Dr Peter Crisp

Springer Lab
University of Minnesota
Department of Plant and Microbial Biology
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Web resources: https://github.com/pedrocrisp



Professional Interests:

As a molecular biologist and geneticist my major interest is in understanding how plant genomes are interpreted and expressed, particularly in the face of challenges posed by the environment. That is to say, how chromatin, gene expression and transcriptional networks shape the interactions between plants and the stressful and dynamic environments they grow in.

My interests span both wet lab and computational biology and I value being able to integrate genetic, biochemical and genomic approaches. From a foundation as a wet lab biologist I now conduct my research using both the bench and bioinformatics. I have expertise in designing bioinformatics analysis pipelines and scripting new computational tools, as well as performing statistical analysis and manipulating big data sets in R. I am broadly interested in developing and applying cutting edge sequencing methods and computational techniques to profile and interrogate genome activity, including transcriptomes (mRNAs, non-coding RNAs, small RNAs and the degradome), chromatin landscapes and the epigenome.

Major Accomplishments

My PhD was recently conferred in July 2016 and I have multiple first author papers in preparation as well as 9 co-author papers including publications in The Plant Cell, PNAS and Science Advances. I am also a reviewer for Science Advances and PLOS ONE.

2016 Science Advances paper on stress recovery and enigenetics covered by popular science media

2016	including The New York Times, New Scientist, IFL Science and Science Friday.
2016	ANU, Earlier Career Researcher Travel Grant, Gordon Research Conference Plant Molecular Biology
2015	PhD accepted without revisions and highest level of commendation from external reviewers.
2012	Poster prize CSH ASIA "Plant Epigenetics, Stress and Evolution" Suzhou, China.
2011	Plant Cell paper ranked as highly cited, describing a complete retrograde signalling pathway.
2011	Australian Society of Plant Scientists student travel grant to International Botanical Congress.
2010	Centre of Plant Energy Biology Postgraduate Scholarship
2010	PhD Research Scholarship holder, Grains Research and Development Council of Australia.
2010	Australian Postgraduate Award (APA)

2009 Dean's prize, top Honours Thesis result in the College of Medicine, Biology and Environment.

2009 Centre of Plant Energy Biology Undergraduate Honours Scholarship

Education and Professional Experience:

2017	Post-doctoral associate, working on the function, regulation and inheritance of epigenetic phenomenon in maize and other crops species, Springer Lab, Department of Plant Biology, University of Minnesota.
2016	Post doctoral research fellow, Australian Research Council Centre of Excellence in Plant Energy Biology, Australian National University, Australia.
Ph.D. (2016)	PhD, Australian National University, Australia; Grains Research and Development Council Scholarship (Advisor Prof Barry Pogson).
B.S. (2009)	Combined Bachelor Science with Honours (highest honours mark in College of Medicine, Biology and Environment), Bachelor Laws with Honours, Australian National University.

Publications:

Google scholar: https://scholar.google.com.au/citations?hl=en&btnA=1&user=BAVfSlIAAAAJ

Pornsiriwong, W. et al. (2017). A chloroplast retrograde signal, 3'-phosphoadenosine 5'-phosphate, acts as a secondary messenger in abscisic acid signaling in stomatal closure and germination. eLife Sciences 6: e23361.

Carmody, M., **Crisp**, P.A., D'Alessandro, S., Ganguly, D., Gordon, M., Havaux, M., Albrecht-Borth, V., and Pogson, B.J. (2016). *Uncoupling high light responses from singlet oxygen retrograde signaling and spatial-temporal systemic acquired acclimation in Arabidopsis*. **Plant Physiol**. pp.00404.2016.

Crisp, P., Ganguly, D., Eitchen, S., Borevitz, J., and Pogson, B., (2016). *Reconsidering plant memory: intersections between stress recovery, RNA turnover and epigenetics.* **Science Advances**, *2*, e1501340.

Chan, K., Phua, S., Crisp, P., McQuinn, R., Pogson, B., (2016). *Learning the Language of the Chloroplast: Retrograde Signaling and Beyond*. **Annual Reviews of Plant Biology**, *67*, 25–53.

Ganguly, D., **Crisp**, P., Harter, K., Pogson, B.J., and Albrecht-Borth, V. (2015). *Genetic suppression of plant development and chloroplast biogenesis via the Snowy Cotyledon 3 and Phytochrome B pathways*. **Funct. Plant Biol.** 42, 676–686.

Bainbridge, K., Bennett, T., **Crisp**, P., Leyser, O., Turnbull, C., (2014) *Grafting in Arabidopsis*. **Methods Mol. Biol**. 1062, 155–163. doi:10.1007/978-1-62703-580-4_7

Jung, H-S, **Crisp**, P, Estavillo, GM, Cole, B, Hong, F, Mockler, T, Pogson, BJ and Chory J (2013) *A Subset of Heat Shock Transcription Factors Required for the Early Response of Arabidopsis to Excess Light*. **Proc. Natl. Acad. USA**, *110*, 14474–14479.

Estavillo, GM, **Crisp**, PA, Pornsiriwong, W, Wirtz, M, Collinge, D, Carrie, C, Giraud, E, Whelan, J, David, P, Javot, H, Brearley, C, Hell, R, Marin, E and Pogson, BJ (2011) *Evidence for a SAL1-PAP Chloroplast Retrograde Pathway that Functions in Drought and High Light Signaling in Arabidopsis.* **Plant Cell** 23: 3992-4012

Faculty of 1,000 citation and Plant Cell Editors Choice; ranked as a "hot paper" by ESI at the ISI web of knowledge website, in the top 0.1 per cent of all papers in "plant and animal sciences" in the two-year period with respect to citations.

Hirsch J, Misson J, **Crisp** PA, David P, Bayle V, Estavillo GM, Javot H, Chiarenza S, Mallory AC, Maizel A, Declerck M, Pogson BJ, Vaucheret H, Crespi M, Desnos T, Thibaud M-C, Nussaume L, Marin E (2011) *A Novel fry1 Allele Reveals the Existence of a Mutant Phenotype Unrelated to 5'->3' Exoribonuclease (XRN) Activities in Arabidopsis thaliana Roots.* **PLoS ONE** 6(2): e16724

Chan, KX, **Crisp**, PA, Estavillo, GM and Pogson, BJ (2010) *Chloroplast-to-nucleus communication: current knowledge, experimental strategies and relationship to drought stress signalling.* **Plant Signal Behavior** 5: 1575-82.

Cazzonelli CI, Cuttriss AJ, Cossetto SB, Pye W, **Crisp** P, Whelan J, Finnegan J, Turnbull C and Pogson BJ. (2009) *Regulation of carotenoid composition and shoot branching in Arabidopsis by a chromatin modifying histone methyltransferase*, *SDG8*. **Plant Cell**. 21(1):39-53.

Specific Expertise:

Computational Biology:

I have specialised using bioinformatics approaches to solve biological questions. I am proficient in writing and implementing bioinformatics tools and pipelines for the analysis of plant transcriptomes and genomes. I can script in bash and R to implement existing tools and also write programs for novel and custom analysis where new challenges arise. For instance, I wrote a tool biaSEQr to analyse RNAseq coverage profiles to analyse the degradome for signatures of miRNA action and mRNA decay intermediates.

- Bioinformatics and statistics
 - o Experienced user of Word, LaTex, Excel, PowerPoint, Photoshop, Illustrator
 - o Intermediate R, Linux, Bash, GitHub user
 - Experience with Partek and CLC genomics software packages
 - Microarray and tiling-array analysis using R and Partek
 - Designed and implemented complete data analysis pipelines for NGS and Microarrays from raw data to publication quality figures

Plant molecular biology:

I also have an expert foundation in wet lab molecular biology specialising in nucleic acid extraction and manipulation (particularly RNA), qPCR and preparation of libraries for Next Generation sequencing. In addition, I have experience in plant physiology and phenotyping.

- Plant physiology and phenomics, in particular photosynthesis and drought phenomics
 - o Instrument and technique experience including PAM, LiCor, Porometer, HPLC, Scanalyser/TrayScan, plant propagation, seed stock databasing and mutant screening.
- Nucleic acid, protein and metabolite isolation and manipulation, in particular RNA biology
 - o Instrument and technique experience including Bioanalyser (and other capillary electrophoresis), Liquid handling robotics (JANUS), Covaris, Qubit, acrylamide gels for RNA and protein, western blotting, chromatography, Mass spectrometry, extensive use of qPCR.
- Cloning, tissue culture and protein expression
- Next Generation Sequencing technologies (NGS)
 - Including standard and custom small RNA, mRNA, PARE, genomic DNA, and methylome library preparation for Illumina Sequencing

Detailed Research Experience:

2010 – 2015 Graduate student, PhD Thesis

Department of Plant Science, Research School of Biology, Australian National University Supervisors: Prof Barry Pogson, Dr Gonzalo Estavillo, Dr Iain Searle

Balancing the messages: RNA metabolism mediates stress-signaling and recovery in plants Publications: Crisp et al 2016, Chan et al 2016, Jung et al, 2013, Estavillo et al., 2011

2009 Undergraduate student, Honours Thesis

Department of Biochemistry and Molecular Biology, Australian National University

Supervisors: Prof Barry Pogson, Dr Gonzalo Estavillo

PAP signals a new line of communication between the chloroplast and nucleus.

Publications: Hirsch et al, 2011; Bainbridge et al, 2014

2007 Undergraduate student

Department of Biochemistry and Molecular Biology, Australian National University

Supervisors: Prof Barry Pogson, Dr Chris Cazzonelli

An Investigation of the Effect of Over-expressing the Carotenoid Isomerase in Arabidopsis

Thaliana.

Publications: Cazzonneli et al, 2009

2006 Undergraduate student

Department of Biochemistry and Molecular Biology, Australian National University

Supervisors: Prof Barry Pogson, Dr Pip Wilson

Stress responses in plants, characterisation of the putative Arabidopsis mutant salk_020882

2006 Undergraduate student

Research School of Chemistry, Australian National University

Supervisors: Dr Hideki Onagi and Prof Chris Easton

Fine tuning a high-powered Molecular Machine: synthesis of 6^A-Deoxy- 6^A-(N-methyl-

nitrocinnamido)- β -cyclodextrin

2005 Undergraduate student

School of Chemistry, Australian National University

Supervisors: Dr Simon Petrie

Salt Dimers New Candidates for Interstellar Detection

Presentations:

Talks:

Rapid recovery gene silencing in response to excess-light stress in Arabidopsis (2016) Peter Crisp, CSIRO Agriculture and Food Seminar Series, Canberra, Australia.

Have plants learned to forget stress? RNA dynamics during stress recovery in Arabidopsis (2016) **Peter Crisp**, **Gordon Research Conference**, **Plant Molecular Biology**, Holderness, NH, USA.

Signaling and RNA dynamics during stress recovery (2016) Plant Energy Biology Annual Conference, Perth, Australia.

Rapid recovery gene silencing: small RNAs and stress recovery (2013) Peter Crisp, Kevin Murray, Gonzalo Estavillo, Iain Searle, and Barry Pogson, Plant Energy Biology Annual Conference, Perth, Australia.

Rapid recovery gene silencing: small RNAs and stress recovery (2013) Peter Crisp, Kevin Murray, Gonzalo Estavillo, Iain Searle, and Barry Pogson, ACT RNA Society, Canberra, Australia.

PAP signals a new line of communication between the chloroplast and nucleus (2010) Peter Crisp, Gonzalo M Estavillo, Wannarat Pornsiriwong, Markus Wirtz, Chris Carrie, Jim Whelan, Barry Pogson, Plant Energy Biology Annual Conference, Perth, Australia.

Poster presentations:

A metabolic message from the chloroplast affects RNA metabolism and gene silencing in the nucleus (2010) **Peter Crisp**, Gonzalo M Estavillo, Wannarat Pornsiriwong, Markus Wirtz, Chris Carrie, Jim Whelan, Barry Pogson, **Keystone Symposia: RNA Silencing Mechanisms in Plants**, Santa Fe, USA.

PAP signals from the chloroplast regulate exoribonucleases, gene silencing and stress responses in Arabidopsis (2010) Crisp, P.A., Estavillo, G.M., Pornsiriwong, W., Wirtz, M., Carrie, C., Hell, R., Whelan, J. and Pogson, B.J. OzBio, Melbourne, Australia.

Transcriptome analysis reveals a novel signalling pathway between the chloroplast and the nucleus (2011) **Peter Crisp**, Marri Shashikanth, Estelle Giraud, Gonzalo Estavillo, Iain Searle, Jim Whelan, Barry Pogson, **AMATA**, Canberra, Australia

PAP signals from the chloroplast regulate exoribonucleases, gene silencing and stress responses in Arabidopsis (2011) **Peter Crisp**, Gonzalo M Estavillo, Wannarat Pornsiriwong, Markus Wirtz, Estelle Giraud, Rudiger Hell, Jim Whelan, Iain Searle, Barry Pogson, **IBC**, Melbourne, Australia.

Transcriptome analysis reveals a novel signalling pathway between plant organelles and the nucleus, (2012) **Peter Crisp**, Estelle Giraud, Marri Shashikanth, Gonzalo Estavillo, Iain Searle, Jim Whelan, and Barry Pogson, **CSH ASIA Plant Epigenetics, Stress and Evolution**, Suzhou, China.

Rapid recovery gene silencing: the role of small RNAs and RNA decay in stress memory and recovery. (2013) **Peter Crisp**, Marri Shashikanth, Gonzalo Estavillo, Iain Searle, and Barry Pogson, **ICAR**, Sydney, Australia.

Have plants learned to forget stress? RNA dynamics during stress recovery in Arabidopsis. (2016) Peter Crisp, Diep Ganguly, Aaron Smith, Kevin Murray, Steve Eichten, Gonzalo Estavillo, Iain Searle, Justin Borevitz, Ryan Lister, Barry Pogson, Research School of Biology Early and Mid-Career Research Conference, Canberra Australia.

Have plants learned to forget stress? RNA dynamics during stress recovery in Arabidopsis (2016) **Peter Crisp**, **Gordon Research Seminar**, **Plant Molecular Biology**, Holderness, NH, USA

Teaching and Supervisory Experience:

Demonstrator and marker for the Biology Course 'Genomics and its Applications' 2009-2013

Students Mentored/supervised

Year	Student	Project
2016 - Ongoing	Aaron Smith (Honours)	Genome-wide profiling RNA Pol II read-through and consequences for chromatin, gene expression and retrograde signaling
2015 – 2016	You Zhang (Honours)	Understanding mechanisms responsible for thermal acclimation of leaf respiration in rice
2015 – 2016	Aaron Smith (Summer scholar)	RNA stability during excess-light stress and mechanisms enabling rapid recovery
2015	Aaron Smith (Undergraduate)	Investigating the role of RNA polymerase II read-through in PAP-mediated gene activation
2014 – Ongoing	Estee Tee (PhD student)	Defining new roles for the retrograde signal PAP in stomatal dynamics and Reactive Oxygen Species regulation.
2014 – Ongoing	Diep Ganguly (PhD student)	Investigating the role of DNA methylation in Stress Response in Arabidopsis thaliana and Brachypodium distachyon
2014	Rebecca Wardell (Undergraduate)	Documenting an RNAseq bioinformatic pipeline for a transcriptomic analysis of xrn2-1xrn3-3 and alx8 mutants
2014	Lauren Ashman (Undergraduate)	A transcriptomic analysis of drought and excess-light stress using RNAseq
2013	Kevin Murray (Honours)	Gene expression variation under dynamic growth conditions in Arabidopsis thaliana
2012	Thomas Brereton (Undergraduate)	Abscisic Acid Signal Transduction: Possible Involvement of the SAL1/PAP/XRN Pathway

2012	Kevin Murray (Undergraduate)	DegradomeAnalyseR: a bioinformatic tool for investigating RNA metabolism and small RNAs
2010-2011	Su-yin Phua (Honours)	Investigating SAL1-mediated drought tolerance in Arabidopsis

Extracurricular Activities:

Lead Organiser of the Plant Energy Biology, Bioinformatics user group 2014-2016, ANU

ACT Science fair volunteer, Plant Energy Biology Outreach Program for primary school students 2009, 2011, 2016.

BioBounce volunteer, Plant Energy Biology Outreach Program, Strawberry Extraction Stall for Primary School Students, Floriade 2013, 2015.

Team Sports:

- -ANU, Life Science soccer team 2011-2016
- -Competitive soccer since 1990 including representing Australia in the under 18 Australian Futsal Center of Excellence Brazil Touring Side 2000.

I also enjoy camping, fishing, snowboarding, fine wine and cooking.

References:

Prof Barry Pogson

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The Australian National University,
Acton, ACT 0200
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E: barry.pogson@anu.edu.au

Dr Gonzalo Estavillo

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Dr Tony Millar

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