AUSTRALIAN PULSE CONFERENCE
12-14 SEPTEMBER 2016 • TAMWORTH
FEED THE FARM - FEED THE WORLD

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The Australian Pulse Conference is proudly supporting the International Year of Pulses 2016 as a Global Signature Event.

For more information please visit www.iyp2016.org
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Welcome to the Australian Pulse Conference

The Australian Pulse Conference follows the highly successful Inaugural Pulse Breeding Australia Conference held in Adelaide in October 2013. The focus of our conference in 2016, the International Year of Pulses, has expanded to look beyond the national breeding programs to address the theme “Feed the farm – feed the world”.

A unique feature of the inaugural conference was the field day which formed an integral component of the conference, allowing delegates to focus on practical issues facing pulse production in the southern region. The success of this model encouraged us to include a field day as part of the 2016 conference and the field day committee has worked very hard to prepare trial sites to showcase pulse production in the northern region and to illustrate some of the issues affecting pulse productivity. This year the field day will be on the final day of the conference, Wednesday 14th September.

Day 1 of the conference, Monday 12th September, begins with a session addressing optimisation of pulse performance in diverse agro-ecological environments and keynote speaker, Dr Vincent Vadez, will speak about linking different research disciplines to provide more targeted and efficient breeding of pulse crops adapted to harsh farming environments. Dr Peter Hayman will follow up with strategies to mitigate unpredictable climate and a range of speakers will present insights into adapting pulses to diverse farming environments. The afternoon sessions will discuss the application of molecular techniques for breeding efficiency, led by Dr Tony Slater and Dr Rebecca Ford, as well as addressing phenotyping methods for biotic and abiotic stresses.

Tuesday 13th September begins with a session addressing the topic “Feed the world: harnessing breeding research to increase global pulse production” and keynote speaker Professor Bert Vandenberg will discuss the importance of maintaining flexibility in breeding programs to adapt to changing environmental and market conditions. This will be followed by Dr Jeff Paull who will speak about the history and successes of the Pulse Breeding Australia breeding model and subsequent speakers will address breeding issues across a range of pulse crop species.

The afternoon session on Tuesday will be a special session to commemorate the International Year of Pulses and will feature keynote speaker Murad Al-Katib and Tim McGreevy, a representative of the Global Pulse Confederation. The IYP session will have a strong industry focus including marketing, farming and agronomic perspectives. Global food and nutrition trends will be addressed by Michelle Broom. The IYP session will culminate with an interactive forum including key conference participants.

This conference has been generously supported by the many sponsors listed in this booklet and the Conference Organising Committee are very appreciative of all support.

On behalf of the Conference Organising Committee, I welcome you to the Australian Pulse Conference and thank you for your participation. I trust it will be a productive, interesting and enjoyable time for all participants.

Phil Davies
Chairperson, Conference Organising Committee
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<th>Time</th>
<th>Speaker</th>
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<td>Matthew Rodda</td>
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<td>Brett Williams</td>
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<td>Mark Norton</td>
<td>Screening for genotypic heat tolerance in lentil.</td>
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<td>Stratified soil pH reduces faba bean nodulation and production potential</td>
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<td>4.45</td>
<td>Lachlan Lake</td>
<td>Negative association between chickpea response to competition and crop yield: phenotypic and genetic analysis.</td>
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<td>5.00</td>
<td>Marty Wilson</td>
<td>Change management.</td>
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A welcome reception will be held in the Town Hall immediately following the conclusion of the day’s proceedings and will include canapés and drinks.
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<td><strong>Chair: William Erskine</strong></td>
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<td>9.00</td>
<td>Bert Vandenberg</td>
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<td>9.45</td>
<td>Jeff Paull</td>
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<td>12.00</td>
<td>Jason Brand</td>
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<td>12.15</td>
<td>Jon Clements</td>
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<td>1.30</td>
<td>Tim McGreevy</td>
<td><strong>INTERNATIONAL YEAR OF PULSES</strong></td>
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<td>1.30</td>
<td><strong>Chair: Gavin Gibson</strong></td>
<td><strong>Examining the production, trade and consumption of pulses for a sustainable and healthy future.</strong></td>
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<tr>
<td>2.00</td>
<td>Murad Al-Katib (Presented by Peter Wilson)</td>
<td>International pulse trade and impact of international trends on the Australian pulse industry.</td>
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<tr>
<td>2.30</td>
<td>Ron Story</td>
<td>Finger on the market pulse.</td>
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<tr>
<td>2.50</td>
<td><strong>Afternoon tea / poster session: Agronomy and GxE</strong></td>
<td><strong>Chair: Nick Goddard</strong></td>
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<td>3.20</td>
<td>Michelle Broom</td>
<td>Global food and nutrition trends driving pulse consumption.</td>
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<td>3.40</td>
<td>Hannah Avery</td>
<td>Technical advantages of pulses in foods for nutritive value.</td>
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<td>4.00</td>
<td>Darryl Bartelen</td>
<td>Pulses in sustainable farming systems.</td>
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<td>4.15</td>
<td>Brad Coleman</td>
<td>System benefits of pulses in farming systems from a technical point of view.</td>
</tr>
<tr>
<td>4.30</td>
<td><strong>Marty Wilson - facilitator</strong></td>
<td><strong>Interactive forum with key conference participants</strong></td>
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<tr>
<td></td>
<td><strong>Feed the farm – feed the world: exploring Australia’s role in lifting pulse production and demand beyond IYP 2016.</strong></td>
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<td>5.15</td>
<td><strong>Close</strong></td>
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**Conference Dinner – Sponsored by Department of Primary Industries**

The conference dinner will be held at Tangaratta Vineyards, 340 Old Winton Road from 6.30pm. Buses will collect participants from their motels and transport them to the dinner venue. Conference Dinner will conclude at 10.30pm. The evening will be hosted by comedian Marty Wilson and will include the presentation of the 2016 Farrer Memorial Medal.
<table>
<thead>
<tr>
<th>Time</th>
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</table>
| 7.45 | Buses pick up from motels  
Indicate to organisers the location of your motel or make own way to Tamworth Agricultural Institute and take a bus for the remainder of the day. |
| 8.30 | **Tamworth Agricultural Institute - NSW DPI**  
Welcome – Guy McMullen (Centre Director)  
Chickpea pathology – Kevin Moore, Sean Bithell |
| 9.30 | Buses leave for Breeza |
| 11.00 | Morning tea |
| 11.15 | **Liverpool Plains Field Research Station – NSW DPI - Breeza**  
Faba Bean/Chickpea virus - Joop van Leur (20 mins)  
Faba Bean Rust - Bill Manning (20 mins) |
| 12.15 | Buses leaves for Nowley |
| 1.00 | Packed lunch |
| 1.15 | Welcome & site management overview - Professor Richard Trethowan, The University of Sydney  
Rabobank - Field Day Sponsor’s address |
| 1.40 | **E. J. Holtsbaum Research Station – University of Sydney, “Nowley”**  
PBA Variety Launches  
Desi chickpea: PBA Seamer release  
Narrow leaf lupin: announcement of the new PBA eastern states variety  
Pulse Breeding Australia |
| 2.10 | Station talks - pick your own program, 4 choices from 6 stations  4 x 20 mins (15 + 5 mins)  
Chickpea plant growth regulators – Northern Grower Alliance (NGA) – Station 1  
Lentil variety demonstration - Matthew Rodda – Station 2  
Fieldpea variety demonstration - Garry Rosewarne, Angela Pattison – Station 3  
Chickpea variety demonstration - Kristy Hobson – Station 4  
Faba bean variety demonstration - Jeff Paull, Kedar Adhikari – Station 5  
Pulse Agronomy and Farming systems - Andrew Verrell – Station 6 |
| 3.30 | Speakers at stations, participants free range |
| 3.50 | On bus to next demonstration |
| 4.00 | **Lupin variety demonstration – Mark Richards and Jon Clements – Station 7** |
| 4.15 | Buses variety for Tamworth |
| 5.45 | Buses arrive in Tamworth and return participants to motels |
Feed the Farm: optimising pulse performance in diverse agro-ecological environments
Linking research disciplines for a more targeted and efficient breeding of legume cultivars for harsh farming environments

Breeding legume cultivars for abiotic constraint: A challenge that takes more than breeding

Vincent Vadez

International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru 502324, Greater Hyderabad, Telangana, India

Pulses are often cultivated on marginal land and breeding cultivars adapted to abiotic stresses, e.g. salinity, heat, drought, soil fertility, is critically needed to sustain pulse productivity. Under such complex constraints, crop improvement, i.e. the science of combining genetics and agronomy to improve productivity, needs a strategy than goes beyond yield-based selection to lay the basis of future gains. Tools from phenomics and genomics offer new opportunities for faster and more efficient breeding but their use is not trivial because the complexity of abiotic stresses first requires a thorough understanding of the biological basis of stress adaptation, and of the genotypic interactions with the environment (E) and management practices (M). Rather than a discipline on its own, breeding will become a crucible where different disciplines interact and iterate toward consensual solutions. I’ll take examples from research on salinity tolerance in chickpea where a better understanding of the biology of salt tolerance has refocused research away from the traditional mineral toxicity towards the plant’s reproductive biology. In relation to temperature stress, yield reductions can be caused by temperature effects on the reproductive biology, the phenological development, or the evaporative demand, and this needs to be carefully sorted out for a targeted breeding effort. In relation to water stress, a small amount of water during reproductive and grain filling is critical for enhancing grain yield under water limited conditions. This is a consequence of plant traits altering the plant water budget, operating mostly in the absence of water stress. Therefore, current efforts aim at cracking the plant water budget into simpler “building blocks”, more amenable to genetic analysis and breeding use. Data will be presented on the genetic variation for these traits, on high throughput methods to measure them, on their use to harness genetic regions. In these efforts, crop simulation modelling is used to characterize prevalent stress scenarios and test the effect of traits / trait-by-management combinations on yield across locations, and then helps bind together the pieces of a multi-disciplinary approach, to guide the choice of key breeding and agronomic management targets. This multi-disciplinary framework opens a new era of “gene-to-phenotype” modelling in support of modern crop improvement programs.
Understanding and quantifying the drivers of seed yield in pulses

Victor Sadras, Lachlan Lake
South Australian Research and Development Institute, Adelaide, Australia

Crop yield depends on the environment (E), technology including the genotype (G) and management (M), and their interactions. In the short to medium term (5-10 years), the environment over-rides technology. In the long-term (decades), technology increases yield, whereas the environment contributes to often significant deviations around time trends. Despite of its importance, the environment is often characterised superficially, e.g. nominally as location and season. In this paper, we discuss established and new methods to quantify probabilistically the water and thermal environments for field pea and chickpea in Australia, and their implications for crop improvement.

The GxE interaction is biologically interesting and agronomically important, as it is often a large component of the phenotypic variance of crop yield. Here we show how an approach based on phenotypic plasticity of crop traits helps to untangle complex GxE interactions in field pea and chickpea. Combining this plasticity perspective with Fst genome scan, we show genetic profiles associated with phenotypic plasticity of yield, nitrogen fixation and carbon isotope discrimination of chickpea crops in diverse water and thermal regimes returning a range of yield from 1.1 to 5.1 t/ha.

Natural selection favours competitive plants whereas selection for seed yield in agriculture favours less competitive types, which conform to the phenotype of Donald’s “communal plant”. Comparison of yield of chickpea under normal crop competition, i.e. central rows in stands sown at 55 plants m$^{-2}$ (Desi) or 30 plants m$^{-2}$ (Kabuli), and yield measured under relaxed competition in border rows showed high-yielding lines are less responsive to competition, in agreement with Donald’s theory. Fst genome scan highlighted the lack overlap in the genetic architecture underlying yield of crop stands and yield under relaxed competition.
Managing pulses in a variable and changing climate

Peter Hayman

South Australian Research and Development Institute, Waite Research Precinct, Adelaide SA

Advances in weather and climate science combined with advances in information and communication technology (ICT) have led to extraordinary access to information. The Bureau of Meteorology has moved to what they describe as the next generation of forecasts, the most notable example is METEYE (1). Farmers and advisers have gone from a shortage of information to a problem of information overload. In understanding what is on offer, it is important to distinguish between a weather forecast, a seasonal climate outlook and climate change projections. Weather is a ‘snap shot’ of the atmosphere at a particular time whereas climate is a composite of weather events. Weather is determined by the timing of individual synoptic events such as a cold front or high-pressure systems and can last between a few hours to a week. New developments such as multi-week forecasts from the Bureau of Meteorology’s models POAMA and ACCESS S (2) blur the distinction between weather and climate.

A useful framework to consider decisions is to consider long term strategic decisions that set the overall direction of the farm, seasonal tactical decisions that respond to prices, the time of the break, stored soil water, disease and weed build up and potentially a seasonal climate forecast. Then in running a farm there are day to day operational decisions. This framework is used in GRDC Business Management Fact Sheets (3).

This presentation will provide an update of weather, seasonal climate and climate change information with an emphasis on the role that seasonal climate information might have on managing the climate risks associated with pulse crops.

Building the base: widening the genetic & adaptive diversity of chickpea

Jens Berger¹, Abdullah Kahraman², Bilal Aydin², Cengiz Toker³, Christiane Ludwig¹, Petr Smykal⁴, Eric JB von Wettberg⁵, Alex Greenspan⁶, Bekir Bekun⁷, Abdulkadir Aydogan⁸, Sergey V Nuzhdin⁹, RV Penmetsa⁶, Douglas R Cook⁸.

1. CSIRO Agriculture & Food, Perth, WA Australia
2. Department of Field Crops, Faculty of Agriculture, Harran University, Sanliurfa, Turkey
3. Akdeniz University, Antalya, Turkey
4. Department of Botany, Palacky University in Olomouc
5. Florida International University, Department of Biological Sciences and International Center for Tropical Botany, Miami, FL USA 33199
6. University of California at Davis, Department of Plant Pathology, Davis, CA USA 95616
7. Faculty of Agriculture, Dicle University, Diyarbakir, Turkey
8. Central Research Institute for Field Crops (CRIFC), Ankara, Turkey, 9 Department of Biological Sciences, University of Southern California, Los Angeles, CA, USA

Chickpea has a narrow genetic base (1): adaptive traits for biotic and abiotic stresses are hard to find, making further improvement difficult. The annual wild relatives have long been recognized as a potential gold mine for improvement, harbouring a useful resistance to a range of stresses (2), but their use is constrained by extremely limited collection. Cicer reticulatum, the wild progenitor of chickpea, and its close relative C. echinospermum (both crossable with chickpea), were only represented by 18 and 10 original accessions in the entire world collection (3). Further collection was difficult because these species reside in SE Anatolia, the site of a long standing conflict between the Turkish government and a Kurdish guerrilla movement.

In 2013, coinciding with a fragile peace accord that lasted 2 years, GRDC funded 3 missions covering much of SE Anatolia that have reversed this collection deficit:

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<thead>
<tr>
<th>Species</th>
<th>Sites</th>
<th>Accessions</th>
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<tr>
<td>C. reticulatum</td>
<td>41</td>
<td>589</td>
</tr>
<tr>
<td>C. echinospermum</td>
<td>17</td>
<td>282</td>
</tr>
<tr>
<td>C. pinnatifidum</td>
<td>25</td>
<td>253</td>
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<tr>
<td>C. bijugum</td>
<td>6</td>
<td>85</td>
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These collections have considerably widened the annual wild Cicer habitat range, sampling a range of locations, altitudes, climates and soil types throughout SE Anatolia, in areas which are once again inaccessible due to the resumption of earlier conflicts. Because collection was made on a single plant basis, within and between population analyses are feasible. Germplasm collected in 2013 has been lodged in the AARI Genebank (Izmir, Turkey) and is now also accessioned in the international genebank network, including the AGG & USDA, where it is driving a range of phenotyping (water deficit response, low pH, cold & heat tolerance, phenology, nematode, Ascochyta, leaf miner) and domestic introgression projects in Australia, Turkey, USA, Canada, India & Ethiopia. The remaining 2014-16 collection is being multiplied, and will be accessioned in AARI in 2016 for subsequent international dissemination. The work has only just begun, but offers an exciting opportunity to test our original contention: that chickpea is constrained by a narrow base. Now that we have widened this base, what does the future hold for chickpea improvement?

A report card on the N2-fixation of field pea in southern Australia

Elizabeth A. Farquharson¹, Ross A. Ballard¹, Nigel Charman¹, Matthew D. Denton²

1. South Australian Research and Development Institute, Urrbrae, SA, Australia.
2. School of Agriculture, Food and Wine, University of Adelaide, Urrbrae, SA, Australia.

Pulses provide an abundant, inexpensive and sustainable source of nitrogen (N) for Australian cropping systems. Cereal and oilseed yields are consistently greater following pulses due to these N inputs and the benefits that accrue from disease and weed breaks and improvements to soil structure and biological function. The potential contribution of fixed N from field pea, which is typically grown on more than 250,000 ha across southern Australia, is examined in this study.

Field trials were conducted at 17 sites in South Australia and Victoria over six years to assess the performance of the pea symbiosis. Uninoculated field peas were sown at each site to provide a measure of their N2-fixation when reliant on the naturalised rhizobia that are present in many soils. Different pea cultivars and inoculation treatments were also examined. Nodulation, dry matter (DM) production, nitrogen (N2) fixation (15N natural abundance method), grain yield and %N in the grain were determined. The data provide a broad picture of the symbiotic performance of field pea in the contemporary farming systems and the potential for improvement.

Average N2-fixation by field pea was 17.7 kg/t shoot DM, which is below the commonly cited benchmark of 20.6 kg of fixed N/t shoot DM for field pea in general (1). Our value may provide a more accurate assessment of field pea in southern Australia and the substandard N2 fixation potentially indicates an opportunity for improvement of field pea symbiosis. A substantial number of the observations fell below 17.7 kg fixed N/t shoot DM and were often associated with low herbage N concentration (N deficiency). Results showed that approximately 50 nodules per plant (10 weeks after sowing) were needed to provide a reasonable likelihood of effective N2-fixation. At fewer nodule numbers, the number of observations where fixed N was below 15 kg/t DM increased.

Variation in field pea nodulation and positive associations between nodule number and grain yield ($R^2 = 0.26, P <0.01$) suggests that there is scope to improve both nodulation and yield. The potential for improvement to the pea symbiosis through cultivar choice, inoculation practice and agronomic management will be discussed.

Effective weed management is critical for successful pulse production and the overall sustainability of Australian cropping systems. Weed control, particularly of broad leaved weeds in pulses is often difficult due to inherent poor plant competiveness and limited herbicide options. Furthermore many registered herbicides have a low safety margin between the target weed and the pulse crop. The development of varieties with improved tolerance to registered herbicides or tolerance to novel herbicides was identified as a likely method for improving weed control in pulse crops. Initial research by Agriculture Victoria using conventional mutagenesis breeding techniques and the chemical mutagen ethyl methanesulfonate (EMS) led to the development of lentil germplasm with improved tolerance to Group B (inhibitors of the enzyme acetolactate synthase) herbicides. Group B herbicides (including imidazolinone (IMI) and sulfonylurea (SU)) applied in cereal phases of the crop rotation can aid broadleaf weed control across the whole farming system due to their residual activity. However, their use can also limit subsequent pulse crops. Following breeding and evaluation of the herbicide tolerant lentil lines by Pulse Breeding Australia (PBA) and agronomic research by the Southern Region Pulse Agronomy program, the lentil varieties PBA Herald XT and PBA Hurricane XT were released with a permit for the post-emergent use of imazethapyr and with improved tolerance to soil residual IMI and SU herbicides. These varieties increased in-crop weed control options in lentil and allowed Group B herbicides to be re-introduced safely into other phases of the cropping rotation. This led to a rapid uptake of this technology in southern Australia with an estimated 50% of the lentil harvest deliveries in southern Australia in 2015 being PBA Hurricane XT.

Commencing in 2010 a PBA-initiated research project led by the South Australian Research Development Institute in collaboration with the University of Adelaide and the Grains Research and Development Corporation created large EMS mutagenized populations of lentil, faba bean and chickpea. These populations were mass field screened in subsequent years for tolerance to a range of herbicides with the aim of identifying lines with improved tolerance. A number of putative herbicide tolerant selections were identified in each crop, including for Group B in faba bean and chickpea, Group C (inhibitors of photosystem II) in lentil and Group I (synthetic auxins) in chickpea, lentil and faba bean. All selections with putative tolerance are being extensively characterized and tolerance levels quantified. PBA breeders are also rapidly incorporating these traits into elite breeding material, with PBA Faba Bean entering an advanced line incorporating Group B tolerance into the National Variety Trialing system (NVT) in 2016. A similar process with field pea has now commenced and the opportunity to develop pulse lines with dual herbicide tolerance is currently being explored with the aim of broadening and extending the life of these technologies for modern, evolving broad acre farming systems.
Application of molecular techniques for breeding efficiency
Application of advanced technologies for pulse improvement through an initiative called PulseBio

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Conventional pulse breeding consists of undertaking crosses, advancing generations through 5-6 cycles of selfing, followed by extensive in field yield testing over multiple years and environments. Finally, better performing individuals are selected as parents for the commencement of the next breeding cycle. Under this scenario, a full breeding cycle may take up to 10-12 years. Molecular markers have been developed and implemented to perform rapid selection in a cost effective manner for some simple traits in pulses, however for complex traits, such as yield or grain quality, traditional marker assisted selection is inefficient. Recent advances in DNA sequencing technology allows the identification of extensive numbers of molecular makers at dramatically reduced costs enabling genomic-assisted breeding that includes genomic selection, which is currently being used in many animal and plant improvement programs, including dairy cattle, sheep, chicken, ryegrass, eucalyptus, pine and maize. Combined with high-quality phenotyping, genome wide markers will capture the majority of the genetic variance in any trait. The sum of the marker effects forms a prediction equation, which can be used to predict the performance of unphenotyped individuals with the genome wide markers. In addition, multiple traits can be selected for simultaneously with the same markers early in the breeding cycle, without ignoring major traits such as yield. Genomic selection allows cost savings by reducing field trials through elimination of individuals of lower genetic merit, whilst also increasing the accuracy of selection through prediction of performance in a range of environments. Genomic selection approaches have been developed for the PBA lentil breeding program and are being applied to identify current elite genetics. Crossing strategies to fast track genetic gain have also been developed and approaches to computationally evaluate and select superior plant genetics to cross are being used. There are several advantages to genomic selection. The main one is that with genome wide markers, the majority of the genetic variance in a trait can be identified, which is especially useful in complex traits such as yield. Secondly, multiple traits can be selected for with the same markers early in the breeding cycle, thus avoiding selection bottlenecks. Finally, considerable cost savings can be achieved by reducing field trials through elimination of individuals of low genetic merit using genomic selection.

In addition to genomic selection, the improvements in imaging sensors and robotics will enable plant phenotyping (phenomics) to make rapid gains in quantifying a plant’s performance more accurately and with lower costs than was previously possible. The development of plant phenomics will also enable novel traits to be screened and selected for in pulse genetic improvement programs.

The PulseBio initiative is specifically designed to develop and implement all these technologies for rapid advances in pre-breeding for the benefit of the pulse industry.
Structure of the Australian chickpea Ascochyta blight population and risk to resistant cultivars through pathogenic fungal adaptation

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The causal agent of chickpea Ascochyta blight, Phoma rabiei (syn. Ascochyta rabiei), in Australia exists as a mainly clonal population with few molecular differences detected among isolates sourced from different growing regions or from different host cultivars between 1998 to present (1). In contrast, there is a broad range of aggressiveness in the population with several highly pathogenic isolates detected in recent seasons. These were not associated with a particular host cultivar or a particular growing region; however under controlled bioassays, they were able to cause severe disease symptoms on the moderately resistant PBA HatTrick and resistant Genesis090 cultivars (4). They were also mostly members of a large haplotype group, occupying over 50% of the fungal population, indicating a founder population that has become widely adapted across regions and hosts. Furthermore, isolates of differing pathogenicities caused significant differences in the expression of key host defence-related genes among resistant cultivars, indicating the breadth of possible interactions among the pathogen and its host, potentially sufficient to overcome currently employed host resistance genes (2).

Management of chickpea Ascochyta blight in Australia is based on an integrated approach utilizing host resistance plus chemical and cultural methods. In 2009, it was recommended that the then new varieties Genesis 090 and PBA HatTrick, with improved resistance, only required a foliar fungicide application at podding, whereas less resistant varieties required applications throughout the growing season. However, by 2011 for PBA HatTrick, a reactive foliar fungicide spray strategy together with at least one pod protection spray was recommended in seasons of high disease pressure due to presence of disease symptoms (3). In 2015, it was recommended that fungicide be applied to PBA HatTrick during the vegetative stage, particularly if inappropriate management had occurred, including lack of sufficient rotation (5). Also, in the 2015 season, disease was observed for the first time in the field on Genesis090 across southern Australia and growers were strongly advised to use foliar fungicides during the vegetative phase.

To date, none of the most pathogenic isolates have been able to cause severe disease on the landrace ICC3996, a major source of resistance upon which a substantial amount of the Australian chickpea industry is reliant. However, it is likely the pathogen is evolving with increased selection pressure towards isolates capable of infecting and reproducing on the dominant cultivars. Indeed, there is a substantially greater frequency of highly pathogenic isolates within the largest haplotype group than across the broad population. If the pathogen is able to overcome these control measures, massive costs to the Australian chickpea industry through loss of quality, yield and grower confidence would ensue.

Understanding the risk that the current and future isolate populations pose to the current resistance sources and control methods used will better inform and prepare breeders and farmers for the best practice disease management necessary to maintain good crop yields and quality. As an immediate preparedness, the highest risk isolates (most frequently detected and most pathogenic on the best resistance sources) are provided annually to the national chickpea breeding program to select the most resistant pre-breeding and breeding material.

Validation and implementation of lentil molecular markers for boron tolerance and ascochyta blight resistance

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Tolerance to abiotic and biotic stresses is a key attribute of cultivars with broad-adaptation and enhanced yield stability. For the Australian growing region, tolerance to elevated soil boron and resistance to the fungal disease ascochyta blight (caused by Ascochyta lentis) are two high priority breeding traits. In the breeding program, extensive phenotyping for boron toxicity tolerance is carried out to select and enrich for this trait, and likewise, for ascochyta blight, multiple years of field phenotyping and controlled environment assays are used to maintain a high level of resistance for the Australian lentil industry. Molecular markers, to more easily and rapidly select for these traits in breeding populations, offer efficiency gains and a higher level of precision in the ability to characterise germplasm. For this reason, a significant amount of resources has been invested in the development of molecular markers for these traits to advance Australian lentil breeding.

Multiple bi-parental mapping populations for ascochyta blight and boron tolerance were utilised to generate molecular maps and identify one major QTL for boron tolerance, from landrace ILL2024, and two important QTLs for resistance to A. lentis from the cultivar Indianhead (IH). Flanking genetic markers for all of these QTLs were identified and subsequently validated in diverse lentil germplasm and within Australian breeding populations. Markers for boron tolerance could not correctly predict phenotype in unrelated, diverse lentil germplasm. The markers were, however, demonstrated to be effective in tracking boron tolerance in crosses with the tolerant parent ILL2024, as well as after subsequent rounds of intercrossing with elite lentil germplasm.

QTL markers for IH resistance genes effectively determined resistance to ascochyta blight in lentil field trials and to recently-isolated, aggressive strains of A. lentis. A major QTL identified in two independent populations (IH x Northfield and IH x Digger) had the strongest effect, alone correctly predicting the resistant phenotype in 84% of a lentil germplasm panel. Phenotyping of breeding lines with A. lentis isolates of alternative virulence patterns also enabled the effect of secondary QTLs to be seen more clearly, with the action of the two resistance QTL seen across isolates. Genotyping and phenotyping of Australian lentil germplasm has revealed evidence of additional, independent resistance genes operating in current breeding material. Additional work is underway to map these additional genes and generate linked markers.
Detection methods for virus diseases of pulse crops in Australia

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Accurate identification of viruses is critical for resistance breeding and for development of management strategies. We are developing improved diagnostics for the luteoviruses / poleroviruses that commonly affect chickpea and pulse crops in Australia. The Tissue blot immune-assay (TBIA) method is routinely used to screen large numbers of samples for viruses in pulse crops. However, some of the antibodies used in TBIA are known to cross react with multiple viruses. Therefore, we use PCR tests in conjunction with TBIA in virus surveys of chickpea and pulse crops from eastern Australia. We use a multiplex PCR for Turnip yellows virus (TuYV), Bean leaf roll virus (BLRV), Phasey bean mild yellows virus (PBMYV) and Soybean dwarf virus (SbDV) to investigate the importance of each virus and their host range from different locations. Important alternative hosts included Malva parviflora which was commonly found to be infected with TuYV from many locations and Medicago polymorpha was a host for BLRV, PBMYV and SbDV.

We have found pronounced differences in the population of viruses infecting pulse crops across regions and seasons. For example, in northern New South Wales pulse crops, SbDV was the dominant virus in the 2013 season but was relatively rare in 2014. In contrast, there were relatively fewer luteo/polero viruses in 2015 but some large outbreaks of other important aphid-transmitted viruses, Alfalfa mosaic virus (AMV) and Cucumber mosaic virus (CMV) in chickpea crops.

Using the virus species-specific PCRs for luteo / polero viruses, we have confirmed that several antibodies used for TBIA provide false positives for TuYV. In addition, we now know that there are at least three genetically distinct viruses infecting a range of pulse crops that make up a complex previously thought to be BWYV. These distinct virus species or strains all have some degree of genetic similarity to the recognised species Turnip yellows virus (TuYV). We have used next generation sequencing to characterise almost complete genomes of three distinct viruses from this TuYV cluster which may have distinct geographical distributions and host ranges. While our knowledge of these viruses is currently limited, we have confirmed they infect crops of chickpea, faba bean, field pea, lentil and canola.

Further work to clarify the Australian luteovirus / polerovirus complex through molecular techniques and investigate biological differences between virus species is in progress.
Queensland’s tropical/subtropical environment, combined with close proximity to key markets, provides an unprecedented opportunity to increase production and export of tropical pulses such as chickpea and mung bean in an increasingly competitive global market. While Queensland has some natural advantages, increasing tropical pulse production is also fraught with inherent challenges. Increasing climate variability and change are major risk factors as are the increasing incidence of pests/diseases and ABARES recently forecasted that agricultural production in Australia could fall by as much as 19 per cent by 2050. The Queensland University of Technology (QUT)-led $4.8 million Queensland Government funded Tropical Pulses for Queensland project is a partnership between QUT and the Queensland Department of Agriculture and Fisheries and aims to address many of these concerns. Key goals of the project are to address risks and challenges associated with growing tropical pulses in Queensland through the development of more productive, profitable and resilient chickpea and mung bean options for growers and industry. This presentation will provide an overview of the Tropical Pulses for Queensland project highlighting the innovative scientific solutions used to improve the productivity and resilience of chickpea and mung bean crops, increase the bioavailability of iron in chickpea seeds, improve the breeding of mung bean and define new opportunities for expanding production of mung bean and chickpea crops in Queensland.
Phenotyping for biotic and abiotic stresses
When good pulses turn bad: root-lesion nematodes in the northern grain region of Australia

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Northern region grain growers love pulses but they hate the root-lesion nematodes that attack their crops. Unfortunately pulses such as chickpea, mungbean and faba bean, are susceptible to the root-lesion nematode, *Pratylenchus thornei*, and cause populations of these nematodes to increase. Three-quarters of grain paddocks in the northern grain region have *P. thornei* and they can cause devastating yield losses of up to 70% in intolerant wheat cultivars and up to 20% in chickpea (1, 2, 3). Successful management relies on the combination of growing tolerant cultivars that do not suffer yield loss and rotation with resistant crops that do not allow the nematodes to reproduce. Decreasing populations of *P. thornei* by growing consecutive resistant crops over several years is a slow process but one that allows growers to diversify crop choices, improve yields and restore balance to the soil’s biology.

We have previously shown that populations of *P. thornei* in field experiments increased from two to eight-fold after growing chickpea, faba bean and mungbean cultivars and caused up to 67% yield loss in the following wheat crop. We will present new results that show there are a small number of cultivars or advanced lines with moderate resistance however, most chickpea, faba bean and mungbean cultivars remain susceptible to very susceptible.

Our research has the potential to identify new sources of resistance to root-lesion nematodes that could be incorporated into breeding programs. If there were more resistant cultivars, pulses could play a central role in helping to reduce the burden of root-lesion nematodes in northern grain region soils. Only then will our growers be able to take full advantage of all of the benefits that pulses offer our farming systems.

Screening for genotypic heat tolerance in lentil

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Heat waves during the reproductive phase of crops poses a significant constraint to agricultural production systems. Pulses, such as lentil are particularly sensitive to high temperature. The current study is investigating the use of genetic solutions for improving adaptation of lentil to heat stress during the reproductive phase. Field-based screening over two consecutive years (2014/15 & 2015/16) during the summer period in western Victoria, tested a broad range of lentil genotypes and commercial cultivars (81 lines), for heat tolerance. Genotypes were selected from a range of climatic zones globally, that targeted regions where high temperatures and low rainfall occur. The screening trials were sown in October and flowering occurred in late November, which coincided with naturally hotter conditions. Lentil were grown in full open environment (heat treatment) and compared with shaded controls. Plots were irrigated to avoid moisture stress. For both years the shade reduced the radiant temperature by 38% and absolute temperature by 2.5°C which resulted in 57% higher average grain yield for the shaded treatments. Seasonal conditions between the two years varied, with the absolute temperature higher in 2015/16 which translated to lower biomass and grain yield across the trial.

In 2014/15, four genotypes (72578, 70549, 71457, 73838) were identified, with improved tolerance to heat compared with the best commercial cultivar, PBA Bolt. These genotypes were tested again in 2015/16 alongside additional genotypes, with 71457 and 72578 showing consistent tolerance. In addition, genotypes 70816, 70874 and 73076, were identified with improved tolerance compared with PBA Bolt. The genotypes with improved tolerance were from regions in Jordan, India, Pakistan and Bangladesh where high temperature during flowering could be expected. They also showed an ability to maintain high grain number under heat treatment. The identification of such genotypes indicates the potential of genetic solutions for improving adaptation of lentil to high temperature during the reproductive phase.
Leaf and canopy traits for heat resistance in field pea

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Field pea (Pisum sativum L.) is grown in western Canada as a dryland summer crop. Several days of heat starting at 28°C cause flower and pod abortion and most cultivars are heat sensitive. Heat can lower yield by 25%. To seek traits for improved heat resistance we measured a 94-member pea collection. Pea cultivars originated from north America, western and eastern Europe and Australia. We tested this collection under high temperatures (38°C and above) in the field in Arizona in 2012, and in Saskatchewan with shorter periods of heat in 2012, 2013 and 2015.

Traits measured included canopy temperature, canopy greenness (SPAD and various vegetation indices), reproductive node number, pod number, seeds per pod, flower abortion rates, ovule retention, and yield. A wide range of vegetation indices were calculated from spectra collected in the field with a handheld spectral radiometer in 2015. Genotypes groupings were based on previous analysis of the pea collection, which is an association mapping panel.

Results will be presented for how cultivar leaf, canopy traits, and genotypic grouping relate to canopy temperature, canopy colour, vegetation indices, and the various yield-based traits. The goal is to identify how various canopy features in pea relate to heat resistance for maintaining cooler canopies and reducing reproductive flower, pod and ovule abortion. Traits that are easy to measure or that can be used in crop management will also be discussed.
Stratified soil pH reduces faba bean nodulation and production potential

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Yields from acid sensitive pulse crops grown on low pH soils of south-eastern Australia are variable. Results from this jointly funded GRDC and NSW DPI project (DAN00191: N fixing break-crops and pastures for high rainfall zone acid soils) indicate that current acid soil amelioration strategies are inadequate and that subsurface acidity is limiting the potential of faba bean crops. Previous studies in this region linked effective nodulation of pulse crops with dry matter production and N fixation and highlighted variable persistence of rhizobia and N fixation in commercial pulse crops (1). Investigation of commercial faba bean crops grown on low pH soils of south-eastern Australia in 2015 showed a strong correlation \( r^2=0.82 \) between low pH and poor nodulation.

During 2015, 12 commercial faba bean crops in NSW, VIC and SA were assessed 2-3 months post sowing for effectiveness of nodulation. Combined 0-10 cm soil test samples were collected in February. Eight crops showing poor nodulation were followed up and more detailed testing of topsoil at 2 cm increments was undertaken using a field pH kit. The study indicated that the adoption of reduced tillage practices has resulted in the development of more defined pH stratification than previously reported (2). Despite widespread use of lime to ameliorate soil acidity, results showed that unincorporated, surface-applied lime produced elevated pH_{Ca} of more than 6.5 at the soil surface (0-2 cm), but less than 5.0 in subsurface layers (below 6 cm). This has negative impacts on nodulation and root development of faba bean crops, and implications for all acid sensitive crops. Growers also need to be aware of the effect elevated pH of the surface soil has on the breakdown of sulfonyl urea herbicides and plant back period for legume species.


Negative association between chickpea response to competition and crop yield: phenotypic and genetic analysis

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Donald’s ideotype and empirical evidence in cereal and oilseed crops indicate high yield is associated with less competitive plants. In this study we grew 20 chickpea lines in six environments to investigate the association between yield and intra-specific competitive ability and its genetic underpinnings using DNA sequencing and Fst genome scan. We measured yield and its components and calculated response to competition (RC) as the ratio between the trait in border rows (lower competition) and the trait in inner rows (higher competition). Crop yield correlated negatively with RC for yield, biomass, harvest index, seed number, and pod number. Fst genome scan revealed 13 genomic regions under selection for response to competition of yield, seed number or biomass, and 7 genomic regions under selection for yield in inner or outer canopy rows. Candidate genes in these regions include members of the nitrate-transporter 1 family, patatin and hormone-related genes. The top genomic regions found to be under selection for yield in inner rows, outer rows or response to competition did not coincide. This genetic architecture provides a mechanistic basis for the observation that phenotypes that are adequate for relaxed competition often perform poorly in dense stands.
Feed the world: harnessing breeding research to increase global pulse production
Flexibility in Breeding to Adapt to Changing Environmental and Market Conditions

Albert Vandenberg  
NSERC Industrial Research Chair in Genetic Improvement of Lentil, University of Saskatchewan

Environmental and market conditions may not just be about climate change, price fluctuation or the legalities of food systems and international markets. Changing perceptions of economic value of a breeding program affect the amount of and return on investment. From the biological perspective, pulses to this point are essentially GMO-free for economic and market reasons. From a genetic technology perspective, investment in pulses has always lagged far behind the world’s major crops like maize and soybean. In spite of that, market perceptions currently indicate that non-animal and non-soy vegetable protein has growing demand. Pulses represent a conglomeration of global niche markets. Flexibility in breeding is an essential requirement for success if the goal is to develop new and improved products, especially if we expect more volatility in weather and climate. To achieve success, this will require expanded investment in development and implementation of new and more efficient breeding technologies, improved technical resources, and linkages to the agronomic and market systems that are linked to breeding systems. Breeders will have to form effective international alliances and linkages in the area of genetic improvement if pulses are to remain competitive.
History and Success of Pulse Breeding Australia

Jeff Paull

School of Agriculture, Food and Wine, University of Adelaide, Glen Osmond, SA, Australia

On behalf of all former and current members of Pulse Breeding Australia.

Pulse production in Australia was at a low level prior to the 1980s and was restricted to field peas and lupins. During the 1980s chickpeas, faba beans and lentils were adopted and there was significant expansion in area sown to all pulses and increased investment in breeding to develop improved varieties. Breeding programs were based in State agencies and Universities and generally had a regional focus. There was a shift to National breeding programs commencing in the mid-late 1990s and Pulse Breeding Australia (PBA) was formed in 2006 as an unincorporated joint venture between GRDC, Pulse Australia, state government agencies and the University of Adelaide with the objectives of improving efficiency and rate of genetic gain of pulse breeding and to remove impediments to exchange of germplasm and IP between partners.

The structure of PBA with a Coordination Group comprised of breeders and researchers, an Advisory Board represented by senior management of each investor, a Coordinator, and individual crop breeding groups, has facilitated communication across all levels of the breeding chain. Examples of communication activities include annual meetings, PBA newsletters, international market/quality fact-finding missions, the Inaugural PBA Conference in 2013 and Technicians Symposiums.

Initially, PBA included faba bean, field pea, chickpea and lentil, while lupin breeding was included in 2011. The breeding programs exchanged ideas, co-located trials where appropriate and shared equipment to improve overall efficiency. A Germplasm Enhancement (GE) program was also included in PBA, and this enabled the breeding programs to prioritise biotic, abiotic and quality traits and technologies that were addressed by the GE program, and for direct adoption of the outputs of the GE program by the breeding programs.

Each crop breeding program selected a commercial partner, following a competitive tender process, to release a pipeline of varieties. This has enabled the commercial partner to contribute earlier in the identification and multiplication of lines thus reducing the time to release. Decisions on lines to progress to release, and management of the release process via a Maximum Adoption Plan, is managed by a Release Advisory Group for each crop. To date, over 30 PBA varieties have been released, with more in the pipeline. These varieties have had a major impact through improvements in yield, disease resistance and seed quality, with the recent introduction of herbicide tolerance, and are now the dominant pulse varieties in production in Australia.
Research innovations transform mungbeans into ‘moneybeans’

Rex Williams
Queensland Department of Agriculture and Fisheries

Our mungbean industry is celebrating the International Year of Pulses (IYP) with a record crop, near record prices and a new range of locally-produced spreadable pastes. Australian ‘clean green’ mungbeans continue to be highly sought after in premium export markets for sprouting and processing as well as locally to produce a nut-free alternative to peanut butter. The rise of mungbeans as a profitable summer pulse crop in the northern grains zone follows innovations in breeding and research that transformed mungbeans in the eyes of growers from ‘mongrel beans’ into ‘moneybeans’.

Vital research has delivered improved varieties and better ways to grow mungbeans in the face of environmental challenges. The integration of improved genetics and best practice management matched with a better understanding of production environments and market needs has revolutionised grower confidence and mungbean profitability.

The Queensland Department of Agriculture and Fisheries (DAF) leads mungbean breeding efforts that continue to improve yields, grain quality and crop resilience in the face of drought and disease. Since 2003, double-digit yield gains in successive DAF-bred varieties have increased grower confidence and doubled industry production from 35,000 to 70,000 tonnes. University research partnerships are further supercharging our mungbean industry. For example, our Queensland Alliance for Agriculture and Food Innovation (QAAFI) is delivering more productive and resilient management options including row spacings. Revolutionary genetic tools and technologies are also being developed and tested with the Queensland University of Technology (QUT). The University of Southern Queensland (USQ) is using expertise in bacterial pathogens to better address challenges from key diseases such as halo blight. Queensland scientists are also a vital part of a new international network that will further improve breeding and research outcomes for our pulse industry and our growers.

Industry partner, the Grains Research and Development Corporation (GRDC), estimated that every dollar invested in the mungbean breeding program alone returned $18 of benefits to the grains industry. Our world-class efforts in mungbean breeding and research provide the key to consistently delivering industry’s bold target of 170,000 tonnes of mungbeans annually. This will ensure we remain the preferred supplier of premium, quality-assured mungbeans in competitive domestic and international markets.
History and Development of Chickpea in the Northern Region - a grower’s perspective

Sam Gourley
Chickpea grower, ‘Eurowie’, Edgeroi, NSW, Australia

Sam will share his experience of being one of the foundation chickpea growers in the northern region and some of the difficulties in the early days. In his presentation he will discuss the following: how he became involved in growing chickpeas, the planting of the first Tyson crop, weed management, harvesting issues, marketing the grain, rotational benefit of chickpea, the impact of new varieties, extension activities, overcoming Ascochyta blight, and his connection with the chickpea breeding program and variety releases.
History and Development of Chickpea in the Northern Region – a breeder’s perspective

Edmund J Knights

Formerly NSW Department of Primary Industries, Tamworth, NSW, Australia

Chickpeas were first tested in the northern region at Warwick and Emerald as part of a preliminary nationwide evaluation initiated from Wagga. (There was no comparable site in northern NSW). Commercial production began in 1979 with the release of an introduced desi variety (Tyson). Desis have dominated production (more than 95 per cent) ever since. State-based programs were replaced by a coordinated NSW (Wagga)/ Qld (Warwick) breeding program in 1982. This was broadened to a national one in 1988, based at Tamworth, with the last iteration (chickpea as a subprogram of Pulse Breeding Australia) in 2006.

The industry has grown steadily since 1979, accelerating recently to approach 700,000 ha which is approximately one quarter of the regional winter crop area. Most production is in northern NSW and southern Qld, with a smaller area on the Central Highlands of Central Qld. Chickpea normally follows wheat or barley in the rotation but is also used opportunistically as a double crop after sorghum to flip the program to a winter cropping phase.

Disease has been the primary production and breeding problem. Phytophthora root rot and Ascochyta blight are the major disease diseases and varieties have now been developed combining moderate resistance to both. The breeding program assigns a high priority to seed quality. An emphasis on seed size, colour and milling quality has enabled regional desi chickpeas to achieve premium status in the Indian market.

Collaboration with growers has been an essential element of the northern breeding effort. Final stage evaluation uses a network of trial sites strategically located on farmer properties across the region. Apart from providing a relevant growing environment, the siting of trials within crop 'heartlands' often provides useful grower feedback and can act as a nucleus for encouraging new converts to the industry.
Developing medium to large seeded kabuli chickpeas with early maturity, improved yield and Ascochyta bight resistance for Australian growers

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Medium to large seeded kabuli chickpeas can be a profitable option for chickpea growers, particularly in south eastern Australia (1). A considerable price premium generally exists for grain greater than 8 mm compared to desi and small seeded kabulis (6-7 mm). Historically Australia’s medium to large seeded varieties have required favourable spring conditions to achieve good yields and seed size greater than 8 mm. In years with short seasons or dry springs, the larger seeded kabuli varieties performed poorly and were therefore considered unreliable and risky, particularly in low to medium rainfall environments. Following the outbreak of Ascochyta blight (AB) in the late 1990’s, the subsequent seven kabuli varieties released were all bred at the International Centre for Agricultural Research in the Dry Areas (ICARDA). These varieties provided the required AB resistance and acceptable adaptation, particularly the smaller seeded varieties Genesis™090 and Genesis™079. The first Australian bred kabuli variety was PBA Monarch released in 2012. PBA Monarch is a medium sized kabuli with early flowering and maturity providing significantly improved yields over current medium and large seeded varieties in short season environments such as the South Australian Yorke Peninsula, Mid North and Victorian Mallee. However its plant type can be prone to lodging under high biomass and it is moderately susceptible to AB.

The Pulse Breeding Australia (PBA) Chickpea program has made a concerted effort to combine improved seed size, AB resistance, erect plant type and earlier maturity using PBA Monarch, elite PBA breeding lines and international germplasm. New breeding lines have been developed and evaluated in yield trials in South Australia, Victoria and northern New South Wales. Multi-environment (MET) analyses were used to identify lines with superior yields and examine how individual environments correlate. The 2015 season featured a very short spring and a number of medium to large seeded lines were identified with increased yield compared to PBA Monarch with an erect plant type. Although some lines had exceptional yields only in the short season 2015 trials, other lines demonstrated wide adaptation and improved yield stability with superior yields in the 2015 trials as well as longer season 2014 trials. Assessment of AB resistance has also occurred and a number of these early maturing high yielding breeding lines have increased AB resistance compared to PBA Monarch.

The development of medium and large seeded kabulis with superior yield and adaptation will provide more reliable and profitable varieties for south eastern Australian chickpea growers. The next challenge for the PBA Chickpea program is to improve the Phytophthora root rot (PRR) resistance to elite adapted breeding lines to provide growers in north eastern Australia improved opportunities in kabuli chickpea production.

Opportunities for Faba Beans in the low rainfall zone Mallee

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Faba bean production in southern Australia has primarily been limited to medium to higher rainfall zones (>400mm/annum) on loam to clay textured soils. It has generally been perceived as unreliable with poor yield and low profitability in the low rainfall zone (300-400mm). However, improved moisture conservation techniques (retained stubble, early sowing and wider row spacing) mean that beans could now be considered as a profitable option within the low rainfall zone farming system, particularly as they are one of the best nitrogen fixing pulses. In addition, the breeding program has made remarkable gains with several lines showing significant improvements in grain yield in dry areas, novel herbicide tolerance to improve weed management options, disease resistance improvements and smaller seed size which will reduce seeding costs. A combination of the improved genetics with modern management is likely to result in improved reliability and profitability of the crop.

From 2013-2015, several field trials have been conducted in the southern and central Mallee of Victoria to investigate new breeding lines and agronomic treatments including row spacing, sowing rate, nutrition and inoculation. In all seasons, despite annual rainfall being 20-40% below average, profitable grain yields of faba beans were achieved. In 2015 (195mm annual rainfall, 40% below average) all of the lines identified for improved dry area adaptation had higher grain yields than PBA Samira, with AF12025 achieving 158% of PBA Samira (0.48t/ha). In addition, all of these lines displayed higher early vigour scores, were 7-11 days earlier flowering and had earlier maturity than PBA Samira. Sowing rate experiments in 2013 and 2015 have indicated that, consistent with recommendations, 20 pl/m\textsuperscript{2} is the optimum density to maximise grain yield in the Mallee. Row spacing from 18 cm to 72 cm had no impact on grain yields in 2014, indicating that wider row spacing could be used to reduce production risks and costs. Neither inoculation or foliar fertiliser treatments affected grain yield in 2015 and differences in nodulation in response to the various inoculation treatments were observed.

These results demonstrate that faba beans can be grown profitably in dry Mallee conditions. Further gains in reliability and profitability are likely to occur with the incorporation of imidazolinone herbicide tolerance to provide an effective ‘in-crop’ control of broadleaf weeds, which has not been previously available in faba beans. This presentation expands on these results and future traits, discussing the opportunities for expansion of faba bean production in the low rainfall zone and potential benefits for the farming system.

Yield progress and trait variation among Australian narrow leafed lupin cultivars from 1967 to 2016

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Narrow-leaved lupin (NLL, Lupinus angustifolius) has been a grain legume of major importance in Australian southern winter cropping rotations on acid sandy soils for the past 35 years. The breeding program in Australia began in the early 1960s through the combining of key domestication genes, producing the first fully domesticated cultivar in 1973 (1). Wild genotypes from several Mediterranean countries were integrated into the breeding program in the late 1970s followed by advances in yield since 1980s coming through intercrossing within advanced lines and varieties (2). Further emphasis on broadening the genetic base began in 2001 with the introduction to the crossing program of new diversity from wild and foreign genotypes. Previous work (2) has demonstrated yield progress until 2007 and has demonstrated the predominance of good general adaptation provided by modern cultivars, with general consensus that the program has produced relatively little specific adaptation to take advantage of wider environment ranges across southern Australia (3).

The present study extends yield progress assessment until 2015, with the release of new varieties over the past few years, culminating in the release of two cultivars in 2016. We also identify range variation available among historical cultivars to 2016 for additional traits, including flowering time, plant and harvest height, seed quality (protein and alkaloids, seed size, seedcoat%), pod shattering and molecular markers for important characters.

International Year of Pulses - Examining the production, trade and consumption of pulses for a sustainable and healthy future.
International Year of Pulses

Tim McGreevy

This abstract was unavailable at the time of printing.
International pulse trade and impact of international trends for the Australian pulse industry

Murad Al-Katib

This abstract was unavailable at the time of printing.
Finger on the market pulse

Ron Story

This abstract was unavailable at the time of printing.
Global food nutrition trends driving pulse consumption

Michelle Broom

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Mega-trends are shaping changes in food consumption around the world. Our global population is expanding from 7.3 billion today to an estimated 9 billion or more in 2050, and more people are living with disease, with an estimated 422 million people currently living with diabetes. Pulses can help address these trends which put a triple challenge on the global food supply: ensuring enough food, producing food within a changing environment and producing healthy food to mitigate the chronic disease burden whilst still addressing malnutrition. Domestically, manufacturers are beginning to explore the potential for using pulses in processed foods to meet consumer demands such as high protein, gluten free and low GI foods. However, manufacturers need to be assured of a safe, consistent supply of raw product to invest in processing. Excellent opportunities exist for these Australian crops to be positioned as superior quality human foods for both domestic use and for export.
Technical advantages of pulses in foods for nutritive value

Hannah Avery

This abstract was unavailable at the time of printing.
Pulses in Sustainable Farming Systems

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The inclusion of pulses on Australian farms has become the norm rather than the exception. The producers who first challenged the status quo by producing pulses would have firstly been challenged by market access and crop profitability. However, this would have been compensated by improving profit margins of subsequent cereal crops. Pulses are useful for reducing soil diseases, opportunity to use robust chemistry to control weeds and improve soil quality by fixing some nitrogen.

Pulse Econ
Until Australian producers could demonstrate to consumers the capacity to annually produce the critical mass and quality expected, markets were limited. Once the industry could ensure consistent quality and tonnage, consumers became more liquid and thus was reflected in prices with increased competition. Today, Australian produced pulses are highly regarded around the world as having excellent quality but we still suffer hiccups with production. Chickpeas are now my “pillar” crop because long term profit margins are superior to all other winter crops produced.

Impact of pulses on the farming system
The challenge of growing pulses with consistent yields year on year is difficult given the vagaries of the weather, disease, soil health and varietal impediments. Over the last 20 years vast gains in achieving more consistent yields has been a result of robust breeding programs, understanding the limitations imposed by soil type/quality, weather, and by identifying the good/bad management practices. If a producer fails to recognise the risks involved and does not take proper actions to mitigate as many as threats possible, pulses can have dramatic negative impacts on farm profitability. Some years, the impacts of weather can be so severe that even the best management practices are not enough to prevent substantial yield loss.

The X-Factor of pulses
While we understand the immediate gains by growing pulses such as N fixation, reduction of soil diseases and opportunity to decrease the weed seed bank of certain species, there is evidence that the benefits are reaped for multiple years. Many years ago, I planted a crop of Koala Lab Lab beside sunflowers in a paddock which were both taken to harvest. With the utilisation of yield maps, a distinct line between the two treatments was very evident for 5 years in subsequent crops. Recently, with the help of DAFF, funding of both large and small scale trials to measure long term impacts summer legume cover crops can provide, were established. The vagaries in weather heavily impacted on this 3 year project however in the last year of the project, better growing conditions provided the opportunity for the multiple legumes to produce good biomass. 2 years after the cover crops were grown, with the use of satellite imagery, we are seeing increased biomass in this year’s chickpea crop and hopefully higher yields. Why the subsequent crops over multiple years are improved is not fully understood. As a grower, I don't need to fully understand the ‘why’, as long as my profits are improved over the long term.

Conclusion
Pulses are very important on our farm currently and in the future could potentially represent 75% of our cropping program. Pulses do offer challenges, but I don't feel the extra attention to management is more difficult than the production and management of cereals are today. Increasingly, global demand for pulses is occurring because consumers are much more aware of the benefits to health and long term environmental impacts. With our enviable global location and with very large importers close at hand the increased demand for our produce will increase our profitability. By further investment into pulse production more growers will be more able to reliably produce profitable pulses which drives long term sustainability.
Looking at the system benefits of pulses in farming systems from a technical pint of view

Brad Coleman

This abstract was unavailable at the time of printing.
Poster Abstracts

Poster abstracts are listed in alphabetical order by first author.
Diversifying the genetic bases of rust (*Uromyces viciae-fabae*) resistance for faba bean improvement in Australia

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Faba bean rust (caused by *Uromyces viciae-fabae*) is a major fungal disease in most of the faba bean growing regions in the world. It is a major disease in the northern grain growing region of Australia where farmers need to spray fungicides 2-3 time in a season to protect the crop from rust. The development of rust resistant varieties can eliminate the need for fungicide spraying. Breeding resistant cultivars relies on the ability to detect the resistant genes and understanding their genetic bases of resistance. Diallel crosses without reciprocals were made among three resistant (AC1227#14908, AC1655 and Doza#12034) and one susceptible (Fiord) genotypes. Seedling tests on F2 and F3 progenies showed three distinct responses: highly resistant, moderately resistant and susceptible. However, no homozygous family with a moderate response was found in the F3 progeny test, hence, this infection type could not be attributed to independent gene(s). The segregation ratio in both F2 and F3 in the population derived from Doza#12034, a selection from the commercial cultivar Doza, and a central European line Ac1655 indicated a single dominant gene responsible for conferring resistance in each of these lines. An allelism test revealed that each of the above resistant parents carried a single and independent gene for resistance.

The other parent AC1227#14908 gave near susceptible reaction at seedling stage, but it was moderately resistant at adult plant stage indicating the adult plant resistance. When it was crossed with the susceptible parent Fiord, all its progeny were susceptible in F3 indicating it had no seedling resistance gene. However, when it was crossed with resistant parents Doza#12034 and AC1655, the F2 progenies segregated in a 9 resistant: 7 susceptible ratio indicating complementary resistance genes. It appears that AC1227#14908 carries a complementary gene which cannot be expressed on its own, but when crossed with another resistant parent gives a resistant reaction. These results clearly showed availability of at least three rust resistant genes for breeders to choose or pyramid for improving faba bean rust resistance in Australia with further indication of an adult plant resistant gene.
Pulse viruses in commercial crops, breeding lines and in pulse seeds in Victoria

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Chickpea, faba bean, field pea, lentil and narrow leaf lupin are the most common winter pulse grain crops grown in Australia. Six economically important viruses are known to infect these crops in Australia. Four are seed-borne: *Alfalfa mosaic virus* (AMV), *Bean yellow mosaic virus* (BYMV), *Cucumber mosaic virus* (CMV) and *Pea seed-borne mosaic virus* (PSbMV) and two are non-seed-borne luteo and polero viruses: *Bean leafroll virus* (BLRV) and *Turnip yellows virus* (TuYV, synonym *Beet western yellows virus* (BWYV)). In this study we investigated the incidence and distribution of pulse viruses in commercial crops, breeding trials and seed lots.

One hundred samples were randomly collected from each of 61 commercial pulse (17 field pea, 14 faba bean, 8 chickpea, 6 lupin and 4 vetch) crops during 2014-15. From breeding trials in 2014, 100 random samples were collected from each of field pea, lentil and chickpea without distinguishing between different breeding lines and in 2015, 10 samples were randomly collected from each of 16 field pea lines, 12 lentil lines and 5 chickpea lines. In 2015, seeds from five field pea varieties (400 seeds from each) and five lentil varieties (400 seeds from each) were sown in seedling trays contained in cages in the glasshouse and the resulting plants were tested for seed-borne viruses. Transmission experiments were conducted to determine the infectivity of a Deniliquin canola isolate of *Turnip yellows virus* (TuYV) in 90 plants of each of the varieties of field pea (Parafield), lentil (CIPAL 1301), faba bean (Farah) and chickpea (Genesis 90) using green peach aphids. For virus confirmation, samples were tested using a tissue blot immunoassay. The incidence of CMV in lentils and BWYV in field pea was higher in commercial crops compared to breeding trials and while PSbMV was only detected in field pea seeds, it was higher in breeding trials than commercial crops. The most commonly detected virus was BWYV in all crops except faba bean and lupin. CMV was detected in some lentil and lupin in both commercial crops and breeding trials but was not detected in seeds. The seed infection of PSbMV was high in some field pea cultivars but this virus was not present in commercial crops. BYMV was only a problem in some lupin crops. AMV was detected in lentil and chickpea with low incidence and BLRV was not found in any crop. TuYV was successfully transmitted to field pea, lentil, faba bean and chickpea.
Effect of frost on biomass production and grain yield in faba bean (*Vicia faba* L.)

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Faba bean is affected by frost both at vegetative and reproductive stages. Yield losses due to frost depend on several aspects such as duration of frost, frequency, intensity, crop sensitivity and plant growth stage. A field experiment was carried out at The University of Sydney, Plant Breeding Institute, Narrabri to identify (1) the effect of frost on physiological parameters, biomass production and grain yield, (2) traits associated with frost tolerance and (3) find frost tolerant genotypes. Fifteen different faba bean genotypes were studied under three sowing dates (17th April, 7th May and 28th May 2015) in three replications. Frost damage in the field was scored by (i) the number of damaged plants/m² at the early stage, (ii) ranking the damage using a visual 1-9 scale at vegetative and reproductive stages (1: low damage, 9: complete damage) and (iii) tagging five random plants/plot. At least three visually damaged flowers/plot were tagged to determine the impact of frost on pod set. Genotypes were differently affected by frost at the early and vegetative stages depending on the sowing date. At early stage, plants in the first sowing were damaged less by frost than in the third sowing, whereas no frost recorded in the second sowing. At reproductive stage, first sowing time showed high flower survival and less frost damage on stems than the second sowing time. The third sowing time escaped frost damage, but the overall yield was low. Genotype 11NF010a-2 showed high frost tolerance in all plant growth stages and had greatest flower survival and grain yield (3.8 t ha⁻¹). In contrast, IX541a-2-8 was the most susceptible to frost damage, with low flower survival rate and yield production (3.2 t ha⁻¹). Frost damage on stems and flower survival were highly negatively correlated with plant height and biomass production at flowering. In contrast, frost damage was positively correlated with plant height, width of first podding node, seed filling duration and final yield. These results indicated a clear relationship of phenological and physiological traits on frost damage providing information to plant breeders to select traits for frost tolerance.
Mapping Phytophthora root rot resistance in chickpea (*Cicer arietinum*)

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Phytophthora root rot (PRR) is a major biotic stress in chickpea caused by the fungus-like Oomycete *Phytophthora medicaginis*. The disease causes significant yield loss in north-eastern Australia and costs Australian growers $8.2 million per year (1). There is no practical in-crop control to prevent the disease in chickpea. Field resistance to PRR has been identified in wild relatives of chickpea, *Cicer echinospermum*, (2) and researchers have incorporated this resistance in some cultivated chickpea varieties such as Yorker. However, under high inoculum load, in poorly drained soils and following high rainfall conditions even Yorker becomes susceptible and large yield losses are common. This necessitates the need for a genetic approach to improve resistance in chickpea against *P. medicaginis*.

Three available recombinant inbred line (RIL) mapping populations developed from a cross between Genesis 114 x Yorker, Rupali x backcross derivative from *C. echinospermum*, and Yorker x backcross derivative from *C. echinospermum* were genotyped using Genotype-by-Sequencing approaches (DArTseq). A high density linkage map for each population was constructed with an overall length spanning 993.8 cM, 1109.7 cM and 1174.1 cM comprising of 573, 4101 and 3933 markers (SNP and silico-DArT), respectively. Phenotypic evaluation was performed under field conditions using a cocktail of 10 *P. medicaginis* isolates. Whole genome quantitative trait loci (QTL) analysis identified two significant PRR resistance QTL on chromosome 4 and 6 at intervals of 1.06 cM and 5.5 cM respectively, explaining 16.9% to 25.0% of genetic variance in Genesis 114 x Yorker. Three major PRR resistance QTL were identified on chromosome 3, 4 and 6 at intervals of 0.8 cM, 0.9 cM and 1.01 cM respectively, explaining 10.1% to 27.3% of genetic variance in Rupali x backcross derivative from *C. echinospernum*. In the Yorker x backcross derivative from *C. echinospernum* population, two major resistance QTL on chromosome 3 and 6 at intervals of 0.8 cM and 1.4 cM respectively, were identified, explaining 9.4% to 25.2% of genetic variance.

The DNA markers located in the PRR resistance QTL region can be used for marker assisted selection in chickpea breeding. Furthermore, these results will be applied to develop populations suitable for high resolution mapping of the resistance loci to determine the mechanisms involved in PRR resistance in chickpea.

Physiology and genetics of salinity tolerance in chickpea from high resolution image phenotyping

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Chickpea is sensitive to salinity (1,2), which can be a major limitation to productivity in arid and semi-arid environments as well as in intensively irrigated lands (3). Salinity management options are expensive and not practical, which necessitates a genetic approach.

The focus of this study is to investigate the physiology and genetics of salinity tolerance in chickpea using data collected from high resolution image phenotyping. Phenotypic data was generated from a collection of 245 diverse chickpea accessions (diversity panel, a subset of the ICRISAT Reference Set) (4) and a biparental population developed from a cross between Genesis 836 and Rupali, two Australian chickpea cultivars that contrast for salinity tolerance. The populations were phenotyped under 0 and 40 mM NaCl (for Reference Set) and 0 and 70 mM NaCl (for biparental population). To quantify relative growth rate due to salinity, plants were imaged for three days at The Plant Accelerator, Adelaide commencing 28 days after sowing, after which salt was added in gradual increments over a period of two days. The plants were then further imaged for 22 days after salt application. In addition to data extracted from high resolution imaging, data on yield and yield components were also taken.

High genetic variation for relative growth rate and seed yield and yield components under both control and salinity treatments was observed. Salinity reduced relative growth rate, shoot biomass and seed yield, with some genotypes affected more than others. Seed number explained 88%-92% of the variation in salinity tolerance. A major quantitative trait locus (QTL) for relative growth rate on chromosome 4 explaining 42.6% of genetic variation was identified by both genome-wide association mapping and linkage mapping using the phenotypic data generated from this experiment combined with SNP data generated from whole-genome resequencing (for Reference Set) and DAriTseq (for biparental population). The QTL was found to co-locate with QTL for projected shoot area, 100-seed weight and seed number under salt. This QTL will be validated in the PBA chickpea breeding program and markers developed for marker-assisted breeding to improve salinity tolerance in future chickpea cultivars.

Monitoring of pathogen populations causing Ascochyta blight in lentils and faba beans in southern Australia.

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Ascochyta blight includes a group of host-specific fungal foliar pathogens causing serious and often devastating disease on pulse crops leading to reduced yield, downgraded seed quality, poor nitrogen fixation for utilization by subsequent crops and ultimately economic loss. Monitoring of pathogen populations of Ascochyta lentis and Ascochyta fabae is critical to successfully manage disease in lentils and faba bean respectively and to ensure sound cultivar recommendations are made each cropping season. Both pathogens have a natural diversity in aggressiveness and are capable of sexual reproduction and recombination leading to new genetic variants. Over the past 18 months, a number of field trials, controlled environment studies and naturally infected stubble experiments have been conducted. These have revealed changes in the virulence of populations of both pathogens with increasingly aggressive isolates identified on previously resistant cultivars. A change in the reaction of the previously resistant lentil cv Nipper just four years after its commercial release has been reported (Davidson et al 2016), and 38 of 40 A. lentis isolates collected in 2015 were highly aggressive on cv Nipper in controlled environment experiments conducted this year. Of concern for the current lentil season is that 11 of 40 isolates collected in 2015 caused low levels of disease on the moderately resistant lentil cv PBA Hurricane XT in controlled environment experiments. This cultivar has been widely planted across southern growing regions in Australia due to the short term attractive high lentil prices and herbicide resistance. This poses a potential longer term risk to the lentil industry where loss of Ascochyta blight resistance could occur when single cultivars are intensively planted. For faba bean, whilst current cultivars remain resistant against A. fabae isolates collected prior to 2012, shadehouse experiments have revealed that isolates collected in 2014 and 2015 from the lower/mid north of SA are increasingly aggressive on some resistant cultivars. Of 31 isolates collected in 2014, 3 were highly aggressive on cv PBA Rana whilst 5 isolates collected in 2015 were highly aggressive on cv Farah and of these, 2 were also aggressive on cv PBA Rana. This research highlights the importance of monitoring Ascochyta blight populations to inform disease management strategies and cultural practices including crop and cultivar rotations in maintaining resistance to Ascochyta blight. Studies are continuing this season including collection of new isolates from growing regions as well as a suite of field trials, controlled environment experiments and stubble pot trials.
Construction of genetic linkage map and QTLs identification for Ascochyta blight (AB) resistance and flowering time in faba bean (Vicia faba L.)

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Faba bean (Vicia faba L.) is a diploid (2n = 2x = 12) legume species with a facultative allogamous reproductive habit, such that rates of outcrossing differ between environments. Faba bean plays an important role in management of soil fertility through crop rotation and nitrogen fixation, hence contributing to agricultural sustainability. The productivity of faba bean is limited due to various environmental factors (such as drought, salinity and frost) and diseases (bacterial, viral and fungal). Ascochyta blight (AB), caused by the fungus Ascochyta fabae is a destructive disease of the crop globally. Moreover, time to flowering is also crucial for the plant adaptation to specific environments. This study presents the development of an enhanced and improved genetic linkage map based on SNP markers and identification of the quantitative trait loci responsible for Ascochyta blight resistance and other traits (such as time of flowering) in faba bean. An intraspecific recombinant inbred line population was developed by crossing Nura (AB susceptible; late flowering) and Farah (AB resistant; early flowering) and a total of 166 F₄ progeny individuals were obtained. The lines were genotyped by Illumina’s Infinium assay with 1,536 SNP markers. A total of 1,105 markers were used for the construction of the genetic linkage map using JoinMap 4.1. Linkage map comprised of 688 non-redundant loci organized into 6 linkage groups representing six chromosomes of faba bean spanning a total of 839.97 cM, with an average inter-marker distance of 1.22 cM. Two phenotypic trials for AB resistance were performed under controlled environment conditions using different pathotypes and disease was scored on a 1-9 scale. Days to flowering were evaluated in three different glasshouse trials. QTL analysis detected multiple regions conferring AB resistance with one common QTL being identified between the two pathotypes. Three different QTLs were identified for days to flowering. Once validated, the associated markers identified in this study can prove to be an efficient tool for accelerating breeding in faba bean.
De novo assembly and characterisation of faba bean (Vicia faba L.) transcriptome using RNA-Seq

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Faba bean (Vicia faba L.) is one of the most important cool-season legume species that is cultivated world-wide to produce protein-rich grain not only for human consumption but also for animal feed. A number of transcriptome sampling studies have previously been performed for faba bean, with an emphasis on specific developmental stages or environmental conditions. However, there is a need to enhance the genetic and genomic resources to allow the construction of a transcriptome atlas for faba bean as previously described for other pulses such as field pea. The enhancement of the genetic resources for faba bean will lead to the identification of the novel genes and alleles for molecular breeding to increase the crop quality and yield. The RNA-Seq method enables the generation of a reference unigene set for a species without the need for a whole genome sequence. The objective of this study was to generate the reference unigene set for faba bean and to characterise it for two distinct genotypes, Doza and Farah. Transcriptome sequencing was performed from multiple tissues including leaves, flowers, stems, pods and roots at various developmental stages. A total of 7 RNA-Seq libraries from each cultivar were sequenced using Illumina-based high-throughput sequencing technology. The de novo sequence assembly resulted in a total of 60,012 and 59,391 transcripts with approximately 67.4 Mbp (N50 1,588 bp) and 65.5 Mbp (N50 1,629 bp) for Doza and Farah respectively. The transcripts generated were compared to the protein and nucleotide databases, as well as to the gene complements of several legume species such as Medicago truncatula and Cicer arietinum. Annotation of unigenes was performed, and patterns of tissue-specific expression were identified. Candidate genes for relevant agronomic traits were identified including winter survival rate, days to flower, field plant height, seed weight and seed yield. The faba bean transcriptome dataset will serve as a highly valuable resource for future genomics-assisted breeding activities in this crop.
Linkage map construction and QTL identification of Ascochyta blight resistance in wild chickpea (*Cicer echinospermum*)

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Cultivated chickpea (*Cicer arietinum* L.) is a highly valuable global food crop that provides a good source of protein, dietary fibre, carbohydrates and minerals. *Cicer echinospermum* is a wild relative of chickpea (*Cicer arietinum* L.) with valuable agronomic traits including resistance to Ascochyta blight (AB). Ascochyta blight, caused by the fungus *Phoma rabiei* is a destructive disease of chickpea affecting the crop yield globally. Therefore, additional sources of AB resistance are required for breeding activities to meet any challenges with potential resistance breakdown. Recent advances in next generation sequencing technologies permit the development of low-cost high-throughput genotyping including genotyping by sequencing (GBS) using RNA-Seq. The study aims at the development of high-density genetic linkage map for chickpea using a GBS approach and identification of quantitative trait loci that are responsible for resistance to Ascochyta blight. An interspecific recombinant inbred line mapping population was developed by crossing a susceptible cultivar, Sonali (*Cicer arietinum*) and a highly resistant line, 04067-81-2-1-1 (*Cicer echinospermum*) for the identification of linked markers for AB resistance. A total of 164 individuals were genotyped using a GBS-transcript approach that generated c. 3,000 segregating markers that could be potentially used for mapping. Approximately 2,000 markers were removed from the final analysis as they represented duplicate loci. A linkage map was constructed using a total of 1,005 non-redundant markers using JoinMap 4.1 that were assigned to 8 major linkage groups and 4 satellites. Total map length was calculated to be 557 cM with an average inter-marker distance of 0.56 cM. Phenotyping was performed under field conditions using a mixed inoculum over two years. Disease symptoms were scored using a scale of 1-9 based on whole plant severity. QTL analysis identified a single QTL for AB resistance from *C. echinospermum* source (AB_echino; Vp = 46%) on Chr4 of chickpea. The markers identified in close linkage to AB resistance genes from this study can be further validated and effectively implemented using marker assisted selection in chickpea breeding programs.
Pests in Australian summer pulses in 2016: current state of play and future challenges

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Pest management in Australian summer pulses is ever challenging because of the number of pests attacking pulses and the low damage thresholds in some crops. This applies especially to pulses grown for human consumption, including mungbeans that currently have a very high farm gate price of >$1000/t. Major pests such as Helicoverpa, podsucking bugs and mirids (Creontiades sp.) remain a constant threat. While all are easily controlled at present with pesticides, resistance management for Helicoverpa and a need for softer sucking pest insecticides (to retain beneficial predators that reduce Helicoverpa) are key issues for the longer term. Challenges have also arisen, including: 1) fluctuating seasonal conditions favouring different pests (e.g. etiella, Etiella behrii, increases in El Niño, whereas bean pod borer, Maruca vitrata, prefers La Niña); 2) the expansion of pulses into new production areas such as the Burdekin; 3) the southward movement of tropical pests such as soybean stemfly (Melanagromyzae sojae), and 4) changing cultural practices, including zero till cultivation (favouring soybean stem borer, Zygrita diva) and narrow row spacing to increase yields (but also increasing the survival of mirids). Finally there is the threat posed by new pest incursions, including very recently the vegetable leaf miner (Liriomyza sativae) on Cape York. Critical for successful summer pest management is knowing what pests might attack, detecting the early stages of pest outbreaks, and knowing when crops are (or not) at greatest risk of economic damage. This paper outlines specific recent pest issues in Australian summer pulses and discusses possible sustainable management strategies to minimise the flaring of secondary pests and to slow the development of insecticide resistance in Helicoverpa.

Stratified soil pH reduces faba bean nodulation and production potential

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Yields from acid sensitive pulse crops grown on low pH soils of south-eastern Australia are variable. Results from this jointly funded GRDC and NSW DPI project (DAN00191: N fixing break-crops and pastures for high rainfall zone acid soils) indicate that current acid soil amelioration strategies are inadequate and that subsurface acidity is limiting the potential of faba bean crops. Previous studies in this region linked effective nodulation of pulse crops with dry matter production and N fixation and highlighted variable persistence of rhizobia and N fixation in commercial pulse crops (1). Investigation of commercial faba bean crops grown on low pH soils of south-eastern Australia in 2015 showed a strong correlation ($r^2=0.82$) between low pH and poor nodulation.

During 2015, 12 commercial faba bean crops in NSW, VIC and SA were assessed 2-3 months post sowing for effectiveness of nodulation (2). Combined 0-10 cm soil test samples were collected in February, 2015. Eight crops showing poor nodulation were followed up and more detailed testing of topsoil at 2 cm increments was undertaken using a field pH kit. The study indicated that the adoption of reduced tillage practices has resulted in the development of more defined pH stratification than previously reported (3). Despite widespread use of lime to ameliorate soil acidity, results showed that unincorporated, surface-applied lime produced elevated pH at the soil surface (0-2 cm). However, the lime had limited effect on pH of the subsurface layers (below 6 cm). This has negative impacts on nodulation and root development of faba bean crops and implications for all acid sensitive crops.

ALOSCA® – A new technology to deliver rhizobia and other beneficial microbes into broadacre agriculture

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ALOSCA® technology was developed to provide a more reliable and end-user friendly delivery system for rhizobia and other beneficial soil microbes. The key feature of ALOSCA® technology is the enhanced survival of microbes during desiccation, which leads to better survival of inoculants and ultimately greater impact on plant growth. The use of ALOSCA® granules eliminates the need for slurry inoculum immediately prior to planting. ALOSCA® granules can be mixed with either seed or fertilizer at seeding and can remain viable in the ground for extended periods. A further advantage of the ALOSCA® technology is the flexibility it affords when fungicide is applied to seeds without adversely affecting the rhizobia which are supplied separately in the clay based granules.

Strategies to regulate water and oxygen gain or loss from rhizobia coated onto seed have been tried, and met with limited success particularly in the harsh Mediterranean climate. ALOSCA® is the first truly dry granule to be commercially released that is suitable for use in Mediterranean agriculture. Current inoculation technology has been sub-optimal in changed farming systems and legume performance often suffers due to poor nodulation, especially following extended periods of dry warm weather before adequate rainfall is received. On many large farms, farmers have a strong desire to dry sow (i.e. before the winter rainfall commences), this is often purely a logistical decision due to time restrictions when winter rainfall commences

ALOSCA® represents a significant development in the delivery of root nodule bacteria to Australian agricultural systems. The nature of the granules gives the bacteria a considerable edge over the traditional peat based system. Moreover, primary producers are no longer required to sow at ideal times to ensure survival of rhizobia, the dry granules offer new degrees of flexibility to sowing times without resulting in diminished nodulation.

QTL detection for flowering time in faba bean and the responses to temperature and photoperiod

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Faba bean (Vicia faba L.) is a grain legume primarily used for animal feed and human food grown in a range of environments, globally. Time of flowering in faba bean is critical for adaptation to specific environments and is controlled largely by ambient temperature and photoperiod. The aim of this study was to investigate the genetic control of flowering in faba bean and the responses of flowering time to ambient temperature and photoperiod, which directly contributes to Milestone 8 of the GRDC project ‘Molecular markers for pulse breeding programs’. A bi-parental recombinant inbred line (RIL) population (Icarus × Ascot) was evaluated over three years in the field and in three controlled environments with varying temperatures and photoperiods. QTL analysis identified eight regions of co-localised QTL associated with days to flower, thermal time to flower and node of first flower; on Chr-I.A/III/V, Chr-I.B.3, Chr-III.1, Chr-III.2, Chr-V.1 and Chr-V.2. The three regions of greatest effect are likely to be identical to those identified in a previous study, while the other five may be novel. For the first time, the associations of these QTL with ambient temperature response and photoperiod response were described. Candidate genes for some of the QTL were identified using the associations with ambient temperature and photoperiod response together with knowledge extended from other legumes that have a syntenic relationship with faba bean. Evaluation of 11 Australian varieties and breeding lines (from both Northern and Southern breeding nodes) grown in controlled environments identified variation in ambient temperature and photoperiod response beyond that of the RIL population and suggested that variation in ambient temperature response stems from variation in optimum temperature, which could have implications for breeding for warmer climates.
Varietal differences in tolerance and the ability to recover from spring radiation frosts in chickpea

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Frost, which is defined when ambient temperature is ≤ 0°C, is a major abiotic constraint not only for winter cereals, but also for chickpea in Australia. In 2015 a limited comparison among six commercial varieties of chickpea (PBA Boundary, PBA Hattrick, Kyabra, PBA Pistol, CICA0912 and Monarch) at 3 field sites in Queensland (Hermitage, Jondaryan and Kingaroy), with and without frost protection, significant variety x frost treatments (unprotected and protected) and location x frost treatment interactions in yield were found. PBA Boundary gave the highest yield at Kingaroy and Hermitage, and Kyabra at Jondaryan. PBA Pistol and Monarch were the lowest yielding varieties under unprotected conditions at all locations. Low yields of PBA Pistol were mainly due to its high susceptibility to frosts, as it was the highest yielding variety when protected from frosts using frost shields in all environments. The yield advantage of frost tolerant varieties ranged 18 to 48% compared to the frost susceptible PBA Pistol. Only the frost events occurring after flowering caused appreciable visual damage to the crop. Visual scores of damage were significantly related to yield at maturity. The relationship between the number of frost events and yield, as expected, was negative with each additional frost event reducing yield by about 5%.

Under unprotected conditions, both PBA Pistol and Monarch made considerable recovery growth, as was evident from their greener appearance compared to their protected treatment. However, their yields were still less compared to Kyabra and PBA Boundary. This suggests that both frost tolerance and the ability to recover from frost damage should be combined together to minimize frost impact on the chickpea crop. A screening method for identifying varieties with both traits has been developed. A larger set of germplasm is now being screened using this method and appreciable differences have been observed. This work on frost in chickpea is supported by GRDC for the project on ‘Developing chickpeas with a better regenerative ability against spring radiation frosts (DAQ00193).
Generation of elite chickpea varieties for enhanced stress tolerance and resistance to *Botrytis cinerea*

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With global demand increasing, Australia has an unprecedented opportunity to significantly increase chickpea production. While we have some natural advantages, increasing chickpea production also has some inherent challenges. Increasing climate variability and change including excessive heat and water deficit as well as the increasing incidence of pests/diseases are major risk factors that affect the industry. By 2070, there may be 40% more months of drought in eastern Australia and conditions will be worse in a high-emissions scenario. In addition to the risk of drought, diseases still play a large role within Chickpea cultivation, which in 2010 witnessed a grey mold (*Botrytis cinerea*) epidemic that caused up to 40% yield losses. Upon abiotic and biotic stress plant cells accumulate large amounts of misfolded proteins that can lead to cell death. To combat these consequences plants have evolved cytoprotective genes that help maintain proper folding of proteins and reduce stress-induced death. The BAG genes are a family of multifunctional stress protective co-chaperones that facilitate protein folding and are conserved in mammals as well as plants. Here we describe the development and assessment of elite GM chickpea varieties expressing BAG genes isolated from *Arabidopsis thaliana* and the Australian resurrection plant *Tripogon loliiformis*. An efficient regeneration and transformation system was established using Agrobacterium—mediated transformation of half embryonic axis of chickpea (variety Hattrick). Using this system we achieved transformation efficiencies of up to 3%. In glasshouse trials, transgenic chickpea lines maintained two-fold higher yields compared to non-transgenic Hattrick controls under both mild and severe drought stress. In addition to increased yields upon stress, the transgenic plants produced higher quality grain with reduced tiger striping and increased size. Challenge with *Botrytis cinerea* (10⁵ spores/ ml) demonstrated that at least two transgenic plants displayed reduced infection (infection score of 2.75/10) compared to non-transgenic control (4/10) three weeks post-challenge. Our results indicated that expression of co-chaperones is a suitable method for the development of elite chickpea varieties that are not only drought tolerant, but also disease resistant. Furthermore, the development of an efficient transformation system provides tremendous potential for the introduction of additional elite traits into chickpea in the future.
Selecting for reproductive frost tolerance in field pea

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Frost at flowering and podding causes significant economic loss to field pea by decreasing yield and increasing the incidence of fungal diseases such as black spot. The frequency of spring frost events is likely to increase in many regions, primarily due to a change in rainfall patterns. This paper describes a method for selecting reproductive frost tolerance in field pea by observing the impact of frost events on pods and seeds. The field-based method uses replicated plantings of germplasm at a frost prone site in the Adelaide Hills. In the 48 hour period following a frost event, large numbers of young flowers and pods are tagged and the survival and damage to flowers and immature pods is recorded after plant maturity. Results over three seasons have shown consistent differences between control varieties and identified germplasm with putative reproductive frost tolerance.

Two traits are measured following a frost event: 1) pod loss (the proportion of tagged pods which survive to maturity) and 2) seed loss (the proportion of damaged seeds in surviving pods). Significant genetic variation was found for both of these traits and the evidence to date suggests that they are inherited independently.

A wide diversity of germplasm has been tested and lines with significantly reduced seed loss and pod loss have been identified. Crosses have been developed to elucidate the genetics of these traits and to transfer them to germplasm better adapted to Australian agronomic conditions.
Early maturity opens up potential for crop topping in chickpea

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Crop topping is a common practice in southern Australian pulse production as a strategic method of controlling Group A herbicide resistant Annual Wimmera ryegrass prior to seed set. The herbicide application timing is critical in pulses, as a crop can incur yield losses, quality down grading and reduced seed viability if it has not reached physiological maturity. Chickpeas are generally considered to be unsuitable for the practice of crop topping, due to their relatively late maturity and higher yield losses in comparison to other pulse crops. However, due to their slow early season growth rates and open plant canopy architecture, chickpeas are widely considered as one of the weaker competitors with ryegrass allowing large seed sets to occur. Trials have been conducted over multiple years on the Yorke Peninsula of South Australia comparing early flowering and maturing breeding lines with commercial varieties to study the impact of crop topping on chickpea grain yield and seed size.

Results showed earlier maturing desi chickpea varieties, such as PBA Striker, were generally less sensitive to crop topping. These varieties incurred minimal yield loss compared to later maturing varieties, such as the widely grown commercial small seeded kabuli variety Genesis™ 090, which incurred a 16 to 36% yield loss across years at the recommended crop topping application timing for effective seed set control in ryegrass. Earlier maturing varieties also incurred smaller reductions in grain weight, used as an indicator of seed size, at this timing compared to Genesis™ 090 where a 7 to 17% reduction in grain weight occurred. Premiums are generally paid for larger seed sizes in kabuli chickpea varieties so avoiding seed size reductions is paramount for maximizing returns to growers.

The Pulse Breeding Australia (PBA) chickpea program is actively developing early maturing chickpea lines for better adaptation to both the southern region environment and the practice of crop topping. To date, the advanced early maturing breeding lines, whilst showing improved suitability to crop topping, have been inferior to commercial varieties in other essential characteristics, such as disease, yield and plant type. A number of targeted crosses to combine the required early maturity traits with good disease resistance and agronomic characteristics has been ongoing in the breeding program. Screening and selection for suitability to crop topping is now routine to identify a high yielding broadly adapted line with characteristics to improve weed control options in kabuli chickpeas.
Characterisation of root architectural responses of mungbean to water deficit

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Research into making agricultural systems more water efficient is becoming more relevant as the majority of climate change scenarios paint a deteriorating picture of fresh water availability. Agriculture accounts for in-excess of 70% of the world’s freshwater usage and this figure is set to increase by another ~19% by 2050. Lack of freshwater has been described as the single biggest problem in meeting the ever-increasing global food requirement. Other abiotic stresses leading to crop losses include salinity, temperature, and chemical toxicity. However, of these, drought and salinity (often occurring in conjunction) are the most costly.

Vigna radiata (mungbean) is one of the most important pulse crops in the world. They are one of the most economical sources of protein (24%) available, contain high levels of dietary fibre, essential amino acids including methionine and lysine, vitamins, minerals and only a small amount of oil. Mungbeans have been commercially grown in Australia since the late 1960s and 1970s. It is believed annual production could see drastic increases if we are able to improve abiotic stress tolerance – particularly drought.

The present study investigates physiological and morphological responses of differentially drought tolerant varieties of mungbean under regulated deficit irrigation (RDI) at the Queensland Crop Development Facility (QCDF). Seed pre-treatment with a novel chemical referred to as ATW1124 was investigated as a putative enhancer of root development for the improvement of adaptability to water limiting conditions. Another pillar of the study is simulating the effects of ATW1124 on mungbean in APSIM to determine potential impacts on production. Finally, RNA-Seq transcriptome analysis will reveal molecular mechanisms underpinning these responses.
Using controlled environment screening of Ascochyta bight in Chickpea (Cicer arietinum L.) to develop chickpea varieties with improved resistance for Australian growers

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Ascochyta blight (AB) is an important disease caused by a fungus (Phoma rabiei) damaging crops, reducing yield and grain quality in most chickpea growing regions of the world, including Australia. The use of a controlled environment (CE) screening for AB resistance enables the rapid selection and phenotyping of breeding lines for future release and selection of parent material, independent of the external environment. Additionally the CE AB screening is being used within the breeding program to phenotype for resistance against single aggressive isolates to assist AB resistance marker development.

Chickpea seedlings are grown to the 3 node stage in potting mix, inoculated with either a single or mixed aggressive isolates selected from the target growing region (1) at a rate of 50,000 conidia/ml. Plants are scored twice, first 10-12 days after inoculation then 3-5 days after the initial scoring.

Pulse Breeding Australia (PBA) chickpea breeding lines are screened annually as part of the program’s efforts to improve AB resistance. In conjunction with the CE AB screening, the breeding program also conducts field AB nurseries at Tamworth (NSW) and Horsham (Vic). At Tamworth in 2014 and 2015, the same mix of isolates were used in field and CE screening. The highest correlation between field and CE scores occurred between the 2014 stage 3 desi field nursery (high early disease pressure) and 2015 CE data (R² = 0.51), with the most resistant and most susceptible lines correlating well in both environments. Most variation between field and CE scores are within moderately resistant/moderately susceptible lines, with increased disease observed in the CE screening. The method has proven effective for rapid identification of high levels of resistance.

Changes in AB reactions of a number of chickpea varieties have been reported in both the northern (1) and southern (2) chickpea growing regions. The PBA Chickpea program will move to single isolate screening in CE to address this emerging issue whilst maintaining mixed isolate screening in field nurseries.

The development of chickpea varieties with improved resistance will require an integrated approach combining breeding, pathology and genomic expertise. The PBA Chickpea program is currently using marker assisted selection to characterise parents using flanking markers (3) generated within the Pulse Marker program in order to identify suitable populations with AB resistance. The program is also involved in the effort to identify new markers for alternative AB resistance sources which provide good levels of resistance.

Resistance of field pea and lentil to the root lesion nematodes *P. thornei* and *P. neglectus*.

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The root lesion nematodes, *Pratylenchus thornei* and *P. neglectus*, cause grain yield losses in cereal crops throughout Australia. Control of these nematodes is achieved through cultivation of resistant crops or varieties which reduce nematode densities. Pulse crops, already sown in rotation with cereals, are most effective at reducing nematode densities. The most resistant pulse crops have previously been reported to be field pea and lentil, but numerous varieties have been released since the resistance screening was conducted and the ratings for these varieties is unknown.

Current field pea and lentil lines were evaluated in replicated field trials, with wheat, barley and fallow control plots included for reference. Nematode multiplication rates were calculated using soil samples taken at sowing and post-harvest. The final levels of nematodes were analysed using linear mixed models incorporating spatial methods and residual maximum likelihood (1) for variance parameter estimation. Nematode multiplication rates were derived from this analysis.

Recently released field pea varieties, including PBA Gunyah and Kaspa were less resistant to *P. thornei* than varieties such as Parafield and Excell tested in the 1990s (2). Field pea resistance to *P. neglectus* was similar between recent varieties and varieties tested in the 1990s (3). In lentils, recently released varieties were found to be resistant (R) or moderately resistant (MR) to *P. thornei*, similar to the lentil varieties tested in the 1990s (2). Recently released lentils were found to be MR to moderately resistant/ moderately susceptible to *P. neglectus* which is similar to previous reports (4).

A decreased resistance to *P. thornei* in recently released field pea varieties highlights the need for routine testing of new pulse varieties for resistance to root lesion nematodes.

These results have been incorporated in disease guides to assist growers in reducing root lesion nematode densities. This will reduce grain yield losses in subsequent cereal crops.

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Virulence status of *Uromyces viciae-fabae* pathotypes in Australia

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Faba bean rust (*Uromyces viciae-fabae*) is an important disease in sub-tropical region of Australia and pathogen variability of this fungus is unknown. Pathotypes (races, strains) are the unique variants of a pathogen that differ in their ability to overcome the resistance in one or more host types of the same species. The ability or inability of rust pathogen to infect a group of host genotypes allows pathotype detection. Three single seedling rust resistant genes have recently been detected in cultivar Doza, European accession Ac1655 and Ac1227#14908 in Australia (1). These three genotypes were used to study the pathogen variability as there are no differentials developed yet for faba bean rust. The detection of virulence involved the collection, purification and multiplication of rust urediospores from single infected lesion followed by infecting a set of healthy seedlings (with known resistance) under controlled environment. The pathotype testing was designed and performed at Cereal Rust Testing Laboratory, Plant Breeding Institute, Cobbitty. The rust urediospores suspended in light mineral oil (Isopar) were misted on the set of resistant plants using ultra low volume applicator (Microfit, Micron sprayer, UK). After inoculation, plants were kept for incubation in dark room with 100% relative humidity for 24 h. Following incubation, plants were moved in microclimate room at 24±2 °C and seedlings were rated for disease resistance. The virulence pattern revealed the faba bean genotypes were uniformly susceptible to rust isolates Uvf-4 and Uvf-5, but variable in their response to the other eight isolates. Six pathotypes were identified based on the virulence/avirulence pattern on these three faba bean genotypes with known resistance, i.e. P-1 (Uvf-1 and Uvf-3), P-2 (Uvf-2 and Uvf-9), P-3 (Uvf-6 and Uvf-8), P-4 (Uvf-4 and Uvf-5), P-5 (Uvf-7) and P-6 (Uvf-10). The rust resistant gene from Doza seems to be more stable and effective in SA and NSW. Furthermore, two of the three pathotypes collected from Queensland were found to be virulent on all genotypes showing a concern for rust resistance breeding for this region.

Identification of QTL associated with metribuzin tolerance in field pea (Pisum sativum L.)

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Field pea is an important grain legume known for its nutritional value and rotational benefits including improving the soil fertility status through nitrogen fixation. However, one of the key constraints to Australian field pea production is weed competition due to the shortage of herbicide control options. Metribuzin is considered a safe herbicide control option for legumes but it can cause phytotoxicity to both weed and crop. Not much data is available on the metribuzin screening in field pea, therefore, a preliminary assay was conducted to optimize the dosage required to differentiate between tolerant and sensitive genotypes. The assay was performed using six different concentrations of metribuzin ranging from 0 ppm (untreated control) to 25 ppm in a sand culture and 10 ppm metribuzin concentration was selected because of its efficacy for discriminating between metribuzin tolerant and sensitive germplasm. Subsequently, using this concentration, a single field pea recombinant inbred line population Kaspa x PBA Oura was screened for tolerance to metribuzin in two individual controlled environment assays. After two weeks of metribuzin treatment, plants were assessed for symptom score on a scale of 0 (no symptoms) to 6 (severe chlorosis and necrosis) and plant damage as percentage of necrosis. The results between the two assays indicated high correlations for symptom score ($r = 0.95; P \leq 0.05$) and the percentage of necrosis ($r = 0.97; P \leq 0.05$). The location and magnitude of effect for QTL was estimated using both simple interval mapping (SIM) and composite interval mapping (CIM) analysis. Plant symptom score and percentage of plant necrosis from both assays were used to perform QTL analysis using a previously published Kaspa x PBA Oura population-derived map. The analysis performed revealed a single genomic region on Ps IV for both assays with gene based flanking markers that are 5 cM apart. The phenotypic variance ($V_p$) explained for plant symptom score and percentage of plant necrosis in both assays was in the 12-21% range. These markers could be further validated and applied in field pea breeding programs.
Optimum sowing time and plant density for irrigated mungbean in central west NSW, 2013/14 – 2015/16.

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Mungbean has regained popularity in northern NSW as a short season, summer opportunity crop for three reasons: reduced irrigation allocations; the release of new varieties with improved yield and disease resistance; and higher prices. This has led to improved profitability of mungbean as a stand-alone crop, in addition to its rotational benefits as a pulse crop. However, adoption in the Macquarie Valley (central-west NSW) is limited by lack of agronomic currency regarding best management practice for new varieties.

NSW DPI, with support from the GRDC funded Northern Pulse Agronomy Initiative project, has conducted variety-specific management experiments at Trangie over the past three summer seasons (2013/14–2015/16). All experiments were sown into a grey vertosol soil under fully irrigated conditions.

The first experiment in 2013/14 compared an older variety Berken, with two new varieties Crystal® (released 2008) and Jade-AU® (released 2013); at four target plant density establishment rates (20, 30, 40 and 50 plants/m²) at a single row spacing (33cm). In this experiment Jade-AU® was the superior variety, with higher yield and larger seed size than Berken or Crystal®.

Follow-up experiments in 2014/15 and 2015/16 seasons therefore used Jade-AU® variety only, to evaluate the interaction between four target plant densities (20, 30, 40, 50 plants/m²) and three row spacings (33, 66 and 99 cm) at two times of sowing (17 December and 19 January in both seasons) for optimum yield response.

In these experiments there was a significant yield response to time of sowing, with the 17 December sowing yielding higher than the 19 January sowing in both seasons. There was also a significant response to row spacing, with higher yields obtained from the narrowest row spacing (33 cm) at both times of sowing in both years. Optimum planting density showed a less significant response in all three experiments – yield responded to increased target densities from 20 to 30 plants/m², but there was no yield response to 40 or 50 plants/m².

Mungbean growers in the Macquarie Valley are therefore advised to choose Jade-AU® variety for its superior yield and disease resistance, sow early on a narrower row spacing (33 cm) and aim to achieve a minimum of 30 plants/m². These updated guidelines will support improved productivity of mungbean in the Macquarie Valley region of NSW.

Varieties displaying this symbol beside them are protected under the Plant Breeders Rights Act 1994.
Identification of quantitative trait loci for agronomically important traits in field pea (Pisum sativum L.)

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Field pea is an annual cool-season legume crop that is grown for either human consumption or livestock feed. In some parts of the world, field pea is also grown as green manure. Agronomic traits have significant influence on the stability and adaptability in pea production, hence understanding the genetic basis of agronomic traits is important. In this study, quantitative trait locus (QTL) analysis of multiple agronomic traits was performed using four recombinant inbred line (RIL) populations derived from crosses between Kaspa and four other genotypes - Parafield, PS1771, Yarrum and PBA Oura that had contrasting agronomic traits. Previously developed SSR and SNP based genetic linkage maps were available for all populations. Twelve agronomic traits including vegetative traits (plant height, internode length, leaf type), flowering traits (flowering time, number of flowers per peduncle), pod and seed traits (pod type, number of pods, seed type, seeds per pod, number of seeds), plant maturity and plant biomass were evaluated. A total of 25 QTLs were detected that explained 8-80% of total phenotypic variation. The QTL that explained the highest level of variation was associated with leaf type. Some of the QTLs were found to be common to multiple RIL populations. Identified QTLs were compared to previously published studies based on common markers and a range of QTLs associated with pod and seed traits were inferred to be at the same genomic locations. The genetic markers flanking the QTL-containing regions identified in this study can be used for the development of linked polymorphisms for marker-assisted selection (MAS) of superior cultivars, based on introgression of QTL-containing genomic regions from donor to recipient germplasm. An integrated genetic map outlining the positions of agronomic QTLs represents a valuable resource for field pea genomics and breeding.
Validation and utilisation of molecular markers for bacterial blight resistance in field pea breeding

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Bacterial blight, caused by Pseudomonas syringae pathovars (pv.s) pisi and syringae, is a serious disease of field pea all over the world. Prevalence of each pathovar varies between regions (depending on the predominant cultivar within that region), and they may occur in the field separately, or in combination. Resistance to pv. pisi is conferred by a specific gene-for-gene interaction mechanism whilst resistance to pv. syringae exhibits continuous variation, suggesting contributions by a number of genes with lower magnitudes of effect, and leading to quantitative inheritance. This pathogen is considered to be the main cause of recent bacterial blight epidemics worldwide. As chemical control options for bacterial diseases are not economic and cultural practices are of partial benefit, the development of field pea varieties with bacterial blight resistant is a high priority for field pea breeding programs. Trait-dissection studies from two segregating recombinant inbred line populations (Kaspa x Parafield and Kaspa x PBA Oura) identified six QTLs for pv. syringae whereas a single common genomic region was identified for pv. pisi Race 3 in both populations. The flanking markers from these QTLs were predictive of the phenotype when validated using a diverse set of germplasm comprising c. 200 lines, representing most of the diversity within the Pulse Breeding Australia field pea breeding program. Marker trait correlations were calculated to be 83% and 84% for pv. syringae and pv. pisi Race 3, respectively. A small number of false positives and negatives were identified that could be explained by either new sources of resistance and/or loss of marker linkage. Our results indicated an adequate level of resistance to Race 3 present within the current field pea breeding program, however, for pv. syringae, there are only a limited number of known sources. This emphasises the need for breeders to incorporate additional sources of bacterial blight resistance for pv. syringae such as PBA-Oura which is rated as moderately resistant. Linked markers for pv. syringae validated in the current study can be used for marker assisted selection to enable introgression of new sources of pv. syringae resistance in a cost-effective and efficient manner.
The narrow genetic base of grain legume cultivars coupled with low utilization of genetic resources are the major factors limiting the breeding gains for these crops globally. Exploitation of new and diverse sources of variation is needed for the genetic enhancement of grain legumes including lentil. Knowledge of genetic variation and genetic relationships between lentil genotypes (wild and cultivated) is important for efficient germplasm preservation, characterisation and subsequent use by breeders. To achieve this, transcriptomes from all lentil wild relatives (c. 200) preserved at Australian Grains Genebank (AGG), as well as a subset of cultivated lines (c. 850) either obtained from the Australian lentil breeding program or the AGG were sequenced using a genotyping by sequencing method. A total of c. 5 million reads were generated from each sample and aligned against PBA-Blitz genome and transcriptome references generated as part of the International Lentil Genome Sequencing Initiative, to identify sequence variations. This data was used to assess genetic diversity between wild and cultivated lentil gene pools and understand genetic relationships amongst all species leading to a pan \textit{Lens sp.} relationship matrix. In addition to this, genomes of \textit{L. ervoides} and \textit{L. nigricans} were sequenced using Illumina paired end and mate pair libraries to c. 30-35x coverage and have been assembled using a range of software tools and pipelines. The draft genome sequences were then compared against the \textit{L. culinaris} genome to identify potential similarities and differences.
Lentil genome sequencing effort: a comprehensive platform for genomics assisted breeding

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The International Lentil Genome Sequencing Initiative, led by the University of Saskatchewan in collaboration with Biosciences Research, Agriculture Victoria, Australia, has recently released a draft lentil genome sequence assembly from CDC Redberry. This significant advance will help in better understanding of the genetic architecture of lentil. As part of this international effort, Biosciences Research sequenced the genome and transcriptome of an important Australian cultivar, PBA-Blitz, which would prove highly beneficial for the Australian national breeding program. The genome sequence assembly consisted of 354,140 scaffolds with N50 of 96,159 bp whilst the assembled transcriptome reference comprised of c. 85K scaffolds and contigs totalling c. 77 Mbp with a N50 of 1,302 bp. Sequencing the lentil genome will enable the identification of key genomic regions that affect important complex traits, such as yield. The availability of the lentil genome sequence will assist in applying genome-wide methods for trait mapping using association studies and genomic selection and when combined with high-throughput phenomics will enable the delivery of improved pulse varieties with better precision. In addition, c. 200 diverse lentil lines have also been sequenced to understand the levels of genetic diversity within key lentil gene pools. A neighbour joining (NJ) tree was generated using the unweighted NJ method. All lentil cultivars were assigned to four major groups along with three small outgroups, that in general reflected the known pedigree relationships of the lines. These resources will help to integrate molecular tools into the PBA lentil breeding programs for the fast delivery of superior varieties with better resistance/tolerance, yield and quality, to Australian growers. This in turn will also increase the competitiveness of the Australian lentil industry and further maintain its position as one of the leading lentil producers and exporters in the world.
Transcriptome profiling as an initial step towards identifying the defence genes that provide resistance to *Ascochyta lentis* in lentil

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Ascochyta blight, caused by *Ascochyta lentis*, causes ~16.2 million dollars of economic loss annually to the Australian lentil industry (1). Sustainability of resistant cultivars may be improved through selection and incorporation of specific genes conditioning the early defence-responses including those associated with recognition, structural and biochemical fortification, and signalling. These genes were captured through the monitoring of changes in the gene expression (transcriptome) patterns via RNA sequencing of a highly resistant accession (ILL7537) and a highly susceptible accession (ILL6002) in response to inoculation with the pathogen. Transcripts were collected and compared at 2, 6 and 24 hours post inoculation with either a highly aggressive isolate (ALP2) or H2O. In total, 175 genes were identified as differentially transcribed and that had previously been associated with plant-pathogen defence (2-7). Of these, 39 were directly associated with resistance to *A. lentis*. Several had previously been associated with this pathosystem using microarray and EST approaches (8). These were categorised into three main physiological classes; 1) primary defence response (recognition), 2) induced defence response, and 3) necrotic structural defence response. Each class comprised specific functional gene groups such as receptors and signalling molecules; structural and biochemical compounds; and systemic signalling and cell death compounds, respectively. These key resistance gene candidates will be investigated further for sustainable functional validation and to determine their genome locations for future selective breeding.

High-throughput screening of lentil for Aluminium tolerance using hydroponic assay

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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 general, legumes are more sensitive to environmental challenges than cereals, and several abiotic stresses such as salinity and boron toxicity, cold, drought, heat and acid soils adversely affect global yields of lentil. Acid soils are a major limiting factor affecting the cultivation and production of the crop worldwide including Australia. In acid soils with pH below 5.5, phytotoxic forms of Aluminium (mainly Al^{3+}) become available and inhibit the root growth which affects water and nutrient uptake resulting in yield loss. Application of lime to manage acid soils is not economical and efficient practice. Therefore, there is a need to identify tolerant genotypes that can grow well in acid soils. The current study reports the development of a high-throughput hydroponic assay system to enable large scale screening of lentil genotypes for Al tolerance. A pilot experiment was conducted using 8 landraces obtained from Australian Grains Genebank (AGG) in a hydroponic assay system in order to optimize Al concentration that can differentiate between tolerant and intolerant genotypes. A known Al-tolerant lentil line, ILL6002 as well as Al-tolerant and sensitive wheat lines (Yitpi and Chara) were included as controls in the experiment. Different Al concentrations (0, 3, 10, 20 and 30 µM) were used to screen 4-day old seedlings for 3 days in a low ionic nutrient solution at pH of 4.5. Relative Root Growth (RRG) was measured and showed significant reduction at 10µm compared to 3µM Al treatment. The known lentil tolerant line ILL6002 showed higher RRG as compared to wheat sensitive line, Chara at 3µM but showed less RRG than wheat tolerant line Yitpi, at all the other concentrations which indicates the reliability and reproducibility of the hydroponic assay. However, the landrace ILL4777 and lentil genotype PI299306 performed better when compared to ILL6002 at all Al concentrations indicating that additional sources for Al tolerance in lentil are present within the AGG germplasm and should be further explored. Based on the initial results, we are planning to screen additional 124 lentil genotypes identified as putative tolerant lines to Al toxicity using the Focused identification of Germplasm Strategy (FIGS). These lines will first be screened using the hydroponic assay and further on, the results will be compared using a pot based trial.
Patterns of temperature for Australian chickpea production

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The environment is the largest component of the phenotypic variance of crop yield with water and temperature playing a major role. There have been studies focussed on the patterns of water deficit for specific crops and regions, but thermal characterisations have not been reported. To quantify the types, spatial patterns, frequency and distribution of thermal regimes for chickpea in Australia, we combined modelling, trial and meteorological data. We used data from National Variety Trials, including sowing time, yield and weather, from 295 production environments across Australia. Associations between actual yield, in a range from 0.2 to 5.2 t/ha, and actual temperature were explored. Yield correlated positively with minimum temperature in the 800 degree-days window bracketing flowering and the correlation shifted to negative after flowering. A negative correlation between maximum temperature over 30°C and yield was found from flowering through to 1000 degree-days after flowering. A wider analysis was performed using crop simulations in 3905 environments (71 locations x 55 years between 1958 and 2013) which identified three dominant seasonal patterns for both maximum and minimum temperature accounting for 77% and 61% of the overall variation. The most frequent environments for minimum and maximum temperature were associated with low actual yield (1.5–1.8 t/ha). For all temperature environment types, we found significant spatial variation that is relevant to the allocation of effort in breeding programs.

Robust associations between yield and crop growth rate in a species-specific critical developmental window have been demonstrated in many crops. In this study we focus on genotype-driven variations in crop growth rate and its association with chickpea yield under drought. We measured crop growth rate using Normalised Difference Vegetative Index (NDVI) in 20 diverse chickpea lines, after calibration of NDVI against biomass accounting for morphological differences between Kabuli and Desi types. Crops were grown in eight environments resulting from the combination of seasons, sowing dates and water supply, returning a yield range from 152 to 366 g m\(^{-2}\). For both sources of variation – environment and line - yield correlated with crop growth rate in the window 300°Cd before flowering to 200°Cd after flowering. In the range of crop growth rate from 0.07 to 0.91 g m\(^{-2}\) oCd\(^{-1}\), the relationship was linear as with other indeterminate grain legumes. Genotype-driven associations between yield and crop growth rate was stronger under water stress than under favourable conditions. Despite this general trend, lines were identified with high crop growth rate in both favourable and stress conditions. We demonstrate that calibrated NDVI is a rapid, inexpensive screening tool to capture a physiologically meaningful link between yield and crop growth rate in chickpea.

This abstract is from a paper that has been submitted to the European Journal of Agronomy for consideration for publication.
Field pea is a major pulse crop in the winter dominant rainfall farming systems of southern Australia and is being increasingly grown in regions where water and heat stress are common. Adaptation to these conditions remains poor leading to unreliable yield. Research looking at adaptive traits for 29 different field pea lines in environments varying for moisture and heat stress found a trait termed ‘pod wall ratio’ (pod wall weight/whole pod weight) which is linked to high yield in stress and non-stress environments. This trait captures variation in seed abortion, seed per pod and pod wall thickness and is relatively easily measured. To investigate the genetic basis of this trait we are studying a mapping population of 120 individuals that has been produced from a cross between two parents contrasting for pod wall ratio (Kaspa and Excel). We multiplied this population in 2014 and carried out a replicated field trial at Roseworthy in South Australia in 2015. This replicated trial is being repeated at Turretfield South Australia in 2016. Phenotypic data have been collected for the 2015 trial showing a good distribution for the pod wall ratio trait amongst the population. Phenotypic data will again be collected in 2016 and combined with genotypic data with the aim of isolating regions of the genome responsible for variation of this trait. Markers will then be developed and provided to breeding programs for use in early generation selection.

Genome-wide association studies identified candidate genes for Ascochyta blight resistance using whole genome re-sequencing data in chickpea

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Next-generation sequencing (NGS) technologies offer a relatively cheap and high-throughput genotyping option to discover genome variation and selection signatures in many crop species, such as chickpea.

Sixty-nine chickpea genotypes were sequenced using whole genome re-sequencing (WGRS), including 48 chickpea cultivars released in Australia from 1978 to 2013, 17 advanced breeding lines, four landraces, and one *Cicer reticulatum*. Alignment of 0.9 billion Illumina paired-end reads to the kabuli reference genome of chickpea resulted in the identification of over 800,000 single nucleotide polymorphisms (SNPs). Population structure analysis revealed two groups of cultivars separated based on their level of Ascochyta blight (AB) resistance and narrow genetic diversity in recently released Australian cultivars. Several regions of the chickpea genome were under positive selection based on Tajima’s D test. Both Fst genome scan and genome-wide association studies (GWAS) identified a ~100kb region on chromosome 4 that was significantly associated with AB resistance. This region was co-located in a large QTL interval of 7Mb~30Mb identified previously in three different mapping populations genotyped at low density with SSR or SNP markers. The 100kb region has been validated by GWAS in an additional 132 advance lines with ~140,000 SNPs. Reduced level of nucleotide diversity and the long extent level of linkage disequilibrium (LD) also suggested this region may have gone through selective sweeps caused by selection of AB resistance traits in breeding. In total, 12 predicted genes were located in this region including NBS-LRR receptor-like kinase, wall-associated kinase, zinc finger protein and serine/threonine protein kinase. One significant SNP located in the coding sequence of NBS-LRR receptor-like kinase led to amino acid substitution. Transcriptional analysis using qPCR shown that some predicted genes were significantly induced in resistance lines after inoculation compared to non-inoculated plants. This study demonstrated the power of combining WGRS data with relatively simple traits in fast developing “functional makers” for marker-assisted selection and genomic selection.
Genome-wide association studies identified candidate genes for yield relative traits under drought prone environments using whole genome re-sequencing data in chickpea

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Drought stress is an important constraint for chickpea production. It is a complex trait controlled by numerous genes and further complicated by environmental conditions [1]. Previous research to improve drought tolerance has been focused on drought escape through selection of early flowering traits; however, little progress is made on breeding drought tolerance per se [2].

To study the genetic basis of drought tolerance, a diverse panel consisting of 132 advanced breeding lines from the Pulse Breeding Australia (PBA) Chickpea breeding program and the International Centre for Research in the Semi-Arid Tropics (ICRISAT) was phenotyped to measure 12 yield and yield-related traits in three drought-prone field environments in Western Australia. Yield was positively correlated with seed size, size number, dry weight, and flowering time, while negatively correlated with the empty pod ratio.

The panel was subjected to whole genome re-sequencing (WGRS) with 5-15X coverage using next-generation sequencing (NGS) technologies. More than 140,000 single nucleotide polymorphisms (SNPs) were discovered using ~1.8 billion Illumina paired-end reads. Population structure analysis revealed that the PBA lines are generally separated from the ICRISAT lines. Combining SNP data with phenotypic data, 35 SNPs significantly (p< 3.45e-07) associated with six traits were identified using genome-wide association studies (GWAS). Among them, a SNP was found to significantly associate with yield. The closest gene near this SNP encodes a protein belonging to ABC transporter B family/p-glycoprotein which regulates auxin transport under abiotic stress response. Among the eight SNPs significantly associated with 100 seed weight, several candidate genes have been identified including one sugar transporter, two nodulin 21/EamA-like transporters, one Lateral Organ Boundaries domain protein and several uncharacterised genes.

This study demonstrated the value of using WGRS data to study complex traits for marker-assisted selection and genomic selection.

Selection for salinity tolerance in lentil

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Like most other crops lentil is susceptible to salinity. However, as salinity and salinity stress is widespread especially in arid and semi-arid regions, the ability to germinate and grow under saline conditions are important traits for selection in lentil. We evaluated genetic variation in salinity stress at germination and investigated traits responsible for salinity tolerance at the seedling stage. Germplasm comprising 128 genotypes from nine countries was examined for salinity tolerance at germination at 0 mM and 150 mM NaCl. Significant difference in germination percentage among germplasm from different countries of origin was observed: Genotypes from Ethiopia and Pakistan had the highest percentage of germination under salinity (98 ± 2% & 99 ± 1%, respectively). In contrast, Turkish germplasm had the lowest percentage of germination (79 ± 2.5%).

Six genotypes identified in the germination test, three tolerant and three susceptible genotypes, and two control genotypes (ILL 2501 and Nugget) were tested in the seedling stage at three NaCl concentrations (0.2-control, 60 and 150 mM NaCl). Salinity treatments were imposed in sand culture for 14 days when plants were 21 days old. All 8 genotypes were significantly affected by the salinity treatments. Root relative growth rate was more affected than shoot growth. Seed can germinate at 150 mM NaCl, but most genotypes only could survive as seedlings at 60 mM NaCl in this study. There was a positive correlation of salinity tolerance at germination and at the seedling stage.

In conclusion, salinity tolerant genotypes - both at germination and at the seedling stage - were identified for use in breeding.
Time of sowing for Faba bean (Vicia faba)

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Faba bean has become a significant rotation crop in northern NSW, used to manage cereal disease inoculum levels, provide nitrogen to the farming system and generate additional income.

Field trials at Breeza and Narrabri in North West New South Wales examined the influence of three sowing dates (early, mid and late) on yield, seed weight, harvest index, and pod distribution at four nodal intervals as well as biomass production at flowering, early podding and maturity. At Breeza the influence of irrigation on these traits was also examined. In addition, tagged plants were used to study the development of flowers into pods at individual nodes in relationship to temperature regimes during the seven days following first flower at specific nodes.

Sowing date had a significant impact on yield. A mid (April) sowing producing the highest yield and seed weight at both sites. At Breeza the latest sowing date produced greater yield than the earliest sowing date, this was associated with very high final biomass at the earliest sowing date (9.8t/ha). At Narrabri the reverse occurred with the earliest sowing date yielding more than the latest. At both sites mid and late sowing dates produced a similar harvest index, being higher than the earliest sowing date. The quickest maturing genotype, IX148f gave the highest yield and seed weight at both sites. Irrigation had no impact on yield but significantly reduced harvest index. Sowing date influenced pod distribution at all nodal intervals at both sites with earlier sowing producing pods at higher nodal intervals. Genotype had a greater influence on pod distribution at Breeza compared to Narrabri, with the quicker maturing IX148f producing more pods at lower nodes.

Production of pods at individual nodes was maximized with average daily temperatures in the range of 12.5-13.5°C, daily maximum temperatures in the range 23.5-25.5°C and daily minimum temperatures in the range of 3-4°C.
Developing herbicide tolerance in faba bean: the response of different biotypes to multiple classes of ALS inhibitors

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Faba beans play an important role in sustainable farming systems, however weed competition, particularly from late emerging broadleaf weeds, is a major limitation in Australian production due to the absence of any in-crop broad leaf weed control options. The development of herbicide tolerance in broadacre crops has become an effective strategy in expanding weed control options, and was identified as a major breeding priority by Pulse Breeding Australia (PBA).

Mutagenesis methods have been successfully used in the development of a number of Imidazolinone (Group B) herbicide tolerant varieties in crops such as wheat, barley & canola. Imidazolinones are a class of acetolactate synthase (ALS) inhibitor herbicides that control a broad spectrum of grass and broadleaf weeds, including a number of key weeds in Australian faba bean production. In this project, mutagenesis methods were used to develop a large mutant (M) population from Nura and over 1 million M2 seedlings were mass field screened using the imidazolinone herbicide imazapyr. Four putative tolerant M2 plant selections were identified (IMI-1, IMI-2, IMI-3 and IMI-4) and tolerance levels to a range of Group B herbicides have been extensively evaluated in both controlled environment trials and field validation. All four selections were found to have a high level of tolerance to the imidazolinone family, however while IMI-2, IMI-3 and IMI-4 showed improved tolerance to herbicides from the sulfonylurea (SU) and triazolopyrimidine (Sulfonamides) families, IMI-1 remained sensitive to both these classes of herbicides. Of all four selections, the IMI-3 biotype showed the highest level of tolerance across the different classes of Group B herbicides. Sequence analysis of the ALS gene compared all four selections to control cultivar Nura and identified two different mutation events to be conferring herbicide tolerance.

All selections have been passed onto the PBA Faba Bean breeding program, however breeding progress has largely focused on the IMI-3 biotype due to its higher tolerance levels and improved agronomic characteristics. Elite lines incorporating the herbicide tolerance traits have been progressed to National Variety Trials (NVT) in 2016. If released, these new traits will help to expand broadleaf control options as well as reduce current plant back limitations, however, given the potential usage of Group B herbicides in other parts of the crop rotation, the adoption of integrated weed management practices is critical to maintaining herbicide efficacy and sustainable farming systems.
Weed the farm – Feed the world: Developing diagnostic molecular markers for Group B herbicide tolerance in three pulse crops

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Weed management is a major issue in all pulses with very few herbicides registered for use on faba bean, lentil or chickpea (1). Historically, acetolactate synthase (ALS)-inhibiting herbicides (Group B) have been registered for several non-pulse crops, including oat, barley, wheat and canola (2). Soil residue can damage emerging pulses and result in yield loss if sown following a crop that has been treated with Group B herbicides (3).

Target site tolerance to Group B herbicides has been reported in many plants and is caused by point mutations in the acetohydroxyacid synthase (AHAS) gene that result in amino acid substitutions in the ALS enzyme. Changes in the residues involved in herbicide binding reduce the efficacy of the herbicide resulting in herbicide tolerance with negligible fitness cost (2). Diagnostic markers based on these genetic mutations have been reported in many crop and weed species. Molecular markers can be a valuable tool to accelerate the introgression of novel traits into elite breeding lines, as well as to monitor resistance in weed populations.

In this project, AHAS mutations at residues 197, 205 and 653 were identified in novel Group B tolerant faba bean, lentil and chickpea germplasm and high-throughput molecular markers were developed and validated for use in pulse breeding programs. Development of faba bean, lentil and chickpea varieties with tolerance to group B herbicides will provide growers with additional weed management options and help to increase yields by reducing weed pressure and plant back restrictions in paddocks that have been sprayed with ALS inhibitors. The molecular markers described in this project will be invaluable tools for incorporating this novel tolerance into existing breeding lines.

Phytophthora root rot in chickpea – resistance and yield loss

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Phytophthora medicaginis, the cause of phytophthora root rot (PRR) of chickpea, is endemic and widespread in Southern QLD and Northern NSW. Although registered for use on chickpeas, metalaxyl seed treatment is expensive, does not provide season-long protection and is not recommended. There are no in-crop control measures for PRR and reducing losses from the disease is based on avoiding risky paddocks and choosing the right variety. Current commercial varieties differ in their resistance to P. medicaginis, with Yorker and PBA HatTrick having the best resistance and being rated MR (historically Yorker has been slightly better than PBA HatTrick), while Jimbour is MS - MR, Flipper and Kyabra are MS and PBA Boundary has the lowest resistance (S).

From 2007 to 2015 PRR yield loss trials at the DAF Qld Hermitage Research Station, Warwick QLD have evaluated a range of varieties and advanced PBA breeding lines. Each year the trial is inoculated with P. medicaginis at planting. There are two treatments, (i) seed treatment with thiram + thiabendazole and metalaxyl and regular soil drenches with metalaxyl and (ii) seed treatment with thiram + thiabendazole only with no soil drenches. The difference in yield between the metalaxyl-treated plots and untreated plots is used to calculate the yield loss caused by PRR.

Yields in metalaxyl-treated plots were close to seasonal averages for the 2015 season with the lowest yielding breeding lines and varieties (CICA1328, Yorker and PBA HatTrick) yielding close to 2.5 t/ha. In 2015 the level of PRR in the trial was considerably higher than those in previous seasons, such as 2014. For example yield losses were greater than 40% for CICA1328 in 2015, but only 1.8% in 2014 and yield losses for PBA Boundary were 94% in 2015 and 74% in 2014. However, the 2015 trial again confirmed that Yorker and PBA HatTrick had better resistance than PBA Boundary, which has been consistent across previous trials. Results for the high PRR disease season of 2015 showed that susceptible varieties sustain substantial yield loss from PRR and that varieties with moderate resistance have reduced losses. The 2015 trial again confirmed the superior PRR resistance of the PBA breeding line CICA1328 which is a cross between a chickpea (Cicer arietinum) line and a wild Cicer species (C. echinospermum).
Identifying leaf level physiological mechanisms of drought tolerance in faba bean

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The ongoing rise in global temperatures owing to climate change is likely to aggravate the negative effects of hot and dry climatic conditions on faba bean farming. Programs aiming at genetic improvement of the drought resistance of this crop are hampered due to lack of high throughput screening methodologies for this crop (1). Genotypic variation in response to drought has been observed in faba bean (2,3,4). Understanding the physiological basis of drought tolerance is essential for the development of cultivars adapted to drought conditions. Experiments were carried out both in the field and control environment to find out leaf level physiological mechanisms of drought tolerance. Primarily, we evaluated 96 diverse genotypes known to vary widely in drought response, and used carbon isotope discrimination (∆13C) to identify genotypes with highly contrasting drought response. Large phenotypic variation was found over a range of 4.39‰ (28.82‰ ~ 24.43‰, equivalent to intrinsic water use efficiency of 98.53-179.75 μmol CO2 mol⁻¹ H₂O) among genotypes. Later five genotypes were evaluated (two drought tolerant, two susceptible and a check) in irrigated and rainfed condition in the field, and 100% and 50% field capacity in the control environment. We used a combination of approaches, including gas exchange, psychrometry and isotope ratio mass spectrometry, to investigate physiological traits. The genotypes showed considerable variation in maturity, relative water content (RWC) and water potential, determined at grain filling stage. Moisture deficits decreased water usage and consequently RWC, water potential and harvest index. In the field there was no yield penalty observed among rainfed and irrigated, but in the control environment yield significantly decreased in drought sensitive genotypes. Further study will be conducted this year to gain a better understanding of drought tolerance mechanisms which will help to develop optimal ideotypes and high throughput phenotyping methods.

Speed breed to meet industry needs

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It is well established that pulses provide crucial disease, pest and weed management options as well as valuable nitrogen within Australian farming systems. Breeding for improved performance under yield-reducing stresses is clearly a high priority to ensure producer uptake. Elite cultivars, which perform even under challenging conditions, are the goal of all pulse breeding efforts underway in Australia.

The University of Western Australia (UWA) has partnered with The Grains Research and Development Corporation (GRDC) to undertake research aimed at speeding the process of developing these elite cultivars.

The long lifecycle of pulses has previously slowed the rate of genetic gain. Currently, one (field) to three (glasshouse) generations are possible in a single year, with six generations generally required for fixation of favourable genes or development of mapping populations.

The research at UWA has led to the development of an ‘in soil’ process that enables turnover of 6-8 generations per year in lentil, chickpea, field pea and lupin. This accelerated single seed descent (aSSD) technology halves the current fastest route to homozygosity and enables a rapid breeding response to emerging production threats.

To capitalise on the advantages of the aSSD technology, we have concurrently developed an integrated screening system to enable selection for key traits during the generation turnover process. A hydroponic selection screen enables discrimination of the sensitivity of individual plants to boron, salinity or aluminium and the identification of tolerant lines within populations derived from immature seed. The hydroponic methodology permits rapid discrimination of traits followed by recovery of plants to allow flowering and viable seed set without affecting the speed of aSSD-based generation turnover.

The aSSD technology is now being employed within the Australian pulse industry to speed the incorporation of key traits. To date, we have partnered with Pulse Breeding Australia (PBA) breeders and GRDC researchers to produce recombinant inbred line populations for metribuzin tolerance, salinity tolerance, chilling tolerance and Ascochyta blight resistance. Further GRDC/UWA investment (2016-2019) will drive enhancement of the aSSD platform to include screening for biotic traits, expansion to include faba bean and efficient integration into pulse breeding and research efforts.
**Beet western yellows virus or Turnip yellows virus: which virus infects pulse crops in Victoria?**

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In 2002, the International Committee for the Taxonomy of Viruses (ICTV) approved a proposal to classify Beet western yellows virus (BWYV) and Turnip yellows virus (TuYV) as two distinct viruses in the genus Polerovirus in the family Luteoviridae (1,2). In Victoria, tissue blot immunoassay (TBIA) is used to test for BWYV/TuYV in pulse crops. However, the antisera used for the TBIA test does not distinguish between the two viruses so it is not clear which of the two viruses is present in Victoria. Eleven pulse samples (4 lentil, 5 pea and 2 chickpea) that were collected throughout Victoria in 2015 and had previously tested positive for BWYV using TBIA were tested using RT-PCR to gain more information about the virus species present. Samples were tested using two different sets of BWYV/TuYV primers that each targeted different regions of the virus genome: the coat protein (CP) region and the ORF0 (P0) region. Five samples (1 lentil, 3 pea and 1 chickpea) tested positive using both sets of primers and the resulting PCR products were directly sequenced (AGRF, Melbourne).

The remaining samples did not give a positive result for BWYV/TuYV using either PCR test. All samples were then also tested using a multiplex PCR test that distinguishes between BWYV/TuYV, Bean leaf roll virus (BLRV), Phasey bean mild yellows virus (PBMYV) and Soybean dwarf virus (SbDV)(3). PBMYV was detected in the 6 samples that tested negative for BWYV/TuYV by PCR but positive by TBIA using BWYV antibodies. This demonstrated that PBMYV was being incorrectly identified as BWYV by TBIA. PBMYV was also detected in 2 of the samples (pea and chickpea) that were co-infected with BWYV/TuYV. These results highlight the need for more specific tests to be able to distinguish between these closely related poleroviruses. Further work, such as transmission tests and next generation sequencing are also being done to further confirm the identity of this BWYV/TuYV that is present in Victoria.

3. Personal communication with Murray Sharman and Fiona Filardo, Department of Agriculture and Fisheries, Brisbane, Queensland, Australia).
Elevated CO$_2$ stimulates nitrogen fixation of two lentil genotypes in a dry-land Mediterranean environment

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Atmospheric CO$_2$ will be rising from currently 400 to 550 ppm by 2050. Elevated CO$_2$ (eCO$_2$) enhances plant growth and yield. However, the stimulation of plant growth at eCO$_2$ requires additional nitrogen (N) and prolonged exposure to eCO$_2$ potentially risking N limitation. Legumes can overcome such limitation by fixing aerial N. Previous studies under Free Air CO$_2$ Enrichment (FACE) show that eCO$_2$ can stimulate N fixation, but it is unknown to which extent this applies to dry-land Mediterranean environment. We address this gap by investigating the growth and N economy of lentils in a FACE facility in water limited, low yielding environment.

We investigated N$_2$ fixation of two lentil cultivars (PBA Ace and HS3010) using $^{15}$N natural abundance with wheat as reference. Water soluble carbohydrates (WSC), total N and free amino acids were determined in leaves, stems, floral organs, roots and nodules. Lentils were grown in elevated CO$_2$ (~550 μmolmol$^{-1}$) and ambient (~400 μmolmol$^{-1}$) in the Australian Grains FACE (AGFACE) at Horsham. Measurements of crop growth were made at flowering.

Lentils grown under eCO$_2$ had on average 21 % greater biomass, greater CO$_2$ assimilation rate (40%), increased concentrations of WSC (20%) and greater nodule numbers (27%) than under ambient CO$_2$. Leaf N and free amino acid concentrations were lower (7%) under eCO$_2$. In contrast, nodules had greater amino acid concentrations (15%) under eCO$_2$. Total crop N increased under eCO$_2$ from 114 to 135 kg N ha$^{-1}$, as did the percentage of N derived from atmosphere (%Ndfa). The amount of N fixed was greater under eCO$_2$, but the amount of N taken up from the soil did not change.

In agreement with studies on soybean and pea (1, 2, 3), eCO$_2$ stimulated growth and N fixation of lentils. Contrary to previous studies, lentils met the greater demand for N arising from eCO$_2$-stimulation of biomass solely through enhanced N fixation (1, 2). Apart from greater nodule numbers, nodule activity may also have been stimulated, supported by increased availability of soluble carbohydrates. Despite increased N fixation, leaf N concentrations decreased under eCO$_2$. Lower free amino acids concentrations in leaves, in conjunction with greater concentrations in nodules, suggest down-regulated supply of organic N to the shoot. Despite the ability of lentils to increase N fixation, leaf N responses were similar to cereals, which also showed decreased free amino acids with decreased leaf N (4). The implications of these changes for lentil grain protein will be discussed.

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Developing a platform for rapid exploitation of beneficial alien genes

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Wild relatives of crop species harbour genes for adaptation to challenging conditions. Of particular interest to us are genes that may be present within chickpea wild relative *Cicer echinospermum* L. These include genes for chilling tolerance at flowering, root lesion nematode resistance and disease resistance. Introgressing these genes into chickpea (*C. arietinum*) can be challenging, due firstly to the difficulty in obtaining hybrids in the first instance and secondly to genetic barriers such as reciprocal translocation, which render a high proportion of the hybrid progeny sterile.

At UWA, we have built upon earlier GRDC-funded work of Dr Heather Clarke to effectively cross domesticated chickpea with accessions of its primary genepool relative *C. echinospermum*, confirming the beneficial effect of applying hormones to the peduncle/stem interface at time of pollen transfer in order to retain hybrid viability. We have cloned the hybrid F₁ material to demonstrate capability to rapidly develop large F₂ populations for single seed descent (SSD) and recombinant inbred lines from the hybrids.

Allied GRDC-funded research at UWA (UWA159) has led to the development of an ‘in soil’ process, termed accelerated single seed descent (aSSD) that enables turnover of 6-8 generations per year in the pulses. Concurrently, we have optimised controlled environment growing conditions to rapidly initiate flowering across a broad range of *Cicer echinospermum* and *C. reticulatum* germplasm. A flow-on benefit from the aSSD research is the development of a modified technique that is applicable to hybrid *Cicer* material. Using a *C. arietinum* x *C. echinospermum* population provided by Dr Jens Berger (CSIRO) we have shown it is possible to turnover 4.5 hybrid generations per year.

To assist in improving fertility in the hybrid progeny, we will backcross the F₄ material to the domestic parent (pers. comm. Mr Ted Knights). It is planned to use aSSD technology to rapidly progress the backcross material to homozygosity, prior to screening for traits of interest and utilisation as parental material. Integration of the crossing protocol, cloning process, aSSD technology and backcrossing program will provide a platform to rapidly introgress beneficial genes from *C. echinospermum* to chickpea.
An Optimal Breeding Design for Pulse Species in the Era of Genomic Selection and Genome Sequencing

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Parental selection and combination in plant breeding has an important impact on the derived progeny and realised genetic gain. However, parental phenotypic performance alone does not provide information about the segregation of complex traits such as grain yield in derived progeny, failing to provide an indication of the true genetic value of a cross. The emergence of genomic selection now enables the accurate calculation of the genomic estimated breeding value (GEBV) of individuals with only genotypic information. In parallel, advances in sequencing technologies have seen draft genome sequences and genome-wide genotyping methods become available for a range of important pulse crops, such as chickpea and lentil. With genomic selection now being established for pulse species, new novel breeding methodologies can be developed to exploit the full benefits of this genomic information. The ability to predict the genetic effects across the whole genome, whilst understanding the structure and physical order of such associated regions, enables computational modelling of segregation patterns, and design optimal crossing strategies to incorporate a range of traits in the most efficient manner. A novel multi-parent pulse crossing and family sub-selection scheme has been designed. A diverse range of elite parental genetics is initially crossed to generate F₁ populations, which are then inter-crossed with other F₁ populations producing a range of individuals, termed F₁i. Specific pairing of the initial parental genetics and subsequent F₁s are chosen based on predictions of the range of potential haplotypes they will contribute to the following generation; selecting those with most optimal haploid value. Specific F₁i individuals are selected for rapid advancement, by simulating potential recombination events in each generation and the GEBVs of the final progeny. This allows breeders to select and design crosses, not only on the additive genetic value of a cross, but also on the potential haplotype combinations in the resulting individuals. This methodology offers the potential to rapidly increase the rate of genetic gain achieved in pulse breeding, through reducing the generation interval, and more accurately introgressing and combining optimal genetics. The proposed scheme is currently being implemented in lentil breeding and is being developed for other pulses, such as field pea and chickpea.
Application of historical data from Australian lentil breeding program to enable rapid implementation of genomic selection

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Genomic selection (GS) has recently emerged as an evolutionary approach in plant and livestock breeding where selection is made on the basis of genomic estimated breeding values (GEBV’s) calculated from genome-wide marker data. GS can outperform conventional marker-assisted selection and phenotyping in terms of gain per unit time and cost. A major advantage of using GS in crop breeding is the acceleration of genetic improvement through the ability to predict the phenotypic performance of individuals early in the breeding cycle, reducing the generation interval. Here we evaluate for the first time its efficacy for breeding lines of lentil from the Australian lentil breeding program. A total of 864 advanced breeding lines along with phenotypic data from 2010-2014 for economically important traits such as grain yield and grain weight were obtained from PBA lentil breeding program. Phenotypic data was corrected for spatial and environmental effects, and G x E effects within years were assessed by fitting an extended factor analytic variance structure.

Weather data, was then used to cluster phenotypic data across years. Genotyping was performed using a whole genome genotyping-by-sequencing transcript approach. Over 200,000 SNPs were initially identified from sequencing key ancestor/founder lines of the PBA breeding program, and were used for SNP variant calling in the breeding lines. The ability to genomically predict the observed phenotypic performance in each progressive year, and within-year clustered environments was explored by using lines from previous years (forward prediction), as the reference population and applying a range a genomic selection models, such as GBLUP, BayesA and BayesB. Accuracies achieved for grain yield and weight were moderate to high (c. 0.35-0.70), reflecting the relative heritabilities of these two economically important traits. The GEBV’s and genomic prediction equations developed are now being implemented within the lentil breeding program to design optimal crossing schemes to increase genetic complementarity, as well as to select elite breeding lines for rapid advancement, reducing the overall generation interval, and increasing genetic gain.
Genebanks are tasked to conserve high viability seed in genetic resource collections for use by researchers and breeders to develop more productive varieties. When viability of an accession falls below 85%, regeneration is required to obtain fresh, highly viable seed. Once seed viability falls below 85%, there is a rapid decline in seed quality, and germplasm can be lost. Major determinants of seed longevity are storage temperature and seed moisture content which are currently being investigated in a long term trial in the Australian Grains Genebank(1). The AGG manages a collection of more than 24,000 accessions of pea, lentil and chickpea to ensure that high viability seeds are always available for the full range of accessions. To optimize the frequency of seed regenerations, it is important to predict when the rapid decline in seed quality will occur.

Variation of seed longevity in 10 genetically unrelated accessions each of lentil, pea and chickpea have been investigated by the AGG. All accessions were grown in the same field under rainfed conditions in 2002 and initial viability was close to 100%. In 2003, seeds were placed in storage under 20°C and ambient seed moisture content to determine storage decline curves. Typically little decline in viability occurs over an initial storage period, and after 8 years, only one lentil and one chickpea accession had declined to below 85%; the remaining accessions maintained 90 - 100% viability. By 2016, there was a considerable range in viability from 0 to 100%. This experiment clearly illustrates the range in seed longevity of seeds at AGG and the challenge to predict when an accession should be regenerated before rapid seed deterioration begins.

An added evaluation of RNA integrity for these same accessions will be assessed in collaboration with the USDA Fort Collins. We are hypothesizing that RNA integrity, analysed predominantly by prevalence of ribosomal RNA fragments may detect early signs of seed aging or, at least, require fewer seeds in testing. Ultimately, we wish to analyse mRNA quality to gain molecular information on gene products that could show different physiological processes and further explain the observed intra- and inter-specific variation in seed longevity from the seed moisture and storage temperature studies.

Assessing a new collection of wild chickpeas for potential sources of resistance to the root-lesion nematodes (RLN) *Pratylenchus thornei* and *P. neglectus*.

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Chickpea (*Cicer arietinum*) is a crop of global importance and is Australia's most valuable pulse crop with current gross production valued at $320 million/year (ABARE 2014/2015). Unfortunately, chickpeas have been shown to be susceptible to the root-lesion nematodes (RLN) *Pratylenchus thornei* and/or *P. neglectus* in Europe, Asia and Australia. *P. thornei* has reduced the yield of some Australian chickpea cultivars by up to 20% (Reen et al 2014, Thompson et al 2011). The aim of our research is to optimise methods for screening chickpea germplasm for RLN resistance and to test a new collection of wild chickpea accessions (*Cicer reticulatum*; *C. echinospermum*) originating in Turkey, to identify new sources of genetic resistance for incorporation into current commercial cultivars by plant breeders. To date, several experiments have been conducted in controlled glasshouse conditions to optimise the screening process for chickpea. Findings show inoculation with rhizobium (Group N) does not appear to influence *P. thornei* reproduction. Optimum fertiliser to distinguish *P. thornei* reproduction in chickpea genotypes of different susceptibilities was a solution-based fertiliser of NPK supplying (mg/kg soil) 200 NO₃-N, 25 P, 88 K, 36 S and 5 Zn compared with slow release Osmocote. The seed dressing P-Pickel T® had no effect on nematode reproduction if separated by a band of soil from the nematode inoculum applied as a suspension (10 mL) at planting. Optimum growing time to distinguish partially resistant and susceptible cultivars was 18 weeks. These results are based on a series of experiments and more research will be conducted to confirm these initial findings. Currently, 151 wild chickpea accessions from the recent collection are being screened for resistance to both *Pratylenchus* species in Australia (University of Southern Queensland) and Turkey (Cukurova University). Additional accessions will be tested in 2017 and it is hoped this research will identify new sources of RLN resistance suitable for Australian and Turkish breeding programs to develop elite chickpea cultivars with improved RLN resistance.

Low red to far red ratio and high intensity in the far red region accelerate flowering in pulses

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Light modulates a wide range of plant physiological responses. Understanding the triggers of floral initiation is key to the broad application of a range of pre-breeding tools. One of these tools, accelerated single seed descent (aSSD), has been developed at The University of Western Australia in partnership with the Grains Research and Development Corporation (GRDC). The aSSD technology is designed to speed generation turnover in pulses, enabling the rapid production of elite cultivars. A crucial part of the development of aSSD technology in pulses has been determining optimal growth conditions for rapid initiation of flowering across broad phenological ranges.

The importance of temperature and photoperiod on triggering floral onset in pulses has been well studied (1). The effect of light quality parameters on flowering induction remains unclear. For this research, early and late flowering genotypes of field pea, chickpea, faba bean, lentil and lupin were grown in controlled environment rooms under a 20 h photoperiod. The photoperiod was provided by various light sources with different light spectra (blue and far red-enriched LED and metal halide lights) and compared with the natural light spectrum. All species and genotypes showed a positive response to a decreasing red (R) to far red (FR) ratio. In general, the longest time to flowering was observed when the R:FR ratio was above 3.5. When comparing environments with a R:FR ratio below 3.5, the environment with the highest number of photons in the FR region of the light spectrum was the most inductive.

We demonstrate the importance of considering both relative (R:FR ratio) and absolute (photons in the FR region) light values for the optimisation of time to flowering in grain legumes. Another key finding was the greater flowering time plasticity exhibited in response to light spectra by late field flowering genotypes compared to early field flowering ones. This enabled us to use our optimised conditions to compress time to floral initiation for the later flowering genotypes to within three to four days of the earlier genotypes for field pea, chickpea, lentil and lupin and to within 12 days for faba bean. The improved understanding of the effect of light quality on flowering regulation will assist the development and exploitation of biotechnological tools for legume breeding.

Maximising chickpea productivity in southern New South Wales

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The major pulse production regions of the world are dominated by alkaline soils, such as those in northern NSW, the Wimmera region of Victoria and Yorke Peninsula of SA, where most of Australian pulse production is concentrated. The unique environment of southern NSW presents new challenges, specifically the dominance of acidic duplex soils and a climate with cool, wet winters and dry, hot springs.

Chickpea research conducted by NSW Department of Primary Industries at the Wagga Wagga Agricultural Institute aims to develop recommendations to maximise chickpea productivity in the southern NSW region. Our variety improvement and agronomy research over the past decade has contributed to yield and crop adaptation through improved plant type, disease resistance and regionally specific guidelines.

Results from chickpea agronomy trials conducted in southern NSW since 2010 highlight key agronomic and management principles, which need to be adopted in order to maximise chickpea productivity in the region.

Sowing time is the most critical management tool for chickpea production in this region. Results from a number of trials at Wagga Wagga and Yenda showed that chickpea grain yields were maximised when sown from 25 April to 15 May. Plants sown in this window establish well in acidic, hard-setting, red-brown earths, before growth is checked by cold in the June/July winter period. Plants sown in this period produced more bulk and height than later sown plants, and were less affected by heat and moisture stress during seed set and pod fill.

Sowing earlier increased dry matter and height but also increased the risk of disease and lodging to the detriment of grain yield. Sowing later resulted in reduced biomass and delayed seed set increased the effect of hot and dry seasonal conditions on pod fill. Results from plant density trials show that plant populations of 30 to 45 plants per m$^2$ are required to maximise grain yield.

When sowing chickpeas at the start of the recommended sowing window or in a paddock where there is a risk of sclerotinia it is recommended to grow a variety with a level of sclerotinia resistance.

The application of chickpea management principles developed specifically for southern NSW will aid in maximising chickpea production in the region.
Marker assisted selection has the potential to reduce costs of multiple trait pyramiding by over 80% in the field pea breeding program

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Development of elite breeding lines and varieties often requires plant breeders to combine desirable traits from multiple genetic backgrounds. The process of combining traits, known as gene pyramiding, can be accelerated by using molecular markers to track individuals that contain the desired allele combinations. Here we report a modelling approach to compare costs of using phenotypic selection versus marker assisted selection (MAS) strategies to pyramid 8 independent loci in field pea. These loci represent multiple traits including tolerance to salinity (2 loci) and boron (1 locus), and resistance to downy mildew (2 loci) and bacterial blight (3 loci). There are well developed, efficient phenotypic assays for all of these traits. Costs for all assays (phenotypic and molecular) were calculated based on consumables and staff time. Phenotypic selection was based on screening populations at each generation from F₂-F₅, in which sequential generations would be screened for selection of different traits followed by a final screening of F₅₋₆ families for all traits to identify homozygous lines. During the generation advancement process, seeds from plants with desired phenotypes would be bulked together to maintain a population size of c. 50 plants. Several strategies for phenotypic selection were investigated and the cheapest was estimated to cost $29,900. Different marker strategies were also investigated based around the number of generations in which MAS was performed. The most efficient MAS strategy was estimated at $5,375 and this was achieved by selecting 50 lines that were heterozygous for all loci in each generation from F₂-F₅. This modelling is based on several assumptions, including that the markers were truly diagnostic of the phenotype, the phenotypic assays were highly accurate on single plants and that the loci targeted by the markers accounted for much of the trait variation. These assumptions may not be completely true as marker development in field peas is still in relative infancy. Therefore we are also developing marker validation strategies that are being implemented side-by-side with the MAS approach. Various selection strategies, the validity of the assumptions and marker validation approaches will be discussed.
Contrasting drought patterns for field pea and chickpea in Australia

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The effect of drought on yield depends on the timing, intensity and duration of stress episodes. For this reason, it is essential to characterise the patterns of drought in these terms, as the traits improving adaptation to, say, early-season drought are different to the traits required for adaptation for seed-filling drought. We modelled the daily water budget for 5616 site-seasons for field pea and 3905 site-seasons for chickpea in Australia using location-specific soil and climate data (1,2). Cluster analysis revealed three major types of drought for field pea and four types for chickpea. In field pea, the most frequent (43% incidence) and most severe drought featured an onset at 400 degree-days before flowering with gradually increasing stress towards flowering, pod set, and seed filling. In chickpea, drought is less severe and all four patterns have an onset of water stress close to flowering and early pod set. We hypothesise that the contrasting drought patterns between the crops derives from differences in their thermal requirements. Owing to the early selective pressures on chickpea as a spring-summer crop and its slower growth under prevailing winter temperatures, crop water deficit is less likely to develop in chickpea in comparison to faster-growing, more vigorous field pea crops. This has implications for breeding for drought adaptation, which should target crop- and environment-specific developmental windows where stress is more likely and severe.

New evidence on the effectiveness of native and commercial rhizobium strains for mungbean

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Expansion of the cultivation of mungbeans in many parts of Queensland could benefit growers by increasing the value and profitability of primary production both through direct sales of grain from this high-value crop, and/or through potential residual fixed nitrogen. Simplifying the operations involved in growing mungbeans, including rhizobium inoculation, may encourage more farmers to include them in their farming system. Anecdotal reports have suggested that native rhizobia are as effective as commercial inoculum for mungbean in the Burdekin region of far north Queensland. To test this hypothesis, nodules were collected from mungbean plants grown in soil from two sites in the Burdekin region. One site had been treated with commercial inoculum CB1015, the other had never been treated with commercial inoculum. Analysis using Matrix Assisted Laser Desorption Ionization Time of Flight Mass Spectrometry (MALDI-TOF MS) (1) showed that up to eight different native strains of *Bradyrhizobium*, distinctly different to CB1015, were present in the nodules of these plants. A different native strain dominated at each collection site. Mungbean plants grown in soils from Millmerran, on the Darling Downs, Qld, on the other hand, hosted only CB1015 when inoculated, and did not nodulate when not inoculated, indicating no native strains were present in this soil. In a controlled glasshouse experiment, mungbeans (cvs Crystal and Jade-AU) and black gram (cv Regur) inoculated with either of the two most dominant native rhizobia strains produced similar biomass compared with those inoculated with CB1015. The plants inoculated with the native *Bradyrhizobium* strains however fixed significantly more nitrogen than those with CB1015.

These results support the belief that native rhizobia are as effective at promoting growth and may be superior in fixing nitrogen in mungbeans as the commercial strain in some parts of Queensland. However, further investigation of the distribution, effectiveness and pervasiveness of these native rhizobia is required before any major practice change could be recommended. The application of commercial inoculum is necessary for a healthy crop in other parts of Queensland, and may still be considered a useful “insurance policy” to ensure healthy nodulation of mungbean crops in the Burdekin catchment area.

Comparative genomics within and between two pathovars of *Pseudomonas syringae*; pv. *syringae* and pv. *pisi*

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*Pseudomonas syringae* is a large species complex of gram negative bacteria comprised of plant-pathogenic and non-pathogenic isolates that cause diseases on many crop species worldwide. Isolates of *P. syringae* are taxonomically subdivided into pathogenic varieties known as pathovars, based largely on their host of isolation. The *P. syringae* pv. *pisi* (Ppi) and *P. syringae* pv. *syringae* (Psy) serve as an interesting area for comparative genomics as both can infect *Pisum sativum* to cause epidemics. Ppi are generally thought to be restricted to this host while Psy isolates are able to infect a number of different hosts. These pathovars also differ considerably in their disease symptoms in pathogenicity assays in controlled environment but under field conditions the symptoms are often indistinguishable. Whole genome sequencing was performed on 19 *P. syringae* isolates, including Psy and Ppi races. Additionally one *P. viridiflava* species was included as an outgroup. These isolates were also tested for their pathogenicity on host plant *P. sativum* susceptible cultivar Kaspa, moderately resistant cultivar PBA Percy and a non-host common bean *Phaseolus vulgaris* to study their host specificity. Principal Components bi-plot clustered the isolates based on their aggressiveness on different hosts. Phylogenetic analysis based on c. 2,000 predicted protein sequences of the Psy and Ppi isolates sequenced in this work and also including publicly available Ppi and Psy genome sequences revealed a large amount of genetic diversity among the Psy isolates. However, the 7 isolates isolated from pea formed a monophyletic clade. Cluster analysis of orthologous proteins between and within the Ppi and Psy isolates revealed significant difference in sizes of core and accessory proteomes; Ppi core proteome contained 4,337 proteins and the accessory proteome contained 2,375. The Psy core proteome contained only 2,642 proteins while the accessory proteome was 10,675. In all Ppi isolates, 20 proteins were found in the core proteome of Ppi strains but not in any Psy strains. Analysis of the Carbohydrate-Active Enzymes (CAZymes) and type three effector content within and between pathovars was also studied and significant differences were observed. Interestingly, the Ppi AN3 group and AN7 groups again clustered into two separate clades based on the presence/absence and abundance of different predicted CAZyme proteins. Notably all members of the AN3 group lacked the GH5 and GH27 predicted proteins found in all of the AN7 isolates.
Development of cost-effective and high throughput genotyping method using next generation sequencing for low diversity species

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Advances in next generation sequencing technologies provide unprecedented opportunities to develop high throughput and cost-effective genotyping assays, that have the potential for simultaneous genome-wide SNP discovery as well as genotyping. Genotyping-by-sequencing (GBS) has emerged as a fast, reliable and robust approach that has many applications in plant genetics and genomics such as association mapping, genetic linkage mapping, genotype screening and purity testing. GBS also provides a rapid and low-cost tool to genotype breeding populations, allowing plant breeders to implement genomics assisted breeding tools including genomic selection. The objective of this study was to evaluate the feasibility and adaptability of some of the new sequencing based genotyping approaches in an important grain legume crop, chickpea (Cicer arietinum). Chickpea is a self-pollinating, diploid crop with a moderate sized genome (c. 740 Mbp). A draft sequence assembly of the chickpea genome has already been generated and is available to be used as a reference to evaluate new high-throughput sequencing and genotyping approaches including GBS-transcript sequencing, genome-based skim sequencing and target enrichment. In this study, a total of 24 chickpea genotypes were selected to evaluate the above mentioned GBS approaches. Target enrichment probe design was based on the draft chickpea genome, aiming 11,221 variants from 8 chromosomes (c. 2.9 Mbp) that represented most of the diversity present in some of the recently released Pulse Breeding Australia cultivars. GBS-transcript sequencing was performed on these 24 genotypes aiming at c. 5-10 million reads per sample. Skim genotyping based on the whole genome was performed aiming at 1x, 2x and 5x coverage. Sequencing data was generated using Illumina HiSeq platform and aligned to chickpea genome to discover and characterise polymorphisms. Evaluation of these GBS methods will enable the development of a rapid, highly effective and low-cost genotyping tool that is suitable for population studies, germplasm characterisation, breeding and trait mapping in chickpea.
Development of gene-based linkage maps and identification of quantitative trait loci for rust (Uromyces viciae-fabae) resistance in faba bean (Vicia faba L.)

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Faba bean (Vicia faba L.) is one of the oldest domesticated plant species and an important food crop worldwide. The main faba bean breeding objectives include yield and seed quality improvement as well as resistance to biotic and abiotic stresses. Among biotic stresses, rust (Uromyces viciae-fabae) is a common fungal disease that can cause up to 70% yield loss in early infections. Chemical control of rust has been reported however, use of genetic resistance is the most practical and efficient method of rust control. To identify the genomic locations controlling rust resistance, two recombinant inbred line (RIL) populations were developed by crossing two different resistance cultivars Ac1655 and Doza and a susceptible cultivar Fiord (Ac1655 x Fiord; Doza x Fiord). Both populations were genotyped with Illumina Infinium® 1536-SNP assay, but the Ac1655 x Fiord had additional genotyping-by-sequencing (GBS) performed. A large proportion of markers were still observed to be polymorphic among the parents but non-segregating within the RIL progeny. This could be due to the genetic constitution of these mapping populations. A total of 332 and 370 SNP markers were grouped into 14 and 12 linkage groups covering 1,250 and 970 cM in Ac1655 x Fiord and Doza x Fiord maps, respectively. The majority of linkage groups could be assigned to specific chromosomes based on common markers. Phenotyping was performed under controlled environmental conditions, where three weeks old seedlings were inoculated with urediniospore suspension. QTL analysis allowed the identification of single independent genomic regions conferring resistance to rust from the resistant cultivars, Ac1655 and Doza. QTLs explained 32% (Ac1655 x Fiord) and 71% (Doza x Fiord) of the phenotypic variance of the trait. Markers flanking the QTL-containing regions identified in this study can be further validated in a diverse set of germplasm and then applied in marker-assisted selection for introgression of such regions derived from parental germplasm in faba bean breeding programs. As two different sources of rust resistance were identified, gene pyramiding to achieve better and durable rust resistance in faba bean is now possible.
Development of genetic linkage maps using genotyping-by-sequencing (GBS) approach and the identification of QTL conferring resistance to downy mildew in field pea (*Pisum sativum* L.)

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Downy mildew, caused by obligate parasite *Peronospora viciae*, causes significant yield losses in all field pea (*Pisum sativum* L.) growing regions of the world. The two common *Peronospora viciae* pathotypes in Australia are Parafield-type (less virulent and infects old conventional type field pea varieties) and Kaspa-type (virulent type and infects both conventional type and semi-leafless field pea varieties). Selection of varieties that are resistant to different pathotypes is the most effective means of controlling this disease. Genetic improvement of traits can be facilitated through the identification and selection of candidate genes using advanced genomic tools. Genotyping-by-sequencing (GBS) is a high-throughput and robust genotyping system that is suitable for population studies, germplasm characterisation, breeding and trait mapping. In this study, a GBS approach was used for large-scale SNP discovery and genotyping of two field pea mapping populations segregating for downy mildew resistance, Kaspa x Parafield and Kaspa x PBA Oura. After stringent filtering, a total of 822 and 1,033 high quality SNPs were selected of which 509 and 853 successfully mapped to the Kaspa x Parafield and Kaspa x PBA Oura maps, respectively. Phenotyping was performed under controlled environmental conditions (at 12/4°C for 12/12-h light/dark cycle in growth chambers), with seedlings being inoculated with spore suspensions from two different pathotypes, Parafield-type (on Kaspa x Parafield population, where Kaspa is resistant and Parafield susceptible) and Kaspa-type (on Kaspa x PBA Oura population, where Kaspa is susceptible and PBA Oura resistant). QTL analysis identified two single independent genomic region conferring resistance to *Peronospora viciae* from the resistant parents explaining 35% and 21% of phenotypic variance in Kaspa x Parafield and Kaspa x PBA Oura populations, respectively. Identification and marker-tagging of genomic regions containing QTLs conferring resistance to downy mildew will facilitate the targeted introgression of this trait into otherwise unadapted germplasm.
Generation and characterisation of a reference transcriptome for lentil (*Lens culinaris* Medik.) and the identification of candidate genes for important traits

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RNA-Seq using second-generation sequencing technologies allows the generation of a reference unigene set for a given species, in the absence of a well-annotated genome sequence. Such a reference set will not only assist in functional genomics and gene characterisation, but also enable detailed expression analysis for the evaluation of specific morphophysiological or environmental stress response traits. Transcriptome sequencing was performed using 7 cDNA libraries generated from different tissues of lentil at various developmental stages. In excess of 0.6 billion sequencing reads were *de novo* assembled into 77,778 contigs and scaffolds. These transcripts were additionally processed and filtered on the basis of read length and gene annotation through assessment of sequence similarity with closely related species, as well as the Nr and Uniref100 databases, resulting in a reference unigene set consisting of 58,986 contigs and scaffolds with an N50 length of 1,719 bp. Comparison both to previously published transcriptomes and a draft genome sequence validated the current dataset in terms of degree of completeness and utility. To characterise gene expression on a tissue-specific basis, the unassembled trimmed sequence reads were aligned to the unigene set. A large proportion (c. 98%) of the unigenes were expressed in more than one tissue at varying levels, while the remaining c. 2% displayed distinct expression patterns in specific tissues. Candidate genes associated with mechanisms of tolerance to both boron toxicity and time of flowering were identified, which can eventually be used for the development of gene-based markers. This study has provided a comprehensive, assembled and annotated reference gene set for lentil that can be used for multiple applications, permitting identification of genes for pathway-specific expression analysis, genetic modification approaches, development of resources for genotypic analysis, and assistance in the annotation of a future lentil genome sequence.
Identification of quantitative trait loci conferring resistance to pea seed-borne mosaic virus in field pea (*Pisum sativum* L.)

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Pea seed-borne mosaic virus (PSbMV), a member of the genus Potyvirus in the family Potyviridae causes significant yield losses in pea. One efficient, environmentally friendly and cost effective approach to control the disease is to breed for resistance. A biparental mapping population obtained by crossing Kaspa (susceptible to PSbMV) and Yarrum (resistant to PSbMV) was used for quantitative trait loci (QTL) analysis. Multiple phenotypic screening trials were performed in both field and greenhouse using a mix of highly aggressive PSbMV P4 pathotype (strains Ps11-10/2 and Ps11-12/7). QTL analysis was performed using a previously published Kaspa x Yarrum linkage map and detected a single genomic region on Ps VI associated with PSbMV resistance, explaining upto 76% of the phenotypic variance (V_p). The BLAST analysis of the sequence underpinning one of the flanking SNP markers revealed annotation as *Pisum sativum* cultivar JI2009 eukaryotic translation initiation factor 4E (SBM-1) mRNA, *sbm-1*-resistant-1 allele. The *sbm* category of recessive genes is known to be conferring resistance to pea mosaic virus. Previously published studies have confirmed the location of these *sbm* genes on different pea chromosomes along with their corresponding pathotypes. The *sbm-1* gene is reported to be located on LG VI of pea and confers resistance to pathotype 4 (P4) of the virus. The QTL detected in the current study was highly comparable to the previously mapped *sbm-1* on LG VI. As PSbMV resistance QTL from this study accounted for large percentage of V_p, it will prove highly useful for introgression of resistance alleles into elite parental background by donor-recipient backcrossing with minimal linkage drag. In addition, the linked marker annotated as *sbm-1*-resistant-1 allele can be used as a diagnostic marker that will facilitate selection processes in field pea breeding programs by direct identification of donor genotypes in germplasm collections and hence reduce duration of the breeding cycle.
RNA-Seq expression analysis of resistant and susceptible field pea (Pisum sativum L.) cultivars after Pseudomonas syringae pv. syringae infection

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Bacterial blight is an economically important disease of field peas caused by Pseudomonas syringae (pathovars pisi and syringae). The molecular basis of resistance and susceptibility of field pea to bacterial blight is largely unknown. In this study, RNA-sequencing (RNA-Seq) was performed to investigate and compare the transcriptional changes in two field pea cultivars, Kaspa (susceptible to Psy) and Parafield (moderately resistant to Psy), in response to inoculation with P. syringae pv. syringae cox-1 strain at various time points (3 hpi, 8 hpi, 12 hpi, 24 hpi, 48 hpi, 5 dpi, 7 dpi and 15 dpi). cDNA libraries from multiple biological replicates of colonised and mock-inoculated plants were sequenced using an Illumina HiSeq2000 platform. Sequence reads from all samples were de novo assembled with a SOAPdenovo-Trans assembler, resulting in 251,330 contigs and scaffolds. The paired end reads from each genotype were reference aligned to the plant and published P. syringae pv. syringae cox-1 references to identify transcripts specific to each field pea genotype. RNA-seq differential expression analysis workflow was performed R specifically using DESeq2 and edgeR. The Nr, Uniref100 and Gene Ontology (GO) databases were further used to annotate differentially expressed transcripts. Among differentially expressed transcripts, pathogen-associated molecular pattern (PAMP) receptors, disease resistance genes and pathogenesis related genes were of particular interest. Other transcripts involved in photosynthesis and hormone signalling pathways were also differentially expressed. In addition, novel transcripts were identified, providing the basis for further characterisation of plant defense-related genes. The present study provided insights into transcriptome responses in the field pea-Psy interaction and proposed candidate genes that contribute to protection against Psy in field pea.
Iron deficiency is a worldwide problem affecting both developed and developing nations. Currently the most common means of combating this issue is supplementation and food fortification. Such measures however, are limited by the economic status of the targeted demographics. An alternative and more sustainable method is to enhance the inherent iron content and bioavailability of crops through biofortification. Iron biofortification through genetic modification has been done in several important crops like rice and wheat; however no such work have been done on pulses despite them being an important secondary staple. Pulses are rich in protein and micronutrients like iron, most of which however, is not bioavailable. This project focuses on the iron biofortification of the pulse crop chickpea through genetic modification. Chickpea is the second most important pulse crop globally and is widely consumed, particularly in India where anaemia is prevalent. Nicotianamine synthase (NAS) and ferritin, two iron homeostatic components successfully used in rice and wheat biofortification, were used to transform chickpea half-embryonic axes via Agrobacterium-mediated transformation. The leaves and seeds of the T1 and T2 progeny were assessed for iron content using LA-ICP-MS (Laser Ablation-Inductively Coupled Plasma Mass Spectroscopy) and ICP-OES (Inductively Coupled Plasma Optical Emission Spectroscopy), the results of which were correlated to the transgene expression levels. Preliminary results show an enhanced iron accumulation of 3-fold in transgenic leaves and 1.3-fold in transgenic cotyledons compared to the non-transgenic controls.
Found it! $FTc1$ is the major gene controlling flowering time variation in Australian narrow-leafed lupin cultivars

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Optimisation of flowering time is essential for adapting crop species to new or changing environments and for maximising yields. In narrow-leafed lupin ($Lupinus angustifolius$ L.), a single flowering time locus named $Ku$ has been strongly selected in the Australian breeding program as a means of successful adaptation to warm, short-season, winter growing environments. This adaptation is achieved by removing the requirement for vernalisation; a prolonged period of exposure to cold winter temperatures that enables flowering. A floral integrator gene $FLOWERING LOCUS T$ ($FT$) was identified as a likely candidate for $Ku$ (1), and the aim of this GRDC funded project (UHS10659) is to obtain biological evidence to determine whether $FTc1$ is the hidden gene at the $Ku$ locus. This will improve our understanding of the genetic control of flowering in narrow-leafed lupin and enable us to use genetics, as opposed to purely phenotypic data, to better match varieties to target environments, returning a more precise control of flowering time.

The temporal and spatial expression of $FTc1$ was assessed in $Ku$ (vernalisation-insensitive) and $ku$ (vernalisation-responsive) types, both grown with and without vernalisation. Gene expression levels were measured using quantitative reverse-transcription PCR (qRT-PCR), and comparison of sample levels was made possible by normalising the data against reference genes (2) we designed for this purpose.

Vernalisation had a dramatic effect on the expression of $FTc1$ in the $ku$ (vernalisation-responsive) type, causing increases of up to 74,000-fold in expression level within the leaves. Contrastingly, vernalisation did not affect $FTc1$ expression in the $Ku$ (vernalisation-insensitive) type, with expression levels remaining equally high in vernalised and non-vernalised treatments. In other words, $FTc1$ expression behaved exactly as would be expected if it is responsible for vernalisation insensitivity in $Ku$ types.

These results indicate the involvement of $FTc1$ in narrow-leafed lupin vernalisation response, complementing genetic and sequence data to confirm $FTc1$ as the gene underlying the $Ku$ locus (3). Further research supported by the GRDC (DAW00238) is now underway to identify other gene variants (“alleles”) at $Ku$, in addition to trying to identify other flowering time genes. This research will make it possible to combine complementary flowering time genes for specific target environments, enhancing yield potential and opening new environments for narrow-leafed lupin production in Australia and beyond.

Could more than one *Diaporthe/Phomopsis* species be associated with stem and pod blight in NSW lupins?

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Phomopsis stem and pod blight of lupins (*Diaporthe toxica*) is a seasonal issue in Australia causing yield losses if environmental conditions are favourable for disease development. Prolonged rainfall favours disease build-up, particularly if crops are planted into or near infected stubble. Outbreaks appear to have been increasing in recent years. Although plants may be infected, lesions are rarely seen when plants are still actively growing, but will rapidly develop on the stems and pods of infected plants if stressed by frost, hot dry conditions or herbicide injury. Lodging, early senescence and subsequent yield losses can result if infection is severe, and the risk of lupinosis developing in stock grazing on the stubble also increases. Lupinosis disease is caused by a toxin produced by *D. toxica* and can cause liver damage, loss of appetite and sometimes death of affected stock.

*D. toxica*, like many *Diaporthe/Phomopsis* species is also an effective saprobe or coloniser of dead plant tissue, so lupin stubble can also significantly aid the survival of this pathogen, thus creating an inoculum reservoir for future crops and considerable risk to grazing stock.

In 2015, *Diaporthe/Phomopsis* species infection caused severe lodging and stem infection in some NSW lupins including varieties previously considered to display moderate tolerance to *D. toxica*. Researchers were concerned that other *Diaporthe/Phomopsis* species may have been involved in the outbreak as recent Australian studies of this group of pathogens have revealed multiple new species with a range of virulences on many other broadacre crops including sunflower, soybean, mungbean and chickpea.

To assess the risk of these new species to lupin, six varieties were selected for susceptibility testing in a glasshouse *Diaporthe* pathogenicity study. A number of the new *Diaporthe/Phomopsis* species were inoculated onto plants of each lupin variety using a recognised stem slit method. Lupin plants were rated for severity of infection and the virulence of each new species was compared to that of *D. toxica*. 
Status and management of *Pratylenchus thornei* in chickpea of Madhya Pradesh (India)

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Similarly to the northern grain region of Australia, root-lesion nematode (RLN), *Pratylenchus thornei*, is an important constraint to chickpea crops in Madhya Pradesh, which is the major chickpea growing state of India. Damaged plants exhibit lesions on the roots, become less efficient in taking up water and nutrients, and thus become intolerant to drought. First signs of RLN infestation in the field include poor emergence and plant establishment and stunting and wilting, despite adequate soil moisture. RLN damage to chickpea occurs in patches, with affected plants showing stunting, leaf chlorosis, root necrosis and reduction of root growth.

Under field conditions in Madhya Pradesh the tolerance limit of chickpea to *P. thornei* was found to be as low as 2 nematodes /cm³ soil. Losses varied in different cultivars; JG 74 (20.0%); JG 315 (16.4%); Annigiri (22.2%). *P. thornei* usually inhabited mixed red and black soil with a percent frequency of occurrence to the extent of 63.3%, relative density 18.8%, total biomass 43 mg, prominence value of 132 and importance value of 54 in Madhya Pradesh. Chickpea crops cultivated in the Budelkhand region of Madhya Pradesh are more prone to losses than other agro-climatic zones of the state (3). *P. thornei* showed interrelationships with *Fusarium oxysporum* and *Rhizoctonia bataticola* (2 and 1). Chickpea accessions viz., ICC (11315,42, 43, 11324, 12233, 112237, 12239, 12245, 12267, 12228, 12242, 1870, 4936, 5534, 5875, 8712, 100519, 10522, 9032), ICCV (90301, 45330), IC (11551, 1164), BG (306, 321, 329 M, 329, 377, 1035), BDNG (25, 355-15), GL (1271, 96152) and GNG (158, 659, 543, 1078) showed resistant reactions to *P. thornei* (3).

Soybean—wheat and sorghum—chickpea rotations resulted in stability of *P. thornei* population development, whereas soybean—chickpea crop rotations showed an increase in *P. thornei* population development. Seed dressing with neem seed kernel powder (10 g/kg seed) coupled with *Trichoderma viride* (10 g) reduced RLN populations with incremental yield improvement. Most chickpea varieties released from the State of Madhya Pradesh have been found to be susceptible to RLN, except Vishal, which was observed to be moderately resistant. Nigella, fenugreek and coriander have been found to be better crop rotation options in Madhya Pradesh to minimize nematode populations in the field, however, ajaiv and soybean are very poor rotation options.

Disease resistance and susceptibility in Ecuadorian faba bean germplasm

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Faba bean (Vicia faba) cultivation is important to small landholders in the High Andes of South America as both a food and cash crop. The plants are grown in a harsh environment characterised by frequent low intensity rainfall (5), which favours the development of fungal diseases. Faba beans were introduced to South America relatively recently after the Spanish colonisation of the continent. Considering the likely narrow gene base it is remarkable how fast a quite unique gene pool that is well adapted to the local growing conditions developed: Local faba bean varieties showed superior resistance to chocolate spot disease (Botrytis fabae) when grown next to introduced germplasm in Ecuador, but also had a number of negative traits, particularly late (220 - 240 days) maturity (7). A highly chocolate spot resistant accession of Ecuadorian origin was identified after screening the faba bean collection of the International Center for Agricultural Research in the Dry Areas (ICARDA) (4). The same accession was also found to be highly resistant to rust (Uromyces viciae-fabae) in Canadian tests (3). Further evaluation of Ecuadorian germplasm confirmed a high frequency of resistance to chocolate spot (1) as well as rust (6), but also showed susceptibility for Ascochyta blight (Ascochyta fabae) (2).

To broaden the genetic base of disease resistance a germplasm collection mission was undertaken in Ecuador in 1996 by the Ecuadorian Instituto Nacional Autónomo de Investigaciones Agropecuarias (INIAP) in collaboration with ICARDA and co-funded by the Grains Research and Development Corporation (GRDC). This mission yielded 137 accessions from a wide range of altitudes (2270  - 3620 masl) with precise information on collection sites. The collection was evaluated for chocolate spot resistance in ICARDA’s disease screening nurseries at Lattakia (Syria) during 1997 and 1998. Accessions and progenies of single plants selected for disease resistance and agronomic traits (particularly earliness) were imported in Australia and tested against local pathogen strains. Superior resistance to chocolate spot and rust was found, but the most resistant lines were the latest for flowering and maturity. Susceptibility to Ascochyta blight was also confirmed and field testing in northern NSW showed a high frequency of susceptibility to Aphanomyces root rot (Aphanomyces euteiches). Testing for virus resistance showed a unique hypersensitive reaction to Bean yellow mosaic virus (BYMV) in some accessions collected in Azuay province.

Pure line selections of superior accessions that combine disease and virus resistance have been made and are now being used in the PBA faba bean crossing program.

Stemphylium blight in faba bean: an emerging disease or an opportunistic saprophytic pathogen?

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Unusually high incidences of leaf blight symptoms have been observed on faba bean (Vicia faba) crops grown in north-eastern Australian during the current (2016) growing season. The blight was characterised by large grey-black necrotic lesions, often starting from the leaf edge. The lesions appeared to be restricted to leaves only and no symptoms on flowers, pods or stems were visible. The appearance and distribution of lesions on leaves and plants was quite different from that of chocolate spot, caused by Botrytis fabae, which is considered to be the major leaf blight in the northern region: chocolate spot typically starts as small discrete reddish-brown leaf lesions that, after extended periods of leaf wetness, increase rapidly in size, move to other plant parts and cause severe leaf necrosis, stem collapse and flower and pod abortion. The symptoms were also different from leaf blights caused by Ascochyta fabae or Cercospora zonata, both important pathogens on faba bean in Australia’s south-eastern grain growing regions, or Alternaria alternata, a saprophytic pathogen that causes brown lesions characterised by concentric brown rings and is often found late in the season.

Suspect leaf samples were incubated in humid chambers at room temperature for 24 hours. This yielded an abundance of spores, which were identified as Stemphylium spp.: brown, highly septate, oblong conidia (fully grown conidia approximately 15 x 25 µm), with a constriction around a central transverse septum. Stemphylium spp. are generally considered saprophytic fungi or weak pathogens affecting a wide range of hosts. However, Stemphylium blight in lentils, caused by Stemphylium botryosum, is considered to be an important disease in the warm growing environments of south-east Asia and becoming increasingly important in Canada (1). Grey leaf spot in narrow-leafed lupins (caused by Stemphylium spp.) has recently increased in importance in Western Australia (2). In faba bean Stemphylium blight is thought to be a minor disease, but high incidences have been reported in Iran (3) and New Zealand (4) and was also noted in commercial crops in South Australia during the 2014 growing season (R. Kimber, pers. com.).

The 2016 growing season in the northern region has been relatively mild with a number of low-intensity and long-duration rainfall events that typically favour development of leaf blights like chocolate spot. However, this cannot fully explain the high incidences of Stemphylium blight observed in a large number of commercial paddocks. An evaluation of 480 faba bean genotypes in a disease screening nursery at the NSW DPI Liverpool Plains Field Station (LPFS) this year showed a non-symmetrical distribution over Stemphylium blight incidence classes, with a relatively low number of severely blighted lines. Large differences in symptom incidences within genotypes, as well as genetic relationships within the group of highly affected lines, indicate genetic control of susceptibility. The recently (2012) released variety PBA Warda (now the most widely grown variety in the northern region) is among the more affected. Disease control trials at the LPFS failed to show adequate control by any of the 5 fungicides (mancozeb, tebuconazole, chlorothalonil, carbendazim and procimidone) currently registered for use on faba bean.

The impact of Stemphylium blight on faba bean yields in the northern region is not yet known. We are planning yield loss experiments and will continue variety screening and fungicide efficacy trials, as well as trials to determine whether other (non-genetic) factors (abiotic stresses, herbicide injury, nutrient deficiencies) play a role in increasing the vulnerability of faba bean to this pathogen.

Effect of plant density on grain yield of chickpea in contrasting environments in northern NSW

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There has been a tendency for growers to reduce sowing rate of chickpea crops, mainly in response to the increasing cost of seed. This has necessitated research to quantify target plant densities for new varieties in different environments.

Whish (1) monitored 52 commercial chickpea crops over three seasons (2002-04) which showed the median plant density on farm fluctuated between 14 and 22 plants/m\textsuperscript{2}. Modelling by Whish (1) suggested that increasing plant density independently of sowing date would improve yields 55\% of the time for crops sown in early June and 60\% of the time for crops sown in mid May.

A series of variety (PBA HatTrick\textsuperscript{TM}, PBA Boundary\textsuperscript{TM}, Kyabra\textsuperscript{TM}, CICA0912 and Genesis\textsuperscript{TM}090) by plant density (5, 10, 15, 20, 30 and 45 plants/m\textsuperscript{2}) experiments were conducted from 2011 to 2015 at two locations at fixed row spacing (0.5 m). The two contrasting environments; Coonamble and Tamworth have long term median growing season (May to November) rainfall of 212 mm and 300 mm, respectively.

There were no significant interactions between variety and plant density at either location, or in any of the years. At Coonamble, grain yield showed a flat response to plant density above 20 plants/m\textsuperscript{2} with a marginal increase in yield from 20-45 plants/m\textsuperscript{2} (335 kg/ha) under high in-crop rainfall (349 mm, 2011). At Tamworth, the wetter of the two locations, yields were more responsive across the range of plant densities over the years. At Tamworth, the optimum plant density was 30 plants/m\textsuperscript{2} irrespective of in-crop rainfall.

When sowing within the optimum sowing window, mid May – early June, where yield potential is ≥ 1.5 t/ha; sow at ≥ 30 plants/m\textsuperscript{2} and where yield potential is ≤ 1.5 t/ha; sow at ≥ 20 plants/m\textsuperscript{2}.

\textsuperscript{d) Varieties displaying this symbol beside them are protected under the Plant Breeders Rights Act 1994

Alternative fungicides provide improved control of ascochyta blight and yield benefit in field peas

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Ascochyta blight (AB) (synonym: blackspot) remains one of the most economically important diseases in field peas often resulting in significant yield losses, either directly through infection, or indirectly through delaying sowing time to minimise infection. Fungicides to control AB can be an important component of disease management and also assist in maintaining yield potential through enabling agronomically optimal sowing times. Previous research by SARDI (1) has shown that a strategy of P-Pickel T® seed dressing followed by two foliar applications of Mancozeb (2 kg/ha at 9 node and early flowering) suppresses AB and is generally economical in crops yielding 1.5 t/ha or greater. The aim of the current project was to test the efficacy of a range of unregistered foliar fungicides, including new actives, against this current strategy.

Field trials were conducted in three major field pea production areas in South Australia; Hart, Pinery (medium rainfall zones) and Minnipa (low rainfall zone). Trials were Randomized Complete Block Design (RCBD), replicated three times with nine treatments including an untreated control. Fungicides were applied either as a seed dressing, as fluid injection, or as combinations of seed dressing and foliar fungicide at 8 weeks after sowing and again at early flowering. fortnightly applications of chlorothalonil were included as a second control treatment. Field pea stubble infested with AB from the previous season was spread adjacent to seedlings (1 to 2 node) at Minnipa only. AB was assessed visually at early bud development as a % AB severity per plot (% of plant diseased x frequency of infected plants) and at mid to late flowering stage as number of girdled nodes on five randomly selected individual plants. A disease index (DI) was developed from these scores. At the first assessment, disease severity differed among the fungicide treatments but the magnitude of these differences was site dependent. In particular at Minnipa disease spread prior to the first foliar fungicide application (8 weeks after sowing), suggesting an earlier timing of the foliar fungicide may be beneficial in high disease risk situations. Similar responses for DI and grain yield were found from all fungicide treatments across the three sites. The new fungicides showed improved efficacy in controlling AB with yield benefits of approximately 15% compared to untreated plots and those treated with Mancozeb. Earlier application timings and further testing across seasons is required to explore the results.

Eliminating grain defects in chickpeas

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Desi chickpea seed is a major Australian pulse export (1), highly regarded in the Indian sub-continent for its good quality. This high quality leads to high prices and greater profitability along the value chain. However, the presence of any grain defects can lead to lower prices or potential rejection of grain at receival. GRDC funded project (DAN00196) is conducting multidisciplinary preemptive research to explore the genetic (G) and environmental (E) components of several grain defects with the aim of eliminating them, where possible, from Australian breeding material.

Research in this presentation will focus on one type of seed defect; seed markings. Seed markings are visual defects that can detract from the attractiveness and marketability of seeds (2). Research has shown that there is a significant genetic component to this defect, and that occurrence is heightened under certain environmental conditions. Factors involved in triggering seed markings have also been investigated. Conventional biometrics is combined with a focus on phenotypic plasticity (3) to untangle GxE. Multiple stress-inducing treatments will now be applied in a controlled environment study that is currently underway. This project will ensure that new Australian varieties are much more resistant to defect incidence, even under stressed environments. This will reduce grower risk and give the entire value chain additional certainty about Australian seed quality to maintain high prices into the future.

Improving the profile of soybean proteins to enhance soy food properties

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Soybean (Glycine max) seeds offer high quality and affordable protein and oil for human consumption and are processed into a wide range of foods. The proteins in the seed have a significant impact on the functional and sensory properties of soy foods. The content and globulin composition of major storage proteins affect gelling, and subsequent textural and water holding, properties of tofu. Lipoxygenases cause lipid oxidation leading to undesirable flavours and taste in soy foods. The Australia Soybean Improvement Program aims to select soybean genotypes with improved protein profiles thereby enhancing soy food quality. We have developed soybeans differing in protein content, globulin subunits (glycinin 11SA4 and/or β-conglycinin 7Sα') or lipoxygenases and investigated their impact and interactions on soy food quality.

Our results from a series of studies (1-5) showed that both protein content and 11SA4 significantly affected tofu properties. Higher proteins content and lack of 11SA4 consistently enhanced two key quality attributes important for tofu manufacturers: texture and water holding capacity, which were positively correlated. Lack of 11SA4 induced compensatory accumulation of 7S globulins, leading to similar amount of these two major groups of storage proteins irrespective of protein content or 11SA4 level in the seed. Soybean lacking lipoxygenases produced soymilk and tofu with decreased negative (grassy/rancid) and increased positive (sweet) aroma (6), making these soy foods more acceptable and potentially broadening soybean utilisation.

Seed Quality Traits of faba bean (*Vicia faba*)

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Faba bean (*Vicia faba*) is one of most important pulse crops in Australia. Most of Australia’s faba bean production is exported to the Middle East where it is a staple food. Hence, the industry requires high quality varieties combined with high yield potential. The preferred size of faba bean seed differs between specific markets and end-uses, while Hydration Capacity (HC – water uptake expressed as a percentage of initial seed weight) is considered an indicator of cooking and canning quality. A high HC and low proportion of unhydrated seeds is preferred. Hydration testing is conducted as an ongoing process in the faba bean breeding program.

Fourteen varieties and breeding lines were included in all trials at two locations, Charlick and Turretfield, South Australia, in 2011-2014 (3 replicates/trial), and were assessed for HC, Unhydrated seed and 100 seed weight. ANOVA (GenStat 14th Edition) indicated that there was a highly significant genetic component for HC, unhydrated seeds and seed weight, but environment (site and season) also had significant main and interaction effects.

An F5:7 RIL population derived from Icarus (green testa, large seed, high HC) and Ascot (buff testa, small seed, moderate HC) was grown at Turretfield for three seasons and assessed for seed quality traits and then subjected to QTL analysis. One highly significant QTL associated with seed testa colour was identified, and this is consistent with major gene control of seed colour. Two significant QTLs associated with HC and two with seed weight were identified in every season. One of the QTLs, on Group 11, was common for the two traits. Several QTLs associated with unhydrated seeds were identified, but were generally of a low LOD score and not consistent across seasons. HC of the RIL population was determined after 2, 4 and 6 hours of soaking and compared with the standard protocol of soaking for 16 hours. HC after each of the short-term treatments was significantly correlated with HC after 16 hours, and the QTLs identified in the 16 hour treatment were also present for the 4 and 6 hour treatments.

These results should assist in improving the efficiency of selection for seed quality traits, and lead to continued improvement of the quality of Australian faba bean varieties.
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