Wednesday, 16 Oct 2019

10:30 - 12:45: Expanding Pulse Production

Paper ID: 90, Progress in Chemical Weed Control in Pulses in western Canada

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Pulse crops are an important contributor to the agricultural economy in the Canadian Prairie Provinces. Approximately four million hectares are seeded annually with lentil (*Lens culinaris* L.) and dry pea (*Pisum sativum* L.) being the most common pulses grown in this area. Soybean (*Glycine max* L.) area has been expanding rapidly over the past decade, with the province of Manitoba being the predominate producer. Chickpea (*Cicer arietinum* L.), fababean (*Vicia faba* L.), and dry bean (*Phaseolus vulgaris* L.) are produced as well but their combined area is usually less than 200,000 hectares. Pulses are generally poor competitors with weeds and are quite reliant on ALS-inhibiting herbicides (Group B) for weed control. Problem weeds in pulse crops that have evolved Group B resistance include kochia (*Bassia scoparia* (L.) A.J. Scott), wild mustard (*Sinapis arvensis* L.) and false cleavers (*Galium spurium* L.). Screening for alternative herbicide mechanisms of action has been ongoing since the inception of the Pesticide Minor Use Program in 2000. Sulfentrazone, a Group G herbicide, was one of the first herbicides introduced for use in chickpea and dry pea, particularly for the control of kochia. Other Group G herbicides that have been registered for use in pulses include saflufenacil and flumioxazin. Pyroxasulfone, a very long chain fatty acid inhibitor (Group K), has also been registered in pulses. Co-packs or mixes of the Group G herbicides combined with pyroxasulfone are also available to provide a broader spectrum of weed control in pulses. All of these herbicides are soil applied; thus, their efficacy is highly dependent on environmental conditions and soil characteristics. The concept of herbicide layering, the application of a PRE- soil herbicide followed by the application of a POST- herbicide with a different MOA, has been proven successful in controlling weeds such as false cleavers in field pea. PRE- applications of either ethafluralin, sulfentrazone, or clomazone (Group Q) followed by a POST- application of imazamox (Group B) and bentazon (Group C) provided higher levels of control of Group B resistant false cleavers in

field pea than the PRE- or POST herbicide applied alone. The search for different mechanisms of action in pulses will continue; however, the success will be dependent on availability of new chemistries.

Paper ID: 111, The Expanding Pulse - Adapting Pulses to Mallee environments

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Northbound Pulses on the march into the semi-arid Mallee region

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Pulses are an important driver of productive, profitable and sustainable farming systems in south eastern Australia. Local applied research has demonstrated the benefit legume crops such as pulses provide to Mallee farming systems. Grain yield increases of 0.5 1.5 t/ha in cereal following a pulse, with an increased profit up to $100/ha per year has been recorded in low rainfall pulse break crop sequences, relative to maintaining continuous wheat (McBeath et al, 2015; Moodie et al.2017). Improved grain yield and profitability was attributed to beneficial effects on the cycling and supply of nutrients, improved grass weed control and reduction in cereal disease.

A roadside survey in 2017 of approximately 800 paddocks across an 1100 km transect has shown that the adoption of pulse crops in the Victorian Mallee region has increased dramatically, from 7% of paddocks in 2006 to 24% in 2017. Lentil (10.6%) was the dominant legume crop in 2017followed by field pea (6.2%), vetch (including for hay) (5.3%), lupin (1.6%) and chickpea (0.7%). The increase in pulse area came at the expense of fallowed paddocks which declined from 18.4% in 2006 to 2.4% in 2017 or regenerating pastures which declined from 18.0% in 2006 to 12.4% in 2017.

Significant agronomic changes in Mallee farming systems have also supported the adoption of pulses in the Mallee. The widespread adoption of no-till and stubble retention farming practices (Llewellyn and DEmden, 2010) have allowed for successful establishment of pulse crops on coarse textured soils, while summer weed control practices increase stored soil water, which moderates risk in semi-arid environments. Strategic and careful use of herbicides across the cropping sequence has helped to avoid problems from herbicide residues in high risk alkaline, low organic matter Mallee soils. These farming systems also

have a strong focus on early sowing to ensure effective utilisation of in-crop rainfall, while minimising effects of drought and heat stress at the end of the growing season. Often a sow by the calendar policy is implemented, which can bring about its own challenges, such as successful inoculation practices in dry soils. There can also be increased frost risk if crops emerge early. Advancement in pulse breeding has also supported the adoption of pulses in the Mallee. Improved traits such as herbicide tolerance, disease resistance, tolerance to subsoil constraints, improved phenology and architecture have provided Mallee farmers with better adapted pulse crop varieties resulting in lower production costs and reduced risk.

To ensure the sustainability of growing pulses in the semi-arid Mallee there are environmental, biotic and abiotic challenges which need to be overcome through improved genetics and crop management. Rainfall is slightly winter dominant, generally low (annual <350mm; GSR < 250mm) and variable, with terminal drought often experienced by crops. Temperatures can vary dramatically throughout the cropping season and particularly in the critical reproductive phase of pulses. Both frosts and heat stress can result in significant grain yield and quality losses. Soil variability is extreme which provides challenges for both crop and variety selection as soil types within paddocks vary from deep infertile sands to clay loams with subsoil constraints.

Diseases above (eg. *Ascochyta sp*. and B*otrytis sp*) and below ground (eg. *Pythium* and *Rhizoctonia*) can pose a significant risk, causing substantial yield loss in these regions depending on seasonal environmental conditions and soil types. Improved tactical disease control strategies are required, as disease outbreaks are infrequent, and the extensive nature of low rainfall farming systems mean expensive inputs are often wasted when farmers follow routine preventive disease control programs. Weed management is also incredibly challenging due to the environmental variability and changing soils, combined with a limited range of registered products, particularly for broadleaf weed control. Moreover, there is a high risk of crop damage from commonly used group C herbicides or herbicide residues in the soil on sandy, low organic matter soils.

There is a significant role for innovative research and development to create solutions that overcome constraints to growing pulses in the Mallee and other low rainfall farming regions. This will see pulses continue their march into the Mallee which will both grow the pulse industry and increase the profitability of low rainfall farming systems.

Paper ID: 56, Using @RISK modelling to examine risk in Mallee cereal and legume rotations

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A model developed by Rural Directions Pty Ltd using @RISK, an add-on to Microsoft Excel, was used to assess risk and net profit associated with rotational sequences in the Northern Mallee of South Australia.

@RISK uses multiple probability Monte Carlo simulation. The model was used to analyse, 5000 seasonal outcomes in relation to yield and price for nine rotational sequences practiced in the northern SA Mallee for a model farm. In comparison, a grower might experience only 40-50 seasons in their entire farming career.

Percentile 10, 50 and 90 yields and prices were inputted into the model, together with variable costs for each crop. Estimated yield benefits and penalties associated with following crops were also considered (i.e. increases in wheat yields following break crops). Estimated fixed costs for the model farm (depreciation, finance costs and overhead costs) for the model farm were also included into the model.

In the simulation, the baseline sequence was continuous cereal with alternating wheat and barley. The continuous cereal sequence was compared with a range of rotational sequences involving legume break crops including field peas, chickpeas and lentils as well as vetch pasture and vetch hay. Sequences including canola and fallow were also analysed.

In the analysis, continuous cereal achieved a profit in 38% of years. The inclusion of pulse crops chickpeas and lentils in rotations improved the risk profile. Crop sequences including chickpeas were profitable in 59% of years and those including lentils were profitable in 53% of years. Average Net profit per hectare per year over the six-year sequence for continuous cereals was -$20.89, whereas sequences including chickpeas and lentils returned $123.13 and $59.86 respectively.

Paper ID: 5, Predictions of optimal chickpea flowering time for better yield

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Chickpea yields are often constrained by miss-match of crop duration with the environment in which it is grown leading to its exposure to frost, drought and heat stress. For achieving higher and reliable production, its duration therefore needs to be optimised for individual environments. We tried to achieve this through a modelling approach. A factorial simulation study was conducted across important chickpea growing regions in Australia, to determine how differences in crop phenology across these regions can affect yield in current and future environments. Based on temperature and photoperiod as the main drivers of flowering time, significant differences in floral initiation (date of first flower) were observed among the sites and between sowing dates. Flowering was earliest at Biloela and Theodore, situated at relatively low latitudes in Queensland, in contrast to Roma, Dalby and Goondiwindi (at higher latitudes in Queensland). Some sites exhibited a wide range in flowering characteristics (e.g. Wagga Wagga (NSW) and Dalby) which may be due to greater fluctuations in seasonal conditions. It is also possible that at these sites, the Agricultural Production Systems sIMulator (APSIM) was not adequately able to account for variation in flowering and pod set due to failure to reconcile with production of sterile (pseudo) flowers in cooler environments which seems to occur due to interactions between soil moisture and temperature. There was a strong latitudinal phenology gradient in flowering, with southern sites being better-suited to earliness to facilitate drought escape during grain-fill, and northern sites better-suited to lateness to maximize biomass production and avoid the fitness penalty associated with the species lack of reproductive chilling tolerance. Indeed, across all sites, yield was most strongly influenced by soil water supply (in-season rainfall) and sowing date. The follow-on challenge from this work is to identify the levels and duration of chilling stress responsible for observed yields that depart from the simulated yields, and to determine how

those chilling indices might be incorporated into the chickpea growth model in future versions of APSIM.

Paper ID: 57, Putting our finger on the pulse - improving mungbean productivity in the paddock

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Across Australia performance of pulse crops can be highly variable and risk of low yields leads growers to the perception that they are a high-risk crop. While high potential profits have encouraged many growers to persist the factors causing yield gaps and variability are poorly understood and a range of abiotic and biotic yield-reducing factors are likely to be important. In the northern grain region new higher yielding mungbean varieties in combination with high marketability have lead to a rapid increase the area planted across the region somewhat overcoming their tradition reputation as mongrel beans. In this study we aimed to use a paddock survey approach across three main mungbean growing areas in the northern grain region to assess yield variability and the effects of paddock conditions on yield gaps. This was combined with simulation modelling approach to determine the water-limited yield potential and estimate yield gaps of mungbean crops across a diverse range of environments and growing conditions. The objective was to identify likely factors that may be related to poor mungbean crop performance.

Key findings include: low yields and high yield gaps were associated with low harvest index, not always low crop biomass; there was no regional differences in the frequency and size of yield gaps for mungbeans and management factors found to significantly increase yield were narrow row spacing (<50 cm and crops sown on a fallow rather than double cropped. Benchmark water use efficiency of approximately 7.5 kg/ha.mm of available water (rain + starting soil water) were found across the data collected. Differences in starting water at this WUE explained observed yield differences between fallow and double crop mungbeans. One third (35%) of crops achieved > 80% water limited yields but 36% yielded < 60% of the water-limited yield potential. Nearly half of all monitored crops had yield gaps > 500 kg/ha. No single biotic or abiotic factor was found to be associated with low mungbean observed crop yields or high yield gaps. However, rather a combination of factors led to farmers losing yield in the paddock. In the paddock, 88% of crops with a high yield gap (< 65% water limited yield) had either *P.thornei* > 3/g or maximum temperatures > 39C during flowering or starting soil nitrate levels below 65 kg N/ha.

Paper ID: 110, Improving pulse nodulation in stressful environments

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New rhizobia to improve the nodulation and production of faba bean and lentil on acid soils

As the area sown to faba bean and lentil expands, crops are being grown in areas where soil acidity (pH less than 5.0, measured in 0.01M calcium chloride) is limiting crop nodulation and performance. Beans in the high rainfall areas of western Victoria and south-east South Australia (SA) and lentils on well drained acid soils in parts of SA and southern NSW are known to be affected. It is likely to become an issue in other areas, if soil pH continues to decline.

The nodulation of faba bean, lentil, pea and vetch by *Rhizobium leguminosarum* bv. *viciae* (*Rlv*) is sensitive to soil acidity. Below pHCa 5.0, proliferation of the rhizobia around plant germination, steps in the nodulation process and persistence of the rhizobia in the soil are detrimentally affected. Since strains of rhizobia can vary in their acidity tolerance, work is being undertaken to determine if there are strains with greater acidity tolerance than WSM1455, the current Group F inoculant strain for bean and lentil.

Strains of *Rlv,* including some sourced from acidic soils, were selected for further assessment, based on their ability to nodulate seedlings growing in hydroponic solutions maintained at pH 4.2.

Promising *Rlv* strains (SRDI-969, SRDI-970 and WSM-4643) have now been tested at up to 19 field locations (mainly in SA and Vic., covering a range of hosts and soil types) to examine their effect on nodulation, crop biomass production, N2-fixation and grain yield. Included are two studies of soil colonisation by the rhizobia. The ability of the strains to survive on seed post inoculation has also been examined.

Pulse crop performance on acid soils was consistently improved by rhizobia strain SRDI-969, compared to WSM1455. Site means for nodulation, legume dry matter, N2-fixation and grain yield were increased on average by +56, +15, +24 and +14 percentage units respectively. The same measures were increased by approximately +30, +7, +6 and +5 percentage units, by strains SRDI-970 and WSM-4643. Regardless of the rhizobia strain used, nodulation was

reduced to negligible levels at pH 4.2, indicating the requirement for liming to increase soil pH above that level.

In acid soil colonisation studies, strains WSM-4643 and SRDI-969 were more persistent and increased nodulation compared to WSM1455. However, soil colonisation by the rhizobia was still limited, indicating that re-inoculation will be needed each time the crop is grown and that there may still be opportunity for further strain improvement.

Survival of the rhizobia strains on seed stored in the laboratory (lentil and bean) varied. In this regard, SRDI-970 survived at highest number. WSM-1455 and SRDI-969 survived at lower but similar number. WSM-4643 survived least well, which may explain reduced nodulation by the strain in some field trials.

Although WSM-1455 has consistently been out-performed, none of the alternative strains performed best across all measures. In terms of crop impact, SRDI-969 has performed best so far, with further evaluation underway in 2019. Pending the outcome of current trials, the replacement of WSM-1455 is planned for 2021.

The efficacy of rhizobial inoculants when sowing pulses into dry soil

With a push to increase the area of pulses cropped in areas traditionally considered marginal comes new challenges. One of these challenges in less reliable rainfall, to help manage this risk farmers often look to dry sow legumes to better manage time demands around sowing and ensure early establishment of crops. However, where legume inoculation is required, there remains a need to improve inoculation guidelines.

A series of greenhouse and laboratory experiments were completed to determine the survival of rhizobia under simulated dry sowing conditions. The three different rhizobia strains assessed (chickpea -Group N strain CC1192, faba bean-Group F strain WSM1455 and lupin-Group G WU425) all had similar survival rates when applied as peat slurry on seed and sown into a dry acid soil (0.5%w/w, pHCa 4.9). Numbers decreased tenfold between 24h and 14 days post sowing. Factors such as soil type, moisture level, temperature, inoculation rate and seed chemical dressing (P-Pickle T) impacted on the survival of bean rhizobia on seed.

Seven field trials were conducted at four field sites in South Australia in 2017 and 2018 to assess the efficacy of a range of inoculant carriers when sown into dry soil. Three trials included multiple times of sowing (ranging from 0-4 weeks in dry soil (<2% w/w) and another three trials included different inoculant rates (peat on seed). Crop differed with site

and included faba bean, lupin, chickpea and field pea. Nodulation (number and/or weight per plant), shoot and root dry weight was measured 10 weeks after crop emergence, peak biomass, shoot % N, %Ndfa (N derived from atmosphere 15N natural abundance technique, Unkovich et al. 1997) was measured at mid pod fill and grain yield.

Standard inoculation (peat slurry on seed) practices did not provide satisfactory nodulation, especially where extended dry conditions (>2 weeks) were combined with other stresses such as low pH. Doubling the rate of peat slurry inoculant applied to seed significantly improved nodulation of bean, lupin and chickpea when sown into dry soil. The performance of granules varied with carrier and year, however granule formulations that delivered high numbers of rhizobia (>400,000 cells/ seed equivalent) improved nodulation of pulse crops under extended dry sowing conditions.

Ref: Unkovich MJ, Pate JS and Sanford P, 1997, Nitrogen fixation by annual legumes in Australian Mediterranean agriculture, Aust. J. Agric. Res. 48, 267-93.

Paper ID: 92, Alternative legume crops for the southern region of Australia

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Grain legume crops constitute 10% of grain production across the south-east region of Australia, with potential to increase this through diversification of available legumes for summer and winter seasons. Grain legume production in the southern region is dominated by winter crops; lentil, chickpea, field pea and faba bean, with limited summer options. Alternative legume crop options could improve the efficiency and profitability of farming systems through access to higher-value markets, increased break crop and fodder options and by maximising resource capture within the system. Alternative legume species being tested include adzuki bean, black gram, black turtle bean, borlotti bean, burgundy bean, cowpea, fenugreek, kidney bean, lab lab, mungbean, narbon bean, navy bean, pigeon pea and soybean. Many of these crops 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.

To assess the agronomic suitability of alternative legume species across a range of agroecological zones (low, medium and high rainfall) in both winter and summer, five early sown winter field trials were established across the southern region. Key issues under investigation include optimal time of sowing, sensitivity to abiotic and biotic stresses, opportunities for grain and graze and management of weeds through herbicide options. Across all trials, good crop establishment (ca 90% at all sites) and early plant vigour was observed for the majority of species, and the effects of cold temperature on subsequent growth are being monitored. Initial observations indicate that the temperature and rainfall gradient has adversely affected plant growth, with greater crop growth occurring under the higher temperatures at the Mallee site.

This research program is also screening a broad range of legume crops from the Australian Grains Genebank (AGG) to identify potential germplasm suited to the southern farming region. This will help define the physiological and phenological traits suited to the southern

region, providing opportunity to increase the adaptation of viable alternative legume crop options through breeding solutions. Remote and proximal sensing technologies are being used to monitor plant growth, vigour and canopy architecture and biophysical modelling used to identify potential growing environments across Victoria. Ultimately, this program aims to identify crops and management strategies that can expand the range of legume crops available to the grains industry for both winter and summer plantings. This will help growers to better manage pests and disease, build soil nitrogen, utilise out of season rainfall and improve farm profitability.

Paper ID: 19, Developing pigeonpea as a new profitable and resilient summer pulse crop for Queensland

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[1] DAF

Pigeonpea (Cajanus cajan) is gaining attention as a potential new pulse crop for summer production in Queensland and northern NSW. Current summer pulse 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. Pulse exporters are also seeking a reliable supply of high quality pigeonpea to service expanding and potentially lucrative market opportunities in South Asia.

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

In response, the Department of Agriculture and Fisheries (DAF) in Queensland is undertaking a major initiative to develop the potential of pigeonpea as a new pulse crop. This project is delivering an integrated platform of R&D to identify potential genetic options and management strategies that could 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 is also fostering 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.

13:30 - 15:05: Value Adding Pulses

Paper ID: 107, New products and Market Opportunities

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[1] Australian Plant Proteins

Australian Plant Proteins (APP) Objective

APPs objective is to develop a premium plant-based protein powder processing, packaging & distribution business for both domestic and international markets. This facility will have the following objectives of:

- supplying protein powder, sourced from only Australian grown raw materials, to a global market to meet the increasing demand for plant proteins; and

- provide R&D capabilities for customers who are seeking plant-based ingredients to meet specific formulation and customer requirements.

APP will sell directly to large consumers of protein powder as well as via an existing plant protein distribution network to smaller customers.

Market Opportunity

Whether for flexitarians, vegetarians, vegans or simply healthy eating consumers, plant-based foods are making inroads.

The worlds population is forecast to increase by 22% between 2010 and 2030, which means an extra1.5 billion people to feed. Changes in dietary habits resulting from rising living standards will also lead to an increase in the demand for food. Given that the majority of the worlds population is currently at the beginning of the first dietary transition, demand for plant oils should increase by 39% by 2030, while demand for plant and animal proteins will increase by 40%.

Benefits of Legumes (Pulses)

The advantages of legumes include the following:

- high protein content and high levels of amino acids that determine protein value

- particularly high soluble fibre content (baroreceptors and key satiating effect of short-chain fatty acids)

- high proportion of resistant starch after cooking

- protease and α-amylase inhibitors (slowed digestion of proteins and carbohydrates)

- long-lasting satiety due to the properties above (they make you feel satisfied and full)

Manufacturing Process

The manufacturing process has been developed and refined in conjunction with CSIRO (Werribee) for the past two years. This proprietary process, owned by APP, extracts high levels of protein and separates out the fibre and starch (by-products) from the protein concentrate.

APP have now established their own R&D manufacturing facility in Werribee, Melbourne.

Target Markets

APP will focus on Australia, UK, Europe and North America for initial market entry. The USA is a market leader in plant-based proteins and many organisations are actively looking for alternative sources of plant proteins for existing and new formulations. Australia is also a progressive plant protein market and an

ideal market for product testing and consumer feedback.

Product Applications

Based on conversations with potential customers, the predominant use for APPs Faba Bean protein will initially be to replace existing plant-based proteins such as Pea and Rice. As companies expand their product offerings and develop new formulations, APP expects that their products will form the basis of these new products as a key protein ingredient.

Examples of potential product applications for Faba Bean as a replacement for Pea, Soya, Rice and Mushroom protein powders.

Some product applications include:
- Breakfast cereals
- Beverages (alcoholic & non-alcholic)
- Meat analogues
- Petcare
- Proteins bars
- Snack foods
- Sugar replacements

Paper ID: 81, Silicon supplementation improved the nutritional potential and sensory properties of drought-stressed lentil seeds as revealed by a novel sensory analysis using non-invasive biometrics from consumers

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Lentil is one of the most important nutritionally rich pulse crops in the world. Despite having a prominent role in human health and nutrition, it is very unfortunate that global lentil production is adversely limited by drought stress, especially in Mediterranean and sub-tropical countries, causing a huge decline in yield and productivity. Furthermore, drought stress can also affect the nutritional profile of lentil seeds. The mineral silicon (Si) is an essential element for plants (especiall under stresses) and a general component of the human diet found mainly in plant-based foods. This study investigated the effects of Si on nutritional (nutrients, antinutrients and antioxidants) and sensory properties of cooked seeds obtained from two lentil genotypes (ILL 6002-drought tolerant) and ILL 7537-drought sensitive) grown in Si-supplied, drought-stressed environment. The sensory properties of cooked seeds (stir-fried and boiled) obtained from lentil plants grown under different drought stress treatments were evaluated using 51 panellists (35 females and 16 males; 20 to 50 years). A novel sensory analysis using an integrated camera system coupled with the Bio-Sensory application was employed to evaluate the unconscious and self-reported responses of the participants. Appearance, color, aroma, flavor, texture and overall liking of samples were rated using a 9-point hedonic scale (1=dislike extremely to 9=like extremely). Biometric measurements (unconscious responses) were acquired from video data acquisition and infrared thermography to obtain a series of physiological (heart rate and skin temperature changes, respectively), emotional and behavioural responses from facial expression analysis (neutral, happy, sad, angry, surprised, scared, disgusted, and contempt, gaze direction and head orientation) from participants during the sample assessments. The facial expressions and emotional responses to different samples were analysed using FaceReader 7.1 software. Significant enhancements in the concentration of nutrients (protein, carbohydrate, total dietary fibre and Si) were found in the lentil seeds along with increase in the antioxidants (ascorbate, phenol, flavonoids and total antioxidant activity). Significant reductions in antinutrients (trypsin inhibitor, phytic acid and tannin) were also recorded (P≤0.05),

irrespective of cooking methods. The results also showed a higher acceptability for lentil seeds obtained from Si treated drought stressed plants with higher flavour, softness and aroma, along with good texture in the stir-frying cooking method. The emotional and physiological responses captured using non-invasive biometrics also lead to similar findings and supported the results from self-reported responses. Principal component analysis explained 88.5% of total data variability along with the covariance matrix ($P \leq 0.05$), showing significant correlations (R=0.6-1) between the nutritional properties of seeds and sensory responses of consumers with the biometric data. Overall, this study demonstrated that Si supplementation of drought-stressed plants can improve the nutritional properties and sensory characteristics of seeds. Thus, this study not only offers an innovative approach in sensory analysis coupled with biometric techniques to accurately assess consumers preference and liking towards tested samples, but also, in the future, would help in making a predictive model for sensory traits and nutritional components in lentil seeds using machine learning modelling techniques.

Paper ID: 35, Influence of processing conditions on pulse flake quality

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Pulses are a healthy and sustainable food source of global significance. Pulse crops like chickpeas and faba beans are gaining popularity with Australian farmers, however, pulse producers face volatile international markets and limited domestic processing markets. Pulse consumption is well below the recommended daily intake in developed countries such as Australia, and the traditional pulse dishes in developing nations are being replaced by ready-to-eat cereals. Therefore, new ways to increase pulse consumption are required, especially in the processed ready-to-eat market. The production of pulse flakes could be a means of increasing pulse consumption if we can address pulse processing challenges such as their structural weakness and long cooking times.

This research investigated the influence of processing conditions on the flaking quality of Australian chickpea and faba bean splits. The process consisted of first conditioning the pulse splits using different steam injection times (one, three or five minutes). Secondly, the softened splits were flaked between two rollers with gap sizes ranging from 0.6 to 1.9 mm. Finally, the rolled pulse flakes were rapidly dried using a fluidised bed drier at either 150C or 200C.

The results demonstrate that the quality parameters of flakes generated using Australian pulses including the degree of cooking, appearance, texture and durability are affected by processing parameters. By optimising processing conditions, it may be possible to produce ready-to-eat pulse flakes that are healthy and add value to pulse grains.

Paper ID: 97, Beyond visual classification: The nutritional value of frost-damaged lentil flour in baked and extruded products

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Lentil (L. *culinaris* Medik.) is a highly nutritious pulse that has long been a traditional food staple throughout the Indian subcontinent and the Mediterranean. Traditionally lentil are prepared through minimal processing and commonly consumed as whole or split. In Australia lentil has become a high-value rotational crop however, unpredictable environmental conditions such as frost events can devalue crops by affecting either the visual appearance of the seed or the seed-size which in severe cases may result in a down-grade to stock-feed value. Todays consumers are well informed and continue to seek food choices based on health outcomes. Consumer choice continues to drive the development of novel food production and pulse flours are being utilised in the manufacture of snack foods, breakfast cereals and pasta products.

This research investigated the potential of using flour derived from frost-affected lentil in the production of composite wheat-lentil bread, cookies and extruded products. Our findings showed that bread, cookies and extruded product made using flour from frost-damaged lentil seed had elevated levels of protein and fibre when compared to wheat only products. No significant difference was observed in the proximal analysis of flour from either premium or frost damaged lentil and confirms the potential application of frost-damaged lentil as a milled flour.

Paper ID: 61, Exploring genetic variation to improve salinity tolerance in faba bean

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Faba bean (*Vicia faba* L.) is one of the most important high protein cool-season grain legumes; however; it is sensitive to salinity stress. Breeding for improved salinity tolerance of faba bean is needed to improve its productivity on saline soils. This study was designed to assess the level of genetic variation for salt tolerance among 22 faba bean genotypes, including 17 Australian varieties, and identification of new genetic resources with desirable combinations of salt tolerance sub-traits. Faba bean genotypes were grown in soil and treated with 0 mM (control) and 100 mM NaCl (salt treated) for 21 days. Salinity tolerance sub-traits related to plant growth (plant height, shoot and root dry biomass), ion accumulation (Na^+, K^+, Cl^- contents in leaf, shoot and root) and photosynthesis (leaf chlorophyll contents, stomatal conductance and leaf chlorosis) were measured in control and salt treated plants. A significant variation was noted amongst the varieties, with PBA Nasma, PBA Zahra, Doza and PBA Samira identified as tolerant varieties and Manafest, Nura and Fiesta as sensitive ones. The most tolerant varieties (PBA Nasma and PBA Zahra) possessed better ability to maintain higher leaf K^+/Na^+, low leaf Cl^- accumulation, lower root K^+/Na^+ and less leaf chlorosis, resulting in higher total (shoot and root) dry biomass production. Leaf and shoot Na^+ and Cl^- contents, considered as major salt tolerance sub-traits, exhibited significant positive correlation with leaf chlorosis, but not with total dry biomass (shoot and root). However, the root Na^+ contents were positively correlated with total dry biomass and negatively correlated with leaf Na^+ level. The ability of plants to accumulate higher Na^+ contents in roots and restrict its transportation to leaves was associated with salt tolerance. These results also suggest that different salt tolerance sub-traits varied independently, and higher salt tolerance could be achieved through different combinations of salt tolerance sub-traits.

Paper ID: 58, Survey of emerging pulse root diseases in South Australia

Tara Garrard[1]

Kelly Hill[1], Laura Davies[1], Blake Gontar[1], Katherine Linsell[1], Daniele Giblot-Ducray[1] and Alan McKay[1]

[1] SARDI

In South Australia the occurrence of pulse root diseases has been increasing with the intensification of pulses in cropping rotations. During the 2018 growing season, SARDI have initiated a pulse root survey to assess the prevalence and distribution of known soil-borne pulse root pathogens and to detect the occurrences of new pathogens. The survey will continue throughout the 2019 and 2020 growing seasons.

Pulse root samples were sent to SARDI by growers and agronomists predominantly from the South East region of SA. Excess soil was washed from the roots and any plant material above the basal stem was removed. Pulse root DNA was extracted from the dry samples and analysed using a test panel of 22 quantitative real time PCR tests. The tests have been developed by SARDIs Molecular Diagnostic Centre for the detection of known pulse pathogens. In addition Next Generation Sequencing was used to identify potential new pathogens.

The survey has so far collected almost 100 samples of pulse roots from crops, most of which were showing signs of poor performance. The crops included chickpea, lentil, faba bean, field pea, lupin, vetch, clover and Lucerne. Canola was also included in the survey.

From the pathogens currently assessed by the pulse test panel, *Pratylenchus neglectus*, *Pythium* clade F and *Didymella pinodes/Phoma pinodella* were the most prevalent in the samples analysed. *Rhizoctonia solani* AG8 and 2.1, *Pythium* clade I and *Macrophomina phaseolina* were also present at significant levels. *Aphanomyces euteiches* was found in 18% of samples, all from faba bean crops experiencing moderate to severe root rot symptoms. There were no detections of *Phytophthora medicaginis*, a known cause of root rot in chickpea, in the samples received despite some samples showing symptoms consistent with the disease.

The Next Generation Sequencing have detected multiple species of *Phytophthora* and *Fusarium*, which could be potential pathogens on pulse crops. This data provides valuable insight into which pathogens are emerging in South Australia and should be further investigated in host range, pathogenicity and disease management work in the future.

Paper ID: 51, Driving research discovery in pulse legumes - current outcomes from the ARC ITRH - Legumes for Sustainable Agriculture

Brent Kaiser[1]

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Legumes for Sustainable Agriculture (LSA) is an ARC Industrial Transformation Research Hub based at the University of Sydney. LSA is co-funded by the Grains Research and Development Corporation and involves seven other university and two state government partners for a collective national research effort in confronting abiotic stress in pulse legumes. LSAs major themes are in the areas of heat, drought and salinity tolerance with below-ground traits exploring nitrogen access and symbiotic partnerships. Over the last three years, using chickpea as a model system, we have made progress in discovering new processes to identify abiotic stress tolerance which can be delivered to pre-breeding activities and eventually made available to breeders for trait incorporation to commercial germplasm improvement programs. In this talk, Ill highlight current research outcomes and the stages of our research program aimed at delivering new research tools and outcomes for the Australian Pulse Industry.

15:40 - 16:25: Pushing Yield Boundaries

Paper ID: 87, The Internet of Things

Mark Gould[1]

[1] Agriculture Victoria

Introduction to the Internet of Things (IoT), addressing the what, why, where, how and when of IoT, including some examples of how IoT can be applicable On Farm. Addressing how IoT devices have come about, what is and isnt an IoT device, and what networks are suitable for IoT.

Paper ID: 24, Expanding pulse production through extension - Pulse Check discussion groups

Prudence Cook[1]

[1] Birchip Cropping Group

The *Building capacity, skills and knowledge for the pulse industry in the Southern Region: Supporting expansion of high value pulses into new areas and ensuring sustained profitability of all key pulse crops in existing areas* project is funded by the Grains Research and Development Corporation (GRDC). The project started in August 2017 and will conclude in March 2020.

The purpose of this investment is to realise the potential long-term farming system and financial benefits of pulse crops in the Southern Region through targeted expansion of pulse crops into new areas while fostering sustainable intensification of pulse crop production in existing areas.

The project aims to improve the skills and knowledge of growers and advisors in the southern region in relation to profitable pulse crop production and agronomy, allowing them to exploit the systems and financial benefits of pulse crops in a sustainable manner. At the projects completion, growers and advisors will have improved confidence in the agronomic management of key pulse crops for their sub-region; an awareness of the major risks associated with production; and appropriate management strategies in place to mitigate risks identified.

A core component of this project is the establishment of Pulse Check discussion groups. These groups have been established in areas where pulses, in particular chickpea and lentil, are not commonly grown and where grower and advisor knowledge of pulse production may be limited. The groups are designed to share learnings (experienced pulse producers and advisors are invited to participate) and address key concerns and constraints to pulse production at the local level, so that future research, development and extension activities can be tailored to local needs.

Twelve groups have been established extending from the Eyre Peninsula to north-east Victoria. Each group is facilitated by a local representative (agronomist, consultant or farming systems group personnel) and meets four times a year. Meetings coincide with the pre-sowing, early post-establishment, pre-canopy closure and pre-harvest periods for each area.

Prior to each round of meetings, facilitators participate in a train-the-trainer webinar with renowned pulse experts so that they can be upskilled in core components of pulse production. Facilitators then design their meetings according to their group needs. Some groups have also taken bus trips to more established pulse areas to learn from long-term growers and local experts.

A key component of the project is the establishment of a local trial site (a complementary GRDC investment). The Pulse Check group have input into trial design and visit the site throughout the season, enhancing their learning through these local trials.

Detailed evaluation of participant practice change will be collected at project completion. The project will also deliver a series of participant case studies and an analysis of the financial risk associated with pulse production in these new, non-traditional pulse areas.

Paper ID: 20, High throughput aluminium toxicity tolerance screening in lentil to expand production area

Vani Kulkarni[1]

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[5] Australian Grains Genebank, Agriculture Victoria, Grains Innovation Park, 110 Natimuk Road, Horsham, Victoria 3400, Australia.

Lentil (*Lens culinaris* ssp. *culinaris*) is one of the oldest domesticated crops, and serves as a valuable source of dietary proteins, minerals, fibre and carbohydrates. In Australia, ~50 Mha of the agricultural soils have a surface pH < 5.5, and 12-24 Mha have pH <4.8. Major grain crops and pulses are affected by acid soils and annual total losses to agriculture is estimated to be AU $9001585 million. Lentil is sensitive to soil acidity and its annual production in Australia comes mainly from north-western Victoria and South Australia. In acid soils with pH below 5.5, phytotoxic forms of Aluminium (mainly Al^{+3}) become available and inhibit root growth, resulting in reduced yields. Development of lentil varieties with Al toxicity tolerance will be the most efficient and economical way to manage acid soil limitations. The results of this research will enable breeding programmes to use AGG germplasm to produce new, more productive lentil varieties and will enable lentil production to be expanded into other areas of Australia with acid soil conditions. In this study a high-throughput hydroponic screening method was developed for Aluminium (Al) toxicity tolerance screening at the seedling stage for lentil. Diverse germplasm of 111 lines including Focused Identification of Germplasm Strategy (FIGS) lines, local landrace varieties and adapted lines from 18 countries were obtained from Australian Grains Genebank (AGG). Uniform 4-day old seedlings were treated in three-day 5m Al treatment and relative root growth (RRG%) was

assessed. Results showed significant variation for Al toxicity tolerance with 26% of the lines with higher RRG% than the known tolerant line ILL6002 (37.9%). Very tolerant lines AGG70137 and AGG70256 with RRG% greater than 52% were identified in the FIGS set. Histochemical analysis supported the hydroponic results with the tolerant lines AGG70137 and Northfield showing less Al accumulation, plasma membrane damage and lipid peroxidation compared to the sensitive Precoz and AGG70530 lines. Screening of a subset of lines in an acid soil in growth chamber differentiated some tolerant and sensitive lines for all the traits tested based on relative performance (as % limed treatment) but these results were not statistically significant due to the complexity of interactions in a soil-based system. Medium correlation ($r^2 = 0.58$, $p<0.001$, n = 15) obtained with RRG% and number of lateral roots showed the effect of Al toxicity in acid soil is more prominent in sensitive lines than the tolerant lines. This work has developed a high throughput screening method for Al toxicity tolerance for lentil and identified new tolerant germplasm lines. This germplasm will be evaluated with a Genome Wide Association Study (GWAS) to identify potential markers/genes for Al toxicity tolerance.

Paper ID: 6, Waterlogging tolerance in lentil

Lachlan Lake[1]

Victor Sadras[1]

[1] SARDI

Lentil is vulnerable to damage and yield loss from waterlogging. Waterlogging can occur at any time in the growth cycle and is common on shallow duplex or poorly drained soils, or in combination with persistent or extreme precipitation. Here we present a pilot study to screen for waterlogging tolerance with a focus on the timing and duration of waterlogging in 10 common Australian lines. Using potted plants, we found measurable responses to waterlogging around 24 days (~ 330 °Cd-1) after emergence for a period of 14 days submergence. We also demonstrate the use of alternative phenotyping techniques.

Paper ID: 49, Exploiting wild germplasmto expand the genetic diversity and enhance the adaptive potential of domesticated chickpea

Lars Kamphuis[1]

Toby Newman[1], Silke Jacques[1], Christy Grime[1], Fiona Kamphuis[1], Rob Syme[1], Yuphin Khentry[1], Kristy Hobson[2] and Robert Lee[1]

[1] Centre for Crop and Disease Management - Curtin University

[2] Department of Primary Industries

Chickpea (*Cicer arietinum* L.) is an important legume crop, which is produced and consumed worldwide, with Australia being the second largest producer and the largest exporter of chickpea [1]. However, chickpea production is constrained by several biotic and abiotic stresses, as well as its particularly narrow genetic base [2].

In order to overcome these limitations and, ultimately, improve the currently stagnant yields of chickpea for Australian growers, wild relatives can be exploited. To this end, we are utilising a collection of wild *Cicer reticulatum* and *Cicer echinospermum* accessions, which are the direct progenitor and a sister species of chickpea, respectively [3].

With a view to expand the genetic diversity of chickpea, diverse wild genotypes have been crossed with an elite Australian chickpea variety, namely PBA HatTrick. Segregating populations derived from these crosses have been assessed in the field for various agronomically important traits, such as flowering time and growth habit. Genotyping of these populations will enable us to investigate the genetic basis of these valuable traits.

In addition to this, we have taken a more targeted approach to improving resistance to ascochyta blight, a devastating fungal disease caused by *Ascochyta rabiei*. Screening of the collection has revealed some promising accessions that displayed resistance against a diverse set of isolates, hinting at possible sources of durable ascochyta blight resistance. Mapping populations are being generated to elucidate the underlying QTLs associated with resistance.

References:

[1] FAOSTAT data, 2017, http://www.fao.org/faostat/en/#data

[2] Abbo S. et al., 2003, Funct Plant Biol 30, 1081-1087.

[3] von Wettberg E.J.B. et al., 2018, Nature Comm, 9, 649.

Thursday, 17 Oct 2019

08:30 - 10:30: Smart Farms And Remote Sensing

Paper ID: 108, Retrieval of physiological plant traits using airborne imaging spectroscopy and thermal data: physical vs. data driven methods

Pablo J. Zarco-Tejada[1]

[1] The University of Melbourne

Progress made in hyperspectral remote sensing methods over the last 20 years has enabled the development of new spectral traits linked to plant functioning, including the quantification of the solar-induced fluorescence. New developments in sensor miniaturization and physical modelling techniques have enabled a fast progress in the estimation of such plant traits and on the early detection of stress as part of precision agriculture and plant breeding efforts. Although a tremendous push in hyperspectral and thermal technology has been achieved, proper interpretation of the spectral signatures is required to quantify traits linked to plant photosynthesis and transpiration. Empirically-based data-driven methods have re-emerged as part of new artificial intelligence algorithms offering new capabilities for the analysis of large spectral datasets. Nevertheless, limitations of these empirical methods exist as they lack proper understanding of the photon-vegetation interactions and the physiological drivers underlying such non-linear relationships. The use of these physiology-based spectral plant traits along with deep-learning algorithms will be described, discussing the successes and limitations for the operational use in plant breeding and precision agriculture.

Paper ID: 96, High-throughput field phenotyping for important crop breeding traits

Sameer Joshi[1]

Joshua Koh[1], Bikram Banerjee[1], Babu Pandey[1], Garry Rosewarne[1] and Surya Kant[1]

[1] Agriculture Victoria, Grains Innovation Park, 110 Natimuk Road, Horsham, Vic 3400, Australia

Precise and rapid phenotyping is critical to speed-up breeding for improved varieties of field crops. Non-destructive phenotyping techniques are preferred over destructive methods as they allow for repeated measurements and more informative data capture in a cost-effective manner. Sensor and camera-based equipment can provide non-destructive, precise and high-throughput measurements of traits for crop breeding. Here, we describe how we have deployed customized aerial imagery platforms and infrastructure. We show examples of application of phenotyping platforms to measure traits such as nutrient and water use efficiency, disease resistance, and screening large reference population to support molecular and genomic breeding and to take informed breeding decisions for the development of improved crop varieties. We also describe how we have developed workflows for image processing and analysis to extract data at the plot level from our aerial imaging platforms, which are equipped with a range of multispectral and thermal sensors, and high-resolution cameras. We currently measure a range of agronomic and growth traits including emergence count, plant height, phenology, canopy coverage, biomass, growth rate and plant health. Our aerial imaging capabilities enable high-throughput phenotyping of large-scale field experiments across the entire growth cycle for a range of crop species including wheat, canola, safflower, field pea and lentil with precision, repeatability, time and cost efficiency compared to conventional phenotyping methods. Results will also be presented for the application of a multispectral camera that gives normalized difference vegetation index to correlate with disease scores for the assessment of bacterial blight in breeding trials.

Paper ID: 86, Lentil sensitivity to frost and rapid detection in field using proximal sensors

Audrey Delahunty[1]

Eileen Perry[1], Ashley Wallace[2], Alexander Clancy[2] and James Nuttall[2]

[1] Agriculture Victoria

[2] Agriculture Victoria - Horsham

Radiant frost limits production and export value of lentil in southern Australia, by reducing grain yield and quality. Increased understanding of the impact of frosts, including severity and growth stage effect will enable effective management and limit associated financial losses. Further, non-destructive measurements (handheld, UAV or satellite imagery) would be useful to assess the extent of frost damage at paddock scales ahead of harvest. To address these research gaps, active frost treatments were applied to field grown lentil at different intensities, using mobile frost chambers, at Horsham (2017) and Ouyen (2018), Victoria. Experimental work in 2017 assessed the response of lentil (cv. Jumbo 2) to 12 frost scenarios, where temperatures below 0C were applied at; flowering, early pod, flat pod, filling-filled pod. This study determined that lentil was most susceptible to frost during the pod filling stage, where for every degree hour below zero, there was a 2% reduction in grain yield. This compared to the response at flowering, where a threshold of 31C.hr (<0C) was reached prior to yield reduction, and thereafter yield decline was 3.8% per C.hr. Experimental work in 2018 (Ouyen) was expanded to assess if Group B herbicide (imidazolinone (imi)) tolerance in lentil was linked to increased sensitivity to frost. Frost was applied at the late vegetative and late podding stage, where four imi lentil varieties (PBA Herald, PBA HurricaneXT, PBA HallmarkXT, CIPAL1721) and two conventional lines (PBA Jumbo 2 and PBA flash) were tested. Under applied frost conditions (severe), conventional and imi lines were equally affected by frost during the late vegetative and reproductive period. This result infers that the increased visual symptoms of frost damage in imi tolerant lines (e.g. PBA Hurricane XT) observed by industry, is unlikely to translate to greater yield loss due to frost. As part of these trials, proximal sensing was used to monitor the crop. A handheld active light fluorometer was used to measure SFR_G, an index related to chlorophyll concentration. Spectral reflectance of the canopy was used to determine the Normalized Difference Vegetation Index (NDVI) and the Photochemical Response Index (PRI). The results show that in addition to the proximal measurements detecting natural senescence occurring during the period from flowering to pod fill, it also detected a decrease in canopy chlorophyll associated with cold

exposure, beyond a threshold cold sum value (5 31C.hr). NDVI from canopy reflectance measurements was related to cold sums across pooled measurement dates with an R^2 value of 0.81. The reflectance index PRI increased with increasing cold exposure (R^2 value of 0.61), indicating changes in photosynthetic efficiency with increasing frost damage. SFR_G from the active fluorometer measurements was related to cold sums with an R^2 value of 0.84 six days following frost application at flowering, and 0.72 eight days following frost at pod filling. Next steps will include assessment of other sensors, additional growth stages, and response to frost for other lentil varieties.

Paper ID: 103, Application of machine-vision to assess admixture and discoloration in lentil and field pea

Linda McDonald[1]

Jason Brand[2] and Joe Panozzo[3]

[1] **Department of Jobs Precincts and Regions**

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Lentil and field pea are typically traded based on broad market classes. Market acceptance is largely driven by the visual appeal of the split or whole-grain product. Colour and uniformity are major indicators of the grain quality however these have traditionally been assessed by subjective visual inspection. Colorimeters have also been used for assessment of grain colour and while these instruments are objective, they are not able to capture the variation and distribution of colour traits across the grains. Moreover, in the context of assessing pulse-specific quality traits, the pre-defined colour spaces used by colorimeters are not always intuitive.

Machine vision systems, comprising image capture and analysis, are becoming increasingly popular for quality evaluation of agricultural products. These systems offer the potential for objective, consistent, high-throughput and non-destructive assessments. Through image analysis visual properties of lentil and field pea grains can be quantified with mathematical models. Size and shape features can be calculated by transformations of the seed boundary coordinates and, provided the image-acquisition light-source is consistent, colour features can also be objectively defined through modelling.

In this study we apply a machine vision approach based on multi-spectral images to assess admixture and quantify the magnitude and distribution of discoloration in lentil and field pea grains. Visual features of the grains relating to size, shape and colour were extracted from digital images and used to train the models. Seed admixture was determined through Linear Discriminant Analysis models for quantifying levels of lentil off-types within lentil samples, field pea off-types within field pea samples and vetch seed within lentil samples. Discoloration of grains was quantified through transformations of modelled visible-reflectance spectra.

Paper ID: 47, High throughput phenotyping for assessment of bacterial blight in field pea

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Bacterial blight is a major disease of field pea that causes significant yield losses worldwide. Breeding resistant cultivars is crucial to minimize yield losses from this disease. Employing high throughput phenotyping methods in breeding programs can save significant time and efforts when assessing the disease across larger breeding trials. In this study, an unmanned aerial vehicle (UAV) mounted with multispectral camera (Micasense Red Edge) was used to acquire images that were processed to generate normalized difference vegetation index (NDVI) from five co-located field pea breeding trials (stage 0 to stage 3 trials and PHISTHO18) at Horsham in 2018. A handheld device Crop Circle (ACS 470, Holland Scientific, USA) was used to record NDVI scores from two trials (stage 2 and PHISTHO18) in 2-15 days interval from 27th August to 5th December. Visual scores bacterial blight disease were also recorded on a 1-10 scale (1=resistant, 10=susceptible) from all the trials. Yields were obtained from machine-harvest of the whole plots. Yield losses were assessed for four check varieties present in all the trials. The check varieties had different levels of disease resistance; PBA Percy (moderately resistant, MR), PBA Oura and PBA Butler (moderately resistant to moderately susceptible, MRMS), and Kaspa (susceptible). Yield losses were estimated as the percentage yield loss in the plot most affected by the disease compared with the one least affected by the disease. The yield losses were, Kaspa 55%; PBA Butler and PBA Oura 22 and 37%, respectively; and PBA Percy 32%.

NDVI had significant positive correlations (r = 0.39 to 0.778) with plot yield and significant negative correlations (r = -0.39 to -0.73) with visual scores of the disease in all the trials except in the stage 3 trial. Correlation analysis of NDVI recorded with Crop Circle at different times showed that the NDVI recorded on 16th October had the strongest correlations with plot yield and visual scores of the disease in stage 2 and PHISTHO18. The second half

of the September suffered from multiple frost events with a cumulative 62 hours of below 0 C temperatures. Strongest correlations of NDVI on 16th October with plot yields and visual scores of the disease possibly was a result of the frost events which consequently exacerbated the disease. Frost driven bacterial blight epidemic is evident from strong correlations among NDVI scores measured on 16th October with plot yields and visual scores of the disease.

The results clearly demonstrated that susceptible varieties suffered substantial yield loss compared with the MRMS and MR varieties in field conditions. In summary, NDVI captured bacterial blight disease scores and could be used as high throughput phenotyping technology to assess the disease in breeding trials.

Paper ID: 79, Do sensors explain the advantage of navy bean intercropped with maize under limited water and N environments?

Abeya Temesgen Tefera[1,2]

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[2] Agriculture Victoria Research

Sensor technology has been widely used under field conditions to improve our understanding of crop stress level to a wide range of production factors. Here we used active and passive sensors, such as infrared thermometer, SunScan canopy analysis system and neutron moisture meter to understand the physiological and environmental drivers of navy bean-maize intercropping advantage as the level of water and N input decreases. Field experiments were carried out at Gatton research station of the University of Queensland in 2011/12 and 2012/13 summer seasons. Navy bean maize intercropping systems and their sole crops were evaluated using automatic rainout shelters in three trials viz., under low water/nitrogen (W/N), medium W/N and high W/N conditions. Sensors were deployed to quantify the aboveground and below ground production factors, viz., plant available soil water, fraction of intercepted photosynthetic active radiation (fPAR), relative humidity and temperature both inside and outside canopy of sole and intercropping systems. Canopy stress index as well as productivity index viz., Land Equivalent Ratio (LER), were computed to assess the stress level of component crops and grain intercropping advantage gained over their sole crops. Resource use (i.e. water, nitrogen and light) and use efficiency were analysed in both intercropping and sole cropping systems. The result indicated that the higher the level of water and nitrogen, the lower the advantage of intercropping system in terms of LER. Under low water and N input, intercrop navy bean had lower canopy temperature and stress index values compared to sole crops. In addition, intercrop system intercepted significantly higher fPAR than both sole crops for long growing period under limited water and N availability. The intercropping advantage (in terms of LER) was directly related to the intercropping advantage on systems water use efficiency (not to water use) and systems N use (not to NUE). However, there was no clear relationship between the intercropping advantage (in terms of LER) and radiation intercepted or use efficiency. Overall, this research has demonstrated that sensors appear to be more applicable in explaining factors driving intercropping advantage as the level of water and N availability decreases. From this finding, it seems that intercropping of navy bean with maize might have maintained navy beans temperature in a water stressed environment.

Further research efforts should be needed to automate the sensors we used for applications at a larger scale in pulse based cropping system.

11:00 - 12:25: Pushing Yield Boundaries

Paper ID: 109, Pea genomics for advanced breeding strategies

Judith Burstin[1]

[1] INRA

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Pea genomics has significantly progressed in the last decade. The recently published pea genome sequence provides an improved reference and allow progressing in the identification of candidate genes, locating QTLs, and predicting genomic-enabled breeding values. We will show examples of how large-scale transcriptome approaches reveal complex regulatory networks at play during seed filling, multi-environment and multi-population studies allow reducing QTL confidence intervals, and genomic selection holds promises for breeding complex traits.

Kreplak *et al*. 2019 A reference genome for pea provides insight into legume genome evolution. Nature Genetics volume 51, pages14111422 (2019)
https://doi.org/10.1038/s41588-019-0480-1

Paper ID: 55, Genomic Selection in pulses

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Genomic selection (GS), which incorporates genome wide marker information to predict the breeding values of individuals in a breeding population, is rapidly becoming an important selection tool in plant breeding. One of the major advantages of using GS in plant breeding is its ability to predict the phenotypic performance of individuals early in the breeding cycle, hence, reducing the generation interval and thus increasing genetic gain. We evaluated its efficacy using c. 2,000 advanced breeding lines from the Australian lentil breeding program. These lines were evaluated annually in a range of environments from 2010-2018 for economically important traits including grain yield, grain weight, disease resistances and abiotic stress tolerances. A genotyping-by-sequencing approach was used to genotype the breeding material and over 200,000 SNPs were identified. The ability to genomically predict the observed phenotypic performance was explored by forward prediction and applying a range of genomic selection models such as GBLUP, BayesA and BayesB as well as incorporating GxE components. Genomic selection has now been fully implemented into the lentil breeding program and prediction equations for yield, grain weight, boron and salt tolerance as well as ascochtya blight and botrytis grey mould resistance have been derived with moderate to high prediction accuracies (0.35-0.70). Optimal crossing schemes have also been designed and applied to increase genetic complementarity, as well as to select elite breeding lines for rapid advancement, reducing the overall generation interval, and increasing

genetic gain. Simulation modelling of the lentil breeding program is currently in progress to design a full GS assisted breeding pipeline.

Paper ID: 99, Transforming Genetic Gain in Pulses

Janine Croser[1]

Federico Ribalta[1], Maria Pazos Navarro[1], Rick Bennett[1], Christine Munday[1], Simone Wells[1], Sabrina Tschirren[1], Kylie Edwards[1], Leon Hodgson[1], Theo Pfaff-Lichtenzveig[1], William Erskine[1] and Judith Lichtenzveig[1]

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Legumes have proven to be useful and, in favourable market conditions, high value components of sustainable cropping rotations. However, the well-known risk of profit margin losses due to market instability, disease, climatic variables, herbicide damage, subsoil constraints coupled with a relatively small research community has moderated their uptake. In the Western Region, the low market price of lupin and competition with oilseeds has decimated the production area of the only widely adapted grain legume option. Producer surveys continue to recognise the development of further legume options as a high priority for weed, pest and disease control and reducing nitrogen inputs. In answer to the need for tools to facilitate the necessary rapid genetic gain in legumes, we began a broad-ranging fundamental and applied seed-to-seed physiology research effort in chickpea, field pea, lupin, lentil and faba bean.

Our findings have enabled the regulation of key components in legume phenology to achieve rapid plant turnover. They include elucidation of biochemistry of seed development for precocious germination (Abstract: Ribalta et al.), understanding the role of light quality when combined with saturation photoperiod and conducive temperatures in the synchronisation and compression of time to flower (Abstract: Bennett et al.) and plant height manipulation for multi-tier, high-density plant growth in controlled environments (Abstract: Munday et al.). The resulting accelerated single seed descent (aSSD) approach enables the turnover of 5-8 generations per year in all the major pulses. In collaboration with breeders and research colleagues, we have successfully integrated marker assisted selection and screening for key production constraints under controlled conditions as part of the aSSD platform. The platform is continuously deployed to accelerate genetic gain within phenotypically diverse segregating breeding populations for our own research and for pulse breeding and research groups nationwide with processing of > 30,000 breeding lines to date.

The knowledge acquired in the domesticated grain legume species provided the basis for fundamental studies into physiology and genetics of phenology in wild *Cicer* species. The

resulting Rapid Gene Introgression (RGI) platform speeds and eases geneflow between the wild relatives *C. reticulatum* and *C. echinospermum* and domestic chickpea enabling seed-cross-RIL interspecific production within two years (Abstract: Pazos-Navarro et al.). The RGI platform has enabled prompt access to inbred wild, cultivated and hybrid accessions and facilitated the evaluation of interspecific geneflow and evolution of wild and cultivated *Cicer* (Abstract: Lichtenzveig et al.). With the aim of expanding the crops adaptation potential, we are currently elucidating the genetic basis of recalcitrant traits, such as response to low temperature (e.g. chilling at reproductive stage). We expect our fundamental studies into genetics and physiology coupled with the aSSD and RGI platforms will have a transformational impact at the farmgate, through both novel gene combinations and rapid delivery of key traits. We acknowledge the continuous support of this research by GRDC investment in partnership with The University of Western Australia.

13:10 - 15:00: Pushing Yield Boundaries

Paper ID: 39, Heterosis and hybrid mimics in lentil

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Heterosis has been used in agriculture for decades making significant contributions to secure global food supply. However, there are drawbacks to using heterosis. One of them is that the hybrid vigor in the F1 generation can only be used for one generation. It is lost because of segregation in the F2 generation. Through strict selection of the best plants over a number of self fertilised generations in Arabidopsis, we have overcome the F1 restriction by generating stable lines with comparable vigor to the F1 hybrid in the F5 and subsequent generations; we designated these lines hybrid mimics. To extend our success to production agriculture, we are attempting to generate hybrid mimics in crops, especially those where a hybrid breeding system does not exist. Our current research is focused on lentils. Lentil is one of the important legumes serving as a main protein resource for a large number of people in many developing countries. As a typical self-pollinated legume, the lentil flowers do not open during flowering until after pollination, which makes it difficult to achieve a hybrid breeding system.

We asked is there any heterosis in lentil? In the evaluation of more than forty different hand pollinated hybrid combinations, including commercial varieties, pre-breeding material and wild species, we found there is seed yield heterosis in lentil. Some hybrids have more than 30% heterosis. We also found that parents differing in flowering time are more likely to have yield heterosis. The next question is whether we can produce stable hybrid mimics. Our results so far are promising. We found several F2 plants which are comparable in yield to the F1 hybrids. A high yielding F3 generation with reduced variation is expected. A more confident statement could only be made when the results of the F5 generation in the middle of next year are available. It would be a great benefit to know if hybrid mimics selection is successful in lentil. It is likely that success in lentil could lead to hybrid mimics in other grain legumes.

Paper ID: 50, GWAS and QTL analyses identify genomic regions associated with resistance to Ascochyta blight in chickpea

Rosy Raman[1]

Annie Warren[1], Jenny Davidson[2], Nicole Dron[3], Niharika Sharma[1], Maheswaran Rohan[3], Kurt Lindbeck[1], Kevin Moore[3] and Kristy Hobson[4]

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Ascochyta blight (AB) - a major endemic disease of chickpea, caused by the fungus, *Ascochyta rabiei* (Pass.) can cause high production losses in all chickpea growing regions worldwide. Deployment of resistant varieties in combination with cultural practices are required for effective management and for long-term sustainability and profitability. Only a few landrace accessions resistant to AB have been identified in the global chickpea germplasm and were subsequently used to introgress resistance in commercial chickpea varieties. The Australian chickpea germplasm is mainly reliant on resistance derived from an Iranian landrace ICC3996. The recent increase in aggressiveness of Australian *Ascochyta rabiei* isolates has resulted in erosion of resistance in current commercial chickpea varieties such as PBA HatTrick. Some of these isolates have also been shown to cause severe disease on ICC3996 as well as the most resistant kabuli variety Genesis090.

The Pulse Breeding Australia (PBA) Chickpea program has made a concerted effort for continued improvement in resistance, by incorporating diverse sources in the breeding pool. As a result, the breeding germplasm has improved levels of resistance to aggressive *Ascochyta rabiei* isolates compared to commercial varieties. The aim of this study was to identify Quantitative trait loci (QTL) and candidate genes associated with AB resistance in the breeding germplasm. We utilised two genome-wide association study (GWAS) panels comprising breeding lines, varieties and landraces and two F$_3$ populations derived from PBA Drummond/CICA1841 and CICA1521/CICA1841 to identify marker-trait associations. The breeding line CICA1841 was identified as moderately resistant to the most aggressive isolates in disease screening nurseries.

All populations were genotyped using genotyping-by-sequencing based DArTseq approach. These populations were evaluated for resistance under field/ glasshouse/shade house

conditions using the most aggressive isolates. The disease severity was measured as percent main stem breakage (MSB), 0-9 rating scale and a disease index (an average of MSB, percent of stems with lesions, side branches with lesions and affected leaf area). QTL and genome wide association analyses identified several genomic regions associated with resistance that were located on all chromosomes with the exception of Ca8. We compared the QTL identified in our study with the previous reports on the basis of the physical locations on the reference CDC Frontier genome assembly v2.6.3. Common genomic regions were identified on chromosomes Ca1, Ca2 and Ca4. In addition to these, we have identified new loci on Ca3, Ca4, Ca5, Ca6 and Ca7. A number of potential candidate genes underlying AB-QTL were also identified. Our study has provided an insight into the genetic basis of AB resistance and identified favourable alleles. The SNP markers associated with AB resistance will increase the selection efficiency of the PBA chickpea program.

Paper ID: 54, Genetic characterisation of synthetic auxin herbicide tolerance in pulse crops

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Weed control remains a major constraint to pulse production in Australia. The rapid adoption of PBA XT lentil varieties and PBA Bendoc faba beans, and the subsequent increase in the use of AHAS-inhibitor herbicides, indicates the industrys desire for herbicide tolerant varieties. It also highlights the need for tolerances to additional modes of action to facilitate best practices of chemical rotation, in order to mitigate the incidence of herbicide tolerance in weed populations.

Synthetic auxin herbicides (SAHs) have been used in Australian farming systems for more than 70 years to control broadleaf weeds in cereal crops. Despite this strong and prolonged selective pressure, weed resistance to these chemistries is surprisingly uncommon compared to other herbicide modes of action, making them an attractive target for herbicide tolerant crop development.

SAHs mimic the plant hormone, indole-3-acetic acid (IAA), binding to the TIR1/AFB subunit of an E3 ubiquitin protein ligase complex, which stimulates the degradation of AUX/IAA transcriptional repressors. This de-repression of auxin-regulated genes results in the expression of herbicide symptoms and eventually leads to plant death.

Through mutagenesis screening techniques, we have identified chickpea, lentil, faba bean and field pea selections with improved levels of tolerance to the SAH, clopyralid (Lontrel). Candidate gene association in bi-parental populations of chickpea and lentil identified a homologue of the *AFB4/AFB5* clade to be associated with the herbicide tolerance trait. Direct sequencing of this candidate gene in multiple tolerant lines identified a range of non-synonymous SNPs in the coding sequence of this gene. Three-dimensional models of the wildtype and mutant AFB proteins reveal that C-terminal truncations are likely to result in a complete loss of function, explaining the herbicide tolerance phenotype. Further genetic and phenotypic characterisation of all tolerant selections is ongoing and is expected to provide a

detailed understanding of the mechanisms of SAH action in pulse crops and allow the rapid and effective incorporation of clopyralid tolerance into new pulse varieties. This is the first report of target-site tolerance to SAHs in any crop species in the world.

Paper ID: 27, Identification and characterisation of a genetic marker for Ascochyta lentis virulence in lentils

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Ascochyta lentis is a necrotrophic fungal pathogen that causes ascochyta blight (AB) in lentil. This pathogen infects all above ground parts of the plant and can reduce grain quality and yield. Our research has focused on the discovery of virulence factors in *A. lentis*, and host specificity in two Australian lentil cultivars, Nipper and PBA Hurricane XT. Recent studies have found many isolates in the *A. lentis* population in Australia that differ in virulence towards these cultivars.

To identify the gene/s associated with virulence, the response of *A. lentis* progeny from a bi-parental population generated from the cross between *Al*Kewell (virulent on PBA Hurricane XT; avirulent on Nipper) and P94-24 (virulent on Nipper; avirulent on PBA Hurricane XT) was evaluated. QTLs in 96 progeny isolates were mapped based on disease response on PBA Hurricane XT and Nipper, and genotyping using ddRADseq. This analysis resulted in the identification of a major QTL, in a region containing a gene with the hallmarks of an effector and was considered the most likely candidate effector for determining virulence. Further investigation of this candidate gene showed major allelic differences between *Al*Kewell and P94-24, with 23 amino acid differences in protein sequence between the two strains for this effector candidate. The two protein forms were designated as K-type (*Al*Kewell) and P-type (P94-24). To validate this as a putative marker, a set of primers were developed to differentiate the two genes using PCR. All 96 bi-parental progeny and a set of *A. lentis* isolates from the SARDI *A. lentis* collection were evaluated and results confirmed that isolates virulent on PBA Hurricane XT or Nipper could be predicted using the PCR marker based on nucleotide polymorphism.

To characterise the proteins for effector activity, agroinfiltration on PBA Hurricane XT and Nipper was performed. Necrosis was observed on PBA Hurricane XT infiltrated with the P-type protein while the K-type protein did not elicit any response from the lentil cultivars tested. Sensitivity of PBA Hurricane XT to the P-type effector from P94-24, which is avirulent on this cultivar, suggests that the P-type effector is an avirulence (Avr) effector.

In this study, we have identified a virulence marker that can be used as a molecular tool to assess *A. lentis* isolates and populations for virulence, while the putative effector can be developed as a valuable resource for effector-guided breeding for AB resistance. It is proposed that two pathotypes in the Australian *A. lentis* population can be designated based on virulence and avirulence responses in these key Australian lentil varieties, and the presence of the K- or P-type effector. A better understanding of the molecular mechanisms of *A. lentis* pathogenesis and the nature by which the pathogen infects its host is key for the development of novel and durable strategies to manage AB in lentil.

Paper ID: 26, Identification and characterization of heterotic genotypes in lentils for enhanced crop productivity

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Heterosis is the superior performance of an F_1 relative to its parents and this phenomenon has been widely studied and commercially used in a range of crop species including maize, wheat, rice and canola. The conventional breeding programme in lentils produces seed yields of 1.5 t/ha and typically experiences increases in yield by 1.13% p.a. Heterosis in other crops has realised increases of c. 20-50%. By applying heterosis and F_1 hybrid breeding to pulses, dramatic increases in productivity, profitability and sustainability could potentially be realised. The current study aims to evaluate hybrid performance across generations (i.e. F_1 to F_6) by identification and quantification of heterotic traits and germplasm in lentil and to understand the underlying genetic and molecular mechanism of heterosis. High yielding genetically divergent parents were selected to make crosses that could produce heterotic F_1s. In a replicated glasshouse experiment, a total of 72 F_1s along with each parent were evaluated for seed number, seed weight, fresh weight, internode number and height. The top three crosses exhibited 62%, 57%, 31% heterosis for seed number and 57%, 50%, 26% for seed weight, respectively with reference to the better parent. The five best performing heterotic crosses were selected (~200 F_2 plants for each line including parents) with a negative control and were progressed to the next generation for phenotypic and genotypic evaluation. The best performing heterotic lines exhibited higher heterotic percentage at F_2 as compared F_1 for all the yield related parameters. In terms of phenotypic evaluation, the F_2 plants were measured for height and internode number during their life cycle at different time points throughout the duration of the experiment. At the time of harvest, the plants were also evaluated for other yield contributing characters to establish an association between different traits. Correlation coefficients were determined, and seed number was found to be positively correlated with seed weight and plant biomass. A strong correlation was not observed for height and internode number with seed number. This phenotypic evaluation suggests an indirect

selection based on component traits. The data across generations will be analysed and compared to understand the phenomenon of heterosis. Based on phenomic observations, genomics of the most heterotic cross shall be analysed through sequencing to determine possible chromosomal combinations that are responsible for causing heterosis.

Paper ID: 76, Identification and characterisation of potential novel sources of resistance to ascochyta blight within the exotic germplasm of lentil

Rama Harinath Reddy Dadu[1]

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Ascochyta blight (AB) caused by *Ascochyta lentis* affects gross profits and yield stability of lentil in Australia. The susceptibility of previously released resistant cultivars (Northfield and Nipper) and a future uncertainty over the resistance status of the few remaining available resistance sources, has necessitated an immediate influx of novel and diverse resistance sources into the Australian lentil breeding program. To aid in this, the potential of exotic germplasm including thirty accessions from five-wild species of lentil collected from Australian grain genebank (AGG), Horsham were screened against two highly aggressive *A. lentis* isolates (FT13037 and FT13038). The bioassay revealed two highly resistant *L. orientalis* accessions (ILWL 180 and ILWL 7) and a ten (*L. nigricans* (6), *L. odomensis* (1), *L. ervoides* (1), *L. lamottei* (1), and *L. orientalis* (1)) moderately resistant accessions. Of these, accession ILWL 180 of *L. orientalis* was the most resistant compared to the control ILL 7537. Apart from validating the symptomatic results, replicated histopathological studies was later carried out to understand the resistant mechanisms underlying lentils defence to *A. lentis* including the assessment of spore germination percentage, germ tube length and timing of appressoria formation of highly aggressive isolate FT13037. This indicates early and rapid recognition of *A. lentis* invasion is likely a major contributor for superior resistance as observed in ILWL 180. Additional evidence of faster accumulation and notably higher levels of reactive oxygen species (ROS; hydrogen peroxide and superoxide) and phenolic compounds in response to *A. lentis* penetration at 12 hours post inoculation (hpi) compared to ILL 7537 confirmed ILWL 180 could be a potential resistant source for future lentil breeding program to develop cultivars with more durable *A. lentis* resistance.

To better understand the genetic basis of resistance, a F_5 recombinant inbred line (RIL) population (N = 140) was constructed from an interspecific cross between ILWL 180 and AB susceptible cultivar ILL 6002 using accelerated single seed descent technology. The RILs and parents were then sequenced through transcriptome sequencing and using 815 high quality single nucleotide polymorphism (SNP) markers generated, a linkage map was constructed. The map stretched 488.02 centiMorgan (cM) along eight linkage groups (LGs) with an 0.66 cM average marker-marker distance. Genetic dissection of the RIL population detected a quantitative trait loci (QTL) on LG5. The identified QTL region stretched 4.93 cM and harboured nine putative candidate genes linked to AB resistance. Of these, five candidate genes were directly related to plant defence responses. Overall, the disease symptomatology, physiological and biochemical responses, and genetic evidence of resistance against AB infection support the conclusion that a stable and novel AB resistance was identified and characterised from ILWL 180. This offers significant potential to improve AB resistance of the existing cultivars within the Australian lentil breeding program.

Paper ID: 82, Growth of pea (Pisum sativum) under conditions for accelerated maturity shifts the expression pattern of key hormones related to embryo physiological maturity

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The University of Western Australia (UWA) has partnered with The Grains Research and Development Corporation (GRDC) to undertake research aimed at delivering rapid genetic gain in pulses through the deployment of an accelerated single seed descent (aSSD) platform. Manipulation of key growth conditions, including photoperiod, light quality and temperature, has enabled the substantial shortening of time to maturity across the five major cool-season pulse species. A key aspect of the aSSD platform research has been determining the timing at which robust precocious germination of the immature seed is achievable. We have previously established sugar and moisture content as indicators of physiological maturity in pea. In the research reported herein, we now address the question of how hormone profiles are regulated by plant growth environment and the relevance of these fluctuations to precocious *in vitro* germination.

Three pea cultivars (PBA Twilight, PBA Pearl and Kaspa) defined as early, mid and late based on field flowering time were grown under two environments. Environment 1 (E1) was a controlled environment room set at a 20 h photoperiod provided by LED AP67 arrays (Valoya, Finland) to promote rapid maturity. Environment 2 (E2) was a glasshouse with a 13-14 h photoperiod provided by natural light. Temperature of 24/20C (day/ night) was constant in both environments. The profiles of key embryo development hormones indolacetic acid (IAA), chlorinated IAA (4Cl-IAA), gibberellins (GA_{20} and GA_1) and abscisic acid (ABA) were measured in the developing seed in a period between the end of embryo morphogenesis (10 days after pollination, DAP) and the attainment of embryo physiological maturity (22 DAP).

Growing plants under E1 conditions altered the seed hormone content by advancing the auxin, GAs and ABA profiles by 4-8 days compared to those of seeds grown under E2 conditions. In E1, there was a synchronisation of auxin peaks across the different pea genotypes. GA_1 was only detected in seeds harvested from the less intensive conditions. The

results point to an acceleration of embryo physiological maturity by up to four days in the intensive environment and the utility of auxin and GA profiles as reliable indicators of seed maturation. A second experiment aimed to *in vitro* germinate seeds harvested at time-points 12-22 DAP, with and without exogenous hormones. The results demonstrated the extent of sensitivity of developing seeds to exogenous ABA was strongly genotype-dependent. Concentrations between 5-10 M inhibited germination of seeds harvested 18 DAP. Germination of seeds harvested 12 DAP was enhanced up to three fold with the addition of 125 M GA_3. These results show for the first time the fluctuations of seed hormone levels across genotypes, stage of seed development and environmental conditions and the influence of these changes on precocious germination competence in pea.

15:40 - 17:20: Pushing Yield Boundaries

Paper ID: 63, Identification of resistance to multiple viruses in lentil germplasm

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Viruses are a major threat to lentil production worldwide with high levels of virus infection regularly found in Australian lentil fields. Losses are likely to increase as lentil cultivation is expanding into environments that are more prone to virus infection that the current production areas.

Cucumber mosaic virus (CMV) is currently the most commonly virus found in Australian lentil crops and its spread is facilitated by high levels of transmission in lentil seed. *Pea seed-borne mosaic virus* (PSbMV) is a major virus in Australian peas, but less so in lentils as, unlike with peas, high levels of PSbMV seed transmission have not been found in commercial seed lots. However, PSbMV strains have been isolated from experimental lentil seed lots that have unique virulences and the capacity to incite severe damage. Spread of these strains into commercial fields will have a major impact on production. *Bean leafroll virus* (BLRV) is particularly dangerous and can cause plant death after early infections. All three viruses are transmitted by aphids and lentils are a preferred host for a number of aphid species.

There is an urgent need to identify genetic sources of resistance to each of these viruses as current Australian lentil varieties are lacking adequate resistance. A program is established to evaluate germplasm using greenhouse (Tamworth Agricultural Institute) and field screening (NSW DPI Liverpool Plains Field Station), the latter being an environment that favours virus and virus vector development. PSbMV greenhouse screening uses mechanical inoculation with highly virulent isolates (lentil seed and pea seed derived strains). CMV screening is done both using mechanical inoculation in the greenhouse and in the field following natural infection. BLRV screening is done in the field using inoculations by viruliferous aphids.

The 2019 trials consisted of 126 germplasm accessions from the Australian Grains Genebank (AGG) with diverse backgrounds from Afghanistan (6), Azerbaijan (4), Chile (3), Ethiopia

(9), India (24), Iran (18), Tajikistan (6), Turkey (50), Yemen (4), Italy (1) and Mexico (1) and 6 established lentil varieties. CMV screening is ongoing, but has so far failed to identify high levels of resistance. BLRV screening showed a clear clustering of resistance in germplasm from Iran and Chile; of the 20 accessions that showed less than 10% BLRV symptomatic plants at the first reading on 29 July, 15 originate from Iran and 3 from Chile. Iranian germplasm also performed outstandingly well in the PSbMV screening; of the 96 accessions tested so far, only 16 showed complete immunity to all PSbMV strains used; 14 from Iran, 2 from Turkey and 1 from Chile. Out of these 11 Iranian accessions and 1 Chilean were also among the best performers for BLRV resistance. Two of the Iranian accessions, AGG72116 (PI432028) and AGG71751 (PI431663) and the Chilean accession AGG71289 (PI299198) have been reported of having resistance to *Pea enation mosaic virus* (PEMV). PEMV has not been reported in Australia and is considered a high biosecurity risk.

The identification of accessions with combined resistance to un-related virus species was unexpected and warrants further investigations.

Paper ID: 75, Walking on the wild side: widening the phenological responsiveness of domestic chickpea

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Mediterranean climates are characterized by cool, wet winters and hot dry summers: stresses that impose considerable selection pressure on native annuals and crops alike. The key adaptation is appropriate phenology that fully exploits growing season rainfall to maximize resource capture and times the reproductive phase to avoid both early frost and terminal drought. Wild and domesticated *Cicer* have undergone contrasting evolutionary histories leading to divergent lifecycles/distributions with different temperatures, rainfall distributions and photoperiods impacting on the optimal flowering window and the environmental signals regulating phenology. Thus, we hypothesize that wild and domestic *Cicer* will differ in their responses to environmental triggers that regulate flowering, and that wild species may harbour a wider array of responses that can be exploited to broaden the habitat range of domesticated chickpea.

Wild and domestic *Cicer* with contrasting phenology was evaluated in factorial experiments examining:

Vernalization response (Temperature (5-15°C) x Time (5-40 days) in a constant temperature glasshouse (21.5^{o}C, ambient photoperiod (10.2-14.2 hr))

Interactions between photoperiod (SD=8, LD=20 hrs), temperature (High=26°C, low=15°C) & vernalization (+/- vern) in controlled environment cabinets

At ambient short-medium photoperiods there is no vernalization response in domestic chickpea, whereas wild *Cicer* have 2 distinct temperature-dependent responses: a stronger, longer-term cold response invoked after 20 days at 5°C, and a weaker, shorter-term cool response after 5-10 days at 10°C.

Wild *Cicer* also have much more dynamic responses to temperature and photoperiod than domestic chickpea, with fascinating redundancy mechanisms regulated by the

presence/absence of vernalization. Unvernalized wild *Cicer* are very photoperiod responsive, particularly at high temperatures, while temperature plays contrasting roles depending on day length: negatively correlated to flowering rate under SD, and strongly positively correlated to flowering rate under LD. Conversely, vernalized wild *Cicer* become *both* strongly photoperiod and temperature responsive, with some accessions flowering earlier than the earliest chickpea under warm LD conditions. Domestic chickpea is less responsive to all phenological drivers than wild *Cicer*.

These wild/domestic differences have arisen as a result of divergent evolution. The lifecycle of domestic chickpea is under control of man where the timing of sowing, vegetative and reproductive phases is proscribed by the interaction of climate and farming system, exposing the crop to a narrower, more predictable set of environmental phenology regulators. Conversely, because of physical dormancy, wild *Cicer* will germinate throughout the Mediterranean growing season and is exposed to a wide range of temperature and photoperiods. Accordingly, the regulation of wild *Cicer* phenology responds to manifold signals with considerable redundancy. Thus, plants emerging in autumn receive the strong, longer-term low temperature vernalization that makes them very responsive to the increasing temperature and photoperiods during spring. In early spring, the weaker, shorter-term vernalization response adds a redundancy mechanism for later emerging wild *Cicer*. Finally, a stronger photoperiod response in unvernalized plants may allow some even later emerging wild *Cicer* to complete their lifecycle within the growing season. This level of redundancy gives the wild *Cicer* unparalleled phenological flexibility that has been lost in domestic chickpea but may help breeders target new environments for the crop.

Paper ID: 34, Establishment and validation of high-throughput screening protocol for salinity tolerance in lentil

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Salt toxicity is recognised as a major constraint to crop production in Australia where c. 32 million hectares of cropland is affected by salt. Accumulation of salt causes inhibition of plant growth and reduces the ability for water and nutrient uptake ultimately resulting in reduced yield. We have developed high-throughput screening protocols using Lemnatec systems that can be deployed in the breeding programs for routine screening of salt tolerance.

In this study, a range of lentil breeding lines with varying levels of salt tolerance (ILL2024, CIPAL 1522, tolerant; PBA Bolt, PBA Hurricane, medium tolerant and PBA Ace, PBA Jumbo2, sensitive) were treated with various salt concentrations; 42.5, 85 and 127.5 mmol NaCl, in LemnaTec system at Plant Phenomics Victoria Bundoora. Imaging was performed at the start of the treatment, then every second day for six weeks. The image scores were used to measure plant pixel area (as a proxy for plant biomass) and plant senescence (as a proxy for plant health). Concordant results with traditional phenotyping were obtained and an optimal concentration of sodium chloride discriminating between the breeding lines was identified.

In a follow up experiment, approximately 190 advanced lines from lentil breeding program including 12 check lines were selected for salt screening in a partial replication (20%) trial. Each of these lines were tested under two conditions, control (zero salt) and treatment (100 mmol NaCl, identified in the pilot study). At the conclusion of the experiment, the above ground biomass of the plants was harvested, oven dried and weighed and correlations to the image scores were drawn. Furthermore, to understand mechanism of salinity tolerance in lentils, leaves (including lower leaves and young shoots), stems and roots were sampled, oven dried and chemical elements including sodium (Na) and potassium (K), as well as P, S, Ca, Mg, Cu, Zn, Mn, Fe, B, and Al were measured by Inductively Coupled Plasma Optical Emission Spectroscopy (ICP-OES)

Paper ID: 93, Are we describing the phenological development of Chickpea and Lentil correctly?

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Understanding the phenological development of a crop is critical to matching genetics to the environment. In Australian pulse research the focus on flowering as a critical development stage has dominated the way we classify cultivars. However, the focus on an open flower is likely to be confounding our perception of when the plant actually enters the reproductive stage. After reviewing and using a range of phenological keys to describe indeterminant plant species, we have modified the BBCH generic pea phenology key to specifically suit lentil and chickpea. Using this key, we have made over two hundred thousand observations in two climatically different environments. Preliminary results suggest that bud development is a much more reliable indicator of the sensitive reproductive phase. The use of clearly defined stages emergence, budding and flowering will more reliably describe crop development in ways that best relate to the sensitive stages of the crop. This will significantly improve advice to growers and consultants to help target critical period into the optimal environmental window.

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The Australian field pea and lentil breeding programs are working to incorporate a range of cutting-edge technologies to improve breeding outcomes. These technologies include advances in statistical design and analysis, genomic selection, accelerated single seed descent (aSSD), high throughput phenotyping and improving genetic diversity. This paper will give an overview of how these technologies can have an impact on responses to selection pressure within the breeding program. This response has been captured in the Breeders Equation, which states:

The response to selection = $(\sigma_g \times i \times r) / L$

Where σ_g = genetic variation, i = selection intensity, r = selection accuracy and L = generation length.

Trial design theory has evolved rapidly in recent years and innovations such as pedigree analysis, partial replication, and more recently, bespoke designs, significantly improve accuracy of yield trials. Genomic selection can have a profound impact on the breeders equation through increasing selection intensity, selection accuracy and aid in the incorporation of genetic diversity, whilst dramatically reducing the generation cycle. The Australian Grains Genebank is continually evaluating diverse germplasm and as this facility is co-located with lentil and field pea breeding programs, the breeders can observe this diversity as it is first entering Australia or while undergoing routine seed replenishment.

aSSD facilitates the production of F_6 progeny from a cross within a single year, and although it is limited to relatively small populations, the effective population size can be dramatically increased if accompanied by trait and/or molecular selection processes being applied throughout generation advancement. Finally, high throughput phenotyping has the potential to characterize a range of traits within breeding germplasm to improve accuracy through the elimination of subjective biases and increase selection intensity by screening larger numbers of lines. Remotely sensed indices are also being developed to capture variation in photosynthetic ability and other production parameters that have previously been unavailable on such large scales. The combination of the above listed technologies can increase the response to selection in the breeders equation by 200-fold over conventional breeding programs.

To maximise the benefit of these technologies, breeders need to define specific crop ideotypes that will reduce input costs for growers, increase the market value of the product or increase yield potential and stability. Examples of where this has occurred in the past will be highlighted, as well as outlining opportunities for future breeding targets in a range of areas. Application of modern breeding technologies will allow us to develop tailor-made varieties much quicker than ever before.