance of the plant. Little has been done towards Jojoba genetic improvement. The exploration of jojoba genetic resources will define a molecular and biochemical fingerprint for jojoba and will aid sustainable crop commercialisation define. In this research, we aim to establish a reference genome database for Jojoba, which will help to facilitate crop improvement. Besides, the contribution to reveal the molecular background of its outstanding drought tolerance using transcriptional profiling during a water stress. RNA sequencing will be performed for samples collected under moderate and severe stress. The genetic database of jojoba will help to reveal the genetic mechanism of response and identify the genes responsible for the drought tolerant phenotype of this crop. Application of this knowledge will support the researchers, farmers, and the jojoba industry.

Aflatoxin contamination of village grains in Central Tanzania: Risky food and agricultural practices and significance to village chicken productivity

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A study was conducted in the semi-arid Manyoni District of Central Tanzania, involving eight village communities to: 1) determine aflatoxin contamination of village grains; 2) evaluate significance of contamination to village chicken performance and 3) gain knowledge on grain food practices and habits associated with aflatoxin risk.

Random immediate post-harvest (n=134) and following 6 month or more after storage grain samples (n=157) were screened followed by quantitative determination of samples containing ≥ 10 $\mu\text{g}/\text{kg}$ total aflatoxins. A 60-day aflatoxicity trial was conducted on 16-day village chicks using concentrations likely to occur under field conditions. Responses were sought from 76 randomly selected adults by a questionnaire covering pre-harvest, harvest and post-harvest practices, food preparation and knowledge on food toxins.

Aflatoxin contamination was particularly more significant in maize and groundnut samples ranging to 192 $\mu\text{g}/\text{kg}$ and 198 $\mu\text{g}/\text{kg}$ (mean=25.46 $\mu\text{g}/\text{kg}$) respectively, in immediate post-harvest grains and up to 213 $\mu\text{g}/\text{kg}$ and 351 $\mu\text{g}/\text{kg}$ (mean=50.83 $\mu\text{g}/\text{kg}$) respectively, in stored grains. Exposure of chicks to feed containing aflatoxin as low as 30 $\mu\text{g}/\text{kg}$ was associated with lesions in organs, reduced feed intake, body weight gain and immunity to Newcastle disease vaccination. Respondent questionnaires revealed farmers: had no knowledge of food toxins; received limited extension services; did not generally use irrigation, fertilisers or pesticides; relied on inadequate harvesting, drying and storage technologies; and frequently consumed unpolished grains.

Village grains in Central Tanzania may contain high concentrations of aflatoxins that may affect community health and hinder village chicken productivity which may be addressed through improving existing practices.

The role of leadership and local ownership in Research 4 Development (R4D) projects

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All researchers for development struggle to achieve lasting results on the ground. Regardless of the introduced technology, the fundamental basis for achieving lasting results involves: 1) strategic project leadership, 2) local ownership of research objectives, research design, outputs and overall results, and 3) local leadership and management of activities and finances. To support lasting results, research tools can assist in communicating the complexities of an introduced technology and can guide stakeholder interactions to bridge knowledge systems and create common understandings and new hybrid knowledge systems. We highlight a transdisciplinary process used to co-create a Research Discussion Tool and identification of 9 thematic areas which, in combination, enabled obstacles to technology uptake to be overcome and farmers to benefit from research-based innovations. The process involved assisting local researchers and extension agents to co-develop solutions, strategies and methods to improve technology uptake by farmers in Lao PDR, using a series of change management interventions. A complex ecology of factors involving farmers' decision drivers and farmers' decision enablers within farmers' production systems influence technology uptake. The relative importance of each factor is dependent on the specific technology that is being introduced. Hence, projects that introduce new technologies grapple to address all relevant factors and often do not have the ability to deal with the complex array of factors that are at play. Co-constructed knowledge embeds local knowledge that becomes accessible to projects. The approach also has the potential to harness collaborative exchanges with other projects in similar geographical regions.

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Grain filling temperature reduces head rice yield through husk enlargement in long grain and grain breakage in medium grain cultivars

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Climate change represents a threat to the productivity of staple crops, including rice (*Oryza sativa*). The impact of a 10-d heat stress event (31/23oC, 33/24oC and 35/25oC: day/night, 12h/12h) from 10 days after anthesis (DAA) to 20 DAA was investigated on grain yields and head rice yield in four rice cultivars. Losses during milling were partitioned into husk losses or grain breakage during de-husking, and bran losses or grain breakage during polishing. While the highest heat stress (35/25oC) reduced grain yields by around 20% compared to control plants, reductions in head rice yield were greater than 50%. In the control treatment, husk losses during milling ranged from 21% (Teqing) to 40% (Lemont) while breakage of white rice during milling ranged from less than 5% in M205 and Lemont to 23% in Teqing. As per reports in the literature, high levels of heat stress led to increased grain breakage during dehusking and/or polishing in cultivars M205, Baru and Lemont. However, heat stress reduced cultivar Lemont head rice yield not by increased grain breakage during polishing but predominantly due to a 59% increase in husk loss. Given husk tissue is not a net carbon source for developing rice grains, this suggests heat stress in Lemont increased carbon partitioning from vegetative tissues to the husk at the expense of the developing caryopsis. Ultimately, our results indicate reduction in head rice yield due to heat stress cannot be attributed solely to greater grain breakage during de-husking and polishing.

Impact of soil water stress at seed development stage on phenology, fecundity and seed dormancy of *Avena sterilis* ssp. *ludoviciana*

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Wild oat (*Avena sterilis* ssp. *ludoviciana* (Durieu) Nyman) is considered the most difficult-to-control winter weed in the north-eastern grain-growing region (NGR) of Australia particularly following the adoption of no-till conservation agriculture and the enhanced reliance on herbicides for weed control. A diversity of survival mechanisms is responsible for its persistence in no-till conservation cropping. Among them long-term, variable seed dormancy is the most important. A number of environmental stresses (for example drought) are known to affect the seed dormancy status. We hypothesized that the increasing frequency of hot and dry period in late winter/early spring season in the NGR might help to mature and shed less dormant wild oat seeds before the wheat crop is harvested. This early shedding of highly germinable seed better aids persistence in no-till conservation cropping systems. Our research show that soil water stress applied at seed development stage resulted in lower number of early maturing less dormant seed. This observation was made for a number of biotypes either coming from within one location or between locations within the NGR. Thus, the frequent hot and dry period at the time of seed development in the northeastern grain region of Australia is responsible for production of less dormant *Avena sterilis* ssp. *ludoviciana* seeds where no-till conservation cropping is helping to retain these seeds on the top soil. Under favourable germination conditions in the following season these less dormant seeds will immediately be available to re-infest the autumn/winter-sown wheat crop.

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Genetic determination sex in Jojoba (*Simmondsia Chinensis*)

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Jojoba (*Simmondsia chinensis*), is a dioecious perennial shrub, originating from North American deserts. Jojoba is a great model because it grows in arid and semi-arid areas and is considered to be resistant to drought and salinity. Jojoba is a crop grown commercially for its seeds, because it contains 50% oil which is a higher amount than that found in most oilseed crops. Jojoba oil is a liquid wax and has a viscosity which is constant with temperature, a very high resistance to rancidity and oxidation, and a high boiling point (398 °C). It has been used for biodiesel production, lubricants, plasticizers, cosmetics and pharmaceutical purposes. However, it is difficult to distinguish the sex of Jojoba plants at the seedling stage, and populations of Jojoba are male biased. This has resulted in cuttings being used for commercial plantations which has caused a narrowing of genetic diversity that may lead to a reduction in seed yield. Efforts have been made using different molecular markers to determine putative sex-specific or sex-linked markers for Jojoba but these have some inherent limitations. Applying modern technologies including next generation sequencing, assembly, annotation, and transcriptome sequencing will allow understanding of the molecular genetic basis of agronomic traits in the Jojoba plant. The goal of this research is to create a reference genome for Jojoba plants and perform transcriptome sequencing from different developmental stages in order to determine the genes expressed differently in male and female Jojoba plants.

Determination of phylogenetic relationships of the genus *Sorghum* using nuclear and chloroplast genome assembly

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Sorghum (*Sorghum bicolor* [L.] Moench) is a multipurpose food crop which is ranked among the top five cereal crops in the world. It serves as a source of food, fodder, feed and bioenergy. The genus *Sorghum* consists of 25 species and is considered as a group of plants with enormous diversity. Crop wild relatives have played significant roles in assessing and utilizing genetic resources which is the fundamental step of crop improvement. Successful examples of introgression of novel alleles from the wild relatives of rice, wheat, maize and sugarcane have been reported, whereas studies on wild sorghum are limited. The wild gene pool of sorghum harbours many useful genes for drought tolerance and disease resistance. However, the phylogenetic relationships in the genus remain unresolved due to the limited availability of sequencing data. The comparison of nuclear genomes along with the chloroplast genomes of sorghum species would expand this knowledge and aid in using these potential genetic resources as well as resolving the vague phylogeny of the genus. To date the chloroplast genome of only four sorghum species have been sequenced. This first of its kind study aims to determine the phylogenetic relationships in the genus *Sorghum* by means of nuclear and chloroplast genome sequencing and assembly of all the 25 known *Sorghum* species. This effort would undoubtedly be a significant step towards exploiting the hidden genetic resources of sorghum in crop improvement.

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Relationships between Iraqi rice varieties at the nuclear and plastid genome levels

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Due to the importance of the rice crop in Iraq, a study was conducted to determine the origin of the major varieties and understand the evolutionary relationships between Iraqi rice varieties and other Asian-rice accessions that could be significant in the improvement of this crop. Five varieties of *Oryza sativa* were obtained from Baghdad, Iraq; among these varieties, one, Amber33, is local and is one of the most highly valued varieties in Iraq because of its fragrance, and two varieties, Furat and Yasmin were introduced from Vietnam while the other two, Buhoot1 and Amber al-Baraka, were improved varieties. Raw sequence reads of 33 domesticated Asian-rice accessions were downloaded from National Centre for Biotechnology Information-NCBI. The sequence of the whole chloroplast genome of 5 Iraqi varieties and 34 domesticated rice accessions was assembled while for nuclear genome analysis, only the sequences of 916 concatenated nuclear genes were assembled. The phylogenetic trees of both the chloroplast and nuclear genomes were similar with insignificant differences at the end of the clades. Two main clusters, Indica and Japonica, and further five subclusters based upon their ecotype, *indica*, *aus*, *tropical japonica*, *temperate japonica* and *basmati* were created. The phylogenetic analysis of both chloroplast and nuclear genomes placed Amber33 in the *basmati* ecotype group as a sister of cultivars from Pakistan and India. This confirms the old traditional story that the Amber variety was transferred by a group of people who had migrated from India (the Southeast) and settled in southern Iraq a long time ago.

Occurrence of phytoplasma in sugarcane with Yellow Canopy Syndrome (YCS) and phloem sap sucking insects in North Queensland, Australia

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Yellow Canopy Syndrome (YCS) is characterised by uneven yellow-green mottling followed by bright yellow-orange regions leading to premature senescing in the mid-canopy leaves of sugarcane. Spread of it from North Queensland to the northern NSW, Australia occurred within less than 6 years. Leaf yellowing is modulated by environmental conditions. Untranslocated sugar and starch were found in affected leaves. Following detection of YCS, several field trials were carried out to explore the possibility of finding a biotic factor. Leaf tissue samples and two types of phloem sap-sucking insects collected from YCS hot spots were used for conventional and nucleic acid based approaches. *Candidatus Phytoplasma aurantifolia* strain belonging to the subgroup 16SrII was detected in symptomatic and non-symptomatic leaf tissues and also in insects collected during the YCS season. During spring and early summer, plants are symptomless and phytoplasma detection level was also low. Results indicate seasonal phytoplasma titre changes possibly due to environmental influence. The possibility of phytoplasma transmission between sugarcane and the insect species tested in this study is discussed.

Single Tube Long Fragment Reads (stLFR): A simple and cost effective method for de novo whole genome sequencing

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Currently de novo sequencing of plant and animal genomes is both costly and challenging. Here we describe a novel technique – single tube long fragment reads (stLFR), which involves the addition of the same molecular barcode sequence to sub-fragments of the original long DNA molecule (DNA co-barcoding) via clonally barcoded beads. stLFR allows for analysis of long DNA fragments (20-300kb) with accurate short-read sequencing technology. Here we show a drastic improvement of de novo assembly results for several economically important plant and pest genomes using co-barcoded long fragment reads (stLFR) with short-read sequencing technology on the MGISEQ-2000. For lettuce (*Lactuca sativa*, genome size 301.6 Mb), we achieved 51Kb for contig N50 and 493Kb for scaffold N50, and for teak (*Tectona grandis*, genome size 276.12 Mb), 74.61Kb for contig N50 and 5.32Mb for scaffold N50. We also sequenced the fall armyworm (*Spodoptera frugiperda*), an invasive pest responsible for a large decline in the world's maize and rice production. Using a combination of stLFR and Hi-C technology, two chromosome scale genomes were assembled, each representing one male (genome size 542.42 Mb, scaffold N50 14.89 Mb) and one female (genome size 530.77 Mb, scaffold N50 14.16 Mb) collected from the Yunnan Province of China. With only 1.5ng of HMW gDNA needed for library preparation within a single tube reaction, stLFR offers a cost effective and simple approach for de novo WGS as well as other long read applications such as haplotype phasing and structural variant detection.

Remobilisation and fate of sulphur in Indian mustard (*Brassica juncea. L*)

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Understanding the basis of sulphur (S) use efficiency in higher S requiring crops such as brassicas can help develop more cost-effective cultivars. Oleriferous brassicas sequester reduced S in the mature seeds mainly as secondary metabolite-glucosinolate (GSL) and seed storage proteins (SSP). Glucosinolates have a wide range of positive aspects in food production, human nutrition and plant defence, and SSPs are a potential source of high quality vegetable proteins for human and livestock consumption. We carried out a developmental S audit to establish the net fluxes of S in two lines of *B. juncea* mustard where the level of seed GSL differed. We quantified S pools (sulphate, GSL and total S) in different organs at multiple growth stages until maturity. We have established that leaf S components accumulated as primary S sinks at early developmental stages in condiment type *B. juncea* become remobilised as a secondary S source to meet the demand of GSL as the dominant seed S sink at maturity. Our evidence for S remobilisation from leaves as primary S sink suggests that up or down regulation of signalling molecules which mediate between secondary S sinks and sources may help modulate economically valuable S compounds in brassica seed.

Land situation and sowing date effects growth and yield of crops in the rice-pulse based cropping systems of coastal India

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The coastal saline zone of West Bengal in India is the home for millions of the world's poorest and most vulnerable people. Due to gradual increase in salt accumulation on soils of the coastal saline zone of West Bengal in India from winter to summer days, cultivation of the second crop in winter season becomes possible in a limited area. To address this issue, field experiment was conducted both in rainy and winter seasons of 2016-17 and 2017-18 in this zone to study the feasibility of incorporating different winter pulses (lentil and grass pea) in the rice based cropping system. The experiment was conducted in strip plot design having two factors namely, Factor I: Six dates of sowing of rice at an interval of one week (2nd week of June to 3rd week of July) and Factor II: Two land situations (Medium-upland and Medium-lowland). Date of sowing significantly influenced dry matter and macro-nutrients (NPK) partitioning in rice. Irrespective of land situation, crop sown on 1st and 2nd dates recorded significantly higher grain yield and macro-nutrient uptake by rice. Date of sowing of rice and land situation also significantly influenced the seed and stover yield of different pulse crops. Pulse crops sown on 1st and 2nd dates recorded significantly higher seed yield in coastal saline ecology of West Bengal, India.

Foliar nutrient management on potato grown under zero tillage and mulching in Coastal Saline Soil of West Bengal, India

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The Coastal Saline Zone (CSZ) of West Bengal, India is dominated by rice-fallow-fallow system cropping system. Only 4% of the cultivated area of the coastal zone can be irrigated with available sweet water. To cope up with the present situation is introduction of new high value crops to catch the fallow winter period emphasizing on water saving technologies. In this way mono-cropped saline soils of coastal region can be converted into multiple cropping through the adoption of zero tillage potato technology. Soils of the CSZ show multi-nutritional deficiencies and these deficiencies adversely affect the crop. To address this issue, field experiment was conducted in winter season of 2016-2018 in CSZ of West Bengal, India with the focal objectives of studying the feasibility of potato under zero-tilled-mulched condition in CSZ of West Bengal; assessing the effect of foliar nutrient management practices on growth, yield, quality and economics of potato. The foliar nutritional supplementation with 2% Urea at 30 & 50 days after planting (DAP) of potato along with 0.1% Boron at 30 DAP not only increased tuber number and yield but also quality parameters of potato tuber such as TSS, tuber hardness, vitamin C etc. were significantly increased. It may thus be concluded that 2% Urea at 30 & 50 at DAP of potato along with 0.1% Boron at 30 DAP as foliar application is the best foliar nutrient management option for potato grown under zero tillage and mulching in coastal saline soils of West Bengal, India.

System identification of linearized rice growth dynamic for precision irrigation

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Modeling crop growth dynamics has been used to predict and analyze the effects of water stress on crop yields for different irrigation managements. In particular, rice, a water intensive crop, has been extensively modeled using simulation software such as ORYZA3, Aquacrop, and WARM. Despite these established simulation models, only soil water balance models are utilized for real time irrigation control. The reasons are twofold: the complexity in incorporating non-linear and highly interactive nature of crop physiological mechanisms in a control framework; and the difficulty in estimating these physiological mechanisms compared to using soil water sensors for soil water balance models. This work developed a system identification technique that improves accuracy in irrigation timing, amount and efficiency by integrating crop growth dynamics to estimate evapotranspiration as feedback in the soil water balance model. Sample simulation runs from ORYZA3 were used to build and validate a water limited growth dynamics. A two level regression technique was used resulting in reduced expressions for leaf area index, biomass, and soil water depletion. With advancements in wireless sensor technologies, the modeling framework maximizes use of field sensor information to adequately estimate the crop state. Thus, it can be adopted in advance control techniques for irrigation.

Evaluation of mungbean varieties for northwest Cambodian lowland rice systems

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Small-scale agriculture is the economic, social and cultural foundation of Cambodian rural communities. Crop diversification is not widespread in these traditionally rice-producing smallholder farms. Rice monoculture has led to a decline in farm productivity and farming household income. Mungbean is emerging as a high-value opportunity for crop diversification in smallholder farms in north-west Cambodia. However, its expansion is being constrained by the low quality of varieties available to farmers. This study aims to evaluate the locally available varieties with others from Cambodia and the region by comparing the varieties' agronomic and economic characteristics. The varieties from Cambodia, CMB-3 and CARDI-Chey, had superior agronomic and quality characteristics compared with the varieties available to farmers. This was reflected in the price estimate and income of both varieties which had the highest gross margins. Hence, the varieties currently available to farmers are unsuitable for continued cultivation in the modern mungbean production environment.

Key Words: Mungbean production, variety evaluation, smallholder, Cambodia

Socio-economics analysis of food insecurity status in rural households in Central Dry Zone, Myanmar

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This paper identifies the key challenges and issues facing the rural households in relation to income activities and food security context, and the key attributes of the households followed by the indicators of household food security in the central dry zone of Myanmar. The findings show rural households depend on on-farm and off-farm activities for earning income for the livelihoods of the households. Land ownership does not comfort for earning enough money for the household to ensure food security. The reasons are due to the higher cost of labor input, fertilizer, seeds, etc. which gave budget pressure in the production cost to the farmers. At the same time, migration was a common issue in the region and it may encounter the farm labor shortage in the rural agriculture sector. Then, skilled local labor scarcity is one of the major constraints in farming for the landowners. It becomes a vicious cycle in rural agriculture. Most of the landowners faced inconveniences to have enough food for the family when the farming started until it harvested, generally from March to July. Differently, the food deficit time for the landless started from January to May when there were no income activities from the farm. Then, they have the constraints in order to have sufficient food for the livelihoods of households, such as low/no income; less employment; lower crop production; lack of money for production; investment in crop production. These limitations occurred from the amount of income they earned and also job opportunity available in the region. To ensure enough food for their daily livelihoods, the rural households have their own strategies at the time of food deficit in rural households. The most common strategies for both landowner and landless to overcome food deficit situation are borrowing food from the others; purchasing staple food, such as rice, cooking oil on credit; reducing the frequency of daily meals, such as 3 times to 2 times a day; consuming less preferred staple food and changing curry or quality with cheap items. However, these are just immediate strategies to overcome short term food deficit problems. To ensure long term food security, there may have better strategies to overcome the challenges occurred in the agriculture sector which will encounter the better livelihoods of rural farmers in the future.

Single cross testers for CIMMYT Heterotic Group B maize germplasm adapted to Mid-Altitudes

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Maize is an important food crop in sub-Saharan Africa providing about 95% of the calories in their diets. Many African countries frequently experience maize shortages and average maize yield is 1.3 t/ha due to drought and low soil nitrogen stress. However, some of CIMMYT-Zimbabwe's efforts are directed towards developing drought and low nitrogen tolerant maize hybrids which adapt to target environments. The breeding program use testers to evaluate the performance of inbred lines which will be used for hybrid make up. The testers used are old, they have been used for over 20 years amid climate change which can render them to become obsolete. This slows the development of hybrids. The objective of this study is to 1) to evaluate testcross performance under optimum, drought and low N stress conditions; 2) to assess combining ability of single cross testers and inbred lines 3) to identify single cross testers for future evaluation new inbred lines. To achieve this, 165 three-way hybrids composed of 162 testcrosses and three commercial hybrids checks were evaluated under 15 locations. Two trials were conducted under managed drought in 2017 dry season, two low nitrogen, four random stress and seven trials for optimum conditions were conducted during 2018 main rain season in Zimbabwe, South Africa and Zambia. Analysis of variance and pattern analysis for grain yield and secondary traits across 15 sites will be done. Significant differences among genotypes for the different traits will enable identification of single crosses that could potentially be used as testers.

Differential gene expression among genotypes of the genus *Saccharum* contrasting in biomass production

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The development of biomass crops aims to meet industrial yield demands to become a profitable and sustainable activity. Achieving these goals in an energy crop such as sugarcane relies on breeding for sucrose accumulation, fiber content and tillering capacity. Sucrose storage depends on transport from leaves to culms driven by enzymes involved in sucrose synthesis and hydrolysis. High biomass genotypes often use photosynthesis products to produce lignocellulosic compounds to form the cell wall. To expand the understanding of the pathways related to these traits, we evaluated gene expression of two groups of genotypes contrasting in biomass yield, as well testing differences among members within a same group. First visible dewlap leaves were collected from six genotypes of each group to perform RNA-Seq. We found evidence that both groups differ with regard to genomic stress caused by polyploidy, as indicated by the enrichment of genes involved in transposition activity and defense response processes. Although carbon assimilation terms were not enriched, genes annotated with such terms were co-expressed with those coding for members of hormonal pathways. Sucrose phosphate synthase and hydrolytic enzymes coding genes were upregulated in leaves of sucrose-accumulating genotypes, as were some genes coding for enzymes involved in the biosynthesis of lignin. Compared to other high biomass accessions, the hybrid US85-1008 presented upregulation of photosynthesis-related genes probably due to its sink demand to store sugar in culms. This study expands the knowledge of gene expression in sugarcane leaves, revealing differences between and within phenotypically distinct groups.

Quantifying gas emissions and denitrifying genes in a salt-affected soil

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Salinity effects on microbial community relative to greenhouse gas emissions are not well understood in salt-affected soils. A better understanding of this interaction would be useful for agricultural practices to reduce nitrogen gas losses and manage environmental pollution. We hypothesized that elevated salinity would increase the abundance of denitrifier genes resulting in a low rate of gas emissions. Objectives of this study were to measure induced-soil greenhouse gas emissions and to quantify denitrifying genes in a salt-affected soil over a 3-week incubation period. This incubation study was conducted by submerging field-moist samples of an acid sulphate soil in different saline solutions. A quantitative polymerase chain reaction (qPCR) was used to quantify the abundance of resident bacterial denitrification genes in the salt-affected soil. It was found that increased salinity caused a decrease in both flux and cumulative emission of N₂₀ from the incubated soil, relative to fresh water. Soil respiration was significantly reduced in salinity treatments compared to the treatment of distilled water. The study results showed that elevated salinity increased the denitrifying genes in the incubated acid sulfate soil. The abundance of the *nir* genes was usually high between the first and second week of incubation, while number copies of the *nosZ* gene were significantly low at those times. The study concludes that salinity controls the biological aspects of denitrification leading to a reduction of greenhouse gas emissions. Findings from this investigation extend our knowledge about the underlying molecular ecological mechanisms of denitrification that manage nitrogen cycling in salt-affected soils.

Key Words: denitrifying genes, gas emissions, nitrous oxide, qPCR, salinity effects.

Financial Support: This project was funded by Australian Centre for International Agricultural Research (ACIAR). Project number: SMCN/2009/021.

Utilisation of sludge from ditches to maintain soil nutrients and increase rice yield in rice-shrimp systems in Vietnam

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An integration of a shrimp production cycle into the traditional system of rice farming is an adopted practice by farmers due to saline intrusion and changes of environmental condition in Vietnam. Aquacultural pond sludge or biological waste has the potential to cause environmental pollution if it is not managed well. However, the sludge from shrimp ponds in rice-shrimp farming systems can provide nutrition and maintain soil fertility for the integrated rice crop production. A randomized block field experiment was conducted on a rice-shrimp farm to test the fertiliser value of sludge for rice over two consecutive seasons in Vietnam. Five treatments of sludge and fertiliser rates were applied in field experiments including control, sludge application alone, recommended fertiliser rate, reduced fertiliser rate, and combination of sludge and reduced fertiliser rate. The results consistently proved that the pond sludge can provide large quantities of plant available nutrients such as ammonium nitrogen, total nitrogen and organic matter. The use of sludge either alone or in combination with the reduced fertiliser rate produced optimal rice yields while fertilizer cost of rice production was reduced. This finding indicates that the use of sludge is able to save cost of production to rice-shrimp farmers and reduce adverse impacts of pond sludge released on the surrounding environment.

Key Words: available nitrogen, mineralisation, organic matter, pond sludge, and rice-shrimp farming systems.

Financial Support: This project was funded by Australian Centre for International Agricultural Research (ACIAR). Project number: SMCN/2010/083.

Effects of pesticides on nitrous oxide production from sugarcane cropping soils

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This study aimed to assess the non-target impacts of pesticides on soil biological processes, particularly N₂O emissions and improve understanding of the contributions of nitrification and denitrification to N₂O production in sugarcane soils. We conducted a laboratory incubation experiment, in which a herbicide Roundup®, an insecticide Confidor®, a fungicide Shirtan®, and a fumigant metam sodium were added to a Ferrosol and then incubated at 25°C for 38 days at 2 moisture regimes (55 % and 90% water holding capacity (WHC)). At day 28, soil water contents in the 55% WHC treatments were also increased to 90% WHC to create a condition to favour denitrification. The 55% and 90% WHC treatments received NH₄SO₄ at 40µg N g⁻¹ dry soil and KNO₃ at 40µg N g⁻¹ dry soil, respectively, with K¹⁵NO₃ added at 2 µg N g⁻¹ of dry soil in all treatments. Compared with the control treatment, Confidor application significantly increased net nitrification rates and N₂O emissions at 55% WHC. After increasing water content from 55% to 90% WHC at day 28, net denitrification occurred in the metam sodium treatment; N₂O emissions increased in the order: metam sodium ↑ Shirtan ↑ Glyphosate treatment, with little changes in the Confidor and control treatments. During the 38-day incubation at 90% WHC, the metam sodium treatment emitted more N₂O emissions than other treatments in the first 15 days of the incubation but no significant differences were observed among the other treatments at the end of the incubation.

Key Words: N₂O production, pesticides, sugarcane cropping soils

Assessment of soil structural properties in relation to land use change in South-East Asia

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For many emerging economies, rapid land use change from forest to farmland is resulting in high levels of land degradation. Farming systems such as maize cultivation under conventional tillage after slash and burn degrade the soil resource through declining soil structural stability. Cultivation enhances mineralisation and hence loss of soil organic matter, which in turn reduces soil structures stability and promotes further carbon losses through soil erosion. Alternative land uses such as fruit tree plantations, or practise change to reduced tillage or conservation agriculture have the potential to counter this spiral of accelerated soil degradation through improving soil structural stability and build-up of soil organic matter. This project assessed how land use influences soil structural stability in Cambodia near Battambang and the North-Western Mountain regions of Vietnam where maize based system are most common. Soil properties measured were: (1) total carbon and nitrogen content analysis, (2) particle and aggregate size distribution using laser refraction, (3) hydraulic conductivity, (4) bulk density and (5) microbial CO₂ respiration. Information on land use history was also collected through farmer surveys. Land use significantly influenced aggregate stability and hydraulic conductivity. This was largely associated with differences in soil organic carbon content. Forest system had the highest, and conventional maize systems had the lowest amount of large aggregates. Fruit tree plantations are relatively new to these regions but they already showed improved soil aggregate sizes though the level of improvement varied and depended on remnant soil degradation from prior land uses and change to reduced tillage systems.

Alternative legume crops for the southern region of Australia

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Pulse production in the southern region of Australia is dominated by the winter crops lentil, chickpea, field pea and faba bean with limited options for summer cropping. Alternative legume crops could improve the efficiency and profitability of farming systems through access to higher-value legumes, increased break crop and fodder options and maximising resource capture within the system. Alternative legume species being tested include adzuki bean, black gram, cowpea, *Lathyrus*, lupin, moth bean, mungbean, narbon bean, Phaseolus, pigeon pea and soybean where many of these are traditionally grown in sub-tropical growing regions; therefore, a key consideration is determining their suitability to the rainfall pattern, photoperiod and temperatures occurring across southern Australia. This work is assessing the agronomic and economic viability of these crops and defining the traits which require greater adaptation to the southern region and support targeted breeding solutions. To identify potential germplasm suited to southern farming systems, a broad range of germplasm from the Australian Grains Genebank (AGG) was screened, where winter sown trials were established at Horsham, Victoria, that included 812 genotypes across the 11 species. Remote and proximal sensing technologies are being utilised to monitor plant growth, vigour and canopy architecture. Preliminary results have shown genetic diversity within species in crop establishment and early season biomass, indicating a potential to increase the adaptation of key alternative legume species to the southern region. Ultimately, this program aims to identify viable legume crop options and management strategies enabling growers to maximise on-farm profitability.

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Simulation of mungbean productivity during the fallow phase on rainfed rice in Central Java, Indonesia

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The processes and potential for modification of mungbean performance to reduce fallow phase in rainfed rice system is limited. Agricultural Production System Simulator (APSIM) has the ability to examine mungbean performance in response to management options to reduce fallow. This study was aimed to evaluate the productivity of mungbean at different management practices across various agro-climatic conditions on a long-term scale during the fallow phase in Central Java, Indonesia based on simulation. Four sites in Central Java (Jakenan, Brebes, Kebumen and Sukoharjo) were selected representing various agro-climatic conditions. Each study site was examined using APSIM in response to sowing times, residue treatments, soil types, plant available water levels, and climate data from 1983 to 2013. The Data were analyzed using two-way (ANOVA) and significant effect continued with multiple range test with an error rate of 5% ($p \leq 0.05$). The probability of mungbean yield for each site was calculated using cumulative distribution functions. The results of this scenario analysis was firstly reported and indicated that mungbean yield was influenced by plant available water levels (10 to 70 mm) and sowing time (early, medium and late sowing time). The highest mungbean yield was achieved at high level of plant available water (70 mm) and late sowing time in August. Further, simulated mungbean yield resulted around 1000 to 1200 kg ha⁻¹ in Brebes, Kebumen and Sukoharjo, whereas in Jakenan mungbean yielded less than 1000 kg ha⁻¹. Based on these results, initial water at sowing and sowing date is important factors in determining mungbean yield.

Key Words: APSIM, Rainfed, Mungbean, Fallow, Central Java

"Toto, I've a feeling we're not in Kansas anymore": Mungbean's journey from the Midwest to the Emerald City and beyond

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Mungbean (*Vigna radiata* var. *radiata* (L.) Wilczek) is a short season tropical grain legume originating from India, though its Australian journey actually started with the introduction of variety 'Berken' from Oklahoma in 1969. Subsequent introductions were followed by public sector investment in agronomy and breeding. In Australia mungbeans have been transformed from 'mongrel beans' into 'money beans' and are firmly established as a vital part of Australia's tropical farming systems.

In global terms mungbeans are no longer considered an orphan crop forgotten by the green revolution. The International Mungbean Improvement Network (IMIN) is an ACIAR collaboration that builds on the World Vegetable Center's global mandate for mungbean improvement and Australia's National Mungbean Improvement Program. IMIN partners Bangladesh, India, Myanmar and Australia are building research capacity, sharing germplasm, new plant breeding tools and conducting multi-location trials in four countries. As such, mungbean improvement now encompasses world leading statistical analysis of plant breeding trials, genetic diversity panels, wild relative and inter-specific crossing, accelerated generation turnover, genomics, pan-genome, physiology, pathology and globally coordinated pre-breeding for key traits.

Like the Wizard of Oz, mungbeans' story is one of self-discovery and the power of collaboration; the journey rather than the destination.

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The economic benefits of improvements in online licencing of the chemical use in Queensland crop industries

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The selective use of chemical products plays an important role in increasing production, improving the quality of Queensland's agricultural produce and enabling producers to earn reasonable returns on their investments. Effective pest management, therefore, helps deliver high quality, healthy and affordable food for all consumers. The efficiency of policy tools such as chemical use licencing hinges critically on supply-side knowledge levels. Although licence applications are available online, information can be difficult to find and often businesses need to contact the state authority to seek further assistance in completing their licence applications.

The aim of this study is therefore to identify the benefits for the users of agricultural chemicals from improvements in licencing application process. Based on a rigorous literature review and statistical analysis of available data, this study modelled the per day / per application value of the use of crop protection products in Queensland.

Results indicate a potential saving by farmers due to a faster process for chemical licence applications. Extreme values of these savings range from \$87 thousand to \$52 million per annum, with actual ones falling in between depending on the coincidence and level of individual risk factors.

Since the chemicals subject to licencing are used beyond agriculture and are utilised not only for crop protection, the results of this analysis are thus underestimated, which implies even greater benefits for the economy. It therefore seems important to update the current licence application platform so that applicants can lodge their application in a more user-friendly and synchronised manner.

Promoting social learning in soil water and nutrients management using farmer - friendly monitoring technology

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Soil water management is typically by trial and error among smallholder farmers. Social learning in the use of farmer - friendly soil-water and nutrients monitoring tools were promoted in Malawi to improve productivity. A simple tool (chameleon) which was designed to fit the mental model of African farmers and to give an output that is linked to action was deployed to 198 farmers in nine irrigation schemes. Chameleon illustrate information on soil moisture status by colours - blue, green and red colours representing adequate moisture, moderate and dry soil status, respectively. The use of colours and not numbers promoted inclusiveness across illiterate and all gender categories. Farmers participated in sensors' installation, soil moisture measurement, data visualization and learning by doing to get insights from their participation. The chameleon was combined with an on-line communication and learning system to improve water management at scheme level. The results indicated that: (1) the tool gave farmers new frames of reference; (2) it improved farmers on time, labour and water saving by reducing irrigation intervals; (3) it gave farmers new reference of experience to change their irrigation traditions; (4) it also reduced conflict for water in irrigation schemes between users apart from improving water productivity. Use of these tools made a rigor that make scientists easily communicate science to lay farmer and initiated the movement of farmers who know how to manage water. Social learning in sensor technology helped to increase farmers' resilience to climate change and shaping the science of the future.

Key Words: irrigation, soil moisture, colour, climate change and water management

Developing climate resilient crops - Bambara groundnut (*Vigna subterranea* (L.) Verdc) as an exemplar crop

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Drought stress is a major constraint to plant growth and productivity. Bambara groundnut (*Vigna subterranea* (L.) Verdc.) is a cleistogamous, underutilised and drought tolerance leguminous crop, capable of growing in marginal and low-input agricultural systems in semi-arid areas. A better understanding of mechanisms involved in drought tolerance will accelerate breeding improvement of bambara groundnut for drought adaptation. A total of 108 F₄ segregating lines derived from a cross between S19-3 (from Namibia, drought tolerant) and DodR (from Tanzania, presumed drought susceptible) were developed to investigate the effect of drought stress on yield components in a rain-out shelter. The experiment was carried out in a randomized complete block design with three replications. Drought stress imposed during vegetative growth significantly decreased ($p \downarrow 0.01$) photosynthesis rate, stomatal conductance, transpiration rate, intracellular CO₂, leaf area and grain yield, however, these traits recovered after normal irrigation resumption. Photosynthesis rate, stomatal conductance, transpiration rate, intracellular CO₂ was significantly ($p \downarrow 0.01$) higher in S19-3 than in DodR under drought stress conditions. Possible transgressive segregation was observed in the F₄ population as some individuals showed superior performance compared to the parents. In addition to advancing these breeding lines for improved cultivars, the segregating populations offer opportunities for genetic analysis of drought tolerance-related traits and yield components in bambara groundnut. The development of drought tolerant materials is essential to cope with the effects of climate change, especially in the tropical arid and semi-arid areas where rainfall is scarce and erratic.

Key Words: Breeding; Drought stress; Stomatal Conductance; Biomass; Grain yield

Genotypic variation in biomass produced is linked to differences in radiation acquisition in mungbean

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Mungbean has become an important cash and legume rotation crop in the Australian Northern grains region. Thus, it is necessary to narrow the gap between potential productivity and actual production through understanding of the crop physiological attributes contributing to the acquisition of radiation, and its conversion into total biomass by the crop. A field experiment was conducted at Gatton, during 2018-19 summer season, growing two commercial varieties of mungbean; Jade and Satin under irrigated conditions. The varieties were planted at 0.5m and 1.0m row spacing. Weekly biomass cuts were taken from a square meter and separated into its components. The area of a green leaf sub-sample was used to compute the leaf area of the canopy. Total shoot dry matter, pod dry matter and leaf area index (LAI) was investigated. There was no significant difference in total dry matter between the two varieties, however, row spacing effects were significant. A highly significant variation in LAI amongst the two varieties and across the row spacing was recorded, with Satin II having a higher mean LAI compared to Jade. Specific leaf area (SLA) differed significantly between the two varieties, with Satin II having a higher average SLA than Jade. There was significant effect of variety and row spacing on pod dry matter. Our data indicate (1) differences in efficiency of conversion of intercepted radiation into dry matter and (2) differences in dry matter partitioning between the two varieties per given LAI. These two parameters need to be investigated further to elucidate the performance of these two varieties under varying environmental conditions.

Diversity of domestication loci in wild rice populations

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Domestication syndrome traits, i.e. seed shattering, seed dormancy and plant architecture have been selected during the domestication of wild rice around 10,000 years ago. These traits evolved through a series of genomic modifications, including selection of nucleotide polymorphisms resulting from spontaneous mutations, recombination, and fixation of alleles and were incorporated into cultivated rice by hybridization or introgression. The Australian wild rice populations are geographically and genetically distinct and free from genetic exchange with cultivated rice unlike the wild populations in Asia. Furthermore, recent studies reveal they have numerous traits of value and unique alleles. Therefore, these populations seem to be suitable to use to investigate the genetic basis of domestication traits as well as other important traits. In this study, we aim to determine the origin and role of domestication loci using two Australian wild populations: Taxa A (like *Oryza rufipogon*) and Taxa B (like *O. meridionalis*) endemic near Cairns, Northern Queensland. To do so, firstly, we will analyse the variation of domestication loci in these two wild populations by the comparison with cultivated rice (*O. sativa* spp. *japonica* cv. Nipponbare) using the whole genome sequencing. Secondly, we will look at the gene expression of the domestication loci at different seed development stages using transcriptomics. Thirdly, we will determine the variation of starch synthesis related genes using whole genome sequencing. Next generation sequencing along with a set of bioinformatics tools will be applied. This research may enlighten our understanding about the domestication process as well as provide insights into how to domesticate these species through genetic manipulation for commercial purpose.

Mungbean pest identification mobile phone application development for Northwest Cambodia

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Cambodian farmers have begun incorporating mungbean into rice cropping systems in response to the need for crop diversification. However, mungbean is facing significant yield loss due to direct impacts of insect and disease pests. Improper pest management has worsened the issue, causing economic losses to farmers and environmental disruption through ill-informed chemical use. Use of broad-spectrum pesticides as a solution to all observed pests is common place in mungbean fields of lowland Cambodia and is associated with unsuitable sources of agricultural information. This project aimed to discover the pest and beneficial species most common in mungbean fields of lowland Cambodia, and to use this information to develop an informative image-rich mobile phone application to aid Cambodian farmers with insect and disease identification, and so provide specific management recommendations applicable to the Cambodian context. This study evaluated the feasibility of the proposed app through a survey with potential users and these responses were incorporated into developing the Pest ID app prototype, which was trialled with farmers and subsequently refined by adding audio content in Khmer. The majority of farmers in this study were unable to distinguish between beneficial and pest insect species. The Pest ID app has been well received by farmers with users seeing its potential to support crop management decisions. This app holds potential as an important agricultural education tool and may be applied to a broader range of mungbean farmers in the future.

Key Words: Sustainable Diversification; Education; Design; Integrated Pest Management.

Investigation of insect resistant components in wild pigeonpea *Cajanus scarabaeoides*

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Cajanus scarabaeoides (L.) Thouars is the closest wild relative to cultivated pigeonpea *Cajanus cajan* (L.) Millspaugh. However, unlike cultivated pigeonpea which is very susceptible to insect, especially *Helicoverpa armigera* (Hubner), wild relative pigeonpea possesses a great insect resistant ability. Since *H. armigera* causes damage to major important crops resulting in economic losses up to 300M USD/year, improvement of resistance to this insect in crops is necessary. This study investigates insect resistant components in *C. scarabaeoides* and the possibility of transferring those insect resistant components to cultivated pigeonpea. Detached leaf assay was used to assess antibiosis and antixenosis resistance mechanisms of *C. scarabaeoides*. Artificial diet supplemented with lyophilised leaf powder was employed to further investigate antibiosis resistance mechanism. Data on larval mortality and larval and pupa weights were collected. Times for neonate larvae growing up to pupate and from pupa to moth were determined through daily observations during experiments. Preliminary results show that *H. armigera* larval weight was significantly reduced and larval period were prolonged when reared on different accessions of *C. scarabaeoides* as compared to the susceptible check *C. cajan* (ICPL 87). Interspecific hybridization was carried out between *C. scarabaeoides* and a commercial pigeonpea variety. Results from insect challenge assays and trichome identification, using a scanning electron microscope, indicate that the hybrid has similar insect resistant level to its wild parent. Proteomic analysis is ongoing for further investigation.

Relationship between biomass composition and enzymatic hydrolysis efficiency in sugarcane

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Meeting future demands for renewable fuels and other bioproducts is dependent on the use of lignocellulosic biomass feedstocks from highly productive crops such as sugarcane. However, the rigid and highly cross-linked cell wall impedes the efficient breakdown of biomass into fermentable sugars necessitating the use of chemical pretreatments to loosen the cell wall prior to enzymatic hydrolysis and subsequent fermentation. Developing sugarcane varieties with altered biomass composition is vital for improving the enzymatic hydrolysis efficiency. With the aim of identifying the major biomass components that influence cell wall recalcitrance, enzymatic hydrolysis efficiency was measured in pretreated leaf and culm tissues of seven sugarcane genotypes that varied in fiber composition. The strongest negative associations with conversion of glucan to glucose were observed for acid-insoluble lignin content (AIL), S/G ratio and xylan content while acid-soluble lignin (ASL) had a strong positive influence on conversion efficiency. Therefore, reducing AIL, S/G ratio and xylan content and increasing ASL content will be key for creating bioenergy varieties of sugarcane.

Comparative analysis and evaluation of handheld X-ray fluorescence spectrometry to measure silicon in crop plants

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Rice, wheat and corn are the three most consumed crop foods worldwide and, as such, are important when considering future global food security. All three species are members of the Poaceae family and are silica accumulators. For those plants that accumulate silica, silica fertilisation is considered to improve plant health and alleviate abiotic and biotic stresses thereby lessening reliance on pesticides and fungicides. Measuring the silicon (Si) content in soils and plants is useful for identifying Si-poor systems; however, traditional chemical digestion methods to measure Si are hazardous and time consuming. Advances in the sensitivity of handheld X-ray fluorescence spectrometers (hh-xrf) create new opportunities for rapid plant elemental analyses. We present a Si analysis of using two handheld X-ray fluorescence devices (SciAps X-300 and the Niton XL3t GOLDD+) compared with a traditional NaOH-digestion method. The SciAps was found to be more accurate than the Niton and the average time taken to analyse Si using the SciAps was four seconds per sample. These data support the use of hh-xrf for rapid analysis of Si and indicate there are additional opportunities for future research to accurately quantify potassium and phosphorus using this technology.

Investigating the effects of pollen and environment on palmitoleic acid and saturated fat content of macadamia nuts

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Palmitoleic acid (PA) and saturated fat content are important quality traits of macadamia nuts due to their impact on human health. Previous studies have indicated that maternal effect plays a major role in determining the oil profile of oilseeds and grains but similar research has not yet been done on macadamia nuts. In order to understand the effect of pollen and environment on PA and saturated fat content of macadamia nuts, fatty acid methyl esters (FAME) analysis using gas chromatography-mass spectrometry (GC-MS) was carried out on eight control-pollinated cultivars and nine open-pollinated cultivars, including replicate trees planted at different locations for most of these cultivars. Statistical analyses including single-way ANOVA and t-tests revealed that the variation of PA and saturated fat content in open-pollinated cultivars were higher than control-pollinated cultivars, suggesting a paternal effect. In addition, a small variation of PA and saturated fat content (statistically significant at $P=0.05$) was detected in replicate trees of both open and control-pollinated cultivars, indicating that environment may affect these quality characteristics as well. This study also revealed that PA and saturated fat content were the highest in pre-mature (mid-development stage) nuts and these traits tend to decrease as the nuts mature, which could be explained by the general fatty acid biosynthetic pathway in higher plants, where the main saturated fatty acid and precursor of PA in macadamia nuts, palmitic acid, is further elongated to stearic acid. These findings may be useful for oil production, plant breeding, and genomic studies.

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How does sugarcane stalk anatomy relate to fibre quality characteristics?

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In recent years in Australia, new sugarcane varieties have been released that due to their poor fibre quality have caused milling problems. These varieties are classified as 'soft' canes and have been rescinded at considerable cost to the sugarcane industry. Since the 1980s, fibre quality has been measured using methods that are expensive, laborious and to some extent unreliable. These methods measure shear strength, impact resistance and short fibre content and are applied around 10 years into the breeding program. This project aims to address the current deficiencies of these methods and to potentially develop a new high throughput tool to enable sugarcane breeders to economically measure the fibre quality of sugarcane genotypes early in their breeding programs. Fibre is the insoluble portion of the sugarcane stalk, derived from the cell walls and typically composed of cellulose (72%), hemicelluloses and lignin (21%). Previous work has shown that variation in stem anatomy including vascular-bundle number per area, fibre-bundle size (near rind), fibre content and rind thickness all contribute to fibre quality. Further work is needed to determine what factors of the cell walls, in the different tissues of the stalk, are producing the differences in fibre quality. Currently our investigation is focusing on a developmental series of internodes from three sugarcane clones: SRA-1 a soft cane, Q208 a cane with good fibre qualities and SRA-5 a high fibre cane. We are examining the anatomical, biochemical and genetic variations of these genotypes, to evaluate associations with fibre quality, and determine what are the differences in the fibre components that are causes milling problems.

The role of farmers' perception of salinity for ensuring food security: Evidence from coastal rice-growing areas of Bangladesh

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Achieving SDGs by 2030 such as “No poverty, zero hunger, good health” is the main priority for policy planning in Bangladesh. Key challenges faced in achieving these goals is encountered in the agricultural sector. This research focused on farmers' perception of salinity and their management strategies, and the implications for policy makers to sustain rice production in the coastal areas of Bangladesh. Household survey data was collected from randomly selected 108 rice farming families from two south-west south-east coastal sub-districts. Semi-structured and pre-tested questionnaire were used to collect data from the respondents. Majority of the respondents (89%) reported that salinity has increased over the last 20 years and they also believe that the current salinity level in their fields are high. In a 2nd field trip 36 farmers from the original sample had soil in their fields measured over two time periods. Farmers' perceived salinity level was then compared with measured field salinity in their rice field. Farmers' perception of soil salinity level in their rice field aligns closely with the measured salinity level in the majority of the cases. It was also observed that farmers' understanding of salinity level is strongly associated with in-field crop condition and soil appearance. 45% of respondents said their main signals of salinity were from the appearance of the plant and 22% of farmers also observed the inflorescence becoming white and grain unfilled in rice crops. Results also suggests that early transplanting of rice seedlings during Boro season rice and use of salt tolerant rice varieties having high tolerance during booting stage along with improved irrigation facilities can substantially reduce rice yield loss from salinity effects.

Perspective of smallholder farmers on smart farming gadgets in Pakistan

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In spite of its importance as a backbone for Pakistani economy, agriculture sector is technologically backward. The sustainability of agriculture depends upon promotion and adoption of new agricultural tools among farmers. As technology adoption is a complicated process because of production and technical factors. The increasing need and use of smart technology in the field of agriculture invites us to make an assessment of the behaviour of farming community about trusting on gadgets or protecting their own traditional knowledge. Participatory action research is appreciated method of promoting new gadgets among farmers as compare to linear model but factors like age, literacy level, shortage of money, family size could hinder the process of engagement of smallholder farmers. Simple random sampling will be used to choose farmers out of one forty-two farming families who are active users of agricultural tools in six districts of three provinces of Pakistan under a project related to enhancement of water management skills of farmers. A mix methodology including surveys and interviews will be used to collect data from the smallholder farmers involved in project activities. The data will be analysed in narrative and tabular form. This research will indicate the trends in adopting smart farming gadgets among smallholder farmers. It will catch the insights from farmers and methods to improve the existing system and ways to deal with challenges to get smart technology gadgets into the hands of farmers. It will provide suggestions for the practitioners of participatory action research.

Distribution and chemical speciation of nitrogen and inhibitors from banded enhanced efficiency fertilizers

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Enhanced efficiency fertilizers (EEFs) are promoted as tools for improving nitrogen (N) use efficiency (NUE) in agricultural systems; however, more information is needed on their behaviour when they are band applied in tropical environments.

Incubation studies using banded, urea-based EEFs with nitrification inhibitor (NI), urease inhibitor (UI) and polymer-coating (PCU) technologies have identified how soil physico-chemical characteristics impact on urea dissolution, hydrolysis, volatilisation and microbial nitrification processes that determine the effectiveness of these products. The extent of the affected zone was dependent on soil type; mineral N species typically diffused further than the inhibitors, resulting in key N transformations often occurring outside the zone of inhibitor influence. The effects of banded UI were transient (ca. 5-9 days) in both soils. More consistent co-location of the NI and nitrifying activity occurred in a clay-rich soil where diffusion was limited by soil properties, and some benefit of the NI was observed late in the incubation. In contrast, PCU slowed the rate of release of N from granules to the surrounding soil solution and delayed N release from granules in concentrated bands was consistent with poorly developed concentration gradients due to close proximity of PCU granules to each other.

Understanding the N dynamics and subsequent transformations of EEFs in soils with different physico-chemical characteristics, and with different fertilizer application methods, will be the key to developing management practices that allow EEFs to have the greatest impact on fertilizer NUE.

A decade of tropical sweet corn breeding using conventional and molecular approaches in Malaysia

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To increase self-sufficiency in sweet corn production in Malaysia, a long-term breeding study was conducted to develop merit inbred lines using conventional and molecular techniques toward production of superior local hybrid varieties. A germplasm consisting of 18 tropical source populations was established and used for inbred line development. Forty tropical inbred lines were developed through continuous self-pollination and selection. Agronomic performance of these newly developed inbred lines was evaluated in replicated blocks in two locations. Significant variations in agronomic performance indicated presence of high genetic diversity among the inbred lines for potential utilization towards hybrid production. In addition, the level of genetic homozygosity for each inbred line and genetic similarities among the inbred lines were estimated through amplification of 100 microsatellite loci. The 40 inbred lines were clustered into five main heterotic groups based on their agronomic and molecular characteristics. Eleven inbred lines were selected to conduct two sets of half-diallel cross (5×5 and 6×6), resulting a total of 25 single-cross hybrids. Greater estimates of GCA mean squares than SCA mean squares showed relatively more important effect of additive gene action in controlling yield and yield components in the hybrids. Genetic distances among the parental lines were used to predict hybrid performance, showing significant positive associations between genetic similarities and SCA estimates. Among the 25 hybrids produced, five hybrids exhibited high and competitive yield performance in comparison to those from the commercial imported hybrids and can be released as new hybrids in Malaysia after evaluation in large scale multi-locational trials.

A pod borer resistant cowpea is one step toward food and nutrition security in West Africa

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Cowpea is the most economically important grain legume in sub-Saharan Africa; however, the legume pod borer (*Maruca vitrata*) reduces farmers' bean yields from a potential 1,500–2,000 kg/ha to only 150–500 kg/ha, representing a 70 to 90% yield loss. Without the availability of resistant varieties, farmers regularly spray with insecticides 5–8 times a season. The Pod Borer Resistant (PBR) Cowpea Project was initiated to control the pod borer pest through the introduction of a Bt (*cry1Ab*) gene, licensed royalty free from Monsanto Company. Efficacy trials with artificial infestation have shown 98–99% reduction in pod and seed damage from the pest in confined field trials in Nigeria, Burkina Faso, and Ghana, and this has been confirmed in confined multi-location agronomic trials in Nigeria. The *cry1Ab* gene has been introgressed into farmers' preferred varieties through conventional breeding and homozygous BC₅F₆ seed has been produced for release. The National Biosafety Management Agency of Nigeria has approved the commercialization of the PBR cowpea and release to farmers is expected in 2020. A second Bt gene (*cry2Ab*) with a different mode of action is being stacked with the *cry1Ab* gene to support a robust insect resistance management strategy.

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Biological control of rice brown spot by *Bacillus* spp. in Thailand

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Rice brown spot (BS), caused by *Bipolaris oryzae* (Breda de Haan) Shoemaker, is a serious disease causing infection in all growth stages of rice and significantly affect to yield and grain quality losses. This study aimed to find effective antagonistic microorganisms to control BS, hundreds of microbial isolates were obtained from rice paddy fields across Thailand. A total number of 31 antagonistic microbes were selected and screened against *B. oryzae* by dual culture technique. The results showed that CRI_15183 has highly percentage of inhibition (67.35%) followed by ACKB03, CRI_15059, CRI_15010, No.33, CRI_15186 and BUDN027 with 57.25, 54.01, 53.28, 52.94, 52.65 and 51.26%, respectively. Then, sequencing of 16S rDNA confirmed two species of *Bacillus* amongst the isolates, *B. subtilis* and *B. amyloliquefaciens*. Three isolates including CRI_15183, CRI_15186 and ACKB03 were formulated with talcum based powder, stored at room temperature and sampled to test their shelf life monthly. In greenhouse experiment, the results revealed that CRI_15186 has highest effective with 14.08 percent of disease incidence followed by CRI_15183 and ACKB03 with 15.06 and 15.98%, respectively. The field experiments will be conducted in wet season this year. There have been only a few reports on the improvement of rice brown spot control involving biological control agents. However, the use of antagonistic microbes can reduced the used of fungicides and developed environmentally safe for the management of rice brown spot disease.

Fusaristatin A production negatively affects the growth and aggressiveness of the wheat crown rot and head blight pathogen *Fusarium pseudograminearum*

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Fusarium pseudograminearum (Fp), the causative agent of the diseases Fusarium crown rot and head blight, is an important pathogen of cereals in many countries including Australia. Fp produces a number of secondary metabolites throughout its life cycle. One of these metabolites, the cyclic lipopeptide fusaristatin A is encoded by a specific gene cluster containing a polyketide synthase and a three module non-ribosomal peptide synthetase. However, a recent survey of Fp populations across Australia suggests that the cluster may only be present in a subset of isolates from Western Australia (WA). In this study, we screened 319 Fp isolates from WA and 110 Fp isolates from the Australian eastern states of New South Wales, Victoria, Queensland and South Australia. The fusaristatin A gene cluster was found to be present in ~50% of Fp isolates from WA but completely absent in Fp isolates from eastern states. Mutants of the fusaristatin A gene cluster were generated by disrupting the non-ribosomal peptide synthetase and polyketide synthase genes simultaneously in two different parental backgrounds. The mutants showed increased growth rates and were significantly more aggressive than their respective parental strains on wheat in both crown rot and head blight assays. This suggested that fusaristatin A has a negative effect on fungal development and aggressiveness. The possible reasons for the geographically restricted presence of the fusaristatin A gene cluster and its role in fungal biology are discussed.

Machinery and labour requirements as influenced by diversified farming systems in the Australian Northern grain production region

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Farming systems in tropical regions of the world have been shown to be underperforming. For instance, recent analysis that only about 29% of current crop sequences in the northern grains region of Australia are achieving 80% of their water-limited yield potential. Consequently, several farming systems analyses have been conducted to enhance soil structure, water and nutrient use efficiency and the resilience of cropping systems to increasing soil-borne pathogens. While biophysical optimisation of the farming system may be possible to improve the efficiency of most farming systems, one key element that is often ignored is how the intensity and diversity of different cropping systems impact on the labour and machinery requirements. Considering these factors is crucial as they can influence the adoption of particular innovations at the farm level.

Here, we combined the Agricultural Production Simulator (APSIM) outputs with farm surveys to examine the machinery and labour requirements of eight crop rotations in the northern cropping zone of Australia. Results showed that the low-intensity systems required 46% less labour per ha than the higher-intensive systems, while the less diverse systems required about 33% less labour per ha than the more diverse systems. Planting and spraying operations respectively represent about 27% and 37% of total fieldwork requirements. We conclude that diverse rotations may create higher labour demand and peak periods that might, in some cases, limit the adoption of diversified crop rotations in some farm businesses, suggesting that labour efficiency can be an important consideration in farming systems research and analysis.

Quantifying forfeited wheat yield due to soil sodicity in the northern grain-growing region of Australia

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Sodicity is a major soil constraint to the growth of wheat (*Triticum aestivum*) in Australia. Objective estimates of the effects of sodicity on wheat yield across large regions—but at a scale fine enough to be useful for on-site management—are difficult to obtain, due to the spatial and temporal variability of climate, management practices and diseases. In this study we have estimated the forfeited wheat yield due to sodicity in the northern grain-growing region (NGR) of Australia, under high-, moderate-, and low-rainfall scenarios, at the *GlobalSoilMap* resolution (3 arc second), through two different approaches: (1) quantify forfeited yield from satellite-based yield predictions at sparse soil locations, then interpolate results over the NGR; (2) examine the relations of monitored yield with interpolated soil maps, then use regression-kriging to predict forfeited yield over the NGR. We also estimated the average annual forfeited yield from 2000 to 2016. We compared the approaches to determine if they were in reasonable agreement, and if they gave a fair assessment of uncertainty. The results of this work complement previous national studies on yield gap of wheat, and provide more detailed information on how soil sodicity impacts yield at the field level. They should prove useful to guide on-farm management decisions so that farmers can better allocate their resources.

Unique genetic resource in perennial wild rice *Oryza rufipogon* Griff., in the Mekong Delta

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Oryza rufipogon Griff. is a perennial species of wild rice widely distributed along the channels and rivers of the Mekong Delta Vietnam. This study attempted to find centers of diversity among wild rice populations in this area and their inter-relationships. The highest genetic diversity was found in the upstream population (Dong Thap) and the lowest in the downstream population (Can Tho). Maternal diversity evaluated using chloroplast INDELs detected ten plastid types, five of which were novel relative to other Asian countries. The mitochondrial genome suggested two unique deletions. One 699bp deletion via short tandem repeats was accompanied by another deletion including orf153. All accessions carrying the mitochondrial type were found in a particular plastid type. This unique maternal lineage was confined to specific channels where it showed vigorous vegetative growth in comparison to upstream areas where various maternal lineages and maximum genetic diversity occurred. This area along the Mekong Delta is a center of not only nuclear but also maternal diversity. Those results yielding a wider picture of natural wild rice resources in this area that would be useful for biological conservation as well as exploitation for rice breeding program.

Autoencoding genetic markers to predict the value of ecophysiological model parameters - proof of concept using a sorghum diversity panel

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Crop growth modelling formalizes the biological processes at which genotype X environment interactions (GxE) are expressed. It has the potential to evaluate, *in silico*, the effect of elementary traits and related genetic factors on phenotype and yield elaborations. Recent studies showed that, by driving the value of crop model parameters using a genomic selection model, yield was predicted more accurately than by a classical genetic model. However these studies dealt with few, integrative parameters and a narrow genetic diversity, i.e. a reduced number of molecular markers. This contrasts with the necessity to make crop models more responsive to climate change variables and thus increase the number of physiological parameters, while studying wider genetic diversity to seek for adaptive markers. With this respect, methods that reduce the dimensionality of the problem are needed. The autoencoder, a semi-supervised machine learning method, can reduce the number of predictors (markers) without prior information, by compressing input data into an encoded neural network layer. Applied to genetic diversity, it should ease modelling and predicting the genetic value of crop model parameters underlying GxE and yield variability, compared to classical regression methods. This study aimed at testing the autoencoding of the genetic data (ca. 1.5M markers) within a West-African sorghum diversity panel of 200 individuals. It evaluated then the relevance of autoencoded data to predict the genetic value of the dozen of crop/plant parameters controlling growth and plasticity in Ecomeristem model, estimated using data from an experiment in the Phenoarch platform.

Background genotypic effects in soybean (*Glycine max (L.) Merrill*) in the presence of Sulfonylurea Herbicides

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Sulfonylurea (SU) herbicides inhibit the Acetolactate Synthase (ALS) enzyme, which is essential for plant growth and development. Normally, soybeans are susceptible to SU herbicides, but two unlinked genes, ALS1 and ALS2, have been identified that confer SU tolerance. In this project we explored the potential of genetic background to affect the expression of SU-tolerance in soybeans. Three lines, carrying both ALS1 and ALS2, were derived by backcrossing three Australian cultivars to the breeding line W4-4 and using markers to select plants homozygous for both genes. These three derived lines plus the ALS donor (W4-4) were then crossed together in a diallel mating design and the six F2 progeny populations screened hydroponically against metsulfuronmethyl herbicide at 4x recommended field rate. The 4x rate was identified in a preliminary study as being sufficient to cause some adverse effects on seedling growth in the presence of both ALS1 and ALS2 but not enough to cause serious damage. Analyses of seedling dry biomass and colorimetric parameters identified statistically significant ($P \leq 0.05$) general combining ability (GCA) and specific combining ability (SCA) effects among the different parental combinations. These effects indicated that genes of minor effect were interacting with and/or combining additively with ALS1 and ALS2 to confer greater or lesser tolerance depending on the parental combination. The results indicate that either the ALS genes interact with their genetic background, or there are minor genes conferring SU tolerance; whatever, selection for these background effects needs to be undertaken in the presence of high levels of herbicide.

Sorghum (*Sorghum bicolor* L.) germination dynamics at extreme temperatures

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Water and heat stressors during flowering are predominant limitations of dryland sorghum yields across Australia's north-eastern cropping zone. Crops sown early could flower before seasonal heatwaves, but the seed must uniformly germinate and emerge at soil temperatures between approximately 10 to 15°C. Furthermore, chemical coatings applied to commercial hybrid seed lots effectively protected the developing crop from pest, disease and herbicide damage but the combined influence of low temperatures and seed coatings on germination of hybrid sorghum seed batches is unknown. In this experiment, germination dynamics were modelled for 10 commercial sorghum hybrid-seed lots (with or without seed coating of a.i. thiamethoxam, oxabtrininil and thiram) incubated at continuous temperatures ranging from 9.4 to 46.1°C. Results also show commercial seed treatments negatively affect final germination proportion especially at sub- and supra-optimal temperatures. Some hybrid-seed lots in current experiment were more sensitive to seed coatings at either sub- or supra-optimal temperatures regardless of seed germination capability (i.e. germination proportion at 25°C). Seeds took 5 days to reach 50% germination (t₅₀) at 9.4°C but germinated within 24 hr at constant temperatures between 20 and 40°C. The spread of germination (time between 10 and 90% germination) increased from 0.5 days at 30°C to 3.8 days at 9.4°C. Therefore, some hybrid-seedlots are suited to early sowing because they can maintain high germination proportion (↑90%) even at soil temperatures (9.4°C) as long as the seedbed remains moist for a least 12 days. Research continues identify the basis of cold tolerance in some-hybrid seedlots.

Nanotechnology promotes R&D of micronutrient foliar fertilizers

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The continuous increase of world population are demanding increasing quantity and quality of food supply, and consequently, efficient and environment-friendly nutrients' supply to the crops. Besides the common NPK nutrients, the micronutrients are also essential to physiological functions in plant metabolism however were taken no account of in many cases. With the increasing awareness of the micronutrients' functions, their fertilizers, especially the foliar ones, have attracted increasing attention over the last few decades as they offer the most efficient way to correct micronutrient deficiencies and enhance the product yield and quality of crops and plants. Here we present our effort by taking the advantages of nanotechnology to design and develop new-generation long-term micronutrient foliar fertilizers. Our opinions for further development and screening criteria of new-generation micronutrient foliar fertilizers have been proposed from the viewpoints of nanotechnology.

Unique secreted in xylem genes in banana-infecting endophytic *Fusarium oxysporum*

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Members of the *Fusarium oxysporum* species complex include pathogenic and non-pathogenic isolates and infect a broad range of plant species. *F. oxysporum* f. sp. cubense (*Foc*) causes the destructive Fusarium wilt of banana, and the recently emerged *Foc* tropical race 4 strain threatens the global banana industry. *Secreted in xylem* (*SIX*) genes encode for *F. oxysporum* effector proteins that are associated with virulence in pathogenic *F. oxysporum*, however they have rarely been reported from non-pathogenic *F. oxysporum* isolates. Our recent survey of asymptomatic banana plants grown in *Foc*-infested fields in Queensland and northern NSW revealed that diverse *Fusarium* spp, including *F. oxysporum*, reside in the plant roots and pseudostem without causing obvious damage to the plant. Intriguingly, we amplified *SIX* genes from several of the putative endophytic *F. oxysporum* isolates identified in the survey and found that they differ in their profile to known *Foc SIX* genes. To study the role of the endophytic *F. oxysporum* isolates in planta and the biological function of their *SIX* genes in more detail, we will re-inoculate commercial and wild diploid banana lines with the endophytic *F. oxysporum* strains under glasshouse conditions to confirm that they are non-pathogenic on banana. Secondly, we will determine whether the endophytic *F. oxysporum SIX* genes are expressed in planta and/or in vitro and look at the transcriptome changes occurring in the host following infection. Finally, endophytic *F. oxysporum* strains transformed with GFP will be used to investigate the extent of fungal colonisation in the plant.

Lying down on the job: A multivariate mixed model approach helps detect important traits underpinning lodging

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Lodging is a major constraint on wheat production in high rainfall or irrigated environments, severely limiting the high yield returns possible under these conditions. Lodging occurs when a plant is unable to remain secured in the soil and falls over, resulting in substantial yield losses. Lodging is driven by both environmental factors (such as soil strength, wind and rainfall/irrigation) and plant architecture (such as stem and root structure). Given the limited control over environmental factors, there is great interest in understanding the plant architecture traits underpinning lodging to better manipulate these in future germplasm. However, modelling large numbers of potentially correlated traits, and identifying those of interest, is a complex process.

A large number of plant architecture traits, along with lodging and yield, were measured in two field trials conducted in South East Queensland over two years. The trials consisted of a diverse set of lines, some already identified as low-lodging with varying plant architecture. A combined analysis of the traits was performed using a linear mixed model framework. This enabled the correlations between traits to be estimated separately for genetic and non-genetic components rather than pooling this variability as in many multivariate techniques. This was especially important given the interest in developing new lodging-resistant germplasm and allowed the identification of the important traits underpinning lodging. This approach revealed that traits relating to root anchorage had a strong relationship with lodging, with lines possessing high rooting depth and root plate spread having lower lodging severity and higher yield.

Performance of sunflower varieties in respect to different planting system in the coastal saline zone of Bangladesh

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A field experiment entitled "Performance of different sunflower (*Helianthus annuus* L.) varieties in respect to planting systems in the coastal saline zone of Bangladesh" was conducted during Rabi 2018 at the farmers field of Dacope Khulna, Bangladesh. The soil of experimental site was clay loam with pH of 7.47, electrical conductivity of 1.64 dSm⁻¹, low in organic carbon (0.36 %), available nitrogen (262 kg ha⁻¹) and phosphorus (29 kg ha⁻¹) and high in potassium (342 kg ha⁻¹). The experiment was randomized complete block design consisting of factor A: variety and factor B: planting system having twelve treatments combinations and replicated thrice. High yielding variety BARI shurjomukhi 2 (V₁) and hybrid variety Hysun 33 (V₂) were the two varieties. Six planting systems were S₁- Flat bed sowing at 40 cm × 25 cm, S₂- Ridge and furrow sowing at 40 cm × 25 cm, S₃- Flat bed sowing at 50 cm × 25 cm, S₄- Ridge and furrow sowing at 50 cm × 25 cm, S₅- Flat bed sowing at 60 cm × 25 cm, S₆- Ridge and furrow sowing at 60 cm × 25 cm. Sunflower was seeded on 24-12- 2018 and harvested completely on 15-04-2019. The results revealed that varieties had significantly influenced growth parameters, yield attributes and yield of sunflower. Hysun 33 secure highest plant height (111.44 cm), leaf area (3307.7 cm²), leaf area index (2.72), root length (43.33 cm), stem girth (7.77cm) and significantly differs over BARI Shurjhomukhi 2 which had plant height (107.88 cm), leaf area (3174.38 cm²), leaf area index (2.60), root length (41.66 cm), stem girth (7.46cm) at 85 days after sowing. Among the planting systems Flat bed sowing at 40 cm × 25 cm had shown highest leaf area index followed by Ridge and furrow sowing at 40 cm × 25 cm and Flat bed sowing at 50 cm × 25 cm had shown highest leaf area followed by Ridge and furrow sowing at 50 cm × 25 cm. In the treatment interaction Hysun 33 and Ridge and furrow sowing at 50 cm × 25 cm had sown best result on leaf area index and leaf area. Hysun 33 produced significantly highest seed yield (2066.47 kg ha⁻¹) over BARI Shurjhomukhi 2 (1253.62 kg ha⁻¹) and Ridge and furrow sowing at 50 cm × 25 cm planting system produced significantly highest seed yield (1974.24 kg ha⁻¹) followed by Flat bed sowing at 50 cm × 25 cm (1791.47 kg ha⁻¹). Hysun 33 and Ridge and furrow sowing at 50 cm × 25 cm planting system produced significantly highest seed yield (2591.08 kg ha⁻¹); stalk yield (3889 kg ha⁻¹) and harvest index (39%). Thousand seed weight, quality parameters viz; oil and protein yield were not significantly influenced by different treatments and due to their interaction. Post harvest soil properties (pH, Ec and OC) and available soil nutrient status did not vary significantly due to different planting system and interaction. Gross returns (79701tk ha⁻¹), net returns (56549 tk ha⁻¹) and B: C ratio (2.8) were highest with Hysun 33 and Ridge and furrow sowing and Hysun 33 and flat bed sowing at 50 cm x 25 cm shown significantly similar results. From the present investigation it can be concluded that hybride Hysun 33 and Ridge and furrow sowing followed by flat bed sowing at 50 cm × 25 cm was ideal for realizing higher sunflower yield and economic returns in the coastal saline zone of Bangladesh.

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Rescheduling of wet season (T. Aman) rice planting for cropping intensification in coastal Bangladesh

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About 1.0 million ha coastal lands in Bangladesh are mono-cropped suffer from varying degree of soil salinity, waterlogging and climate vulnerability. Low yielding, traditional T. Aman rice is grown only in wet season. Growing non-rice crop after late harvested T. Aman rice is not profitable. This study was aimed to introduce high yielding, short duration T. Aman rice varieties for advancing its harvesting time and to make the avenue for timely establishment of dry season crops. Varietal trials were made at Dacope and Amtali under ACIAR funded project during 2016-2018 and compared with local cultivars. Among tested varieties BRRI dhan76 followed by BRRI dhan77 and BRRI dhan54 in Dacope and BRRI dhan77 followed by BRRI dhan76 and BRRI dhan54 in Amtali were preferred for 0.5-1.0 tha⁻¹ yield advantage and 15-25 days earliness compared to traditional varieties. Early harvesting of T. Aman created the avenue of timely establishment of rice and non-rice crops depending on availability of fresh water and thus crop intensification and land productivity was improved. The new cropping system increased annual rice yield and farmers' profits by 1.5- to 2-folds compared with traditional system without environmental degradation. This technique can be replicated in similar coastal zones of Bangladesh.

Assessing the use efficiency of Enhanced Efficiency Nitrogen Fertilisers (EENFs) in irrigated maize

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Improving nitrogen use efficiency (NUE) in agricultural systems is a key challenge and represents a win-win-win for society (improved yields, food security), the economy (farmer profitability) and the environment (improved water quality, climate change mitigation). Enhanced Efficiency Nitrogen Fertilisers (EENFs) attempt to improve NUE by synchronizing N supply with crop N demands. This research evaluated the relative performance of a range of EENF technologies compared to standard urea applied at rates equivalent to 125 and 250 kg N/ha. The EENF products included controlled-release (CR) coatings and microbial inhibitors (urease, UI, or nitrification, NI, inhibitors), the target crop was maize and the experiment was conducted under field conditions. Grain yield did not differ significantly between EENFs at 250 kg N/ha, but at sub-optimal N rates (125 kg N/ha), inhibitor-based (UI and NI) products produced significantly higher grain yield than urea. The CR products yielded relatively poorly in this study. Grain N concentrations significantly increased with increased N application rates, with no significant differences between EENFs. Higher amounts of residual mineral N (primarily NO₃-N) were recorded for EENFs compared with urea. The differences in residual soil N between urea and EENFs potentially provide an opportunity to decrease fertiliser N requirements in subsequent crops, depending on the fate of that N during the fallow period. The role of the timing of fertilizer N application in what appeared to be a mismatch between N supply and demand for CR products is under active investigation.

Morphological characterization of root trait variability in bambara groundnut (*Vigna subterranea* (L.) Verdc) landraces – implication for drought adaptation

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Efforts to improve bambara groundnut (*Vigna subterranea* (L.) Verdc.) are currently underway. This underutilised, African grain-legume has limited established varieties with most accessions existing in the form of landraces. Empirical evidence suggests the crop to be drought tolerant, giving better yields relative to other grain legumes, although the adaptive mechanisms deployed are not fully understood. We quantify the variation among eight diverse bambara groundnut landraces and classify the root development observed at the flowering stage. Plants were grown under natural conditions in polyvinyl chloride (PVC) pipes of 20×110cm, diameter and length respectively, packed (1.6g cm⁻³) soil bulk density and roots quantified at different soil depths. Thirty-six root-related traits were characterised, 23 of which had coefficients of variation (↑20%). The Pearson correlation matrix showed a strong correlation among most of the selected traits (P < 0.05). Principal component analysis (PCA) revealed four principal components capturing 94% of the variation. An agglomerative hierarchical clustering, based on root trait variation, identified four landrace groups. The group composition reflected environmental adaptation of landraces. Bambara groundnut sourced from drier regions of Sub Saharan Africa had 21-fold more root growth in deeper soil layers. In contrast, bambara groundnut landraces, from wet-humid regions in South East Asia and West Africa, exhibited shallow-highly-branched root growth. Taken together, our results suggest deep rooting to be an important strategy for improved adaptation of bambara plants growing in water-limited environments. We propose specific bambara groundnut landraces as donors in root trait driven breeding programmes to improve water and nutrient use efficiency.

The relationship between bulb yield and allicin concentration in garlic varieties

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Garlic (*Allium sativum* L.) is used as a vegetable and medicinal plant. It is a rich source of organosulfur compounds, in particular allicin, which contributes to the flavour and health benefits. Although worldwide garlic production is increasing, demand continues to outstrip supply. Improving the yield of garlic will address the increasing demand, while increasing allicin concentration will improve its potential health benefits and flavour. It is unknown if increasing garlic bulb size (yield) has a negative effect on allicin concentration of garlic. Therefore, a fundamental understanding of the relationship between yield and allicin concentration is required.

A field experiment was conducted at Gatton (QLD, Australia) with 32 varieties, of which 29 varieties were sourced from World Vegetable Centre and 3 varieties from existing Queensland sub-tropical varieties. The garlic cloves were planted in March 2018 with 4 replicates in a randomised complete block design and harvested when garlic had 70% senescence.

Varieties showed large variation in bulb size, ranging from 35 to 120 g, with fresh yield ranging from 5.5 to 16 t/ha. The allicin concentration ranged from 3.3 to 6.6 mg g⁻¹ fresh weight (FW) between varieties and more than 50 % of varieties were under the minimum pharmaceutical standard for allicin concentration (≥4.5 mg g⁻¹ in FW). Across varieties there was an inverse relationship between yield and allicin concentration. However, there were some varieties which had both high allicin concentration and yield. Current field trials investigate the effect of agronomic practices on yield and allicin concentration in garlic varieties.

Ecophysiology of *Sorghum bicolor*'s Australian wild relatives

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Sorghum bicolor is grown in semi-arid regions for grain and livestock forage, and is the fifth-most important cereal crop, in terms of usage, globally. It is especially useful for its drought tolerance, which allows it to be grown in conditions which are unsuitable for other cereals and forage crops. However, concentrations of the cyanogenic glucoside dhurrin, a precursor to the production of toxic hydrogen cyanide, increase in *S. bicolor* under drought and temperature stress. Cyanogenic glucosides are found in more than 10% of angiosperms, and appear to have evolved as a herbivore defence. *Sorghum*'s wild congeners store much lower concentrations of dhurrin than *S. bicolor* whilst maintaining high drought tolerance, making this a useful clade for studying the evolutionary purposes of dhurrin production, or lack thereof. These species also represent potentially useful sources of genes for crop improvement, however, their conservation statuses remain largely unknown. Five wild Australian *Sorghum* species were selected alongside *S. bicolor* to investigate the effects of nitrogen supplementation on growth and dhurrin production. Plants were grown for six weeks under deficient and excess nitrogen treatments, with total plant nitrogen, concentrations of stored dhurrin and nitrates, growth rate and photosynthetic parameters measured for each species. This study gives insight into how species can maintain high growth rates without storing harmful concentrations of dhurrin, with implications regarding the effects of cyanogenic glucosides on plant ontogeny and plant-herbivore interactions, and the improvement of food security and safety through genetic enhancement of sorghum crops.

Impact of agroforestry practice on soil conservation- Initial assessment in Northwest Vietnam

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In the Northwest Vietnam, traditional maize (*Zea mays*) cultivation practices of farmers mainly based on sole cropping, intensive tillage combined with burning crop residues on steep slopes. These cultivation practices resulted in severe erosion, soil degradation, reducing crop production and un-sustainable production systems. It requires assessing of the impact of agroforestry practice on the soil conservation in the context of the upland areas in Northwest Vietnam. This study has been carried out since 2017 to present the actual impact of agroforestry practice including longan (*Dimocarpus longan*)+mango (*Mangifera indica* L.)+maize+forage grass strips (*Guinea - Panicum maximum*) on soil conservation. The assessment based on quantifying soil loss by soil traps and evaluating terrace's formation by erosion pins placing above forage grass strips. The sole maize system had been using for the comparison. The initial results showed that the evaluated agroforestry practice reduced soil loss from 18.3 to 37.4% in compared with the sole maize system in 2017 and 2018, respectively. In the second year (2018), the deposition of sediment on the front and rear pins at the above grass strips was 0.81 and 0.41 cm, respectively. It indicated the increment in soil surface at the above grass strips. In contrast, the negative value of the deposition of sediment was recorded in the sole maize system. We are continuing to monitor the impact of agroforestry practices on reducing soil loss and terrace formation, and evaluate the function of the system on soil fertility improvement, nutrient use efficiency and economic profitability.

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Heterobeltiosis in banana and genetic gains through crossbreeding

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Heterosis, or hybrid vigour, is the superiority of the hybrid for a certain trait over the mean of its two parents. Heterobeltiosis is a form of heterosis where the hybrid is superior to its best parent. Banana breeding is a tedious, time-consuming process, taking up to two decades to develop a hybrid. Understanding heterosis in banana breeding will contribute to selecting right breeding materials for further crossing, thus increasing banana breeding efficiency. Here we document heterobeltiosis by using the recently bred NARITA 'Matooke' hybrids and their ancestors. NARITA hybrids, their parents (4x and 2x), grandparents (3x and 2x), and local 3x 'Matooke' cultivar checks were planted in a rectangular lattice design with two replications. Yield and other agronomic data were collected at flowering and harvest. The NARITAs were compared with their 3x 'Matooke' grandmothers. Heterobeltiosis on bunch weight was calculated with the data of 3 cycles. All the NARITAs showed heterobeltiosis for bunch weight. NARITA 17 had the highest grandparent heterobeltiosis (ca. 250%). Genetic gains due to crossbreeding were determined for fruit yield considering three generations: matooke cultigen (C_0), primary tetraploid hybrids (C_1) and secondary tetraploid hybrids (C_2). The average genetic gain (from C_0 to C_2) rates for bunch weight (kg) and yield potential ($t\ ha^{-1}year^{-1}$) were 1.4% and 1.3% per year, respectively.

Participatory variety selection for enhanced promotion and adoption of improved finger millet varieties: A case for Central Tanzania.

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Participatory variety selection (PVS) is an approach that provides a wide choice of varieties to farmers to evaluate in their environment using own resources for increasing production. It enhances farmer's access to diverse crop varieties, increases production, ensures food security and helps faster dissemination and adoption of pre and released varieties. It allows timely and cost-effective varietal selection in targeted areas, promoting community seed production and community seed banks. Therefore, a variety developed through PVS usually meets the demand of different stakeholders. Farmers in Singida and Iramba districts in central Tanzania were found to be growing landraces which were low yielding, long maturing, drought and disease susceptible, as no variety had previously been released in Tanzania. Through PVS a broader choice of varieties matching farmer needs in adaptation and quality traits was offered for evaluation. PVS was used to introduce, evaluate, release and promote for adoption finger millet varieties in Central and Northern Tanzania. Farmers selected and adopted new varieties of a higher utility (a combination of improved agronomic traits, higher yield, and improved quality). Through PVS Tanzania released her first finger millet varieties (U15 and P224). Adoption of the varieties was very high as farmers associated with the varieties; the affordable high-quality seed was made available as Quality Declared Seed (QDS) produced by target farmer groups. Preferred traits differed between the gender groups; women preferred risk averting traits like short duration, drought tolerance, compact heads, and disease resistance while male preferred market-related traits (high yield, brown, and big head).

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Hedging your bets: The importance of flowering time and agronomic practise in the search for the ideal Australian hempseed cultivar

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Cannabis is a versatile plant that has been grown for millennia for a variety of uses, including fibre, food, and medicine. It is divided into two groups based on cannabinoid content: the narcotic type, which contains high levels of psychoactive tetrahydrocannabinol (THC); and the hemp type, which contains low levels of THC. Research on the crop has been severely limited due to drug restrictions. Presently, a range of countries are starting to legalize *Cannabis* for industrial, medicinal, and/or recreational purposes, paving the way for a renewed interest in hemp research for crop improvement and commercial use. Past research focused mainly on varietal selection for increasing hemp fibre production. Studies dealing with the specific effects of environmental cues and agronomic practises on the flowering time are relatively scarce. Additionally, the genetic mechanisms that control flowering in *Cannabis* are currently unexplored. This study aims to investigate the effects of decreasing day length and temperature, and the effects of the agronomic practise called "hedging" on the flowering time and seed yield of hemp. The study will look at variability in flowering emergence, branching, and plant biomass, as well as seed yield and seed nutrient quality. As a first step towards elucidating the genetic control of flowering in hemp, this study will also try to identify key candidate flowering control genes, specifically the hemp orthologues for: FT – mobile flower promoter signal that induces flowering, CONSTANS – one of the regulators controlling the activation of FT, and FLC – floral inhibitor by inhibiting the activation of CONSTANS.

Sustainable carbon alternatives from agriculture for a better tomorrow

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The impact of global warming on agriculture, humans and the ecosystems has become so prominent that it creates economic inequalities among nations and hence, access to affordable, reliable, sustainable, and modern energy for all has become a sustainable development goal of the United Nations. The alarming rise in the atmospheric CO₂ concentration to its historic high levels necessitates comprehensive and cost effective mitigation strategies. Alternate plant based sources of carbon have become a viable option for a greener planet in order to reduce the dependence on depleting fossil fuels and to mitigate climate change. The transition to a renewable carbon regime requires optimum combination of dedicated lignocellulosic feedstocks and conversion technologies. The structural diversity and complexity of plant cell walls pose technological and scientific bottlenecks in the efficient utilization of plant biomass. The relative composition and content of the major cell wall components such as cellulose, hemicellulose and lignin determines the downstream utility of plant biomass. Lignin bestows plants with mechanical strength, however its presence in the secondary cell walls is a major hindrance in the effective processing of lignocellulosic biomass. Targeted manipulation of the central carbon metabolism in plants can make them better candidates for the production of renewable fuels or novel chemicals. Bioengineering of lignin biosynthetic genes using novel genetic approaches to alter the lignin profile of biomass crops can facilitate biomass processing. Emerging approaches such as gene editing can improve the cell wall composition and plant architecture to suit the changing goals for a sustainable future.

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Understanding sclerotinia risks associated with growing peanuts in the South Burnett Area

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Sclerotinia Blight, caused by ascomycete fungal pathogen *S. minor* (Jagger), is a serious soil-borne disease of peanut crops within the South Burnett area in Queensland, Australia. The pathogen can infect root, stem and foliage tissues, forming characteristic fluffy white mycelial growth on stems leading to tissue wilting and necrosis. The disease can cause significant yield reductions and, in some cases, complete crop losses in peanut production. Outbreaks occur in cooler weather (under 18°C) with high humidity levels (above 95%) as the higher humidity levels promote germination of sclerotia (Smith 2003, Maas, Dashiell et al. 2006). Therefore, knowledge of inoculum levels prior to sowing could enhance cropping systems through enhanced capacity to predict outbreaks.

The South Australia Research and Development Institute (SARDI) offers a new soil test for Sclerotinia sp., called PreDictaB, available for farmers to assess inoculum levels pre-planting as a crop risk assessment tool. This project validated the accuracy of the PreDictaB test for Sclerotinia inoculum levels in the South Burnett soils, while gathering paddock and weather data to identify key characteristics linked to high risk of Sclerotinia Blight incidence to be transposed in a pre-season risk matrix model.

Results demonstrated a close positive relationship between the level of Sclerotinia in the soil pre-planting and the paddock disease severity observed at harvest. The significance of the results for future research into potential management strategies is discussed. This new test has the potential to reduce the impact and presence of Sclerotinia in the field within the South Burnett region.

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Analysis of differences in gene expression associated with variation in biomass composition in sugarcane

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Sugarcane has a high potential to support second-generation ethanol production and environmentally friendly by-products for use in chemical, pharmaceutical, medical, cosmetic and food industries.

A crucial challenge for a long-term economic viability is to optimise the crop for production of a biomass composition that will ensure maximum economic benefit.

Transcriptome data analysis provides a relevant explanation of phenotypic variances and gives a more accurate prediction of phenotypes than genomic information.

This multi-omic approach, with an integrated transcriptomics and metabolomics analysis may reveal details of biological mechanisms and pathways.

A global view of transcriptional regulation and the identification differentially expressed genes (DEGs) and metabolites may help the feasibility of tailoring engineering targeted biosynthetic pathways to improve the production of these bio-products from sugarcane.

We propose a profiling analysis workflow (pipeline) to generate empirical correlations between gene expression, metabolites, proteins and phenotypic traits and pathway analysis, with a highlight focus on data visualisation.

This study of genetic variation in gene expression and correlations with metabolic and protein phenotype relies on high-throughput methodology, measurement and analysis of 360 samples, 24 commercial sugarcane cultivars with different phenotypic characteristics at 5 different development stages with 3 replicates.

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Host plant resistance to *Helicoverpa.armigera* has been observed in Australian wild *Cajanus (Pigeonpea) species*

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Pigeonpea (*Cajanus cajan* (L) Millspaugh) is extensively grown in tropical subtropical and warmer equatorial regions of the world and ranking 6th in the global legume production (6.8MT; 2017). It is consumed by billions of people as a major source of protein in developing countries. Despite the increasing demand the crop is facing severe yield losses (2.4 billion US\$/Annum) due to the insect pest *Helicoverpa.armigera* (68% globally). As this pest is polyphagous was exposed to several pesticides and gained strong resistance, it necessitates a strong need for identifying host plant resistance towards this pest. Australia is the second hub with 15 out of 32 *Cajanus* species next to Asia. This is the pilot study exploring the potential of Australian *Cajanus* species as wild were proven sources for potential trait information in many other crops. My study firstly characterized the Australasian wild species and their derivatives for phenotypic variation and secondly tested for their resistance to *Helicoverpa armigera*. My research demonstrated a very high levels of resistance to *Helicoverpa armigera* in some of the Australian wild species and some of their derivatives, compared to cultivated species. This research also revealed a high levels of total phenolic compounds in the wild species and a significant negative correlation of total phenols with the pest survival. We were successful in identifying the major phenolic compound in resistant species. Exploring the role of that specific compound related to host plant resistance and identifying the genetic markers associated with phytochemicals triggering the pest resistance is underway.

Genotypes with deep roots are associated with high yield in aerobic rice production

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Aerobic production (well-watered, non-flooded) has been adopted in the developing rice industry in northern Queensland and has been proposed for southern NSW to improve water productivity where the availability of irrigation is limited. However, current varieties used have mainly been bred for continuously flooded growing conditions and as such their suitability to aerobic production needs to be explored. One trait believed to be associated with aerobic performance is deep rooting as it makes a plant less susceptible to fluctuations in water availability in the top 20cm of the soil profile. Three aerobic field experiments were conducted over two years at Gatton, Queensland examining genetic variation and relationship between root traits and grain yield. Two experiments were conducted in 2017-18 and consisted of 20 genotypes, while the experiment in 2018-19 consisted of 48 genotypes. Highly significant genetic variation existed for grain yield and root traits. Several genotypes had predicted grain yields above 7.5 t ha⁻¹ including current Australian varieties Sherpa and Langi which suggest that they are suitable for aerobic production. Rooting depth contributed to grain yield in all experiments with moderate genetic correlations observed between grain yield and the percentage of the number of roots below 20cm ($r_g=0.27-0.56$). Australian varieties, Sherpa and Langi, displayed high yields but had only moderate deep rooting and the incorporation of deep root characteristics from suitable donors (i.e. IRAT109 and Lemont) into the varieties may have the potential to increase yield in an aerobic environment.

Going underground: Root and stool architecture traits to improve sugarcane productivity

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Sugarcane growth is fuelled by the stool; a complex branched structure of underground internodes and associated roots. Recruitment of basal stool buds for stalk growth underpins the success of a ratoon crop. Root systems are then critical in determining yield through their role in nutrient and water uptake, early vigour, stool anchorage at harvest, and interaction with soil microbes. A better understanding of root and stool growth has the potential to improve productivity and overcome soil constraints.

Studying underground organs has always been challenging and is especially complicated in sugarcane because of the size of the plant and the long growing season. We developed analysis frameworks to study sugarcane stool and root systems at different levels, from root anatomy for carbon economy traits, to root morphological traits, and stool and root system architecture.

Using our toolkit of methods, we screened for diversity in a collection of Australian varieties to provide a baseline understanding of the range and variation of traits. We then defined the impact of constraints including reduced tillering, nitrogen limitation and compacted soils, by combining glasshouse trials, field sampling and physiological modelling. For field sampling, we developed a fast and specific method for quantifying live sugarcane roots in soil samples. With the new methods and knowledge of trait plasticity, we can now start to test which traits provide a benefit in various agronomic situations and develop an integrated understanding of root/stool health which can be used to monitor soil health and promote the adoption of better agronomic practices.

Geographic Information System (GIS) techniques to tackle unsustainable agriculture practices in Madagascar

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One of the major causes of deforestation in Madagascar is the conversion of forest land into crop fields by practicing slash and burn agriculture locally named "Tavy". Rice is the staple food for Malagasy people but local production grown on wetland and flat terrain is not sufficient enough to feed one household of six family members. Cash crops such as vanilla, coffee, cocoa and cloves are the main sources of income that allow them buy rice after all the harvests have been consumed. Sometimes, these crops are grown illegally inside or on the edge of humid rain forests, despite topographical constraints and where trees are cut down and burnt and where remaining organic materials are transformed into fertilizers for paddy fields. The aim of this paper is to describe GIS (Geographic Information System) technique to tackle conflicts between agriculture and forest conservation in Madagascar. These techniques include satellite image processing and on ground zonation using satellite receivers (GPS: Global Positioning System) and local surveys. Landsat satellite images of 30m resolution were used to produce a land use map. SRTM (Shuttle Radar Topography Mission) images have been processed to draw ridgeline, rivers and watersheds. Pre-processed maps are verified and accepted by local communities. Zonation identifies areas important for retaining habitat quality and connectivity for different species but also areas where local agriculture is permitted to be conducted. Locally produced maps will help communities to manage sustainably natural resources, patrol illegal activities inside the forests and find suitable land for cash cropping.

Utilization of forgoing coastal rice fallow lands of Bangladesh with zero tillage potato cultivation using different rates of residues

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An experiment was conducted in south-western coastal saline area of Khulna district of Bangladesh (22°35'N latitude and 89°27'42.617" E longitude) during the period from December 2018 to March 2019. The experiment was laid out in two factor Randomized Complete Block (RCB) design with three replications. Factor A included two potato varieties (V₁ = BARI Alu-72 and V₂ = BARI Alu-73) and factor B consisted with three rates of rice straw mulch viz. M₁ = 4 ton ha⁻¹, M₂ = 7 ton ha⁻¹ and M₃ = 10 ton ha⁻¹. Average thickness of mulch treatments were 11 cm, 13 cm and 15 cm, respectively. Mulch rate had significant effect on different soil and crop parameters, however there was no significant effect observed in variety and variety vs mulch rate. At harvest, highest plant height (50.7 cm), stem dry weight (1.33 g plant⁻¹) and leaf dry weight (7.29 g plant⁻¹) were recorded from M₃ treatment. In case of yield components and yield, M₃ treatment gave highest value for number of tuber per plant (7.11), individual tuber weight (59.38 g), tuber yield (15.62 t ha⁻¹), haulm yield (2.26 t ha⁻¹). Significantly highest moisture was conserved by M₃ treatment (27.13%) at harvest as well effectively controlled salinity (EC_e) increase (only 1.25% increase than initial). So, it is observed that rice straw @ 10 t ha⁻¹ is most suitable for zero tillage potato cultivation in the coastal area of Bangladesh. We estimated that, dry rice straw from about 3.18 hectare land is needed to meet 10 t ha⁻¹.

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Technology package for sustainable productivity and resiliency to climate variability: The proof from SIMLESA studies in Tanzania

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The agricultural sector in Tanzania is mainly rain fed and are dominated by smallholder farmers unreliable rainfall, short than normal duration of cropping season and fluctuations of onset and end of cropping season are main challenges facing small scale farmers. The increased frequency and intensity of droughts, unpredictability of weather, shorter than normal duration of cropping seasons have significant impact on farmers' resilience, production practice and season timing. This paper report study on Conservation agriculture for Sustainable Intensification (CASI) technology package tested on farm for productive, resilient and sustainable smallholder maize-legume cropping systems in 5 districts.

Three practices namely Conservation practice (CA), Current applied recommended practice (CONV. or sometimes referred to as IMPROV) and primitive farmers practice (FP) were compared in an experimental plots at farmers' environment. Improved (DT maize and Pigeonpeas) was intercropped in all practices. Only CA and CONV practices were statistically compared, whereas FP was for farmer's visual observations and comparisons. Data recorded were, soil carbon, moisture, yields and economic analysis.

Results showed that, the average maize yields for 4 seasons in CA and CONV doubled and for tripled.

An average of 30.5% hours was saved in CASI relative to non CASI practice.

The benefit cost ratio of maize-pigeonpea intercrop under CASI was 2.1 as compared to 1.4 in conventional agriculture.

Institutionalization of CASI at local and national policy decision levels is utmost important for sustainability of the effort and resources invested in developing CASI technology package in Tanzania.

Key Words: Sustainable, Resilience, Productivity, Variability.

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Pedigree data analysis of a wheat population

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Genetic diversity is an essential part of successful crop development and can be evaluated by different methods, e.g. the Coefficient of Parentage (COP). This coefficient is established on pedigree data and the pedigree is an illustration of the genetic connection among individual lines, their parents and progeny. COP has been used to analyse the genetic diversity in a variety of crops, as it measures the probability of two alleles in two different individuals being identical by descent. This method can determine the variation among genotypes without the influence of environment effects as would be the case for field data. This study measured genetic diversity among 317 wheat cultivars from a population generated by the speed breeding technique. Using pedigree data, we determined the associations between parents and individuals, and then used the pattern analysis techniques of principal component analysis and clustering. The results enabled an appropriate graphical representation of the 317 lines of wheat cultivars. This information is useful for selecting future parents in breeding programs. This demonstrates that using COP is a viable way to evaluate diversity among genotypes, especially in inbred populations.

Unravelling the complex genetic architecture of spot blotch resistance in barley

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Bipolaris sorokiniana is a necrotrophic fungus which is the causal organism of spot blotch disease of barley (*Hordeum vulgare*). In Australia, the majority of two rowed spring barley cultivars are susceptible to this foliar disease and deployment of genetic resistance is regarded the most efficient and ecofriendly strategy for control. The aim of this study was to dissect the genetics of spot blotch resistance and provide useful tools for breeding resistant cultivars. We employed a multi-pronged approach, initially applying GWAS to Australian elite barley breeding populations and a novel method that explores genome-wide linkage disequilibrium (LD) patterns to identify additional genetic factors with smaller effects that underlie disease susceptibility. Secondly, we evaluated a large multi-parent nested association mapping (NAM) population and analyses revealed key genomic regions associated with resistance that displayed strong interactions with both the environment and genetic background. Lastly, in order to diversity resistance factors in elite breeding material novel resistance genes are needed, thus we performed genetic characterisation using bulked segregation analyses targeting novel landrace sources from China, Pakistan etc. countries. The new insight, resistant germplasm and molecular markers identified as part of this study is anticipated to help plant breeders assemble new barley cultivars incorporating effective genetic resistance to *Bipolaris sorokiniana*.

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Integrated high-throughput phenotyping with high resolution multispectral, hyperspectral and 3D point cloud techniques for screening wheat genotypes under sodic soils

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Wheat production in southern Queensland, Australia is adversely affected by soil sodicity. Crop phenotyping could be useful to improve productivity in such soils. This research focused on adapting high-throughput phenotyping of crop biophysical attributes to monitor crop health, nutrient deficiencies and plant moisture availability. We conducted an aerial and ground based campaign during several wheat growing stages to capture soil and crop information for 18 wheat genotypes at a moderately sodic site near Billa Billa in southern Queensland. Three techniques were employed to monitor crop condition and predict yield multispectral, hyperspectral, and 3D point cloud. Spectral information and vegetation indices (VI) such as, normalized different vegetation index (NDVI), modified soil adjusted vegetation index (MSAVI), and leaf area index (LAI) were derived from multispectral imagery and compared with ground-based agronomic data for biomass, nutrients, leaf area, and yield. Significant correlations were observed between NDVI and yield ($R^2 = 0.81$), LAI ($R^2 = 0.74$), and biomass ($R^2 = 0.65$). Partial least square regression (PLS-R) modelling using hyperspectral spectroscopy data (400-900 nm) provided crop yield predictions that correlated significantly with observed yield ($R^2 = 0.65$). The 3D point cloud technique was effective with comparison to in field manual measurements of crop architectural traits height, volume, and foliage cover (eg. for height $R^2 = 0.73$). For, this study multispectral techniques showed greater potential to identify wheat varietal tolerance under moderately sodic soils than hyperspectral technique. In future, the genotypes will be tested under more severely sodic soils to monitor crop performance and predicting yield.

Key Words: Wheat genotypes, Phenotyping, Vegetation indices, Multispectral, Hyperspectral, 3D point cloud, Sodic soils.

Analyzing the climate change impact and farmer's adaptability strategies in Khyber Pakhtunkhwa, Pakistan

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The agriculture sector is deemed as more vulnerable to climate change as its variation can directly affect the crop's productivity. However, climate change impact and farmers adaptation strategies were not figured out in Khyber Pakhtunkhwa Province, Pakistan by previous researchers and formed the rationale for this research endeavor. This research has assessed the Climate Change impact on wheat productivity and farmers adaptability strategies. The non-climatic variables (wheat yield and area under wheat cultivation) and climatic variables (temperature, precipitation and humidity) were taken into consideration. The Panel Data of thirty years (1985-2015) about non climatic and climatic variables was obtained from different secondary sources; however, primary data was collected from sampled farmers. The econometric diagnostic tests were encompassed to confirm the validity of the data. Chow test was used to underscore the structural breaks. Fixed Effect Model was adopted as suggested by Hausman Test. The salient findings express that temperature has inverse relationship with wheat productivity. This implies that by soaring one Celsius degree Centigrade ($^{\circ}\text{C}$) temperature can plunge down the wheat productivity by 0.074 percent. Similarly, the association of precipitation was also observed negative with wheat. Contrary to this, humidity is observed as positively associated with wheat. The study concludes the substantial association of climate change with wheat crop, whereas, farmers had less awareness about the adaptability strategies. It is recommended that high temperature resistant wheat varieties may be provided to farmers and disseminates the exalted adaptation strategies with respect to climate change to overhaul their existing crop management practices.

Does pulses cultivation uplift the farmer's livelihood in Khyber Pakhtunkhwa Province, Pakistan?

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The major pulses grown in Pakistan are chickpea, gram, lentil and mung-bean. However gram and chickpea together accounts 76 percent of the total pulses production of the country. The recent estimates have shown a decline of 17.7 percent in gram's production during last few years. Therefore, this study has aimed to measure the technical efficiency of chickpea growers in district Karak, Khyber Pakhtunkhwa, Pakistan. The primary data was gleaned from 120 chickpea respondents by employing multistage sampling technique in three focused villages. Stochastic Frontier Production Function of Cobb-Douglas type was encompassed to compute the technical efficiency of chickpea growers. The salient findings of Stochastic Frontier Model divulged that most of the variables were statistically significant. However, surprisingly the overall contribution of the explanatory variables ratifies decreasing returns to scale (Elasticity of inputs = 0.58 \downarrow 1) in the study area. The mean technical efficiency was observed as 80 percent portraying that chickpea growers could improve their crop production by further 17 percent. The total cost of production was estimated as AUD 454.69 per hectare and net revenue from chickpea was computed as AUD 547.98 per hectare. The study has concluded that due to competing crop, no support price and manual management practices for chickpea crop, farmers has curtailed their field area for pulses. It is recommended that farmers should be equipped with modern mechanization tools and major crop's inputs may timely be available in the crop season. Moreover the government may ensure the rational prices of basic pulses inputs.

Economic analysis of cotton crop production in District Dera Ismail Khan, Khyber Pakhtunkhwa, Pakistan

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Cotton crop contributes 5.5 percent in agriculture value addition sector by providing input to the textile realm of Pakistan. This research endeavor is designed to analyze the efficiency of cotton growers in district Dera Ismail Khan, Khyber Pakhtunkhwa, Pakistan. Primary data was collected from the total of 110 cotton growers of the study area. The Cobb-Douglas type Stochastic Frontier function was estimated to investigate the technical efficiency of the cotton growers. The mean technical efficiency was estimated as 77 percent, implying that the farmers can still boost production by 22 percent with the current set of inputs and technology. Results further revealed that Seed, Labour days, Urea, Pesticide and Irrigation play significantly role to boost yield of cotton but tractor hours and DAP show insignificant effect on cotton yield. Cotton growers in the research area received increasing return to scale as summation of elasticity of production was computed as 1.803 which is greater than 1 (1) confirming economies of scale exists. This scenario indicates that if cotton crop's input increase by 1 percent, the cotton yield will be increased by more than 1 percent. Gamma value was observed as 0.83 that demonstrates 83 percent variation in the yield was due to technical inefficiency effect and remaining 17 percent variation due to the uncertainty. Further results reveal that growers with more education and more farming experience were observed as more efficient. The study suggests that the government may conduct training sessions to enhance the capacity building of the cotton growers.

Cropping system intensification for increasing crop productivity in salt-affected coastal zones of Bangladesh

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In Global Climate Risk Index 2019, Bangladesh has been ranked seventh among the countries most affected by extreme weather events. The salinity intrusion has increased by 27% from 1973 to 2009 in coastal areas of Bangladesh due to impacts of climate change. The cropping intensities of the coastal zones are below than the country's average intensity (195%), which causes severe food insecurity. In southern coastal zone, soil and water (river/canal) salinity remain the minimum (\downarrow 4 dS/m) during in July/August but attain the maximum (upto 11 and 25 dS/m, respectively) in March/April. Farmers grow single T.aman rice a year. Therefore, five cropping patterns were tested under ACIAR funded project in Amtali (Barguna district) and Dacope (Khulna) upazilas during 2016-2017 and 2017-2018 irrigating with low salinity surface water (canal/pond) to increase crop productivity. In Amtali, T.aman-Potato-Mungbean-T. aus cropping pattern gave the highest (20.18 t/ha) rice equivalent yield (REY), which increased 360% REY over the farmers' practice (T.aman-fallow-fallow). However, in Dacope, T.aman-spinach-fallow showed the highest REY (14.00 t/ha) that increased 207% REY compared to farmers' practice. The improved cropping patterns can be practiced within the polder (embankment for water control) for increasing crop productivity and profitability in salt-affected coastal zones of Bangladesh.

Zero tilled-paddy straw mulched potato (*Solanum tuberosum*) cultivation in the coastal saline soils reduce soil salinity, increase yield and profitability

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In the coastal saline region of West Bengal, India, rice is the predominant crop during wet season (July-December) and majority land remain fallow during dry season (January-June). Sustainable intensification needs improved package of practices which conserve soil moisture, facilitate early crop establishment, ensures profitability and has positive effect on soil health. To achieve these objectives in a rice-based cropping system, we evaluated seven treatments for potato crop during the dry season viz. T1: ridge sowing (control), T2: Zero tillage (ZT) sowing with 9 t ha⁻¹ paddy straw mulching (PSM), T3: T2 + foliar spray of nutrients, T4: ZT sowing with 12 t ha⁻¹ PSM, T5: T4 + foliar spray of nutrients, T6: ZT sowing with 15 t ha⁻¹ PSM, T7: T6 + foliar spray of nutrients in randomized block design with five replications. Cost of cultivation of potato reduced by about 27% due to ZT sowing (₹ 81,287 ha⁻¹) compared to ridge sowing (₹ 1,11,260 ha⁻¹). Tuber yield, net return and irrigation water productivity was significantly increased in T5, T6 and T7 over other treatments. There was reduction in soil salinity (EC_e reduced from 5 to 3 dS m⁻¹), bulk density (from 1.49 to 1.44 Mg m⁻³), irrigation water use (less 20 cm), conservation of soil moisture (4-8%), and increase in organic carbon (0.39 to 0.44%) due to ZT sowing with PSM. Rice-ZT potato-green gram cropping system was the most profitable one with highest net return (₹ 1,71,752 ha⁻¹), however, the benefit-cost ratio was highest (2.33) with Rice-ZT potato cropping system.

Modelling yield and seasonal soil salinity dynamics in Rice-Grasspea cropping system for the Coastal Saline Zone of West Bengal, India

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Due to seasonal dry-season salt accumulation in the coastal saline zone (CSZ) of West Bengal, India, the cultivation of winter crops (following summer rice) is rare. To address this issue, field experiments were conducted over two years (2016-18) in the CSZ to study the feasibility of cropping system intensification through incorporating grass pea into the dominant rice-fallow rotation. The experiment was conducted in strip plot design with two factors namely, Factor A: Six dates of rice sowing (at one-week intervals - 2nd week of June to 3rd week of July) and Factor B: Two land situations (Medium-upland and Medium-lowland). The experiment was simulated using APSIM (Agricultural Production Systems simulator) utilizing the APSIM-SWIM water balance module to understand the mechanisms of seasonal soil salinity dynamics and the associated crop responses. The results suggest that irrespective of land situation, early sown rice (2nd week of June) produces higher dry matter and yield compared to late sown crops. This early rice sowing also facilitated better subsequent grass pea performance, by avoiding the worst of the salinity build-up and drought stress later in the winter. The model performed well in simulating the observed rice and grass pea yields (R² = 0.97 with low bias (slope, $\hat{\theta}$ = 0.93, intercept, $\hat{\theta}$ = 149 kg ha⁻¹), RMSE = 558 kg ha⁻¹). It may be concluded that APSIM-SWIM is an effective tool to understand, assess and predict the complex bio-physical mechanisms of ground water and soil salinity dynamics in rice-pulse-based cropping systems of CSZ of West Bengal.

Performance of garlic (*Allium sativum*) varieties under zero tillage mulch condition in southern coastal region of Bangladesh

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The experiment was carried out under ACIAR-KGF project at farmers' field of Tildanga village at Dacope Upazilla under Khulna District during rabi season of 2018-19 after harvest of previous transplanted aman rice to find out the suitable variety of garlic (*Allium sativum*) for cultivation in southern coastal region of Bangladesh and to observe the effect of straw mulching on the yield of garlic. The experimental area faces slight to moderately drought and saline prone at later part of winter season and beginning of summer. The salinity causes unfavorable environment and hydrological situation restricting the normal crop production. Farmers generally cultivate only single transplanted aman (T.aman) rice in a year at south and south-western coastal saline areas. Garlic is one of the important spices crop in Bangladesh. The treatments of the experiment were five garlic varieties viz., V1=BARI Roshun-1, V2 = BARI Roshun-2, V3 = BARI Roshun-3, V4=BARI Roshun-4 which were developed by Bangladesh Agricultural Research Institute (BARI) and V5= Local cultivar. The experiment was laid out in a randomized complete block design with three replications. All five varieties of garlic were sown on 17 December 2018 under zero tillage condition. BARI Roshun-1 gave the highest number of bulb/m² (57), pseudostem height (37cm), weight of individual bulb (7.65g) and bulb yield (5.81 t/ha). BARI Roshun-3 gave the lowest yield (3.87 t/ha). It was also observed that the soil moisture of the farmers' field were higher during sowing of garlic which was not suitable for ploughing the land. So timely establishment of garlic is possible by following hand dibbling methods under zero tillage condition on the muddy soil surface and also cost effective. Mulching can protect the evaporation loss and reduces the salinity stress which ultimately influence the crop establishment and yield. Earlier farmers of Tildanga at Dacope under Khulna District had no idea about the cultivation of garlic under zero tillage along with straw much. When the experimental results were demonstrated and discussed about the technology to the farmers gathering during Field Day then they were impressed and interested to grow garlic. Fallow land of coastal areas of Bangladesh could be utilized through disseminating this technology and ultimately cropping intensification increased.

Key Words: garlic, coastal zone, saline soils, zero tillage

Effect of straw mulch and irrigation on sunflower and maize cultivation in no tillage systems of coastal heavy soils

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Three constraints affect the growth of crops in the rabi (dry) season in southern Bangladesh: these are the clay nature of the soils which decreases the infiltration of water, the conserving of soil moisture with the increasingly dry conditions and the accumulation of salts on the soil surface through capillary from saline groundwater. Field experiments were conducted in the salt-affected areas of southern Bangladesh. The objectives of the study were to: (i) evaluate the effect of straw and irrigation frequency on crop growth and yield in maize and sunflower, and (ii) determine the combined effect of straw and irrigation frequency on the salinity, osmotic potential and moisture of soils. The experiment was carried out in farmers' fields with eight treatments and was replicated three times during the dry (rabi) season of 2018-2019. There were two rice straw treatments (with or without straw), and 4 irrigation frequencies (at intervals of 5-7,10-12,15-17 or 20-25 days). Maize and sunflower seeds were sown by dibbling in no-tilled systems. The results showed that rice straw significantly affected the crop growth and yield, increasing the yield of maize and sunflower by 22% and 4.3% compared to treatments of without residue. The irrigation treatments also significantly affected crop yields. There was no interaction between straw levels and irrigation. The causes of these effects appeared to be improved water relations: rice straw and more frequent irrigations both reduced the salinity and osmotic potential of soils compared with treatments without straw while the soil moisture was greater in rice straw treatments and increased with the increased soil layers. We conclude that straw mulching and irrigation management practice could be used in coastal saline of heavy soils to reduce soil salinity, osmotic potentials thereby increasing crop yields in no-tilled systems.

Effects of fresh and saline water irrigation for maize in coastal areas of Bangladesh

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Farmers are being encouraged to represent the conjunctive use of fresh water (FW) and saline water (SW) irrigation for the future agriculture in the coastal saline prone areas of Bangladesh where the scarcity of FW. Therefore, the effects of fresh and saline water irrigation for maize was performed on the crop performances, water use, water productivity (WP), soil salinity and scope for maize cultivation in coastal areas. The experiment was carried out at farmers' field at two locations with six irrigation treatments and replicated thrice during 2016-2017 and 2017-2018. Results showed that the effect of FW (0.5 \leq salinity \leq 1.5 dS/m) at early growth stages and SW (1.5 \leq salinity \leq 5 dS/m) at later growth stages had insignificant difference compared to the treatment of FW irrigation. Yield slightly increased with increased number of irrigations but there was no significant differences among the treatment. WP significantly affected by irrigation frequency in both locations, decreasing greatly with increasing amount. The more changes in soil water occurred at upper layer than lower depth of soil profiles. The highest changes soil salinity (EC_e) occurred at mid-February of the crop growing season compared to the beginning and later growth stages of maize in 60 cm soil profiles. The technique of fresh and saline water irrigation at different growth stages of maize in coastal regions could be an alternative irrigation scheduled and method for increasing yield and WP through establishment of maize compared to no crops at fallow lands during *rabi* (dry) season in the salt affected areas of Bangladesh.

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Yield response of sunflower to sowing dates and NPK rates under zero tillage in wet soil of southwestern coastal Bangladesh

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The low cropping intensity in the southwestern coastal Bangladesh is constrained by excess wetness of soil, low fertility and scarcity of fresh irrigation water. Fallow-fallow-T. *aman* is the main cropping pattern in this region. In the recent years some winter (dry season) crops (wheat, sunflower, maize etc.) have been introduced. Among them sunflower is best suited as it can be established in wet soil and also having the capacity to tolerate salinity and drought to some extent. The fertility of soil of this area is low particularly nitrogen (N). There is no fertilizer recommendation for sunflower in this area. Thus it is necessary to develop a fertilizer recommendation for sunflower. To develop this, a set of field experiments were carried out during winter season (2018-19). In these experiments, the major nutrients [nitrogen (N), phosphorus (P) and potassium (K)] were varied in early (by November) and late (end of December) sown (dibbled) sunflower. Results showed that early sown sunflower produced higher seed yield with lower amount of N than that of late one. In case of P, unlike N, yield increase was not at par with the increase of P rates indicated residual P that applied to previous rice crop supported the sunflower. Potassium rates have little effect on yield increase. Based on the average yield (~3.5 t/ha) of the variety (Hysun-33) N, P and K @ 120-150, 40-50 kg/ha and 50-60 kg/ha was produced highest yield in early sown sunflower in excessively wet soil of southwestern coastal Bangladesh.

Prototype tool kit to identify yellow canopy syndrome in the field

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Yellow canopy syndrome is a condition that is evident as yellowing in the mid-canopy (leaf # 3-7) of sugarcane across all varieties and regions in Queensland. Initial signs of the syndrome are evident by a golden yellow colour usually on one side of the midrib. A characteristic of YCS is the accumulation of sucrose and D-glucans in the mid-canopy leaves. Previous work has shown that once a sucrose threshold level is reached, PSII in particular is disrupted and the density of reaction centres decrease. A consequence of the accumulation of sucrose in the leaf is that reduced carbon is redirected to other pools such as soluble and insoluble D-glucans. Misidentification of YCS is common as there may be many types of leaf yellowing present in a crop at any one time. To identify YCS correctly and to predict its onset will better assist industry to manage the syndrome in the absence of a known cause. The identification of significant accumulation of insoluble D-glucan (starch) in the lamina and midrib led to the development of a quick and easy test that is user friendly. Starch within the midrib veins (vascular bundles) is easily visible when stained with iodine solution. There is a strong correlation between midrib staining, starch content, YCS development and expression. This inexpensive in-field "Prototype YCS Investigative Tool for Industry and Researchers" is currently undergoing field validation.

Understanding how PHOTOPERIOD1 and FLOWERING LOCUS T2 regulate flowering time and spike development in wheat

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To maximise yield, the transition in plant development from vegetative to reproductive growth is coordinated to coincide with the optimal time of the growing season. Cereals detect seasonal changes in day length through the photoperiod pathway in which *Photoperiod1* (*Ppd1*) and *Flowering Locus T* (*FT*) have been shown to be important. In this study we have developed a series of loss of function mutants for key genes in the photoperiod pathway, to investigate how these genes interact. In wheat under long day (LD) conditions, *Ppd1* promotes FT, which travels to the shoot apical meristem (SAM) to promote flowering. Under LD conditions, flowering was delayed but still occurred with loss of *Ppd1* function, despite *FT1* not being expressed. This suggests the presence of an alternative pathway through which flowering is regulated. *FT1* belongs to the PEBP family of which there are at least six *FT*-like genes in wheat. *FT2* is the most similar of the *FT*-like family to *FT1* and therefore may have a similar function. Our results suggest that *FT2* plays an important role in spike development and a more limited role in the regulation of the initial transition of the SAM to the reproductive phase.

Characterizing genetic variation in late, deep wheat root architecture to improve yield and yield stability under terminal water stress

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Root systems play an important role in crop performance particularly under rain fed conditions. Root architecture is key in determining the ability of crops to extract water at various soil depths. In many rain fed production regions, opportunities to improve yield through changes in management practices are limited. Thus, genetic solutions to improve yield under water limitation are required. We postulate that in drought-prone environments, genotypes with greater yield and yield stability can be developed by breeding for genotypes with favourable root systems.

We studied wheat root architecture late in the developmental cycle. Narrow and deep root systems may help wheat to extract more water at depth late in the season and give an advantage to yield and yield stability where crops rely on stored moisture deep in the soil.

To improve yield stability in rain fed regions, an effective phenotypic method is needed. However, studying root traits in mature field-grown crops is extremely challenging. A PVC tube method was developed and has been used to identify genotypic differences in root architecture late in crop development.

Identification of root traits to improve deep water uptake late in crop development and the development of phenotypic methods to identify genetic sources of such traits will assist breeders to improve yield and yield stability in water-limited environments.

Building climate resilience and reducing yields gaps in the wheat belt of South Asia: Can it be achieved at scale?

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By 2050, India needs an additional 44 million tonnes of wheat while environmental externalities and resources depletion concerns are drawing into question the long-term viability of sustaining current production levels in the 'breadbasket' region of NW India. Eastern India has the highest density of rural poverty and food insecurity in the region, but yield gaps for cereal staples ($\uparrow 70\%$ for wheat) are also higher than elsewhere in South Asia. As such, increasing staple food production in Eastern India is a development imperative at the local to national scales. Suboptimal crop management is prime cause for low wheat yield. Here, we established that sowing dates explains 50% of contemporary wheat yields achieved by farmers. By assessing planting dates and production practices through landscape diagnostics, we estimate that feasible adjustments to the timing of wheat sowing can contribute to closing about 30% of the current wheat yield gap. Nevertheless, timely wheat sowing is often impeded by late rice harvests; as a consequence, system level interventions are a most to improve wheat productivity. Simulations results also suggest that early wheat sowing will confer greater resilience to the rising temperatures observed and anticipated in the region. We are working on research-based strategies that permit early planting together with companion management strategies (e.g. genetics, irrigation, conservation agriculture-based management) that promise to further reduces yield gaps. By bringing wheat sowing in Eastern India States by 5 days can increase wheat yield by 0.2 t ha^{-1} , generating an additional farm profitability of 136 million USD.

Response of mungbean root system architecture to phosphorus application methods

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In recent years phosphorus application methods have become an important management strategies for optimising the uptake of immobile phosphorus nutrient. Root system architecture (RSA) could also play an important role in the uptake of phosphorus, a key nutrient for the grain legumes. Objective of this study was to understand the response of mungbean root system to phosphorus application methods. Contrasting mungbean varieties were grown in purpose-built soil filled root chambers with five phosphorus application methods. Phosphorus treatments consisted of a control (no application of P compared with 30 mg/kg soil applied P for other treatments and a high P treatment), shallow dispersed, deeper dispersed, deep band and high P dispersed. After 50 days of growth, plant were destructively harvested and shoot and root parameters were measured. Mungbean varieties responded differently to P application methods, where Jade and Berken varieties showed greater root proliferations at depth and greater shoot growth in response to banded and deeper dispersed P applications, compared to a late maturing variety Putland. Surface applied and no-P control both resulted in poor root growth for all the genotypes, except Celera II, which did not respond to P rates or placement. Results suggest that P application strategies may need to vary with variety to maximize the uptake of P.

Low cost protective structures providing suitable growing conditions for vegetable crops year-round in the tropics

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Vegetable production is an important activity, source of food and income for farmers. Vegetables are grown in many regions in Lao PDR. There is a large range of agro-climatic conditions between the two seasons - wet and dry. The dry season is suitable and favourable for vegetable production. However, the wet season has high temperature, high relative humidity, high soil moisture content and heavy rain. These conditions cause several negative impacts for vegetable production such as, low vegetable productivity and poor quality. Higher application of pesticides can also lead to food safety issues and high input cost of cultivation. These challenges could impact to inadequate domestic supply of vegetables in rainy season, low economic returns from vegetable production, and increased imports of vegetable from other countries. NAFRI and ACIAR have cooperated to research and develop a design of greenhouse structure that is economical and provides suitable growing conditions in the wet season to help farmers to mitigate the multiple constraints and successfully grow vegetables year-round. The new design was constructed and tested with several types of vegetable crops including coriander, lettuce, spring onion and tomato during 2015 -2018. Evaluation was made against ambient conditions, crop needs and also a comparison with several other protected cropping designs was conducted. The new design provides improved, cooler and more suitable growing conditions for a range of crops, increasing productivity and quality of vegetable in the wet season.

Key Words: Productivity, vegetable, greenhouse structure, Lao PDR

Genetic elucidation of glucosinolates in a diverse collection of Indian mustard (*Brassica juncea* L.)

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Glucosinolates (GSLs) are secondary metabolites produced by members of the genus *Brassica*. These compounds impart the pungency to brassica vegetables and oils. Due to their health benefits, which include anti-cancer and anti-fungal properties, they have been attracting interest in research. Indian mustard (*B. juncea* L.), used as condiment and oil crop has high natural levels of seed glucosinolates and displays exploitable natural variation in this trait. In this study a diverse collection of 161 mustard lines originating from 21 countries, will be genotyped and phenotyped. Traits of interest include seed GSLs (sinigrin, gluconapin, progroitin, epi-progoitin and glucoiberin), oil and protein content, as well as basic agromorphological performance such as height, flowering time and yield. Current knowledge on GSL biosynthesis and its genetic regulation mostly relies on data from *Arabidopsis thaliana*. We aim to elucidate the genetic architecture of GSL content and composition in relation to other seed traits (oil and protein content) in our diversity panel through association mapping. Additionally, we are aiming to resolve genome complexity of GSL genes in mustard genome in contrast to *A. thaliana* by identifying gene copy number through *in silico* analysis. Outcome of this study will help streamline the breeding and product development for either high GSL mustard lines for condiment use or low GSL lines for canola-type oil use. Our preliminary data on seed GSLs seems to reflect the historical use of mustard in different geographical regions. Chinese and European lines featured higher GSL while lines from the Indian subcontinent displayed lower GSL contents.

Affordable, Accessible, Asian (AAA) Drought Tolerant Maize specifically developed for poor-resource smallholders; a collaborative program between CIMMYT and SYNGENTA

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In 2010, CIMMYT and SYNGENTA decided to co-develop a specific maize breeding program to make hybrids of tropical maize accessible at an affordable price to poor-resource smallholder farmers. The objective was to create drought tolerant hybrids that yield about two times of widely used OPVs or at least 80% of some of the popular, low-priced hybrids, commonly cultivated in rain-fed, drought prone areas in India.

The development opportunity for AAA maize in the specific targeted geographies: South Rajasthan, East Gujarat and West Madhya Pradesh is evaluated at 0,6M ha meaning 8000 Tons of seeds.

The ultimate goal is to increase poor-resource smallholder farmers yield from 1.5T/ha to 2.5T/ha, and generate an additional net income of \$100/ha

After several years of intense R&D activity, the program team has selected the variety TA5084, and launched it during the 2018 Kharif season (30 Tons). Around ten key seed partners in India are already testing and promoting this new resilient hybrid on a larger scale.

Considered as International Public Goods (IPG), AAA maize hybrids are made publicly available to the seed partners. SYNGENTA and CIMMYT are co-owners of the hybrids: SYNGENTA owns the female and CIMMYT owns the male. CIMMYT is entitled to make its parental line available to third parties for further breeding, production and commercialization in South Asia and South East Asia. CIMMYT licenses the male to the seed partners – royalty free while SYNGENTA licenses the female with a discounted royalty rate of 2% of the Net Selling Price instead of 5-6% (seed industry practice) in order to contribute to the expansion of AAA maize considered as IPG. This would create a strong impact assuming we aim converting 50% of the OPV targeted geographies and reaching 200.000 smallholder farmers.

Control of sugar and fibre: Insights from sugarcane transcriptome analyses

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Sucrose and fibre in sugarcane share a very dynamic relationship depending largely upon the genetic makeup of the genotypes and growth environment. To investigate the molecular basis of carbon flux into sucrose and fibre that makes the genotypes high sugared or high fibred, or dual purposed, an extensive transcriptomics study was undertaken using a set of sugarcane genotypes differing in sugar and fibre contents. Differential gene expression analyses were performed using 50 transcriptomes revealing a complex network of transcripts associated with growth, defence, vacuole, sucrose and fibre. Rather than merely being a storage sugar of the culms, sucrose might play a significant regulatory role in controlling the expression of several thousand genes including those related to fibre. The high sugar genotypes were not always low in fibre and the fibre might to an extent provide structural framework for maintaining high sugar levels as seen by the high expression of fibre related genes. The study suggests that there could exist certain threshold levels of sugar or fibre contents beyond which an inverse relation would occur. In addition, analysis of the transcriptomes resulted in the identification of a new isoform of sucrose synthase genes, SuSy 7 that was not reported earlier. With the availability of a monoploid reference genome, there is a need for in-depth transcriptome studies to understand and identify finer details of genes, and their transcripts in entirety and regulatory elements of sugarcane genome which is challenging the current capabilities of sequencing technologies unlike any other plant genomes sequenced thus far.

Isolation and characterization of full-length phenylalanine ammonium lyase and cinnamyl alcohol dehydrogenase genes involved in lignin biosynthesis of *Erianthus arundinaceus*

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Lignocellulosic biomasses available in abundance is the promising raw material for alternate energy production considering the issues of dwindling oil prices, and global warming. Recently, *Erianthus arundinaceus* has been identified as a potential target for second generation biofuel crop due to its high biomass production, and adaptability to extreme growth environments. Lignin is a major plant cell wall polymer indispensable for plant growth and development, however it hinders the saccharification of lignocellulosic biomass. Based on the previous transcriptome studies in a set of sugarcane genotypes differing for lignin content, genes encoding cinnamyl alcohol dehydrogenase (CAD), and Phenylalanine ammonium lyase (PAL) genes playing major roles in genetic regulation of lignin production have been cloned and characterized from an *Erianthus clone* IK 76-81. The genomic region of EriCAD was 3524 bp sequence containing four exons and three introns, among which the exon 1&2 of 88 and 80 bp were conserved with sorghum and Miscanthus CADs. The coding region of CAD was identified with 1086 bp open reading frame (ORF), a 68 bp 5' untranslated region (UTR), and a 86 bp 3' untranslated region (UTR). In the PROSITE analysis, a zinc-containing alcohol dehydrogenase signature (GHEVVGVEVGPEV) and an NADP-binding domain motif (GLGGLG) was identified. Similarly sequence analysis of PAL showed an ORF of 2,106 bp encoding for 702 amino acid residues. It was flanked by 172 bp of 5' UTR and 121 bp of 3' UTR. This sequence information on PAL and CAD from *Erianthus* might be useful for subsequent research on lignin modification for improved biomass conversion.

Building farming resilience to climate change: Upland crop production in Northwest Cambodia

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Production of upland crops such as maize, cassava, soybean, mungbean, peanut and sesame contribute importantly to Cambodia's economy and food security, especially for those who live in the upland areas in almost every province of Cambodia. The upland farmers are highly vulnerable to climate variability and climate change due to low adaptive capacity and high dependence on rainfed crop production for livelihood. This study involved in-depth review of literature, conducting on-farm experiments, downscaling climate projections from General Circulation Models (GCMs), running Agricultural Production Systems sIMulator (APSIM) simulations and farmer consultation to define climate impacts and explore adaptation options that could build farming resilience to the existing and projected climate change scenarios for upland cropping farmers in Northwest Cambodia. Insufficient water and nutrient depletion were the main production risks and yield limiting factors. On-farm adaptation options such as modifying sowing windows, crop rotation with legumes and additional fertiliser application are likely to substantially minimise risks from climatic impacts, and increase and sustain returns. Additional adoption of conservation agriculture practices – including reduced tillage, crop residue retention that enhance soil structure, soil water holding capacity and reduced soil erosion should enhance productivity and incomes, while making the farming systems more resilient to the existing and projected climate variability and climate change, and other production stressors.

Agroforestry suitability mapping for the northwest provinces of Vietnam

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This study aims to assess the potential development of selected agroforestry options for three provinces in the Northwest of Vietnam. Available spatial data including Land use/land cover maps and forest inventory maps were used as the base maps in combination with supplementary data and field survey to determine the potential agroforestry areas. Soil types, soil depth, soil texture, elevation, slope, temperature and rainfall were used to evaluate the biophysical suitability of ten typical agroforestry options in the study region. For assessing the impact of climate change to agroforestry suitability in the future, temperature and precipitation data extracted from two climate changes scenarios (Representative Concentration Pathway 4.5 and 8.5 in 2046-2065) were used. The results showed that the suitable areas for agroforestry development in Dien Bien, SĐn La and Yen Bai provinces were 267,74.01 ha, 405,597.96 ha; and 297,995.55 ha, respectively. Changes in temperature and precipitation by 2 climate change scenarios affected significantly to the suitability of *Docynia indica + livestock grass*, *Teak + plum + coffee + grass* and *Plum + maize + livestock grass* options. The map of agroforestry suitability can be served as a useful source in developing and expanding the area of agroforestry in the target provinces, and can be applied for other provinces in the same region in Vietnam.

Large scale genome-wide association study reveals drought induced lodging in grain sorghum is mainly driven by remobilisation and plant height

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Sorghum is generally grown in water limited conditions and often lodges under post-anthesis drought, which reduces yield and quality. Due to its complexity, our understanding on the genetic control of lodging is very limited. We dissected its genetic architecture in grain sorghum through genome-wide association study (GWAS). GWAS was conducted on 2308 unique hybrids grown in 17 Australian sorghum trials over 3 years. The GWAS detected 213 QTL, the majority of which showed a significant association with leaf senescence and plant height (72% and 71% respectively). Only 16 lodging QTL were associated with neither leaf senescence nor plant height. The high incidence of multi-trait association for the lodging QTL indicates that lodging in grain sorghum is primarily driven by carbohydrate remobilisation and height. This result supported the selection for stay-green (delayed leaf senescence) to reduce lodging susceptibility, rather than selection for short stature and lodging resistance per se, which likely reduces yield. Additionally, our data suggested a protective effect of stay-green on weakening the association between lodging susceptibility and plant height. Our study also showed that lodging resistance might be improved by selection for stem composition but was unlikely to be improved by selection for classical resistance to stalk rots.

Adopting and adapting the principles of participatory guarantee systems for local quality assurance systems in conventional agriculture

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Participatory Guarantee Systems (PGS) are locally focused quality assurance systems established out of the global organic movement in 2004. PGS was seen as an affordable, credible and alternative system to third-party organic certification for small-scale farmers. Based on active participation of stakeholders and built on a foundation of trust, social networks and knowledge exchange, PGS has become instrumental in opening unregulated markets to small-scale farmers who cannot afford third-party certification. However, since then there has been a broadening of the term PGS in the agribusiness community and including those not practicing organic agriculture. We discuss here our findings on the local perceptions of the meaning and application of PGS, which include its use in organic and conventional agriculture. Drawing parallels from the misuse of the term *organic* and the impacts of this on the organic movement, we discuss here problems associated with applying the term PGS in conventional systems; these include confusion by the traditional users of the term, inability to distinguish quality assurance efforts in organics from non-organics and more importantly, undermining the credibility of the growing organic movement in Fiji and the Pacific. We suggest here a possible solution in adopting a similar PGS-like approach and term, for those involved in conventional agriculture and seeking to have a local quality assurance system recognized and accepted.

A novel biomarker test for sugarcane yellow canopy syndrome

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Yellow canopy syndrome (YCS) is a condition that affects sugarcane crops throughout Queensland, and is most apparent in the warmer summer months when plants are actively growing. Key symptoms of YCS include a yellowing of the mid-canopy leaves, and the accumulation of sucrose and D-glucans in the lamina, midrib and sheath tissue. As no cause for the syndrome has yet been found, a biomarker test for identifying YCS, as distinct from other conditions that cause leaf yellowing, is important to enable early detection before any signs of visual yellowing. This will inform YCS management practices, and drive the research forward. We used an RNAseq and bioinformatic approach to identify six YCS-specific biomarker candidate plant transcripts that were uniquely and consistently up-regulated in YCS. We designed primers against these transcripts, and developed a novel reverse-transcriptase polymerase chain reaction (RT-PCR) test to identify sugarcane plants affected by YCS. The YCS biomarker test is showing early signs of success and is undergoing further validation, with the aim of correctly identifying YCS-affected sugarcane plants before symptoms become apparent. This poster outlines the biomarker candidate discovery and test development process.

Plant and seed mortality of fireweed *senecio madagascariensis* following herbicide application

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Fireweed (*Senecio madagascariensis* Poir), is a weed of National significance and one of the worst weeds of coastal pastures in South Eastern Australia. Chemical control has been found to be effective in killing plants but there is no information on the effect of herbicides on the seeds that may be present on plants at the time of application. Consequently, a study was undertaken to determine the effect of five selective herbicides 1) on plant mortality at different life stages and 2) on the viability (as assessed by germination) of fireweeds seeds at different stages of maturity. Potted plants of the required growth stages were obtained through several collections of different sized seedlings from a field site near Brisbane. Before herbicide application, in the mature plant cohort the inflorescences were tagged according to their maturity as being either immature (IM) or intermediate (INT). Plants were sprayed with either fluroxypyr/aminopyralid (HotShot™) (A), bromoxynil (Bromicide® 200) (B), metsulfuron-methyl (Brush-Off®) (C), triclopyr/picloram/aminopyralid (Grazon™ extra) (D), triclopyr/picloram/aminopyralid (Tordon™ regrowthMaster) (E) at the recommended dosage, with untreated control plants of the three growth stages also included for comparison. All herbicides killed fireweed seedlings and juvenile plants, but only treatments A, D and E gave high plant mortality (↑80%) of mature plants. All herbicides also caused nil germination of seeds collected 30 days after spraying, except for a small percentage (8% germination) of mature seeds from Bromoxynil treated plants. These results have identified several herbicides capable of killing mature fireweed plants and minimizing replenishment of soil seed reserves.

Developing pigeonpea as a sustainable new field crop for Australia

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Pigeonpea (*Cajanus cajan*) provides a major opportunity as a highly profitable grain legume for summer production in QLD and northern NSW. Current options such as mungbean, peanut and soybean each have their specific niches. However, growers also need a resilient, drought-tolerant grain legume like pigeonpea to increase broad-acre pulse production. Exporters are also seeking a reliable supply of high quality pigeonpea for expanding and potentially lucrative market opportunities in South Asia.

Pigeonpea as a crop is currently not without its problems for mechanised agriculture. Small areas of this pulse crop are already grown in Australia to provide insect refuges within GM cotton, but not for premium grain.

In response, the Department of Agriculture and Fisheries (DAF) is undertaking a major new 'Pigeonpea Initiative'. This is delivering an integrated platform of R&D that is identifying potential genetic options and management strategies to maximise crop yields, reduce production risks and ensure reliable supplies of high quality pigeonpea for premium commodity exports and food.

This highly focused 'proof of concept' R&D is also identifying the key research questions, opportunities and targets for a larger and more comprehensive project on pigeonpea. This will foster vital collaboration between researchers, research agencies, growers and industry to ensure potential benefits from pigeonpea as a new pulse crop can be realised.

Developing pigeonpea as a resilient and productive new summer pulse crop for Australia promises to underpin enhanced productivity, profitability and sustainability for our northern grains region.

Estimating soil organic carbon under different land-use types in Australia's Northern Grains Region using mid-infrared spectroscopy

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Land-use type is known to affect levels of soil organic carbon (SOC). However, the degree to which SOC is affected by land-use type over the short- (↓10-years) and long- (↘10-years) term remains relatively uncertain. Moreover, there is limited data on the distribution of SOC across particulate (POC), humus (HOC) and resistant (ROC) fractions, and the responses of these fractions to land-use. Using mid-infrared spectroscopy (MIR) coupled with partial least squares regression (PLSR) algorithms generated from the Australian Soil Carbon Research Program (SCaRP), soil organic carbon (TOC, POC, HOC and ROC) was estimated across 280 paired samples across Australia's Northern Grains Regions. Our analysis covered five land-use types: remnant native vegetation, long-term pasture (↘10-years), short-term pasture (↓10-years), short-term cropping (↓10-years) and long-term cropping (↘10-years). All land-use types except long-term pasture generated significant declines across all SOC fractions compared with native vegetation. Long-term cropping resulted in the greatest declines, with an average decrease of 6.25 g TOC/kg soil relative to native vegetation. Long-term cropping also reduced POC (-0.71 g/kg) and HOC (-3.19 g/kg) below that of short-term cropping. In addition, the ROC fraction responded to land-use type, with native vegetation and long-term pasture maintaining greater ROC compared with other land-use types. The results demonstrate substantial reductions across all SOC fractions with long-term cropping. The ability of long-term pastures to maintain levels of SOC similar to that of native vegetation indicates the importance of limiting soil disturbance and maintaining more continuous living plant cover within cropping systems.

Grain oats - an alternative winter cereal for the Australian sub-tropics?

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Current production of oats for grain in Queensland is minor due to unsuitable varieties bred for different climates, and high disease pressure from leaf and stem rust late in the growing season. A range of grain oat breeding lines developed by the Federal University of Rio Grande do Sul in Porto Alegre, Brazil, was screened for leaf rust resistance and subsequently identified as potential grain oat cultivars for sub-tropical Queensland. The evaluation of these grain oat lines from Brazil may provide an opportunity to re-establish oats as a winter grain crop in central and southern Qld and northern NSW. Two replicated trials were established near Toowoomba in Qld and Grafton in NSW to assess grain yield and agronomic characteristics. These trials showed significant differences in grain yield within the set of Brazilian grain oat lines, compared with the Australian cultivars, showing the potential for selection of higher yielding lines. The Brazilian line coded UFRGS037031-3 was the highest yielding line in both high yielding conditions at Grafton and moisture stressed conditions at Wellcamp, and should be the focus of any further evaluation. The Brazilian grain oat lines have very strong resistance to leaf rust compared with Australian cultivars. Further research is needed to determine the potential demand for grain oats as a feed grain in Queensland and to determine the profitability of grain oats to farmers as an alternative winter cereal.

NT native rice - commercial use, regulation and benefit sharing

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We explore benefit sharing, for the commercial use of native rice in the NT, Australia. The study specifically investigates the perspective of Indigenous enterprise developers. How can Indigenous suppliers and/or users of these resources, ensure they share the benefits flowing from a range of commercial uses?

Traditional Owners in the NT are interested in the benefits of commercial use of native species. This interest is matched by that of consumers in native plant products, which attract premium prices because of their nutritious status and cultural identification. Resource supply ranges from wild harvest to cultivation. Native species underpinning new products and markets include wild relatives of crop species. Thus, they also present valuable genetic resources for plant breeding.

Collecting, use and transfer of wild species requires regulation, permits and benefit sharing agreements under NT acts and regulations. Commercial uses of resources from native title lands may activate additional demands via *Aboriginal Land Rights Act 1976*. The Nagoya Protocol aims to ensure benefits to indigenous people who supply resources for commercial use. "Rice" is named in the *International Treaty on Plant Genetic Resources for Food and Agriculture*. In agricultural settings, materials transfer agreements are used to track the movement of materials (and benefits) among parties involved in crop development.

How does this dense landscape - of (a) regulations, permits and agreements, (b) cultural, genetic and economic values, and (c) benefit sharing - hinder, help or protect the interests of Indigenous enterprise developers using or sharing species resources?

Indigenous enterprise developers explain.

Commercial use of native species by Indigenous enterprises - a case study of native rice in the NT

Dr Sean Bellairs¹, Dr Penny Wurm¹

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We explore benefit sharing relating to the commercial use of native rice in the Northern Territory (NT), Australia. This study specifically investigates how to ensure Indigenous land owners and Indigenous suppliers of these resources share in the commercial benefits.

Traditional Owners in the NT are interested in the benefits of commercial use of native species. Consumers desire native plant products, which attract premium prices because of their nutritious status and cultural identification. Resource supply ranges from wild harvest to cultivation, and includes wild relatives of crops, valuable genetic resources for plant breeding.

The legislative landscape is complex. The Northern Territory Biological Resources Act (2006) promotes the conservation and sustainable use of biological resources, while requiring benefit sharing agreements occur between land holders and those using biological resources. Collecting, use and transfer of wild species requires regulation, permits and benefit sharing agreements under NT Acts and Regulations. Commercial uses of resources from native title lands may activate additional demands via the *Aboriginal Land Rights Act 1976*. The *Nagoya Protocol* seeks to ensure benefits for indigenous people who supply resources for commercial use. "Rice" is named in the *International Treaty on Plant Genetic Resources for Food and Agriculture*. In agricultural settings, materials transfer agreements seek to control benefits among parties involved in crop development.

How does this dense landscape of (a) regulations, permits and agreements, (b) cultural, genetic and economic values, and (c) benefit sharing - hinder, help or protect the interests of Indigenous enterprise developers using or sharing species resources?

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Novel source of biotic stress resistance identified from brassica species and its wild relatives

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In rapeseed and mustard, the major diseases (downy mildew, white rust, *Alternaria* blight and *Sclerotinia* stem rot) cause 37-47% loss in pod formation and 17-54% reduction in grain yield. The identification of new sources of resistance is a high priority in breeding programs. About 3000 germplasm accessions of Indian mustard were evaluated under multiple environments (3 seasons) at hot spots (4 locations) and under artificial epiphytophic conditions against insect pests and diseases (aphids, white rust, powdery mildew and *Alternaria* blight). Accessions IC265495, IC313380, EC766091, EC766133, EC766134, EC766192, EC766230, EC766272 were identified as highly resistant to white rust (*A. candida*) with disease severity reaction (Percent disease severity Index, PDI = 0) across the locations and under artificial inoculation. Accession RDV 29 showed the inheritance of resistant source for powdery mildew in Indian mustard. Screening of brassica wild relatives (about 25 species) for white rust found that *Brassica fruticulosa*, *Brassica tournefortii*, *Camelina sativa*, *Diplotaxis assurgens*, *D. catholica*, *D. cretacia*, *D. Erucoides*, *D. Muralis*, *Lepidium sativum* had highly resistance (PDI=0) to Delhi isolates of white rust. Several traits identified from cultivated and related species will be useful for genetic improvement of rapeseed and mustard.

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Wxlv, the ancestral allele of rice Waxy gene

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In rice endosperms, the *Waxy* (*Wx*) gene is important for amylose synthesis, and various *Wx* alleles control the amylose content and affect the taste of cooked rice. Herein, we report the cloning of the ancestral allele *Wx^{lv}* of the *Wx* locus, which affects the mouthfeel of rice grains by modulating the size of amylose molecules. Using evolutionary analysis, we demonstrated that *Wx^{lv}* originated directly from wild rice, and the three major *Wx* alleles in cultivated rice (*Wx^b*, *Wx^a*, and *Wxⁱⁿ*) differentiated after the substitution of one base pair at the functional sites. These data indicate that the *Wx^{lv}* allele played an important role in artificial selection and domestication. The findings also shed light on the evolution of various *Wx* alleles, which have greatly contributed to improving the eating and cooking quality of rice.

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Is broadcasting mung bean into rice crops a useful practice in Timor-Leste?

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Mung beans (*Vigna radiata*) are a potential crop in rotation with rice on the south coast of east Timor. When Mung beans are planted after rice, the soil is cultivated after rice harvest, before mung beans are planted by hand with the use of a dibble stick. This paper looks at the cost and benefits of broadcasting mung beans into rice just prior to or just after rice harvest. Broadcast mung beans requires much less labour than planted by dibble stick. Broadcast mung beans require more seed, and can be more difficult to weed. Based on a gross margin analysis mung bean yield could be 35% lower and be as profitable as conventionally grown mung beans.

National level economic and environmental benefits of rice hull biochar in Timor-Leste

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Rice hull biochar has been proven to be a potent and very effective soil ameliorant in soils in Timor-Leste. A series of experiments have demonstrated large consistent increases in yields of rice crops and upland crops when supplied with rice hull biochar. This research shows that if half of the rice hulls in Timor were returned to rice fields, the average rice yield would increase 0.3%/year in the first year, and increase national rice income by \$150,000. Using biochar on horticulture crops would produce a higher financial return, increasing horticulture production by about \$1 million. In addition to the economic returns, the return of rice hull biochar to cropping fields would reduce the national emissions by 7,600 t of CO₂ equivalents about 2% of the emissions of TL.

Physiological response of 20 Bambara groundnut (*Vigna subterranea* L. Verdc) to intermittent periods of water stress during different growth stages

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Drought stress is a limitation to bambara groundnut (*Vigna subterranea* L. Verdc.) production in the drought prone areas of Ghana, accounting for up to 50% yield losses reported. Landraces grown by farmers are low yielding. Invariably, introduced genotypes have low adaptation. This study was therefore, undertaken at CSIR-Crops Research Institute in a controlled environment to identify Bambara genotypes that will be tolerant to drought, good crop development and high yielding in the Forest Transition agroecological zone of Ghana. Nineteen Bambara genotypes from Botswana, Tanzania, Swaziland, Nigeria, Burkina Faso, Namibia, Kenya, Mali and Ghana were screened for drought tolerance at vegetative and reproductive stages. The experiment was designed as a factorial laid out in randomized complete block arrangement, 19 genotypes of bambara groundnut and three water stress levels with all factorial combinations replicated three times in a screen house. The bambara genotypes showed considerable variability in tolerance to drought stress. Stressing plants at vegetative and reproductive stages resulted in a decline in relative water content of leaf, chlorophyll content and leaf area index. Genotypes were significantly different for dry matter production ($P \leq 0.01$), maturity days ($P \leq 0.05$) and harvest index. A maximum seed yield was achieved by local landrace under fully irrigated condition. Genotypes Uniswa Red, S19-3 and Nav Red gave relatively high yields under stress and no stress conditions, maintained above mean seed yield and thus were tolerant to drought stress induced at both vegetative and reproductive stages.

Assessment of genetic diversity of Bambara groundnut (*Vigna subterranea* (L) Verdc.) accessions for the development of drought tolerance lines

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Genetic diversity studies are used in crop improvement to aid selection of important traits that can lead to an improved yield, selection for better crop performance and resistance to stresses. Here, 138 accessions of Bambara groundnut (BG) (*Vigna subterranea* (L) Verdc.) were planted in 2018 rainy season at three contrasting geographical locations in Nigeria

Phenotypic descriptors for BG and Single Nucleotide Polymorphisms (SNPs) markers were used to assess the genetic diversity amongst the accessions. The experiment was arranged in a randomized complete block design of three replications.

High quality DNA was extracted from the young healthy-looking BG leaves and sent for DArT seq genotype-by-sequencing at DArT Pvt Ltd, Canberra, Australia. A total of 24,386 SNPs generated and filtered to give a core set of 5.4k SNPs. Heterozygosity, genotype call rate, polymorphic information content, reproducibility and genetic distance were obtained using DArTsoft v.14. Principal component analysis and Neighbour-Joining cluster analysis were used to analyze the genetic relationship among the accessions. Phenotypic data results were analyzed; clustering analysis grouped the total accessions into seven clusters of 2-47 members. The first five principal components axes explained 94% of the total phenotypic variation. There was significant ($P \leq .001$) variation within and across locations. Correlation between number of petiole per plant and seeds per plant has significant. Accession TVsu-11 and S19-3 showed high seed yield and were the most stable accessions across locations. Number of petiole per plant, plant height are among parameters that could be used for indirect selection for yield performance in BG landraces

Demand driven common bean variety development and promotion for enhanced productivity and production

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Common bean research program of Ethiopia aimed at development of demanded variety for enhanced adoption, improve food and nutrition security as well as to boost income of smallholder farmers thereby enhancing foreign earnings of the country. To achieve these aim, the breeding program use different strategies. These includes, importing demanded variety and fast-track testing release, introducing bean germplasm and release stable variety and participatory variety selection for incorporating growers traits on variety selection. Accordingly, bean improvement program selected six major bean products that includes, small/large white beans, speckled bean, small/large reds and mottled beans. During variety selection stakeholders' choice and trait of preference has been incorporated during interactive consultative forums of the value chain actor at bean innovation multi-stakeholder platform. Apart from bean variety development, integrated crop management technologies has been developed to implement good agricultural practice. To facilitate common variety adoption, bean seed system have been enhanced through integration of early generation seed production with formal and informal seed production of public and private seed producers. These efforts has enhanced transformed productivity from 0.7 to 1.5t/ha and area expanded from 150,000 ha to 520,121 ha and total production up to 568,243t. Due to this fact bean export has been increased up to 100-150 million USD per annum. Generally, the demand led breeding and value chain approach, synergetic and innovative technology generation and promotion has transformed bean productivity, area produced and market; consecutively livelihood of growers and income of the country has been enhanced.

Key Words: Common bean, demand led breeding, seed system, multi-stakeholders, platform

Response of grain legume species to terminal drought in Timor-Leste

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Growth, development and yield of three-grain legumes (mung bean [F1], soybean [F2] and grass pea [F3]) following rice crop to enhance grain production was studied in a paddy field in the northern Timor-Leste. A split plot design was used with three water treatments (well-watered [W0], water withheld at flowering [W1] and after germination [W2]). Interaction between water treatments and species on dry matter production ($P < 0.001$) and seed yield ($P = 0.005$) was observed. In control, the highest seed yield was F1 (1.2 t/ha) followed by F2 (1.1 t/ha) and F3 (0.4 t/ha) respectively. There was a steady reduction in seed yield in F1 from W0 to W2, but almost fifty percent reduction in F2 under W1 and W2 compared to W0. F3 had little difference between water treatments. The W1 and W2 reduced number of filled pods per plant in all species compared to control (W0). Between the species, F3 had the highest filled pods per plant followed by F2 and F3. The W1 and W2 reduced seeds per pod of F1; however, it did not effect F2 and F3. There were interactions between water treatment and species on 100 seeds weight. The heaviest seeds were in F2 in the control plants, but in the F2 drought treatments (W1 and W2) seed weight were less than F3. The lowest seed weight was in F1, but there was no impact of the terminal droughts on its seed weight.

Jatropha curcas development as intervention potential to tackling land, energy and food challenges of rural communities in dryland sub-Saharan Africa

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Global population growth is placing increasing pressures on land for food and feed production as well as energy security. In particular in sub-Saharan Africa (SSA), these issues require urgent attention. This is clearly stated in The United Nations Global Goals for Sustainable Development emphasizing the importance of sustainable use of land resources to increase food productivity and energy requirement. SSA lags behind most regions of the world in household food security and access to energy. The rural agriculture-dependent communities of SSA are the hardest hit by food and energy scarcity and the impact is felt most by communities in the dryland farming areas. In terms of energy supply appropriate measures and interventions are required to address this challenge. *Jatropha curcas* L. oil fast tracked itself from obscurity to prominence. Its main advantage is the high content of methyl ester (or bio-diesel). It conforms to EN 14214 specifications, exhibiting emission reduction potential and qualifying as a lucrative bio-diesel alternative to fossil diesel. This paper proposes a focus on *Jatropha* technology as a holistic approach to tackling the land, energy and food degradation challenges in unison for dry-land SSA. The new *Jatropha* strategy would be innovative and environmentally friendly soil resource recapitalization and supply feed stock for rural energy generation while fulfilling the criteria of delivering other benefits, such as addressing land use conflict for food and energy production.

Suitability Evaluation of Underutilized crops under future climate change using ecocrop model: A case of bambara groundnut in Nigeria

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The agricultural crop system depends on a few major staple crops such as rice, maize, wheat, sorghum, soybeans amongst others for food production leaving certain crops underutilized. Even though of these underutilized crops have the potentials of diversifying and sustaining food and nutrition system, while presenting different resilience to climatic conditions. As world's population increases, and climate change keeps occurring, these major staple crops are being negatively affected by climate change resulting to low yield. Hence, this study will be focusing on testing the spatio suitability of Bambara groundnut (*Vigna subterranea* (L.) Verdc.), an indigenous underutilized African legume under current and projected future climate scenarios.

This study is based in Nigeria, West Africa where farmers depend mostly on rainfed agriculture. Spatial suitability of Bambara groundnut will be computed according to the FAO Ecocrop suitability database under the following climate scenarios: historical (1980-2010), near future (2010-2040), mid-century (2040-2070) and end of century (2070-2099). Climate datasets were sourced from the Coordinated Regional Climate Downscaling Experiment (CORDEX) Africa project and use multiple downscaled Global Climate Models from SHMI-Swedish Meteorological and Hydrological Institute, RCA4 under a Representative Concentration Pathway (RCP) 8.5 emission scenarios.

With studies indicating low spatial and temporal suitability of major staple crops, the results of this study are expected to show the changes in spatial suitability of Bambara groundnut in the country in comparison to the staple crops. The study will contribute to the discussions of increasing the number of agricultural crops cultivated under the varying climate as an adaptation strategy towards ensuring a resilient agriculture and sustainable food system.

Developing plantain for resistance to banana aphids by RNA Interference

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Banana Bunchy Top Virus (BBTV) is one of the world's invasive species. Banana aphid (*Pentalonia nigronervosa*) is found in all banana producing areas and it is the insect pest known to transmit BBTV causing Banana Bunchy Top Disease (BBTD) in bananas and plantains (*Musa* spp.) and can cause a significant yield loss of up to 100% in severe cases. Controlling the spread of BBTD has been very challenging since there is no known endogenous gene in the *Musa* germplasm that could confer resistance to BBTV. Excessive dependence on insecticides for disease control is detrimental to the environmental and off-target-organisms. The objective of this study was to use RNA interference (RNAi) targeting AChE gene in banana aphid to develop farmer preferred plantain cultivars that are resistant to banana aphid. This could help sustain smallholder farmers in areas where BBTD is an epidemic. To achieve this, plantain cultivars were initiated using plant tissue culture techniques and rapidly multiplied using Temporary Immersion Bioreactor. This was followed by generation of embryogenic cell suspension (ECS), *Agrobacterium*-mediated transformation of banana ECS using a plasmid construct (PNXT 35s ACE hp) harbouring *acetylcholinesterase* (AChE) and molecular characterization of putative transgenic lines. ECS of plantain cultivars was generated and 1 ml settled cell volume could generate over 11,000 plants. Molecular characterization confirmed 80% transgenic lines. Preliminary screening gave about 40% potential lines that are resistant to banana aphids. The first report on using RNAi to target AChE gene for developing plantain cultivars that are resistant to banana aphids.

Performance of zero tillage potato cultivation with different mulch materials in the south-western saline area of Bangladesh

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Crop cultivation in the coastal saline area of Bangladesh during *rabi* season is limited due to late harvest of *Aman* rice, shorter winter period, difficulty in tillage, soil salinity, lack of fresh irrigation water etc. Zero tillage potato cultivation with mulching could minimize these obstacles and thereby increase system productivity. However, selection of mulching material is crucial for higher yield and economic return. An experiment was conducted at coastal saline area of Bangladesh during *rabi* 2018-19 to observe zero tillage potato performance under different mulch materials. Three locally available mulch materials were employed in the trial viz. rice straw (T₁), rice husk (T₂) and compost (T₃) as control. Additionally, treatment T₁ and T₂ also received same amount of compost as T₃. Results from single factor randomized complete block design with three replications showed that leaf dry matter, leaf area index and number of tuber per plant did not varied significantly. Significantly highest stem and root dry matter were found from T₁ (69.56 kg ha⁻¹) and T₃ (138.92 kg ha⁻¹), respectively. Rice husk (T₂) produced numerically highest leaf dry matter (372.74 kg ha⁻¹) and significantly lowest root dry matter (87.92 kg ha⁻¹), which ultimately produced highest tuber yield (13.99 t ha⁻¹) followed by rice straw (T₁) (11.08 t ha⁻¹). However, weed growth was highest in rice husk (1.16 t ha⁻¹). Mulch treatments conserved 3.5 to 7.45% more moisture and 4.3% less salinity than control. Between two mulches rice straw is suggested for its profitability since it remains unused and readily available.

Effect of mulch materials and nitrogen source on the performance of tomato in the south-western coastal area of Bangladesh

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The major cropping pattern in the South-western coastal area of Bangladesh is transplanted *aman* rice followed by fallow during the *rabi* season (November to March) and kharif-I (April-July) season. Crop production during *rabi* season is limited due to various ecological factors including soil salinity, lack of fresh irrigation water, short winter period, late harvest of previous *aman* rice, heavy clay soil etc. Tomato is a popular winter crop in that area which is mainly cultivated around homestead and ridges of fish pond, where soil salinity and tillage is not a major problem. An attempt was taken to grow tomato in Khulna district of Bangladesh after T. Aman rice harvest during 2018-19 in order to investigate tomato performance at different mulch materials and Nitrogen sources. The two factors experiment was carried out in randomized complete block design with three replications. Mulch materials viz. rice straw (M₁), black polythene (M₂) and no mulch (M₃) were employed as factor one and nitrogen source viz. prilled urea (N₁) and urea super granule (N₂) were assigned as factor two. Results showed that there was no interaction effect of mulch and nitrogen treatments. Single effect of mulch and nitrogen treatments showed that highest fruit yield was found from rice straw (M₁) (17.32 t ha⁻¹) and prilled urea (N₂) (15.64 t ha⁻¹), respectively. So, tomato can be grown with rice straw mulch along with prilled urea for higher economic return (MBCR 2.24).

The effect of water stress combined with a heatwave on reproduction and yield of Roma-VF tomatoes

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Tomato (*Solanum lycopersicum*) is one of the most consumed fruits, supplying humanity with both economic and nutritional benefits. However, its production is affected significantly by climatic conditions especially extreme weather events, such as heat waves, flooding and drought. The objective of this study was to evaluate the additively combined effects of heat and water stresses on the reproductive traits and yield of Roma-VF tomato variety. Pollen morphology, number of developed flowers, fruits and aerial biomass were monitored. At five weeks after sowing, the tomato plants were subjected to day/night temperatures of 28/20°C as a control treatment and 35/23°C as the heat stress treatment. The water stress was imposed by reducing the water received by plants in each 10-litre plastic pot to 70% soil field capacity (moderate stress) and 40% (severe stress). The stress lasted for eight weeks, which was followed by five weeks of recovery period. Our results showed that plants under additively combined heat stress with either moderate or severe water stress produced flowers with no single pollens during the treatment period. We also found that Roma-VF tomato has a high plasticity in response to this particular heat stress for vegetative growth when well irrigated, but when heat and water stresses were additively combined the plants became highly susceptible. This is also the first report of yield response of Roma-VF tomatoes to the additively combined effect of heat and water stressors.

Challenges to increasing production and standardizing fruit quality of Calamansi (*Citrofortunella microcarpa*) towards geographic branding in Mindoro Island, Philippines

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Calamansi or calamondin (*Citrofortunella microcarpa*) is an indigenous fruit that dominates citrus industry in the Philippines. It's small sour fruits is used fresh or processed. Calamansi is a traditional home remedy for common coughs and colds. The fruit is rich in Vitamin C, calcium, zinc and iron. The scent alleviates depression and neutralizes bad smell. The essential oil has anti-bacterial property used as additive to cleansing products and mouthwash. The lead producer of calamansi is the island province of Mindoro, contributing 54% to national production. There is a distinct buyers preference for quality and longer shelf life of Mindoro grown calamansi, and this led to the goal towards its geographic branding. However, on farm level, existing status of calamansi farms and lack of research pose many challenges in achieving this goal, among which are: need for rehabilitation of typhoon damaged trees, old tree rejuvenation, prevalence of chronic pests and diseases, and highly fluctuating prices. While 72% of production is during the peak season, price is only 15% during lean months. Thus, even seasoned calamansi farmers have started shifting to other crops, just when the market demand for both fresh and processed products is increasing. Three municipalities produced more than 80% of the calamansi in the province, hence, upgrading the production system of these core areas will contribute significantly to the industry's sustainability. Developing and making farmers adopt improved and standard good management practices in crop production is key towards achieving the dream of geographic branding for Oriental Mindoro calamansi.

Four new macadamia varieties for the Australian industry

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Four Macadamia varieties have been released by Queensland Department of Agriculture and Fisheries (DAF) after eight years of Regional Variety Trial (RVT) evaluation at eight Queensland (QLD) and New South Wales (NSW) sites. The field trials were planted in 2008 and consisted of 20 superior clones derived from populations bred by the Commonwealth Scientific and Industrial Research Organisation (CSIRO), five standard industry varieties, 'HAES 741', 'HAES 344', 'HAES 816' and 'A16', and five Hidden Valley Plantation selections. The trials were planted over a range of 1400 Kms from the northern most site at Mackay in central Qld to the southernmost site at Macksville on the mid-north coast of NSW. Multi Environment Trial analysis using Best Linear Unbiased Predictions for nut in shell (NIS) yield, kernel yield, kernel recovery (KR) and tree volume, and economic traits modelling to year 20, aided in selecting new varieties for industry release. Discounted Cash Flow (DCF) estimates have been calculated for a 30 ha farm using economic modelling of NIS over 20 years. The average DCF of the four new industry varieties compared with the average of the five standard varieties shows an increased profitability of 11%.

Global scale GxE for Eucalyptus dunnii growth traits

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The amount of genetic gain from elite germplasm deployment is proportional to the accuracy of selection. It is critical to determine the phenotypic response of families to each environment and estimate the genotype by environment interactions. Significant interactions can result in type-B correlations of seed lot performances across sites and can require optimisation of seed lot deployment to each site.

A population of *Eucalyptus dunnii* selected for pulp wood production was evaluated in 17 open-pollinated progeny trials located in Australia, Uruguay, China, Argentina and Spain for diameter at breast height and height between the ages of 12 and 70 months. To handle the complexity of the data we extend the generality of the factor analytic approach to accommodate unbalance in treatment effects and traits by modelling each dimension of the genotype covariance matrix as a unique combination of location, age and trait. This generality supports the estimates of unique variances for each dimension and individual pair-wise correlations, whilst maintaining a positive definite covariance matrix.

Genetic correlations between growth traits, between trials and between ages were generally high with some exceptions. Repeatability of seed-lots varied from 0.05 – 0.18 for both traits. Genotype by environment interactions were low and indicated that genetic gains could be achieved by deploying the highest ranked seedlots in different countries and regions within Uruguay.

Secreted-in-xylem genes as targets for the diagnostics of different races of *Fusarium oxysporum* f. sp. *cubense* infecting bananas

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Fusarium oxysporum f. sp. *cubense* (Foc) tropical race 4 (TR4) is the most threatening pathogen to commercial banana production worldwide due to the lack of effective disease management. The centre of origin of TR4 is Southeast Asia, and over the last two decades the disease has spread widely in Asia but is now also present in India, Pakistan, the Middle East and Africa. An important strategy to protect disease-free areas from new incursions is reliable diagnostics for the early containment of the pathogen. Here we report a novel molecular diagnostics toolbox which is able to detect strains of TR4, subtropical race 4 (STR4), race 1 (R1), and R4 vegetative compatibility groups (VCGs) 0121 and 0122. Our assays include a range of duplex and simplex PCRs targeting different Secreted-in-Xylem genes, with some of the latter involving a restriction digestion step. We validated our assay as being fit-for-purpose using a total of 250 *Fusarium* isolates. Our assay validation takes into consideration a range of parameters to detect strains of Foc and demonstrate the constraints to detect R1 strains given its polyphyletic origin. Our study proposes for the first time specific diagnostic assays for Foc strains associated with VCGs 0121 and 0122. These strains are especially relevant as they are able to cause disease in Cavendish banana in the tropics but express symptoms that are less severe compared with those of TR4. This diagnostic toolkit has the potential to support decision-making by the banana industry stakeholders in any growing region around the globe.

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Aligning Pacific cocoa genetics to productivity and quality for the craft speciality chocolate market

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Cocoa (*Theobroma cacao* L.) is an important agricultural export of South Pacific countries, providing livelihoods for an estimated 310,000 people. The wet tropical coast of Far North Queensland has also started producing cocoa for a local boutique chocolate making industry. Although the volumes of cocoa produced are small by global standards, Pacific island and north Australian cocoa is well placed to compete in the high-value, low-volume markets – based on fine flavour, unusual genetic resources and novel 'single origin' branding.

A member of the *Malvaceae* family, cocoa has its origins in Central and South America. First domesticated over 2,000 years ago, cocoa's global dispersal was mediated by humans and cultivation is now widespread across the humid tropics.

The use of molecular markers to characterize the diversity of genetic resources available and identify superior genetic material is vital to the continued improvement and selection of clones. This work used single nucleotide polymorphism (SNP) markers to identify the parentage of Pacific island cocoa selections in relation to the 10 distinct cocoa families formerly identified from the original Central and South American populations.

On farm collections from Pacific island countries has revealed distinct geographic cocoa populations. Specific populations show strong Criollo parentage, a source of fine flavour qualities, while others exhibit a high component of Amelonado parentage. Small populations show a higher percentage of IMC, Parinari, National or Scavina parentage was identified.

Production and quality data linked to these populations is used to identify superior parentage to enable local programs to rapidly bring these into commercial production thereby improving cocoa productivity and quality in the Pacific.

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Horticulture innovation

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The horticulture industry is highly dynamic. The global horticulture sector is expected to be sustained by Innovations from pre-to-post harvest handling and management of horticultural produce. The world population is estimated to reach 9 billion by 2050, which makes horticultural innovations relevant to meeting global demand for food and nutrition security. According to the United Nations, world food production should be boosted to 60% by the year 2050 if mass unrest in the form of social, political and civil disturbance as well as terrorism is to be avoided.

Innovations in horticulture are essential to address the major threats to global food security such as drought which leads to a shortage in water for human and animal usage including crop production due to global warming and change in weather patterns; emerging diseases caused by new pathogen strains; soil depletion and over-reliance on fertilizers. Postharvest losses, insect damage and poor seed quality for horticultural crops require innovations to address. Innovations being promoted in some developing countries include the zero-energy cold storage chamber for storage of fresh horticultural produce on the farm, the CoolBot technology for reducing the cost of cold storage of horticultural produce, pest exclusion nets and innovative seed drying beads. Other innovations include precision horticulture, protected cultivation, resistant rootstock development, growth regulators, irrigation technology, organic production, crop stress management, molecular markers, and produce marketing are innovations that could enhance horticulture. The ultimate benefit of horticultural innovation would be efficiency in input usage for increased Total Factor Productivity and increased yield.

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The effect of heat treatments and drip line placements on the yield and quality of garlic

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Despite garlic being a crop with significant economic value, the plant has severe productivity constraints and challenges that contribute to low yield and quality. One of the main difficulties in garlic production is Fusarium basal rot (FBR) caused by *Fusarium oxysporum formae speciales cepae* (FOC). The soil-borne fungus infects the roots and basal plates of alliums causing delayed emergence and bulb rot at pre- and postharvest stages. The incidence of the pathogen is increasing and is expected to increase further due to growth being promoted under warmer temperatures associated with climate change. Management of the pathogen is difficult because it produces chlamydospores that can survive for years in the soil. Potential practices for reducing FBR in garlic are hot water or dry heat treatments applied to cloves at 50°C or 45°C, respectively, for 30 minutes prior to planting, and controlling irrigation using single or double drip line placement for 1.5m wide beds with two rows of garlic. The current study investigated the impact of controlled irrigation on FBR prevalence. These chemical-free practices are relatively easy to apply and could be effective for managing FBR in conventional and organic grown garlic.

Analysis of gross margins in Queensland tomatoes

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Tomato is an important vegetable crop that contributes significantly to income security and healthy diets of people worldwide. Queensland produces the majority of tomatoes for fresh consumption accounting for 40 per cent of national supply in Australia.

The purpose of this study is to provide an analytical summary of the Queensland tomato supply chain, by focusing on margins along the supply chain. For that, a representative tomato gross margin model in Southern Queensland was used to analyse the estimated income, grouped variable costs and the gross margin for four tomato varieties: gourmet, round, grape, and cherry.

The mean yields of the sampled varieties varied considerably, depending on climatic conditions, pests and diseases, the season and whether tomatoes are grown on the ground or trellises. Driven by high revenues and relatively low freight costs, grape tomatoes have the highest gross margin (\$73 thousand per hectare) as well as the highest market price at \$4.64 per kilo compared to other varieties. The cost of growing the crop up to harvest can exceed \$10,000 per hectare with high labour requirement for harvesting and packing.

While costs for machinery, fertiliser, herbicide, weed control, insecticide, and fungicide largely remain constant across four tomato varieties, it is planting and irrigation that makes a difference. With average value of \$9,303 per hectare, planting costs range from \$5,134 for round tomatoes to \$12,241 for cherry tomatoes.

The results of this gross margin analysis can be helpful to explore profitability at the farm level, allowing regional and international comparisons.

Solanaceous plants respond to tospovirus infection by accumulation of small interfering RNAs homologous to both viral sequences and endogenous transcripts

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Tospoviruses infect numerous crops worldwide, including solanaceous species. As a defence mechanism, plants use RNA interference (RNAi) to generate viral small interfering RNAs (vsiRNAs), which target viral RNAs for degradation. Here, we show that infection by tomato spotted wilt virus (TSWV) or capsicum chlorosis virus (CaCV) of three solanaceous species, capsicum, tomato and *Nicotiana benthamiana*, resulted in similar vsiRNA profiles across viral genome segments, though some variation was observed in the abundance of specific vsiRNAs. Interestingly, TSWV and CaCV viral load remained high in capsicum and *N. benthamiana* despite the presence of abundant vsiRNAs. Furthermore, with the exception of an *N. benthamiana* accession lacking a functional *RDR1* gene, the three solanaceous host species generated highly-abundant virus-activated small interfering RNAs (vasiRNAs) against a subset of endogenous genes. Analysis of vasiRNA-associated endogenous transcripts revealed a strong enrichment for ribosomal protein-encoding transcripts and for transcripts encoding proteins involved in protein processing in the endoplasmic reticulum, suggesting that vasiRNA biogenesis is dependent on the sub-cellular localisation of the targeted transcript. Although the *N. benthamiana* accession possessing a functional *RDR1* capable of vasiRNA biogenesis demonstrated increased viability relative to the vasiRNA-free accession, viral titre was the same. Moreover, with the exception of *Heat shock cognate 70*, vasiRNA target transcripts were similarly upregulated in both the *N. benthamiana* accession with a functional *RDR1* gene and vasiRNAs, and the accession lacking *RDR1* and vasiRNAs. Thus, while *RDR1* was associated with both improved TSWV resistance and vasiRNA biogenesis, a functional role for vasiRNAs is still to be demonstrated.

Insight into the role of FT in macadamia

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Macadamia is an important commercial evergreen nut crops in Australia. Flowering is a crucial stage, for fruit production, and Flowering Locus T (FT) is recognised as a pivotal floral inducer in the Arabidopsis flowering network system, as well as in other species including crop trees. FT is induced in leaves and moves to axillary buds to promote flowering. We identified two FT homologue genes (*FTa* and *FTb*) in macadamia and found that the expression of *FTa* was higher in buds than in leaves during the assumed period of flower initiation suggesting that bud may be the site of floral induction in macadamia. To further understanding the role played by FT gene in Macadamia (*MacFT*) in flowering regulation, *MacFT* gene expression pattern in leaves and buds were analysed to confirm in dormancy to confirm whether the FT expression in leaf and buds is consistent with the previous experiment. The overexpression of *MacFTa/b* using the CaMV 35S promoter with GFP demonstrated that *MacFT* was localised in the nucleus and suggested their transcriptional factor role. Transient expression in pea, confirmed their involvement in flowering. Finally, in-silico analysis of *MacFT* gene showed high similarity to the transcription factors distribution within the promoter of FT gene in Arabidopsis. These results indicated that *MacFTa/b* encodes a protein closely related to Arabidopsis FT and that the function of FT is conserved in macadamia.

Lime and fertiliser applications increase yield of leafy vegetable crops in Cambodia

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Growing vegetables after rice harvest allows Cambodian farmers to use land that would otherwise be unproductive between rice crops. Producing vegetables on these soils is limited by low soil pH, low cation exchange capacity and limited nutrient retention capacity. Soil pH in the top 20 cm is generally low (5.5) and may limit the availability of nutrients.

Farm-based trials in Siem Reap and Kampot provinces assessed the effect of lime and fertiliser on leafy vegetable crop growth and yield. At lime-only sites, lime was applied at rates of 0.5, 1.0 and 2.0 tonnes per hectare (t/ha) in conjunction with farmer practice fertiliser rates. For sites with lime and fertiliser treatments, combinations of farmer practice and optimal fertiliser rates, no lime and 2.0 t/ha of lime were applied. Two consecutive crops were planted to examine the residual effect of lime on soil pH and crop yield.

At lime-only sites, all crops responded to lime application with yield increases of up to 100%. For sites that assessed combinations of lime and fertiliser, the treatment of lime and optimum fertiliser rates showed the highest yield increase (92%). First crop yields were higher than subsequent crop yields in all trials.

Application of 2.0 t/ha lime increased soil pH by approximately 1.0 unit. This effect was still evident after the second crop. For the 0.5 t/ha lime treatment, an initial soil pH increase of 0.4 units had reduced to 0.2 units after the second crop. Long-term field trials are needed to examine residual lime effects.

Light relation in intensive mango orchards

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The amount of light intercepted by a tree and its distribution within the canopy is critical in optimizing tree performance, from photosynthesis efficiency to carbon partitioning and productivity. Here we documented light relations in high-density training systems in comparison with current commercial orchards. The baseline study showed that light interception in commercial orchards reached maximum level at around 67 % at the age of 26-31 years when canopy volume reached about 15,187 m³/ha canopy volume. Light interception did not significantly increase beyond 67 % regardless of increase in canopy volume per hectare or the increase in orchard age. Maximum yield was around 16000 kg/ha when light interception reached around 49 % and declined at the high levels of light interception. In small tree high density training systems, the light interception increased with canopy volume, with high density training systems intercepted more available lights compared to medium density training systems and low density conventional training trees. Yield per ha increased close to 50t/ha in espalier trained, high-density orchard systems grown where light interception and canopy volume reached around 40 % and 5000 m³/ha at 5 years of age. Single leader trees and espalier trees had more evenly distributed light in the inner canopy compared to conventionally trained trees. Overall, increased canopy volume and light interception in current commercial orchards had no benefit to increase economic returns whereas small tree high density training systems increases yield around four times at their early age. However, further tree management and yield observation are need as trees are still growing to fill their allocated space.

RNAi-mediated management of whitefly *Bemisia tabaci* by oral delivery of double-stranded RNAs

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The whitefly, *Bemisia tabaci* (Hemiptera: Aleyrodidae) is a significant global pest of economically important vegetable, fibre, and ornamental crops. Whiteflies directly damage the plants by piercing and sucking essential nutrients, indirectly through honeydew secretion and by transmitting more than 200 plant viruses that cause millions of dollars in produce losses per year. Whitefly management is mostly reliant on the heavy use of chemical insecticides. However, this ultimately leads to increasing resistance development, detrimental effects on beneficial insects and biomagnification of ecologically harmful chemicals in the environment. Responding to consumer demands for more selective, less toxic, non-GM insect control strategies, RNA interference (RNAi) has emerged as a potential game-changing solution. The RNA interference (RNAi) is a homology-dependent mechanism of gene silencing that represents a feasible and sustainable technology for the management of insect pests. In the present study, twenty-two whitefly genes were selected based on their essential function in the insect and tested in artificial diet bioassays for mortality and gene silencing efficacy. The nine most effective dsRNA constructs showed moderate-to-high whitefly mortality as compared to negative controls six days post-feeding. qPCR analysis further demonstrated significant knockdown of target gene mRNA expression. Additionally, uptake and spread of fluorescently labelled dsRNA was evident beyond the midgut of the whitefly supporting the systemic spreading of RNAi effectors. Taken together, the oral delivery of dsRNA shows effective RNAi mediated gene silencing of target genes and offers a viable approach for the development of dsRNA biopesticides against hemipteran pest.

Variations in macadamia varietal susceptibility to *Phytophthora multivora* and *P. cinnamomi*

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Incidence of diseases caused by various *Phytophthora* spp. in macadamia is increasing worldwide, often resulting in severe yield loss and death of both juvenile and old macadamia trees. In Australia, *P. cinnamomi* and *P. multivora* has been identified to cause severe stem canker in macadamia orchards. Currently, various varietal improvement research programs on macadamia are underway, not only to obtain high-yielding and precocious macadamia germplasm but to develop macadamia genotypes with acceptable levels of tolerance/resistance to pests and diseases. In this study, we selected macadamia genotypes for their acceptable levels of tolerance/resistance to *Phytophthora* infection, after screening about 360 macadamia genotypes against to *P. cinnamomi* and *P. multivora*, using a rapid detached leaf and plant inoculation assays. These macadamia plant materials were collected from a major macadamia arboretum in Queensland.

Our results revealed segregation of macadamia genotypes into two spectrum of susceptible and tolerant macadamia genotypes. Hence, strong representatives within the tolerant and susceptible spectrum were further investigated in order to understand if the basis of the differential response is driven by a variation in structural, physiological or genetic markers, following a challenge with *Phytophthora* spp. Our result revealed a marked variation in structural response during the infection process, between the selected susceptible, 'HAES816' and tolerant germplasm and 'HAES344'. This information will provide evidence to support potential preferential selection of tolerant macadamia genotypes potentially useful for breeding against *Phytophthora* diseases. Further studies will characterize tolerant macadamia progenies to develop marker-assisted selection protocols for resistance, and explore defence mechanisms response.

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Dependence on cross-pollination in macadamia and challenges for orchard management

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Cross-pollination is essential for the reproduction of self-incompatible plants and it improves the yield and fruit quality of some self-compatible plants. Cross-pollination of clonal horticultural crops is achieved only when pollen from one cultivar reaches the stigma of another cultivar. We quantified self- and cross-fertilization rates in macadamia nuts (*Macadamia integrifolia*, *M. tetraphylla* and hybrids) that were harvested at different distances from a cross-pollen source in two different plantation designs (mixed blocks of multiple cultivars vs. pure blocks of a single cultivar). We also estimated the distance of effective pollen movement, evaluated how different pollen parents affect nut quality, and assessed whether distance from a cross-pollen source affected the number of nuts harvested. We found that almost all nuts resulted from cross-pollination in both plantation designs, with almost all nuts being cross-pollinated even at 23 rows from another cultivar. However, most pollen did not travel far, and nearby cultivars were usually the pollen parent. Cross-pollination increased nut mass and changed the nutritional quality of the nut. The number of nuts harvested decreased with increasing distance from a cross-pollen source in large pure blocks, but not in mixed blocks. Dependence on cross-pollination coupled with low distances of pollen movement may cause suboptimal fruit set. Our results suggest that fruit set in macadamia plantations comprised of large single-cultivar blocks is limited and that plantations can benefit from closer interplanting of different cultivars.

Shoot borer *Earias vittella* – a threat to the indigenous vegetable Pele *Abelmoschus manihot* in the Pacific

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The indigenous vegetable *Abelmoschus manihot* (Malvaceae) is one of the staple crops in the Pacific island countries. It is known by various local names, including Pele (Samoa, Tonga), Bele (Fiji), Aibika (Papua New Guinea), and slippery cabbage (Solomon Islands). The Food and Agriculture Organisation (FAO) has recommended this as one of the top crops for nutritional security. The leaves of *A. manihot* are consumed raw, in soups and in various local cuisine. Herbivory is a major problem in growing *A. manihot*; however, farmers are reluctant to use pesticides. We examined the damage caused by the shoot borer *Earias vittella* (Lepidoptera: Noctuidae) to three common *A. manihot* varieties, Green (GN), Red Broad (RB) and Red lobed (RL) in Samoa. In both field and laboratory assessments, *E. vittella* attacked all the selected varieties. Female lay eggs on shoot tips, and the hatched larvae bore into young shoots. The succulent green variety was found to be more susceptible to the borer attack than red varieties. In field assessment, RL was the least attacked by the borers. In the laboratory bioassay, the larvae that developed on RL were much smaller and weaker than those on the other varieties. In sensory testing, the shoot tips of RN were found to have a tougher/fibrous texture that probably made RN undesirable to the borer. Furthermore, the taller plants were found more vulnerable to borer attack. The study suggests that pruning *A. manihot* could minimise borer attack; and that RN is a potential variety for future breeding programmes.

Performance and genetic diversity among a collection of *Stevia rebaudiana* Bertoni Accessions using microsatellite markers in Malaysia

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The plant *Stevia rebaudiana* Bertoni (2n=22) is a native of certain regions of South America particularly in Paraguay. It is a short-term plant and needs three months to complete one cycle of vegetative growth and flowering. With days less than 13 hours in tropical countries, stevia plants flower early, resulting in low yield. In addition, the early bud emergence under the short-day length condition causes the sugar content in stevia leaves to reduce drastically, making them no longer valuable for commercial use. The stevia accessions available in Malaysia today are limited in number and poor in performance, emphasizing the necessity of varietal improvement programs. Assessment of genetic variability, diversity and intrarelationships is an essential step for such breeding programs. This study aims to evaluate agronomic performance of among 21 stevia accessions, namely SRBA-1 to SRBA-21, collected from different origins and to reveal genetic diversity utilizing 52 novel microsatellites. Evaluation of agronomic traits revealed wide range of variation in leaf weight, dry leaf weight, plant height, number of branches, stevioside; rebaudioside A (Reb A), rebaudioside C (Reb C) and total steviol glycosides (TSG). The total genetic diversity detected among the accessions through amplification of the 43 polymorphic microsatellites showed that almost all markers had deviation from Hardy-Weinberg equilibrium ($H_o \uparrow H_e$). Three distinct heterotic groups were identified among the accessions based on their agronomic performance and molecular characteristics. Crosses among different accessions coming from different heterotic groups can be further used to produce potential stevia variety for plantation in Malaysia.

Introducing new improved variety of mangoes into the market: a preliminary consumer study at a shopping mall in Bogor, Indonesia

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Mango is one of the important tropical fruit in Indonesia. There are many species and variety of mango both commercial and still grow wild in the forest. Indonesian Center for Horticulture Research and Development with the Indonesian Tropical Fruit Research Institute as the institution under the coordination of the Indonesian Ministry of Agriculture has developed some new improved mango varieties which are the result of some breeding program for several years. A preliminary study of consumer preference was conducted to find out about the initial information about consumer's opinion for some attributes of new mango varieties. This study was conducted at a shopping center in Bogor, Indonesia, together with an exhibition that carried out by the Indonesian Ministry of Agriculture. Four new improved mango varieties such as Garifita Merah, Garifita Kuning, Agri Gardina-45, and Gadung-21 were introduced in this exhibition. A total of 31 respondents of the exhibition visitors were intercepted and asked to assess their preferences for the color, aroma, size, taste, and texture of those four mango varieties. Most of the respondents were given a positive rating to the attributes of the mangoes introduced. There was also some opinion from the respondents about the uniqueness of the new improved variety that give new sensation in taste and appearance which different from common mango variety that marketed in Indonesian local market.

The effect of medium type and subculture frequency on the formation of friable embryogenic callus for coconut cell suspension culture

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Coconut, a multipurpose palm, is facing an increasing demand for its fruit as well as the pressure from industries to produce coconut-derived products. However, coconut production has been declining and about half of the planted palms are facing senility in the producing countries. This condition will not be alleviated with the continual practice of traditional breeding method which produce only one seedling per fruit. Hence, coconut cloning by somatic embryogenesis process is the focus of the present work. Although this has been attempted over 60 years ago, improvements are still needed to increase the production rate. Therefore, a cell multiplication step to increase the production of embryogenic cells through cell suspension culture is proposed because the establishment of cell suspension culture and its regeneration in oil palm and date palm have been achieved with great success. Hence, the establishment of coconut cell suspension culture is anticipated to bring a leap to the production. The initial plant materials for the initiation of cell suspension culture is the friable embryogenic callus. As the nature of the embryogenic callus is often compact, the effect of medium type and subculture frequency on the induction of friable embryogenic coconut callus is studied. Based on the results, their effects on the friable embryogenic callus formation are minimal. However, there were effects on callus and embryogenic callus formed and the cultures in solid media require less subculture than those in liquid media. Therefore, the formation of friable embryogenic callus is likely to depend on other key factors.

Macadamia genetics: Linkage mapping and genome anchoring

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Background and Aims: Current knowledge of recombination and the functional genes of macadamia is incomplete. Genetic linkage maps and an anchored genome sequence are important genetic tools for future breeding and crop improvement. The aim of this project was to develop genetic linkage maps in order to anchor and orient a chromosomal scale sequence assembly.

Methods and results: DNA was extracted from mapping populations including open pollinated, bi-parental and self-pollinated progeny. Sequence based DArT markers were used to construct parental genetic linkage maps each with 14 linkage groups, consistent with the haploid chromosome number for macadamia. These included '741' self, '741' and 'A268' maternal and '741', 'A4' and 'A268' paternal maps and were used to anchor the *Macadamia integrifolia* '741' v2 genome assembly to pseudo-chromosomes.

The consensus genetic linkage map consisted of 4,208 unique markers and successfully anchored 1,467 scaffolds totalling 521 megabases (MB) in length. The 14 pseudo-chromosomes range in size from 28.2 to 77.7 Mb and represent 70% of the sequenced genome.

Conclusions: The genetic linkage maps and reference macadamia genome developed through this project will enable the identification of DNA markers and genes underlying important crop traits such as pest and disease resistance, quality and yield. Understanding the location and distribution of trait loci is crucial for breeding to accelerate the development of new varieties.

Genetic tolerance in capsicum chinense to low pH constraints on root growth.

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Peppers (*Capsicum* spp.) are valuable cash crops in developing countries of the tropics and sub-tropics where acidic soils represent a substantial amount of arable land. The optimal soil pH for pepper production is about 6.0 to 7.5 and soil acidity causes significant production losses. Soil acidification is aggravated by high inorganic nitrogen fertiliser input which is a critical component in maximising pepper yields. Application of lime can effectively amend the pH but it is a major cost to poor farmers in developing countries. The opportunity to identify pepper genotypes with resistance to low pH can reduce production costs whilst increasing yield.

A glasshouse solution culture experiment was conducted to investigate the effects of pH on root elongation of two commercial cultivars Warlock and Plato (*C. annuum*) and eight wild chilli accessions (*C. chinense*). The experimental design was a randomised complete block with six pH treatments (6.0, 5.4, 5.1, 4.8, 4.5 and 4.2) and three replicates. After germinating seeds in a rolled-towel, the plants were transplanted to 30-L plastic containers containing dilute nutrient solution when the average radicle length was 25-40 mm. At 14 days after transplanting the length of the longest root was determined individually. Root elongation was expressed relative to that in the pH 6.0 treatment.

The relative root length of three wild accessions was substantially greater than that of the commercial cultivars at pH 4.8 to 4.2. Two wild accessions had considerably higher mean root lengths than that of Warlock and Plato at pH 4.5 and 4.2.

Nanobubbles in hydroponics

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Maintaining oxygen levels in the nutrient solution of hydroponic systems, particularly those using the deep flow technique (DFT), is essential for root uptake of nutrients and for cellular respiration. However, more frequent, extreme and longer heatwaves, as a result of climate change, are posing a threat to outdoor hydroponic growers because oxygen levels in the nutrient solution decrease as temperature increases. Low dissolved oxygen (DO) levels can adversely affect growth rates and yield, making it difficult for growers to meet customers' demand. Current strategies for increasing DO include cooling the solution, introducing oxygen into the nutrient tank using air pumps with air stones and surface contact with atmospheric oxygen. However, nanobubbles could be a more effective solution for raising the DO level when the nutrient solution temperature is over 30 DegC. Nanobubbles (↓200nm in diameter) are generated using a nanobubble aerator and can exist in liquid for several weeks to several months due to a negative surface charge and high gas solubility in water. This study investigated the stability of air nanobubbles in distilled water at 14-48°C and in nutrient solutions with pH levels of 5.0, 6.0 and 7.0 at 20, 30 and 40°C. Air nanobubble water could be effective for managing DO levels in conventional and organic hydroponic systems in regions where temperatures are predicted to rise.

Pilot-scale market survey of mango postharvest diseases in Fiji

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A pilot-scale market survey was conducted to determine the major causes and incidence of postharvest disease losses for small holder mango supply chain in Fiji. Five vendors at each of five urban municipal markets, as well as 10 roadside stall vendors, were selected for the survey. From each vendor, ten fruits of each cultivar available at the stall were collected, stored at 23°C and assessed at the eating ripe stage for anthracnose and stem end rot. Some cultivars were much more readily available at the time of the survey (e.g. 'Maqo Dina' and 'Maqo Uto') than others (e.g. 'Kensington Pride').

The incidence of anthracnose varied considerably depending on cultivar, with nearly 100% of 'Parrot', 'Kensington Pride' and 'Maqo Dina' mangoes on average affected by anthracnose body rots at the eating ripe stage, compared to 54% of 'Salusalu' fruits.

Stem end rot caused by the Botryosphaeriaceous fungus was also very common in Fiji marketplaces. Once again, the cultivars 'Parrot' and 'Kensington Pride' had very high disease levels, with stem end rot incidences of approximately 75 and 70% respectively, when averaged over all survey sites. In contrast to trends seen for anthracnose, 'Dina' mangoes had the lowest incidence of stem end rot (19%).

Overall, this study highlights that both anthracnose and stem end rot are highly prevalent in the Fijian mango supply chain. While disease incidence varied considerably according to cultivar, even the lowest disease incidence values recorded exceeded acceptable levels.

Phylogenetic relationship among *Macadamia integrifolia* and *Macadamia tetraphylla* wild accessions

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Two of Australia's endemic rainforest species, *Macadamia integrifolia* and *M. tetraphylla*, produce edible nuts with high-value kernel. The majority of commercial varieties are based on the limited gene pool of *M. integrifolia* and hybrids between *M. integrifolia* and *M. tetraphylla*. An understanding of the existing genetic diversity within the species can be utilized for future genetic improvement. Aiming to identify the genetic diversity, we conducted phylogenetic analyses of 98 wild accessions of *M. integrifolia* collected from 23 population sites, and 94 accessions of *M. tetraphylla* from 21 sites using 2,872 high-quality DArTseq-based SNP markers. The phylogenetic tree clearly distinguished clades of the two species. Within species, most of the accessions from the same population clustered together. Genetic and geographic distances among *M. integrifolia* populations were positively correlated ($r = 0.26$, $p = 0.01$), whereas the correlation was poor and not significant among *M. tetraphylla* populations ($r = 0.08$, $p = 0.13$). The relationship between genetic and geographic distance allows evaluating the relative influences of gene flow and drift on population structure within and between regions.

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Analysis of the temporal and spatial distribution patterns of abnormal vertical growth in commercial macadamia orchards in Australia

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Abnormal vertical growth (AVG) syndrome, which has an unknown aetiology, is a serious threat to the Australian macadamia industry. AVG is characterized by vigorous upright growth and reduced flowering and nut set that results in over 70% yield loss. However, there is a deficiency in knowledge about the distribution of AVG. In this study, we used spatial analysis to provide insights into the distribution and spread of AVG in commercial macadamia orchards in Australia. Using binary data of AVG occurrence from large-scale surveys of six affected commercial orchards in Queensland (five orchards) and New South Wales (one orchard) in 2012 and 2018, spatio-temporal dynamics of AVG was evaluated. Data were subjected to point-pattern and geostatistical analyses using the R package EPIPHY. The Fisher's index of dispersion of all orchards showed aggregated patterns of affected trees in both years, with statistical significance ($P \downarrow 0.01$) of chi-square test. Goodness-of-fit comparisons of incidence data of all orchards with \mathbb{D} -binomial distributions showed that AVG incidence increased by 64% over the six-year period. AVG distribution and the \mathbb{D} -binomial parameters exhibited strong heterogeneity, which indicates high degree of aggregation and increasing spread of AVG over time. In addition, binary power law and spatial hierarchy tests confirmed the patterns of aggregation in all orchards. These results implicate a biotic agent as the cause of AVG.

Genetic diversity and population structure of field isolates of *Ganoderma boninense* from oil palm plantation in Solomon Islands

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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. Oil palm is the most efficient oil producing plant, with an annual production per hectare more than five times that of any other vegetable crop. Unfortunately basal stem rot (BSR), caused by fungus *Ganoderma boninense*, poses a major threat to the oil palm industry and hence to farmers' livelihoods. The only long-term control for this disease is through improving cultural practices and the use of more resistant planting material. *Ganoderma* causes white rot in both felled palm logs and in living palms. It has been suspected that *Ganoderma* found on logs is an inoculum source for infection of living palms. In this study we used 13,000 GBS markers, to analyse a population of 300 isolates from an oil palm plantation in Solomon Islands (SI). The isolates were collected from fruiting bodies found on felled logs (saprophytes) and on living palms (pathogens). Isolates from Australia and Papua New Guinea (PNG) were included for comparison. Phylogenetic analysis revealed that overall there is large genetic variability among the isolates, as expected of a sexually reproducing organism. The SI isolates fell into two clades. A third of the SI isolates clustered with Australian and PNG isolates, indicating some gene flow between the countries. Our results confirm the suspicion that *Ganoderma* on felled logs is indeed a source of inoculum for BSR infection of living palms, which in turn has implications for disease management.

Investigating new methods to increase adventitious root formation

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Modern agricultural improvements rely on the planting of elite crop lines to maximise the productivity of available agricultural land. Elite tree propagation is done through grafting selected scions onto available rootstocks; however in many species rootstocks are only available from seeds. Seed rootstock production requires land, water and other natural resources, as well as seasonal yield being reliant on weather and climate. Clonal rootstock propagation relies on efficient tissue culture protocols, however many tree crop species are bottlenecked at adventitious root formation. Finding new methods to increase adventitious root formation in plants will remove the need for field nurseries for rootstock production, taking us one step towards maximising yield from available agricultural land.

My research has focused on manipulating Auxin signalling pathways and Jasmonic acid recognition pathways, as both of these hormones are integral to adventitious root initiation and outgrowth. In my work I have identified two different chemicals that interfere with Auxin accumulation and degradation, increasing adventitious root formation in the model species *Arabidopsis*. I have also investigated applying exogenous dsRNA to temporarily silence negative regulators of adventitious root formation as a method to increase root formation in *Arabidopsis*.

Avocado genome sequencing and development of genetic markers for breeding and germplasm identification

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Avocado (*Persea Americana* Mill.) is an economically important edible fruit-tree species from angiosperm Family Lauraceae. The Australian avocado industry produces 77K tonnes of fruit with a market value of \$557 million, of which 62% is contributed from Queensland. Every year demand for avocado increases ~10%, due to a growing awareness of its nutritional benefits. Despite the booming popularity of avocado, relatively few commercial cultivars exist. At present 80% of commercial avocado fruit production is of the Hass cultivar, which is clonally propagated by grafting onto rootstocks selected for various qualities including salinity, cold or disease tolerances. Breeding for new improved varieties of avocado, particularly fruit, is complicated by its long juvenile phase and requirement for resource-intensive field selection. In addition, a major research and breeding barrier is the relatively limited publically available genomic information at present. Well annotated genomic information can benefit industry by enabling association of genomic markers or genes with traits of interest, directing early trait selection. It also facilitates plant evolutionary studies and analysis of germplasm diversity for preservation purposes. This project aims to produce a complete chromosome level reference genome, plus a comprehensive reference transcriptome, for Hass using long-read, single molecule technologies. Moreover, resequencing data for 17 varieties of importance to Australia will be used to develop genetic markers for breeding and tree/germplasm identification purposes.

New achievements for diagnostics of banana streak virus

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Banana streak virus (BSV) remains one of the most challenging viral pathogens of banana to detect and most diagnostic assays rely on serological methods. The BSV capsid protein contains an N-terminal, intrinsically disordered (NID) domain that is surface-exposed on the virion and likely is multifunctional and plays important roles in viral replication and transmission. The immunodominant continuous epitopes on the virion are also located in the NID domain, and therefore this domain is of great interest from a diagnostics perspective. Using chemically synthesized peptides to mimic the continuous epitopes of five BSV species including BSMYV, BSOLV, BSIMV, BSGFV and BSCAV, antisera have been raised in rabbits, and shown specificity to each virus species and sensitivity in a range of assay formats such as Western Blot, ELISA, immunosorbent electron microscopy and immunocapture PCR. This work confirmed the applicability of synthesis epitopes/peptides to produce anti-peptide antibodies for BSV diagnostics when the native protein is absent.

The Oxford MinION Nanopore sequencing system is a promising new technology for point-of-care diagnostics. We have successfully used this system and generated long reads with greater than 99% accuracy, allowing accurate and sensitive detection of BSV. The long reads allow episomal from endogenous sequences to be differentiated.

Optimization of coconut micropropagation via somatic embryogenesis

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Coconut (*Cocos nucifera* L.) is one of the most important tropical palm crops worldwide, but the gap between decreasing productivity and expanding demand is growing and is now becoming a major problem. The global coconut industry is threatened not only by palm senility but by pests/pathogen attack which is becoming exacerbated by climate change. However, conventional breeding methods cannot provide sufficient new planting materials to meet the replacement of senile and damaged palms. Hence, coconut clonal propagation via somatic embryogenesis (SE) is being developed to help meet the demand of the growing market. However, with refined medium composition, improved technical skills, optimized environmental conditions, proper acclimatization steps employed and the application of a cell suspension culture step, a much higher multiplication rate can be predicted. Several factors that affect the rate of clonal propagation are being studied: 1) determination of the effect of a non-activated charcoal (AC) medium and 2) the development of culture induction medium composition with a reduced auxin concentration. Results of the study so far show that a non-activated charcoal medium with more frequent subculture (monthly) and a lower auxin concentration is an efficient alternative approach to the traditional mainstream AC-containing medium for the initiation of embryogenic callus. With a better understanding of the callus induction medium composition, and with a liquid cell suspension culture step medium to be applied in the future, should elevate the multiplication rate of clonal plantlet production.

BioClay: Topical RNAi for tomato spotted wilt virus resistance in crops

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The future of agriculture is under threat by the escalating war between crop growers and the plant diseases they have to contend with. Tomato Spotted Wilt Virus (TSWV) is the perfect example of this war. Current management methods for TSWV include using disease-resistant crop cultivars and pesticides to reduce populations of thrips, the insect vector of this disease. However, evidence has shown that TSWV can evolve to overcome common resistance genes in plants, and thrips are highly adept at developing resistance to chemical insecticides. Without innovation in our management strategies, viruses such as TSWV have the potential to devastate marketable crop yields.

RNA interference (RNAi) offers a novel method of crop protection. RNAi allows a plant to control expression of its own genes, using double-stranded RNA (dsRNA) to target a matching mRNA sequence, silencing the associated gene. This mechanism can be exploited to silence the critical genes of invading viruses, shutting down expression before they can infect the plant. By spraying plants with dsRNA matching a critical TSWV gene, it can become resistant to the virus for a limited time. Mixing that dsRNA with a clay nanoparticle creates BioClay, a non-GM, non-toxic, environmentally friendly spray product to provide our crops with viral protection over an extended period of time. Results are presented to demonstrate the efficacy of topical RNAi in providing crop plants with significant resistance to TSWV.

Characterization of Heterotrimeric G Protein Alpha Subunit in Tomato

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Heterotrimeric G proteins, comprised of three subunits, G α , G β and G γ , are involved in signal transduction pathways that mediate a vast number of processes across the eukaryotic kingdom. 23 G β subunits are present in humans whereas most plant genomes encode for only one canonical G β . The disparity observed between *Arabidopsis*, rice, and maize G β -deficient mutant phenotypes suggests that G β functions have diversified between eudicots and monocots during evolution. Alternatively, since the only G β mutations available in dicots have been produced in *Arabidopsis*, the possibility exists that this species might be an exception to the rule. In order to test this hypothesis, we studied the G protein G β subunit (TGA1) in tomato. Four *tga1* knockout lines were generated in tomato cv. Money maker using CRISPR/Cas9. The *tga1* mutants exhibit a number of auxin-related phenotypes including changes in leaf shape, reduced plant height, fruit size and number of seeds per fruit. In addition, *tga1* mutants have increased sensitivity to ABA during seed germination and reduced sensitivity to exogenous auxin during adventitious root formation from cotyledons and excised hypocotyl explants. Our results suggest that G β mutant phenotypes in tomato are very similar to those observed in monocots, i.e. rice and maize, and cast doubts about the validity of using *Arabidopsis* as a model system for plant G protein studies.

Breeding for resistance to husk spot disease in macadamia

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In Australian macadamia orchards, significant decreases in saleable nuts have been reported due to husk spot caused by a fungal pathogen, *Pseudocercospora macadamiae*. In some cultivars, husk spot is able to induce early fruit abscission, which may result in less developed nuts and consequently, increased proportions of commercial rejects. While fungicides are able to reduce impacts of husk spot, breeding for resistance offers a more cost-effective and sustainable control option. Previously published methods used to screen for varietal susceptibility require a delay of several years while waiting for the trees to produce their first fruits. However, in recent years, relationships between macadamia fruit stomatal abundance and husk spot intensity parameters have been reported. This study aims to investigate stomatal characteristics of fruit and leaves to determine whether there is a correlation that will enable leaf stomatal abundance to be used as a pre-fruiting indicator for disease susceptibility. Progeny and parents from the Australian macadamia breeding program will be screened for disease resistance. The degree of genetic control involved in stomatal characteristics and in husk spot resistance will be calculated to determine the appropriateness of these traits for selection in breeding. Inoculation methods will be compared with the aim to increase accuracy of future trials. Finally, a meta-analysis of existing phenotypic and genotypic data will be explored in order to determine whether genetic markers associated with susceptibility groups can be discovered and utilised in future marker assisted selection. Outcomes of this study will guide future breeding for resistance.

The use of sucrose and cold pre-treatments for cryopreservation of avocado (*Persea americana* Mill.) cultivars 'Velvick' and 'Reed'.

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Cryo-protocols that use vitrification solutions usually cause high mortality. Avocado is highly susceptible to osmotic stresses upon vitrification. To date there are no reports of survival/regrowth of in vitro cryopreserved shoot tips. This study aimed to optimize sucrose and cold pre-treatments to sustain shoot tip survival/regrowth after cryopreservation.

In vitro shoots of cultivar 'Velvick' were pre-treated for 2 weeks on 0.3 M sucrose and 100 mg/L Ascorbic acid containing media to be compared with normal sucrose concentration of 0.09 M. Shoots of cultivar 'Reed' were pre-treated at 10°C with normal sucrose concentration of 0.09 M. For cryo-treatments shoots were dissected to obtain 1 x 1 mm shoot-tips. When treated with PVS2 and evaluated for survival, pre-treated shoots of cultivar 'Velvick' displayed higher survival 83%, higher regrowth 73% with vigorous green cultures and appeared morphologically normal. In contrast non-precultured shoots-tips recorded 70% survival, 23% regrowth resulted in stunted yellow-brown and less vigorous cultures. Very interestingly, after liquid nitrogen treatment pre-treated shoot-tips showed 60% survival while no sugar treatment led to 0% survival. For cultivar 'Reed' a survival of 86% and a regrowth of 80% was achieved after treatment with PVS2. Shoot tips of cultivar 'Reed' were recovered after LN with a regrowth of 40%. The cryopreserved shoots of 'Velvick' developed into green proliferating clumps after 8 weeks in culture, while shoots of 'Reed' developed into plantlets after 16 weeks rewarming. This result is the first report of successful regrowth and proliferation of cryopreserved in vitro shoots of avocado.

Assessing the interaction between fig size and wasp abundance in a fig-wasp community at Moonbi range, New South Wales

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Ficus belongs to one of the most widespread genera of terrestrial plants. Over the years, its interaction with fig wasps has been an interesting area of study. It is believed that each fig is pollinated by a distinct species of wasp from the family *Agaonidae*, while the wasp relies on fig for reproduction. However, the dynamics of this mutualism is still under-studied. This study evaluates the interaction between wasp abundance and fruit size in *Ficus rubiginosa*, family *Moraceae*, collected in New South Wales, Australia. It aimed to determine the interaction between fig fruit size and wasp abundance within Moonbi range. Fig samples were collected at D stage (larger, yellow in colour and soft to touch), measured and stored in ethanol for emergence. Normality test was insignificant at $p = 0.06$. The distribution of wasp and fruit sizes within a fig-wasp community was evaluated using Friedman rank sum test which was significant at $p = 0.0001$ and chi square 14.7. Linear regression model of the interaction was insignificant at $p = 0.25$ and $r = 0.07$ indicating, that fig fruit size has no significant effect on the quantity of wasps present in it. This result supports the idea, that wasp abundance could be influenced by fig receptivity regardless of the fruit size.

Do GAP practices improve market access for vegetable farmers? A case study from Vientiane Capital, Laos

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A case study on Good Agricultural Practices (GAP) of vegetable was conducted in 2018, with an objective to understand whether GAP practices improve market access for vegetable farmers in the Lao PDR. The case study was conducted in Nasala Village, Xaythany District, Vientiane capital, Lao PDR. The data was collected using 10 semi-structured interviews and one group discussion with Nasala farmers. The results were summarized based on the themes such as community characteristics, market access and farmers' perception about GAP. The Nasala community has 585 households, majority being farmers with 50% of them growing vegetables with an average farm size of 1.5 hectare. District Agriculture and Forestry Office (DAFO) introduced GAP practices as a pilot project to 28 farmers in Nasala in 2014 through farmer trainings. The DAFO pilot project enabled Nasala farmers to export Thorny Coriander to Japan during 2016-2017. Nasala farmers sold 50 kg/day of Thorny Coriander for about one year at the price of 15000 kip/kg in comparison to 7000-10000 kip/kg at the local market. Farmers agreed that they were motivated by the market incentives and collectively sold the produce by alternating production for continuous supply. This export opportunity was withdrawn after the pilot period resulting in no incentives to practice GAP. Farmers agreed that GAP enabled them to produce better quality, healthier and safer vegetables. However, the barriers to GAP are lack of government policies, institutional support, inadequate incentives and complex certification process. To enable farmers to continue GAP practices appropriate supporting system must be developed.

Biosecurity capacity for the Australian avocado industry

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The geographic isolation of Australia, complemented with strict quarantine and biosecurity procedures, has facilitated protection from exotic pests and diseases that are threats to agricultural industries. The Australian avocado industry is at an increasing risk of exotic pest and disease incursions due to global trade and the accessibility of international travel. Biosecurity monitoring with novel surveillance tools and diagnostic tests, and the capacity to respond to potential incursions, are required to protect the industry and maintain pest-free status. This poster summarises the biosecurity innovations that are being adopted in Australia including i) industry use of digital social networking tool, 'Checkpoint™', for avocado pest and disease surveillance; ii) new real time RT-qPCR and qPCR assays for rapid detection of biosecurity threats, Avocado sunblotch viroid (ASBVd) and avocado scab fungus, *Elsinoë perseae* (syn. *Sphaceloma perseae*); and iii) an experimental investigation of the fungal species associated with branch dieback vectored by ambrosia beetles viz. Tea Shot Hole Borer (TSHB) (*Euwallacea fornicatus*). In a survey of horticultural and ornamental tree species including avocado, mango, macadamia and tuckeroo (*Cupaniopsis anarcardiodes*) in the avocado growing regions of Queensland, 140 fungal isolates were collected from tree branches showing symptoms of ambrosia beetle-vectored dieback. Fungal isolates were also collected from TSHB beetle specimens captured in traps or in branch galleries. The identities of the isolates were determined with multi-gene sequencing and phylogenetic analyses and the genera included *Fusarium*, *Bionectria*, *Colletotrichum*, *Lasiodiplodia*, *Phomopsis*, *Nectria* and *Nigrospora*. New fungal species will be described and pathogenicity tests on avocado will be conducted.

Artificial microRNA (amiRNA) strategies for broad-spectrum resistance to tospoviruses

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Tospoviruses infect and cause damage to a wide range of valuable horticultural crops, resulting in reduced yields and economic losses for these industries. Tomato spotted wilt virus (TSWV) is an economically important species globally while Capsicum chlorosis virus (CaCV) impacts Asia and Australian regions. Additionally, Groundnut bud necrosis virus (GBNV) causes damage in countries across Asia, and is a potential biosecurity threat to the Australasian region. Tospoviruses are transmitted by thrips and consist of a tripartite single stranded RNA genome. These viruses are difficult to control, due to a wide host range and ability of different tospovirus species to recombine genome segments. Artificial microRNA (amiRNA) is an emerging technology for combating plant viruses. Specifically, this technology genetically manipulates plants to produce 21nt small RNA molecules which silence complementary viral RNA transcripts. We have developed an amiRNA strategy for broad range resistance across multiple strains within a species by targeting highly conserved regions of the tospovirus N gene, which is critical for viral replication. Furthermore, we have generated transgenes simultaneously producing unique amiRNAs against CaCV, TSWV and GBNV N genes, potentially preventing breakdown of resistance due to recombination between different tospovirus species.

Air temperature an influential climatic factor for growth and reproduction of dry flower pathogens of macadamia

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In order to assess the influence of climatic factors on abundance of conidia of dry flower pathogens, *Pestalotiopsis macadamiae* and *Neopestalotiopsis macadamiae*, Hirst spore trap was used to determine daily aerial conidia concentration at Alstonville (28.852°S, 153.456°E), NSW, Australia. Weather data including minimum and maximum air temperatures, rainfall, wind speed and relative humidity were obtained from an automated weather station at the same location. The effect of each and the combined climatic parameters on conidia abundance was analysed using the GLM procedure for the all-subset regression link functions. A model containing weekly maximum temperature and weekly rainfall produced the best significant effect on conidia abundance ($R^2 = 72.7\%$, $P = 0.003$) compared with the model containing daily data of both climatic parameters ($R^2 = 35.4\%$, $P = 0.000$). *In vitro* assays were established to examine the effect of different temperatures (12, 19, 22, 25, 29, 33, 37 and 41 °C) on growth and reproduction of the pathogens. The results showed that maximal mycelial growth, conidia production and germination occurred at 25°C and declined significantly ($P \downarrow 0.05$) at cooler and warmer temperatures. Temperatures above 40°C were lethal for growth and functioning of the pathogens. The results confirmed that air temperatures significantly influenced growth and reproduction of both dry flower pathogens. The findings would underpin development of a disease prediction model for dry flower in macadamia.

Dynamics of seedlings and mango varieties: A case study of breeders in mango production center in Majalengka, West Java, Indonesia

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Mango is a favorite tropical fruit in both domestic and international markets. Mangoes are easily cultivated and more resistant to pests and diseases than other fruit plants, so it has a higher success rate in producing its seeds. Mango seedling in Indonesia generally faces the constraints of the lack of use of quality and certified seeds that actually affect the productivity of mangoes. This is because nurseries are still difficult to get superior mango seeds labeled, to look for entres they still use entres from their respective parent trees. The results of Indohort's research in 2016 which was a collaboration between ACIAR, ICHORD and the University of Adelaide showed that the development of mango seedling business capacity between 2011 and 2016 decreased, in 2011 the specialization in the production of mango seeds compared to other fruit crops was 32%, and in 2016 decreased to 19%. The mango variety that is the most preferred in Indonesia is Harumanis, but its production share has decreased, in 2011 it reached 89%, decreased in 2011 to 65%, this was due to changes in consumer preferences towards other mango varieties. The development of mango market network needs to be done because most of the mango seeds are sold to the seedling trader in the same village as a nursery, this shows that the majority of seed breeders do not sell directly to consumers but through middlemen.

Comparative genomics of macadamia species

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Macadamias (*Macadamia integrifolia*, *M. tetraphylla* and hybrids), are native to Australia and, have a significant and growing economic value in the worldwide food market. The genus *Macadamia* belongs to the Proteaceae family and has four species: *Macadamia integrifolia*, *M. tetraphylla*, *M. jansonii* and *M. ternifolia*. Of these four species, *M. integrifolia* and *M. tetraphylla* produce edible nuts, and hence, most of the commercial cultivars belong to either of these two species or their hybrids. The other two species, *M. jansonii* and *M. ternifolia*, have not been used due to their bitter inedible nuts. The majority of global macadamia production relies upon a limited gene pool and is comprised mostly of *M. integrifolia*. Whereas, most of the wild genetic resources are still under-utilised, though they are a potential resource for improving crop yield. Until recently, due to paucity of genomic data, macadamia improvement programs were mostly dependent on pedigree analysis and phenotypic characterization, which were subjected to inaccuracy. Therefore to improve accuracy and to harness the advances in genomic technologies, as an initial strategy, reference genomes of all the four species will be generated using long read sequencing technologies. Comparative genomics analysis will be performed to identify the useful genes from all these species, responsible for adaptation and crop improvement. Detailed comparison of similarities and differences in the relevant genes will provide useful insights into developmental processes.

Brassica biofumigants for improved soil health

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Biofumigation involves growing specialised cover crops that have the ability to suppress certain soil-borne diseases. Species such as those in the *Brassicaceae* family, (e.g. radish, mustard and rocket) are known to have this capability. Biofumigation activity is initiated by the degradation of glucosinolates within the tissues of the plant when the crop is incorporated into the soil at approx. 25% flowering rate. In this experiment, nine bio-fumigant varieties were assessed over six planting dates for biomass yield, irrigation management, glucosinolate concentration and efficacy against three soilborne pathogens, namely; *Sclerotium rolfsii*, *Sclerotinia sclerotiorum* and *Macrophomina phaseolina*.

Preliminary results showed incorporation dates varied across varieties and planting times. Winter planting had highest biomass yield across all varieties, compared with the summer plantings (e.g. 14.82 t/ha in winter, versus 5.02 t/ha in summer for Caliente). The efficacy of disease suppression was variable between variety and planting date. For example, Nemfix and BQ Mulch produced a higher percentage mortality rate (100% and 98%) against *S. sclerotiorum*, compared with autumn (22% and 12%) and winter (37% and 13%) planting.

High glucosinolate production was observed during the summer plantings, where irrigation treatments including drought conditions (Low; 0.75 ML/ha), moderate watering (Medium; 2 ML/ha) and field capacity (High; 2.5 ML/ha) were applied. Increased glucosinolate concentrations were observed in the Low irrigation treatments (e.g. Mustclean; 32.31 $\mu\text{mol/g DW}$), versus High irrigation (e.g. Mustclean; 17.11 $\mu\text{mol/g DW}$). Summer data pending analysis. These findings can help growers to identify biofumigant varieties that compliment rotation program and optimise disease management practices.

Low cost glad wrap film packaging delays postharvest senescence and maintains fruit quality of eight commercial Chili cultivars of Pakistan

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Green chilies are highly perishable with limited postharvest life which substantially affects its quality and market potential. The present study was part of an ACIAR funded project aiming at evaluating the effect low cost glad wrap film packaging (GWFP) on commercial green chili cultivars (Kunri-1, Longi, Talhari, Skyline 1 and 3, Super-hot, Advanta and BSS-410) to help improve shelf life and quality during ambient storage at 18 ± 2 °C. Chilies were weighed and filled in polyvinyl trays and wrapped with glad wrap film. Chilies kept in glad wrap film packaging improved the marketability index and shelf life for 9 to 15 days compared to open top trays (control) with shelf life of 3 to 6 days depending on cultivar. GWFP storage of chili fruits markedly reduced weight loss, decay, disease incidence, wrinkling, red chili percentage and relative electrolyte leakage as compared with control. It was noted that chilies stored under GWFP displayed significantly higher firmness, soluble solid contents, acidity, ascorbic acid with maintained radical scavenging activity. In addition, total phenolic contents, enzymatic essays i.e. superoxide dismutase (SOD), peroxidase (POD), polyphenol oxidase (PPO) catalase (CAT) and ascorbate peroxidase (APX) activities were significantly higher in GWFP kept chilies. Conclusively, the low cost glad wrap film packaging can be employed as promising technique to reduce postharvest losses, extend shelf life and maintain the postharvest quality of chilies leading to more profit for the growers and linked stakeholders.

Optimizing planting method and fertilizer application rate for producing high quality nursery of onion cv. Phulkara

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Onion (*Allium cepa* L.), locally famous as "Piaz", occupies a prominent place among commercial crops of Pakistan, by supplementing the income of small/marginal land-hold farmers. One of the major constraints of onion farming in Pakistan is poor nursery due to adoption of old planting methods and overfertilization, which ultimately increases cost of production and loss of resources. The current study was carried out at Vegetable Area, University of Agriculture Faisalabad, to determine the most suitable nursery raising system and fertilizer application rate for onion nursery in order to get maximum plant population and optimal shoot/ root length. The first experiment comprised of four different nursery growing methods: 1) flat bed + broadcast sowing, 2) flat bed + line sowing, 3) raised bed + broadcast sowing, and 4) raised bed + line sowing. The largest plant population, highest plant fresh and dry weights were obtained on flat beds under line sowing. The smallest plant population was obtained on raised beds under broadcast sowing, however, the lowest fresh and dry weights of seedlings were found with flat beds under broadcast sowing. The second experiment comprised of three diammonium phosphate (DAP) application rates (50 g, 100 g and 150 g per 272.25 ft². applied at one-week interval) and a control. The maximum shoot/ root lengths and fresh/ dry weights were obtained with 100 g DAP 272 ft². In conclusion, line sowing on flat beds and application of 100g DAP 272 ft² at one-week interval produced high quality nursery of onion cv. Phulkara.

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Assessing food safety and quality compliance: An evidence from vegetable industry

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The aim of present research was to assess and document the practices for prevailed food safety and quality standards as employed by small scale growers and market managers in the vegetable supply chains of Pakistan. For this purpose, cross-sectional data were collected from two provinces (Sindh and Punjab) of Pakistan targeting commercial vegetables, i.e., potato, tomato, onion, and chilies. Information regarding the food safety and quality were recorded during field survey from all the supply chain participants, i.e., growers, harvesters, processors, traders, and exporters through well-designed questionnaires. The collected data adherence with the standard requirements and identifying constraints of chain actors were analyzed using descriptive analysis. Results showed that many practices such as soil and ground water contamination, pesticide and fungicide residuals, microbial contaminants, infected labour, diggers, packaging migrants, clothes, surfaces and non-food grade containers may enhance the chances of food borne diseases among consumers. Therefore, training needs have been identified for all stakeholders that need to be addressed which will develop their understanding about the quality requirements and safety regulations. It will create opportunity in the advanced markets at national and international levels and new opportunities may arise to enhance stakeholders' income.

Postharvest innovation to maintain vegetable quality in developing countries with inaccessible cool chain facilities

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Vegetable is becoming more of a focus in research and development to meet the safety and quality needs of consumers and market demands. In developing tropical countries, postharvest losses can be up to 40% across the supply chain and high temperature exposure after harvest is one of the main factors causing the loss. As cool chain facilities are mostly unavailable in these countries, low-cost intervention to maintain produce quality at ambient temperature is important. Using plastic crates to pack vegetables instead of plastic bags could minimise the mechanical damage. Applying passive cooling by covering the crate with a wet microfibre towel can lower the temperature around vegetables by 3-6°C and quality was maintained over a 300 km supply chain trial conducted in Cambodia. Ethylene causing undesirable ripening is another challenge across the supply chain for produce under tropical conditions. Inclusion of ethylene absorbent sachets in a box containing 10 kg green tomato in Lao PDR significantly delayed ripening over a 9 day storage period at 26-37°C. To meet an acceptable market outcome, it is assumed that the box should contain 75% green tomato at delivery. Product with the ethylene absorbent sachet included, can satisfy this requirement over a 7 day supply chain/storage period which is double the 3.5 days for tomato packed without a sachet. These innovative technologies show great potential for developing countries in the tropical regions. The applicability to a larger scale of transportation and to a range of markets needs to be confirmed. Evaluation against the economic benefits and accessible technological resources in these countries would also be necessary.

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RNA sprays to combat plant pathogenic fungi

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RNA interference (RNAi)-inducing sprays are a new non-toxic, non-transgenic, environmentally friendly strategy that has the immediate potential to revolutionise crop protection against insect-transmitted plant viruses, and facilitate a transition away from the use of chemical insecticides in agriculture. The approach, which involves spraying plants with virus-specific dsRNA, triggers and augments systemic RNAi, the plant's natural defence mechanism against viruses. When applied in combination with stabilising nanoclay, in the formulation known as BioClay, dsRNA can provide virus protection to plants for more than 20 days, making a single spray a commercially feasible and lasting approach to protect crops from viruses. The aim of the present work is to develop BioClay-based RNA sprays to protect avocados, pineapples and Australian Myrtaceae species from pre- and post-harvest fungal diseases. This will lead to clean green safe produce from pre- to post-harvest, from field to supermarket trolley, safeguarding Queensland horticulture and ecosystems.

Investigating the sporulation of *Metarhizium anisopliae* formulated in calcium alginate in soil

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Wireworms have the potential to cause significant damage to sweetpotato, particularly late in the season. Whilst several insecticides are registered for use under minor permits, grower concern over the development of resistance has highlighted the need for alternative chemistry and management options. Entomopathogenic fungi like *Metarhizium anisopliae* have been shown to cause wireworm mortality in both laboratory and field conditions. Maintaining the abundance and persistence (i.e. resporulation) of fungi in soil is important for insect control; however, survivability declines in soils when the fungi is inundatively applied because the growth of fungi is limited and can also be parasitised or inhibited by other soil microbes. In this study, to mitigate this *fungistasis*, conidia of *M. anisopliae* were encapsulated in calcium-alginate granules with nutrients for the fungi in the form of corn starch or autoclaved baker's yeast or combination thereof. Combined corn starch and baker's yeast yielded the highest sporulation (granule denoted as CAG_{Ma+Cs+By}). This study further investigated the infectivity of sporulated CAG_{Ma+Cs+By} for mealworms, and resporulation of CAG_{Ma+Cs+By} in field-collected soils that were either sterilised or not. Sporulated CAG_{Ma+Cs+By} caused ↑90 % mealworm mortalities over 7 days bioassay. After 4 weeks incubation, resporulation of CAG_{Ma+Cs+By} in sterile soil was significantly greater (P value ↑0.05) compared to that observed in non-sterile soils. Further work is required to identify other additives that could be incorporated into granules to decrease the effect of fungistasis, to encourage entomopathogenic fungi to better establish in soil and to enhance the biological control of wireworm in sweetpotato.

Evaluation of the effect of organic fertilisers on lettuce yield in Lao People's Democratic Republic (PDR)

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Production of leafy vegetables, such as lettuce, in Lao People's Democratic Republic (PDR) is limited by low nutrient soils. Organic fertilisers or composts made from agricultural residues may provide Lao PDR farmers with economical and environmentally sustainable alternatives to chemical fertilisers. Research is needed to increase awareness and knowledge of organic fertilisers suited to vegetable production in Lao PDR.

An experiment at the Horticultural Research Centre (HRC) in Vientiane assessed the effect of four organic fertilisers on growth and yield of lettuce. Two commercially available fertilisers (fermented manure compost and an organic fertiliser) were compared with a mixture of cow manure plus rice husks, and a fourth compost made from vegetable leaves, straw and cow manure at the HRC. The experimental design was a randomised block with four replicates for each fertiliser treatment. Lettuce was grown in raised beds with 10 tonnes per hectare (t/ha) fertiliser applied before seedlings were transplanted.

The fermented manure compost treatment had the highest yield (1.95 kg/m²) and was significantly higher than the other three treatments ($p \downarrow 0.001$). Growth rates were also highest for the fermented manure compost at all measured growth intervals (14, 28 and 45 days after transplanting).

Rapid nutrient release from fertiliser is important for short-term crops. The higher growth rates and yields found for the fermented manure compost indicate that nutrients were released sooner and were more readily available compared to the other treatments. Mature compost releases nutrients more rapidly than compost that contains partially decomposed rice husks, vegetable leaves and straw.

Evaluation of the effect of lime and irrigation on lettuce yield in Laos

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Diversification of food sources and agricultural production systems has potential to enhance domestic supplies and provide export market opportunities for Laos. Major constraints to agricultural productivity are related to soil management and include inefficient irrigation, poor soil structural stability, low pH and nutrient availability.

An experiment at the National University of Laos (NUOL) in Vientiane assessed the effect of lime and irrigation scheduling on growth and yield of lettuce. The soil was a sandy clay loam with pH 4.89 (H₂O) in the top 15 cm. Lime (CaCO₃) was applied at rates of 2 and 4 tonnes per hectare (t/ha). Irrigation scheduling was based on calculated evapotranspiration (ETc) with frequencies of either twice daily, once daily or alternate days. Urea, chicken manure and rice husks were added to soil in all trial plots. The experimental design was split-plot with two treatments (lime and irrigation scheduling) and four replications.

The combination of 4 t/ha lime and irrigation every second day had the highest yield (mean ↑2 kg/m²). The combined treatment of irrigation once a day and no added lime showed significantly higher leaf number ($p=0.01$) and plant height ($p\downarrow 0.001$) compared to the other treatment combinations. However, increased biomass of individual plants did not translate into increased marketable yield per square metre. The application of lime raised the pH of soil but the effect on plant growth and yield was not conclusive. Separation of the two treatments into single factor trials is needed to elucidate the effects of individual treatments in future trials.

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Investigating capacities to change soil and irrigation practices in vegetable production in two provinces in Cambodia

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Improving vegetable production in Cambodia offers a pathway to grow domestic consumption and exports, and improve nutrition, profits, and livelihoods. Interviews with 120 growers and 5 focus group discussions within 5 villages investigated growers' capacity to change soil and irrigation management in their Chinese cabbage, Petsai, Cucumber, Cauliflower, Lettuce and other vegetable crops. Low or no profitability (34% participants), insect pests (59%) and dry periods (18%) were growers' major limitations, with small farm size (0.08 ha) and limited schooling (21-36% had no schooling) contributing to the scenario. High cost of inputs is a limitation to making farming system changes, with most growers using their own funds and less than 10% borrowing funds to pay for crop inputs.

Communication and planning for vegetable growing occurred almost exclusively within families (93%), with 7.5% of participants discussing with other farmers. Lack of time (43%) and knowledge about farmer group activities (30%) limited ongoing group learning opportunities. Although very traditional, 28% of participants had tried new practices; 42% of participants indicated they will try new practices after exposure to a soil and irrigation research trial. The participants were keen learners, and after exposure to the research, 58% believed that liming improves yields and 18% prefer to evaluate this on their farms. Information sources about vegetable growing are limited, and growers had complex information needs. Facilitating and mentoring ongoing local support and technical information networks, and enhancing capacity and communication are seen as key strategies for empowering long term ability to change.

Linkages for life: Assessing tomato value chain pathways and opportunities for better livelihoods of marginal and vulnerable groups in Pakistan

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This case study offers insights into assessing tomato value chain to improving rural livelihoods of marginal and vulnerable groups in rural Punjab, Pakistan. This research is based on qualitative data collected through Focused Group Discussions (FGDs) in two pilot villages of district Muzaffargarh with men and women farmers separately. The research aims to explore the pathways, linkages and new avenues and opportunities for marginal and vulnerable groups especially women to increase their household incomes under a collaborative Pakistan-Australia Strengthening Vegetable Value Chain Project (SVVCP). It is imperative to identify effective linkages between farmers and other chain actors to have a comprehensive understanding of how these works and what roles public and private actors play in making them work more effectively to plan and implement the project activities with farmers, for farmer and by farmers. It was found that most of farming households operate less than an acre of land and supplement their income with farm labour and small businesses. Both men and women farmers indicated lack of linkages and opportunities for them besides their limited access to agricultural knowledge, skills and resources. Men have diverse linkages with male dominant institutions such as agriculture and marketing. In contrast, women have no linkages with viable economic institutions such as production and marketing and tend to be associated with domestic and community affairs. The findings suggest that, it is imperative that farmers must have access to required information and skills and opportunities for networking to build sustainable linkages with value chain actors.

Postharvest loss improvement in cabbage and cai meo in Son La, Vietnam

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Postharvest losses (PHLs) adversely affects food security and farmers' revenue, especially in developing countries. White cabbage (*Brassica oleracea var. capitata*) and Cai Meo (*Brassica oleracea*) are the main produce along with other fresh leafy vegetables in Son La, Vietnam due to their high demand. However, a significant loss in postharvest quality is causing constraints in generating income for local people. The research aims to identify the major causes of PHLs in cabbage and Cai Meo production in Son La, Vietnam. Data collection was implemented by measuring produce quality and interviews with key respondents. In addition, data was recorded from temperature logging, hand-held core temperature sensors and weight loss measurements. Lack of temperature control and poor postharvest management practices were identified as the two major causes of current PHLs in cabbage and Cai Meo. Practical improvements were recommended for farmers to maintain produce quality, including appropriate harvesting time and technique, proper handling, storage and transportation.

Distribution of the smut fungus *Ustilago cynodontis* within couch grass (*Cynodon dactylon*) plants

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The basidiomycete fungus *Ustilago cynodontis* causes couch smut, a common disease of couch grass (*Cynodon dactylon*). The disease causes significant economic losses to the turf industry as the rate of stolon extension is reduced by up to 50%, leading to turf that is less tolerant of trampling and has slower rates of recovery. High incidences of disease are also associated with larger amounts of wastage during cutting and rolling, as the turf roll frequently breaks at points of infection, presumably due to the shorter and weaker stolons. Effective disease management strategies are currently lacking due to limited understanding of the pathogen biology and disease epidemiology. One of the knowledge gaps is what parts of a plant *U. cynodontis* can enter and what controls movement in the plant after infection. We have developed a nested PCR assay targeting the internal transcribed spacer (ITS) region to allow detection of the fungus even in the absence of disease symptoms. Results show that the fungus moves systemically within the plant and latently infects all organs, including flowers, leaves, stolons, rhizomes and roots. Future experiments are planned to investigate points of entry in order to assess whether mowing contributes to dispersal of the fungus. The nested PCR will also be a useful tool to assess the efficacy of fungicides to cure the plant of infection.

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Back to basics: Does seed size affect germination and plant uniformity in broccoli (*Brassica oleracea* var *Italica*)?

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Hand harvested crops, such as brassicas and lettuce, are prone to high levels of variability during growth and at harvest. This necessitates multiple harvest passes and substantially increased labour costs for the grower. Both biotic and abiotic factors contribute to this lack of field uniformity.

The main objective was to evaluate the impact of broccoli (*Brassica oleracea* var. *Italica*) seed size variability on germination, subsequent crop growth and harvest uniformity. An initial experiment was conducted where germination counts across three seed-size categories including, 2.0mm (SS1), 2.3mm (SS2) and 2.45mm (SS3), were recorded at 3, 7, 10 and 14 days after sowing (DAS). At 14 DAS, germination was greater in the SS1 (95%) and SS2 (91%) than the SS3 (66%) ($P \downarrow 0.005$).

A second experiment evaluated the same seed categories planted under direct seeded (DS) and transplanted (TR) conditions to identify differences in crop growth and development. At 49 DAS, DS plant counts per plot were lowest for the SS3 (54.5 plants plot⁻¹) compared with the SS1 (70.5 plants plot⁻¹) and SS2 (64 plants plot⁻¹). This could be attributed to the reduced seed coat thickness evident in the SS3 (66.3 μm) which can potentially lead to increased damage and mortality of the seed, compared with the SS1 (79.3 μm) and SS2 (73.1 μm). The TR treatment gave greater uniformity with no significant difference ($P \downarrow 0.05$) in plant populations across seed size categories (SS1 = 95, SS2 = 90 and SS3 = 96 plants plot⁻¹).

Modification of *in vitro* bioassay for screening *Musa* species against *Fusarium oxysporum f. sp. cubense*

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So far, there are three types of early bioassays for screening *Musa* genotypes against *Fusarium oxysporum f. sp. cubense* (*Foc*): pot system, hydroponic system, and *in vitro* bioassay. Compared with the other two systems, *in vitro* bioassay is a totally closed system and characterized by *in vitro* inoculation of banana plantlet grown on modified medium for interaction system (MIS) without a carbon source. Twenty-four days after inoculation with *Foc* tropical race 4 (TR4) at 10⁶ conidia/ml, disease severity was rated on a scale of 1 to 6. It was observed that the final disease severity was mainly affected by pathogenicity of *Foc* TR4 strain (degenerated strain, the first-generation rejuvenated strain, and the third-generation rejuvenated strain), sporulation medium (Armstrong's *Fusarium* medium, Richard's liquid medium, and potato dextrose water), MIS composition (Murashige and Skoog salts without organic elements, half-strength Murashige and Skoog salts without organic elements, half-strength Murashige and Skoog salts with organic elements), and growing time of banana plantlet on MIS before *in vitro* inoculation (1 to 3 weeks). The effects of the four factors on final disease severity were studied by using orthogonal design. The variance analysis of data showed that all the four factors significantly affected the development of *Fusarium* wilt on banana plantlets. Among them, pathogenicity of *Foc* TR4 strain was the most important factor. The optimum factor combination for rapid screening was the third-generation rejuvenated strain, potato dextrose water, half-strength Murashige and Skoog salts without organic elements, and one-week growth on MIS before *in vitro* inoculation.

Using demand-led approaches to improve tomato productivity in Ghana

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Tomato is one of the most cultivated and consumed vegetable in Ghana. Being an important source of vitamins, minerals antioxidants.

Any attempt to salvage the tomato industry in Ghana must be holistic, involving contributions from all actors in the value chain including government policy makers and officials. We have engaged all key and catalysed funding for PhD postgraduate. Research is focussing on virus-resistance, heat-tolerance, shelf-life and processing. Best practices in demand-led breeding are being used to ensure that modern varieties from these programmes will match the needs and stimulate tomato industry. Here, we report some of the successes and challenges encountered, and highlight opportunities for developing improved varieties of tomato to increase productivity and incomes in Ghana.

Impact of pre-processing blanching treatment on lipophilic pigments and antioxidant property

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Traditional leafy vegetables including pumpkins (*Cucurbita moschata*) provide a rich source of phytonutrients associated with human health benefits. The aim of the study was to investigate the effect of different blanching treatments on the colour and antioxidant property of pumpkin leaves. The leaves were subjected to blanching, microwave pre-cooking and steaming at 95 °C for 1, 3 and 5 min using a lemon based juice solution (at 5%, 10% and 20%). Steaming with the 20% lemon juice solution for 1 min gave leaves with the best dark green colour retention and the highest content of chlorophyll content. However, the phenols, flavonoid and antioxidant activity were highest in leaves steamed in 5% lemon juice solution for 5 min. Samples subjected to steam blanching treatment showed a significant reduction in antinutritive compounds as blanching time and lemon juice concentration increased. It is evident that the steam blanching using 5% lemon juice solution as blanching medium for 5 min can be recommended for the utilisation of the pumpkin leaves as a dietary supplement.

Impact of pre-processing blanching treatment on metabolites and glycoalkaloids in African nightshade (*solanum retroflexum dun*)

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Vegetable pre-processing entails the use of heat treatments to inactivate enzymes while fixing the colour and nutrient retention. Night shade leaves were subjected to pre-processing treatments by (i) blanching at 95 °C in water bath, (ii) microwave pre-cooking and (iii) steaming at different time intervals (1, 3 and 5 min) using a lemon based juice solution (5 %, 10%, 20%). The best pre-processing conditions for each treatment were selected for comparison and further analysis. These treatments included blanching with 10% lemon juice solution at 95 °C, steaming with 20% lemon juice solution for 5 min and plain water was used as a control. Metabolites chemical classes including organic acid (citric acid), phenolic acids (neochlorogenic, chlorogenic, and caffeoylmalic acid), flavonoids component (kaempferol O-rhamnosyl hexoside, and rutin) were predominantly identified in raw and blanched samples. Blanching treatment enhanced the accumulation of caffeoylmalic acid, rutin, chlorogenic acid, neochlorogenic acid, cryptochlorogenic acid, and kaempferol O-rhamnosyl hexoside in Nightshade leaves. Concentration level of caffeoylmalic acid, rutin, chlorogenic acid neochlorogenic acid, cryptochlorogenic acid and kaempferol O-rhamnosyl hexoside in blanched samples ranged from 894.4-1258.5 mg/kg, 414.2-500.4 mg/kg, 69-446 mg/kg, 40.9-139.7 mg/kg, 14.4-104.5 mg/kg and 35.9-55.5 mg/kg. Overall, the content of all quantified metabolites was higher in blanched samples than in raw samples. Unsupervised principle component analysis (PCA) demonstrated that the metabolic composition in raw and blanched samples of nightshade varied remarkably. Moreover, blanching treatment increased the concentration of different glycoalkaloids (antinutritive compounds).

Bacteriostatic effect of egg albumen from hens of different feed efficiencies

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Egg albumen contains lysozyme and ovotransferrin, bacteria-inhibiting proteins which play important roles against egg contamination especially under tropical conditions. Previous work has shown that albumen quality differs based on hen feed efficiency, where eggs from highly feed efficient (HFE) hens had a greater albumen height and amino acid concentration compared to those from low feed efficiency (LFE). This study investigated the bacteriostatic effect of egg albumen from hens of varying feed efficiencies, against select bacterial species of importance to egg safety.

A total of 22 eggs, (n = 11 eggs from each group) were collected from the HFE (FCR $\nless 1.8$) and LFE (FCR $\nless 2.1$) hen cohorts at 98 weeks. Blank antibiotic susceptibility discs were soaked in individually homogenised albumen and placed in three replicates onto Mueller Hilton plates which were inoculated with either *Salmonella typhimurium* or *Staphylococcus aureus*. Plates were incubated for 24 hours and zones of inhibition were measured under a light microscope. Data were analysed using the using the GLM procedure in SAS. Differences in means with a statistical difference of $P \nless 0.05$ were considered significant.

For staphylococcus, eggs collected from HFE hens had a higher zone of inhibition than LFE hens (2.19mm vs 1.73mm; $P = 0.02$). The inhibition zone for *Salmonella*, was also higher in eggs from HFE hens compared to eggs from LFE hens (2.09mm vs 1.66mm, $P = 0.04$). This study suggests, that albumen from HFE hens have a stronger bacteriostatic effect against *Salmonella* and *Staphylococcus*, than albumen from LFE hens.

Consumer preferences analysis for animal section at the markets (Mandis) under religious meat value chain

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Small ruminants and their meat (mutton) is a highly valued and culturally prominent part of Pakistan's livestock industry. Four interlinked mutton value chains (VC) exist: traditional wet market, new domestic (supermarkets), export, and religious slaughter, and smallholder farmers (SHF) supply all VCs. The religious VC is the largest trading 9 million of the 25 million animals slaughtered annually, and the highest demand is at Eid-al-Adha.

A cross-sectional survey of 53 potential customers was carried out at three mandis just prior to Eid-al-Adha. All customers were male and over half (56%) were aiming to buy only one animal. Preferences were for two-toothed (one year-old) and phenotypically "attractive white" or single coloured animals; 43% of customers had a specific breed in mind. There was a huge variation in willingness to pay from 15,000-60,000 Pakistani Rupees (PKR), but most (62%) were looking to pay between 20,000 to 30,000 PKR (~2.5x prices of traditional domestic VC). The main challenges for purchasing were high prices (56%) and difficulty finding desired animals (45%). Over half of consumers were looking for animals between 21 to 30kg carcass weight, and 96% had a carcass weight in mind. Carcass weights were estimated on visual assessment with liveweights unavailable.

Communicating VC specifications to farmers and extension officers will be a key activity in our project. SHFs supplementary feed select animals for Eid-al-Adha, so understanding VC specifications could lead to better price outcomes and encourage more strategic selection and investment in preparing animals for sale.

Genotypic divergence of *Avibacterium paragallinarum* isolates with different nicotinamide adenine dinucleotide requirements for growth

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In 2017, we reported atypical variants of *Avibacterium paragallinarum* with different NAD dependency characteristics for the first time in Korea. The present study was conducted to characterize 24 isolates of *Av. paragallinarum* obtained from chickens during 2011-2016 in Korea, which included the four variants reported previously. The variants showed genetic differences from the typical NAD dependent isolates and also formed genetically divergent patterns. Most of typical isolates (19/20) showed a unique ERIC-PCR pattern and there were no ERIC patterns in common between the typical isolates and the variants. Also, the variants shared no ERIC patterns among themselves. All the typical NAD-dependent isolates belonged to the same phylogenetic group based on either 16S rRNA or *hagA* gene sequences. In contrast, the four variants were distributed into two groups which were distinct from the typical isolates. In the 16S rRNA phylogenetic analysis were not closely aligned to all other *Av. paragallinarum*, although they were clearly members of the genus *Avibacterium*. All the variants had a deletion of TTTT at position 182-186 in 16S rRNA gene of the Modesto reference strain AY499870. Based on the analysis of 16S rRNA and *hagA*, similarities of nucleotide sequence between typical isolates and the variants of *Av. paragallinarum* reached 97.3-98.2% and 95.2-97.2%, respectively. In addition, the similarities among variants were 98.3-100% and 96.5-98.4%, respectively. Our results indicate that variants of *Av. paragallinarum* showing changes in NAD requirements for growth are genetically highly divergent from typical NAD-dependent isolates.

Cattle integration in Indonesian oil palm plantations: impact on soil properties, oil palm yield, and understory plant composition and biomass

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Population growth and improving living standards have led to a growing demand for beef in Indonesia. The local livestock industry is unable to keep up with consumer demand for beef, largely due to low feed availability and poor feed quality. The understory in Indonesia's 11 million hectares of oil palm plantation represents a potential source of cattle feed. Even though cattle-oil palm integration has the potential benefit of increasing beef production, the impact on soil properties, oil palm productivity and oil palm understory (the forage resource) is uncertain. These impacts need to be quantified to ensure the sustainability of grazing in plantations. Cattle directly and indirectly affect soil properties, through trampling and urine/manure deposition respectively. Such soil property changes may benefit or adversely affect oil palm productivity. Furthermore, understory plant species composition and biomass are altered through grazing, potentially compromising future regrowth of desirable plant species. If the understory ground cover becomes low, soil is susceptible to water erosion. To be able to understand the impact of cattle grazing in oil palm plantations, the first essential step is to appreciate cattle management in the integrated cattle-oil palm farming systems. This poster presents the preliminary results from interviews with 39 smallholder plasma farmers of the Buana Karya Bhakti commercial oil palm plantation in South Kalimantan, Indonesia. Cattle management in these smallholder systems is described, as well as the rationales behind the adopted cattle management models.

Understanding the impact of on-farm animal wastage on productivity and livelihoods of smallholder goat farmers in Punjab and Sindh, Pakistan

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Reproductive efficiency is an important driver of productivity in small ruminant farming systems worldwide that is affected by both doe/ewe reproduction and offspring survival. These measures were evaluated through interviews gathering stock tally data from 114 smallholder farmers in Pakistan (51 Punjab, 63 Sindh), providing previously unpublished insights into herd demographics and productivity issues that currently constrain farm income and livelihoods.

Breeding does were kept by 73% of households and 24% kept both goats and sheep. Average breeding herd size was 10 does and/or 4 ewes per household, and many households (n=36; 31%) had 5 or fewer breeding females (15 in Punjab and 21 in Sindh). Annual doe/ewe mortality was 0-15%, and four villages reported average doe mortality ↑14%. Herd/flock reproductive efficiency was generally low. Although two villages reported average birth rates ↑1.5 kids/doe/year, it was ↓1 kid/doe/year in 11 villages. Reported kid mortality was often high, ∼ 10% p.a. in 14/24 villages, including 6 villages ↑20% (maximum 36%). Combining doe/ewe birthing percentages and offspring mortality showed that overall reproductive efficiency was poor. In 58% of villages, average production of 'saleable' offspring was ↓ 1 per breeding female per year and no villages produced ↑ 1.5 saleable offspring/breeding female/year.

Improving overall reproductive success would reduce significant wastage, substantially improve household income from existing livestock holdings, and meet untapped national demand for goat and sheep meat. Current practices and specific interventions to improve breeder reproduction and/or offspring survival are currently being assessed on smallholder farms in Punjab and Sindh.

Adaptive and productive sheep breed for changing climate

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Sheep in semi-arid environments are likely to be affected by warming environment due to climate change. To identify genotypes best suited to warmer climates we assessed thermotolerance and meat quality of 5 female sheep of each of 4 breeds (Merino, Wiltshire, Dorper, and Southdown) under simulated summer conditions. The sheep were housed in metabolic crates within climate-controlled rooms and were exposed to thermo-neutral (TN; 18-21°C and 40-50% relative humidity) or cyclic heat stress (HS; 28-40°C and 30-40% RH) conditions for two weeks. Physiological responses were recorded 3 times daily, and brown fat tissue temperature was measured by data loggers inserted into the brisket. Sheep were slaughtered at an abattoir as per standard commercial procedure and samples obtained for carcass and meat quality attributes. When exposed to HS, Dorpers and Merinos exhibited lower respiration rate (151, 142 breaths/min, respectively) and rectal temperature (39.39, 39.32 °C, respectively) ($P \downarrow 0.05$) than Southdowns (192 breaths/min, 40.05°C) and Wiltshires (200 breaths/min, 39.91°C). Dorper and Wiltshire ($n=3$) showed lowest sternal fat temperatures during HS indicating inherent differences in thermogenesis. HS had significant effect ($P \downarrow 0.05$) on post mortem muscle pH decline which was slower than TN sheep, except in Dorper again indicating better thermotolerance. There were significant ($P=0.03$) breed effects on meat cooking loss % such that Southdown showed minimum cooking loss (17%) while Merino showed the greatest loss (24%). These results suggest that there are genetic (breed) differences in thermotolerance and meat quality of sheep, providing an opportunity to select best sheep suited to a warming climate.

Genetic control of fertility traits across species: association of genes controlling age at menarche and puberty in women and heifers

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Fertility traits are of paramount importance for humans and cattle. In humans, they greatly impact population growth and in cattle, they are one of the main profit drivers in the industry. Using data from genome-wide association studies (GWAS) from both species, we estimated the effect of bovine orthologous of genes associated with age at menarche in women (AaM) in the genetic variance of age at puberty (AaP) in heifers. We found that variants within 100Kb of AaM bovine orthologous genes explained 11.2% of the additive genetic variance of heifers AaP. This represented about twice the variance explained by random gene-sets of similar size and number of variants. Our work highlights the potential of cross-species analyses to increase the cattle industry's productivity.

Improving productivity on Sri Lankan small-holder dairy farms: The Sri Lanka Dairy Excellence Training Initiative

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Dairy development has been given a high priority by the government of Sri Lanka as a means to improve income and nutritional status in rural areas. The productivity of Sri Lankan small-holder dairy farms is generally poor, with milk production averaging 2.2L/cow/day, and calving intervals often greater than 2 years.

Sri Lankan vets and Livestock Development Instructors (LDIs) are responsible for animal health, extension services and farmer training. However, training often focuses on herd improvement and animal health, with little emphasis on profitability and productivity. Additionally, although there is a high level of technical knowledge amongst the vets and LDIs, effective knowledge transfer to farmers resulting in on-farm improvement is inadequate.

The Dairy Excellence Training Initiative is a collaboration between the New Zealand and Sri Lankan Governments to introduce New Zealand approaches to on-farm extension. New Zealand consultants provided training for 11 Sri Lankan Master Trainers (MTs) in milk quality, feed and farm systems, farm business, reproduction and dairy extension. Particular emphasis was placed on the concepts of a whole farm systems approach and peer-to-peer farmer learning.

Ninety vets and LDIs then attended block courses run by the New Zealand consultants in conjunction with the MTs. The main focus of these courses was on starting New Zealand style farmer discussion groups adapted to a Sri Lankan context. Farmer engagement with these groups has been positive so far.

The aim is for the Master Trainers to continue training further groups of vets and LDIs, ensuring the sustainability of the project.

Use of point-of-care tests for detection of pig pathogens

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Detection of pig pathogens is a major challenge. The process includes proper collection of samples and application of suitable diagnostic methods. Current generation diagnostic tests are typically limited to costly and highly technical laboratory-based assays. Point-of-care or pen-side (POC) testing may provide greater access to effective diagnostic services for both small-holder and commercial pig farms. This work aimed to develop a POC test for detection of pig pathogens (using porcine circovirus type 2 (PCV2) as a model pathogen) and to validate the use of oral fluids (OF) as samples. OF samples were collected by placing cotton ropes inside the pig pens. These samples were diluted to overcome possible inhibitors and spiked with known concentrations of PCV2 artificial target DNA (from 10^{11} to 10^4 copies of PCV2 DNA per ml). Nucleic acid extraction was done using a novel cellulose dipstick and validated using a commercial extraction kit. The target DNA was amplified using quantitative real-time polymerase chain reaction (qPCR) and conventional PCR using a portable miniPCR machine. The results showed that the novel cellulose dipstick method was capable of extracting DNA from PCV2-spiked and non-spiked OF samples. The validation tests using qPCR showed almost the same Ct values ranging from 15.22 up to 36.82 with the spiked diluted OF and spiked PBS. Conventional PCR using the portable miniPCR machine also amplified DNA from dipstick extractions up to 10^6 copies per ml from spiked OF. Further work is in progress to optimise the assay for use in the farm setting.

Evaluation of copra meal (CM) in corn-animal protein meal-based diets and enzyme on broiler performance

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The effects of increasing CM level in corn-animal protein-based diets and enzyme supplementation in broilers was investigated in a 30-day experiment. A total of 168, one-week old Cobb broilers were assigned to 8 diets consisting of 2 controls (with and without enzyme) and 6 other diets with 15, 30 and 45% CM levels with and without enzyme in a completely randomized design. Results showed significant interactions effects on growth parameters, fat digestibility, White Blood Cell (WBC) count, Saturated Fatty Acids (SFA) and Mono Unsaturated Fatty Acid (MUFA) ($P \leq 0.05$). Feed intake and WG were reduced on 30 and 45% diets ($P \leq 0.05$). Fat digestibility was improved on control and 30% CM diets with enzyme ($P \leq 0.05$). Higher WBC counts were recorded in control and 15% CM with enzyme ($P \leq 0.05$). Higher SFA and lower MUFA were on 15 and 45% diets ($P \leq 0.05$). In the main effects, feed intake and weight gain (WG) were reduced and feed conversion ratio (FCR) increased with increasing level of CM above 15% ($P \leq 0.05$). The diet with 45% CM showed lower SFA ($P \leq 0.05$) compared to 15% CM diet, MUFA and PUFA reduced with increasing CM levels ($P \leq 0.05$). Enzyme supplementation reduced SFA and MUFA content ($P \leq 0.05$) but improved crude fibre and fat digestibility of broilers ($P \leq 0.05$). In conclusion, 30% dietary CM inclusion is detrimental in terms of WG but has no effect on the fatty acid composition of broiler meat. More research into enzyme source and concentration above 30% CM is recommended.

Preliminary investigations in giant taro (*Alocasia macrorrhiza* L.) corn meal as energy source in poultry diets

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Giant taro (*Alocasia macrorrhiza* var. Tonga) grows wild in Pacific Island countries and has become invasive in most countries. Proximate analysis of giant taro (GT) corn at USP Alafua Central Laboratory showed ~12MJ ME/kg, 127 g crude protein/kg DM. Currently however, the crop has low food value in the region and its use in poultry feeding is still limited because of the acrid taste due to the presence of calcium (Ca) oxalate. Two preliminary studies (PS) were conducted to evaluate the feeding value of GT for poultry. Study 1 investigated the effect of coconut oil addition on the utilisation of GT corn meal by layers and broilers. Replacing dietary maize with whole GT corn meal at 200 g/kg adversely affected performance of broilers and layers ($P \leq 0.05$). Addition of coconut oil at 9: 1 (corn meal: oil) improved utilisation of the meal by laying hens but not in broilers. Study 2 investigated the effect of peeling and inorganic calcium addition on the utilisation of GT corn meal by laying hens. Results showed that feeding whole GT corn meal at 200 g/kg diet had adverse effects on egg production and egg qualities ($P \leq 0.05$) but peeling or increasing dietary Ca carbonate level from 40 to 60 g/kg improved the utilisation of whole or peeled corn in terms of egg production and egg qualities. In view of the ready availability and low food value, more research is recommended into processing and diet formulation to improve the utilisation of GT corn meal by poultry.

Blood phosphorus concentration as an indicator of phosphorus deficiency in growing cattle

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Inadequate intakes of phosphorus (P) by cattle can cause P deficiency and severely reduce productivity. Blood inorganic P concentration (Pi) is often used as an indicator of P deficiency. Results from two experiments (E1 and E2) with young cattle grazing tropical P-deficient rainy season pastures without or with additional P, or fed in pens on higher energy pelleted diets ranging in P concentration (E3), were used to examine the relationships between Pi and liveweight (LW) gain. When Pi was \uparrow 2.0 mmol/L average LW gains were 0.71, 0.85 and 1.04 kg/day in E1, E2 and E3, respectively. These differences between experiments were most likely associated with diet limitations other than P. LW gain was related curvilinearly in E1 and E2, and linearly in E3, with Pi. The Pi ranged from ca. 1.0 mmol/L through to 2.5-3.0 mmol/L in each experiment. The reductions in LW gains from the maximum at Pi \uparrow 2.0 mmol/L for several lower Pi concentrations were calculated from these relationships. At Pi = 1.0 mmol/L the LW gains were 36-60% of the maximum, at Pi = 1.5 mmol/L LW gains were 59-84% of the maximum, and at Pi = 2.0 mmol/L the LW gains were 82-98% of the maximum. The reductions in LW gain at each Pi were substantially greater for E3 than for E1 and E2. It is concluded that the Pi threshold indicative of P deficiency varies with the diet quality and that the threshold values are substantially higher with higher diet quality.

Multi-trait genomic predictions for a novel age-at-puberty phenotype in tropically adapted beef heifers

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Heifers that reach maturity at an earlier age often experience an increased potential for greater lifetime productivity, and selection has been shown to be an effective way to reduce heifer age at puberty. Here we demonstrate that reproductive maturity score (RMS), a newly developed, industry applicable measure of age at puberty, is highly correlated with age at first corpus luteum (AGECL), a more intensively collected but precise measure of puberty. This suggests that RMS is a good indication of heifer age at puberty and may be used to assess maturity as a component of heifer fertility. This is highly beneficial as RMS is a more commercially relevant adaptation of AGECL, and may be more easily adopted by the extensively operated properties of northern Australia. In a multivariate prediction model containing both traits, the accuracy of genomic estimated breeding values (GEBV) improved in comparison to univariate models. This indicates that there is potential for RMS and AGECL to be used together to increase the accuracy of prediction for heifer maturity traits and that moving forward, RMS should be included with AGECL when predicting GEBV for heifer age at puberty. This represents a new, effective way to select for reduced age at puberty and improved heifer fertility in tropically adapted beef cattle.

Ensiling unsalable vegetables with crop sorghum to produce high quality feed

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Vegetables regarded as unsalable at processing often undergo disposal into landfill, threatening food security and increasing emissions through decomposition. Ensiling vegetables with forage crops is a suggested method of waste reduction that could also double as a livestock feed. Carrot or pumpkin, ensiled at 0%, 20% or 40% DM with crop sorghum, and with or without a second-generation silage inoculant were assessed for nutritive composition, organic acid profiles, aerobic stability and *in vitro* rumen fermentation characteristics. Silage was sampled after 70-days ensiling for nutrient composition, 14-day aerobic stability, organic acid profiles and microbial diversity. Sorghum ensiled with carrot or pumpkin at 20% or 40% DM increased crude fat ($P \leq 0.01$) and decreased ($P \leq 0.01$) silage surface temperature upon aerobic exposure compared to the control. Bacterial communities analyzed through 16S rRNA gene sequencing linearly increased ($P \leq 0.01$) in diversity as vegetable proportion increased in the silage; dominated by *Lactobacillus* species. Upon assessment *in vitro*, there was an increase ($P \leq 0.04$) in *in vitro* digestibility and some CH₄ parameters (% CH₄, and mg CH₄/g DM), with no effect ($P \geq 0.17$) on remaining CH₄ parameters (mL CH₄/g DM, mg CH₄/g DM), gas production or pH. However, increasing vegetable proportion decreased acetic and increased propionic acid concentrations respectively, decreasing A:P ratio and total VFA as a result ($P \leq 0.01$). Results from this study indicate including carrot or pumpkin at 20% or 40% DM in a sorghum silage can produce a highly digestible, microbially diverse and energy-rich livestock feed whilst acting as a method of waste diversion of considerable environmental benefit.

Biopolymer composites for slow release to manage Pimelea poisoning in cattle

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Cattle grazing the pastures of inland Australia can be poisoned by ingestion of certain native *Pimelea* plant species, particularly *Pimelea trichostachya* and *Pimelea simplex*. The *Pimelea* toxin, simplexin, causes often fatal restriction of the pulmonary venules, with resultant heart impacts and characteristic fluid accumulation (oedema) of the jaw and brisket regions. In certain years heavy livestock losses can occur. Currently, there is no effective vaccine or antidote for pimelea poisoning and the only management strategy is to reduce contact between toxic plants and susceptible stock, for beef producers to avoid potentially devastating poisoning events. Nevertheless, previous research has demonstrated that prolonged low dose feeding diminished the effect in animals.

It was postulated that the animal exposed to prolonged low doses developed a mechanism for detoxifying simplexin, possibly through adaptation of the rumen microbial environment.

The present study seeks to investigate the use of a biopolymer/toxin composite to foster toxin-degrading microbe populations. The objectives are to manufacture biopolymer composites based on biodegradable polylactic acid (PLA), polyhydroxyalkanoates (PHAs) and/or polycaprolactone (PCL), as toxin slow-release systems for the rumen that would have broad utility across a range of plant toxins and other beneficial rumen compounds. The poster covers the manufacturing, characterisation and performance of the biopolymers in a simulated rumen environment. Preliminary results of different biopolymers/composites containing *Pimelea* material and toxin extracts in an *in vitro* simulated rumen environment for up to 30 days are presented. It was found that the release rate could be tailored by choosing the right type of biopolymer.

Selection of small SNP panels to predict dairy breed proportions of African crossbred cattle

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Crosses between exotic dairy cattle and indigenous populations have long been used in African countries to improve productivity. High-grade dairy crosses, however, are superior only if kept under optimal environments. The suboptimal environments of the majority of smallholder farms are better suited for crossbreds with lower exotic breed proportions, with the ideal composition depending on the environment. But most farmers do not know the breed composition of their crossbreds to make appropriate mating decisions. High density genetic markers provide accurate estimates of breed composition. However, for routine application genotyping costs need to be low, which restricts the number of markers that can be genotyped. We determined the accuracy of small SNP assays with 100 to 1,500 markers for estimating total dairy breed proportion of 3,139 crossbred cows from East and West Africa. Markers were selected from around 40k SNPs based on the largest absolute allele frequency differences between pure ancestral breeds. In general, panels with larger proportions of markers differentiating African *Bos taurus* breeds from exotic taurine dairy breeds performed better compared to panels where most markers were selected to distinguish *Bos indicus* from exotic dairy breed proportions. Overall, markers selected for largest allele frequency difference between West African indigenous breeds and exotic dairy breeds performed best or near best across all crossbred populations irrespective of their origin with the range of accuracy of prediction (r^2) of breed composition being 0.895 to 0.966 (200 SNPs), 0.917 to 0.974 (400 SNPs), and 0.962 to 0.990 (1500 SNPs), respectively.

Adsorbents for the sequestration of the Pimelea toxin, simplexin

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Pimelea poisoning affects cattle grazing arid rangelands of Australia, has no known remedy and significant outbreaks can cost the industry \$50 million per annum. Poisoning is attributable to consumption of native Pimelea plants containing the toxin simplexin. Charcoal, bentonite and other adsorbents are currently used by the livestock industry to mitigate the effects of mycotoxins. The efficacy of such adsorbents to mitigate Pimelea poisoning warrants investigation. Through a series of *in vitro* experiments, different adsorbents were evaluated for their effectiveness to bind simplexin using a simple single concentration, dispersive adsorbent rapid screening method. Initial experiments were conducted in a rumen fluid based medium, with increasing quantities of each adsorbent: sodium bentonite (Trufeed®, Sibelco Australia), biochar (Nutralick®, Sibelco Australia) and Elitox® (Impextraco, Belgium). Data showed the unbound concentration of simplexin decreased with increasing quantities of each adsorbent tested. Sodium bentonite performed best, removing ~95% simplexin at 12 mg/mL. A second experiment using a single amount of adsorbent included two additional adsorbents: calcium bentonite (Bentonite Resources, Australia) and a synthetic adsorbent (Waters, USA). The concentration of simplexin remaining in the solution after 1 h, the amount able to be desorbed off the adsorbent-toxin matrix with replacement fresh fluid, and the amount remaining bound to the adsorbent were measured. All samples containing an adsorbent were statistically different compared to the blank ($p \downarrow 0.05$), indicating some binding activity. Future work will explore the binding mechanisms and behaviour of the toxin-adsorbent complex in the lower gastrointestinal tract.

Drought impacts on grassland productivity: the role of plant-soil feedbacks

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Drought influences pasture productivity with potentially severe impacts on livestock. However, not all plant species are impacted equally indicating that plant community composition can be managed to improve resistance to drought. We conducted a plant-soil feedback (PSF) experiment to assess impacts of drought at the species and community level. We grew twelve plant species representing C3 and C4 grasses, forbs and legumes in monocultures and in 4-species mixtures (one from each functional group) in soils with a legacy of ambient or drought (5 years) conditions for two generations. We measured plant biomass in the second generation to calculate PSF. Species with positive PSF under drought are likely to be more resistant to drought than those with negative PSF. Under ambient rainfall PSFs were generally negative for C3 grasses, positive for C4, forbs and legumes. Drought promoted negative PSFs in C3 grasses and forbs, but positive PSFs were observed in C4 grasses and legumes. These results indicate that C3 grasses and forbs are likely to be sensitive to drought while C4 grasses and legumes will be less negatively impacted by drought due to changes in PSFs. PSFs at the community level were positive at the community level under ambient but shifted towards neutral under drought indicating that drought may destabilise plant communities. Our results indicate that the presence of C4 grasses and legumes may reduce drought impacts providing a tool for future pasture management for healthy livestock production in Australian rangeland.

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Farmer perception and resources for calf fattening under smallholder production system

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In Pakistan, smallholder farmers are mainly engaged in dairy farming while keeping beef animals as secondary product. Farmers have poor production due to lack of focus on beef farming, traditional calf rearing practices and limited resources. The objective of this study was to understand the perceptions of smallholder farming households of beef production and the available resources for farmers to engage in beef fattening to increase overall farm profitability. Data was collected using a focus group discussion approach, from farming households in villages across Punjab (n=7) and Sindh (n=8). An integrated framework incorporating gender and value-chain considerations was used as a tool to assess farmer interest, goals and resources for rearing livestock. The data was analysed using content analysis. Majority of the farmers interested in calf fattening were more resource rich, with livestock as their primary source of income. A smaller proportion of farmers, with limited resources, also took interest in calf fattening. Women from a few villages mentioned that they were reluctant to be involved in beef businesses due to an emerging focus on childhood education as well as a lack of agency for livestock sales and control over income. Other factor contributing to farmer perception of beef included their enterprise focus (dairy or cropping). Overall, the smallholder farmers perceived that calf fattening could be a profitable business if calves were reared properly, had adequate feed resources and good market return. Training and farm support targeting these areas is critical for calf fattening to become a profitable market strategy.

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Linking smallholder farmers to potential beef markets: A case study of livestock farmers in Pakistan

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In Pakistan there are no dedicated beef breeds consequently beef meat is a by-product of the dairy industry in the form of cull cows and male calves. Smallholder farmers supply up to 80% of animals slaughtered and decisions to sell their animals is driven by a need to generate cash in a time of necessity rather than in response to market signals. The aim of this study was to identify and evaluate beef market opportunities for smallholder farmers with the objective of increasing their income from their beef animals. Using a rapid value chain assessment seven potential beef markets in Punjab and Sindh were assessed and one was studied in detail to evaluate the opportunities and risks for smallholder farmers in beef value chains. Semi-structured interviews were conducted with beef value chain actors including; consumers (10), retailer (1), traders (12), feedlot farmer (1) and smallholder farmers (9). The interview data was analysed using content analysis within value chain framework comprising of different flows (product, information and financial) and relationships among the chain actors. The results indicated that supplying directly to the retailer was indeed a potential opportunity for smallholder farmers provided they can meet product specifications. This study describes what capacity building support would be required to enable smallholder farmers to implement more focused and cost-effective rearing strategies leading to a reliable and consistent supply for this retailer. If successful, this could be used as a model for market interventions for other farmers leading to increased beef production and profitability.

Shining a light on *Haemonchus contortus* in sheep

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Heavy infestations of the Barber's pole worm, *Haemonchus contortus*, can cause severe wasting, morbidity and mortality in animals if not promptly treated. The current detection methods for this blood-sucking parasite involve faecal worm egg counts and diagnosis of anaemia, both of which are time consuming and require expertise. As blood is detected in sheep faeces sooner during infection than worm eggs, quantitative evaluation of blood may serve as a sensitive indicator of *H. contortus* infection. Here we investigated the feasibility of rapid estimation of haemoglobin (Hb) in sheep faeces using visible near-infrared spectroscopy. Haemoglobin (Hb) was assessed at various concentrations in moist sheep faeces using portable visible near-infrared (vis-NIR) spectrometers. Calibration models were developed for the region of 400-600 nm, where Hb absorption bands can be found. Within this wavelength region, Hb in sheep faeces can be estimated with minimal interference from background moisture (970 nm) or chlorophyll (670 nm), suggesting that difference in diets in sheep will have minimal effect on prediction accuracy. Predictions for sheep faeces based on a drenching threshold of 3 µg Hb/mg faeces showed high levels of accuracy with minimal sample preparation (Sensitivity = 89%, specificity = 80%). The success in detecting Hb in sheep faeces indicates the potential of vis-NIR spectroscopy as a rapid, on-farm diagnostic method for predicting blood in sheep faeces, and timing treatment of *H. contortus* infections.

Establishing the underlying genetic basis of phenotypic resistance in *Avibacterium paragallinarum*

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Avibacterium paragallinarum is an avian respiratory pathogen that causes infectious coryza in chickens. The presence of this disease has a great impact on the poultry industry due to decreased egg production and reduced growth in young birds. Most farms employ prophylactic measures like vaccination to prevent outbreaks of coryza. However, some commercial poultry farms in developing countries utilize antibiotics as preventive measure. This practice contributes to the increase and dissemination of antibiotic resistance currently being observed in *Av. paragallinarum*. In the current study, forty overseas isolates of *Av. paragallinarum* that exhibited phenotypic resistance to penicillin, ampicillin and tetracycline were screened for the presence of antimicrobial resistance genes for the corresponding antibiotics. The *bla*_{ROB-1} gene was detected in two isolates that exhibited ampicillin resistance. Nineteen out of the twenty tetracycline resistant isolates were positive for *tetB* resistance gene. None of the isolates were positive for the *bla*_{TEM} resistance gene. The tetracycline resistant isolate that was not positive for *tetB* did not harbour any of the other eight *tet* genes screened for in this study. No genes were detected that could possibly explain the observed penicillin resistance. The main aim of the current study was to determine if an association exists between the phenotypic resistance observed in *Av. paragallinarum* and the resistance genes tested. Additional studies using new molecular assays and potentially whole genome sequencing would be necessary to determine the genes or mechanisms underpinning antimicrobial resistance to *Av. paragallinarum*.

Mitigating the effects of the toxin simplexin in pimelea poisoning of cattle by development of a microbial probiotic

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Pimelea poisoning of cattle (also known as St. George disease or Maree disease) is a disease unique to Australia. Native Pimelea pasture species were found to be responsible for the poisoning with the culprit toxin isolated and characterised as the novel diterpenoid orthoester simplexin. A previous cattle feeding trial reported that cattle fed a diet containing increasing low doses of simplexin showed reduced poisoning symptoms over time. It is hypothesised that rumen microorganisms in the cattle could adapt and detoxify simplexin. To this date, no studies have been conducted on rumen microbial detoxification of simplexin. The project aim is to develop a microbial probiotic able to detoxify simplexin thus allowing cattle to consume Pimelea without adverse effects. Studies are ongoing to investigate the fate of simplexin incubated in in vitro rumen fluid fermentations fed daily with *P. trichostachya* and a salts solution. Preliminary experiments showed decreases in simplexin levels during fermentation suggesting the possible involvement of rumen microorganisms in simplexin degradation. Studies of simplexin hydrolysis using acid and commercial enzymes are being conducted to identify possible simplexin metabolites to create a metabolite database for the in vitro fermentation studies and future simplexin degradation pathway studies. Simplexin and its predicted metabolites are analysed by high-resolution, accurate-mass liquid chromatography-tandem mass spectrometry methods, which also enable molecular formula calculations for detected unknown metabolites. Further studies are planned including incubating simplexin in cultures of micro-organisms isolated from the in vitro fermentation studies and full characterisation of products from the chemical and enzyme hydrolysis studies.

Buffalo flies receptive to Wolbachia infection: An opportunity to population control?

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Buffalo flies, *Haematobia (irritans) exigua* (BF), are obligate haematophagous ectoparasites of cattle that cause significant economic and welfare impacts in northern Australian cattle. With climate change and the development of resistance to commonly used chemicals, BF are rapidly spreading southwards. *Wolbachia* is a maternally transmitted bacterial endosymbiont of insects that induces a range of effects on its host, including cytoplasmic incompatibility (male sterility), reduced fitness, and inhibition of pathogen transmission. We are examining the potential for use of *Wolbachia* in area-wide control of BF. Following a survey of Australian BF populations that showed *Wolbachia* was not present, we have tested embryonic microinjection, pupal injection and injection of adults as a first step towards the development of a *Wolbachia* infected BF line. Here we report distribution and growth of *Wolbachia* in somatic and germline tissue of BF injected with the three *Wolbachia* strains; wAlbB, wMel and wMelPop. Our results to date suggest that pupal or adult injection may be a more suitable method for transfecting BF than embryonic microinjection. We also demonstrate *Wolbachia* induced fitness effects in injected BF including shortened lifespan, decreased pupal emergence, and reduced egg production. Future work will focus on establishing a stably infected BF strain, towards the design of *Wolbachia* - based control programs for BF.

Investigating host biomarkers associated with cattle tick resistance

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The cattle tick *Rhipicephalus microplus* is a blood-feeding ectoparasite that threatens livestock production in tropical countries worldwide. Heavy tick burden causes weight loss and anaemia in animals and poses a risk for the transmission of blood parasitic diseases such as babesiosis and anaplasmosis. Ticks are an economically important pest in Australia, especially in Queensland and the Northern Territory where ticks are controlled with chemical treatments and vaccination, which do not guarantee full protection. Tick spreading and outbreaks can be further controlled with the use of tick-resistant cattle (*Bos indicus*) which performs better at subtropical conditions. Crossbreeding and the introduction of more *Bos taurus* genetics to improve beef production comes at the expense of reducing host resistance. In the field, resistant animals are hard to identify without previous exposure to tick infestation especially in large crossbred herds. Thus, there is a need to develop cost-effective methods to select for resistant animals, yet little is known about the biological process behind host resistance in bovines.

Previous work has shown that ticks are rejected primarily at the larval stage and that taurine cattle develop a strong hypersensitivity reaction at the tick attachment sites, whereas indicine cattle display a suppression of the cell-mediated inflammatory response. However, the mechanisms by which animals acquire and sustain high levels of tick resistance are not yet fully understood. In this project, 35 Brangus animals are being investigated for differentially expressed biomarkers associated with tick resistance using high-throughput transcriptomics.

Topical RNAi for Sustainable Animal Health

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Animal health measures mainly rely on vaccination or chemical control for major pests and pathogens, causing issues of residue, toxicity and development of resistance. For example, control of Sheep flystrike and lice-infestation affecting the Australia's sheep/wool industry (↑3.5B) have developed resistance to nearly all control chemicals used in the past. BioClay technology uses clay nanoparticles to deliver double stranded RNA (dsRNA), the key trigger molecule of RNA interference pathway. However, the instability of dsRNA under environmental conditions is a major bottleneck with a protection window only lasting 5-7 days. Loading of the dsRNA on clay particles overcomes issues of instability, facilitating slow release of the active molecules, ensuring ingestion of dsRNA/BioClay by the pests. As an early proof of concept work we have investigated the stability dsRNA loaded on two types of BioClay: BioClay 1 (releases dsRNA under acidic conditions) and BioClay 2 (releases dsRNA under alkaline conditions) at room temperature and 40C. Cattle skin was treated with Cy3 labelled dsRNA on BioClay1 or BioClay2; the treated skins were imaged using confocal microscope. The imaged skin samples were washed and stored at room temperature for 5 days and imaged again for the presence of fluorescent signal. Our results, show that the dsRNA when loaded on BioClay is stable unlike naked dsRNA which showed degradation and was not visible after washing. This increased inherent stability of the dsRNA molecules, combined with the environmental stability afforded by the BioClay, offers promise to further exploit this distinctive technology for improving animal health.

Effects of nano- pesticide formulation parameters on insecticidal effects against sheep blow fly (*Lucilia cuprina*) larvae

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Flystrike, caused by the Australian sheep blowfly *Lucilia cuprina* (Wiedemann), is a major production and welfare issue in Australian sheep flocks. The availability of effective chemical products is critical for the prevention of breech strike, particularly in unmulesed flocks. There is a history of development of resistance to blowfly control products and few new actives in the pipeline. Advances in formulation technology, particularly in the area of nanotechnology, can greatly increase the utility and effectiveness of insecticidal actives and facilitate the development of optimal resistance management programs.

We have developed mesoporous silica nanoparticles with structural characteristics that can be tuned to provide the desired loading of actives and varied release profiles. We investigated the relative toxicity of different sizes of silica nanoparticles, loaded with ivermectin before and after artificial weathering. Bioassays were conducted using two test systems, a standard chromatography paper assay and a wool-serum assay to determine formulation parameters that provide the best effect against first instar *L. cuprina* larvae. This study will assist the development of novel and labour efficient options for managing flystrike and countering resistance in sheep blowflies.

Climate change adaptation through planted forages in Southern Highlands, Tanzania

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The current production for dairy products in Tanzania has not kept up with the demand. With a population of 53 million that is expected to more than double by 2050 and a natural resource base already under pressure, dairy production in Tanzania urgently needs to sustainably intensify. In addition, the impacts of climate change are projected to leave smallholder farming systems ever more vulnerable. Improving the resilience of these farming systems requires context-specific solutions. This study looks at how smallholder dairy farms in the southern highlands of Tanzania can adapt to changing climate through planted forages. Household surveys, forage trials, and feed and milk analyses were conducted, and three representative dairy intensified farms were selected by identifying the mean values of household survey data in the Mufinidi, Njombe and Rungwe regions of Tanzania. The Integrated Analysis Tool (IAT) model integrates biophysical (crop, animal, forage) and socio-economic (labour, financial resources). The model was used to simulate the performance of smallholder farming systems in 2018, 2030 and 2050 under different climate scenarios with and without the introduction of planted forages. The data collected was used to assess baseline performance and trade-offs in the three different scenarios with the indicators of socio-economic (gross margins, labour days) and productivity (meat and milk production). Recommendations resulting from this study can inform dairy policy development in Tanzania, as well as developing partners with the goal of promoting sustainable dairy intensification.

Key Words: Climate change, Smallholder dairy

Development of a bead-based identification assay for bacteria associated with bovine respiratory disease

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Bovine respiratory disease (BRD) is a major problem in feedlot cattle as it causes serious economic losses due to mortality, antibiotics, labour, reduced growth performance and carcass scores. Bacterial species, such as *Bibersteinia trehalosi*, *Histophilus somni*, *Mannheimia haemolytica*, *Mycoplasma bovis* and *Pasteurella multocida*, are frequently involved in BRD.

Australian studies of the bacterial species involved in the BRD complex are very limited. This project set out to develop a bead based platform assay which involved a multiplex PCR with the amplified products being hybridised to beads analysed on a Luminex machine. The assay was developed for *B. trehalosi*, *H. somni*, *M. haemolytica*, *M. bovis*, *Trueperella pyogenes* and *P. multocida* and tested on the reference strains for each species bar *M. bovis*. As well, 85 field isolates (26 isolates of *P. multocida*, 19 of *H. somni*, 28 of *T. pyogenes*, 8 of *M. haemolytica*, 3 of *B. trehalose* and 1 of *M. bovis*) were tested.

All isolates gave the right result in the Luminex assay. However, the assay could not differentiate between *M. haemolytica* and *M. glucosida* despite trying 16 primers targeting different genes. To differentiate the two *Mannheimia* species, a single-plex was developed that was able to differentiate both species as a follow up assay. This assay will enable us to look at the prevalence of these species to better understand the cause of BRD and to understand the risk of BRD at Australian feedlots. The assay will pave the way to vaccine development and prevention of BRD at feedlots.

Detection of *Stephanofilaria* (Nematoda: Filariidae) in buffalo fly lesions

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Haematobia irritans exigua, commonly known as buffalo fly (BF), causes economic losses of about AUD \$100 million per annum to the Australian cattle industry in terms of decreased production and costs of control. Lesions associated with BF infestation range from raised, dry, alopecic, hyperkeratotic or scab encrusted to severe hemorrhagic areas of ulceration which represent a major animal welfare concern. BF transmits a filarial nematode, *Stephanofilaria* sp., which has been speculatively associated with BF lesion development. The existing literature indicates that the sensitivity of currently used diagnostic techniques to detect *Stephanofilaria* in skin lesions is low and that there is currently no sequence for *Stephanofilaria* available on GenBank. Our objective is to develop a PCR method to detect *Stephanofilaria* in BF lesions.

Skin biopsies were collected from 10 freshly slaughtered cattle hides having obvious BF eye lesions. Samples were collected from the center and the edge of the BF lesion as well as from adjacent normal tissue. Each skin punch was cut into 5-6 slices and immersed in normal saline before incubation overnight at 22°C. Eight nematodes were recovered from the saline by microscopic examination and preserved in ethanol. Nematode DNA will be extracted using conventional extraction methods. Specific primers will be used to amplify the ITS regions of rDNA and *cox1* region of the mtDNA and the amplified DNA will be sequenced. Primers will be designed from these regions to detect the presence of *Stephanofilaria* and used in PCR studies to clarify the etiology and epidemiology of BF lesions.

Predicting age of livestock from DNA hair samples

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DNA methylation occurs predominantly on the cytosine nucleotide in CpG dinucleotides. In humans, the methylation state of CpG sites changes with age and can therefore be utilized as an accurate biomarker for aging. To date, four epigenetic clocks have been developed and used to predict age in humans. In animals, epigenetic clocks have been investigated and tested in dogs, wolves and mice. However, relatively little is known about DNA methylation patterns in livestock. In order to develop a prediction of age from the methylation patterns in bovine DNA we generated DNA methylation profiles from the tail hair of cows of known age. Four different technologies, the Oxford Nanopore technology MinION, human methylation EPIC array, reduce representation bisulfite sequencing and whole genome bisulfite sequencing, were evaluated for their ability to profile DNA methylation patterns. Oxford Nanopore sequencing, a very recently developed technology, showed the most potential to accurately identify large numbers of methylated sites (up to 20.4 million methylated sites). Using the methylation data samples were clustered using principal component analysis. Samples showed clustering based on age. This confirms that DNA methylation profiles do differ between young and old animals. This is the first time age related methylation differences have been demonstrated in cattle.

Effective host depletion and microbial enrichment method for bovine genital tract microbiome research

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In 2016–2017, the Australian beef industry gross value was \$A16.85 billion, which is 20% of the total farm production in Australia (\$62b). Overall beef production is dependent on the lifetime reproductive efficiency of the cow, as the relative cost of raising a breeding female decreases with increased calving. It has been estimated that neonatal calf mortalities, pestivirus and bovine genital campylobacteriosis (vibriosis) collectively contribute to ~\$236m in production losses in Australian cattle industries each year. Genital tract microbiome has a direct impact on bovine reproductive health and susceptibility to infectious diseases which may be associated with infertility and pregnancy losses.

16S ribosomal DNA amplicon sequencing has been utilized to characterize both human and bovine vaginal microbiomes and has generated confident characterization of representative microorganisms for different gynaecological and obstetric conditions. It is accepted that there is an underlying bias in 16S metagenomic sequencing. Hence, shotgun whole-metagenome sequencing (WMS) is proposed for this study to overcome this bias. Additionally, shotgun WGS generates more valuable insights into the phylogenetic composition, metabolic capacity and functional diversity. The major challenge in using WGS from clinical samples is the large amount of host genetic material present in these samples.

We conducted a preliminary study to examine the effects of four host depletion and microbial enrichment methods on cattle genital tract samples. Soft-spinning and benzonase extraction were shown to be the most efficient host elimination methods, yielding more comprehensive taxonomic and functional profiles for the microbiome in bovine genital tracts than the other depletion methods evaluated.

Effect of feeding different cultivars of *Leucaena leucocephala* on rumen-based in vitro anaerobic fermentations.

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The leguminous forage shrub, *Leucaena leucocephala*, is one of the few nutritional options available to significantly improve beef productivity in Northern Australia. A mixed bacterial rumen inoculum for the detoxification of mimosine (present in *Leucaena*) and its toxic derivatives 3,4 DHP and 2,3 DHP has been produced in an anaerobic fermentor for the last 23 years by the Queensland Department of Agriculture and Fisheries, using the commercial cultivar Cunninghamii. The development and release of a new psyllid-resistant cultivar 'Redlands', offers potential for increasing uptake by the beef industry but brings unanswered questions about its impact on the survival of the toxin degrading bacteria *Synergistes jonesii* and the overall efficacy of the current inoculum. A series of 30-day anaerobic fermentations were undertaken using the same starter cultures used in the production of commercial inoculum but fed daily with one of three *Leucaena* cultivars: Cunninghamii, Redlands or Wondergraze. Populations of *S. jonesii* were monitored daily using a quantitative PCR assay and the ability of the fermentation to detoxify mimosine and its derivatives were assayed on days 10, 15, 20, 25 and 30. Feeding the new Redlands cultivar had a negative impact on *S. jonesii* numbers and the ability to detoxify 3,4 DHP. However, as fermentation time increased, the *S. jonesii* populations adapted to the Redlands cultivar. A follow-on fermentation using a starter culture obtained from Day 30 of a Redlands fermentation, showed an immediate increase in *S. jonesii* populations and was able to detoxify mimosine and its toxic derivatives.

Flight zone as an alternative temperament assessment to predict animal efficiency

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Animal temperament evaluation can be included in the cattle selection program also because of an existing correlation with performance. However, there are different assessment methods such as flight speed (time and speed that an animal takes to leave the crush) and exit score (indicating in which pace it does). Flight zone (FZ) refers to the distance that an animal allows human proximity without signs of fear (e.g. moving away and/or aggression) and it was used in this study as an alternative approach to measure temperament without putting cattle through the crush. Apparently, there is no study correlating FZ with performance. Therefore, a pilot trial was conducted to evaluate the correlation between average daily gain (AVG), dry matter intake (DMI) and feed conversion ratio (FCR) of ten Brahman steers. Steers were classified into temperament groups (Docile ≤ 2 m; Moderate between 2 to 2.9 m; and Lively ≥ 3 m). Even though no significant differences were found for ADG (P=0.65), DMI (P=0.36), and FCR (P=0.46), the docile group gained 133 grams/day more than lively counterparts, most likely because of the extra 50 grams consumed. Furthermore, lively steers required an extra 1 kg of feed per kg of gain in comparison to docile animals, 8.24 vs. 7.28 kg FCR, respectively. These results are promising and indicate that FZ could be an efficient way to measure temperament in cattle. Thus, in order to confirm these findings, a new experiment with a more representative number of steers (n=30) will be conducted.

Milk delivery in tropically-adapted neonatal beef calves

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Across beef breeding herds of northern Australia, poor pre-partum nutrition of cows is consistently associated with increased calf wastage between confirmed pregnancy and weaning. With key nutrients at play (especially energy, protein, phosphorus and water) also being associated with milk yields, a specific problem mediating calf mortality is likely to be low milk production and delivery during the highest-mortality-risk period that is the first week after birth. Recent research demonstrated that milk-deprived newborn calves die of dehydration within 1-3 days. Newborn Brahman and tropical composite calves across three grazing herds (n=75) and two penned herds (n=106) were investigated. Calf milk uptake during the first 1-2 days of life was measured by plasma immunoglobulin (IgG) levels and overall milk uptake and health during the first two weeks of life was measured by growth rate from birth. Grazing calves with average IgG levels of 2247, 2508, and 2656 mg/100mL had respective average growth rates of 0.5, 1.0, and 1.4 kg/d. Penned calves with average IgG levels of 2064, 2498 and 2504 mg/100mL had respective average growth rates of 0.6, 1.0, and 1.4 kg/d. The association between calf immunoglobulin uptake and initial growth demonstrates individual variation between tropical beef calves for early milk uptake and that risk factors limiting milk delivery in the first days of life would place calves at greater risk of poor health and mortality.

Delay in progesterone decline before parturition is connected with failure of passive immune transfer in tropical composite beef calves

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A shortage of nutrients during the final period of gestation can decrease secretion of colostrum, which is critical to newborn calf survival. The physiological mechanism modulating the nutritional control of colostrum secretion is poorly understood. Because the decline in progesterone before parturition is required for lactogenesis to occur, the objective was to evaluate the correlation between prepartum progesterone in cows and plasma immunoglobulin-G1 (IgG1) concentration in neonatal calves. From 135 pregnant cows, successful data on both prepartum progesterone and calf IgG1 was collected from 59 cow/calf pairs. The cow/calf pairs were classified into three categories according to the transfer of passive immunity: low (n=19), medium (n=18), or high (n=22). Plasma IgG1 was 1025, 2395, and 3347 mg/dL for the low, medium, and high groups, respectively. Plasma progesterone 1 day prepartum was 18.3, 14.2, and 12.4 nmol/L for the low, medium and high groups, respectively. This indicates that calves with failure of passive transfer were born from cows with higher prepartum progesterone, compared to calves with high IgG1 (P = 0.05). Non-linear modelling of the progesterone data indicated the moment that progesterone started to decline [change-point]. Change-point was 0.8, 2.5, and 2.4 days before parturition for the low, medium, and high groups, respectively. There was a delay in progesterone decline in the Low group compared with the High group (P ↓ 0.05). These results corroborate the hypothesis that the delay in progesterone decline before parturition is responsible for the failure of IgG1 transfer from cows to calves.

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CLEM (Crop Livestock Enterprise Model) – a bio-economic model simulating changes to the whole of farm

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The Crop Livestock Enterprise Model (CLEM) is a bio-economic farming systems model that simulates the effects of a range of activities on resources at the whole farm scale. CLEM evolved from the IAT (Integrated Assessment Tool) and NABSA (Northern Australia Beef Systems Analyser) models, which have been successfully used in subsistence smallholder crop-livestock systems in developing countries and in large beef production agribusinesses in northern Australia, respectively. CLEM has a similar tree structure to the APSIM Next Generation (Agricultural Production Systems sIMulator) model, runs on a monthly timestep, and is designed to be flexible and easy to use for researchers.

CLEM can be used to examine the long-term production risk and variability of a range of farming systems under different distributions of resources or assets (e.g. crops, fodder, livestock, land, labour or capital), changing climates, or changes to management practices. Examples include improving animal genetics or crop varieties, changing animal nutrition, healthcare and reproduction, or altering fertiliser and tillage regimes. CLEM tracks environmental factors such as water and greenhouse gases as well as physical components such as equipment and products. Current model development is focusing on including human nutrition and food security components, adding non-ruminant (poultry, pigs etc) modules, and accounting for animal diseases. Our poster will illustrate a variety of farming system simulations and show the extent of the simplified output and reporting available.

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DNA testing and genetic evaluation for poll breeding in tropically adapted beef cattle

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In beef cattle, horn management is practiced to physically or surgically remove horns for the safety of animals and workers. However, invasive practices of dehorning and disbudding are a great threat to animal welfare, health, production and human safety, as well as labour intensive and costly. The most effective way to limit the impacts and costs of horns is to prevent their occurrences by breeding naturally polled (hornless) herds. Horn development is complex, although two mutually exclusive genetic variants (Celtic and Friesian) have been found prevalent on each copy of chromosome 1 in most polled cattle. Predicting genotypes in an animal is challenging. Available genetic testing assays were often limited in tropically adapted beef cattle. In this study we present a new optimized poll testing (OPT) assay, which has been bundled with SNP genotyping arrays being used for genomic evaluation in cattle. Breeding schemes can profile future parents for pure-polled stock based on the OPT results. We also evaluated the factors causing complexity in horn conditions. Thus, we coupled OPT predictions with head-status and sex distributions, by modelling genetic and non-genetic impacts, revealing that genetics, sex and sex hormones control horn ontology. Finally, concerns of polledness adversely affecting production and reproduction were investigated by using estimated breeding values of several beef traits. We found no detrimental effects of polledness on production or reproduction. Overall, this research concludes that genetically polled cattle will minimize issues about animal welfare and management costs without reducing production potentials in the tropically adapted beef cattle.

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Proteomics as a potential tool for identifying biomarkers for host resistance to cattle tick

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The cattle tick, *Rhipicephalus microplus*, and the diseases it transmits lead to massive economic losses to cattle industries in tropical and subtropical countries. The emergence of widespread resistance to acaricide drugs and the absence of an effective vaccine for tick control had led to genetic selection of host resistance as a method of choice for non-chemical control of cattle tick. Research to identify host genetic markers associated with tick susceptibility or resistance has been limited to the comparison of local breeds in specific geographic regions. Previous studies have also focused on gene expression profiles, localizing cellular and humoral immune responses, and genome-wide association studies (GWAS) to identify functional genetic variants associated with tick resistance/susceptibility. Given the fact that gene expression results and actual dynamics occurring at the protein level often do not correlate due to post-transcriptional, posttranslational and degradation regulation. Host proteomics may provide reliable biomarkers to assist in selection to support traditional breeding programs. The present study aims to investigate the variation in protein profiles among tick resistant and susceptible cattle following tick infestation. Preliminary findings suggest that different serum proteins exist between tick resistant and susceptible cattle. This research is supported by Meat & Livestock Australia.

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Sequencing *Bos indicus* bulls using long reads to solve the poll locus

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Brahman cattle (*Bos indicus*) are adapted to thrive in tropical environments. Since their introduction to Queensland in 1933, Brahman's ability to grow and reproduce on marginal lands has proven their value in the tropical beef industry. As a result, Australia's Northern beef industry is almost exclusively Brahman or derivatives thereof such as Droughtmaster.

The poll phenotype is characterized by the absence of horns. Horns cause bruising of meat estimated to cost \$22.5 million AUD in Australia annually. Dehorning is a common practice, although leads to an average weight loss of 4.3%. The polled mutation in cattle has been mapped to chromosome 1. The causative mutation, a series of copy number variants (CNV) in other breeds, is not fully characterized in Brahman cattle. The Celtic allele, a 212bp duplication replacing a 10bp segment (P_{212ID}) is thought to be the most likely causative mutation. Oxford Nanopore Technology's (ONT) minION (Figure 2) is reportedly capable of read lengths in excess of 3 Mb, ideal for characterizing CNVs. Results suggest the Celtic allele is responsible for the poll phenotype in Australian Brahman cattle. Sequencing of additional Poll Brahman's is necessary yet to validate this result and ascertain the prevalence of the Celtic allele in the population.

The Brahman Genome: A platinum quality genome for tropical beef production

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Bos indicus cattle, the result of an independent domestication in the Indus Valley, are adapted to harsh tropical environments and are widely used in beef and dairy production in Northern Australia, the southern USA, Africa, Asia and South America. Brahman are a *B. indicus* breed developed in the southern USA through cross-breeding four *B. indicus* breeds: Ongole, Guzerat, Gir and Krishna.

A reference sequence for Australian Brahman cattle has been assembled using 195Gb of Pacbio Sequel long read data, with Chicago and Hi-C long range mapping. Gaps were closed with multiple rounds of PBJelly and error correction performed with Arrow. The resulting genome has all autosomes and the X chromosome at full length, with only 403 unfilled gaps in the entire assembly.

Long read Pacbio sequence data has allowed the examination of genome elements for which short read data is inadequate. In addition to annotations acquired from UMD3.1, the Brahman genome includes annotations of transposable elements, simple sequence repeats and structural variants up to 79,000bp in length. Comparisons between the Brahman and Taurine genomes provide insight into tropical adaptation, an important trait as our environment becomes more variable.

Additionally, methylation, whole length transcript sequences and other long read sequence data reveals that there is substantial within breed variation in epigenetic, expression and structure of the Brahman genome. This information brings provides the northern beef industry a detailed understanding the Brahman genome.

Cassava-based diets increase live weight gain of Cross Bred bulls in small fattening systems in Malang, East Java

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Traditional farmers usually use local feed ingredient based on cheapest ingredients without considering the importancies of feed conversion ratio to maximise cattle growth. The experiment was conducted to determine the growth of crossbred bulls fed on a cassava by product based diet and local concentrate. Fifty cross bred bulls aged of 1.5 - 2 years were used in this study. The bulls were divided into five groups; they were offered 1% and 2% local concentrate (T1 and T2), 1% and 2% cassava-based diet (T3 and T4) and current feeding system (CFS) by farmers (T0) as control. Local concentrate was bought from Blitar while cassava-based diet contained 50% cassava, 25% copra meal and 25% palm kernel cake. No interventions were made to the CFS. However, some farmers in T0 not only used local forages and agricultural by-products such as rice bran and pollard bran as a feed, but they also added local concentrate the same as used by T1 and T2 farmers. The average daily gain were 1.13 kg/head/day (T0), 1.09 kg/head/day (T1), 1.38 kg/head/day (T2), 0.8 kg/head/day (T3) and 1.23 kg/head/day (T4). The study found that local concentrates promoted high average daily gain and that traditional feeding systems (CFS) performed well when farmers saw other farmers feeding better diets.

Key Words: Smallholders farmer, Cross bred, Fattening, Cassava, Concentrate.

Modelling and real-time optimisation of air quality predictions for australia through artificial intelligence algorithm

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Air pollution causes more than 3000 premature deaths in Australia. Annually, this health issue cost Australians \$24.3 billion in public health expenses. This calls for a prompt action to have efficient air quality regulating mechanism. Accurate predictive models are important for regulatory plans for the public and different vulnerable groups such as children, pregnant women and the elderly. A pertinent air pollutant responsible for recurrent health-care costs with increased respiratory induced mortality in Australia is Particulate Matter (PM). In such a pressing public health problem, artificial intelligence can provide promising solution via developing models to obtain predictions through novel learning algorithms. This research project, unique in its own kind, focuses on generating real-time air quality forecasts of PM_{2.5}, PM₁₀ and the overall lower atmospheric visibility. To establish a robust optimisation model, an online sequential-extreme learning machine (OS-ELM), a powerful artificial intelligence algorithm was integrated with improved empirical mode decomposition with adaptive noise (ICEEMDAN) as a data pre-processing tool. The resulting novel data-driven, hybrid predictive model: ICEEMDAN-OS-ELM registers good predictive ability, particularly appropriate for near real-time forecasts of PM_{2.5}, PM₁₀ and visibility at key test sites in Australia. The excellent performance of the OS-ELM hybrid model indicates its suitability as a decision-support systems tool in air quality monitoring, forecasting and subsequent health risk mitigation. Future study aspires to develop robust predictive frameworks in facilitating air quality strategies in mitigating Australia's public health risks in a coordinated way through advanced practical development of artificial intelligence approaches.

High level of energy and protein supplementation effect on feed intake and liveweight gain of Bali bulls fed elephant grass

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This research was carried out on-farm at Malonas village, Central Sulawesi, Indonesia to examine the effect of high level supplementation of by-products formulated for high ME and CP. Feed intake, faecal pH and liveweight gain of Bali bulls was observed. The basal diet was elephant grass, and supplements were rice bran (RB), cassava (C), palm kernel meal (PKM), gliricidia (G) and urea.

Fifty Bali bulls (weight 168±4.48 kg) were housed in individual pens for 18 weeks (2 introductory and 16 experimental) and allocated into five treatments: A= elephant grass (EG) *ad libitum*, B= EG offered at 1%W/d, plus 2.5%W/d mixed RB:G, (1:1), C = EG offered at 1%W/d plus 2.5%W/d mixed RB:PKM(1:1), D = EG offered at 1%W/d plus 2.5%W/d mixed C:G (1:1), E = EG offered at 1%W/d plus 2.5%W/d mixed C+urea: PKM (1:1). Faecal pH was measured at weeks 3, 9 and 15.

Bali bulls fed B, C, D and E, consumed supplement at the rate of 2.15, 2.19, 2.09 and 2.29 %W/d, respectively. Total feed intake was 2.47, 2.98, 2.99, 2.93, 3.13%W/d, liveweight gain was 0.30, 0.57, 0.60, 0.66, 0.69 g/d and faecal pH was 6.93, 6.76, 6.65, 6.45, 6.33 for treatment A, B, C, D, and E, respectively. Supplementation increased significantly (P<0.05) total feed intake, liveweight gain, but reduced faecal pH. The highest total feed intake and liveweight gain was achieved by treatment E. It is concluded that cassava can be provided at 1.15%Wd in combination with protein supplement for high liveweight gain of Bali bulls.

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A multiplex molecular assay for *Glaesserella australis*

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Isolates of a new bacterial species, unofficially named *Glaesserella australis*, have been collected from the abattoir and from sick pigs at the farm at the ages of 12 to 20 weeks. Isolates isolated at the abattoir had lesions very similar to those caused by *Actinobacillus pleuropneumoniae*, prompting an investigation to determine the prevalence of this species. For this investigation, a multiplex PCR was developed that can identify *G. australis*, *A. pleuropneumoniae* and *Pasteurella multocida*, all bacterial species that are observed in pigs in the age bracket this new species was discovered. This multiplex has been validated on pure cultures.

A total of 26 isolates of *G. australis* including the candidate type strain and field isolates were used. Isolates of the other two species in this PCR were also tested with 15 reference serovar strains and one field isolate of *A. pleuropneumoniae* and 16 reference serovar strains plus the type strain of *P. multocida*.

To assure specificity, 47 related species including type strains and field isolates were tested in the PCR.

All the *G. australis*, *A. pleuropneumoniae* and *P. multocida* reference, type and field strains were correctly amplified by the PCR. The PCR did not amplify any of the related strains/isolates.

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Assessing the value of whole genome sequence data in selecting for age at puberty in tropically adapted beef heifers

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Age at puberty has been shown to be heritable in tropically adapted beef breeds, but it is both a difficult and expensive trait to measure. Studies have shown that genomic selection may be used to select for age at puberty, however, the accuracy of selection has been low. In this study, we investigate whether whole genome sequence (WGS) genome wide association study (GWAS) results can be used to improve the accuracy of selection for age at puberty using various methods of single nucleotide polymorphism (SNP) inclusion and different densities of SNP panels. Our results, in large cohorts of tropically adapted beef cattle, demonstrate that the use of WGS data in the genomic prediction of age at puberty in a multi-breed population can improve the accuracy of prediction of GEBV in comparison to high density SNP panels alone, in some cases, particularly for low density panels.

Identification of *Lonepinella*-like species in oral cavity of koalas using housekeeping gene for phylogenetic analysis

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The current taxonomy of genus *Lonepinella* under the *Pasteurellaceae* family is not well-studied or defined, with the only current species being *Lonepinella koalarum*. *L. koalarum* was first described based on isolates obtained from the faeces of koalas. *L. koalarum*-related isolates were found in faeces and oral cavity of koalas, as well as, in koala bite wound infections in humans. A number of possible *Lonepinella* isolates was recently encountered while sampling koalas as part of a project looking at the presence of *Pasteurellaceae* in the oral cavity of marsupials. In this current exploratory study, isolates collected in the previous study from koalas at different wildlife centres in Australia were further investigated using amplification and sequencing of the housekeeping gene, *recN*. A total of 23 isolates fitted the basic phenotypic criteria and were included in the molecular analysis. The sequence data of the isolates were analysed and used to produce a phylogenetic tree. The results show that two out of the 23 investigated isolates were highly similar (99% identity) to the *Lonepinella*-like bacteria responsible for causing wound infections by koala bites in humans. None of the investigated isolates appeared to be closely related (ranging from 57% to 85% identity) to the *L. koalarum* type strain. However, the investigated isolates formed four different clusters consisting of two, three, seven and seven isolates respectively. The results of this study strongly suggest that three clusters represent novel taxa, possibly new species within *Lonepinella*, or even a novel genus in the *Pasteurellaceae* family.

Development of a bead based molecular serotyping assay for *Glaesserella parasuis*

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Multiplex PCR serotyping assays are problematic when multiple serovar specific bands need to be recognised to differentiate serovars. To overcome this problem, a bead-based multiplex assay was used to differentiate the 15 serovars of *Glaesserella parasuis*. The assay consisted of a multiplex PCR assay followed by hybridisation to XMAG beads which were then analysed on the Luminex machine. The assay was compared to the conventional multiplex serotyping PCR and traditional phenotypic serotyping. The bead-based assay worked very well for the reference strains but when used on the Australian field isolates displayed some problems. One of the main problems was with the serovar 4 field isolates and to some extent the serovar 7 and 14 isolates. The advantage of the bead-based PCR was the ability to differentiate between serovar 5 and 12 which the conventional multiplex PCR could not. Serovar 4 has been noted to have a high diversity and that isolates from different countries are very diverse. This indicates that the diversity of isolates has to be taken into account when developing a molecular assay. It may be necessary to have assays that are specific for the diversity present in specific geographical regions.

Modelling the controlled release of toxins in a rumen environment

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Pimelea poisoning in grazing cattle, also known as St George or Marree's disease, has been a long-time pestilence for the pastoral industry throughout arid regions of inland Australia. The causative species *Pimelea* (Thymelaeaceae), native to Queensland, New South Wales and South Australia, have been confirmed, with the secondary metabolite simplexin, a daphnane orthoester, being extracted and identified as the principal toxin. Despite the lack of effective prevention or treatment for Pimelea poisoning, naïve calves have previously been demonstrated to develop detoxification capability following prolonged low-dose simplexin intake. A variety of composites are being fabricated by encapsulating *Pimelea* plant material or a crude extract in biodegradable and biocompatible polyesters, aiming to develop a sustained toxin release mechanism. Studies on screening potential rumen microflora able to decompose simplexin during rumen-fluid fermentation are being conducted simultaneously. In this project, a quantification method for simplexin within these biocomposites was developed and validated utilising solid phase extraction combined with UHPLC-Q-Orbitrap MS/MS. Reliable simplexin measurement in matrices will allow investigations into the material composition, geometry and rumen microorganism's effects on the controlled release kinetics of simplexin *in vitro*. The degradation patterns of toxin delivery systems when exposed to simulated rumen environments will also be thoroughly assessed on both microscopic and chemical scales. Mathematical models of the underlying mass transport mechanisms will ultimately be established through approaches ranging from simple empirical correlations to stochastic simulations, which hold the potential to facilitate future design, optimisation, and prediction of other intra-ruminal devices based on biodegradable polymers.

Nutritional composition of solid-state fermented camelina meal (an enriched protein source for broiler chickens)

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Camelina (*Camelina sativa*) also known as false flax or gold of pleasure is an oilseed crop of the Brassica (*Cruciferae*) family. Camelina is not a food crop, however, the by-product (meal or cake) obtained from the pressing of camelina seeds is useful as animal feed because of its moderate crude protein content. The dietary use of camelina meal in broiler diets is limited to low inclusion due to the presence of anti-nutritional factors such as fibre, phytic acid, glucosinolates and tannins which have negative effects on broiler performance. Solid-state fermentation (SSF) is a suitable processing method for enriching agroindustrial by-products since it offers several cost-effective and practical advantages. In the present study, the effect of SSF on the nutrient composition, phytic acid and total phenolic contents of expeller-extracted camelina meal was evaluated. *Aspergillus ficuum* (ATCC 66876) was used for SSF under aerobic conditions at 30°C for 7 days. Raw and fermented camelina meals were analyzed for dry matter, crude protein, crude fat, crude fibre, total sugar (sucrose) and starch as well as for pH, phytic acid and total phenolic contents. Crude protein was improved by 6.79% while total sugar and starch were reduced by 90.99% and 75.78%, respectively in the solid-state fermented camelina meal. Phytic acid and total phenolic contents were also decreased by 39.17% and 56.11%, respectively. This study revealed that SSF could be used to improve the nutritional quality of camelina meal for improved use in poultry feed formulation.

Near infrared spectroscopy reflectance (NIRS) to evaluate seasonal relationship between crude protein and digestibility of forages

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Understanding forage quality is key to meeting the nutritional needs of ruminants, for optimal performance, efficiency and profitability of livestock systems. The objective of this study was, to analyse the seasonal relationship between crude protein and digestibility concentrations of forages, using the near infrared spectroscopy technique (NIRS). Forage samples were collected from seven properties, each having four randomly selected paddocks. Herbage consisted of mixed pasture, Lucerne, grazing wheat, oats, rape and vetch. The interaction between crude protein and digestibility of forages across seasons was determined for dried samples. A quadratic model was fitted and the relationship between crude protein and digestibility based on seasons was significant at $p=2.2e-16$, $r=54\%$ and $se=7.8\%$, expressed by the equation $D=bx^2+cx+d$. The relationship between crude protein and digestibility was linear in winter and expressed as $-57.93CP^2+146.55CP+58.63$. While in spring, summer and autumn, relationship was quadratic, expressed as $-57.93 CP^2+146.55CP + (58.63+3.70)$; $-57.93 CP^2+146.55CP + (58.63+2.27)$ and $-57.93 CP^2+146.55CP + (58.75+1.53)$. Digestibility was predicted to be 59% in winter and for every 1% increase in digestibility, crude protein increased by 1.5% in autumn, 3.7% in spring and 2.3% in summer. All assumptions made in fitting the model were met and results predicted forage quality across seasons, however interactions may be influenced by other factor unaccounted for in this study.

Association of thermotolerance with milk production, feed saver, fertility and fat percentage breeding values in Holstein Friesian dairy cattle

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In Australia, heat waves are becoming hotter and longer, and more frequent, compromising dairy cattle welfare and productivity. Selection for heat tolerance (HT) may help to ensure sustainability of production under hot summer conditions. In a study at the University of Melbourne's Dookie Robotic Dairy Farm, we identified the 20 most heat-sensitive and 20 most heat-tolerant cows in a herd of 150 Holstein Friesian lactating cows based on phenotypic responses (increase in body temperature, panting score, and decline in milk production) of dairy cows grazing pasture and given concentrate at milking during hot summer conditions for 3 months. Hair samples were collected from the tip of the tail according to a standard protocol for genotyping (Zoetis). Results based on 36 successfully genotyped cows indicated a significant variation in feed saved (FS) genomic estimated breeding values (GEBVs) across age indicating a potential for its selection. The thermotolerant group had relatively higher GEBV for FS and fat% but lower milk production potential. Highly significant ($P \leq 0.05$) negative correlations (-0.39 to -0.69) were observed between heat tolerance and current dairy industry economic indices (Balanced Performance Index (BPI), Type Weighted Index (TWI), Australian Selection Index (ASI) and milk production), while positive correlations exist between HT and feed saved (0.44) and fertility (0.27). These findings indicate a positive association between HT and feed saved, fertility, and fat percent breeding values. However, a more extensive study including large number of lactating cows is required to confirm these genomic associations and incorporating in future breeding objectives.

Impacts of heat stress on the physiological and production responses of lactating dairy cows grazing pastures over hot summer months

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Heat stress (HS), a major challenge for sustainable livestock production justifies the need for productive thermotolerant cattle. We measured body temperature (non-invasively using a FLIR T1200 thermal imaging camera), respiratory rate and panting scores of 120 Holstein Friesian cows at the University of Melbourne Dookie Dairy Farm weekly during the summer period (December 2018-February 2019). The effect of Temperature-Humidity Index (THI) on milk production, protein content, fat content was also measured. We categorized THI as low (≤ 72), moderate (73-82) and high (≥ 83) and observed a highly significant ($P \leq 0.01$) effect of THI on respiratory rate (66.7, 84.7 and 109.1/min), panting scores (1.4, 1.9 and 2.3) and average body temperature of cows (38.4, 39.4 and 41.5). Average milk production parameters were also significantly ($P \leq 0.01$) affected by THI: daily milk production dropped by 14% from high to low THI, milk temperature and fat% increased by 3% whilst protein% increased by 2%. Highly significant ($P \leq 0.01$) positive correlations were obtained between THI and milk temperature, fat% and protein% whilst the reverse was observed between THI and milk yield, feed intake and rumination minutes. Under moderate and high THI, most cows sought shade, spent more time around watering points and showed signs of distress (excessive drooling and open mouth panting). These findings clearly indicate that lactating dairy cows grazing summer pastures experience severe HS compromising their welfare. The quantum of production losses, though significant may however be lower than previously reported in studies using climatic chambers.

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Impact of innovative non-thermal technologies on anti-nutrient levels and functional properties of wattle seeds

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The Wattle plant, generally known as *Acacia spp.*, is an indigenous Australian legume with the seeds from up to 40 species commonly consumed by Aboriginal people in Australia. Wattle seeds (WS) are rich in nutrients particularly, protein and dietary fiber. However, the seed contain several anti-nutritional compounds such as trypsin and chymotrypsin, which if not removed through appropriate processing could reduce the absorption of other nutrients.

Thermal treatment (roasting, dry heating, boiling and autoclaving) can effectively reduce the levels of anti-nutrients in WS. However, the high temperature applied can denature the protein of WS, which may affect the functional properties of the protein thereby limiting its use as functional ingredients in foods. Moreover, traditional non-thermal methods such as soaking and germination are not sufficiently efficient to lower the anti-nutrient contents in WS.

In order to minimize this effect, innovative non-thermal technologies that can effectively reduce the anti-nutrient levels in different varieties of WS and also minimize the loss of the native structure of the protein will be presented. This information will enhance the production of WS protein that is both safe for consumption and that exhibits functional properties for potential use in food formulations.

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Women empowerment and poverty reduction in rural Okara, Punjab Pakistan

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In Pakistan, women have limited access to credit, property, education, skill, paid job and land. There are many hindrances in women empowerment in rural such as socio-economic and cultural values, norms, patriarchal structure of society. Research was planned to analyze different determinants of empowerment of rural women for poverty reduction in agrarian communities by taking the case study of rural Okara, Pakistan. Multistage random sampling technique was used for data collection at different stages. Okara was selected through simple random sampling technique and four union councils and then eight villages were selected randomly. Twenty five from each village were selected through convenient sampling thereby making total sample size of 200 women. Most important finding of the study that the households where women have higher decision making authority are better-off and in other words women empowerment is likely to reduce poverty and increase wellbeing. The results also revealed significantly positive relationship between women age, education, decision making authority and paid work involvement with empowerment and poverty reduction. It is also concluded that education is the most important factor in empowerment but majority (64.5%) of respondents had only up to 5 year education. Respondents had very limited decision making authority and control over economic resources mostly significant and important decisions and resources are controlled by the male members. Though rural women have great contribution in poverty reduction but majority of them were facing the problems of low education, wages, less control over resources, freedom of mobility and lack of decision making authority.

Determinants of food inflation in Pakistan: Empirical evidences

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Today food inflation is a rising issue. The world food problem is getting more complicated as the world population is increasing more rapidly than food production. Pakistan being a developing country is a victim of higher food prices. The present study is an attempt to identify main determinants affecting food inflation in Pakistan. The study is based upon the time-series data from 1997 through 2017, collected from secondary sources including published issues of Economic Survey of Pakistan, Agricultural Statistics of Pakistan and annual reports of State Bank of Pakistan. Method of OLS (Ordinary Least Square) was applied by developing an equation for food price inflation and five major determinants; food imports, food exports, wheat support price, value-added in agriculture and money supply respectively. These variables were regressed with CPI (Consumer Price Index) food, the measure of food inflation. The results indicated that agricultural value addition is highly significant and negatively affecting the food inflation while Food imports have most significant positive effect on food inflation. Supply of money in the country and wheat support price are effecting food inflation significantly. The study suggested that increase in agricultural output and tight monetary policy are the key factors to decrease food inflation. The government should adopt measures to improve the productivity of agricultural sector, encourage agro-based industry, moderation in government administered price and should control the supply of money in the country.

Key Words: Determinants, food inflation, inflation, Pakistan

Dubai Municipality initiative to reduce food loss

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Food imports are the main source of food in the Emirate of Dubai. Imported foods are monitored through the ports of entry by the competent authority of the Dubai Municipality. If food consignments meet Dubai Food Safety Department requirements, consignments are allowed to enter. However, if the consignments do not meet requirements, the consignment will be refused entry. Previously, consignments not meeting requirements were confiscated and sent to the Dubai landfill. In addition to that, when food traders held large quantities of stock that was approaching its expiry date, Dubai Municipality previously allowed this food to go to landfill. Now, with a new initiative to reduce negative environmental impacts, the Dubai Municipality has developed new solutions to minimize the quantity of food going to landfill. Food loss has been diverted to the Emirates Food Bank, recycling or to animal feed, resulting in a 93% reduction in food loss over 3 years.

In 2018, food recycling reached 5.4 tons with approximately 679 tons of food being diverted to animal feed, and 2.3 tons of food being sent to the UAE Food Bank after ensuring that it was fit for human consumption.

This new program has significantly reduced the amount of food going to landfill. The Dubai Municipality has also clarified the requirements of importing food to Dubai and developed a training program for importers to reduce food waste at points of entry.

Screening of probiotic lactic acid bacteria and prebiotics to select for effective synbiotics

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One of the popular functional foods available in the market has been probiotic-fermented milks. The activity and the survival of the probiotic bacteria in fermented food may improve by the addition of prebiotics. The aim of this study was to evaluate the potential prebiotic effects of kakadu plum (KP), Fructooligosaccharides (FOS), Inulin, arabinose, rhamnose and galacturonic acid on selected probiotics in milk samples. Four *Lactobacillus* strains, *Lactobacillus rhamnosus* GG, *Lactobacillus plantarum* 299v, *Lactobacillus acidophilus* ATCC 4356 and *Lactococcus lactis* 537 were cultured anaerobically for 24 h in UHT skim milk containing 3% (w/v) arabinose, rhamnose, KP, inulin and FOS. Their growth and milk pH were determined at 0h and 24h of the incubation period. The viability of the two strains, *Lactobacillus acidophilus* ATCC 4356 and *Lactococcus lactis* 537 were determined after 12 days of storage at 4°C in the presence of three different concentrations 1%, 2% and 3% of prebiotics. In general, the growth of the strains was improved in UHT skim milk supplemented with KP. The pH of UHT skim milk ranged from 6.37 (*Lactococcus lactis* 537 with rhamnose) to 4.07 (*Lactobacillus plantarum* 299v with KP) after the incubation period. The viability was enhanced with the addition of some prebiotics, and a higher viability was observed when both strains were grown in the presence of 3% prebiotics compared to 1% and 2% of the prebiotics. The findings of the study clearly show that the growth and the survival of lactobacillus strains in prebiotic fermented milk were strain specific.

A systematic approach to defining nutritional quality of underutilised crops

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Underutilised crops contribute only marginally to global food and nutritional security, despite their regional nutritional, economic and cultural significance. Their potential to make a greater contribution is often overlooked, in part due to the scarcity of data reflecting the range of nutritional variation. Bambara groundnut (BG; *Vigna subterranea* (L.) Verdc.), a pulse native to West Africa has been proposed as an exemplar underutilised crop. We analysed variation in the major nutritional components of 98 BG accessions of diverse geographical origins, and compared these values with representatives of four related pulse crops. We found considerable intra-species variation for major components: 13.8 - 26.4% protein, 4.6 - 8.2% oil, 0.9 - 12.9% total dietary fibre, and 47.8 - 71.4% available carbohydrate. The range in seed protein and oil concentrations were comparable to that measured in chickpea and mungbean. Linoleic (C18:2, n-6) accounted for up to 48% of total fatty acids in BG seed oil, and oleic (C18:1, n-9) up to 28%, with palmitic (C16:0) representing the other major component. Principal component analysis indicated that oleic, behenic (C22:0) and lignoceric (C24:0) acids are strongly associated with seed oil concentration. These data were obtained from material where there has been no systematic selection for enhancement of nutritional composition. The range of variation suggests that there is potential within the genepool to develop distinct sets of high-protein, high-oil cultivars. With the addition of more detailed genomic information, this could follow similar breeding approaches that have been successfully adopted for crops such as cowpea and soybean.

Kakadu plum (*Terminalia ferdinandiana*) - a native Australian fruit with functional properties

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Kakadu plum (KP), a native Australian fruit, is a rich source of vitamin C, minerals and phenolic compounds. A better understanding of the (phyto)chemical composition and biological properties of KP will facilitate the development of functional KP products for the food, pharmaceutical, nutraceutical and cosmetic industry. KP is usually harvested wild and hence, its composition and functional properties may vary considerably depending on the cultivar, maturity, environmental conditions as well as post-harvest treatment. The present study aimed to assess the levels of ascorbic acid (AA) and ellagic acid (EA), the main bioactive compounds in KP, in a commercially available freeze-dried KP powder. The functional properties of a polyphenol-enriched extract obtained from this product were also evaluated. AA and EA were quantified by UHPLC. The polyphenol-enriched extract was tested for in vitro antioxidant and antimicrobial properties using the DPPH radical scavenging assay and Agar well diffusion, respectively. Total AA content in the freeze-dried powder was 200 mg/g dry weight (DW) and total EA was 4.66 g/100 g DW. The polyphenol-enriched extract had a high DPPH radical scavenging capacity and strong antimicrobial activity against methicillin resistant *Staphylococcus aureus*. Our findings demonstrate that AA and EA, the main bioactive compounds in KP, are retained at high levels in the freeze-dried fruit powder. Furthermore, the polyphenol-enriched KP extract has the potential to be used as a natural preservative in the food industry due to its strong antioxidant and antimicrobial activity.

Exploring the nutritional and functional properties of two understudied Australian endemic plants: *Diploglottis bracteata* and *Syzigium aqueum*

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Despite the growing national and international interest for Australian traditional plant foods, information on nutritional and functional properties of many endemic species is limited. This restricts their incorporation in food, beverage and nutraceutical applications. This pilot study explored the phytochemical profiles and antimicrobial activity of two Australian endemic fruits: *Diploglottis bracteata* and *Syzigium aqueum*, to explore their marketability.

Profiling of major bioactive phytochemicals showed the presence of 3 anthocyanins in *S. aqueum* (delphinidin-3-glucoside, cyanidin-3-glucoside and peonidin-3-glucoside) and four carotenoids in *D. bracteata* (lutein, zeaxanthin, β -cryptoxanthin and β -carotene). The total carotenoid content was comparable to that of orange coloured carrots, an important dietary source of carotenoids.

Elemental analysis revealed that, compared to blueberry (a popular dietary source), *D. bracteata* had 4.5 times higher potassium, and 3.7 times higher magnesium content. Calcium levels of *S. aqueum* was 4.9 times higher than blueberry.

Methanol, acetone and water extracts of both fruits were analysed for total phenolic content (TPC) and antimicrobial activity. TPC of *D. bracteata* and *S. aqueum* methanolic extracts were 2.9 and 1.4 mg gallic acid equivalents/g FW which is in the same range as blueberry, a popular dietary source of bioactive phenolic compounds.

Antimicrobial analysis showed methanol, acetone and water extracts of both fruits have strong inhibitory effects against both Gram positive (*Staphylococcus aureus*) and Gram negative (*Escherichia coli*) bacteria, but no effects against fungi (*Candida albicans*).

These promising initial results, diverse phytochemical profiles and strong antibacterial activity, warrant further investigation.

Speciation and bioavailability of Zn in sweetcorn and maize kernels at different maturity stages

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Understanding the speciation of Zn in edible parts of crops helps identify the most effective biofortification strategies that will increase the supply of nutrients for improving the health and nutrition of consumers. Kernels of twelve sweetcorn and three maize (*Zea mays*) varieties were analysed for Zn concentration and content. The Zn speciation in the embryos, endosperms and whole kernels at 21, 28 and 56 days after pollination (DAP) was examined for each of a maize and a sweetcorn variety using synchrotron-based X-ray absorption spectroscopy. Averaged across all sweetcorn and maize varieties at 21 days after pollination, the embryo contributed 27% of the whole kernel Zn and endosperm contributed 73%. While sweetcorn embryos represented a consistently lower proportion of kernel Zn than in maize, the proportion of total Zn in the embryo increased as kernels aged for both varieties. On average, 90% of the Zn in the embryos was Zn-phytate, while in the endosperm, the Zn was present mainly as Zn complexed with a N-containing ligand. However, for maize, as the kernel matured, the proportion of Zn present as Zn-phytate increased, indicative of decreasing bioavailability. It is estimated that a single cob of sweetcorn or maize can only provide ↓10% of the recommended daily Zn intake. Greater biofortification effort is needed to improve these crops as a source of important human dietary Zn.

Source-sink dynamics influence sweetcorn kernel Zn concentration

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Nutrient concentration and yield in crops are usually inversely correlated. Understanding this relationship underpins biofortification efforts that aim to identify potential parents with superior nutrient accumulation capacity for selective breeding. Sink size, expressed as kernel number per cob was manipulated by controlling the time when the silks of 14 sweetcorn (*Zea mays*) varieties were exposed to pollen. The concentration of Zn in embryo, endosperm and whole kernel tissue was determined. Results showed that within varieties, kernel Zn concentration decreased as kernel number increased. However, total Zn accumulation per cob increased with kernel number since the small decrease in Zn concentration was more than offset by the large increases in kernel number. Across the 14 varieties, kernel number and Zn concentration were also inversely correlated. A subset of four varieties were identified as good accumulators of kernel Zn as they expressed higher Zn concentration than expected at a given kernel number. However, the relative distribution of kernel Zn between embryo and endosperm tissues was independent of kernel number. In conclusion, source-sink dynamics resulted in significant decreases in kernel Zn concentration with increasing kernel number, as more kernels competed for a limited pool of Zn distributed to the cob.

A new method for the authentication of Australian honey

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The honey bee industry in Australia is small but has a big impact. Alarmingly it was recently reported that an international laboratory specialising in honey authentication found that almost half the 28 blended and imported honey samples selected from Australian supermarket shelves were “adulterated”.

The Official method of honey analysis (AOAC 998.12) is based on the stable-isotope ratio mass spectrometry analysis of $\delta^{13}\text{C}$ value of honey/ $\delta^{13}\text{C}$ of honey protein to detect the addition of C₄ plant derived sugars, such as cane sugar or high fructose corn syrup. This test is used as the primary C₄ sugar adulteration test around the world, but honey derived from some Australian plants, particularly Manuka (*Leptospermum* species), fail this test.

Our research aims to examine the characteristics of Australian honey and develop a honey analysis test that is fit for purpose, particularly where honeys derived from *Leptospermum* species are concerned. We have focused on the isotopic values of “proteins” precipitated using the standard AOAC method and “proteins” precipitated after incorporation of a further modification step which removes insoluble material (including pollen) from the honey before precipitation. Our modified method also includes analysis of different isotopes of the precipitated protein, sugar profiles and Manuka markers. A key advantage of the proposed method modification is that it does not preclude the detection of residual sugar feeding of bees or extension of honey with C₄ sugar. This proposed modification to the AOAC test will reduce false identification of C₄ sugars and improve the overall reliability of honey authentication.

Dietary alternative protein sources modulate intestinal microbiota and its relationship with apparent nutrient digestibility in farmed yellowtail kingfish *Seriola lalandi*

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Replacement of fishmeal (FM) by alternative protein sources is one of the key to sustainable aquaculture development. The present study aimed to investigate the effect of alternative protein sources on intestinal microbiota and analyzed its relationship with apparent nutrient digestibility in farmed yellowtail kingfish *Seriola lalandi*. Two 4-week trials were conducted to evaluate 8 protein sources including fish meal (FM), two sources of poultry by-product meal (PBM-1 & PBM-2), blood meal (BLM), faba bean meal (FBM), corn gluten meal (CGM), soy protein concentrate (SPC) and wheat flour (WH). Intestinal microbial community was characterized by high-throughput sequencing of V3-V4 hypervariable region of the 16S rRNA gene. The apparent nutrient digestibility were determined using yttrium oxide (Y_{203}) as the inert marker. The greatest change in the microbiome occurred in fish fed diets containing CGM and BLM, characterized by a reduction of Chao-1 diversity index and a clear differentiation in the intestinal microbial populations ($P < 0.05$), which associated with low apparent nutrient digestibility of these dietary alternative protein sources. Additionally, *Proteobacteria* phylum, *Vibrio* and *Clostridium* genera were positively whereas *Enterobacteriaceae* family and *Ralstonia* genera were negatively correlated with protein and energy digestibility. Taken together, these findings suggest that the inclusion of CGM and BLM had negatively affected the intestinal microbial community which could be one of the reasons for the reduced digestibility of those protein sources. We also demonstrated that there is a relationship between intestinal microbiota and apparent nutrient digestibility, this suggests that manipulations of microbial population can improve digestibility.

Optimizing the antimicrobial activity of Tasmanian pepper leaf oil emulsion as a natural preservative for capsicum

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The aim of this study was to produce and optimize Tasmanian pepper leaf (*Tasmannia lanceolata*; TPL) oil contained emulsion using sonication and Response Surface Methodology (RSM). Encapsulating hydrophobic bioactive components is influential in enhancing their applicability as well as their respected antimicrobial activity. The antimicrobial activity of investigated emulsions was evaluated through well diffusion assay against four different spoilage microorganisms isolated from fresh-cut capsicums. In order to optimize the preservative emulsion for further in vivo application, Box-Behnken design with three factors of TPL oil, Tween 80, and citric acid was used. According to the results, bacterial and fungal growth inhibition activity of the investigated emulsions was enhanced through increasing the concentration of citric acid and TPL oil, respectively. Optimization of the investigated variables was conducted after model fitting according to desirability function of Design Expert software. Our main goal was to obtain the maximum inhibitory effect against microbial growth. Therefore, the calculated optimum values were TPL at 1.08%, Tween 80 at 0.15%, and citric acid at 1.50%, with the desirability of 0.978. By and large, the susceptibility of yeast (i.e. *Rhodotorula diobovata*) against TPL contained emulsions showed to be the highest, which was followed by mold (i.e. *Alternaria* sp.), Gram-positive bacteria (i.e. *Bacillus subtilis*), and Gram-negative bacteria (i.e. *Pseudomonas viridiflava*), with predicted inhibition zones of 46.41, 33.03, 13.10, and 11.33 mm. Optimized emulsion using Box-Behnken design is capable of inhibiting the growth of spoilage microorganisms in capsicum, and this understanding can help develop a natural-based preservative for fresh-cut capsicum.

Measures with a human-centred design approach to increase the effectiveness of washing vegetables in Cambodia

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Before consumption, most vegetables need to be washed, since they are grown near, or in the ground. This, and the inadequate use of composted manure, general hygiene, presence of animals etc. leads to increased risk of microbial and parasite contamination, especially in countries like Cambodia.

Traditional washing systems use small bowls or washing in ponds on farms, which adds unacceptable risks of contamination. Washing in non-potable water or using the same water for large volumes of product also increases contamination. To counteract the problem of washing in unsanitary environments, we have developed and tested a prototype washing table with four sinks and shower systems at the start and end.

For further refinement, a human-centred design (HCD) approach was taken in collaboration with iDESIGN (iDE). HCD is based on the concept of involving those who are to use the solution, by hearing what their needs, aspirations, barriers and motivations are, then creating a variety of possible ideas, which can be quickly tested on simple prototypes and then developed through a series of designs. For the CQH project a stainless steel washing table was designed. The table has five washing and rinsing steps which have been shown in several washing trials to reduce bacterial and parasite loads.

The table is already being used by four commercial partners involved in the project to wash their produce before entering the market. This system makes the use of the washing system a cost-effective option towards safer vegetables in Cambodia and other developing countries.

Roadmap for researchers studying northern Australian endemic plant foods

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This review and roadmap analyses policies, approval requirements and laws that food scientists need to comply with to study endemic plant foods from northern Australia. Australia contains many endemic plants that have been used as foods by Australian Indigenous people which are largely unstudied by modern food science. The aim of this study was to provide a review and concise summary of the legal, policy and approval requirements that food scientists must follow and obtain to be able to collect and study these plant foods. These include upholding the rights of Indigenous peoples as outlined in the *UN Declaration of the Rights of Indigenous Peoples*. Complying with International treaties including the Convention on Biological Diversity, the *Convention on International Trade in Endangered Species of Wild Fauna and Flora* (CITES) and the *International Treaty on Plant Genetic Resources for Food and Agriculture*. Following the relevant Queensland, Northern Territory and Western Australia state government laws and the Commonwealth government laws. The relevant ethics guidelines, their main themes and the approvals required are outlined. This roadmap clarifies for scientists and policymakers current requirements so that research into these valuable, unique and exciting plant foods can take place.

Analysis of environmental contaminants in Australian honey and comparison to stingless bee honey from Queensland and Malaysia

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Honey is a widely available natural sweetener containing sugars, and small quantities of vitamins and minerals, proteins, amino acids and fatty acids. Owing to its nutritious components, commercial honeys are sold in bulk blends or as trendy and premium products. Meanwhile, honey bees are considered as environmental monitors and have the potential to transfer environmental contaminants, if present, to honey. In high density urban and industrial environments polycyclic aromatic hydrocarbons (PAHs) and heavy metals can be prevalent, whilst pesticides and mineral and trace elements are ubiquitous. Honey hives are traditionally located in rural and forested areas, but there is a growing trend to locate hives in urban areas. This project has investigated the presence of environmental contaminants in honey samples from high density urban, peri-urban as well as rural areas.

Australian honey samples (n=211) were purchased between 2016 and 2018, including 52 honeys claiming to be of urban origin purchased online. Stingless bee honeys (n=36) from Queensland and Malaysia were compared. Processed samples were analysed by UHPLC-MS/MS (herbicides), GC-MS/MS (pesticides and PAHs) and ICP-MS and ICP-OES (elemental analyses). The results showed low or negligible pesticide, herbicide, and PAH contamination, and that these low results were similar regardless of urban or rural origins. Wide variations of essential trace element (Fe, Zn, Cu, Mo, Co, Mn, Cr) and mineral levels (K, Na, P, Mg, Ca) were found in honey products, which are a good dietary source of K and Zn. Relatively low levels of toxic heavy metals were found in honeys.

Proteogenomics: An approach to integrate OMICS data for exploring functional genes responsible for stress tolerance and wax quality in Jojoba

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In recent years, emergence of new genomics technologies such as DNA long reads have provided a great potential to sequence and explore new genes responsible for many agronomic and breeding traits of importance. Other technologies such as RNA-Seq have facilitated the expression analysis of genes in contrasting environments, leading to recognition of many novel genes. Most of these robust techniques have been applied to the human genome, where they produce very large datasets. They generally include thousands of functional genes and SNPs, many of which do not express at the protein level. Moreover, they may create modified isoforms or protein complexes at the post-translational stage, which cannot be linked to the reference genome. However, after using all of these high-throughput technologies, the main question may still exist. Which gene or cluster of genes have had higher impact on plant phenotype and trait of interest? Proteogenomics analysis has facilitated integration of genomics, transcriptomics and proteomics data, by which a funnel shape workflow can be established to prioritise the genes responsible for traits of interests. In this study, we show development of a bioinformatics approach to integrate genome, transcriptome and proteome (metabolome and other Omics) data in Jojoba plant. This approach can prioritize genes and SNPs affecting traits (Phenotype). It also can annotate and predict novel genes/proteins that may not be recognised through any Omics individually. The workflow and tools in this study can be applied to any other plant species.

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The effect of post-harvest storage on the physicochemical properties and phytochemical content of Queen Garnet Plum

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The Queen Garnet Plum (QGP), a cultivar of Japanese plum (*Prunus salicina* Lindl.) was developed as a high anthocyanin plum in a Queensland Government breeding programme. Anthocyanins have been associated with various health attributes, including diabetes control, cardiovascular disease prevention and anti-inflammatory activity. This study was aimed at identifying the changes in physicochemical properties and important phytochemicals of QGP when stored under two storage temperatures. QGP from two growers were stored at 4 and 23°C for 0, 4, 7, 10 and 14 days. At the end of each storage period the peel, outer flesh (up to 7 mm from the peel) and inner flesh were separated and analysed for chroma, total soluble solids (TSS) and titratable acidity (TA). The grower source had a significant effect on the measured parameters when considered as a covariate. Chroma values of the peel, inner and outer flesh were significantly different ($P \downarrow 0.05$) at 4 and 23°C, after 14 days. There was no significant difference in the inner flesh TSS (IF-TSS) and outer flesh TSS (OF-TSS) between the different storage temperatures, but compared to day 0, after 14 days IF-TSS and OF-TSS were significantly lower. TA of the inner and outer flesh were significantly different at the two storage temperatures, but only the inner flesh TA was significantly different after 14 days. Further analysis is in progress for anthocyanins, total phenolics, carotenoids, folates and vitamin C. The current study indicates that QGP is climacteric and grower source, storage temperature and time and tissue location can significantly affect the studied physicochemical parameters.

Nutritional profile of high-amylose wheat starch: In vitro digestion and fermentation

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Increasing fibre intake is an important public health target. Starches with elevated levels of amylose are rich in resistant starch (RS), and can be a convenient route for increased fibre intake. The recent development of high-amylose wheat now allows formulation of major wheat-based products with higher fibre contents. This study focused on the nutritional profile of high-amylose wheat starch (HAWS). Noodles made of HAW contain 8-times-higher RS than the wild-type flour. Similarly, isolated HAWS both in native and cooked forms are more resistant to *in vitro* digestion. The enhanced resistance of cooked HAWS is proposed to be largely physical in nature, the ability of HAWS to retain granular structure during cooking limiting the access of digestive enzymes to the glucans. Further, the evolution pattern of starch structure during digestion, from size exclusion chromatography (SEC) before and after debranching, was different between wild types and HAWS. In debranched SEC, wild-type starch residuals have similar profiles, suggesting the branches are evenly digested. In HAWS, however, elongated amylopectin and amylose branches were digested relatively faster than shorter branches. The uneven digestion of HAWS suggests that native granules of HAWS could contain heterogeneous crystalline regions, including a previously unreported arrangement of branched glucans which is more resistant to enzymatic digestion. The starch molecular structural changes during *in vitro* colonic fermentation are different to those from digestion: D-limit dextrin was produced during digestion, but was further degraded during fermentation. This difference is attributed to starch-degrading enzymes other than D-amylose being produced by the colonic microbiota.

Indica SSIIa allele partially recovers the altered starch properties of down-regulated SBEIIb japonica rice without change its high amylose content

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Starch synthase IIa (SSIIa) and starch branching enzyme IIb (SBEIIb) are two starch biosynthetic enzymes required in the formation of short and intermediate length glucan chains of amylopectin. In rice, inactive SSIIa cultivars and SBEIIb recessive variants exhibit a range of alterations in grain phenotype, starch morphology, starch granule bound proteins, starch structure and functional properties. However, the interactions between the two enzymes have not been exhaustively investigated in rice yet. In this study, we analysed recombinant rice lines having down-regulated *SBEIIb* expression (*SBEIIb*⁻) with either *indica* or *japonica* type SSIIa (*SSIIa*^{ind} or *SSIIa*^{jap}) by crossing a *SSIIa*^{ind} Nipponbare inbred line to a *SBEIIb*⁻ Nipponbare transgenic line. Our results showed that two increased abundance protein bands (SSI and SSIIa) and seven additional proteins were found inside *SBEIIb*⁻ rice starch granules by SDS-PAGE followed by MS analysis. The amount of SSIIa was higher in *SSIIa*^{ind}*SBEIIb*⁻ than *SSIIa*^{jap}*SBEIIb*⁻, which indicated that *indica* type SSIIa was extensively involved in starch biosynthesis in the *SBEIIb*⁻ endosperm, possibly additional *indica* type SSIIa was involved in the monomer form. Furthermore, compared with *SSIIa*^{jap}*SBEIIb*⁻, *SSIIa*^{ind}*SBEIIb*⁻ starch had higher total starch content, increased starch granule particle size, and higher swelling power, reduced amylose-lipid complexes dissociation enthalpy, but remained the same level of the gelatinization temperatures, enthalpy and apparent amylose content. This suggests *SSIIa*^{ind} can partly recover the alteration of starch synthesis resulting from *SBEIIb* down-regulation in *japonica* background without reducing its amylose content.

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Comparison of antioxidant properties of coconut testa flour of selected local coconut cultivars of Sri Lanka

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Coconut testa is the thin brown colored outer skin of coconut endosperm. It is often peeled off from the kernel during coconut processing due to unfavorable brown colour it might impart on finished products. An attempt was made to utilize coconut testa to produce defatted flour as a substitute for wheat flour in bakery products. Aim of this study was to compare the total phenolic content (TPC) and ferric reducing antioxidant power (FRAP) of coconut testa flour of four local cultivars namely san raman (SR), gon thembili (GT), ran thembili (RT), TallxTall (TxT) against the commercial hybrid (COM) grown in Sri Lanka.

Hundred grams of coconut testa flour produced from partially defatted coconut pairings was extracted with 70% ethanol-water mixture. The TPC and FRAP assays were conducted using a 96 well micro plate reader.

Percentage yield (%) of crude extracts of SR, RT, GT, TXT and COM were 8.26, 6.87, 7.66, 8.06 and 11.17, respectively. The maximum TPC content was observed in TXT (62.58±5.99 mg GAE/g of extract) while the minimum TPC content was recorded for GT (27.53±4.54 mg GAE/g of extract). The lowest FRAP value was observed for SR (0.26 ± 0.02 mmol FeSO₄/g of extract) while the highest FRAP value was observed for COM (0.67±0.00 mmol FeSO₄/g of extract) variety.

In conclusion, coconut testa flour is a rich source of phenolics and antioxidants. The presence of these bioactives would make it a potential functional ingredient in food processing industry.

Key Words: Coconut testa, phenolic, antioxidants, extract, yield

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Aquaculture production for the rural population

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The global fish production from wild fisheries is on a declining trend with minimum signs of recovery. Agriculture is the foundation of rural development through creation of employment and generating income directly or indirectly through the value addition chain. The local food production is a basis for sustaining and caring for the people and environment.

Majority of the world population stay in the rural areas with many in urban areas being unable to eat fish due to the high prices, for it is seen as food for the rich. As the world population increases, so there is the need to increase fish production to meet the nutritional demand that is measured as a per capita fish consumption. Aquaculture in rural economies improves nutrition and helps in diversification of income and food sources, strengthens marginalised communities through creation of employment and reducing food prices.

There is need for investment in the aquaculture sector so that they can realise these benefits. The rural areas are endowed with land, with some having suitable natural sites for production. In addition, there can be a modification to unsuitable sites to avert the unpredictable weather patterns. Potential farmers should have easy accessibility to quality farming inputs (seeds and feeds) so that they are guaranteed of returns. Combining this with modern technologies and models in aquaculture will ensure that rural populations are contributing to the economy and feeding the community and nation as well.

Key Words: Aquaculture, nutrition, economy, employment, farming inputs

Photosensitization, a green treatment for the inactivation of *Aspergillus flavus* in peanuts mediated by curcumin

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The aim of this study was to investigate the efficiency of curcumin-based photosensitization (CUR-PS) in inactivating *Aspergillus flavus* spores and in turn reducing the aflatoxin B₁ production and extending the shelf-life of raw peanuts. The inoculated peanuts with *A. flavus* spores were illuminated for 15 min at 420 nm (Xenon Arc light source) using three different curcumin concentrations of 50, 75, and 100 µM. The highest reduction in *A. flavus* spores on peanuts (1.7 log CFU) was obtained by 50 µM curcumin ($p \uparrow 0.05$). Interestingly, shelf life of treated peanuts with 75 µM curcumin was extended by 7 days. In order to evaluate the influence of CUR-PS treatment on aflatoxin B₁ generation, treated and untreated peanuts were analysed after 20 days of storage 25°C. Results showed that the average level of aflatoxin B₁ in untreated (control) peanuts was 800 mg/kg, while light treatment of peanuts reduced the aflatoxin production to the level of 296 mg/kg. A significant reduction in aflatoxin production was observed in curcumin (75 µM) treated peanuts, where 38.3 and 41.1 mg/kg aflatoxin were detected in illuminated and not-illuminated peanuts, respectively. Moreover, 59.2 and 58.1 mg/kg aflatoxin were detected in CUR-PS treated peanuts with 50 and 100 µM curcumin, respectively. However, not illuminating curcumin treated peanuts with 50 and 100 µM showed higher levels of aflatoxin, 108.8 and 105.3 mg/kg, respectively ($p \uparrow 0.05$). This study demonstrated the efficiency of CUR-PS treatment as a safe and green technology to control fungal growth and mycotoxin production in agro-food sector.

Understanding the metabolic fate and bioactivity of dietary anthocyanins

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Anthocyanins are plant pigments and dietary phytochemicals, and may have potential health benefits. There is emerging evidence from epidemiological and experimental studies that suggests a higher consumption of anthocyanin-rich foods is associated with a reduced risk of heart disease and diabetes. To better understand the observed beneficial effects of anthocyanins and their underlying mode of action, bioavailability and metabolic fate needs to be studied in more detail. Healthy human subjects (10–12 in two different studies) received red grape pomace (700 mg anthocyanins/mainly as malvidin-3-glucoside) or Queen Garnet plum (QGP) juice (426 mg anthocyanins/mainly as cyanidin-3-glucoside) and an anthocyanin-free control in a randomised crossover design. Malvidin- and cyanidin-glycosides are common in many fruits and beverages such as red grapes, red grape juice, red wine, blueberry, cherry, elderberry, (Japanese) plum and are therefore of dietary significance. 24-hr urine samples were collected and analysed for anthocyanins and metabolites by UHPLC-PDA-MS. Methylated, glucuronidated and sulphated anthocyanins could be identified as characteristic metabolites in both studies. Furthermore, the increase in urinary hippuric acid (microbial/hepatic metabolite) was considerable in both studies after the consumption of red grape pomace or QGP juice (1.8–4.5-fold vs. control; $p \downarrow 0.05$). These findings suggest that structurally different anthocyanins are exposed to a similar extensive metabolism by enzymes and the gut microbiome and that the generated metabolites are most likely the bioactive compounds *in vivo*. Therefore, more human studies are warranted to investigate the metabolic fate of dietary anthocyanins and the bioactivity of generated metabolites.

Effect of photosensitization on inactivation of *Aspergillus flavus* in maize

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Mycotoxins are naturally occurring toxins produced by certain types of fungi that contaminate food and feed, posing serious health risks to human and livestock. Photosensitization is a light-based technique, which has emerged as a novel and promising green technology to control microbial growth in food and feed. This study aimed to evaluate the effect of solvent medium including ethanol (EtOH), 50% (v/v) propylene glycol (PG), 20 % (v/v) tween 20 (TW-20), and 20 % (v/v) tween 80 (TW-80), on curcumin-mediated photosensitization to inactivate *Aspergillus flavus* spores *in vitro* and on the surface of yellow and white maize kernel and flour. Results showed a reduction in the phototoxic activity of curcumin in TW-20 and TW-80. However, curcumin-based photosensitization using EtOH and PG as solvents led to a significant decrease in the colony forming ability of *A. flavus* spores *in vitro*, up to 2.04 and 3.33 log colony-forming unit (CFU), respectively. Interestingly, fungal growth was delayed in photosensitized maize kernel and flour for 14 and 7 days, respectively, which were stored at 25°C. Consequently, no Aflatoxin B1 (AFB1) was detected in maize kernels after 20 days of storage at 25°C, whereas accumulation of the toxin was reduced by 91% in photosensitized flour. Thus, photosensitization showed to be a potential alternative to reduce *A. flavus* contamination on maize kernel and flour, giving rise to low concentrations of AFB1. This technique has the potential for use in feed applications resulting in the reduction of post-harvest losses in maize.

Relationships between perceived satiation, subsequent satiety, and plant-based food features

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Satiation and satiety play major roles in controlling food intake in humans, with plant-based foods a key contributor. Although many factors have been shown to influence satiation and satiety, the relationships between perceived satiation, perceived satiety, and plant-based food features are not well understood. We aimed to identify relations between perceived satiation and subsequent satiety, and with the composition, architecture and oral processing of six diverse plant-based foods (apple, avocado, banana, carrot, chickpea, macadamia) using a trained panel and a complete crossover randomized design. The perceived satiation and satiety were calculated from perceived fullness ratings measured using a labelled magnitude scale. Food was served as a mid-morning snack *ad libitum* over 20 minutes until panellists were comfortably full, and subsequent satiety was monitored for up to 180 minutes. Carrot and macadamia had significantly higher perceived satiation, but also significantly lower subsequent satiety per gram of food than other foods. From Principle Components and Pearson correlation analysis, satiation and satiety are negatively related. Food energy factors had no strong relationship with satiation, but were significantly positively related with satiety. Mastication number had significant effects on both satiation and satiety, in negative and positive ways respectively. This study shows how portion control through satiation for different plant-based snacks can influence both energy intake and subsequent satiety.

Purple sweetcorn - an innovative horticultural product - consumer views

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Purple sweetcorn has been conceptualized as an innovative premium horticultural product that may provide consumers with the potential health benefit of anthocyanins. Gathering consumer insights is crucial to inform the breeding program to obtain a purple sweetcorn product closer to consumer's requirements.

Thirty-six non-food neophobic sweetcorn consumers participated in a focus group session on the concept of purple sweetcorn, as well as visually evaluating early breeding lines. Consumers were very positive about the concept of purple sweetcorn and had clear ideas of potential uses. Consumers preferred that purple sweetcorn taste different to commercial yellow sweetcorn, and that health claims would support a premium price position. A small scale follow up consumer study (n=10) was carried out where consumers were asked to rate acceptability for visual (raw and cooked), flavour, textural and overall of two purple sweetcorn breeding lines (reddish-purple and purple) and compared against commercial yellow sweetcorn. Visual acceptability scores were higher for purple than the reddish-purple lines for both cooked and raw forms, but the yellow cobs were the most preferred. In contrast, flavour and overall acceptability scores were higher for the reddish-purple and yellow cobs than the purple lines. It was also noted that the reddish-purple and purple lines had a slight raspberry flavour. Consumer's discussions outcomes from both studies were that consumers preferred better colour coverage across the kernel, which will be the direction in continuing the development of purple sweetcorn lines. This study demonstrated there is a market for a premium purple sweetcorn product among consumers.

Nutritional characteristics of Australian grown Feijoa (*Acca sellowiana*) and its antimicrobial activity

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The present study determined the chemical composition, bioactive compounds and biological properties of Australian grown feijoa (*Acca sellowiana*) (including whole fruit with peel, fruit peel and pulp) in order to assess the nutritional quality and antimicrobial activity of this tropical fruit. Polyphenolic compounds and vitamins were determined by UHPLC-PDA-MS/MS, showing that the feijoa fruit not only contains a high amount of antioxidant flavonoids, but is also a rich source of vitamin C (63 mg/100g FW in the whole fruit and 95 mg/100g FW in the peel; Recommended Dietary Intake (RDI) for adults: 45 mg/day). The proximate, essential minerals and selected trace elements indicate that feijoa fruit is a valuable source of dietary fibre and potassium. The edible fruit peel possesses significantly more antioxidant flavonoids and vitamin C than the fruit pulp.

This is most probably the reason for the observed strong antimicrobial activity of feijoa peel-extracts against a wide-range of microorganism responsible for food spoilage and food poisoning. The consumption of feijoa, whole fruit with peel, can deliver a considerable amount of bioactive compounds such as vitamin C, flavonoids and fibre, and therefore, may contribute to a healthy diet. Furthermore, the potential use of feijoa-peel as a natural food preservative needs to be investigated in follow-up studies.

Impact of photosensitization on physicochemical properties in strawberries

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Strawberries, depending on the cultivar and environmental conditions, can be a rich source of nutrients like folates and vitamin C as well as bioactive phytochemicals, mainly polyphenols. But at room temperature, this fruit is highly perishable and has a relative short shelf life of only a couple of days. An innovative, cost effective and environmentally friendly technique, photosensitization, has been applied with the aim to extend the shelf life of strawberries and to minimize the loss of nutrients and also phytochemicals. Photosensitization works based on the combined action of photosensitizer, light and oxygen, which produce reactive oxygen species that inactivate microorganisms. Curcumin, known for its antifungal activity was used as the photosensitizer in this study. To see the effect of photosensitization, physicochemical parameters of both fresh and photosensitized strawberries have been tested. There were no significant ($p \downarrow 0.05$) changes in pH, titratable acidity, total soluble solids and moisture content between treated and untreated (control) strawberries. However, total sugar content of photosensitized strawberry was significantly ($p \downarrow 0.05$) higher than that of the control (5.3 ± 0.3 g/100g FW vs. 4.12 ± 0.1 g/100g FW). No significant difference was observed in the total phenolic content of the treated (192.9 mg gallic acid equivalents (GAE)/100g FW) and the control (195.8 mg GAE/100g FW) samples. These preliminary findings show that photosensitization could be a promising technique that has the potential to be used in the horticulture industry to extend the shelf life of fresh produce such as strawberries.

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Lemon Myrtle (*Backhousia Citriodora*: Unique Australian native superfood & cosmeceutical active

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Lemon myrtle (LM) has been used by the Aboriginal Australians in cooking, tea and as a remedy for cuts and abrasions for thousands of years. It was named as *Backhousia citriodora* after James Backhouse in 1853. Schimmel and Co of Dresden Pharmaceutical Company isolated and identified the high (90-97%) of citral content in the leaf oil in 1888. From the early 1900's, the foliage was harvested from LM trees in Queensland and the distilled LM oil was exported to Europe and the United States. During WWII LM leaf oil was used in soft drinks by Tarax Pty Ltd and exported to the Australian troops in the Pacific.

LM is a highest source of citral (90-96%) as compared to lemon oil (3-10%), lemon balm oil (64%), lemongrass (70-80%) and May Chang (70-85%). LM leaves and oil exhibits excellent antibacterial, antimicrobial and antifungal properties. Its antioxidant property is greater than green tea and its antimicrobial property is greater than tea tree oil. It is rich in minerals such as zinc, magnesium and calcium and antioxidants such as lutein (a carotenoid important for the eye health), Vitamin A and Vitamin E. Therefore, LM can be used as a superfood in food and nutraceutical industry and a multifunction active for skincare (cosmetic and pharmaceuticals) products.

Exploring the nutritional profile and bioactive potential of Australian grown Saltbush (*Atriplex sp.*)

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Plant foods play a vital role in human nutrition due to their diverse range of macro- and micro-nutrients, fibre and phytochemicals. However, more than 90% of the plant-food demand is satisfied by less than 0.1% of the edible plant species available. Moreover, none of the highly consumed 'food-plants' can survive without freshwater irrigation. As the world's population rises and food sources become limited, alternative avenues for achieving the world's food demand are necessary. This persistent situation urges the domestication of wild terrestrial salt tolerant (halophytes) edible plants, of which saltbush (SB) was found as a valuable source of protein (14-21%), digestible carbohydrates (15-24 %) and minerals (particularly Na, K, Mg, and Cl). It has been reported that SB leaves show potential beneficial effects against diabetes, heart disease and rheumatism. These biological activities are most likely attributed to its phytochemicals. Most of the SB species have a long history of use as animal feed and soil erosion control, while very little scientific information is available on their nutritional profiles and dietary relevance. Therefore, the present study will assess the nutrient and phytochemical composition of selected Australian grown SB cultivars to better understand their nutritional 'value' and potential bioactivity. In addition, the development of new SB based food products and commercial applications for the food industry will be explored.

Antimicrobial activity and ellagitannins from *Terminalia ferdinandiana*

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Extracts were prepared from *Terminalia ferdinandiana* (Kakadu plum) fruits, leaves, seedcoats, and barks using accelerated solvent extraction with methanol, ethanol, water, acetone, and hexane. Antioxidant activity was assessed using the 2, 2-diphenyl-1-picrylhydrazyl (DPPH) free radical scavenging assay and by determining the total phenolic content (TPC). Methanol fruit extracts had the strongest free radical scavenging activity and the highest TPC (12 g/100 g DW). The antimicrobial activity of all extracts (except hexane) was analysed by agar disc diffusion. Fruits and leaves showed larger inhibition zones against foodborne bacteria *Listeria monocytogenes*, *Bacillus cereus*, methicillin resistant *Staphylococcus aureus*, and clinical isolates of *Pseudomonas aeruginosa* compared to seedcoats and barks. The minimum inhibitory and minimum bactericidal concentration of the extracts ranged from 1.0 to 3.0 mg/mL against the tested microorganisms. Scanning electron microscopy images of bacteria treated with the extracts showed morphological changes consistent with cell death. A new UHPLC-MS/MS method for the determination of punicalagin and castalagin, bioactive ellagitannins, was developed and validated. Punicalagin contents in the fruits and leaves were 74 and 49 mg/100 g DW whilst castalagin contents were 1.1 and 0.8 mg/100 g DW. To the best of our knowledge, this is the first report about punicalagin and castalagin concentrations in Kakadu plum fruits and leaves. These initial findings are very promising in regards to the potential use of Kakadu plum fruit and leaf extracts as natural preservatives in the food industry.

High-amylose rice: Starch molecular structural features controlling cooked rice texture and preference

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Cooked high-amylose rices have slower digestibility, giving nutritional benefits, but inferior eating qualities. In this study, Rapid Viscosity Analysis, quantitative descriptive sensory analysis with all panellists from China and Textural Profile Analyser (TPA) have been used to measure rice texture and eating quality of cooked rice. Molecular structural mechanisms for this inferior eating quality are found here using structural analysis by size-exclusion chromatography of both the parent starch and starch leached during cooking. All commonly-accepted sensory attributes of cooked rice were characterized by a trained human panel. Hardness, with the strongest negative correlation with panelist preference, is the dominant but not sole factor determining palatability. Rice with larger amylopectin size can bond more water, thereby have lower hardness value. Meanwhile, hardness is controlled by the amounts of medium and long amylopectin chains and amylose in the starch, and by amylose content and amount of longer amylopectin chains in the leachate. With this, it is concluded for the first time that rice containing 19–25% amylose content are most preferred by the panel. Meantime, it is showed that breakdown viscosity and swelling power of native rice flour can be and should be used as indicators for predicting rice eating quality. This gives knowledge and understanding of the molecular structural characteristics of starch controlling cooked-rice preference: not just high amylose but also other aspects of molecular structure. This can help rice breeders to target starch-synthesis genes to select slowly digested (healthier) rices with acceptable palatability.

Differences in the anthocyanin profile of different tissues of the strawberry fruit

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Strawberries are most commonly red in colour, which is largely due to the anthocyanin, pelargonidin-3-glucoside, a bioactive flavonoid with potential health benefits. Variation in the intensity of red colour across strawberry varieties, from a light pink to a deep cherry colour, is solely associated with a change in concentration of this single anthocyanin, rather than the synthesis of an anthocyanin with a different colour. In this study, the anthocyanin profiles of the two constituent edible tissues of strawberry fruit were determined. The main tissue of the strawberry consists of a swollen fleshy receptacle. The second tissue consists of the achenes, visible on the surface of the strawberry, with each achene consisting of a dry single-seeded fruit formed from a fertilised ovule. The current study showed that the anthocyanin profile of a strawberry achene is totally different from that of the receptacle. While red-coloured pelargonidin-3-glucoside is the main anthocyanin component (about 94%) in the receptacle, purple-coloured cyanidin-3-glucoside accounts for approximately 90% of the anthocyanin content in the achene. This would indicate that flavonoid 3'-hydroxylase (F3'H), the enzyme responsible for shifting anthocyanin biosynthesis towards cyanidin and away from pelargonidin, is functional in strawberry achene tissue, but not in the receptacle tissue. This may indicate that other factors, such as transcription factors, can modulate the anthocyanin profile of different strawberry tissues, rather than strawberries having a non-functional F3'H gene. However, the relevance of these findings for potential strawberry breeding programs and subsequently the nutritional quality of strawberry fruit needs to be investigated further.

Indigenous vegetables in Vietnam: The nutritional and use values

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Vietnam is situated in the tropical region with hot and humid climatic conditions. It possesses highly diverse flora and is also recognized as a culturally diverse country with many ethnic minority communities. Each community possesses its traditional knowledge for the utilization of these unique flora, both in terms of farming practices and culinary preparation. Due to the need for conservation of biodiversity of agricultural plants, as well as maintaining existing indigenous knowledge for these unique vegetable species, we conducted surveys and collected information to initially determine the nutritional values of the following species: *Colocasia esculenta* (L.) Schott, *Momordica charantia* L. var. *minima* Will. et Ng., *Brassica campestris* L., *Lycium chinense* Miller, *Brassica oleracea* L. var. *capitata* L. forma *alba* DC; These species were analysed for moisture content, protein, fat, carbohydrate, Vitamin B1, Vitamin B2, Vitamin C, dietary fiber, potassium, iron, calcium, β -carotene, lutein, and the energy content was calculated. There was a large range in the proximate composition of most nutrients; for example, moisture content ranged from 71.1 to 86.2 g/100 g⁻¹, protein 2.6 to 3.6 g 100 g⁻¹, dietary fiber 0.8 to 3.0 g 100 g⁻¹ and energy 21.0 to 157.0 kJ 100 g⁻¹. Apart from use as food, these vegetables have potential medicine value such as heat-relief, detoxification, increase body resistance, antioxidant, anti-inflammatory. Further research and evaluation of these herbaria should be invested in order to improve the delivery of indigenous vegetable products to the market.

Discerning wine astringency sub-qualities by tribological approaches in a model system – what is the role of saliva?

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Astringency is an important indicator of wine sensory quality. As a complex sensation that the loss of in-mouth lubrication is recognised as an important mechanism, astringency can be perceived as a set of different sub-qualities. In addition to sensory evaluations, chemical approaches measuring interactivity of astringents-proteins have provide ways of astringency quantification, but they do not capture how specific wine components elicit those sub-qualities. In this study, we developed several tribological approaches, which considered saliva interactions, in an effort to explore if any salivary lubrication change is linked to different sensorily perceived wine astringency sub-qualities. In model wine systems with defined matrix compositions, we found that model wines with equivalent responses in chemical assay for astringency possessed various astringency sub-qualities. In particular, the sub-quality Drying corresponded to samples exhibiting higher boundary friction. High-acidity matrix induced Pucker, which is found to be independent of Drying. It was also linked to a faster salivary film collapse. The Rough seemed to be a secondary astringency sub-quality combining Drying and Pucker, because these 2 sensations were found either elicit Rough independently. Polysaccharide reduced the Drying in a low-tannin-high-acidity matrix. This is the first study demonstrating that astringency sub-qualities are likely to have different perceptive mechanisms by using tribological measures. The outcomes would provide insights into employing those tools to help manage wine matrix to attain preferable mouthfeels and astringency characteristics.

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Exploring common bean fresh pod market in East African region: A case of Uganda

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Common bean fresh pod is a niche market product consumed worldwide including in Eastern Africa region. It is more preferred to dry bean due to the fresh taste and ease to cook. A lot of research has been done on production and disposition of dry bean product; however, little information is available on production and marketing of fresh bean pod in Uganda. The general observation indicates wide consumption of fresh bean pods however, there is limited information on its entire value chain, yet, its value cannot be undermined. Based on this background, a reconnaissance study was undertaken in Mpigi district, a major fresh bean growing area and eight retailing markets within Uganda's capital, Kampala, to understand the economic feasibility of fresh bean pod market. Using qualitative approaches, farmer and market analysis was conducted to explore and understand fresh bean market dynamics. The results show that there are over 10 varieties being sold for fresh pod, unstandardized weight measures are being used, and price variation of over 50%. Additionally, unsatisfied demand for fresh pod beans is 45%. The results indicate existence of a lucrative fresh pod market valued at more than USD 2.0 million within Kampala and suburbs. It was also revealed that production faces significant gaps in seed availability to ensure consistent quality supply to the market while at selling points, bronzing effect was a major challenge leading to product deterioration. Thus, interventions are needed to eliminate the existing production and marketing challenges for a sustainable fresh bean pod business.

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The performance of locally developed incubators for increased food and income security

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The study was conducted on-station to determine the hatchability rate of locally manufactured incubators. In rural societies of northern Ghana where a household of averagely 5 persons live on about \$5.00 per day, poverty is endemic. One of the livelihood options is the rearing of poultry mostly the local fowls and guinea fowls. An adult female guinea fowl (guinea hen) can incubate and hatch about 20 eggs within 28-days. Guinea keets mortality doubles as a serious challenge in the production of guinea fowls. This figure is not encouraging as the guinea fowl eggs are seasonal too, lowering the number of incubations that can be done by the guinea hen. To hatch more eggs therefore, one need to have at least 5 productive guinea hens. This is usually difficult to obtain in the rural societies. To solve this problem, Animal Research Institute of the Council for Scientific and Industrial Research have developed local and manually operated incubators with egg-capacities of 300-600 for smallholder farmers. There are some on-station for incubating eggs, at a fee, for farmers who are unable to obtain an incubator. If all conditions for incubation of eggs are observed, the hatchability rate fluctuates from 65-85%. This technology has been helpful to local and commercial farmers for the past years of its operation since they can now incubate more eggs and obtain more guinea keets.

Economic, environmental, and social sustainability assessment of Queensland industries

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In 'Our Future State: Advancing Queensland's Priorities' the Queensland Government outlined how industries and government should contribute to community well-being. Agriculture's contribution lies in generating economic activity, job creation and the Great Barrier Reef protection.

While lack of data prevents the measurement of some attributes in the government plan, composite sustainability indices have been used worldwide to represent the wider objectives of "triple bottom line" economics (growth and throughput), social justice (fair and equitable distribution of the wealth) and environment-friendliness (compatibility with the preservation of natural ecosystems).

One such approach is an innovative self-designed iSENSE index – indicators of Sustainability: ENvironmental, Social, and Economic – that is based on 15 indicators with a maximum overall score of 30. The featured indicators are based on a literature review and represent commonly accepted parameters.

In this study, iSENSE indicators have been enumerated for the analysis of three Queensland sectors: Agriculture, Mining, and Manufacturing. The results show that while Mining leads the group in terms of economic indicators, it is Agriculture that is the most socially oriented and environment-friendly. Overall, iSENSE score is equal 16 for both Agriculture and Mining, whilst Manufacturing stands at 13.

While these results should be taken with caution, they can be used as a guidance for prospective policy proposals in conjunction with the sound *ex post* impact assessments around Queensland industries. Applying composite assessment tools can help to identify challenges related to environmental, economic and social impact, in the course of developing sustainable agriculture.

Digital twin for the future of orchard production systems

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The evolution of orchard production systems towards higher density layouts, makes monitoring of canopy and disease increasingly important. Technological advances over the last few years have greatly increased our ability to collect, collate and analysis our data per tree basis on a large orchard scale. We call this the Digital-Twin Orchard.

A digital-twin is a virtual model of every tree and surroundings. The pairing of the virtual and physical worlds allows analysis of data and continuous monitoring of orchards production systems to predict stress, disease and crop losses, develop new opportunities for end-to-end learning.

Monitoring of orchards is not a new concept but the digital-twin is a continuously learning system that could be queried automatically to analyse specific outcomes under varying simulated-environmental and orchard management parameters. Digital-twin enables improvement of production and dynamic prediction of disease, stress and yield gaps using an end-to-end AI platform.

In this paper, we present our AgScan3D+: an automated dynamic canopy monitoring system to generate a digital-twin of every tree on a large orchard scale. AgScan3D+ consists of a spinning 3D LiDAR plus cameras that can be retrofitted to a farm vehicle and provides real time on-farm decision support by monitoring the condition of every plant in 3D such as their health, structure, or stress, fruit quality, and more. The proposed system has been trialed in mango, macadamia, avocado and grapevines orchards and generated digital-twin of 15000 trees. The results were used to model canopy structural characteristics such as foliage density and light penetration distribution.

Predicting a path to increased genetic gain using artificial intelligence

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The rate of genetic gain in wheat must be doubled over the next 2-3 decades to secure global food supply. Production trends worldwide suggest that current breeding strategies need to be improved in order to achieve this goal. One of the most critical steps in a wheat breeding program is to select parents for targeted crossing but strategies for decision support are not readily available. Conventionally, parents are selected based on their performance *per se* or their breeding value which limits the inference that can be made about the probability for maximising the number of favourable chromosome segments in the offspring of a given cross. This is particularly challenging when a combination of quantitative traits (yield) and mono- or oligogenic traits (e.g. disease resistance, quality) are considered simultaneously. This problem is well suited to evolutionary computation approaches, where algorithms inspired by biological evolution, such as reproduction, mutation, recombination, and selection are employed to find solutions to complex problems. In this ongoing study, we use evolutionary computing in a large commercial data set comprising more than 34,000 genotyped breeding lines which have been tested over multiple years and locations across Australia. The algorithms predict optimal crosses that most efficiently stack complementary alleles for quality, disease resistance and yield. Generated offspring from those crosses is advanced through "speed breeding" which allows a rapid turnaround of several generations and breeding cycles per year. Finally, these approaches will be compared for efficiency with alternative breeding strategies, such as standard genomic selection and phenotypic selection.

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Connectivity in Northern Australia

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Families and businesses across Northern Australia (NA) are looking for a reliable and affordable internet connection, however, it is becoming recognised that the requirements of rural and regional areas can be different to their urban counterparts, and a lack of connectivity is significantly restricting education, social cohesion and daily business right across the North. Premise are talking with producers in NA of differing sizes and in different industries who have successfully developed and installed strategic, professional and business-quality connectivity solutions for their business that deliver integrated voice, internet and data channels. Ag tech companies and connectivity providers are also being interviewed to learn about additional communication options available and the connectivity requirements needed to support the new technologies available now and on the horizon for NA. The themes from our discussions were developed into case studies, with additional information included as a technical note, to directly assist producers in NA assess their own connectivity needs, and identify potential solutions, for themselves. This work has been funded by the CRCNA, and is being undertaken in collaboration with QUT, as part of the larger *Northern Australian Communication Analysis* project.

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Towards on-field diagnostics: Equipment-free nucleic acid purification in 30 seconds

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Nucleic acid amplification is a powerful tool in molecular diagnostics but requires labour-intensive, time-consuming nucleic acid extraction process, limiting its use in poor resource settings. To address this issue, we investigated a variety of materials to test their ability in nucleic acid extraction. We found that untreated cellulose-based filter paper can bind DNA within seconds and retained sufficient DNA for amplification after washing step, while contaminations existing in biological samples were removed. Based on this knowledge, we created equipment-free nucleic acid extraction dipstick methodology that utilise dipstick containing cellulose-based nucleic acid binding area and a waterproof handle to extract nucleic acid by rapidly moving dipstick among extract, wash buffer and amplification reaction successively. This method can obtain amplification-ready DNA or RNA from plants, animal, microbes or even difficult biological samples, such as mature tree leaves and human blood in less than 30 seconds. The simplicity, rapidness, low cost, availability of suitable material (e.g. common paper towelling) makes nucleic acid purification more accessible and affordable for researcher and the broader community. When combined with loop-mediated isothermal amplification (LAMP) and naked eye colorimetric assay, the dipstick extraction technology makes it achievable to perform molecular diagnostics outside modern laboratory environments, such as field-based environments and developing countries.