21st International Conference on Arabidopsis Research

Pacifico Yokohama, Japan
June 6-10, 2010
http://arabidopsis2010.psc.riken.jp

20th International Conference on Arabidopsis Research

20th International Conference on Arabidopsis Research

Edinburgh, Scotland, United Kingdom

30th June - 4th July 2009

Edinburgh 2009 Conference

Welcome

Dear Delegate,

Welcome to the 20th International Conference for Arabidopsis Research (ICAR).
Following on from previous conferences in Montréal, Beijing and Madison, we are celebrating the 20th Anniversary of ICAR in the beautiful and historic city of Edinburgh.

From its inception, ICAR has brought together scientists from across the globe to meet and discuss their work and establish new collaborations and ventures and I hope that this years' meeting will continue to fulfil these ideals.

The conference has attracted over 850 delegates from more than 37 countries. There will be over 70 lectures and approximately 600 posters reflecting the wealth and breadth of Arabidopsis research that is undertaken across the world.

I would like to thank all the Chairs of the scientific sessions and members of the organising committee for their help and enthusiasm in preparing the programme. I would also like to thank the BBSRC and other sponsors for their kind support.

I hope you enjoy the 20th ICAR and your stay in Edinburgh.

Ruth Bastow
On behalf of the UK Scientific and Organising Committee

Organising & Scientific Committee

Dr Anna Amtmann – University of Glasgow

Dr Ruth Bastow – GARNet

Prof Jim Beynon – University of Warwick

Prof Brendan Davies – University of Leeds

Dr Alessandra Devoto – Royal Holloway University of London

Prof Paul Dupree – University of Cambridge

Prof Julie Gray – University of Sheffield

Prof Claire Grierson – University of Bristol

Prof Claire Halpin – Scottish Crop Research Institute

Prof Patrick Hussey – University of Durham

Prof Jonathan Jones – Sainsbury Laboratory

Dr Stefan Kepinski – University of Leeds

Prof Sean May – Nottingham Arabidopsis Stock Centre

Prof Andrew Millar – University of Edinburgh

Dr Robert Sablowski – John Innes Centre

Dr Miltos Tsiantis – University of Oxford

Dr Alex Webb – University of Cambridge

Dr Zoe Wilson – University of Nottingham

Prof Philip White – Scottish Crop Research Institute

Table of Contents

At a Glance Programme

Tuesday 30th June 2009

14:00 - 19:00	Registration
16:00 - 17:30	Workshops
17:30 - 19:00	Opening Ceremony and Keynote Lectures
19:00 - 21:00	Welcome Drinks Reception

Wednesday 1st July 2009

08:00 - 18:00	Registration
09:00 - 10:30	Plenary Session 1
10:30 - 11:00	Refreshment Break, Posters and Exhibition
11:00 - 12:30	Plenary Session 2
12:30 - 14:00	Lunch, Posters and Exhibition
14:00 - 15:30	Concurrent Session A
14:00 - 15:35	Concurrent Session B
15:30 - 16:00	Refreshment Break, Posters and Exhibition
16:00 - 18:00	Concurrent Session C
16:00 - 18:00	Concurrent Session D
18:00 - 20:00	Poster Session 1

Thursday 2nd July 2009

08:30 - 18:00	Registration
09:00 - 10:30	Plenary Session 3
10:30 - 11:00	Refreshment Break, Posters and Exhibition
11:00 - 12:30	Plenary Session 4
12:30 - 14:00	Lunch, Posters and Exhibition
14:00 - 16:00	Concurrent Session E
14:00 - 16:00	Concurrent Session F
16:00 - 16:30	Refreshment Break, Posters and Exhibition
16:30 - 18:00	Workshops
18:00 - 20:00	Poster Session 2

Friday 3rd July 2009

08:30 - 18:00	Registration
09:00 - 10:30	Plenary Session 5
10:30 - 11:00	Refreshment Break, Posters and Exhibition
11:00 - 12:30	Plenary Session 6
12:30 - 13:30	International Vision for Plant Science 2009
12:30 - 14:00	Lunch, Posters and Exhibition
18:00 - 20:00	Poster Session 3

Saturday 4th July 2009

08:30 - 18:00	Registration
09:00 - 10:30	Plenary Session 7
10:30 - 11:00	Refreshment Break, Posters and Exhibition
11:00 - 12:30	Plenary Session 8
12:30 - 14:00	Lunch, Posters and Exhibition
14:00 - 16:00	Concurrent Session G
14:00 - 15:45	Concurrent Session H
15:45 - 16:30	Refreshment Break, Posters and Exhibition
16:30 - 18:00	Workshops
19:30 - 23:00	ICAR 2009 Conference Dinner

ICAR 2009 Programme

Tuesday 30th June 2009

14:00 - 19:00	**ICAR 2009 Registration**	*Strathblane Hall*
16:00 - 17:30	**Workshops**	
	1. **Plant Proteomics - Breakthroughs in studying intra-cellular dynamics and environmental response in the Arabidopsis proteome**	*Tinto*
	2. **Assaying for hallmark features of Programmed Cell Death**	*Moorfoot*
	3. **Quantitative modelling of signalling systems** (This workshop will start at 15:45)	*Kilsyth*
17:30 - 19:00	**Opening Ceremony and Keynote Lectures**	*Pentland Auditorium*
	Prof Andrew Millar - University of Edinburgh, UK Welcome	
	Prof David Baulcombe FRS - University of Cambridge, UK Food for thought or thought for food?	
	Prof Wayne Powell - IBERS, University of Aberystwyth, UK The role and importance of crop science and plant breeding	
19:00 - 21:00	**Welcome Drinks Reception**	*Strathblane and Cromdale Halls*

ICAR 2009 Programme

Wednesday 1st July 2009

08:00 - 18:00	**ICAR 2009 Registration**	*Strathblane Hall*
Plenary Session 1	**The RNA World - Epigenetics and Genomics** Co-Chairs - David Baulcombe and Marjori Matzke	*Pentland Auditorium*
09:00 - 09:30	**Prof Jian Kang Zhu** - University of California, Riverside, USA Mechanism and function of active DNA demethylation	
09:30 - 10:00	**Prof Jurek Paszowski** - University of Geneva, Switzerland DNA methylation and transgenerational epigenetic inheritance	
10:00 - 10:30	**Prof Herve Vaucheret -** INRA Centre de Versailles, France Specificity, redundancy and antagonism among plant small RNA pathways *This session is kindly sponsored by Roche*	
10:30 - 11:00	**Refreshment Break, Posters and Exhibition**	*Strathblane and Cromdale Halls*
Plenary Session 2	**Development** Co-Chairs - Keith Lindsey and Vivian Irish	*Pentland Auditorium*
11:00 - 11:30	**Dr Xuemei Chen** - University of California, Riverside, USA Regulation of floral stem cells	
11:30 - 12:00	**Prof Ben Scheres** - Utrecht University, The Netherlands Architecture from stem cell centred feedback networks	
12:00 - 12:30	**Prof John Bowman** - Monash University, Australia Evolution of patterning genes in land plants *This session is kindly sponsored by NAASC*	
12:30 - 14:00	**Lunch, Posters and Exhibition** *Lunch is kindly sponsored by Bayer*	*Strathblane and Cromdale Halls*
Concurrent Session A	**Hot Topics** Co-Chairs - Ottoline Leyser and Philip Benfey	*Pentland Auditorium*
14:00 - 14:15	**Dr Stig Uggerhøj Andersen** - University of Aarhus, Denmark Next-generation genetics: mapping and mutant identification in one step by deep sequencing	
14:15 - 14:30	**Dr Rebecca A Mosher** - University of Cambridge, UK Uniparental expression of PolIV-dependent siRNAs in developing endosperm of Arabidopsis	
14:30 - 14:45	**Prof Ian Small** - University of Western Australia, Australia Roles for RNA editing factors in leaf development	

ICAR 2009 Programme

Wednesday 1st July 2009 continued

Concurrent Session A — **Hot Topics** — *Pentland Auditorium*
Co-Chairs - Ottoline Leyser and Philip Benfey

14:45 - 15:00 — **Alexander Graf** - John Innes Centre, Norwich, UK
The circadian clock controls carbohydrate metabolism and hence growth rate in Arabidopsis plants at night

15:00 - 15:15 — **Renhou Wang** - Max Planck Institute, Cologne, Germany
Control of perennial flowering and perenniality in *Arabis alpina*

15:15 - 15:30 — **Dr Kirsten Bomblies** - Max Planck Institute, Tuebingen, Germany
Local-scale population structure and outcrossing in *Arabidopsis thaliana*

This session is kindly sponsored by the Plant Journal — the plant journal

Concurrent Session B — **Environmental Responses** — *Sidlaw Auditorium*
Co-Chairs - Steven Penfield and Paloma Más

14:00 - 14:25 — **Dr Paul Devlin -** Royal Holloway – University of London, UK
FHY3 and FAR1 mediate red light input to the Arabidopsis circadian clock

14:25 - 14:50 — **Prof Julian Schroeder -** University of California, San Diego, USA
Identification of CO_2-binding proteins that function as upstream mediators of CO_2-induced stomatal movements

14:50 - 15:05 — **Dr Harriet McWatters** - University of Oxford, UK
Membranes, temperature and the plant clock

15:05 - 15:20 — **Dr Jose Dinneny** - National University of Singapore
Towards a spatiotemporal understanding of the salt stress response

15:20 - 15:35 — **Dr Motoaki Seki -** RIKEN PSC, Japan/Yokohama City University, Japan
Novel RNA- and chromatin remodeling-mediated regulatory mechanisms in plant abiotic stress responses

This session is kindly sponsored by Plant Cell and Environment — Plant, Cell & Environment PC E

15:30 - 16:00 — **Refreshment Break, Posters and Exhibition** — *Strathblane and Cromdale Halls*

ICAR 2009 Programme

Wednesday 1st July 2009 continued

Concurrent Session C — **Novel Tools and Resources** — *Pentland Auditorium*
Co-Chairs - Sean May and Blake Meyers

16:00 - 16:30 — **Prof Joe Ecker** - Salk Institute, USA
Sequencing across the genome-phenome divide

16:30 - 17:00 — **Dr Sean Cutler -** University of California, Riverside, USA
Sidestepping genetic redundancy with small molecules

17:00 - 17:15 — **Dr Anna Amtmann -** University of Glasgow, UK
EZ-Rhizo: New software for fast and accurate measurement of root system architecture

17:15 - 17:30 — **Dr Jun Cao** - Max Planck Institute, Tuebingen, Germany
One genome is not enough: Genome-species genome variation in *Arabidopsis thaliana*

17:30 - 17:45 — **Dr Neil Graham** - University of Nottingham, UK
Evidence of neutral transcriptome evolution in plants

17:45 - 18:00 — **Dr Susana Garcia-Sanchez** - NEIKER Institute-Tecnalia, Spain
Wide screening of phage-displayed protein libraries to draw plant-pathogen interaction maps

This session is kindly sponsored by the Plant Journal — the plant journal

Concurrent Session D — **Development** — *Sidlaw Auditorium*
Co-Chairs - Gwyneth Ingram and Miltos Tsiantis

16:00 - 16:30 — **Prof Rüdiger Simon** - Heinrich-Heine University, Germany
Signalling modules controlling the stem cell niche in Arabidopsis

16:30 - 17:00 — **Dr Gwyneth Ingram** - University of Edinburgh, UK
PHYTOCALPAIN as a key regulator of growth in plants

17:00 - 17:15 — **Dr Dominique Bergmann** - Stanford University, USA
Asymmetry, pattern and renewal in Arabidopsis stomatal development

17:15 - 17:30 — **Dr Ji-Young Lee** - Cornell University, USA
Tissue patterning and growth coordinated by a mobile microRNA and SHORT ROOT in the root

17:30 - 17:45 — **Kensuke Kawade** - University of Tokyo, Japan
Leaf size is regulated by a cell-autonomous system linking cell proliferation and post-mitotic cell enlargement

17:45 - 18:00 — **Dr Carla Galinha** - University of Oxford, UK
Repression of apical HD-ZIP III homeobox genes is required for Arabidopsis embryonic root development

18:00 - 20:00 — **Poster Session 1** — *Pentland Auditorium*
Odd numbered poster abstracts to be presented.
Drinks will be served during this session.

This poster session is kindly sponsored by NAASC — NAASC

ICAR 2009 Programme

Thursday 2nd July 2009

08:30 - 18:00	**ICAR 2009 Registration**	*Strathblane Hall*
Plenary Session 3	**Environmental Responses** Co-Chairs - Alistair Hetherington and Sally Assmann	*Pentland Auditorium*
09:00 - 09:30	**Prof Alistair Hetherington** - University of Bristol, UK The responses of stomata to environmental signals	
09:30 - 10:00	**Prof Sally Assmann** - Pennsylvania State University, USA ABA and G-protein signalling in Arabidopsis guard cells	
10:00 - 10:30	**Dr Julia Bailey-Serres** - University of California, Riverside, USA Low oxygen stress: What is more important cell identity or survival? *This session is kindly sponsored by the New Phytologist Trust*	
10:30 - 11:00	**Refreshment Break, Posters and Exhibition** *This refreshment break is kindly sponsored by ISPMB*	*Strathblane and Cromdale Halls*
Plenary Session 4	**Plant Defence** Co-Chairs - Jonathan Jones and Jim Beynon	*Pentland Auditorium*
11:00 - 11:30	**Prof Corne Pieterse** - Utrecht University, The Netherlands Networking by small-molecule hormones in plant immunity	
11:30 - 12:00	**Dr Cyril Zipfel** - Sainsbury Laboratory, UK Deciphering PAMP-triggered immunity in Arabidopsis	
12:00 - 12:30	**Prof Murray Grant** - University of Exeter, UK Effectors affect distal effects; plant systemic reprogramming associated with defence and disease *This session is kindly sponsored by Plant Biotechnology*	
12:30 - 14:00	**Lunch, Posters and Exhibition**	*Strathblane and Cromdale Halls*
Concurrent Session E	**Plant Defence** Chair - Jane Glazebrook	*Pentland Auditorium*
14:00 - 14:30	**Prof Jonathan Jones** - Sainsbury Laboratory, UK Using pathogen effectors to understand host resistance mechanisms	
14:30 - 15:00	**Prof Jim Beynon** - WHRI, University of Warwick, UK Pathogen effectors and host responses	
15:00 - 15:15	**Dr Nicolas Frei dit Frey -** Max Planck Institute, Cologne, Germany Endocytic trafficking: New players in FLS2/flagellin signalling	

ICAR 2009 Programme

Thursday 2nd July 2009 continued

Concurrent Session E	**Plant Defence** Chair - Jane Glazebrook	*Pentland Auditorium*
15:15 - 15:30	**Steven Spoel** - University of Edinburgh, UK Post-translational modifications of the transcription co-activator NPR1 regulate plant immunity	
15:30 - 15:45	**Dr Fumiaki Katagiri** - University of Minnesota, USA New classes of proteins forming complexes with resistance proteins	
15:45 - 16:00	**Dr Morten Petersen** - Copenhagen University, Denmark Autophagic components contribute to hypersensitive cell death in Arabidopsis *This session is kindly sponsored by Plant Physiology* Plant Physiology	
Concurrent Session F	**Plant Growth Regulators** Co-Chairs - Stefan Kepinski and Joe Kieber	*Sidlaw Auditorium*
14:00 - 14:30	**Prof Joe Ecker** - Salk Institute, USA Untangling transcriptional regulatory networks modulating hormone responses	
14:30 - 15:00	**Dr Zhiyong Wang** - Carnegie Institution, USA The brassinosteroid signal transduction pathway	
15:00 - 15:15	**Prof Joseph Kieber** - University of North Carolina, USA Cytokinin signaling: Two-components and more	
15:15 - 15:30	**Dr Karim Sorefan** - John Innes Centre, UK A regulated auxin minimum is required for tissue patterning in Arabidopsis fruit	
15:30 - 15:45	**Emanuele Scacchi** - University of Lausanne, Switzerland Dynamic, auxin-responsive plasma membrane to nucleus movement of Arabidopsis BRX	
15:45 - 16:00	**Dr Daniela Dietrich** - University of Nottingham, UK Divide et impera – cell division in the root and its control through ABA *This session is kindly sponsored by ISPMB* ISPMB	
16:00 - 16:30	**Refreshment Break, Posters and Exhibition**	*Strathblane and Cromdale Halls*
16:30 - 18:00	**Workshops**	
	1. Stomata - the ins and outs	*Tinto*
	2. Root system architecture	*Moorfoot*
	3. Putting TAIR to work for you - hands-on workshop for beginning and advanced users	*Kilsyth*
18:00 - 20:00	**Poster Session 2** Even numbered poster abstracts to be presented. Drinks will be served during this session.	*Pentland Auditorium*

ICAR 2009 Programme

Friday 3rd July 2009

08:30 - 18:00	**ICAR 2009 Registration**	*Strathblane Hall*
Plenary Session 5	**Natural Variation** Co-Chairs - Caroline Dean and Magnus Nordborg	*Pentland Auditorium*
09:00 - 09:30	**Prof Magnus Nordborg** - Gregor Mendel Institute, Austria Genome-wide association study of 100+ phenotypes in a common set of *Arabidopsis thaliana* inbred lines	
09:30 - 10:00	**Prof Caroline Dean** - John Innes Centre, UK Natural variation in Arabidopsis vernalization response	
10:00 - 10:30	**Prof Joanna Schmitt** - Brown University, USA Predicting flowering time in changing climates *This session is kindly sponsored by Plant Cell* THE PLANT CELL	
10:30 - 10:40	**Presentation of Plant Methods Poster Prize**	*Pentland Auditorium*
10:30 - 11:00	**Refreshment Break, Posters and Exhibition**	*Strathblane and Cromdale Halls*
Plenary Session 6	**Cell Biology** Co-Chairs - Claire Grierson and Jiri Friml	*Pentland Auditorium*
11:00 - 11:30	**Prof Ian Moore** - University of Oxford, UK Small GTPases in post-Golgi and endocytic membrane traffic in Arabidopsis	
11:30 - 12:00	**Dr Silke Robatzek** - Max Planck Institute, Tübingen, Germany Cellular dynamics in plant immunity	
12:00 - 12:30	**Prof Jiri Friml** - VIB and University of Gent, Belgium Auxin transport – connecting cell polarity and patterning *This session is kindly sponsored by Plant Cell* THE PLANT CELL	
12:30 - 13:30	**International Vision for Plant Science 2009** **Prof Andrew Millar** - University of Edinburgh, UK **Prof Joe Ecker** - Salk Institute, USA	*Pentland Auditorium*
12:30 - 14:00	**Lunch, Posters and Exhibition**	*Strathblane and Cromdale Halls*
	Afternoon off to enjoy Edinburgh Pre-booked tours will depart from the front of the EICC at 13:30	
18:00 - 20:00	**Poster Session 3** All poster abstracts to be presented. A bar will be available during this session.	*Pentland Auditorium*

ICAR 2009 Programme

Saturday 4th July 2009

08:30 - 18:00	**ICAR 2009 Registration**	*Strathblane Hall*
Plenary Session 7	**Signalling in Development** Co-Chairs - Dr Karen Halliday and Dr Stacey Harmer	*Pentland Auditorium*
09:00 - 09:30	**Dr Stacey Harmer** - University of California, Davis, USA Timing is everything: exploring links between the circadian clock and hormone signaling	
09:30 - 10:00	**Prof Nicholas Harberd** - University of Oxford, UK Growth regulation by GA-GID1-DELLA and beyond	
10:00 - 10:30	**Dr Christian Fankhauser** - University of Lausanne, Switzerland Regulation of shade avoidance by a network of bHLH class transcription factors	
10:30 - 11:00	**Refreshment Break, Posters and Exhibition**	*Strathblane and Cromdale Halls*
Plenary Session 8	**Systems Biology** Co-Chairs - Andrew Millar and Philip Benfey	*Pentland Auditorium*
11:00 - 11:30	**Prof Enrico Coen** - John Innes Centre, UK Development of shape in plants	
11:30 - 12:00	**Prof Mark Stitt** - Max Planck Institute, Golm, Germany Systems analysis of the diurnal regulation of metabolism and growth	
12:00 - 12:30	**Prof Andrew Millar** - University of Edinburgh, UK Unwinding the circadian clock with systems biology	
	This session is kindly sponsored by the Centre for Systems Biology Edinburgh and the Centre for Plant Integrative Biology	
12:30 - 14:00	**Lunch, Posters and Exhibition**	*Strathblane and Cromdale Halls*

ICAR 2009 Programme

Saturday 4th July 2009 continued

Concurrent Session G	**Systems Biology** Co-Chairs - Reka Albert and Christophe Godin	*Pentland Auditorium*
14:00 - 14:30	**Prof Przemyslaw Prusinkiewicz** - University of Calgary, Canada A level-set model of leaf form development	
14:30 - 15:00	**Prof Reka Albert** - Pennsylvania State University, USA Dynamic modeling of the signal transduction network corresponding to abscisic acid induced stomatal closure in *Arabidopsis thaliana*	
15:00 - 15:15	**Sarah Robinson** - John Innes Centre, UK Modelling cell division in the Arabidopsis leaf epidermis	
15:15 - 15:30	**Dr Adrienne Roeder** - The California Institute of Technology, USA Timing of cell division determines the relative cell size pattern in Arabidopsis	
15:30 - 15:45	**Dr Miguel Moreno-Risueno** - Duke University, USA A systems biology approach to understanding the root clock	
15:45 - 16:00	**Julia Rausenberger** - University of Freiburg, Germany From protein dynamics to physiology: phytochrome B mediated photomorphogenesis	
Concurrent Session H	**Bioenergy** Chair - Paul Dupree	*Sidlaw Auditorium*
14:00 - 14:30	**Prof Henrik Vibe Scheller** - Lawrence Berkeley National Laboratory, USA Arabidopsis as a model for cell wall biosynthesis in bioenergy crops	
14:30 - 15:00	**Dr Ruben Vanholme** - Ghent University, Belgium Systems biology of lignification and relevance to biofuels	
15:00 - 15:15	**Dr Kerrie Farrar** - IBERS, University of Aberystwyth, UK Exploiting model species to increase biomass yield in energy crops	
15:15 - 15:30	**Dr Raymond Wightman** - University of Manchester, UK Assembly of the Cellulose Synthase Complex occurs within a specialised compartment that is derived from the endoplasmic reticulum	
15:30 - 15:45	**Dr Thorsten Hamann** - Imperial College London, UK Using *Arabidopsis thaliana* to improve feedstock quality *This session is kindly sponsored by Plant Physiology* Plant Physiology	
15:45 - 16:30	**Refreshment Break, Posters and Exhibition**	*Strathblane and Cromdale Halls*
16:30 - 18:00	**Workshops**	
	1. Anther/pollen development	*Tinto*
	2. Ambient temperature	*Moorfoot*
19:30 - 23:00	**ICAR 2009 Conference Dinner** The Conference Dinner will take place in the Cromdale Hall with pre-dinner drinks in the Strathblane Hall from 19:30.	*Strathblane and Cromdale Halls*

ICAR Supporters

ICAR 2009 gratefully acknowledges the generous contributions of the following organisations:

Abcam

Bayer

Biobase

BBSRC

Centre for Plant Integrative Biology

Centre for Systems Biology Edinburgh

Company of Biologists

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Plant Methods

Plant Physiology

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Roche Diagnostics Ltd

The Plant Cell

Wiley Blackwell

General Information

Registration

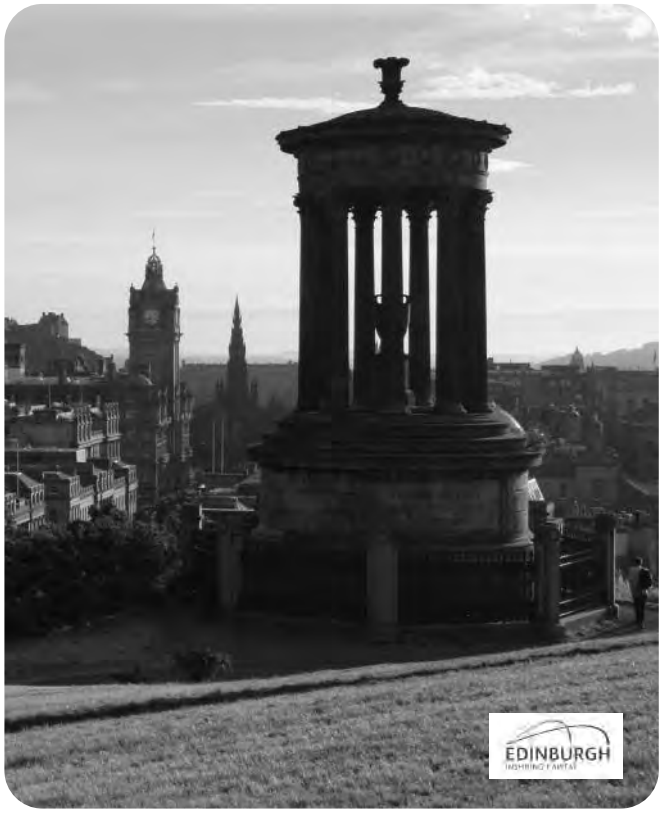
ICAR Conference Registration will take place in the Strathblane Hall on Level 0 of the Edinburgh International Conference Centre and will be open at the following times:

Tuesday 30th June	14:00 - 19:00
Wednesday 1st July	08:00 - 18:00
Thursday 2nd July	08:30 - 18:00
Friday 3rd July	08:30 - 18:00
Saturday 4th July	08:30 - 18:00

Venue

Edinburgh International Conference Centre,
The Exchange, Morrison Street, Edinburgh,
EH3 8EE.
Tel: 0044 (0) 131 300 3000
Fax: 0044 (0) 131 300 3030

ICAR 2009 will be held at Edinburgh International Conference Centre (EICC), situated in the city centre. The EICC's striking circular design has made it one of Edinburgh's most distinctive landmarks. The centre has hosted many high profile congress and events since opening in 1995. As you would expect from a world-class venue, the technical, presentation and communications facilities are modern, efficient and adaptable.



Exhibition

The ICAR 2009 Exhibition will be held in the Cromdale Hall on Level -2 of the EICC from Tuesday 30th June to Saturday 4th July.
All delegates are invited to visit the exhibition.
The opening times of the exhibition are as follows:

Tuesday 30th June	14:00 - 21:00
Wednesday 1st July	09:00 - 20:00
Thursday 2nd July	09:00 - 20:00
Friday 3rd July	09:00 - 14:00 and 18:00 - 20:00
Saturday 4th July	09:00 - 14:00

Refreshment Breaks

Coffee and tea will be served in the both the Strathblane and Cromdale Halls at the following times:

Wednesday 1st July	10:30 - 11:00 and 15:30 - 16:00
Thursday 2nd July	10:30 - 11:00 and 16:00 - 16:30
Friday 3rd July	10:30 - 11:00
Saturday 4th July	10:30 - 11:00 and 15:45 - 16:30

Lunches

Lunch is included in the registration fee and will be served in both the Strathblane and Cromdale Halls. Lunch breaks will be at the following times:

Wednesday 1st July	12:30 - 14:00
Thursday 2nd July	12:30 - 14:00
Friday 3rd July	12:30 - 14:00
Saturday 4th July	12:30 - 14:00

Posters

Posters will be displayed in the Strathblane and Cromdale Halls. Poster numbers on the boards relate to the poster numbers in this programme and in the book of abstracts. Presenting authors are required to attend their posters during the poster sessions on Wednesday (odd numbers), Thursday (even numbers) or Friday evening (all poster numbers) respectively. Velcro to mount the posters can be obtained from the registration desk.

Conference Abstracts

All delegates will have received, in their delegate bags, a memory stick containing all the abstracts

of the conference. Hard copies of the Book of Abstracts have been available to purchase in advance and a few may be available to purchase onsite at the Finance Desk. Producing the abstracts this way reduces organisational costs, as well as reducing paper and printed materials.

Social Event Tickets

There are a limited number of tickets available to purchase for the conference dinner and optional tours. Please see the staff at the Finance Desk as early as possible if you would like to purchase a ticket.

Message Board

Messages and news for the Conference delegates will be published on a message board next to the registration desk and on screens around the EICC.

Delegate Badges

For security purposes, delegate badges must be worn at all times.

General Assistance

Please go to the ICAR 2009 Registration Desk in the Strathblane Hall if you have any queries.

Speakers

The Speakers' Preview Area will be in the Lomond Foyer on Level 0 of the EICC. Speakers should visit this area, preferably at least 2 hours prior to the start of their session, to organise the material for their presentation. The desk will be open from 14:00 - 19:00 on Tuesday 30th June and from 08:30 - 18:00 from Wednesday onwards.

Currency

Currency exchanges are available at Bureaux de Change throughout the city and at all major UK airports including Glasgow and Edinburgh and in Edinburgh Waverley Train Station. Delegates will also be able to exchange currency in most Edinburgh city centre banks.

Credit Cards

Most credit cards are accepted in the UK. However it is best to pay cash in smaller shops.

Banking Hours

Normal bank opening hours are Monday to Friday from 09:00 - 17:00.

Shopping

Opening hours: Monday to Saturday 09:00 - 17:00. Late night shopping on Thursdays until 19:30 or 20:00. Some shops are open on Sundays from 12:00 - 16:00.

Language

The official language of the Conference will be English – there will be no simultaneous translation in conference sessions.

Business Centre

The EICC Business Centre offers facilities including internet access, fax machine, PC/printer and photocopier. Secretarial services are also available.

Internet Access

Delegates can access the wireless internet service by collecting log in details from the registration desk.

Parking

There are three car parks all within two to five minutes walking distance from the EICC. Please view the website for detailed information about car parking – www.eicc.co.uk

Transport

Taxi service is an easy way to travel around Edinburgh. It is best to agree an approximate fare at the start of the journey. There are also good bus routes throughout the city. The main bus terminal is in St Andrew's Square. Buses are operated by Lothian Buses (www.lothianbuses.com) and First Buses (www.firstgroup.com/ukbus).

Telephones

Public telephones for domestic and international calls are located in the Strathblane Hall on Level 0 of the EICC.

Mobile Phones

Out of courtesy to speakers and other delegates, mobile phones and pagers must be switched off or to silent mode before entering sessions.

Smoking

It is against the law to smoke in any enclosed public area in Scotland.

Social Programme

Tuesday 30th June 2009

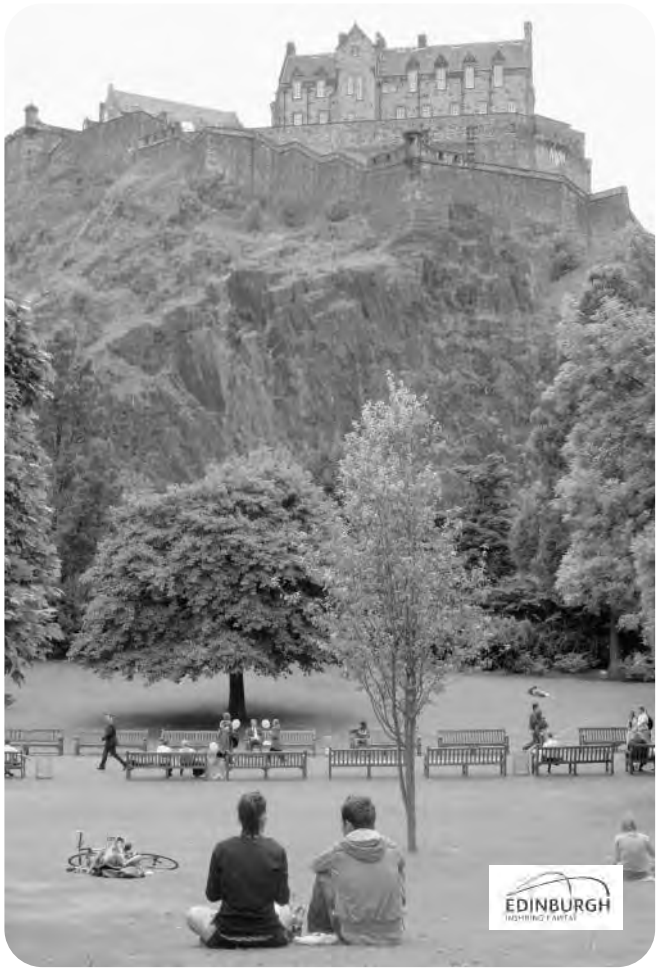
Welcome Reception
19:00 - 21:00

Strathblane and Cromdale Halls
All delegates welcome
The Opening Ceremony and Keynote Presentations will be followed by the Welcome Drinks Reception to be held from 19:00 - 21:00 hours in the Strathblane and Cromdale Halls.

Wednesday 1st July 2009

Poster and Exhibition Session 1
18:00 - 20:00

Strathblane and Cromdale Halls
All delegates welcome
The first poster and exhibition session of the conference will take place in the Cromdale and Strathblane Halls from 18:00 - 20:00, during which drinks will be served. Odd numbered posters will be presented.



Thursday 2nd July 2009

Poster and Exhibition Session 2
18:00 - 20:00

Strathblane and Cromdale Halls
All delegates welcome
The second poster and exhibition session of the conference will take place in the Cromdale and Strathblane Halls from 18:00 - 20:00, during which drinks will be served. Even numbered posters will be presented.

Friday 3rd July 2009

Poster and Exhibition Session 3
18:00 - 20:00

Strathblane and Cromdale Halls
All delegates welcome
The final poster and exhibition session of the conference will take place in the Cromdale and Strathblane Halls from 18:00 - 20:00, during which a bar will be available. All posters will be presented.

Saturday 4th July 2009

ICAR 2009 Conference Dinner
19:30 - 23:00

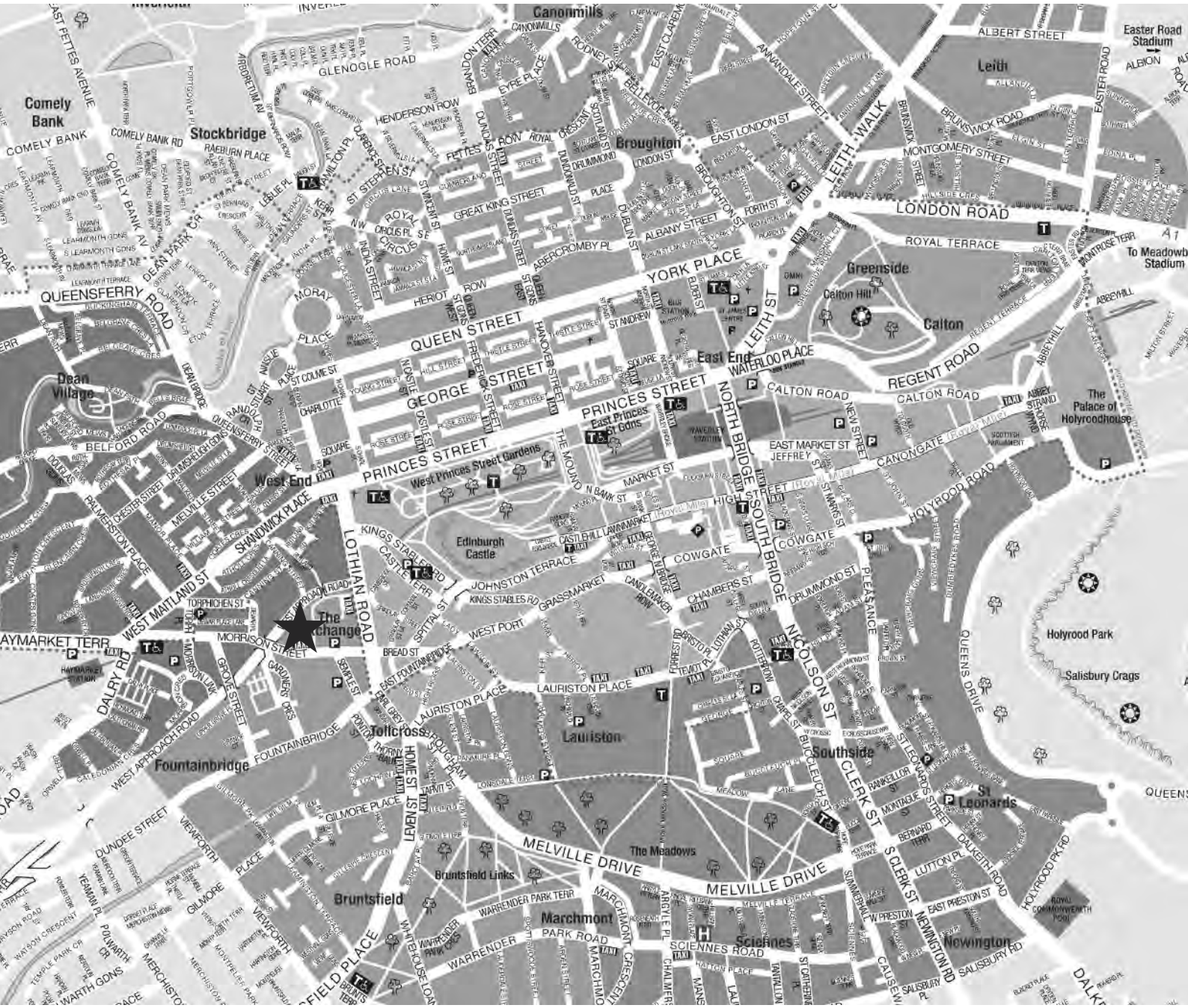
Strathblane and Cromdale Halls
Ticket required
The Conference Dinner will take place in the Cromdale Hall. Delegates will be able to enjoy pre-dinner drinks in the Strathblane Hall from 19:30. Dinner will be followed by a Ceilidh in the Strathblane Hall.
Dress code: smart/casual

Local Information

Welcome to Edinburgh, Scotland

Edinburgh, the Capital City of Scotland is a city filled with historical sights and stories. The Old Town was developed from the 11th century, originally within defensive walls, around the rock on whose peak is situated the famed Edinburgh Castle. From here, the historic Royal Mile sweeps down to the Palace of Holyrood House, the Queen's official royal residence in Scotland. The new Scottish Parliament building is also situated near Holyrood House at the bottom of the Royal Mile. There are also many art galleries located around the city.

Princes Street and George Street are the main shopping areas in the city centre and there are a large number of restaurants in the city centre. An essential guide of Edinburgh is included in delegate bags to provide further information about the city.



★ - EICC

Optional Tours

Friday 3rd July

Coaches for the tours will leave from the front of the EICC at 13:30. Tickets for these tours will be issued with delegate badges.

Edinburgh City Tour

From the comfort of your touring coach discover the history and beauty of Edinburgh. Start the tour visiting the Georgian New Town, with it's sweeping crescents and terraces, then move on to the historic Royal Mile with it's enchanting wynds and closes. A visit to Edinburgh Castle affords wonderful panoramic views of the city skyline along with the chance to see the "Honours of Scotland" – Scotland's Crown Jewels.

Malt Whisky Tour

From Edinburgh we travel southwards to the pretty village of Pencaitland, where we visit Glenkinchie Malt whisky distillery. After a tour of the distillery there is a "wee dram" to sample a taste of the finished product, before having the chance to visit the specialist whisky shop.

Stirling Castle

Travelling from Edinburgh we pass historic Linlithgow, where we can see Linlithgow Palace, the birthplace of Mary Queen of Scots.Soon we will arrive in historic city of Stirling, once the home of the Scottish Kings and Queens. In addition to a guided tour of the Castle, set high on a hill above the ancient town, there will be some free time to explore Stirling itself.

Keynote Speakers

Professor David Baulcombe

David Baulcombe has wide interests in plant molecular biology. Currently he works on RNA-silencing systems that protect against viruses and mobile elements of DNA. His group has identified many components of the RNA silencing machinery and a key discovery was the short RNAs that are the specificity determinant. The recent work in David's group embraces a systems level analysis of RNA silencing and its influences – direct or indirect – on gene expression. Most of his work involves Arabidopsis but he has started to explore the role of RNA silencing in a crop plant (tomato) and in a unicellular alga (Chlamydomonas). David also has interests in disease resistance and he is a member of a consortium investigating ways to mitigate the effects of a sweet potato virus disease.

Until August 2007 David was a senior research scientist in the Sainsbury Laboratory, Norwich. He then became the Professor of Botany at Cambridge University and Royal Society Research Professor. He is a Fellow of the Royal Society and a foreign associate member of the US National Academy of Sciences. His awards include the 2008 Lasker Award and the 2006 Royal Medal of the Royal Society. Extramural activities include membership of the Biotechnology and Biological Sciences Research Council and chairing a Royal Society Policy study on the contribution of biological science to food crop productivity.

Professor Wayne Powell

Professor Wayne Powell has more than 25 years' experience working in the field of contemporary plant genetics. Before being appointed as Director of IBERS at the University of Aberystwyth, he was Director and CEO of NIAB in Cambridge. Previously he was Professor and Foundation Head of the School of Agriculture and Wine, University of Adelaide, Australia. He was Deputy Director of the Scottish Crop Research Institute (SCRI), Dundee, UK, from 2000-2004 and was responsible for leading and facilitating the development of the Institute's scientific vision, with overall responsibility for the Institute's research programmes. Between 1998 and 2000 Professor Powell worked at the Du Pont Company in Wilmington, Delaware, USA, where he gained exposure and experience of operating in a global private sector organisation. Professor Powell's personal research interests are at the interface of plant genetics, genome science, plant breeding and conservation of genetic resources with a strong emphasis on the delivery of 'public good' outcomes.

CSBE

CENTRE FOR SYSTEMS BIOLOGY AT EDINBURGH

The Centre for Systems Biology at Edinburgh, CSBE, is a Centre for Integrative Systems Biology funded by BBSRC and EPSRC. CSBE's research goal is to develop broadly-applicable methods and large-scale infrastructure for modelling the temporal aspects of biological phenomena.

- **Link diverse data and models**
- **Through multiple iterations**
- **Static to kinetic models**
- **Cross multiple scales**

This work is being informed by three biological exemplar projects which have been chosen to exercise all aspects of the modelling process: the circadian clock in *Arabidopsis*, RNA metabolism in yeast and Interferon signalling in macrophages. This continuum of modelling approaches reflects the realistic evolution of a systems-level approach to any and all biological problems. Our philosophy is strongly collaborative; open source and open access and we welcome opportunities for new partnerships.

For experimental projects, a data repository and growing range of model-building and analytical tools. Also, the ability to access our cutting-edge laboratory facilities (robotised qPCR, surface plasmon resonance and Isothermal Calorimetry analysis, LTQ Orbitrap XL mass spectrometer).

Best fit: projects with partly overlapping biological area/data types/analytical requirements.

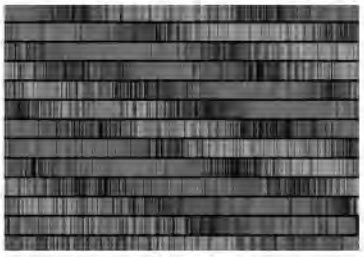
For theoretical projects, a repository of network models linked to diverse underlying data, software tools for modelling and high performance computing. Also the ability to use our modelling expertise as a contract modelling team.

Best fit: projects on complementary analytical or informatic methods.

For further information, in particular to explore research collaboration with CSBE, please contact the Centre Co-Directors or Centre Manager:

Prof. Andrew Millar (Biological Sciences) **e**: andrew.millar@ed.ac.uk
Prof. Igor Goryanin (Informatics) **e**: goryanin@inf.ed.ac.uk
Dr. Liz Elliot **e**: elizabeth.elliot@ed.ac.uk





THE UNIVERSITY OF EDINBURGH

www.csbe.ed.ac.uk

Plenary Abstracts

Mechanism and function of active DNA demethylation

L01

Wednesday 9:00 - 09:30
RNA World

Active DNA demethylation is involved in many vital developmental and physiological processes of plants and animals. Genetic and biochemical studies in Arabidopsis have demonstrated that a subfamily of DNA glycosylases function as DNA demethylases through a base excision-repair pathway. These specialized bifunctional DNA glycosylases remove the 5-methylcytosine base and then cleave the DNA backbone at the abasic site, resulting in a gap that is then filled with an unmethylated cytosine nucleotide by as yet unknown DNA polymerase and ligase enzymes. Evidence suggests that active DNA demethylation in mammalian cells is also mediated at least in part by a base excision repair pathway where the AID/Apobec family of deaminases convert 5-methylcytosine to thymine followed by G/T mismatch repair by the DNA glycosylase MBD4 or TDG. I will present recent work from my lab on the dynamic regulation of gene expression in Arabidopsis by RNA-directed DNA methylation and by ROS1-mediated active DNA demethylation.

Jian Kang Zhu

Institute for Integrative Genome Biology
Department of Botany and Plant Sciences
University of California Riverside
CA 92521
USA

Specificity, redundancy and antagonism among plant small RNA pathways

L02
Wednesday 09:30 - 10:00
RNA World

MicroRNAs (miRNAs) and short interfering RNAs (siRNAs) are involved in a variety of phenomena that are essential for genome stability, development and adaptive responses to biotic and abiotic stresses. Their mode of action also is diverse. They guide DNA elimination during the formation of the macronucleus in protists and heterochromatin assembly in fungi and plants. They target endogenous mRNAs for cleavage and translational repression in plants and animals, and protect both plant and animal cells against virus infection through an RNA-based immune system. They also control the movement of transposable elements at the transcriptional and posttranscriptional level in plants and animals. Here I will present specificities, redundancies and antagonisms among the various plant small RNA pathways.

Herve Vaucheret

Laboratoire de Biologie Cellulaire
Institut Jean-Pierre Bourgin
INRA
78026 Versailles Cedex
France

DNA methylation and transgenerational epigenetic inheritance

L03

Wednesday 10:00 - 10:30
RNA World

Jerzy Paszkowski

In mammals, cytosine is methylated essentially only in CpG sequences (mCpGs). In plants in addition to mCpGs, mC is found also at mCpNpG or mCpNpN sites (N = A or T or C). Interestingly, the maintenance of mCpGs, which is achieved by similar mechanisms in plants and mammals, is essential for plant and mammalian development. The primary focus of my presentation will be on the role of mCpGs in transgenerational epigenetic inheritance in Arabidopsis. Evidence for dynamic interrelationships and feedback regulation of mCpGs and DNA methylation outside CpGs, nuclear architecture and other epigenetic marks will be provided. Deficiencies in mCpGs result in epigenetic and genetic instabilities, activation of epiallelic interactions and uncoordinated activities of compensatory epigenetic mechanisms. Thus in plants mCpGs patterns provide the blueprint coordinating stability of epigenetic inheritance, however epigenetic information can be readily transferred between different epiallelic forms of loci.

Laboratory of Plant Genetics
University of Geneva
Geneva
Switzerland

Regulation of floral stem cells

L04
Wednesday 11:00 - 11:30
Development

Lijuan Ji
Xigang Liu
YunJu Kim
Xuemei Chen

Botany & Plant Sciences
University of California
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CA 92521
USA

An Arabidopsis flower consists of a fixed number of floral organs derived from stem cells in a floral meristem. Unlike stem cells in the shoot apical meristem, which maintain their stem cell identity throughout plant development, those in the floral meristem are terminated upon the production of the final floral organs, the carpels. The floral homeotic transcription factor AGAMOUS (AG) not only specifies the identities of the reproductive organs but also terminates the floral stem cells by repression of the expression of *WUS*, a gene that promotes stem cell identity. The regulation of WUS by AG, however, is unlikely to be direct. We are striving to understand how AG terminates floral stem cells. We isolated an *ag* allele, *ag-10*, which is completely functional in organ identity specification but is occasionally defective in floral determinacy. We performed a genetic enhancer screen in the *ag-10* background and isolated mutations in several complementation groups that enhance the floral determinacy defect. Cloning and analysis of these genes have implicated small RNA- and chromatin-based regulation of floral stem cell termination.

Architecture from stem cell centred feedback networks

L05
Wednesday 11:30 - 12:00
Development

Ben Scheres

Utrecht University
The Netherlands

Like in many animal systems, plant stem cells reside in niches and are maintained by short-range signals emanating from organizing centres. The Arabidopsis *PLETHORA* genes encode transcription factors required for root stem cell specification. *PLT* expression is induced by the indolic hormone auxin, depends on auxin response factors and follows auxin accumulation patterns.

The *PLT* gene clade extensively regulates expression of the PIN facilitators of polar auxin transport in the root and this contributes to a specific auxin transport route that maintains stem cells at the appropriate position. We are addressing the properties of the *PLT*-PIN feedback loop by gene and protein network analysis and computational modelling. The emerging picture is one in which flexible feedback circuits translate auxin accumulation into region- and cell type specification patterns. The *PLT* network interacts with the SHORTROOT-SCARECROW transcription pathway that plays a role in patterning the root stem cells and in providing mitotic potential to the stem cell daughters that form the proximal meristem. This interaction involves the conserved RETINO BLASTOMA-RELATED pocket protein, and we are investigating links between the RBR pathway and upstream patterning genes.

Evolution of patterning genes in land plants

L06

Wednesday 12:00 - 12:30
Development

John Bowman1,2
Sandra Floyd1
Keiko Sakakibara1
Karen Yip2
Chris Zalewski2
Eduardo Flores1
Pia Sappl1
John Alvarez1
Dyani Lewis1

1Monash University,
Melbourne
Victoria
Australia

2UC Davis
Davis
CA
USA

As more plant genome sequences become available, researchers are increasingly using comparative genomics to address some of the major questions in plant biology. Such questions include the evolution of photosynthesis and multicellularity, and the developmental genetic changes responsible for changes in body plan and the origin of important plant innovations such as roots, leaves, and vascular tissue. We have focused on tracing the evolutionary history of genes involved in pattern formation. In particular, we have investigated the history of genes involved in establishing leaf polarity in Arabidopsis. We find that some genes are evolutionarily recent, evolving coincident with the evolution of leaves in seed plants. However, other genes predate the evolution of leaves, implying a co-option from a more ancestral role.

Expression and functional studies in early diverging lineages of land plants provide clues as to ancestral functions, and thus to the evolution of land plant morphology. For example, Class III HD-Zip genes act to promote meristem development, adaxial leaf development and vascular development in Arabidopsis. Since the latter two tissues do not exist in early diverging land plant lineages, apical growth and meristem development may represent an ancestral function. Expression analyses in moss and liverworts support this hypothesis, but also suggest a more direct role in response to light, an environmental parameter that is key in molding the plastic development of plants, and establishing polarity in liverworts in particular. Thus, ancestral roles of patterning genes may lie in interactions with environmental parameters critical in the transition from an aquatic algal ancestor to a land plant.

The responses of stomata to environmental signals

L07

Thursday 09:00 - 09:30
Environmental Responses

Stomata are pores found on the surfaces of plant leaves. They control the uptake of carbon dioxide for photosynthesis and the loss of water vapour during the process of transpiration. The aperture of the stomatal pore is governed by the state of turgor of the two guard cells that surround the stomatal pore. When the guard cells are fully turgid the pore gapes open allowing gas exchange and conversely stomatal closure is associated with a loss of turgor. A wide range of environmental signals control the aperture of the stomatal pore and the number of stomata that form on the epidermis. This lecture will use examples from light, carbon dioxide, relative humidity and ABA signalling to illustrate how these signals bring about alterations in stomatal aperture and development.

Alistair M Hetherington

School of Biological Sciences
University of Bristol
Woodland Road
Bristol
BS8 1UG
UK

ABA and G-protein signaling in Arabidopsis guard cells

L08
Thursday 09:30 - 10:00
Environmental Responses

Regulation of stomatal apertures by the phytohormone abscisic acid (ABA) promotes plant water conservation under drought conditions. ABA induces stomatal closure via an intricate cellular signaling network. We have applied systems biology methods to model this process (Li *et al*, PLoS Biology, 2006), and have recently characterized the Arabidopsis guard cell proteome with the goal of identifying new candidate stomatal signaling proteins (Zhao *et al,* Plant Cell, 2008). Heterotrimeric G proteins, composed of alpha, beta, and gamma subunits, are important secondary messengers in ABA signaling (e.g. Fan *et al*, PNAS, 2008). Most recently, we have identified two new ABA receptors that exhibit attributes of both G-protein-coupled receptors (GPCRs) and classic G-protein alpha subunits (Pandey *et al*, Cell, 2009). The biochemical and molecular genetic characterization of these proteins will be described.

Sarah Assmann

Biology Department
Penn State University
University Park
PA
16802
USA

Low oxygen stress: What is more important cell identity or survival?

L09

Thursday 10:00 - 10:30
Environmental Responses

Julia Bailey-Serres

Department of Botany and Plant Sciences
University of California
Riverside
CA 92521
USA

Arabidopsis thaliana was used to elucidate responses to low oxygen (hypoxia) stress from the organ to cell-type specific level. We used transgenics expressing a FLAG epitope-tagged ribosomal protein (RPL18B) to immunopurify ribosome-associated mRNAs from crude cell extracts of cryo-preserved samples. First, a 35S:FLAG-RPL18 line was used to obtain total and polysomal mRNA populations from seedlings to evaluate the dynamic response to 2h or 9h of hypoxia as well as re-oxygenation (9h hypoxia + 1h air). The changes in translated mRNAs and metabolites exposed a rapid and reversible reconfiguration of carbon and nitrogen metabolism that augments anaerobic ATP production. A major energy conserving mechanism was the inhibition of translation of over 60% of the cellular mRNAs. This sequestration was rapidly reversible, with 90% recovery of polysomes within 10 min of reoxygenation. Remarkably, some strongly induced transcripts were only recruited to polysomes upon reoxygenation. Second, to identify organ and cell-specific distinctions in response to hypoxia, 13 promoters with regional or cell-type specific expression were used to drive FLAG-RPL18B. This collection of lines permitted the comparative profiling of cell-specific mRNA populations in the seedling root apex, whole root and shoot. For each promoter:FLAG-RPL18B line, ribosome-associated mRNAs were evaluated under control conditions and after 2 h of hypoxia, producing a highly informative dataset for >17,000 genes. Transcription factor mRNAs provided a complex fingerprint for individual cell types under control conditions. The transcription factor mRNA population in ribosome complexes was generally perturbed by hypoxia, indicating that the stress largely overrides cell-specific patterns of protein production. We found that all organs and cell types invoked a core response to hypoxia, including increased translation of ~50 mRNAs, of which half are proteins of unknown function. Specific responses to hypoxia in the root, shoot and individual cell-types were resolved that provide new insight into the intricacies of the response to low oxygen stress. (Funding: NSF 2010 IBN-0420152 and IGERT DGE 0504249).

Networking by small-molecule hormones in plant immunity

L10

Thursday 11:00 - 11:30

Plant Defence

Corné Pieterse
Antonio Leon-Reyes
Dieuwertje Van der Does
Adriaan Verhag,
Annemart Koornneef
Saskia Van Wees

Utrecht University
Utrecht
The Netherlands

Plants live in complex environments in which they interact with a broad range of pathogens and insects. Various genomics approaches expanded our understanding of the molecular mechanisms by which plants tailor their defense response to harmful attackers. Diverse small-molecule hormones such as salicylic acid (SA), jasmonic acid (JA) and ethylene (ET) play pivotal roles in the regulation of the defense signaling network.[1] Their signaling pathways cross-communicate, providing the plant with a powerful capacity to finely tailor its immune response to the attacker encountered.[2] Our research is focused on the antagonism between SA and JA signaling. Using a pharmacological approach to dissect the kinetics and mechanisms underlying SA-JA crosstalk, we demonstrated that SA-JA antagonism is conserved among Arabidopsis accessions, highlighting the importance of this mechanism for plant survival. The kinetics of SA and JA signaling appears to play an important role in the outcome (antagonistic, synergistic) of the SA-JA interaction. The antagonistic effect of SA on JA-responsive gene transcription appears to be linked to SA-induced changes in the cellular redox potential, suggesting that SA-JA cross-talk is redox regulated. Several key regulatory proteins involved in pathway cross-talk have been identified, including the redox-sensitive protein NPR1. ET appears to act as an important modulator of NPR1 function in SA-JA crosstalk. Furthermore we showed that SA-mediated suppression of JA signaling acts downstream of SCF-COI1-JAZ components of the JA signaling pathways and is directly targeted at GCC-box containing promoters of JA-responsive genes. Molecular mechanisms of SA-JA crosstalk will be discussed.

1 Pieterse, Leon-Reyes, Van der Ent, Van Wees (2009). Networking by small-molecule hormones in plant immunity. Nature Chem. Biol., in press.
2 Koornneef and Pieterse (2008). Cross-talk in defense signaling. Plant Physiol. 146:839-844.

Effectors affect distal effects; plant systemic reprogramming associated with defense and disease

L11
Thursday 11:30 - 12:00
Plant Defence

Plant systemic acquired resistance (SAR) is classically recognized as a key defense mechanism elaborated following recognition of a pathogen effector by a plant disease resistance protein. A local signal(s) is generated and translocated to distal naïve tissues where it is decoded to activate a signaling network that confers broad spectrum immunity to a wide range of normally virulent pathogens. Elevated SA levels in distal responding leaves are central to SAR but our knowledge of the nature of the translocated signals, their perception in distal leaves and the response networks that propagate SAR is sparse and in cases contradictory. Using a combination of whole genome transcriptome profiling, targeted metabolite profiling and real time imaging we will describe our efforts to reconstruct the series of events that lead to systemic immunity in *Arabidopsis thaliana* following recognition of an avirulent strain of *Pseudomonas syringae*. In particular we will focus on an emerging role for plant hormones in establishment of effective SAR. Recent data imply that plants also respond systemically to pathogen associated molecular patterns and pathogen effectors. Our experiments show that signals arising from a compatible interaction also reconfigure transcription in systemic tissues, activating networks associated with disease development in infected tissue.

William Truman1
Bing Zhai1
Mark Bennett2
Marta de Torres Zabala1
Colin Turnbull2
Murray Grant1

1School of Biosciences
Univeristy of Exeter
UK

2Division of Biology
Imperial College
UK

Deciphering PAMP-triggered immunity in Arabidopsis

L12
Thursday 12:00 - 12:30
Plant Defence

Cyril Zipfel

The Sainsbury Laboratory
Norwich Research Park
Norwich
NR4 7UH
UK

In plant innate immunity, the first line of microbial recognition relies on the perception of pathogen-associated molecular patterns (PAMPs) by pattern-recognition receptors (PRRs) leading to PAMP-triggered immunity (PTI). In Arabidopsis, the leucine-rich repeat receptor kinases EFR and FLS2, in association with BAK1, mediate recognition of the bacterial PAMPs EF-Tu and flagellin, or their peptide surrogates elf18 and flg22 respectively. Despite the critical role of PRRs in anti-microbial immunity, only limited knowledge exists on how they function at the molecular level and on their downstream signalling events. By forward genetics, we have identified 160 *elf18-insensitive (elfin)* mutants; 57 corresponding to *efr* mutants. The identification and characterisation of six *ELFIN* genes shed light on how EFR protein expression is controlled, as well as on immediate downstream signalling. We describe an unexpected sub-specialisation of the ER quality control (ER-QC) machinery for innate immunity, and the first demonstration of a physiological role of the ER-QC in trans-membrane receptor function in plants. In addition, we identified a new *bak1* allele that impacts differentially the requirement of BAK1 in PTI and brassinosteroid signalling. We are using a combination of genetic, cell biology and biochemistry to unravel the molecular mechanisms underlying this puzzling phenotype. This study should reveal how BAK1 interacts with different signalling pathways in plants. Our quest to decipher PTI signalling is complemented by the search and characterisation of EFR-interacting proteins (EIPs) in yeast and *in planta*. We are also describing the feasibility of trans-family heterologous expression of PRRs to engineer broad-spectrum disease resistance in plants.

Genome-wide association study of 100+ phenotypes in a common set of *Arabidopsis thaliana* inbred lines

L13
Friday 09:00 - 09:30
Natural Variation

Magnus Nordborg

Gregor Mendel Institute
Dr Bohr-Gasse 3
030 Vienna
Austria

Arabidopsis thaliana is ideally suited for genome-wide association (GWA) studies in that it naturally occurs as inbred lines, which can be genotyped once and phenotyped repeatedly. We demonstrate the power of this approach by carrying out a GWA study of 107 different phenotypes in a common set of 96-192 inbred lines (the number of lines varies between phenotypes) genotyped for 250,000 SNPs using a custom Affymetrix chip. The results varied considerably between phenotypes. A minority yielded unambiguous results in the form of distinct, obviously significant associations, usually corresponding to single genes, and often to *a priori* candidates. The majority of phenotypes, however, yielded results that were harder to interpret because the combination of complex genetics and confounding by population structure made it difficult to distinguish true from false associations. *A priori* candidates are strongly overrepresented among these associations as well. Our results are dramatically different from the results of human GWA studies in that we identify a large number of loci with major effect size, and that we often explain a considerable fraction of the phenotypic variation. Our study clearly demonstrates the feasibility of GWA studies in *A. thaliana,* and suggests that the approach will be appropriate for many other organisms.

Natural variation in Arabidopsis vernalization response

L14

Friday 09:30 - 10:00
Natural Variation

Vincent Coustham1
Peijin Li1
Clare Lister1
Svante Holm2
Magnus Nordborg3
Caroline Dean1

1John Innes Centre
Norwich
Norfolk
UK

2University of
Mid-Sweden

3University of Southern
California
USA

Plants are excellent systems in which to dissect the molecular basis of adaptation. Variation in flowering time is a key factor in adaptation as flowering in favourable conditions is so important for reproductive success. We are analysing vernalization, the acceleration of flowering by prolonged cold, and its role in adaptation. In Arabidopsis vernalization involves the cold-induced repression and epigenetic silencing of the floral repressor *FLOWERING LOCUS C (FLC).* We are dissecting the mechanism of this cold-induced Polycomb-mediated epigenetic silencing and will present our current understanding of the three main phases of vernalization - the triggering of *FLC* transcriptional repression by prolonged cold; the nucleation and epigenetic stability of chromatin changes at *FLC*; and the spreading of the silencing signal. This mechanistic understanding is being linked with population and ecological genetic analysis in Arabidopsis accessions from different parts of the world. Our analysis so far suggests that molecular variation at *FLC* itself can contribute to variation in vernalization response. It appears that this variation has arisen independently in different accessions and we are now determining which phase of vernalization is affected for each accession and the responsible cis polymorphism. We are also analysing the distribution of the different alleles within Arabidopsis populations and monitoring individual populations at three ecologically distinct sites in Sweden in order to fully understand the evolution of this adaptive trait.

Predicting flowering time in changing climates

L15
Friday 10:00 - 10:30
Natural Variation

Johanna Schmitt1
Liana Burghardt1
Amity Wilczek1
Martha Cooper1
Stephen Welch2

In order to flower during favorable seasonal conditions, plants must integrate and respond appropriately to multiple environmental signals, such as day length, ambient temperature, and vernalization. However, little is known about the balance and sensitivity of different pathways to complex environmental cues under variable natural conditions in different climates and seasons, or how natural variation in flowering genes is expressed in natural environments. To measure the sensitivity of flowering time to perturbations in different signaling pathways in natural seasonal environments, we grew a set of 320 Arabidopsis ecotypes as well as mutants of key flowering time genes under natural conditions in replicated field experiments in 5 sites spanning the species' native European climatic range. Using detailed temperature and light environments experienced by plants throughout the growing season in each site, we have created a genetically informed photothermal model of development which accurately predicts time to bolting of flowering time mutants under field conditions, and shows that flowering time in the field depends critically upon seasonal timing of germination. In late summer and early autumn, germinating a week later can cause a transition from rapid cycling to winter annual life histories. The model predicts that the switch occurs earlier in the season for genotypes with high initial vernalization requirements. To predict responses to future climate change, we converted predicted air temperature from global climate models under a mid-range scenario of global warming into photothermal inputs to our model. The model predicts that in Norwich, England, this predicted warming scenario for 2099 will cause a seasonal delay in the switch between rapid cycling and winter annual life histories and reduced effects of natural genetic variation in the strength of the initial vernalization requirement.

1Brown University
Providence
RI
USA

2Kansas State University
Manhattan
KS
USA

Small GTPases in post-Golgi and endocytic membrane traffic in Arabidopsis

L16
Friday 11:00 - 11:30
Cell Biology

Ian Moore

University of Oxford
UK

The endomembrane organelles and their associated trafficking pathways synthesise some of the most biologically and commercially important structures in plants. Circumstantial evidence suggests that intracellular membrane trafficking pathways diversified independently in the plant kingdom but documented examples are rare. Rab GTPases are essential regulators of membrane identity and membrane targeting specificity in eukaryotic cells. Rab GTPase families have diversified independently in the animal and plant lineages. We show that in Arabidopsis root tips, the Rab-A2 and Rab-A3 subclasses define a novel post-Golgi membrane domain that communicates with the plasma membrane and early endosomal system and contributes substantially to the cell plate during cytokinesis. In contrast to the Rab-A2 and –A3 subclasses, Rab-A5 proteins define compartments with a distinct and apparently unique distribution at the periphery of root meristematic cells.

We have also employed a screen based on accumulation of secreted GFP to identify mutations that affect biosynthetic membrane traffic in Arabidopsis. Using this screen we identified mutants in the GBF-family Arf GEF GNOM-LIKE1 (GNL1). We show that GNL1 is a BFA-resistant GBF protein that functions together with a BFA-sensitive Arf GEF both at the Golgi and in endocytic trafficking of PIN2 but not of other plasma-membrane markers. The evolution of endocytic trafficking in plants was apparently accompanied by neofunctionalisation within the GBF family while in other kingdoms it occurred independently by elaboration of additional Arf GEF families. A TILLING screen of additional seedling-lethal secretory mutants suggests that several will identify components of the trafficking machinery that are not previously well characterised.

Cellular dynamics in plant immunity

L17
Friday 11:30 - 12:00
Cell Biology

Silke Robatzek
Nicolas Frei dit Frey
Yi-Ju Lu
Susanne Salomon
Thomas Spallek

Max-Planck-Institute for
Plant Breeding Research
Carl-von-Linne-Weg
1050829 Cologne
Germany

Plant defence in response to pathogen infection is tightly associated with reprogramming of vesicle trafficking pathways. These include exocytic/secretory routes for focal accumulation at pathogen penetration sites, and endocytic pathways. To better understand the contribution of endocytic trafficking in plant immunity we combine molecular and genetic approaches with cell biology. We monitor, for example, defence reactions of mutants in known endocytosis components upon pathogen infection. Previously, the FLS2 receptor responsible for perception of bacterial flagellin (flg22) was demonstrated to undergo induced internalization. In an attempt to identify molecular components of FLS2 endocytosis we isolated FLS2 interacting proteins. FIP1 localizes to the plasma membrane and like FLS2 accumulates into endosomes upon flg22 elicitation. The function of FIP1 function in plant development and immunity will be discussed. To additionally elucidate the role of endocytic vesicle traffic during plant defence we established a genetic screen for endocytosis mutants and applied high throughput quantitative confocal laser microscopy (QCLM), which will be described. We identified 12 *fel* mutants (*fel* = FYVE endosome levels) with elevated or reduced vesicle numbers. Interestingly, *fel4* not only displayed increased vesicle numbers but also enlarged vesicles, while *fel5* exhibits tissue-specific differences in endosomal numbers. Characterization of *fel* mutant phenotypes will be presented.

Auxin transport – connecting cell polarity and patterning

L18
Friday 12:00 - 12:30
Cell Biology

Auxin is a prominent intercellular signal in plants and acts as a versatile trigger of developmental change. Directional, active, cell-to-cell transport over short distances mediates differential auxin distributions within tissues (auxin gradients) that are required for various patterning processes, including apical-basal axis formation, organogenesis and tropisms. Various environmental and endogenous signals can be integrated into changes in auxin distribution through their effects on intercellular auxin transport. Differentially expressed auxin transporters of the PIN family, each with specific polar, subcellular localization form a network for directional auxin distribution and formation of these local gradients. The activity of PIN proteins can be regulated at the single cell level by changes in their vesicle trafficking-dependent polar targeting. PIN proteins undergo cycles of a clathrin-dependent endocytosis and ARF GEF-dependent recycling that serves to feed-back regulate throughput and directionality of intercellular auxin flow. Thus, the PIN-dependent auxin transport network, whose directional throughput is modulated by both endogenous and exogenous signals, provides one of the mechanisms underlying the plasticity and adaptability of plant development.

Jiri Friml

Department of Plant
Systems Biology
VIB
and Department of Plant
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Ghent University
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Belgium

Timing is everything: exploring links between the circadian clock and hormone signalling

L19
Friday 09:00 - 09:30
Signalling in Development

The circadian clock modulates many aspects of plant growth and development. Hormone signaling similarly plays an essential and dynamic role in these processes. Using genomic and physiological approaches, we have found interactions between the circadian clock and stress and hormone signaling pathways. Follow-up studies on links between clock and auxin signaling revealed that plant sensitivity to auxin varies with the time of day and led to the identification of a molecular node acting between the clock and auxin pathways. These studies suggest that many aspects of plant physiology not previously thought to be under circadian control may show time-of-day-specific sensitivity, with likely important consequences for plant growth and environmental responses.

Stacey Harmer1
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Growth regulation by GA-GID1-DELLA and beyond

L20

Friday 09:30 - 10:00
Signalling in Development

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The DELLA proteins (DELLAs) are a subfamily of the plant-specific GRAS family of putative transcriptional regulators that regulate plant growth in response to the phytohormone gibberellin (GA). The DELLAs restrain growth, and GA promotes growth by opposing DELLA function. Essentially, GA binds to a specific GA-receptor protein (GID1), thus stimulating a GID1-DELLA protein-protein interaction. This interaction itself promotes specific targeting of DELLAs for destruction in the proteasome via the SCF^{SLY1} E3 ubiquitin ligase. Additional signalling pathways, such as those associated with phytohormones other than GA, and environmental variables such as light, temperature and nutrient status, also influence plant growth via effects on the GA-GID1-DELLA growth-regulatory mechanism. A genetic approach to identifying novel growth-regulatory factors via mutagenesis of a DELLA-deficient mutant line will be outlined. The concept that the DELLAs are integrators of multiple plant growth regulatory signalling inputs will be explored, and the broader biological significance of DELLA function will be illustrated, with particular emphasis on the question of how the GA-GID1-DELLA growth-regulatory mechanism arose during land-plant evolution.

Regulation of shade avoidance by a network of bHLH class transcription factors

L21

Friday 10:00 - 10:30

Signalling in Development

Christian Fankhauser
Patricia Hornitschek
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Light is a source of energy for plants, but also an important source of information about the surrounding environment. Since plants are sessile organisms it is of major importance that they adapt growth to changing light conditions. One well-studied phenomenon is the shade avoidance response. In high vegetational density the red:far-red (R:FR) ratio decreases, because photoactive pigments of neighboring plants absorb R light, whereas FR light is mainly transmitted and reflected. In *Arabidopsis thaliana* this change of light quality is detected by R/FR photoreceptors known as phytochromes (phyA-phyE) and leads to the shade avoidance response. In order to reach direct sunlight several morphological and molecular changes take place. At the phenotypical level, shade avoidance is characterized by elongation growth of stems and petioles at the expense of leaf development. In addition plants have elevated leaf angles (hyponasty) and an increased apical dominance leading to reduced lateral branching. At the molecular level shade rapidly upregulates the expression of a number of transcription factors including *HFR1*, *ATHB2* and *PIL1*.

The Phytochrome-Interacting Factors PIF4 and PIF5 interact with the light activated photoreceptor and promote growth responses under vegetational shade. In direct sunlight they interact with phytochrome resulting in rapid degradation of those bHLH class transcription factors. In shaded conditions the phytochrome photoequilibrium shifts towards the inactive form of the photoreceptor, that does not interact with PIF4 and PIF5. PIF4 and PIF5 thus accumulate in low R:FR and lead to elongation growth responses. The related bHLH class transcription factor HFR1 (long Hypocotyl in FR 1) limits excessive shade-induced responses. We have studied the relationship between PIF4, PIF5 and HFR1 during shade avoidance at the molecular and physiological levels.

Development of shape in plants

L22
Friday 11:00 - 11:30
Systems Biology

Enrico Coen

The John Innes Centre
Norwich
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UK

Much progress has been made recently in our understanding of how genes control patterns of cell types or regional identities with in an organism during its development. However, the link between this process of patterning and growth or morphogenesis is much less well understood. Bridging this gap requires a quantitative understanding of how genes modify growth of multicellular tissues in 3D space at multiple scales. We have been addressing this problem using a combination of genetic, morphological, computational and imaging approaches in collaboration with Andrew Bangham (University of East Anglia) and Przemyslaw Prusinkiewicz (Calgary). The results provide new insights into how genes interact with patterns of growth at various scales to modify shape. The talk will illustrate how integrating biological and computational methods may lead to a quantitative mechanistic framework for development.

Systems analysis of the diurnal regulation of metabolism and growth

L23
Friday 11:30 - 12:00
Systems Biology

Mark Stitt

Max Planck Institute of
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Golm
Germany

Plants grow continuously changing conditions. Every day they alternate between photosynthesis in the light and respiration in the dark. Conditions also change from day to day, and on a seasonal basis. We want to understand how plants gauge their rate of growth to fluctuating resources. Our starting point is to ask how they balance their carbon budget over a 24 hour cycle. Some photosynthate is stored as starch in the light, and remobilised at night to support respiration and growth. This process is precisely regulated, such that starch just lasts till dawn. The rates of starch synthesis and breakdown and, by implication, the rate of carbon use for growth are adjusted to allow this balance to be maintained across a very wide range of photoperiods. This provides an excellent system to understand how plants gauge allocation and growth to the carbon supply. We have accumulated a large body of data about transcript levels, enzyme activities, polysome loading, metabolite levels and growth rates during the perturbations of the diurnal cycle in the reference Arabidopsis accession. These traits have also been analysed in a set of genotypically-diverse Arabidopsis accessions, which grow at different rates. I will discuss how we are using various sorts of models to integrate these large and multi-level datasets.

Unwinding the circadian clock with systems biology

L24
Friday 12:00 - 12:30
Systems Biology

Andrew J Millar1
Kieron D Edwards1
Ozgur E Akman1
John O'Neill1
Carl Troein1
Treenut Saithong1
Kevin Stratford2
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Systems biology approaches are helping us to understand the complexity of circadian clock mechanisms, as one of three pilot projects in CSBE. To develop mathematical models of the clock, we combine timeseries of molecular data and luciferase reporter imaging, with analysis of clock mutants, and computational parameter estimation. The models have predicted the properties of unidentified regulators in the clock and the photoperiod sensor.

Models are now refined by direct comparison to data, and tested for their robustness to parameter variations. This prioritises our experiments, including measuring biochemical parameter values (Finkenstadt *et al,* Bioinformatics 2008; O'Neill, unpublished).

Mathematical analysis helps us to understand the broad lessons from the models, and their detailed mechanisms. Single measures of global properties are useful to compare across species or mutants (flexibility dimension of Rand *et al*, Interface 2004, or the functional robustness of Kitano, Mol Syst Biol 2007). To unpick the biochemistry, we measure how one process, at one time, affects one specific output. I will illustrate: 1. how the flexibility of timing favours clocks with multiple feedback loops (Rand *et al,* J. Theor. Biol. 2006), 2. how complexity in both the clock and the light input pathways reconfigures the Arabidopsis clock under different photoperiods (Edwards, Akman and Troein, unpublished), and how this affects photoperiodism, 3. a new and simpler experimental organism that facilitates the testing of systems biology models, and that will be broadly applicable to plant systems biology at the cellular level.

ICSB edinburgh 2010

10 - 16 October 2010

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Concurrent Abstracts

Next-generation genetics: mapping and mutant identification in one step by deep sequencing

C01
Wednesday 14:00 - 14:15
Hot Topics

Identification of causative point mutations after forward genetic mutant screens typically begins with genetic mapping, followed by transformation rescue or candidate gene sequencing. We present a one step alternative: performing hundreds of thousands of genotyping assays while sequencing all candidate genes. This is accomplished by deep sequencing of a pool of F2 progeny obtained by crossing to a polymorphic strain and does not require prior knowledge of mapping markers. The application of high-throughput sequencing shortens the overall time required for genetic mapping from months to weeks and, importantly, greatly reduces investigator hands-on time. The steps requiring investigator input are: DNA isolation (1 day), library preparation and validation (4 days), Illumina cluster generation and sequencing (2 days), and data analysis (1 day). Once the mapping population has been established, the present method therefore allows a single investigator to identify a causative mutation within only eight working days – approximately an order of magnitude faster than with conventional methods.

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Trine Juul2
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Uniparental expression of PolIV-dependent siRNAs in the developing endosperm of *Arabidopsis*

C02

Wednesday 14:15 - 14:30
Hot Topics

Most eukaryotes produce small RNA (sRNA) mediators of gene silencing that bind to Argonaute proteins and guide them, by base pairing, to an RNA target. Micro(mi)RNAs that normally target mRNAs for degradation or translational arrest are the best understood class of sRNAs. However, in *Arabidopsis thaliana* flowers, miRNAs account for only 5% of the sRNA mass and less than 0.1% of the sequence complexity. The remaining sRNAs comprise a complex population of more than 100,000 different small interfering (si) RNA transcribed from thousands of loci. The biogenesis of most of the siRNAs in Arabidopsis are dependent on Polymerase IV (PolIV) – a homologue of DNA-dependent RNA polymerase II. A subset of these PolIV-dependent (p4)-siRNAs are involved in stress responses and others are associated with epigenetic modifications to DNA or chromatin but the biological role is not known for most of them. Here we demonstrate that the predominant phase of p4-siRNA accumulation is initiated in the maternal gametophyte and continues during seed development. Expression of p4-siRNAs in developing endosperm is specifically from maternal chromosomes. Our results provide the first evidence for a link between genomic imprinting and RNA silencing in plants.

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Roles for RNA editing factors in leaf development

C03

Wednesday 14:30 - 14:45
Hot Topics

Anne Bersoult
Anne-Laure Chateigner-Boutin
Kamel Hammani
Aaron Yap
Etienne Delannoy
Sabine Kahlau
Ian Small

ARC Centre of Excellence in Plant Energy Biology
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RNA editing alters transcripts to differ from the DNA sequence they were transcribed from, and thus breaks one of the central tenets of molecular biology - that protein sequences can be predicted from the genes that encode them. Over 600 cytidines in Arabidopsis organellar transcripts are specifically deaminated to uridine by a process that is not fully understood. In the last year, we have identified 14 pentatricopeptide repeat (PPR) proteins that specify editing of target nucleotides in chloroplast or mitochondrial mRNAs. A failure to edit a specific organellar RNA can give rise to phenotypes that are unobtainable by any other means, given the intractability of Arabidopsis organelle genomes to the usual genetic tools. The extent of editing of some sites varies from 0% - 100% depending on tissue-type, developmental stage or growth conditions, suggesting RNA editing may be a novel means of controlling gene expression. As just one example, the PPR protein *FLAVODENTATA (FLV)* is required for editing of *rpoC1*, encoding a subunit of the plastid RNA polymerase. A failure to edit *rpoC1* leads to delayed chloroplast biogenesis in leaf margins and characteristic alterations in leaf morphology and symmetry. The target site for *FLV* shows variable editing in wild-type plants, and the extent of editing can be manipulated by altering *FLV* expression. The results imply previously unsuspected routes by which nuclear and chloroplast gene expression are coordinated.

The circadian clock controls carbohydrate metabolism and hence growth rate in Arabidopsis plants at night

C04
Wednesday 14:45 -15:00
Hot Topics

Using the model plant Arabidopsis, we have revealed the mechanism by which the circadian clock optimises plant growth and productivity. We show that the circadian clock has a central and previously unreported function in controlling carbohydrate availability in leaves at night. Signals from the clock set the rate of starch mobilisation to available sugars, so that plants are depleted of starch precisely at the anticipated dawn. This timing is vital for the normal growth of the plant: if starch reserves are exhausted before dawn there is a massive transcriptional “starvation response” and growth stops.

By utilizing a combination of abnormal photoperiods, mutants defective in central elements of the circadian clock and mutants defective in conversion of starch to sugars we demonstrate unambiguously that 1) the rate of conversion of starch to sugars in leaves at night is set by the circadian clock and 2) failure to set the correct rate leads directly to reductions in plant growth rate.

Our results provide a new and unexpected perspective on the function of the plant circadian clock, and are relevant to circadian biology in general. They also have important implications for understanding plant productivity.

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Control of perennial flowering and perenniality in *Arabis alpina*

C05

Wednesday 15:00 - 15:15
Hot Topics

Renhou Wang1
Maria Albani1
Sara Farrona1
Coral Vincent1
Anika Joecker1
Heiko Schoof1
Franziska Turck1
Carlos Alonso-Blanco2
George Coupland1

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Annual plants complete their life cycle in one year and initiate flowering only once, whereas perennials live for many years and flower repeatedly. Perenniality of higher perennial plants is closely related to their specific flowering behaviours. Although the molecular mechanism of flowering-time control has been extensively studied in annual *Arabidopsis thaliana*, little is known in perennials. We have developed a perennial model *Arabis alpina*, which is a relative of *A. thaliana,* to study perennial specific flowering time control and perenniality related issues including seasonal flowering, juvenility and polycarpy. We identified the *A. alpina* mutant *perpetual flowering 1 (pep1)*, and found that *PEP1* contributes to seasonal flowering by restricting flowering to spring and adds to polycarpic growth habit by preventing flowering in some branches. The *pep1* mutation is in the orthologue of the Arabidopsis *FLC* gene. In contrast to the stable epigenetic silencing of *FLC* caused by vernalisation, *PEP1* is only transiently repressed by low temperatures, causing repeated seasonal cycles of repression and activation of *PEP1* transcription that allow it to carry out functions characteristic of the cyclical life history of perennials. The patterns of chromatin modifications at *FLC* and *PEP1* differ correlating with their distinct expression patterns. Thus we describe a critical mechanism by which flowering regulation differs between related perennial and annual species, and propose that differences in chromatin regulation contribute to this variation.

Local-scale population structure and out-crossing in *Arabidopsis thaliana*

C06

Wednesday 15:15 - 15:30
Hot Topics

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Arabidopsis thaliana is increasingly employed to investigate questions in evolution and ecology. It is thus critical to understand population structure and dynamics of wild populations at a scale relevant to individuals. We collected seeds from >1000 individuals in 78 populations within 25 km of Tuebingen, Germany. We genotyped all plants at 436 single nucleotide polymorphism (SNP) markers distributed across all chromosomes. We found pronounced variation among sites in genetic diversity and heterozygosity. About 70% of sites contain at least two distinct genotypes. Sites were strongly isolated and genetic identities of individuals spaced more than a few dozen meters apart were very rare. Distinct genotypes within populations tended to be more closely related than those from different populations. Pairwise genetic distance comparisons among genotypes in neighboring populations were often lower than comparisons among more distant populations and nonparametric clustering often groups individuals from nearby populations together. Some populations had surprisingly high estimated outcrossing rates – up to 20% - while others were completely homozygous with no evidence of past or ongoing outcrossing. We observed striking differences between sites in rural and urban settings. Rural sites have more distinct genotypes, higher genetic diversity, higher heterozygosity, and evidence of past recombination. The picture emerging from our work, together with other studies, is that *A. thaliana* exists in the wild in isolated populations that differ greatly in structure, stability and natural history. Outcrossing is sufficiently high in some populations to maintain overall genetic variation and generate novel haplotypes with a regional stamp. These patterns have implications for sampling for natural variation and ecological adaptation studies.

FHY3 and FAR1 mediate red light input to the Arabidopsis circadian clock

C07

Wednesday 14:00 - 14:25
Environmental Responses

Paul Devlin
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Royal Holloway
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London

The circadian clock is tightly tied to the light environment. Transcriptional feedback loops are able to generate a self-sustaining rhythm of approximately 24 hours, which impinges on almost every aspect of physiology in higher organisms. However, light signals are essential to maintain an exact 24 hour rhythm.

In Arabidopsis an endogenous circadian rhythm is generated by a set of interlocked transcriptional feedback loops. Light directly affects the level of a number of the clock components in plants. The photoreceptors involved have been well characterised but the way in which they affect clock components is only beginning to be understood.

The transcription factors, FHY3 and FAR1, play a key role in red light input to the clock. We have shown that FHY3 and FAR1 positively regulate transcription of key clock components in red light. As a result, *fhy3* and *far1* mutant seedlings specifically display aberrant circadian rhythmicity under these conditions. Moreover, this specific action of FHY3 and FAR1 has revealed novel interactions between the various clock loops and has given us new insights into the mechanism by which light can fine-tune the clock throughout the cycle of day and night.

Identification of CO_2-binding proteins that function as upstream mediators of CO_2-induced stomatal movements

C08

Wednesday 14:25 - 14:50
Environmental Responses

Guard cells form stomatal pores in the plant epidermis that allow CO_2 influx for photosynthesis and transpirational water loss from plants. The continuing rise in atmospheric CO_2 causes closing of stomatal pores in leaves and thus globally regulates CO_2 influx into plants, leaf heat stress, and plant water use efficiency. However, the CO_2 binding proteins and mechanisms that control this CO_2 response remain unknown. Moreover, the cell type that responds to CO_2 - mesophyll cells or guard cells - and whether photosynthesis mediates this CO_2 response remain matters of debate, with a need for genetic investigation. New findings will be presented showing that Arabidopsis mutant plants in leaf-expressed CO_2 binding proteins (CO_2 Responsive Protein: CORP) display strongly impaired CO_2 -regulation of gas exchange and CO_2 -regulated stomatal movements, but retain functional abscisic acid and blue light responses. Data will be presented demonstrating whether CORP-mediated stomatal CO_2 signaling is directly linked to photosynthesis and which leaf cell type mediates this response. Interestingly, tissue-specific targeted over-expression of CORP in wild-type plants greatly enhances water use efficiency. These findings, together with epistasis and biochemical CO_2 response analyses demonstrate that CORP functions early in the stomatal CO_2 signaling pathway and initiates CO_2 control of gas exchange between plants and the atmosphere.

Julian Schroeder
Honghong Hu
Aurélien Boisson-Dernier
Maria Israelsson-Nordström
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Membranes, temperature and the plant clock

C09

Wednesday 14:50 - 15:05
Environmental responses

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Circadian clocks are an important adaptation to life on a rotating planet and are found in all eukaryotes. The cycle of day and night is the major signal used by a clock to synchronise with its environment. Temperature cycles can entrain the Arabidopsis clock in constant light or dark, hence the circadian system also integrates information from daily changes in temperature. However, no temperature receptor is known in higher plants. Preliminary experiments have revealed that the viscosity of wild type Arabidopsis plant cell membranes alters across the day and this response is changed in plants with mutations in fatty acid biosynthesis pathways *(fatty acid desaturase (fad)* mutants). We have examined the circadian phenotypes of a range of *fad* mutants and found a subset have temperature-sensitive circadian phenotypes and changes in temperature compensation. Hypocotyl growth and flowering time are affected in the same mutants, suggesting that *fad* mutations cause pleiotropic effects in a range of light and clock pathways. This is suggestive that the membranes are involved in temperature sensing. Given the apparent requirement for normal lipid synthesis for temperature compensation of a fungal clock, this work will allow a comparative view of ‘thermometer’ function in circadian clocks.

Towards a spatiotemporal understanding of the salt stress response

C10

Wednesday 15:05 - 15:20
Environmental Responses

Jose Dinneny1
Xie Fei1
Penny Chan2

Plants are intimately associated with their environment and have developed complex mechanisms to perceive, respond and adapt to fluctuations that may arise. Recently, several studies have revealed the important contribution that cell identity has in guiding the response to salt stress and other environmental stimuli. While this work has revealed the vast complexity of the transcriptional response, very little is known regarding the molecular mechanisms that control these changes and how the initial responses assayed ultimately lead to stable changes in the plant that enable adaptation. To shed light on these areas, we are utilizing mutants defective in cell-type specification to determine what role each cell layer plays in affecting salt response. Using the genetic pathway controlling ground tissue development, we have been able to show that SHORTROOT, a GRAS-family transcription factor, is necessary for responses to salt in the cortex and epidermal cell layers. Furthermore, our preliminary data indicate that SHR regulates the expression of ethylene biosynthetic genes in internal tissue layers of the root, which may account for the non-cell-autonomous role of SHR in the salt stress response. We have also expanded our studies to examine the temporal regulation of salt response. Based on previous microarray analysis, we have found that salt stress is characterized by waves of transcriptional activity. We have used this temporal dynamism to identify “marker genes” whose expression is associated with particular phases of the salt response. We are analyzing the temporal expression of these markers under various salt treatments to understand how the time course is modified. These studies are accompanied by live-imaging analysis of roots to determine how the changes in the transcriptional program correlate with the observed phenotypic changes. Our results indicate that the concentration of salt has an important role in determining the timing of transcriptional events.

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Novel RNA- and chromatin remodeling-mediated regulatory mechanisms in plant abiotic stress responses

C11
Wednesday 15:20 - 15:35
Environmental Responses

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Masanori Okamoto1
Taiko Kim To1
Eiji Nambara2
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Plants respond and adapt to drought, cold and high-salinity stresses. Many stress-regulated genes have been identified by the expression profiling studies. However, we think that novel non-coding RNAs and chromatin remodeling mechanisms have additional functions in the regulation of plant stress responses.

We applied Arabidopsis tiling arrays to study the whole transcriptome under drought, cold, high-salinity stress and ABA treatment conditions[1] and showed that 7,719 non-AGI transcription units (TUs) exist in the intergenic regions. These include 1,275 TUs that are induced by the treatments. Most of the non-AGI TUs are hypothetical non-coding RNAs. About 80 percent of the non-AGI TUs belong to pairs of the fully-overlapping sense-antisense transcripts (fSATs). High-correlation between the expression ratios (treated/untreated) of the sense TUs and the ratios of the antisense TUs was observed in the SATs of AGI code/non-AGI TU. We found that the expression of sense TUs is necessary for the stress- or ABA-inducible expression of the antisense TUs in the fSATs (AGI/non-AGI).

We determined the temporal and spatial changes in levels of lysine modifications in histone H3 N-tail on the drought stress-inducible genes under drought stress by ChIP analysis.[2] Enrichments of H3K4me3 and H3K9ac correlate with gene activation in response to drought stress in all genes studied. Interestingly, establishment of H3K4me3 occurs after accumulation of RNAPII on the coding regions of *RD29A* and *RAP2.4*. Enrichment of H3K23ac and H3K27ac occurs under drought stress on the coding regions of RD29B, *RD20* and *RAP2.4*, but not on the coding region of *RD29A*. These results indicate that histone modifications are altered with gene activation on the drought-responsive genes under drought stress.

1 Matsui *et al* (2008) PCP 49:1135.
2 Kim *et al* (2008) PCP 49:1580.

Sequencing across the genome-phenome divide

C12
Wednesday 16:00 - 16:30
Tools and Resources

Joseph Ecker

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The development of DNA sequencing technologies producing vast amounts of sequence information has triggered a paradigm shift in biology, enabling massively parallel surveying of complex nucleic acid populations. The diversity of applications to which these technologies have already been applied demonstrates the immense range of cellular processes and properties that can now be studied at the single-base resolution. As part of the Arabidopsis 1001 genomes project (http://1001genome.org project), we have carried out both resequencing and de novo sequencing and assembly of several accessions. In parallel, we developed RNA-Seq and MethylC-Seq methods which now allow sequence-level maps of the transcriptome and cytosine DNA methylome, respectively. When combined with the genome sequences, an in depth view of the relationship between genetic and epigenetic variation and their effects on gene expression can be obtained. In addition, we have applied now-generation DNA sequencing approaches to identify the sites of insertion of T-DNA in large populations of arrayed plants. This approach should enable completion of the Arabidopsis Unimutant Project, which aims to identify sequence-indexed homozygous insertion mutations for all genes in the Col-0 genome (see http://signal.salk.edu). Finally, a major deficiency in the repertoire of plant genomic resources is the paucity of large-scale protein-protein and protein-DNA information for Arabidopsis or any plant system. Genome-wide molecular interaction maps (interactomes) are an indispensible tool for systems biology, aid focused biological studies, provide network information for topological analysis and aid the development of large-scale dynamic models. We have created a first generation plant interactome map in a collaboration led by the Center for Cancer Systems Biology. Utilizing both high throughput, high-quality yeast-2-hybrid and improved protein array technologies, a 9k by 9k binary interaction map has been developed using a recombination-vector based ORFeome collection of sequence-validated Arabidopsis open reading frame (ORF) clones. Properties of this first generation plant protein-protein interactome map, examples of its utility and examples of novel biological insights derived from it will be described.

Sidestepping genetic redundancy with small molecules

C13

Wednesday 16:30 - 17:00
Tools and Resources

Genetic redundancy is pervasive in plants and can limit the ability of forward genetic analysis to identify factors in a pathway. Small molecules can combat this genetic redundancy, because their variable selectivity can illuminate functions for otherwise redundant gene products. For example, an antagonist with low selectivity can perturb the function of an entire protein family, while a selective agonist can illuminate the function of one member of normally redundant receptors, as we describe with our work on the selective ABA agonist pyrabactin. Pyrbactin acts through *PYRABACTIN RESISTANCE 1 (Pyr1)*, the founding member of a family of START proteins called PYR/PYLs, which are necessary for both pyrabactin and ABA signaling *in vivo*. Our data show that ABA binds to PYR1, which in turn binds to and inhibits PP2Cs. We conclude that PYR/PYLs are ABA receptors that function at the apex of a negative regulatory pathway that controls ABA signaling by inhibiting PP2Cs. When assayed for ABA sensitivity, Pyr/Pyl genes show redundancy, which we suggest prevented these genes from emerging in ABA screens conducted over the last 20 years. Pyrabactin's selectivity for a subset of the PYR/PYL family enabled us to bypass this redundancy, which masks ABA phenotypes in single mutants. Thus, our results demonstrate the power of synthetic molecules to expose phenotypes for otherwise redundant genes.

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EZ-Rhizo: New software for fast and accurate measurement of root system architecture

C14
Wednesday 17:00 -17:15
Tools and Resources

Patrick Armengaud1
Kevin Zambaux1
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Root system architecture (RSA) is a quantitative and dynamic output of the signalling pathways that enable plants to sense and respond to changes in nutrient supply. Considering that RSA is a complex trait composed of many parameters that are interconnected through growth, development and information flow it is very likely that many of its genetic determinants remain uncovered unless we measure RSA comprehensively.

To allow fast and comprehensive measurement of RSA we have developed the new software tool EZ-Rhizo.[1] EZ-Rhizo detects roots from scanned images (e.g. of *Arabidopsis thaliana* plants grown on vertical agar plates), and automatically measures a set of primary and derived RSA parameters including path length, vector length, straightness and angle of main and each lateral root as well as number, position and density of (higher order) lateral roots. EZ-Rhizo deposits all measured data into a database, which can subsequently be queried by the user for individual parameters and/or metadata (e.g. genotype, growth conditions, time point). We have already demonstrated the usefulness of EZ-Rhizo for quantifying natural variation of RSA among *A. thaliana* ecotypes and for extracting spatial and kinetic information on root growth.[1] A free download of EZ-Rhizo is available to the scientific community from our web page.[2] For demonstration and training visit our computer station in the poster hall!

1 Armengaud, P. *et al* (2009) EZ-Rhizo: integrated software for the fast and accurate measurement of root system architecture. Plant Journal 57, 5, 945-956
2 http://www.psrg.org.uk/

One genome is not enough: Genome-species genome variation in *Arabidopsis thaliana*

C15

Wednesday 17:15 -17:30
Tools and Resources

Genome-wide sequence variation among populations reveals the history of evolutionary processes and ecological forces that molded species. In the “post-genomic” era, sequencing multiple natural strains from diverse populations has becoming increasingly desirable in a broad areas such as evolutionary, ecological and systems biology. As part of the 1001 genome project (http://1001genomes.org), which aims to sequence at least 1001 strains of *Arabidopsis thaliana,* we have completed a first pilot project, with 80 natural strains from across Eurasia. Each strain was sequenced to 5- to 12-fold genome coverage using Illumina’s sequencing-by-synthesis (SBS) technology. A comprehensive inventory of sequence variation including single-nucleotide polymorphisms (SNPs), small insertions/deletions (INDELs) and structural variation were generated. The effects, patterns and distribution of sequence variation have been analyzed and their population genetic implications will be discussed.

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Evidence of neutral transcriptome evolution in plants

C16

Wednesday 17:30 - 17:45
Tools and Resources

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An organism's transcriptome is its set of gene transcripts (mRNAs) at a defined spatial and temporal location. Since gene expression is affected markedly by environmental and developmental perturbations, transcriptome divergence among taxa will evolve through adaptive phenotypic selection. Here we show that stochastic, evolutionarily neutral processes also drive transcriptome divergence in plants. Among 14 Brassicaceae (cabbage family) taxa, transcriptome divergence correlates positively with evolutionary distance between taxa and with gene expression diversity within replicate samples. Remarkably, the transcriptomes of functionally homologous tissues sampled from different taxa have diverged more than the transcriptomes of functionally discrete – and highly specialised – tissues from one taxa. These observations are consistent with neutral evolutionary theories. Analysis at the individual gene level has been performed using the 'analysis of trait' module of the Phylocom software package, which is designed for the analysis of community phylogenetic structure and character evolution. This has identified genes whose expression level is under phylogenetic constraint and 'Phylogenetic independent contrasts' have been used in parallel to calculate evolutionary correlations of gene expression across the Brassicaceae. Correlation analyses can then be used to infer gene interaction networks that are evolutionary conserved. Web based tools will be developed to enable users to identify genes that are evolutionary correlated with their gene of interest.

Broadley *et al* 2008, New Phytologist: 180, 587-593

Wide screening of phage-displayed protein libraries to draw plant-pathogen interaction maps

C17

Wednesday 17:45 - 18:00
Tools and Resources

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The interactions between plants and microorganisms in nature are complex and diverse. In Arabidopsis, the availability of post-genomic tools makes possible novel approaches to discover the molecular players involved in this diversity. We have used a phage-display strategy to express Arabidopsis proteome during microbial infection and to select for proteins able to bind microbial components. To rapidly identify microbe-bound proteins in different plant pathosystems, we developed a monitoring method using microarrays. This combined strategy allowed for a genome-wide screening of plant genes involved in microbial recognition.

Three phage-displayed libraries were constructed upon Arabidopsis infection with *Pseudomonas aeruginosa* PA14, the virulent isolate DC3000 from *P. syringae Pto* and an *Avr* isolate. These pathosystems represent different degrees in the specificity of the plant-microbia interactions, which presumably involves a large number of plant proteins. The libraries contain up to 2x10E7 plant transcripts that are expressed as functional proteins fused to the capsid of T7-bacteriophage. These proteins and their corresponding genes have been rescued by the ability of phagemic particles to bind living Pseudomonas cells, in a so-called “biopanning” selection. Bound and unbound proteins have been monitored along biopanning rounds by hybridisation of biopanned phage DNAs with microarrays. This has lead to a set of 205 proteins that are potential targets for microbe binding. The set includes BAK1 and FRK1, two previously known receptors of bacterial effectors, the plant defensin PDF1.2 and several NBS-LRR proteins, which are predicted to be involved in pathogenesis. The set also contains 28 unknown proteins, which have been first related to pathogenesis in this work. Our results show the potential of this phage-display-based strategy for wide exploration of plant-microbia interactions and provide a new tool for post-genomic research in plants.

Signalling modules controlling the stem cell niche in Arabidopsis

C18

Wednesday 16:00 - 16:30
Development

Stem cell fate in shoot and root meristems is controlled by the interaction with the stem cell niche. Several genes (encoding transcription factors or signalling molecules) have been identified in recent years that are essential to promote or restrict stem cell fate. I will discuss some of the mechanisms regulating stem cell fate, and present recent data addressing commonalities and differences between root and shoot meristems.

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PHYTOCALPAIN as a key regulator of growth in plants

C19

Wednesday 16:30 - 17:00
Development

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Co-ordination of cell division and expansion between different cell types (such as epidermis and mesophyll) is critical for the efficient functioning of plant organs, and is likely to be effected by multiple interlinked mechanisms allowing adaptation to both exogenous and endogenous cues. Here we show that DEK1 (also known as PHYTOCALPAIN), a unique plant-specific protein, plays a fundamental role in regulating both cell division and cell expansion in Arabidopsis organs. DEK1 contains a domain showing high homology to animal cysteine proteases of the calpain family. Unlike animal calpains, DEK1 has a highly extended N-terminal region containing numerous predicted trans-membrane spans. In plant tissue, the DEK1 calpain domain is released from the full-length protein by autocatalytic processing. Expression of the active calpain domain alone is sufficient for full complementation of the early embryo lethality caused by loss of DEK1 function. Thus, as reported in some animal systems, cleaved calpain may represent the activated form of the protein. Although decreased accumulation leads to severe epidermal abnormalities, phenotypes generated by over-expression of the active calpain domain show that DEK1 it does not directly regulate epidermal cell fate. Instead we hypothesise that aspects of growth-co-ordination which are critical for maintenance of epidermal integrity during development are compromised by loss of DEK1 activity. Ongoing research into understanding the mechanisms underlying DEK1–mediated growth control will be discussed.

Asymmetry, pattern and renewal in Arabidopsis stomatal development

C20
Wednesday 17:00 - 17:15
Development

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Stomata are epidermal pores found on the surfaces of the aerial portions of most land plants that function to regulate gas exchange between the plant and the atmosphere. We use the development of stomata as a model for the generation of cell fates and pattern during development. Stomatal guard cells are created via a stereotyped set of asymmetric cell divisions whose number and orientation are dictated by local cell-cell interactions and longer range signals from the environment. We are interested in the nature of the positive and negative inputs into this system and how they are integrated; to this end we have focused on three major elements: (1) a set of related bHLH transcription factors that regulate the cell divisions associated with establishing, maintaining and terminating the stomatal lineage, (2) a negative regulatory circuit previously defined by receptor-like proteins and a Mitogen Activated Protein Kinase (MAPK) cascade, and (3) novel proteins that carry out the asymmetric division process. We have established direct regulatory relationships between the MAPK kinases and one of the bHLHs and will discuss how stomatal development provides a test system for deciphering complex regulatory networks. We will also introduce the novel and asymmetrically localized protein BASL and a model for its activity in differentiation and self-renewing cell divisions.

Tissue patterning and growth coordinated by a mobile microRNA and SHORT ROOT in the root

C21
Wednesday 17:15 - 17:30
Development

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One main interest in developmental biology is to understand the positional information for tissue patterning in developing organs. In plants, regulation of tissue patterning has to be coordinated with cell division to assist post embryonic growth.

Here, we present a novel crosstalk mechanism mediated by SHORT ROOT (SHR) that regulates root tissue patterning and growth. SHR proteins, produced in the xylem and procambium of Arabidopsis roots, move to the rest of vascular cylinder cells, endodermis, and QC. In the endodermis and QC, SHR directly activates *SCARECROW (SCR)* and together forms a complex. SHR/SCR complex regulates not only the development of ground tissues and QC but also the cell proliferation and patterning in the vascular cylinder. In the *shr* or *scr* mutants, fewer cell files form in the vascular cylinder and ectopic metaxylem develops in the place of the protoxylem. We found that SHR/SCR regulate these by directly activating a subset of *miR165/166* genes in the endodermis. *MiR165/166* produced in the endodermis moves into the vascular cylinder and restricts mRNA domains of *PHABULOSA (PHB)* and other class III HD-ZIP transcription factors to the center of the vascular cylinder. In *shr phb* double mutant, the protoxylem and cell proliferation were recovered in the vascular cylinder. Furthermore, the root apical growth was also largely recovered without the recovery of QC, suggesting the contribution of PHB mediated cell proliferation in the vascular cylinder for apical root growth.

This novel crosstalk mechanism provides new insight into the patterning and growth of developing organs.

Leaf size is regulated by a cell-autonomous system linking cell proliferation and post-mitotic cell enlargement

C22
Wednesday 17:30 - 17:45
Development

Kensuke Kawade1
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During leaf development, a defect in cell proliferation often triggers enhanced post-mitotic cell enlargement. This phenomenon is termed compensation. For example, a *Kip-related protein2* overexpressor (*KRP2* o/x) and an *angustifolia3* (*an3*) mutant show atypical compensation. In leaf primordia, differentiating cells and proliferating cells are found in the apical and basal regions, respectively. Until now, how, where and when cells in leaf primordia recognize the defect of cell proliferation remained to be elucidated. In particular, whether compensation is induced non-cell-autonomously or not is totally unknown. To solve these questions, we designed an experimental system, which can make mosaic leaves expressing *KRP2* or *AN3* by CRE/Lox.

First, we assessed the functionality of our system. When *KRP2* overexpression was shut off within the whole very young leaf primordium, compensation was restored, suggesting that the system was functional. We next examined whether *KRP2* directly regulates enhanced cell enlargement. When *KRP2* overexpression was induced in the postmitotic cells, cell enlargement was not enhanced, supporting the idea that enhanced cell enlargement was not a direct function of *KRP2* but caused by a defect in cell proliferation. As for cell autonomy, we analyzed cell size in mosaics. We found that *KRP2* mosaics contained two distinct cell-size classes that were equivalent to wild-type and *KRP2* o/x in size, respectively. This fact indicated that compensation in *KRP2* o/x is induced cell-autonomously. Indeed, in the boundary of mosaics, size of genotypically wild-type and *KRP2* o/x cells are not affected by the other genotype. Our results suggested that the activity of cell proliferation is memorized in each cell at least in the case of *KRP2* o/x. We will discuss the system behind the compensation based on these results and data from *AN3* mosaics now being characterized.

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Repression of apical HD-ZIP III homeobox genes is required for Arabidopsis embryonic root development

C23
Wednesday 17:45 - 18:00
Development

Development of seed plant embryos is polarized along the apical-basal axis. This polarization occurs in the absence of cell migration and culminates in the establishment of two distinct pluripotent cell populations; the shoot and root apical meristems (SAM, RAM), which post embryonically give rise to the entire shoot and root systems of the plant. The acquisition of genetic pathways that delimit root from shoot during embryogenesis must have played a pivotal role during land plant evolution because roots were likely derived from shoots of ancestral vascular plants. However, such pathways are very poorly understood. Here we show that RAM establishment in the model plant *Arabidopsis thaliana* requires restriction of the Class III HOMEODOMAIN-LEUCINE ZIPPER (HD-ZIP III) proteins PHABULOSA (PHB) and PHAVOLUTA (PHV), which direct both SAM development and shoot lateral organ polarity. Failure to restrict PHB and PHV expression via a microRNA (miRNA)-dependent pathway prevents correct elaboration of the root development programme. As such, repression of a fundamental shoot development process is essential for correct root development.

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Using pathogen effectors to understand host resistance mechanisms

C24

Wednesday 14:00 - 14:30
Plant Defence

Plant pathogens use small molecules and also proteins to render their hosts susceptible. Many bacteria and other pathogens use a specialized secretion system to deliver proteins into host cells that interfere with host defence. We have taken advantage of the bacterial type III secretion system (T3SS) to investigate effectors from filamentous pathogens such as oomycetes. We are using T3SS delivery of oomycete effectors from *Pseudomonas* sp to investigate the effector complement of the downy mildew pathogen *Hyaloperonospora parasitica (Hpa)*. I will report recent data on *Hpa* effector functions and on the use of the Solexa/Illumina sequencing instrument to advance our understanding of *Hpa* pathogenicity. We are using Illumina paired read sequencing and Velvet software (Zerbino and Birney, Genome Research, 2008) to assemble sequences of multiple races of another oomycete pathogen, *Albugo candida*, which is particularly effective at shutting down host defence. The analysis of its effectors is likely to provide very interesting new insights into host defence mechanisms. In addition, we are using T3SS delivery of oomycete effectors to investigate the molecular basis of pathogen/host specificity and non-host resistance. An update on recent progress will be presented.

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Pathogen effectors and host responses

C25

Thursday 14:30 - 15:00
Plant Defence

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To enable a pathogenic lifestyle many organisms produce a repertoire of proteins that enable them to colonize host tissue. These proteins, effectors, are likely to be targeted to suppressing host immune mechanisms and redirecting nutritional resources to benefit the pathogen. We are studying the interaction between the downy mildew pathogen *Hyaloperonospora arabidopsidis* and Arabidopsis. We have just completed the sequencing of the *H. arabidopsidis* genome and it reveals a gene content that suggests that it has been adapted to a biotophic lifestyle. It has a very large effector content that suggests complex mechanisms of interaction between host and pathogen. We are analyzing the role of individual effector proteins in interacting with the host plant immune system. Finally, we are analyzing the role nature of the host plant response to biotic and abiotic stress using systems biology approaches.

Endocytic trafficking: New players in FLS2/ flagellin signaling

C26

Thursday 15:00 - 15:15
Plant Defence

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Cell surface receptor kinases serve as sensors for internal and external stimuli that trigger signaling cascades and are evidently important for developmental regulation and self from non-self discrimination. Active defenses are initiated upon receptor-mediated perception of so-called pathogen-associated molecular patterns (PAMPs). One of the best-studied PAMPs is bacterial flagellin (flg22), which is recognized by the receptor kinase Flagellin Sensing 2 (FLS2). Upon flg22 sensing, FLS2 elicits an array of defense responses, which enhance plant immunity to prevent bacterial infection and proliferation. Concomitantly, activated FLS2 translocates to an endosomal pool reminiscent of receptor-mediated endocytosis. Although both, PAMP perception and receptor trafficking became a focus of research in the past years, there is largely nothing known about downstream molecules of receptor signaling and regulatory components of receptor endocytosis.

To identify such components we searched for FLS2 Interacting Proteins (FIPs) by yeast split-ubiquitin screening. *FIP1* is a member of a gene family encoding transmembrane proteins, which potentially regulate cellular Ca^{2+} levels. Using chemical interference we showed that flg22-triggered FLS2 endocytosis requires changes in the Ca^{2+} distribution. FIP1-GFP was clearly localized to the plasma membrane and notably, was internalized into endosomes upon flg22 treatment. We will further discuss *in planta* interaction and co-localization of FLS2 and FIP1. Moreover, mutant plants devoid of *FIP1* and its close homologue *FIP1-like* are impaired in flg22-triggered responses, which was confirmed by chemical inhibition of FIP1 activity. This suggests that FIP1 is a critical component of FLS2 signaling. A detailed characterization of *fip1/fip1-like* phenotypes will be presented. Unlike *FIP1, FIP2* appeared to mostly localize to the cytoplasm. It codes for a soluble kinase and currently, we are addressing the relevance of FIP2 in FLS2 signaling and endocytosis.

Post-translational modifications of the transcription co-activator NPR1 regulate plant immunity

C27
Thursday 15:15 - 15:30
Plant Defence

Systemic acquired resistance (SAR) is a plant immune response effective against a broad-spectrum of pathogens. Activation of SAR is associated with dramatic transcription reprogramming of over 2,200 genes to prioritize defense responses over normal cellular functions. The transcription co-activator NPR1 directly or indirectly controls the expression of most of these genes. In the cytoplasm of resting cells, NPR1 forms an oligomer through redox-sensitive intermolecular disulfide bonds. Upon induction of SAR, changes in cellular redox result in the release of NPR1 monomers, which translocate to the nucleus and modulate gene transcription. To gain a better understanding of transcriptional regulation in SAR, we investigated pathogen-induced changes in the equilibrium between NPR1 oligomer/monomer conformations and studied the behavior of NPR1 in the nucleus. We found that distinct post-translational modifications of NPR1 control its activity. In the cytoplasm, S-nitrosylation of NPR1, a process in which nitric oxide is covalently attached to a cysteine thiol, promotes oligomer formation, while thioredoxins (TRX) facilitate the opposite oligomer-to-monomer reaction. Moreover, in the nucleus NPR1 activity is regulated by cycles of site-specific phosphorylation coupled to ubiquitin-mediated degradation by the proteasome. Degradation not only restricted the activity of NPR1 in the absence of pathogen threat, it surprisingly also played a critical role in promoting co-activator activity upon induction of SAR. The intimate interplay between different post-translational modifications and their dynamic effects on NPR1 activity will be fundamental to our discussion of regulatory mechanisms that govern plant immune responses.

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New classes of proteins forming complexes with resistance proteins

C28
Thursday 15:30 - 15:45
Plant Defence

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Resistance (R) proteins directly or indirectly recognize cognate pathogen effectors, thereby activating effector-triggered immunity (ETI). Two types of proteins have been reported to form complexes with the NB-LRR class of R proteins before R proteins are activated by the effectors: chaperone-type proteins such as RAR1 and SGT1; and protein targets (or decoys) of the effectors, such as RIN4. We used a biotin affinity-purification tag to purify R protein complexes (Qi and Katagiri, Plant J. 57, 932 (2009)) and identified new classes of candidate proteins forming complexes with the NB-LRR proteins RPS2 and/or RPM1 before R protein activation. One class consists of the hypersensitive response-induced reaction (HIR) proteins, which is characterized by the stomatin/prohibitin/flotillin/HflK/C (SPFH) domain motif. A close physical association between RPS2 and a HIR protein was confirmed by fluorescence resonance energy transfer (FRET) after transiently expressing RPS2::CFP and HIR::YFP in *N. benthamiana.* In addition, HIR proteins make homo- and hetero-HIR protein complexes. As HIR proteins are localized in lipid rafts in the plasma membrane, RPS2 may also be localized in lipid rafts prior to activation. We will report other classes of proteins in resistance protein complexes in addition to the HIR proteins.

Autophagic components contribute to hypersensitive cell death in Arabidopsis

C29

Thursday 15:45 - 16:00
Plant Defence

Recent studies implicate autophagy as a pro-survival mechanism in plants that restricts programmed cell death (PCD) associated with the pathogen-triggered hypersensitive response (HR). This model is based on the observation that HR lesions show unrestricted spreading in tobacco and Arabidopsis plants with RNAi-mediated reduction of autophagy gene expression. We examined HR PCD responses in autophagy-deficient Arabidopsis knockout mutants (*atg*), and report that infection-induced lesions are contained in *atg* mutants. HR PCD conditioned by one class of innate immune receptors through the defense regulator EDS1 is suppressed in *atg* mutants. Furthermore, we demonstrate that PCD triggered by immune receptors via NDR1 is either autophagy-independent or engages autophagic components with cathepsins and other unidentified cell death mediators. Thus, autophagic cell death contributes to HR PCD and can function in parallel with other pro-death pathways.

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Untangling transcriptional regulatory networks modulating hormone responses

C30

Thursday 14:00 - 14:30
Plant Growth Regulators

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The phytohormone ethylene plays critical roles in growth, defense and a myriad other plant processes by regulating the expression of large and diverse sets of genes through control of protein stabilization of the master transcriptional regulator EIN3. Using ChIP-Seq and RNA-Seq methods, we found that EIN3 is involved in a feedback loop that controls both positive and negative components in ethylene signaling. Several ethylene receptor genes are direct EIN3-binding targets, along with genes encoding CTR1 protein kinase and EBF1/EBF2, EIN3-binding F-box proteins, EER5, a proteasome-related signalosome subunit that is proposed to be involved resetting the ethylene-signaling pathway, as well as RAN1 a copper transporter involved in ethylene receptor function. We also identified a number of positive regulators in the ethylene signaling pathway components among the list of EIN3 direct target genes. Confirming that a massive transcriptional cascade is a critical aspect of the diverse responses mediated by ethylene output pathways, we identified many AP2/ERF and WRKY transcription factors as direct EIN3 binding targets; several of which are known to be involved in mediating responses to pathogens. In addition, we identified key points of hormone crosstalk of ethylene with other hormones. Direct EIN3 targets included several of the master regulatory transcription factors controlling growth regulation by other hormones, revealing new (and direct) connections among these signaling pathways. Additional EIN3 targets include enzymes for hormone biosynthesis or conjugation, further supporting the existence of connections among hormone pathways. Finally, we merged the EIN3-target information with global gene expression information and a large protein-protein interaction network (Braun *et al*. CCSB-Harvard/Salk, unpublished) to establish a first generation hormone interactome network map. As indicated by the multitude of connections between different nodes in the network, EIN3 targets encompass numerous hormone biosynthesis and signaling pathways which can now be further explored.

The brassinosteroid signal transduction pathway

C31

Thursday 14:30 - 15:00
Plant Growth Regulators

Molecular genetic studies in Arabidopsis have identified several brassinosteroid (BR) signaling components and provided an outline of the BR signal transduction pathway from the cell surface receptor to nuclear gene expression. When BR levels are low, the BIN2 kinase phosphorylates the BZR1 and BZR2 (also named BES1) transcription factors to inhibit their DNA binding and reduce their nuclear localization through the phosphopeptide-binding 14-3-3 proteins. BRs bind to the BRI1 receptor kinase at the cell surface and activate a signalling cascade that leads to dephosphorylation and activation of the BZR1 and BZR2 transcription factors, presumably by inhibiting the BIN2 kinase or activating the BSU1 phosphatase. How activation of BRI1 leads to inhibition of BIN2 or activation of BSU1 has remained a major gap in our understanding of the BR signalling pathway. This gap is now filled by proteomic and biochemical studies. Using quantitative proteomic studies we identified a class of BR signalling kinases (BSKs) as BRI1's substrates. Biochemical studies demonstrated that BRI1 phosphorylation of BSKs promotes BSKs' interaction with a downstream component that inactivates BIN2 by dephosphorylation. Our study has thus closed the last gaps in the BR signalling cascade from receptor kinases to transcription factors. Furthermore, we have performed chromatin immuno-precipitation-microarray (ChIP-chip) and identified about a thousand BZR1-target genes that are regulated by BR. These primary targets of BR signalling include key components of other signalling and developmental pathways as well as specific cellular structure and functions, providing a global map of steroid actions in Arabidopsis. As such, a complete BR signalling pathway from signal perception at cell surface to gene expression and cellular and developmental responses is emerging.

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Cytokinin signaling: Two-components and more

C32

Thursday 15:00 - 15:15
Plant Growth Regulators

Cytokinins have been implicated in a wide variety of plant growth and development processes and have been shown to interact with various other signals. Recent studies have demonstrated that cytokinin signal transduction occurs through a classic bacterial two-component signaling system, in which signal propagation relies on the transfer of phosphates between alternating histidine and aspartic acid residues. Genes encoding proteins corresponding to each of these two-component elements have been identified in Arabidopsis. Using molecular, genetic and biochemical approaches, the roles of the Arabidopsis two-component genes in plant growth and development have been defined. There is extensive functional redundancy in these gene families. Analysis of lines harboring multiple disruptions in multiple two-component genes has indicated that these elements play roles in various signaling pathways. The effect of these loss-of-function mutations on various aspects of growth and development and on the response to environmental interactions will be presented. We have also identified a number of transcription factors that are regulated by cytokinin using a variety of approaches. The analysis of the role of these transcription factors in cytokinin function will be discussed.

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A regulated auxin minimum is required for tissue patterning in Arabidopsis fruit

C33
Thursday 15:15 - 15:30
Plant Growth Regulators

Local hormone maxima are essential for the development of multicellular structures and organs. For example, steroid hormones accumulate in specific cell types of the animal foetus to induce sexual differentiation and concentration peaks of the plant hormone auxin direct organ initiation and mediate tissue patterning. Here we show the first example of a regulated local hormone minimum required during organogenesis. Our results demonstrate that formation of a local auxin minimum is necessary for specification of the valve margin separation layer where Arabidopsis fruit opening takes place. Consequently, ectopic production of auxin, specifically in valve margin cells, leads to a complete loss of proper cell fate determination. We demonstrate that the valve margin identity factor INDEHISCENT (IND) is responsible for forming the auxin minimum by altering the polarity of PIN auxin efflux carriers. IND re-localises PINs by directly regulating expression of the genes encoding the PINOID kinase and the close relative, WAG2, which have been shown to direct PIN polarity. We propose that the simplicity of formation and maintenance make local hormone minima particularly well-suited to specify a small number of cells such as the stripes at the valve margins. To our knowledge this is the first report of a regulated signalling minimum in plants or animals.

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Pedro Robles4
Carlos Galván-Ampudia5
Remko Offringa6
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Dynamic, auxin-responsive plasma membrane to nucleus movement of Arabidopsis BRX

C34
Thursday 15:30 - 15:45
Plant Growth Regulators

In Arabidopsis, interplay between nuclear auxin perception and trans-cellular polar auxin transport determines the transcriptional auxin response. In *brevis radix (brx)* mutants, this response is impaired, this is thought to be an indirect effect of disturbed crosstalk between the auxin and brassinosteroid pathways. Here we provide evidence that *BRX* protein is plasma membrane-associated, but transfers to the nucleus upon auxin treatment to modulate cellular growth. Application of the specific polar auxin transport inhibitor naphthalene phtalamic acid (NPA) results in increased *BRX* abundance at the plasma membrane. Thus, nuclear translocation of *BRX* could depend on cellular auxin concentration or on auxin flux. Supporting this idea, NPA treatment of wild type roots phenocopies the brx root meristem phenotype. Moreover, *BRX* is constitutively turned over by the proteasome pathway in the nucleus. However, a stabilized C-terminal *BRX* fragment significantly rescues the brx root growth phenotype and triggers a hypocotyl gain-of-function phenotype, similar to strong overexpressors of full length BRX. Therefore, while *BRX* activity is required in the nucleus, excess activity interferes with normal development. Finally, similar to PIN-FORMED (PIN) auxin efflux carrier, *BRX* is polarly localized in vascular cells and subject to endocytic recycling. Expression of *BRX* under control of the PIN1 promoter fully rescues the *brx* short root phenotype, suggesting that the two genes act in the same tissues. Collectively, our results suggest that *BRX* may provide a contextual read out to synchronize cellular growth with the auxin concentration gradient across the root tip.

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Julien Beuchat
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Divide et impera – cell division in the root and its control through ABA

C35

Thursday 15:45 - 16:00
Plant Growth Regulators

Daniela Dietrich1
Susana Ubeda-Tomas1
Rishikesh Bhalerao2
Malcolm Bennett1

Abscisic acid (ABA) is primarily known as a stress hormone that relays the plants responses to environmental signals such as drought, salt stress or cold. Increases in ABA concentration lead to inhibition of root growth but it is unclear what the underlying cellular and molecular mechanisms are. Detailed analysis of root growth and cell division markers revealed that ABA regulates growth of primary and lateral roots by influencing cell division rates. Further analysis of cell cycle component mutants provide the first evidence for a molecular mechanism connecting the ABA signal with the cell cycle machinery.

We are also interested where in the root the ABA signal is perceived and have used a transactivation approach to investigate whether any root tissue is particularly important for ABA signal perception. Results will be presented that show that it is indeed possible to render the whole root ABA insensitive by blocking ABA perception in one cell file. Cell division rates in the root apical meristem have to be orchestrated between cells of different identities, sizes and shapes and the wider implications of this finding on the control of cell division in the root will be discussed.

In summary, we show some of the mechanisms by which ABA integrates environmental responses into the root developmental growth program and thus shapes root growth.

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A level-set model of leaf form development

C36

Saturday 14:00 - 14:30
Systems Biology

Przemyslaw Prusinkiewicz1
Miltos Tsiantis2

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Alberta
Canada

2University of Oxford
UK

A key question in biology is to understand how organismal form is generated through the process of development. Here we focus on the development of leaves. To this end, we integrate developmental genetics and computational modeling to compare the mechanisms that shape the simple leaf of the model plant *Arabidopsis thaliana* and the compound subdivided leaf of its close relative *Cardamine hirsuta.* The models capture the feedback between the dynamic emergence of auxin convergence points on the leaf margin, and the development of leaf shape. Following the level-set methodology, this development is simulated as the propagation of leaf margin over time. The propagation rates are informed by the interplay between auxin and gene expression in the leaf margin. We test and validate these models by interrogating experimental data for *A. thaliana, C. hirsuta* and their mutants and transgenic variants.

Dynamic modeling of the signal transduction network corresponding to abscisic acid induced stomatal closure in *Arabidopsis thaliana*

C37
Saturday 14:30 - 15:00
Systems Biology

Reka Albert
Song Li
Assieh Saadatpour-Moghaddam
Zhongyao Sun
Biswa Acharya
Sarah Assmann

Pennsylvania State University
University Park
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USA

During drought, the plant hormone abscisic acid (ABA) inhibits stomatal opening and promotes stomatal closure, thereby promoting water conservation. This talk will present a discrete dynamic model of ABA-induced stomatal closure based on a reconstruction of the signal transduction network corresponding to this process. Our model captures the regulation of more than forty identified network components, and accords well with previous experimental results at both the pathway and whole cell physiological level. By simulating gene disruptions and pharmacological interventions we find that the network is robust against a significant fraction of possible perturbations. Our model predicts that the disruption of membrane depolarizability, anion efflux, actin cytoskeleton reorganization, cytosolic pH increase, the phosphatidic acid pathway or of K^+ efflux through slowly activating channels lead to the strongest reduction in ABA responsiveness. We experimentally tested and validated one of these predictions. We are currently extending the model by performing protein-protein interaction assays, by theoretical analysis of the dynamical behaviors allowed by the model, and by synthesizing the signal transduction network corresponding to light induced stomatal opening. Our model offers a roadmap for the identification of manipulations that have the best chance of conferring increased drought stress tolerance and for the prioritization of future experiments. Several steps of this work have now been formalized into software applications.

1 Li, S., Assmann, S. M. & Albert, R.2006. Predicting essential components of signal transduction networks: A dynamic model of guard cell abscisic acid signaling, PLoS Biology 4: e312.
2 Kachalo, S., Zhang, R., Sontag, E. D., Albert, R., DasGupta, B. 2008. NET-SYNTHESIS: A software for synthesis, inference and simplification of signal transduction networks. Bioinformatics 24:293-295.
3 Albert, I., Thakar, J., Li, S., Zhang, R. and Albert, R. 2008. Boolean network simulations for life scientists, Source Code for Biology and Medicine 3, 16.

Modelling cell division in the Arabidopsis leaf epidermis

C38
Saturday 15:00 - 15:15
Systems Biology

Sarah Robinson1
Pierre Barbier de Reuille2
Samantha Fox1
Grant Calder1
Andrew Bangham2
Przemyslaw Prusinkiewicz3
Enrico Coen1

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2University of East Anglia
UK

3CPSC
University of Calgary
AB
Canada

The Arabidopsis leaf epidermis is a tissue consisting of a single layer of cells of various sizes, shapes and functions, arranged in an intricate two-dimensional pattern. We aim at understanding this pattern with a combination of time-lapse imaging and computational modeling techniques.

We have developed the ability to image Arabidopsis seedlings continuously for up to seven days using time-lapse confocal microscopy. The resulting movies capture the dynamic nature of the leaf development. From these movies we extract the information about cell growth, timing of cell divisions and placement of division walls, which is used to produce an initial descriptive model. We then gradually replace direct data with hypothetical deterministic rules of cell division within a growing leaf epidermis, and verify the results by comparing the output to the data.

The model has already made it possible to test existing theories of how and when cells divide, and resulted in the falsification, in the case of Arabidopsis leaves, of several rules previously reported in the literature. We have verified rules that predict the position of dividing walls in non-differentiated cells. The model is currently being extended to include rules for the timing of cell division and the differentiation of stomata. The model thus provides a framework for understanding how complex patterns of epidermis cells develop and accommodate differentiated cells, and suggests that the observed complexity may by an emergent property of a small set of simple, possibly deterministic rules.

Timing of cell division determines the relative cell size pattern in Arabidopsis

C39

Saturday 15:15 - 15:30
Systems Biology

Adrienne Roeder1
Vijay Chickarmane1
Alexandre Cunha1
Boguslaw Obara2
Tigran Bacarian3
Aida Sun1
B S Manjunath2
Eric Mjolsness3
Elliot Meyerowitz1

1California Institute of Technology

2University of California Santa Barbara

3University of California Irvine

A fundamental question in biology is how a pattern of different cell types develops from a field of relatively uniform cells. Developmental decisions take place in a dynamic environment, but in most cases it is not known how the growth and proliferation of cells contribute to pattern formation. In Arabidopsis, one such pattern is seen on the sepal epidermis where highly elongated and polypoid giant cells are interspersed between smaller pavement cells. We have used a combination of live imaging, image processing, modeling, and genetic approaches to determine how this pattern is established. We predict by modeling that the relative cell size is determined by the time at which individual cells make a stochastic decision to exit the cell division cycle and continue to grow and replicate their DNA without dividing, through endoreduplication. We have tested the model using live imaging and shown that giant cells start to endoreduplicate early during sepal development whereas the neighboring cells undergo multiple divisions. The model predicts that the probability that cells enter endoreduplication is a major determinant of pattern, with a higher probability causing over-production of giant cells and a lower probability resulting in the absence of giant cells. We show that these predicted phenotypes are produced by overexpressing the cell cycle inhibitor KRP1 (Bemis and Torii, 2007) and loss of function mutations in a cell cycle inhibitor gene that we name *LOSS OF GIANT CELLS FROM ORGANS (LGO)*, respectively. We demonstrate that the timing of endoreduplication is perturbed accordingly. Thus in the Arabdisopsis sepal, a key determinant of pattern formation is a stochastic decision by equivalent cells whether to divide or endoreduplicate.

Bemis, S.M., and Torii, K.U. (2007). Dev Biol 304, 367-381.

A systems biology approach to understanding the root clock

C40
Saturday 15:30 - 15:45
Systems Biology

In Arabidopsis, lateral roots are formed through the production of new meristems from pericycle cells located at the xylem poles. Using an *in vivo* imaging system we observed that positioning of these new meristems and the wave pattern formed by the primary root follow a temporal periodic distribution with an associated period of around 6 hours. However, the mechanisms that lie behind the initiation of lateral root primordia and the selection of only some pericycle cells to undergo dedifferentiation to form a new root are not known. Previous reports have shown that expression of the auxin response reporter DR5 correlate with lateral root initiation and that auxin production in pericycle cells is sufficient to initiate a new lateral root. Our results indicate that DR5 expression in the basal meristem oscillates following the pattern of a wave propagating along the longitudinal axis of the primary root. To further understand this oscillatory mechanism and lateral root positioning we performed microarray analyses of two different root segments, the basal meristem and the adjacent upper region, of 40 individual roots. Our results show two sets of genes oscillating in opposite fashion. We hypothesize these genes are the basis of the molecular mechanism determining lateral root positioning, and therefore make up a clock that establishes lateral root initiation time. Other computational approaches as well as analysis of several mutants, impaired in lateral root formation and other developmental process, suggest that this clock might be also regulating other periodic processes in the root, such as waving.

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Jaimie Van Norman
Philip Benfey

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NC
USA

From protein dynamics to physiology: phytochrome B mediated photomorphogenesis

C41
Saturday 15:45 - 16:00
Systems Biology

Plants have evolved a variety of sophisticated mechanisms to respond and adapt to exogenic factors in their natural environment. Multiple photoreceptors regulate the plant's development according to the spectral quality and light intensity. In a combined experimental and theoretical approach we gain new insights into the phytochrome B controlled signal transduction system in *Arabidopsis thaliana*. By suggesting a multiscale approach we connect the mesoscopic phytochrome B protein dynamics to the macroscopic response. Using the protein dynamics in combination with a model for hypocotyl growth, we estimate the relevant dynamic parameters of the phytochrome pathway and the growth kinetics. We challenge the model by predicting the fluence rate response behavior for an over-expression line. Furthermore, we predict from the theoretical considerations that the hypocotyl length depends on the total phytochrome amount in an algebraic manner. Using experimentally measured phytochrome levels of different mutants and the corresponding hypocotyl lengths, we find an excellent agreement between our theoretical prediction and the experimental results. Hence, our multiscale approach captures the main features of phytochrome B mediated photomorphogenesis in Arabidopsis.

Julia Rausenberger[1]
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Stefa Kircher[2]
Ferenc Nagy[3]
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Arabidopsis as a model for cell wall biosynthesis in bioenergy crops

C42
Saturday 14:00 - 14:30
Bioenergy

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Ai Oikawa1
Anongpat Suttangkakul1
Naomi Geshi2
Yves Verhertbruggen1
Michelle Truong1
Lan Yin1,2
Jacob K Jensen1
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Yumiko Sakuragi2
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2Department of Plant Biology and Biotechnology
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Declining sources of fossil fuels, global warming and political instability in oil producing regions have led many countries to develop strategies for alternative energy. Plant biomass is a convenient way to harness solar energy and photosynthesis, and biomass is already an important supplement to fossil fuels. However, the energy efficiency of biofuel production is low, and environmental impact can be high. There is a great need to develop new technologies that can provide fuels, especially liquid fuels for transportation, in an efficient and environmentally friendly way.

Plant cell walls are composed mainly of polysaccharides and production of biofuels from biomass requires decomposition of the polymers. Many of the polymers are recalcitrant to degradation and some degradation products cannot be converted efficiently into fuels or may even be inhibitory. Better understanding of the biosynthesis of the cell wall polysaccharides may enable development of crops with improved properties as biofuels feedstocks. Despite rather detailed information on the structure of the cell wall polysaccharides, little is known about their biosynthesis. The key enzymes are glycosyltransferases (GTs) and plants need a large number of GTs to synthesize the complex polysaccharides present in the walls. However, only a few GTs have had their activity demonstrated. In Arabidopsis, approximately 450 GT genes have been identified, and The Joint Bioenergy Institute has undertaken a systematic analysis of these enzymes. Biosynthesis of hemicelluloses is particularly important since they are the most abundant non-cellulosic component in biomass.

Systems biology of lignification and relevance to biofuels

C43

Saturday 14:30 - 15:00
Bioenergy

Ruben Vanholme
Veronique Storme
Kris Morreel
Jorgen Christensen
Antje Rohde
Geert Goeminne
Rebecca Van Acker
Eric Messens
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With increasing concerns about global warming and energy security, it is important to reduce dependence on fossil fuels. Biofuels are widely accepted to be a valuable alternative to achieve part of this objective. Bioethanol, as one of the major biofuels, is nowadays mainly made from food crops such as maize and sugarcane. However, much higher energy efficiencies are expected when bioethanol could be derived from lignocellulosic material such as wood or straw. This process, which includes fermentation after acid or enzymatic hydrolysis of the cell wall polysaccharides, is expensive due to some practical hindrances. One of the major barriers is lignin, an aromatic polymer and important component of the secondary cell wall. Lignin reduces access of enzymes and chemicals to cell wall polysaccharides, thus reducing the efficiency of hydrolysis. A solution to this issue is designing tailor-made lignin in biomass crops, in order to make the cell wall more applicable for processing, without introducing detrimental effects on plant growth. To succeed in this fragile balance-exercise, system-wide knowledge about lignification is needed.

We used Arabidopsis as a model species to determine the effects of altering lignin composition and content on both plant growth and biofuel processing efficiency, and to obtain insight into the cross-talk between lignin biosynthesis and other metabolic pathways and processes. A complete set of mutants, each defective in a lignin biosynthetic step, is investigated by transcriptomics (via microarrays) and metabolomics (via GC/MS and LC/UV-MS). The data reveal that genetic modification of monolignol biosynthesis in the cell wall has wide-ranging consequences on a number of metabolic processes. Molecular insight into these pleiotropic effects is essential if we want to design cell walls for end use applications.

Exploiting model species to increase biomass yield in energy crops

C44

Saturday 15:00 - 15:15
Bioenergy

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Sarah Hawkins
Elaine Jensen
Paul Robson
Ruth Sanderson
John Clifton Brown
Iain Donnison

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There is an urgent need to generate higher yielding energy crops in order to mitigate fossil fuel usage whilst minimising competition with food production. In contrast with model species, there is very little known about these novel crops. Molecular breeding relies on good understanding of the interaction between the genotype and the phenotype, so a combination of molecular approaches and intense phenotyping are required in order to achieve improved genotypes in the near future.

Miscanthus is a tall grass from South East Asia, which can grow to over 3m and produce yields of up to 14t/ha in the UK. Current plantings consist of a single sterile genotype M.x giganteus. The collection based at IBERS, Aberystwyth, comprises several hundred different genotypes comprising a wealth of diversity, which is ideal for genetic studies and forms the basis of the Miscanthus breeding program.

A number of key traits have been identified for increasing biomass yield, including spring emergence, light interception, stem morphology and flowering time. Genetic information from other species is used to select candidate genes for use in association studies using the Aberystwyth collection. Linking genotype to phenotype provides fundamental understanding of how a giant perennial plant develops. Using this knowledge to generate molecular markers for alleles conferring desirable traits will accelerate the breeding cycle and thereby allow more rapid development of lines adapted for their environments and end usage.

Assembly of the Cellulose Synthase Complex occurs within a specialised compartment that is derived from the endoplasmic reticulum

C45
Saturday 15:15 - 15:30
Bioenergy

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Aleksandr Mironov
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Cellulose is synthesised at the plasma membrane by a large multiprotein complex termed the Cellulose Synthase Complex (CSC). In cells that undergo deposition of a secondary cell wall, the CSC is assembled from three different CesA subunits; CesA4, CesA7 and CesA8. Previous work has shown the CSC to be found in the Golgi[1] and a small compartment that resides directly below the sites of secondary wall synthesis.[2] We have recently developed a method to visualise individual CSCs directly using Transmission Electron Microscopy. We have observed CSCs to be arranged in a very large 3-dimensional array within a membrane bound compartment. The identification of these CSC-containing arrays is further supported from immunogold labelling and mutant analyses. Characterisation of this compartment suggests that it is a specialised ER body and is the likely location for the synthesis and assembly of the CSC. The results have identified an entirely novel pathway for membrane protein trafficking in which a membrane-bound protein is able to avoid co-translational insertion into the ER membrane, instead passing through into the lumen of the ER. These results have profound implications for protein trafficking in general, but in particular for how the CSC assembles and functions at the plasma membrane.

1 Wightman, R., and Turner, S. R. (2008). The roles of the cytoskeleton during cellulose deposition at the secondary cell wall. Plant J 54, 794-805.
2 Wightman, R., Marshall, R., and Turner, S. R. (2009). A cellulose synthase-containing compartment moves rapidly beneath sites of secondary wall synthesis. Plant Cell Physiol 50, 584-594.

Using *Arabidopsis thaliana* to improve feedstock quality

C46

Saturday 15:30 - 15:45
Bioenergy

Thorsten Hamann
Lucy Denness
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Priya Madhou
Alexandra Wormit

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Feedstock quantity and quality fundamentally influence the efficiency with which energy can be produced from biomass. Biomass quality is determined by composition and structure of plant cell walls. Evidence has accumulated that a mechanism exists in plants capable of monitoring and maintaining the functional integrity of plant cell walls by changing their composition and structure. Functionally characterising the genes involved in this mechanism opens up the possibility of using their orthologs in future bioenergy crops like poplar, willow or miscanthus to improve feedstock quality. In order to identify genes involved in the cell wall integrity (CWI) mechanism, time course expression profiling experiments were performed using Arabidopsis seedlings treated with isoxaben (a highly specific cellulose biosynthesis inhibitor, CBI). This treatment causes cell wall stress by preventing formation of the load bearing cellulose microfibrills in elongating cells. The expression analysis has identified several candidate genes that are involved in the response to CBI. We will show how different tools have been adapted for functional characterisation of a larger number of candidate genes and present results regarding genes of interest.

North American Arabidopsis Steering Committee

NAASC

On behalf of the Arabidopsis community, the NAASC extends their appreciation and best wishes to Dr. Randy Scholl for 18+ years of service as the Director of the Arabidopsis Biological Resource Center.

ABRC, established in 1991, has been an invaluable resource to thousands of researchers worldwide. Randy's involvement in establishing and maintaining ABRC has been essential to its success in serving the worldwide community.

Randy Scholl, ABRC Director
1991 - 2009

Congratulations on your retirement!

2008 - 2009 NAASC Members

Joe Kieber Xuemei Chen (2005 - 2009)	George Haughn Scott Poethig (2007 - 2011)
Caren Chang Julian Schroeder (2006 - 2010)	Jane Glazebrook Mark Estelle (2008 - 2012)

NAASC is pleased to announce this year's recipients of underrepresented minority conference funding:

Luz Maria Borelli
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Allison Mello
Patricia Montano
Cristina Moreira
Kathleen Szick-Miranda

Award funding generously provided by the U.S. National Science Foundation

The Arabidopsis conference returns to the United States in 2011 (Madison, WI)

NAASC: http://www.arabidopsis.org/portals/masc/countries/NAASC_Info.jsp

Posters

Genome organisation

Arabidopsis whirly proteins maintain genomic stability in plastids **P001**
Jean-Sebastien Parent, Alexandre Marechal, B Franz Lang, Normand Brisson

Manipulating meiosis: crossovers from Arabidopsis to crops **P002**
Claire Halpin, Abdellah Barakate, Robbie Waugh, Luke Ramsay, Glyn Jenkins, Dylan Phillips, Sue Armstrong, James Higgins, Chris Franklin

An orthologous transcriptional signature differentiates responses among closely related chemicals in *Arabidopsis thaliana* and *Brassica napus* **P003**
Malay Das, Georg Haberer, Jay R Reichman, Gerhard Welzl, Felipe F Aceituno, Michael T Mader, Lidia S Watrud, Tom G Pfleeger, Rodrigo A Gutierrez, David M Olszyk, Anton R Schaffner

Investigating novel potential regulators and signalling components in phosphate stress responses of *Arabidopsis thaliana* **P004**
Magdalena Musialak-Lange, Rosa Morcuende, Wolf-Ruediger Scheible

Generation and transcriptome analysis of autotetraploid *Arabidopsis thaliana* **P005**
Zheng Yu, Kristina Haage, Michaela Matthes, Verena Streit, Georg Haberer, Klaus F X Mayer, Alfons Gierl and Ramon A Torres-Ruiz

Intron retention in Arabidopsis mRNA transcripts **P006**
Craig G Simpson, Maria Kalyna, John Fuller, Diane Davidson, Andrea Barta, John WS Brown

Arabidopsis PTB-like 1 (AtPTBL1) negatively regulates splicing inclusion of a plant mini-exon **P007**
Craig G Simpson, Sean Chapman, Michele Liney, Diane Davidson, Dominika Lewandowska, John WS Brown

Development

Dynamic changes of histone H3K27 tri-methylation during plant development **P008**
Marcel Lafos, Phillip Kroll, Daniel Schubert

Signaling triggered by activation of CC-NB-LRR-related UNI affects SAM activity in a non-cell-autonomous manner involving ERECTA receptor kinase **P009**
Naoyuki Uchida, Kadunari Igari, Masao Tasaka

The trihelix transcription factor AtGTL1 controls ploidy-dependent cell growth in the Arabidopsis trichome **P010**
Christian Breuer, Ayako Kawamura, Takanari Ichikawa, Rumi Tominga-Wada, Takuji Wada, Youichi Kondou, Shu Muto, Minami Matsui, Keiko Sugimoto

Proliferation and cell fate establishment during Arabidopsis male gametogenesis depends on Retinoblastoma **P011**
Zhong Chen, Said Hafidh, Shi Hui Poh, David Twell, Frederic Berger

Novel MAG2-interacting proteins are involved in vacuolar sorting of seed storage proteins **P012**
Lixin Li, Tomoo Shimada, Hideyuki Takahashi, Baoyu Tu, Hongmin Jin, Baoda Han, Junpei Takagi, Maki Kondo, Mikio Nishimura, Ikuko Hara-Nishimura

A timing mechanism for stem cell maintenance and differentiation in Arabidopsis flower development **P013**
Bo Sun, Yifeng Xu, Kian-Hong Ng, Toshiro Ito

Expression control of the central growth regulator *BIG BROTHER* involves parallel function of independent transcriptional inputs **P014**
Holger Breuninger, Michael Lenhard

Auxin-independent regulation of IAA12/BDL expression during embryo development **P015**
Ive De Smet, Steffen Lau, Jasmin Ehrismann, Ioannis Axiotis, Marika Kientz, Dolf Weijers

Regulation of floral patterning by flowering time genes **P016**
Chang Liu, Wanyan Xi, Lisha Shen, Hao Yu

A link between ANGUSTIFOLIA3 and the adaxial/abaxial patterning of leaves through ribosome-related processes **P017**
Gorou Horiguchi, Naoko Ishikawa, Minoru Kubo, José Manuel Pérez-Pérez, María Rosa Ponce, José Luis Micol, Taku Demura, Hiroo Fukuda, Hirokazu Tsukaya

***AtNUFIP*: a key gene controlling the biogenesis of snoRNPs and scaRNPs directing methylation of rRNA and snRNA and its impact on plant development** **P018**
Julie Rodor, Edouard Jobet, Jonathan Bizarro, Christel Carles, Manuel Echeverria

Epigenetic regulation of cartenoid composition and plant development by a chromatin modifying histone methyltransferase, SDG8? **P019**
Christopher Cazzonelli, Barry Pogson

Polarised vascular cell divisions are controlled by the CLE41-PXY ligand-receptor pair **P020**
Peter Etchells, Simon Turner

In Arabidopsis, a novel binding site for AP2 is important for AG regulation **P021**
Thanh Theresa Dinh, Xuemei Chen

Establishing regulatory models for anther endothecium development and the regulation of dehiscence **P022**
Caiyun Yang, Jie Song, Zoe A Wilson

ChIP-Seq and inducible gene expression reveal direct targets of the flowering pathway integrator FD **P023**
Levi Yant, Anusha Srikanth, Felix Ott, Christa Lanz, Frank Küttner, Markus Schmid

Control of embryo development by the CUL4-DDB1 complex **P024**
Eva Dumbliauskas, Jean Molinier, Pascal Genschik

Ribosome heterogeneity in the plant cell - what is its function? **P025**
Peta Bonham-Smith

The *KAONASHI4* gene encoding a putative β1,3-galactosyltransferase is required for the thickening of the pollen exine structure in *Arabidopsis thaliana* **P026**
Toshiya Suzuki, Kenzo Nakamura, Sumie Ishiguro

Coordination of dispersed stem cell activity in Arabidopsis **P027**
Derek White

Establishment of the winter-annual growth habit by *FRIGIDA*-mediated histone methylation in Arabidopsis **P028**
Danhua Jiang, Xiaofeng Gu, Yuehui He

Morphology and molecular regulation of programmed cell death in xylem elements **P029**
Charleen Courtois, Edouard Pesquet, Sunil Kumar Singh, Benjamin Bollhöner, Minako Kaneda, Lacey Samuels, Hannele Tuominen

CKH1/EER4/AtTAF12b and CKH2/PKL may function together to regulate cytokinin responses of calli in Arabidopsis **P030**
Kaori Furuta, Minoru Kubo, Taku Demura, Tatsuo Kakimoto

Paternal regulation of maternal gene expression may provide adaptive developmental strategies in Arabidopsis **P031**
Maria Cartagena, Jonathan FitzGerald

Global identification of targets of the MADS-domain protein AGL15 **P032**
Yumei Zheng, Sharyn Perry

Chloroplast biogenesis and retrograde signalling in seedlings **P033**
Veronica Albrecht, Klaus Apel, Murray Badger, Barry Pogson

TCTP, a putative upstream component of the TOR signalling pathway, controls tip growth and root development in Arabidopsis **P034**
Oliver Berkowitz, Ricarda Jost, Stephan Pollmann, Josette Masle

The MAR binding protein AHL16 controls flowering time by regulating chromosome structure of the *FLC* locus **P035**
Yifeng Xu, Toshiro Ito

Arabidopsis SHEPHERD, an Hsp90-like molecular chaperone resident in the endoplasmic reticulum, buffers against a harmful genetic mutation in *CLAVATA2* **P036**
Tomoko Niwa, Kumiko Oba, Kenzo Nakamura, Sumie Ishiguro

Interaction between the ubiquitination and the miRNA pathways in the regulation of flower development **P037**
Zinnia Haydee Gonzalez-Carranza, Xuebin Zhang, Janny L Peters, Jeremy A Roberts

Ribosomal proteins regulate Arabidopsis leaf dorsoventral polarity **P038**
Pascale Rossignol, Peter Etchells, Mary Byrne

Functional analysis of CYP98A8 and CYP98A9 in Arabidopsis **P039**
Michiyo Matsuno, Vincent Compagnon, Nawroz Abdul Razzak, Daniéle Werck

A systems approach reveals new roles for SHORTROOT and SCARECROW in plant dvelopment and physiology **P040**
Hongchang Cui, Mikhail Kovtun, David Orlando, Philip Benfey

The role of auxin in Arabidopsis late stamen development **P041**
Valentina Cecchetti, Giuseppina Falasca, MariaMaddalena Altamura, Karin Ljung, Paolo Costantino, Maura Cardarelli

PERIANTHIA in proliferation and differentiation of stem cells **P042**
Annette T Maier, Sandra Stehling-Sun, Sarah Schilli, Jan U Lohmann

Molecular and genetic control of endosperm growth in Arabidopsis **P043**
Jing Li, Frederic Berger

The volumetric component of individual leaf expansion: taking into account sub-epidermal tissues in the description of leaf expansion over time **P044**
Nathalie Wuyts, Genevieve Conejero, Jean-Luc Verdeil, Catherine Massonnet, Jean-Luc Regnard, Evelyne Costes, Christine Granier

Probing phenotype and molecular profile reproducibility: a comparison of Arabidopsis leaf growth across ten laboratories **P045**
Catherine Massonnet, AGRON-OMICS Consortium

CHD3 proteins and Polycomb group proteins antagonistically determine cell identity **P046**
Ernst Aichinger, Corina Belle Villar, Lars Hennig, Claudia Köhler

Definition of the quiescent center in the root meristem of Arabidopsis adventitious roots **P047**
Federica Della Rovere, GiuSeppina Falasca, Laura Fattorini, Maria Madalena Alta Mmura

Functional characterization of membrane proteins expressed in the Arabidopsis phloem **P048**
Rozenn Le Hir, Dipankar Chakraborti, Mathieu Castelaim, Peter Immerzeel, Thomas Moritz, Sylvie Dinant, Catherine Bellini

Regulation of KNOTTED1 cell-to-cell trafficking by a chaperonin protein **P049**
Xianfeng (Morgan) Xu, Jing Wang, Yoselin Benitez, David Jackson

BLADE-ON-PETIOLE1 and 2 control Arabidopsis leaf morphogenesis through regulation of *YABBY* and *KNOX* genes **P050**
Chan Man Ha, Ji Hyung Jun, Jennifer Fletcher

BLADE-ON-PETIOLE (BOP1) and BOP2 regulate Arabidopsis leaf morphogenesis by directly controlling *AS2* expression along the proximal-distal axis **P051**
Ji Hyung Jun, Chan Man Ha, Jennifer Fletcher

***DORNROESCHEN* and *DORNROESCHEN-LIKE* function with the *CUC* genes and MP in modulating embryo symmetry via auxin-dependent pathways** **P052**
John Chandler, Melanie Cole, Petra Comelli, Wolfgang Werr

Could the extent of cell division, cell expansion and endoreduplication in a leaf be controlled by leaf expansion itself? **P053**
Catherine Massonnet, Sébastien Tisné, Juliette Fabre, Nathalie Wuyts, Denis Vile, Myriam Dauzat, Christine Granier

Analysis of the impact of cellular processes on leaf growth of *Arabidopsis thaliana* by a high-throughput mutant approach **P054**
Catherine Massonnet, Alexandra Tinaut, Denis Vile, Juliette Fabre, Nathalie Wuyts, Alexis Bediée, Christine Granier

Comprehensive mapping of *ARF* expression reveals novel auxin responses in the plant embryo **P055**
Eike H Rademacher, Barbara Möller, Annemarie S Lokerse, Dolf Weijer

Molecular control of secondary growth initiation in the Arabidopsis shoot **P056**
Silvia Herold, Eva Maria Sehr, Raffael Lichtenberger, Jiri Friml, Javier Agusti, Thomas Greb

Targets of PLETHORA, master regulators of Arabidopsis root development **P057**
Marijn Luijten, Inez Terpstra, Anja van Dijken, Maartje A Gorte, Guy Wachsmann, Vera Jansweijer, Kalika Prasad, Pankaj Dhonukshe, Ben Scheres, Renze Heidstra

The multifaceted role of Lon protease in organelle biogenesis and post-germinative growth of *Arabidopsis thaliana* **P058**
Stamatis Rigas, Gerasimos Daras, Costantinos Fasseas, Lee Sweetlove, Polydefkis Hatzopoulos

BOB, a new triple fluorescence clonal deletion system **P059**
Guy Wachsmann, Ben Scheres, Renze Heidstra

The D-type cyclin *CYCD4;1* controls pericycle cell size in the root apical meristem and lateral root density in Arabidopsis **P060**
Jeroen Nieuwland, Spencer Maughan, Walter Dewitte, Simon Scofield, Luis Sanz, Jim Murray

Redundancy of CVP2 and CVL1 reveals a link between phosphoinositide signaling and the ARF GAP, SFC/VAN3 in establishment of foliar vein patterns **P061**
Francine Carland, Timothy Nelson

Stem cells, epigenetics and root regeneration **P062**
Giovanni Sena, Xiaoning Wang, Hsiao-Yun Liu, Pui-Leng Ip, Hugo Hofhuis, Kenneth D Birnbaum

The SHR/SCR pathway directly activates genes involved in asymmetric cell division in the Arabidopsis root **P063**
Rosangela Sozzani, Miguel Moreno-Risueno, Wolfgang Busch Jaimie Van Norman, Teva Vernoux, Siobhan Brady, Walter Dewitte, Jim Murray, Philip Benfey

Genomic dynamics in a cyclin mutant: limited progressive duplications and a rapid decay **P064**
Yixing Wang, Ajay Jha, Rujin Chen, John Doonan, Ming Yang

From Arabidopsis to crop plants-conserved transcriptional features of shoot apical meristem **P065**
Prem Bhalla, Annie Wong, Dacheng Liang, Farzad Haerizadeh, Mohan Singh

The last common ancestor of ferns and seed plants contained all three clades of the *WOX* gene family including a WUS/WOX5 ancestor **P066**
Judith Nardmann, Pascal Reisewitz, Wolfgang Werr

FPA controls pre-mRNA 3' end site selection **P067**
Csaba Hornyik, Lionel Terzi, Katarzyna Rataj, Jacqueline Marshall, Gordon Simpson

Investigating the role of Tre6P in the shoot apex of *Arabidopsis thaliana* **P068**
Vanessa Wahl, Markus Schmid, Luise H Brand, Regina Feil, Ursula Krause, Mark Stitt, John E Lunn

***MINIYO* links transcriptional elongation to stem cell progeny differentiation** **P069**
Maite Sanmartín, Michael Sauer, Alfonso Muñoz, Jan Zouhar, Angel Ordóñez, Wilhelmina van de Ven, Elena Caro, María Paz Sánchez, Natasha V Raikhel, Crisanto Gutiérrez, José J Sánchez-Serrano, Enrique Rojo

Characterization of CDPKs in flower onset and timing **P070**
Julia Legen, Susanne Matschi, Joachim Kurth, Fiona C Robertson, Helen Briggs, Alex AR Webb, Tina Romeis

Cutting to the chase: Using laser-capture microdissection and transcript profiling to reveal biological insights about Arabidopsis seed development **P071**
Ryan Kirkbride, Mark Belmonte, Sandra Stone, Julie Pelletier, Jiong Fei, Meryl Hashimoto, Anhthu Bui, Brandon Le, Chen Cheng, Min Chen, Jungim Hur, Robert Goldberg, John Harada

Production of superoxide in the Arabidopsis root tip is the result of photomorphogenesis **P072**
Irina Strizh, Andrey Buglak

Analyzing a novel root cell elongation regulator, UP BEAT1 **P073**
Hironaka Tsukagoshi, Siobhan Brady, Philip Benfey

MicroRNA-regulated SBP-Box genes control fertility in Arabidopsis **P074**
Shuping Xing, Vanessa Quodt, Susanne Höhmann, Nora Bujdoso, Arne Grande, Maria Salinas, Rita Berndtgen, Heinz Saedler, Peter Huijser

Integrating the genetic and physical maps of Arabidopsis: Identification of mapped alleles of cloned essential *(EMB)* genes **P075**
David Meinke, Colleen Sweeney, Rosanna Muralla

Analysis of the Arabidopsis homologs of the LST8 protein, a conserved partner of the TOR kinase complex **P076**
Manon Moreau, Gilles Clément, Marianne Azzopardi, Christophe Robaglia, Christian Meyer

***EARLY IN SHORT DAYS 7 (ESD7)* encodes the catalytic subunit of the DNA polymerase epsilon and is required for flowering repression through a mechanism involving epigenetic gene silencing** **P077**
Ivan del Olmo, Leticia Lopez-Gonzalez, Manuel A Pineiro, Jose A Jarillo

Expression of *SHORT INTERNODES/STYLISH* family genes in auxin biosynthesis zones of aerial organs is dependent of a GCC-box-like regulatory element **P078**
Magnus Eklund, Izabela Cierlik, Veronika Stålda, John Chandler, Eva Sundberg

Arabidopsis leaf phenomics **P079**
José Manuel Pérez-Pérez, Silvia Rubio-Día, Diana Hernández-Romero, Joaquín Sánchez-Soriano, Stijn Dhondt, Gerrit Beemster, María Rosa Ponce, José Luis Micol

14-3-3 Proteins and their importance for plant development **P080**
Katrin Weckermann, Claudia Oecking

New interaction partners for 14-3-3 proteins **P081**
Marion Grieser, Stephan Müller, Claudia Oecking

Identifying miRNA regulatory networks in the Arabidopsis root **P082**
Natalie Breakfield, Juthamas Sae-Seaw, Jalean Petricka, David Corcoran, Molly Megraw, Xuan Ding, Philip Benfey

Hormonal effect on root regeneration competence **P083**
Lihua Shen, Giovanni Sena, Xiaoning Wang, Pui-Leng Ip, Kenneth Birnbaum

The plant specific BPC/BBR family of GAGA-repeat binding proteins **P084**
Ulrich Bloss, Mareike L Hohenstatt, Sabine Hummel, Klaus Harter, Dierk Wanke

Floral transition in the shoot apical meristem of Soyabean **P085**
Annie Wong, Mohan Singh, Prem Bhalla

Small RNAs profiling of the shoot apical meristem **P086**
Prem Bhalla, Annie Wong, Xiujie Wang, Jerry Zhao, Farzad Haerizadeh, Bernard Carroll, Mohan Singh

The MCM helicase-binding protein ETG1 supports in sister-chromatid arm cohesion necessary for post-replication repair **P087**
Naoki Takahashi, Veit Schubert, Tim Lammens, Klaas Vandepoele, Ingo Schubert, Dirk Inzé, Minami Matsui, Lieven De Veylder

Identification and characterization of suppressors downstream of the IDA signalling pathway in Arabidopsis **P088**
Chun-Lin Shi, Grethe-Elisabeth Stenvik, Ane Kjersti Vie, Atle M Bones, Reidunn B Aalen, Melinka A Butenko

A transcriptomic approach to identify light quality specific responses during early stages in seedling development **P089**
Florian Peschke, Thomas Kretsch

Senescence in Arabidopsis siliques: its role in seed development and nutrition **P090**
Carol Wagstaff, Thomas JW Yang, Erold Namob, Jerry Roberts

Novel interacting factors of CDD complex, a negative regulator of photomorphogenesis **P091**
Tomoko Igawa, Masayuki Fujiwara, Yoichiro Fukao, Xing Wang Deng, Yuki Yanagawa

Studies on the regulatory role of light in leaf primordia initiation **P092**
Saiko Yoshida, Cris Kuhlemeier

Functional characterization of the Arabidopsis mutant *calmodulin2* **P093**
Michela Landoni, Alessandra De Francesco, Chiara Tonelli

Cell-type specfic auxin responses in the Arabidopsis root **P094**
Bastiaan Bargmann, Kenneth Birnbaum

Epidermal cell density is regulated by a negative feedback loop involving the secretory signaling peptide EPIDERMAL PATTERNING FACTOR 2 **P095**
Kenta Hara, Toshiya Yokoo, Ryoko Kajita, Takaaki Onishi, Kylee M Peterson, Keiko U Torii, Tatsuo Kakimoto

Lipid profiling during Arabidopsis reproductive processes **P096**
Yuki Nakamura, Zhi Wei Teo, Siou Ting Gan, Guanghou Shui, Ryota Koizumi, Hiroyuki Ohta, Markus R Wenk, Toshiro Ito

Functional analysis of *LSH* genes that are direct targets of CUC1 transcription factor controlling organ boundary formation **P097**
Seiji Takeda, Keiko Hanano, Yuka Tsubakimoto, Ayano Kariya, Satoko Shimizu, Masao Tasaka, Mitsuhiro Aida

The ASH1 HOMOLOG 2 (ASHH2) histone H3 methyltransferase is required for ovule and anther development in Arabidopsis **P098**
Paul E Grini, Tage Thorstensen, Vibeke Alm, Gema Vizcay-Barrena, Susanne S Windju, Zoe A Wilson, Reidunn B Aalen

LC-MS-based proteomics of Arabidopsis phloem sap **P099**
Zaidah Rahmat, Mark, H Bennett, Colin, GN Turnbull

Genetic screen for stem cell regulators **P100**
Ta-Fang Lin, Jinhui Chen, Alicja Dolzblasz, Ivo Rieu, Thomas Laux

Identification and analysis of second site mutations that suppress the defective phenotypes of the sterol biosynthetic *dry2/sqe1-5* Arabidopsis mutant **P101**
Veronica Gonzalez-Doblas, Vitor Amorim-Silva, David Pose, Omar Borsani, Herlander Azevedo, Victoriano Valpuesta, Rui Manuel Tavares, Miguel Angel Botella

Characterization of *Arabidopsis thaliana* orthologues of GAAP, a Golgi-localized anti-apoptotic protein **P102**
Maija E Sierla, Bart J Feys

Transcriptional regulation of *GIGANTEA*, a circadian-clock regulated flowering time gene in *Arabidopsis thaliana* **P103**
Markus C Berns, Frédéric Cremer, Ingmar Bürstel, George Coupland

Analysis of the Arabidopsis 4CL-like *ACYL-CoA SYNTHETASE5* gene and co-expressed genes reveals an ancient biochemical pathway required for pollen development and sporopollenin biosynthesis **P104**
Sung Soo Kim, de Azevedo Souza Clarice, Stefanie Koch, Lucie Kienow, Katja Schneider, Che Colpitts, Dae-Yeon Suh, Erich Kombrink, Carl J Douglas

Functional characterization of a microtubule-associated protein, MAP20, in Arabidopsis and Poplar **P105**
Manoj Kumar, David Ohma, Tuula Teeri, Ines Ezcurra, Totte Niittylä, Björn Sundberg

Spermidine hydroxycinnamoyl transferase (SHT) – a BAHD acyltransferase involved in pollen development **P106**
Etienne Grienenberger, Sebastien Besseau, Pierrette Geoffroy, Delphine Debayle, Michel Legrand

Biosynthesis of phenylpropanoid polyamine conjugates in flower buds of *Arabidopsis thaliana* **P107**
Christin Fellenberg, Christoph Bötcher, Thomas Vogt

Characterization of two *NF-Y A* genes in *Arabidopsis thaliana* **P108**
Monica Fornari, Valentina Calvenzani, Katia Petroni, Chiara Tonelli

Analysis of RBR1 protein level and phosphorylation status in auxin-treated Arabidopsis roots **P109**
Pál Miskolczi, Krisztina Ötvös, Errin Johnson, Zoltán Magyar, László Bakó

***Cis* element and transcriptome-based screening of novel root hair-specific genes and their functional characterization in Arabidopsis** **P110**
Su-Kyung Won, Yong-Ju Lee, Yoon-Kyung Heo, Misuk Cho, Hyung-Taeg Cho

Resetting and regulation of *Flowering Locus C* expression during Arabidopsis reproductive development **P111**
Jean Choi, Youbong Hyun, Min-Jeong Kang, Hye In Yun, Jae-Young Yun, Clare Lister, Caroline Dean, Richard M Amasino, Bosl Noh, Yoo-Sun Noh, Yeonhee Choi

Finding new developmental genes – a reverse genetics approach on Polycomb group protein (PcG) target genes **P112**
Julia Engelhorn, Julia Reimer, Sara Farrona, Ulrike Góbel, George Coupland, Franziska Turck

SAUL1, a novel E3 ubiquitin ligase, is required for suppression of premature senescence and cell death **P113**
Gabriele Drechsel, Sabine Raab, Florian Bittner, Stefan Hoth

EPF2 regulates stomatal development **P114**
Lee Hunt, Julie Gray

SQUINT is required for proper CLAVATA signalling **P115**
Nathanaël Prunet, Patrice Morel, Priscilla Champelovier, Anne-Marie Thierry, Ioan Negrutiu, Christophe Trehin

The role of a novel transcriptional complex in maintaining leaf polarity and meristem activity in Arabidopsis **P116**
Melissa Stahle, Janine Kuehlich, Lindsay Staron, Albrecht von Arnim, John Golz

***In vivo* targets of FPA, an RNA binding protein controlling Arabidopsis flower development** **P117**
Lionel C Terzi, Gordon G Simpson

The role of *P5CS1* and *P5CS2* in the flower transition of *Arabidopsis thaliana* **P118**
Roberto Mattioli, Stefania Nigro, Franco Abbate, Giuseppina Falasca, Maria Maddalena Altamura, Paolo Costantino, Maurizio Trovato

DETORQUEO, QUIRKY, and ZERZAUST, novel components involved in organ development mediated by the receptor-like kinase STRUBBELIG **P119**
Lynette Fulton, Martine Batoux, Prasad Vaddepalli, Ram Kishor Yadav, Wolfgang Busch, Stig Anderson, Sangho Jeong, Jan Lohmann, Kay Schneitz

Novel regulators and interactions controlling plant architecture and development **P120**
Enriqueta Alos, Philip A Wigge

Dissecting the transcriptional cascade in auxin-induced cell fate re-specification **P121**
Shuai Yuan, Bastiaan Bargmann, Puileng Ip, Kenneth Birnbaum

Identification of genes implicated in lateral root development in *Arabidopsis thaliana* **P122**
Concepcion Manzano, Bert De Rybel, Tom Beeckman, Carlos Del Pozo

Towards the identification of egg cell regulators **P123**
Ronny Völz Rita Gross-Hardt

The role of NF-Y transcription factors in flowering **P124**
Roderick Kumimoto, Yan Zhang, Nicholas Siefers, Ben Holt III

Kiss of Death (KOD) is a novel peptide regulator of programmed cell death in Arabidopsis **P125**
Bennett Young, Robert Blanvillain, Patrick Gallois

SIAMESE cooperates with a CDH1-like protein to establish endoreplication in Arabidopsis trichomes **P126**
John Larkin, Remmy Kasili, Jason Walker, Alice Simmons, Jing Zhao

Functional domains of PETAL LOSS, a trihelix transcription factor in *Arabidopsis thaliana* **P127**
Tezz L Quon, David R Smyth

The role of INSENSITIVE TO LOW TEMPERATURE 3 (ILT3) in the control of flowering time by ambient temperature in Arabidopsis **P128**
Jeong Hwan Lee, Kyung Eun Kim, Richard G H Immink, Jong Seob Lee, Ji Hoon Ahn

A disease resistance regulator, MAP kinase 4, is required for male-specific cytokinesis in Arabidopsis **P129**
QingNing Zeng, Brian E Ellis, Jin-Gui Chen

Arabidopsis DNA contains very few putative G-quadruplex sequence motifs **P130**
Ayami Nakagawa, Hiro Takahashi, Nobuo Sato, Shoko Kojima, Byung Yoon Cha, Je-Tae Woo, Yasunori Machida, Chiyoko Machida

SD5, a homologue of spliceosome subunit, regulates proliferation in post-seedling development **P131**
Takeshi Yoshizumi, Hiroaki Hongo, Takashi Kuromori, Yoko Horii, Yuko Imura, Asako Kamiya, Hiroaki Shimada, Minami Matsui

Functional characterization of BPEp bHLH transcription factor and its interacting protein, two transcription factors involved in the control of petal growth in *Arabidopsis thaliana* **P132**
Florian Brioudes, Emilie Varaud, Caroline Joly, Judit Szécsi, Julie Leroux, Floriant Bellvert, Cédric Bertrand, Mohammed Bendahmane

TIME FOR COFFEE promotes the morning phase of the circadian clock by interacting with transcription factors **P133**
Jieun Shin, Alfredo Sanchez-Villarreal, Zhaojun Ding, Seth J Davis

Transcription factor-hormone cross-talk in LEAFY COTYLEDON1 mediated embryogenesis **P134**
Astrid Junker, Twan Rutten, Gudrun Mönke, Helmut Bäumlein

A search for mutations suppressing the morphological phenotype of *argonaute 1* **P135**
Verónica Aguilera, Patricia Quinto, Rosa Micol-Ponce, José Luis Micol, María Rosa Ponce

Regulation of *AHP6*, a main player in Arabidopsis root vascular development **P136**
Ana Campilho, Ykä Helariutta

Analysis of SCI1 - a novel Pc-G protein? **P137**
Mareike Hohenstatt, Daniel Schubert

Divergent and redundant roles of the homologous BAH-PHD-containing proteins SHL and EBS in the regulation of developmental transitions in Arabidopsis **P138**
Leticia Lopez-Gonzalez, Laura Narro-Diego, Jose A Jarillo, Manuel Piñeiro

CLI1 - a novel component in cell fate determination **P139**
Nicole Schatlowski, Justin Goodrich, Daniel Schubert

Identification of root vascular patterning mutants **P140**
Jan Dettmer, Robertas Ursache, Ana Camphilo, Ykä Helariutta

The role of APL as a transcriptional regulator in specifying vascular tissue identity **P141**
Raffael Lichtenberger, Satu Lehesranta, Ove Lindgren, Sari Tähtiharju, Ykä Helariutta

SKP2A, an F-box protein that regulates cell division **P142**
Silvia Jurado, Zamira Abraham, Carlos del Pozo

Identification of novel factors involved in vascular development **P143**
Katrin Ollram, Thomas Greb

Over expression of a plant homolog of the human tumor suppressor PTEN leads to flower sterility **P144**
Rodnay Sormani, Anne Pribat, Mathieu Rousseau, Ludivine Taconnat, Jean Pierre Renou, Christian Meyer, Christophe Rothan, Véronique Germain

Functional characterization of Metacaspase 9 in *Arabidopsis thaliana* **P145**
Sunil Kumar Singh, Benjamin Bollhöner, Luis Muñiz, Hannele Tuominen

Investigation of the physiological function of sink-related sucrose transporters in *Arabidopsis thaliana* **P146**
Bianca Schmitt, Inga Barth, Stefan Meyer, Norbert Sauer

Novel role for a pair of NAC-like genes in regulating shoot architecture in Arabidopsis **P147**
Ching-Fang Shih, Jian-Shin Lin, Chang-Hsien Yang

GIGANTEA mediates senescence and oxidative response in plants **P148**
Yu-Yun Chang, Ya-Chun Li, Ching-Fang Shih, Emily Chin-Fun Chen, Muthu Thiruvengadam, Chang-Hsien Yang

The flower development size-clock **P149**
Susana Sauret-Gueto, Jerome Avondo, Andrew Bangham, Enrico Coen

Functional analysis of a Trithorax group (TrxG) gene *ASHH1* in *Arabidopsis thaliana* **P150**
Ya-Chun Li, Chun-Yuan Lin, Chang-Hsien Yang

Phosphoinositides system in Arabidopsis flower development **P151**
Kazue Kanehara, Yuki Nakamura, Zhi Wei Teo Wei Fun Cheong, Guanghou Shui, Siou Ting Gan, Markus R Wenk, Toshiro Ito

A putative CHD3 chromatin remodeling gene implicated in seed maturation and germination **P152**
Nirmala Sharma, Yarnel Bender, Maureen Anderson, Kerry Sproule, Kasi Williams, Pierre Fobert

Insights into the *Arabidopsis thaliana* trehalose-6-phosphate phosphatase family **P153**
L López, L Vandesteene, T Beeckman, P Van Dijck

MicroRNA profiling of *Arabidopsis thaliana* mature pollen **P154**
Gael Le Trionnaire, Robert Grant-Downton, Said Hafidh, Ralf Schmid, Hugh Dickinson, David Twell

***duo pollen 4* – a novel gametophytic mutant blocking male germ cell division in Arabidopsis** **P155**
Hoda Khatab, Tony Wardle, David Twell

Tissue layer-specific rescue of organ form in Arabidopsis revealed by the cell autonomous action of ANGUSTIFOLIA **P156**
Yang Bai, Stefanie Falk, Arp Schnittger, Marc Jakoby, Elena Galiana' Jaime, Martin Hulskamp

***PIGGYBACK6* is required for apical embryo patterning in Arabidopsis** **P157**
Dora Szakonyi, Mary Byrne

In search of interaction partners for 14-3-3 protein ε **P158**
Christian Throm

TEM analysis reveals plasmodesmata structure is important for function **P159**
Tessa Burch-Smith, Patricia Zambryski

Functional redundancy and spatial expression of the *FLOWERING LOCUS T (FT)/TERMINAL FLOWER 1 (TFL1)* gene family in *Arabidopsis thaliana* **P160**
Seong Jeon Yoo, Kyung Sook Chung, Hanna Lee, Ji Hoon Ahn

Plant specific signalling outputs of the TOR kinase growth regulatory pathway **P161**
Natasha Forester, Karen Wilson, Bruce Veit

Live-organ-imaging of auxin responses with the luciferase reporter gene **P162**
Masaaki K Watahiki, Kotaro T Yamamoto

The *MAB/ENP* family genes involved in auxin-regulated morphogenesis **P163**
Masahiko Furutani, Shuhei Yoshida, Masao Tasaka

The abaxial-side specific expression of *MIR165/166* clearly marks off the PHB-expression domain from the FIL-expression domain in Arabidopsis leaf primordial **P164**
Kiyoshi Tatematsu, Keiro Watanabe, Koichi Toyokura, Toshiaki Tameshige, Kiyotaka Okada

***UNICORN*, a negative regulator of YABBY gene *INNER NO OUTER* in Arabidopsis ovule integument development** **P165**
Balaji Enugutti, Kay Schneitz

Seeking a meiotic trigger in Arabidopsis **P166**
Liz Alvey, Ian Henderson

Members of the AP2/ERF family of transcription factors act in vascular development **P167**
Ziwei Song, Simon Turner, Peter Etchells

Gibberillins control fruit pattering in *Arabidopsis thaliana* **P168**
Nicolas Arnaud, Thomas Girin, Karim Sorefan, Tom Wood, Robert Sablowski, Lars Østergaard

Modelling dynamic growth maps of leaf development **P169**
Erika Kuchen, Samantha Fox

Characterisation of Arabidopsis Cathepsin B involved in programmed cell death **P170**
G E Yuan, L Bonneau, VE Rotary, A Danon, B Turk, P Gallois

Role of polycomb-group genes in commitment to flowering in Arabidopsis **P171**
Ralf Müller, Daniel Schubert, Justin Goodrich

CAST AWAY, a receptor-like cytoplasmic kinase, regulates floral organ abscission **P172**
Christian Burr, Michelle Leslie, Michael Lewis, Stephanie Hasty, Patrick Healy, Sarah Liljegren

The essential role of VLCFAs for cell plate establishment during cell division in *Arabidopsis thaliana* **P173**
Liên Bach, Louise Michaelson, Richard Haslam, Yannick Bellec, Lionel Gissot, Jessica Marion, Jean Pierre Boutin, Martine Miquel, Frederique Tellier, Frederic Domergue, Jonathan Markham, Frederic Beaudouin, Jonathan Napier, Jean Denis Faure

Physical interaction between ABBERANT TESTA SHAPE/KANADI4 and AUXIN RESPONSE FACTOR3/ETTIN mediates integument development in Arabidopsis **P174**
Dior Kelley, Alexandra Arreola, Charles Gasser

Interaction of *INDEHISCENT* and *SPATULA* for the valve margin formation in the Arabidopsis fruit **P175**
Thomas Girin, Karim Sorefan, Teodora Paicu, Martin O'Brien, Tom Wood, David Smyth, Lars Østergaard

Identifying the location of GAL4-GFP enhancer trap lines using TAIL-PCR in *Arabidopisis thaliana* **P176**
Jessica Diaz, MariaElena Zavala

Functional analysis of transcripts repressed by the presence of the female gametophyte in the ovule of *Arabidopsis thaliana* **P177**
Alma Armenta-Medina, Jean-Philippe Vielle-Calzad

Arabidopsis *VEN3* and *VEN6* encode carbamoyl phosphate synthetase subunits **P178**
Almudena Mollá-Morales, Raquel Sarmiento-Mañús, Rebeca González-Bayón, Pedro Robles, Víctor Quesada, Matthew Hannah, Lothar Willmitzer, José Manuel Pérez-Pérez, María Rosa Ponce, Jose Luis Micol

The expression pattern of *AGP18* reveals coordinated sporophytic and gametophytic control during ovule development in Arabidopsis **P179**
Edgar Demesa-Arévalo, Jean-Philippe Vielle-Calzada

Characterization of a gene homologous to AT1G74730*(BnMicEmU)* upregulated in embrogenic *Brassica napus* microspore cultures **P180**
Fariba Shahmir, Peter Pauls

The role of the trehalose-6-phosphate sugar signal in coordinating leaf development to plant sugar status in *Arabidopsis thaliana* **P181**
Alexander Ivakov, John Lunn, Vanessa Wahl, Mark Stitt

GPCR-type G proteins are essential for normal growth and development in Arabidopsis **P182**
Felix W Jaffé, Gian-Enrico C Freschet, Billy M Valdes, Jonathon G Jerram, Matthew J Terry, Lorraine E Williams

Environmental Responses

Dynamic interactions of vernalization and photoperiod determine local adaptation of flowering time independent of latitude in *Arabidopsis thaliana* **P207**
AM Lewandowska-Sabat, S Fjellheim, P Winge, A Bones, T Sparstad, CG Fossdal, JE Olsen, OA Rognli

The dynamic nature of molecular responses to cold and their interaction with diurnal regulation **P208**
Carmen Espinoza, Takayuki Tohge, Andrea Leisse, Thomas Degenkolbe, Alisdair R Fernie, Lothar Willmitzer, Dirk K Hincha, Matthew A Hannah

Transcription factors coordinating the salt stress response mediated by the OsRMC peptide: identification and characterization **P209**
Tania Serra, Ana Paula Santos, Margarida Oliveira, Nelson Saibo

Functional dynamics in plant mitochondrial metabolism **P210**
ChunPong Lee, Holger Eubel, Nicolas L Taylor, A Harvey Millar

Implication of CLCc in salt stress resistance in *Arabidopsis thaliana* **P211**
Mathieu Jossier, Benoît Guillemardet, Hélène Barbier-Brygoo, Geneviève Ephritikhine, Sophie Filleur

Adaptation of Arabidopsis leaves to moderate drought stress depends on their developmental stage **P212**
Aleksandra Skirycz, Stefanie de Bodt, Toshihiro Obata, Alisdair Fernie, Dirk Inze

A cytosolic ABA receptor **P213**
Arthur Korte, Yue Ma, Izabela Szostkiewicz, Alexander Christmann, Erwin Grill

The Arabidopsis C/S1 bZIP transcription factor network controls reprogramming of metabolic gene expression in response to energy deprivation **P214**
Katrin Dietrich, Fridtjof Weltmeier, Andrea Ehlert, Johanna Lendner, Klaus Harter, Wolfgang Dröge-Laser

The endogenous *GL3*, but not *EGL3* gene, is necessary for anthocyanin synthesis as induced by nitrogen depletion in Arabidopsis rosette stage leaves **P215**
Dugassa Feyissa, Trond Løvda, Kristine Olsen, Rune Sliimestad, Cathrine Lillo

AtGTL1 transcription factor regulates drought tolerance and water use efficiency **P216**
Chan Yul Yoo, Jing Bo Jin, Kenji Miura, Mike Gosney, Yinhua Jin, Paul M Hasegawa, Michael V Mickelbart

Dissonant circadian clock in early-standing magnesium deficient leaves **P217**
Christian Hermans, Marnik Vuylsteke, Dirk Inzé, Nathalie Verbruggen

Analyzing the molecular differences of the *SPA* genes that cause distinct functions - The dark side of *SPA2* **P218**
Kirsten Fittinghoff, Ute Hoecker

Analysis of suppressor mutants of a PARN deficient mutant, *ABA hypersensitive germination2-1* **P219**
Takashi Hirayama, Shimpei Hayashi

Involvement of amine oxidases in nitric oxide (NO) biosynthesis and in NO-mediated abiotic stresses **P220**
Rinukshi Wimalasekera, Corina Villar, Tahmina Begum, Günther Scherer

DNA damage signaling controls the expression level of B2-type CDK in *Arabidopsis thaliana* **P221**
Sumiko Adachi, Masaaki Umeda

Phosphatidic acid regulates protein kinases in Arabidopsis responses to salt **P222**
Fionn McLoughlin, Carlos Galvan-Ampudia, Christa Testerink

Is ZIF1, a critical component of Zn and Fe homeostasis, a nicotianamine transporter? **P223**
Mike Haydon, Ute Kraemer

Role of the Ca^{2+}-dependent protein kinase CPK3 in the Arabidopsis salt-stress response **P224**
Norbert Mehlmer, Daniela Hofmann-Rodrigues, Bernhard Wurzinger, Andrea Mair, Markus Teige

The major flowering time gene, *Flowering Locus C*, regulates seed germination in *Arabidopsis thaliana* **P225**
George CK Chiang, Deepak Barua, Elena Kramer, Richard Amasino, Kathleen Donohue

Ethylene plays a role in the root phenotype of the *arm* mutant **P226**
Christian Hermans, Simona M Cristescu, Frans JM Harren, Filip Vandenbussche, Dominique Van Der Straeten, Nathalie Verbruggen, Daniel R Bush

Osmotic stress-induced signals control root growth **P227**
Carlos S Galvan Ampudia, Christine Zalejski, Laszlo Bogre, Remko Offringa, Christa Testerink

A role for carbon metabolism in leaf growth response to soil water deficit? An integrated perspective **P228**
Irène Hummel, Florent Pantin, Ronan Sulpice, Gaëlle Rolland, Maria Piques, Myriam Dauzat, Mark Stitt, Yves Gibon, Bertrand Muller

Two novel proteins, POPEYE and BRUTUS, play opposing roles in regulating root responses to iron deficiency **P229**
Terri Long, Jean Wang, Philip Benfey

Hypoxia responsive ERF transcription factors involved in low oxygen signalling in *Arabidopsis thaliana* **P230**
Francesco Licausi, Joost T van Dongen, Beatrice Giuntoli, Antonietta Santaniello, Peter Geigenberger, Pierdomenico Perata

OPEN STOMATA 3, an ABC transporter implicated in ABA signalling, drought and light response **P231**
Aleksandra Wasilewska, Nathalie Leonhardt, Marta Riera, Christiane Valon, JérômeGiraudat, Sylvain Merlot, Michael R Blatt, Jens Uwe Sutter, Jeffrey Leung

Phosphatidic acid, a lipid second messenger involved in early abiotic stress signaling **P232**
Fionn McLoughlin, Henk L Dekker, Magdalena M Julkowska, Dieuwertje van der Does, Chris G de Koster, Christiane Laurière, Grazyna Dobrowolska, Michel A Haring, Teun Munnik, Christa Testerink

The tonoplast nitrate transporter AtCLCa is involved in stomata movement and its activity is regulated by phosphorylation **P233**
S Wege, S Filleur, A De Angeli, S Thomine, F Gambale, H Barbier-Brygoo

QTLs underlying the response of leaf expansion to drought in *Arabidopsis thaliana* highlight different processes by which leaf area can be maintained or increased **P234**
Sébasttie Tisné, Denis Vile, Matthieu Reymond, Myriam Dauzat, Marjorie Pervent, Christine Granier

QTL analysis of developmental and environmental effects on mineral accumulation in Arabidopsis **P235**
Artak Ghandilyan, Luis Barboza, Myriam Olortegui, Dick Vreugdenhil, Sébasttien Tisné, Christine Granier, Umit B Kutman, Ismail Cakmak, Henk Schat, Matthieu Reymond, Maarten Koornneef, Mark GM Aarts

Stability of heritable stress-induced loss of gene silencing **P236**
Christina Mladek, Olga Popova, Marc Berlinger, Kathrin Kiok, Werner Aufsatz, Claudia Jonak, Christian Luschnig, Marie-Theres Hauser

Is OST1/SnRK2.6 a physiological target of PP2Cs in ABA signaling? **P237**
Florina Vlad, Sylvain Merlot, Pedro L Rodriguez, Jeffrey Leung, Christiane Laurière

***Arabidopsis halleri* as a model organism to study the extreme complex trait of metal hyperaccumulation** **P238**
Ute Krämer, Marc Hanikenne, Juergen Kroymann, Ina Talke, Mike Haydon, Christa Lanz, Patrick Motte, Detlef Weigel

Endocycle regulator DEL1 represses PHR1, a UV-induced DNA-damage repair gene **P239**
Amandine Radziejwoski, Kobe Vlieghe, Tim Lammens, Sara Maes, Marcel Jansen, Claudia Knappe, Andreas Albert, Harald Seydlitz, Werner Heller, Günther Bahnweg, Dirk Inze, Lieven De Veylder

Two new clock proteins, LWD1 and LWD2, regulate Arabidopsis photoperiodic flowering and circadian clock **P240**
Ying Wang, Jing-Fen Wu, Shu-Hsing Wu

A functional role for TOC1 in abscisic acid signalling **P241**
Tommaso Legnaioli, Juan Cuevas, Paloma Mas

Lipophilic components of the brown seaweed, *Ascophyllum nodosum*, enhance freezing tolerance in *Arabidopsis thaliana* by priming osmolyte accumulation and enhancing fatty acid unsaturation **P242**
Prasanth Rayorath, Junzeng Zhang, Christopher Kirby, Bernhard Benkel, Mark Hodges, David Hiltz, Alan Critchley, Balakrishnan Prithiviraj

Disentangling *Arabidopsis thaliana* responses to combined drought and thermal stresses **P243**
Denis Vile, Marjorie Pervent, Michaël Belluau, Jean-Jacques Thioux, Jérôme Joubès, Christine Granier

Modulations of *AtGSTF10* expression induce stress tolerance and BAK1-mediated cell death **P244**
Sun Young Kim, Hyun Kyung Kang, Hee Young Ryu, Hyun Mi Park, Ji Young You, Beg Hab Kim, June Seung Lee, Kyoung Hee Nam

Enolase, a cross-link between glycolysis and stress response **P245**
Nina Jaspert, Katrin Weckermann, Markus Piotrowski, Claudia Oecking

Functional analysis of ARR4 in different subcellular compartments **P246**
Janika Witthöft, Virtudes Mira-Rodado, Klaus Harter

Characterization of *Arabidopsis thaliana* Condensin II mutants in B toxicity **P247**
Takuya Sakamoto, Yayoi T Inui, Toru Fujiwara

Nitrogen-regulated transcription factor, AGL21, controls lateral root development in Arabidopsis **P248**
Akinori Suzuki, Mayu Miyamoto, Brian G Forde, Hideki Takahashi

Investigation of genetic influence on the responses of Arabidopsis to environmental change **P249**
Tebogo Selebatso

Role of *Arabidopsis thaliana* stress-response genes in heavy metal tolerance **P250**
Vanessa Menezes-Oliveira, Darlan Quinta, Susana Loureiro, Paula Duque, Amadeu M V M Soares

Protein phosphorylation and a 14-3-3 protein binding in Arabidopsis guard cells in response to ABA **P251**
Yohei Takahashi, Yuta Ebisu, Toshinori Kinoshit, Ken-ichiro Shimazaki

Arabidopsis activation tag lines in studying Zn efficiency **P252**
Gokhan Hacisalihoglu

Characterization of a CNG channel subfamily in *Arabidopsis thaliana* **P253**
Annette Kugler, Barbara Köhler, Petra Dietrich

Analysis of the Arabidopsis *AtMYB60* promoter, specific for guard cell expression **P254**
Eleonora Cominelli, Alessandra Albertini, Priscilla Francia, Massimo Galbiati, Chiara Tonelli

Overlapping function of ZTL, LKP2 and FKF1 in the Arabidopsis circadian clock **P255**
Antoine Baudry, Shogo Ito, Takatoshi Kiba, Sheen Lu, Nam-Hai Chua, Elaine M Tobin, Steve A Kay, Takato Imaizumi

Evidence for gravity-induced calcium response in Arabidopsis under microgravity condition **P256**
Masatsugu Toyota, Takuya Furuichi, Hitoshi Tatsumi, Masahiro Sokabe

OST1 kinase controls ABA dependant gene expression in stomata via the phosphorylation of conserved sites in ABF/AREB transcription factors **P257**
Caroline Sirichandra, Marlène Davanture, Benoit Valot, Michel Zivy, Benjamin Turk, Jeffrey Leung, Sylvain Merlot

Physical interaction between a pseudo-response regulator and a calmodulin-like protein involved in abiotic stress and ABA responses **P258**
Alexandre Perochon, Stefan Dieterle, Didier Aldon, Jean-Philippe Galaud, Martine Charpenteau, Benoit Ranty

Mapping genes involved in growth response to potassium starvation **P259**
Aina Prinzenberg, Hugues Barbier, Maarten Koornneef, Matthieu Reymond

Light signalling pathways mediate cold acclimation in Arabidopsis **P260**
Rafael Catala, Joaquin Medina, Julio Salinas

The critical role of the Arabidopsis circadian clock at high temperature **P261**
Nicola Costa, James Hartwell, Anthony Hall

***TIME FOR COFFEE* sets the circadian clock at dawn by integrating metabolic signals** **P262**
Alfredo Sanchez Villarreal, Seth J Davis

The role of stomatal density in governing growth and competitive interactions in relation to water stress: experimental observations with Arabidopsis **P263**
Ángel Ferrero-Serrano, James Hartwell, Martin Mortimer

Prediction of interaction networks using transcriptional co-regulation algorithms **P264**
Achim Hahn, Joachim Kilian, Dierk Wanke, Klaus Harter, Kenneth W Berendzen

The role of plant synaptotagmins in plasma membrane integrity and cell survival **P265**
Arnaldo L Schapire, Alicia E del Valle, Julio Salinas, Victoriano Valpuesta, Miguel A Botella

Characterising the function and regulatory pathways controlling gene expression of mitochondrial stress induced proteins in Arabidopsis **P266**
Vindya Uggalla, Olivier Van Aken, Monika Murcha, Rachel Clifton, Kristina Kuehn, Chris Carrie, Estelle Giraud

Dissection of the effects of light input signals to the genetic network of the circadian clock **P267**
Kirsten Knox, John O'Neill, Andrew Millar

Arabidopsis as a tool to define the role of programmed cell death in cassava deterioration **P268**
Kimberly Jones, John Beechin

Functional characterisation of four GDSL-lipases in *Arabidopsis thaliana* **P269**
Peter Huppenberger, Birgit Kemmerling, Klaus Harter, Christopher Grefen

The effect of transcriptional adaptor proteins ADA2a, and ADA2b on plant light responses **P270**
Konstantinos Theodoropoulos, Athanasios Kaldis, Konstantinos Vlachonasios

Overexpression of *AtPCS1* affects Cd tolerance in *Arabidopsis thaliana*: Changes in intracellular Cd and root system morphology **P271**
Letizia Zanella, Patrizia Brunetti, Maura Cardarelli, Sylvia Lindberg, Luigi Sanità Di Toppi, Maria Maddalena Altamura, Giuseppina Falasca

Towards a function of a stress inducible glycosyltransferase using non-targeted metabolome analysis **P272**
Veronica v Saint Paul, Basem Kanawati, Theresa Faus-Keßler, Phillippe Schmitt-Kopplin, Anton Schäffner

Characterisation of putative targets of AtMYB60, an Arabidopsis guard cell specific transcription factor **P273**
Alessandra Albertini, Massimo Galbiati, Eleonora Cominelli, Chiara Tonelli

Control of EIN3 stabilization upon ethylene signalling **P274**
Bureau Marina, Lamy Geneviève, Genschik Pascal, Potuschak Thomas

Mediation of plant stress responses via mRNA turnover **P275**
Justin Walley, Katayoon Dehesh

Establishment of a novel gain-of-function resource for functional analysis of transcription factors and analysis of novel transcription factor related with hypocotyl growth under light conditions **P276**
Youichi Kondou, Takeshi Yoshizumi, Mika Kawashima, Tomoko Kuriyama, Yukako Hasegawa, Shu Muto, Nobutaka Mitsuda, Yuko Takiguchi, Masaru Ohme-Takagi, Minami Matsui

Role of dioxygenases in the phytoremediation of polycyclic aromatic hydrocarbons (PAHs) using the plant *Arabidopsis thaliana* as a model system **P277**
Juan Carlos Hernandez-Vega, Elizabeth Smith, Dawit Bezabih, Adán Colón-Carmona

Cell expansion drives ethylene-induced differential petiole growth in *Arabidopsis thaliana* **P278**
Joanna Polko, Martijn van Zanten, Laurentius ACJ Voesenek, Anton JM Peeters, Ronald Pierik

Nitrate transporter and pathogen resistance **P279**
Julie Dechorgnat, Mathilde Fagard, Anne Krapp, Françoise Daniel-Vedele

UBP14 is involved in root hair development under phosphate starvation in Arabidopsis **P280**
Margarete Müller, Thomas Buckhout, Thomas Altmann

Identification of hyperactive forms of Arabidopsis MAP Kinases for the study of their target genes **P281**
Souha Berriri, Heribert Hirt, Jean Colcombet

Control of nitrogen remobilisation during leaf senescence and plant reproduction **P282**
Jeremy Lothier, Céline Diaz, Thomas Lemaitre, Laure Gaufichon, Anne Guiboileau, Céline Masclaux-Daubresse

Functional analysis of a plant specific RNA binding protein PSRP1 in Arabidopsis **P283**
Zhe Wu, Danling Zhu, Qian Yang, Takashi Aoyama, Tomohiko Tsuge, Li-jia Qu, Hongya Gu

TINY GUY (TG), a DREB subfamily transcription factor, is potentially involved in stress response in Arabidopsis **P284**
Danling Zhu, Zhe Wu, Jigang Li, Jia Wei, Haiyang Wang, Takashi Aoyama, Tomohiko Tsuge, Hongya Gu, Li-jia Qu

Phenotypical, molecular and biochemical characterization of new members from a TTL family involved in osmotic stress responses and ABA sensitivity **P285**
Naoufal Lakhssassi, Veronica Gonzalez-Doblas, Alicia Esteban, Julio Omar Borsani, Miguel Angel Botella Mesa

Circadian-regulation of wound responses as a potential mechanism to increase plant fitness **P286**
Michael Covington

Biochemical characterization of two wheat phosphoethanolamine N-methyltransferase isoforms with different sensitivities to inhibition by phosphatidic acid **P287**
Ricarda Jost, Oliver Berkowitz, John Shaw, Josette Masle

Cell-type specific transcriptional stress responses in Arabidopsis roots **P288**
Anjali Iyer-Pascuzzi, Terry Jackson, Philip N Benfey

FIONA1 controls the *CONSTANS (CO)* and *FLOWERING LOCUS C (FLC)* in summer annual **P289**
Miji Yeom, Jeongsik Kim, Yumi Kim, Hyunmin Kim, Hong Gil Nam

Phosphoregulation of calcium dependent protein kinases (CDPKs) and changes in protein levels during ABA signaling mapped by mass-spectrometry **P290**
Maik Böhmer, Onur Erbilgin, Julian Schroeder

Light and temperature inputs into the circadian clock **P291**
Julia Foreman, Kelly L Stewart, Karen J Halliday

The activity of the bHLH transcription factor HFR1 is dependent on light and temperature **P292**
Henrik Johansson, Julia Foreman, Karen J Halliday

Photosynthesis light response curves in Arabidopsis plants under different water availability **P293**
João Lucas Coito, Jorge Faria, Jorge Marques da Silva, Ana Rita Matos, Adalcina Casimiro, Anabela Bernardes da Silva, Maria Celeste Arrabaça, João Daniel Arrabaça

Perturbing the Arabidopsis circadian clock system by limiting its light inputs **P294**
Bénédicte Wenden, László Kozma-Bognár, Qian Xing, Andrew Millar

Metabolomics of ecotypic response to environmental variation **P295**
Chris Stewart

Toward the reconstruction of transcriptional regulatory pathways associated with hypoxia in Arabidopsis **P296**
Fu-Chiun Hsu, Hsin-Ru Hung, Hsiao-Ping Peng, Ming-Che Shih

Isolation and characterization of Arabidopsis mutants with defects in acquired thermotolerance **P297**
Tsung-yuan Lee and Yee-yung Charng

FKBP proteins are important determinants of intracellular acid stress tolerance in yeast and in Arabidopsis **P298**
Gaetano Bissoli, Regina Niñoles, Consuelo Montesinos, Guillem Hueso, M Dolores Planes, Ramón Serrano, José M Mulet

Isolation and characterization of an *Arabidopsis thaliana* mutant resistant to norespermidine **P299**
Rosa Porcel, Carolina Abril, Santiago Alejandro and Ramón Serrano

Arabidopsis *wat1-1D* mutant reveals a role of a C2 domain containing protein in intracellular pH homeostasis **P300**
Regina Niñoles, Santiago Alejandro, Christoph Plieth and Ramón Serrano

Local and systemic regulation of phosphate starvation responses in Arabidopsis **P301**
Margarete Müller, Thomas Buckhout, Bikram Datt Pant, Wolf-Rüdiger Scheible, Thomas Altmann

Expression of alternative oxidase genes in Arabidopsis leaves under progressive drought stress **P302**
Ana Rita Matos, Dave Pinxteren, João Lucas Coito, Anabela Bernardes da Silva Jorge Marques da Silva, Maria Celeste Arrabaça, Adalcina Casimiro, João Daniel Arrabaça

The *early bird 1* reveals a new cog in the circadian clock **P303**
Mikael Johansson, Harriet McWatters, László Bakó, Anthony Hall, Andrew J Millar, Maria E Eriksson

Plant Defence

Metabolite screening to identify *in vivo* ligands for glutathione transferases **P304**
David Dixon, Robert Edwards

TGA transcription factors negatively regulate PAMP signaling cascades **P305**
Katja Rindermann, Christiane Gatz

A member of the Arabidopsis polygalacturonase gene family modulates leaf development and responses to biotic and abiotic stress **P306**
Rana Poor Aiiouby, Sven Friehe, Elmon Schmelzer, Alan Slusarenko, Nikolaus L Schlaich

Subtle changes in the sequence of the *as-1-like* element have a strong impact on the regulation of the *PR-1* promoter **P307**
Sebastian Pape, Corinna Thurow, Christiane Gatz

The RNA silencing suppressor protein encoded by cucumber mosaic virus perturbs host jasmonate and salicylate responses **P308**
Mathew G Lewsey, Alex M Murphy, Daniel MacLean, Neil Dalchau, Mark Bennett, Michael Moulin, Alison G Smith, Glen Powell, David E Hanke, John P Carr

Dissection of RPM1-mediated disease resistance using a novel genetic screen **P309**
Mindy Roberts, Tim Eitas, David Hubert, Jeff Dangl

The role of protease inhibitors in the genetic network restricting pathogen-induced necrosis **P310**
Kristin Laluk, Hongli Luo, Fengming Song, Tesfaye Mengiste

Ecological genetics of microbial sensing in British populations of *Arabidopsis thaliana* **P311**
Eric Holub, Robin Allaby, Laura Rose

Regulation of a bean proline-rich protein gene expression during defense response in transgenic Arabidopsis **P312**
Songhita Das, Mona Mehdy

The Arabidopsis CBP60g and h proteins define a critical node in salicylic acid signalling **P313**
Lin Wang, Kenichi Tsuda, Masanao Sato, Fumiaki Katagiri, Jane Glazebrook

MKK1 and MKK2 synergistically regulate developmental and disease resistance **P314**
Peter Morris, Jin-Long Qiu, Lu Zhou, Byung-Wook Yun, Henrik Nielsen, Berthe Fiil Klaus Petersen, Gary Loake, John Mundy

GABA regulates E-2-hexenal responses and Pseudomonas susceptibility **P315**
Rossana Mirabella, Duck Hwan Park, Han Rauwerda, Michel Haring, Alan Collmer, Robert Schuurink

Multiple hormone signaling sectors are shared among various types of inducible defense **P316**
Kenichi Tsuda, Masanao Sato, Thomas Stoddard, Jane Glazebrook, Fumiaki Katagiri

Genetic analysis of salicylic acid perception **P317**
Juan Vicente Canet, Alejandra Roig, Albor Dobón, Pablo Tornero

Site of action of salicylate antagonism in the jasmonate signaling pathway **P318**
Antonio Leon-Reyes, Dieuwertje Van der Does, Annemart Koornneef, Laurens Pauwels, Hana Návarová, Saskia Van Wees, Elvira S De Lange, Alain Goossens, Johan Memelink, Tita Ritsema, Corné Pieterse

Sensitive and fast laser-based techniques to monitor signalling molecules in Arabidopsis **P319**
Simona Cristescu, Frans Harren

Transcript profiling of chitosan-treated Arabidopsis seedlings **P320**
Giovanni Povero, Elena Loreti, Chiara Pucciariello, Donatella Di Tommaso, Gianluca Di Tommaso, Alberto Piaggesi, Pierdomenico Perata

DIACYLGLYCEROL KINASE 5 is required for SA responsiveness and disease resistance in Arabidopsis **P321**
Saskia CM Van Wees, Bas Van Schooten, Corné MJ Pieterse, Teun Munnik

SSV1 and ATL6 as C/N regulatory E3 ligase, are also involved in immune response system in Arabidopsis **P322**
Shugo Maekawa, Takeo Sato, Yutaka Asada, Shigetaka Yasuda, Midori Yoshida, Junji Yamaguchi

Three *Hyaloperonospora arabidopsidis* RXLR effector proteins interact with members of the Arabidopsis prenylated Rab acceptor PRA1 family **P323**
Jens Steinbrenner, Mary Coates, Susan Donovan, Tina Payne, Peter Bittner-Eddy, Sarat Bimanadham, Volkan Cevik, Jim Beynon

Functional analysis of differentially expressed proteins of *Arabidopsis thaliana* after infection with the pathogenic fungus *Verticillium longisporum* **P324**
Christine Druebert, Saskia Floerl, Andrea Polle

Functional analysis of transcriptional Repressors DEAR1 and ERF9 in terms of plant defense in Arabidopsis **P325**
Yutaka Asada, Natsuko Yamoto, Kazuma Takahashi, Kuniaki Katsumata, Junji Yamaguchi

Systemic disease resistance conferred by the mycorrhiza fungus *Piriformospora* indica requires jasmonic acid signaling and the cytoplasmic function of NPR1 **P326**
Alexandra Molitor, Elke Stein, Karl-Heinz Kogel, Frank Waller

The WRKY33 transcription factor of Arabidopsis is involved in balancing the hormone signaling pathways and adjusting the metabolic response to *Botrytis* infection **P327**
Rainer Birkenbihl, Imre Somssich

Involvement of autophagy in plant defense **P328**
Heike D Lenz, Andrea A Gus, Thorsten Nürnberger

The oxidative pentose phosphate pathway and plant defense responses **P329**
Zhonglin Mou, Yuqing Xiong, Christopher DeFraia, Donna Williams, Xudong Zhang

Analysis and comparison of regulatory mechanisms of *PR-4* genes in Arabidopsis and wheat **P330**
Silvia Proietti, Sjoerd Van der Ent, Antonio Leon-Reyes, Corné MJ Pieterse, Laura Bertini, Carlo Caporale, Carla Caruso

A family of ubiquitin ligases transmits ROS signals in plant cell death induction and stress response **P331**
Karolin Eifler, Wolf-Rüdiger Scheible, Nikolaus Schlaich, Dieter Ernst, Maria Novatchkova, Robert Konrat, Marcus Garzón, Kerstin Luxa, Andreas Bachmair

Additive effects of RNAi-mediated plant resistance against root knot nematodes **P332**
Wayne L Charlton, H Yael Meller Harel, Manjula Bakhetia, Jennie K Hibbard, Howard J Atkinson

The *Arabidopsis thaliana* protein phosphatase PP2C5 is a novel MAPK phosphatase regulating ABA signalling **P333**
Anita Brock, Roland Willmann, Laure Grefen, Dagmar Kolb, Irute Meskiene, Alois Schweighofer, Thorsten Nürnberger, Andrea Gust

Effect of the Geminivirus C2/L2 protein on the CSN complex **P334**
Rosa Lozano-Durán, Alberto P Macho, Giuliana Gusmaroli, Ana P Luna, Adela Zumaquero, Carmen R Beuzón, Xing Wang Deng, Eduardo R Bejarano

Plant SUMO paralogs have distinct functions in development and innate immunity **P335**
Harrold A van den Burg, Harrold A van den Burg, Ramachandra Kini, Pierre J GM de Wit, Frank LW Takken

Identification of PAMPs from *Xanthomonas axonopodis* pv *Citri* **P336**
Martin Lipschis, Georg Felix

Keeping up multiple biotic stress responses **P337**
Mieke de Wit, Sjoerd van der Ent, Laurentius ACJ Voesenek, Ronald Pierik

Hunting jasmonate targets with the yeast three-hybrid technology **P338**
Stephanie Cottier, Katja Schneider, Zheming Wang, Markus Kaiser, Erich Kombrink

Cloning ATR5 from Arabidopsis downy mildew pathogen *Hyaloperonospora arabidopsidis* **P339**
Kate Bailey, Volkan Cevik, Nick Holton, Eric Holub, Mahmut Tor

Structural and functional analysis of the type III secretion system effector AvrRpm1 **P340**
Karen Cherkis, Jeffery Dangl, John Sondek

Control mechanisms for activation of a novel CC-NBS-LRR protein, UNI-mediated signals that induce both SA-dependent defense and CK-dependent morphological signals **P341**
Kwi Mi Chung, Kadunari Igari, Masao Tasaka

A proteomic approach to discover biosynthetical and regulatory protein complexes in plant secondary metabolism **P342**
Jan Geerinck, Maarten Dedecker, Eveline Van de Slijke, Geert Persiau, Yelle Buffel, Dominique Eeckhout, Laurens Pauwels, Sofie Tilleman, Dirk Inzé, Geert De Jaeger, Alain Goossens

The SUMO protease OTS1 is a novel component affecting the SA-mediated response **P343**
Lucio Conti, Andrew Love, Elisabeth O'Donnell, Byung-Wook Yun, Gary Loake, Joel Milner, Ari Sadanandom

An E3 ubiquitin ligase triplet negatively regulates PAMP-triggered immunity in Arabidopsis **P344**
Marco Trujillo, Kazuya Ichimura, Catarina Casais, Ken Shirasu

Microbe-associated molecular pattern-induced Ca^{2+} signalling in *Arabidopsis thaliana* **P345**
Stefanie Ranf, Justin Lee, Dierk Scheel

Genetic analysis of *Burkholderia* elicitor responses in Arabidopsis **P346**
Natalia Dinischiotu, Bart Feys

Arabidopsis class II TGA transcription factors are essential for the jasmonic acid/ethylene-induced PDF1.2 expression **P347**
Mark Zander, Sylvain La Camera, Olivier Lamotte, Jean-Pierre Métraux, Christiane Gatz

Natural Variation

Patterns of shared polymorphism between *Arabidopsis halleri* and *A. lyrata*: the role of demographic and selection processes P370
Camille Roux, Xavier Vekemans, Vincent Castric

Cell Biology

A tripartite SNARE-K^+ channel complex involved in Arabidopsis potassium nutrition P371
Annegret Honsbein, Sergei Sokolovski, Prisca Campanoni, Rejane Pratelli, Manuel Paneque, Ingela Johansson, Michael R Blatt

Dissecting endomembrane trafficking underlying gravitropic responses in *Arabidopsis thaliana* via chemical genomics P372
Michelle Brown, Georgia Drakakaki, Stephanie Robert, Anna-Maria Szatmari, Eugenia Russinova, Jiri Friml, Natasha Raikhel, Glenn Hicks

Functional modules in the Arabidopsis core cell cycle binary protein-protein interaction network P373
Joanna Boruc, Hilde Van den Daele, Jens Hollunder, Stephane Rombauts, Evelien Mylle, Rebecca de Clerq, Pierre Hilson, Dirk Inze, Lieven De Veylder, Eugenia Russinova

Why tetraploid cells are larger than diploid cells in Arabidopsis? Application of an artificial tetraploidization method to Arabidopsis research P374
Hirokazu Tsukaya

Functional analysis of fused-kinase signalling in gametophytic cytokinesis P375
Trudie Allen, Sung-Aeong Oh, Anna Sidorova, David Twell

***AtPP1* encoding a peptidyl-prolyl cis/trans isomerase regulates flowering time in Arabidopsis** P376
Yu Wang, Daiwen Yang, Hao Yu, Yih-Cherng Liou

Molecular chaperones and their receptors in posttranslational protein targeting P377
Verena Kriechbaumer, C Ottilie Freiin Loeffelholz von Colberg, Rowena Shaw, Anne-Marie Harrison, Ben M Abell

Arabidopsis LIM domain proteins P378
Monika Dieterle, Clément Thomas, Jessica Papuga, Stéphane Tholl, Céline Hoffmann, Flora Moreau, André Steinmetz

The exocyst in *Arabidopsis thaliana* - characterisation of Exo84 homologues P379
Elizabeth Turner, Steve Baldwin, Alison Baker

The Arabidopsis CBP20 targets the cap-binding complex to the nucleus and is stabilized by CB P380
Daniel Kierzkowski, Maciej Kmieciak, Paulina Piontek, Anna Kapczynska, Przemyslaw Wojtaszek, Zofia Szwejkowska-Kulinska, Artur Jarmolowski

Integrity of the plant golgi apparatus P381
Carmen Faso, Ya-Ni Chen, Kentaro Tamura, Aurelia Boulaflous, Federica Brandizzi

Mechanistic framework for polar PIN targeting P382
Jurgen Kleine-Vehn, Jiri Friml

Genomic and non genomic effect of auxin on PIN auxin efflux carrier trafficking P383
Stephanie Robert, Jurgen Kleine-Vehn, Thomek Paciorek 1, Jiri Friml

Synthesis and trafficking of the tonoplast potassium channel AtTPK1 P384
Marie Maitrejean, Michael M Wudick, Camilla Völker, Katrin Czempinski, Emanuela Pedrazzini, Alessandro Vitale

Analysis of R-SNAREs mediating endosomal/vacuolar membrane fusion in *Arabidopsis thaliana* P385
Kazuo Ebine, Masaru Fujimoto, Tatsuaki Goh, Jun Ito, Tomohiro Uemura, Akihiko Nakano, Takashi Ueda

Influence of reduced UDP-glucose dehydrogenase activity on *Arabidopsis thaliana*: new cell wall mutants P386
Rebecca Reboul, Claudia Geserick, Ursula Lütz-Meindl, Raimund Tenhaken

A tight balance between cyclin-dependent kinases and their inhibitors controls male gametophyte development in Arabidopsis P387
Xin'ai Zhao, Hirofumi Harashima, Nico Dissmeyer, Stefan Pusch, Nicolas Baumberger, Moritz K Nowack, Pascal Genschik, Arp Schnittger

Characterization of the *LEA18* gene family of *Arabidopsis thaliana* P388
Margarita Santiago, Maria Patricia Romero, Dayan Sanhueza, Herman Silva

The Dof family of plant transcription factors: Insights into the evolution of non-cell-autonomous function P389
Munawar Ahmad, Yeonggil Rim, Won Kyong Cho, Hyosub Chu, Yeonhwa Jo, Xuping Zhao, Che Ok Jeon, Hye-Jin Kim, Jong-Chan Hong, William J Lucas, Jae-Yean Kim

Metabolomics analysis of Arabidopsis suspension cultured cells that overexpress a putative vacuolar membrane transporter P390
Koh Aoki, Ryosuke Sasaki, Miwa Ohnishi, Aya Anegawa, Yuko Sugiyama, Yoko Iijima, Nozomu Sakurai, Mami Yamazaki, Tetsuro Mimura

Isolation and identification of ubiquitin-related proteins from Arabidopsis seedlings **P391**
Tomoko Igawa, Masayuki Fujiwara, Hirotaka Takahashi, Tatsuya Sawasaki, Yaeta Endo, Motoaki Seki, Kazuo Shinozaki, Yoichiro Fukao, Yuki Yanagawa

Analysis of interactions between Arabidopsis CAX1 and CAX3 Ca2+ transporters **P392**
James Connorton, Jian Zhao, Ying-qing Guo, Toshiro Shigaki, Kendal Hirschi, Jon Pittma

Analysis of the protein association of the ribosomal lateral stalk by immunoprecipitation of epitope tagged 12-kDa P-proteins **P393**
Luz Maria Borreli, Kathleen Szick-Miranda

Synthesis of very long chain fatty acids in the epidermis controls cell division in Arabidopsis **P394**
Takashi Nobusawa, Yoko Okushima, Masaaki Umeda

Cohesin gene defects impair sister chromatid alignment and genome stability in *Arabidopsis thaliana* **P395**
Veit Schubert, Andrea Weissleder, Hoda Ali, Inna Lermontova, Joerg Fuchs, Ingo Schubert

Function of NimA-related protein kinases in Arabidopsis **P396**
Hiroyasu Motose, Takahiro Hamada, Takehide Kato, Takashi Hashimoto, Yuichiro Watanabe, Tatsuya Sakai, Taku Takahashis

Functional analyses of cell wall genes involved in physical properties of supportive tissue in the Arabidopsis stem **P397**
Ryusuke Yokoyama, Kaori Sato, Kento Koizumi, Miki Nogami, Kazuhiko Nishitani

Determining primary and specific effects on the nuclear transcriptome in response to inhibition of plastid translation in Arabidopsis **P398**
Katharine Howell, Ralph Bock

StSEBF-homologs in *Arabidopsis thaliana* **P399**
Janina Fuss, Kirsten Krause

Drought stress-induced Rma1H1, a RING membrane-anchor E3 ubiquitin ligase homolog, regulates aquaporin levels via ubiquitination in transgenic Arabidopsis plants **P400**
Hyun Kyung Lee, Seok Keun Cho, Ora Son, Zhengyi Xu, Inhwan Hwang, Woo Taek Kim

AtBG2, a ß-glucosidase homolog localized in the vacuole increases cellular ABA via hydrolysis of ABA-GE **P401**
Zhengyi Xu

AtENT1, an adaptor for clathrin-mediated endocytosis, may play a role in the endocytic pathway during plant cytokinesis **P402**
Kyungyoung Song, Hyangju Kang, Eunhye Kwon, Inhwan Hwang

Characterization of DAD1-like acylhydrolase related to seed viability in Arabidopsis **P403**
Eun Yu Kim, Young Sam Seo, Soo-Jin Kim, Woo Taek Kim

Tail-anchored proteins in plants **P404**
Emanuela Pedrazzini

AtKCO3 potassium channel and tonoplast biogenesis **P405**
Giuseppe Grassi, Alexandra Grippa, Alessandro Vitale, Katrin Czempinski, Emanuela Pedrazzini

A constitutively active phyA mutant is deficient in nuclear transport **P406**
Anja Possart, Wiebke Nordmeier, Eberhard Schaefer, Andreas Hiltbrunner

Enzymatic characterization of DAD1-like acylhydrolase families targeted to the chloroplast in Arabidopsis **P407**
Young Sam Seo, Eun Yu Kim, Jeong Hoe Kim, Woo Taek Kim

Iron loading during embryogenesis in Arabidopsis at tissue, cellular and sub-cellular levels revealed by *in situ* histochemical staining **P408**
Hannetz Roschzttardtz, Geneviéve Conéjéro, Catherine Curie, Stéphane Mari

Systematic protein localization in Arabidopsis **P409**
Tao Zheng, Konstantinos Alexiou, Max Bush, Cristina Pignocchi, John Doonan

Alterations in the cellular distribution pattern of AnnAt1 upon NaCl and ABA treatment **P410**
Malgorzata Lichocka, Dorota Konopka-Postupolska

An investigation into poly(ADP)ribosylation in *Arabidopsis thaliana* **P411**
Mai-Britt Jensen, Sarah Henry, Susan Rosser

Artificial microRNA specifically down-regulates cysteine synthesis in mitochondria **P412**
Florian H Haas, Corinna Heeg, Markus Wirtz, Rudiger Hell

Spatial regulation of ROP4 and GDI1 in root hair growth **P413**
Xin Chen, Claire S Grierson

Functional analysis of GONST3 and 4, nucleotide-sugar transporters of *Arabidopsis thaliana* **P414**
Michael Handford, José Patricio Miranda, Diego Ampuero, Mariela Huichalaf, Sebastian Febres

Systems Biology

Shedding light upon the plant circadian clock: Models including explicitly the dynamics of the photoreceptor phyB **P437**
Christian Fleck, Andrew Millar, Eberhard Schafer, Stefan Kircher, Ferenc Nagy

Light induced degradation of the transcription factor PIF3 **P438**
Christian Fleck, Sebastian Sonntag, Stefan Kircher, Eberhard Schafer

The Arabidopsis circadian clock: Insights from mathematical modelling **P439**
Ozgur Akman, John O'Neill, David Rand, James Locke, Andrew Millar

Dissection of endomembrane sorting using bioactive chemicals **P440**
Stephanie Robert, Georgia Drakakaki, Brown Michelle, Szatmari Anna-Maria, Friml Jiri, Russinova Eugenia, Natasha V Raikhel, Glenn R Hicks

Under the skin: transcriptional subnetworks in the Arabidopsis root **P441**
Jalean J Petricka, Philip N Benfey

An Arabidopsis genetical genomics approach to improve phytonutrient quality in Brassica vegetable crops **P442**
Wessel van Leeuwen, Ric CH de Vos, HK Kim, Rob Verpoorte, Ronny VL Joosen, Kim Boutilier, Frank Johannes, Ritsert C Jansen, Mark GM Aarts

Large-scale analysis of Arabidopsis transcription reveals a basal co-regulation network **P443**
Osnat Atias, Benny Chor, Daniel A Chamovitz

Multiple alternative splicing events in individual transcripts; analyses using full-length cDNAs and tiling arrays **P444**
Kei Iida, Shuji Kawaguchi, Kousuke Hanada, Kaoru Fukami-Kobayashi, Atsushi Toyoda, Yoshiyuki Sakaki, Masatomo Kobayashi, Motoaki Seki, Kazuo Shinozaki, Tetsuro Toyoda

ARTADE2.0: A mathematical integration of tiling array, CAGE and sequence data to elucidate the transcriptional systems dynamics of *Arabidopsis thaliana* **P445**
Shuji Kawaguchi, Kousuke Hanada, Kei Iida, Yoshiki Mochizuki, Akihiro Matsui, Masanori Okamoto, Motoaki Seki, Kazuo Shinozaki, Tetsuro Toyoda

A one-loop model of the *Ostreococcus tauri* circadian clock **P446**
Carl Troein, Andrew Millar

Comprehensive analysis of Arabidopsis expression level polymorphisms with simple inheritance **P447**
Stéphanie Plantegenet, Johann Weber, Darlene R Goldstein, Georg Zeller, Cindy Nussbaumer, Jérôme Thomas, Detlef Weigel, Keith Harshman, Christian Hardtke

Control of the accumulation of major flavonol glycosides by R2R3-MYB production of flavanol glycosdies regulators in adult *Arabidopsis thaliana* plants **P448**
Ralf Stracke, Matthias Keck, Antje Bluemke, Karsten Niehaus, Bernd Weisshaar

Using synthetic biology and a marine algae to simplify the study of light entrainment to the Arabidopsis circadian clock **P449**
Laura Dixon, Florence Corellou, François-Yves Bouget, Andrew Millar

Quantification of BAK1 and BRI1 receptors **P450**
GW van Esse, JW Borst, C Albrecht, M de Gee, J Molenaar, SC de Vries

Transcription regulatory programs of cell cycle control in the root vascular tissues **P451**
Sarit Weissmann, Je-Gun Joung, Zhangjun Fei, Yra Helariutta, Ji-Young Lee

Composite module analysis using BIOBASE ExPlain™ plant identifies factors, which may influence *ms1* pollen and tapetum developmental phenotypes **P452**
Raymond DiDonato, Ruy Jauregui, Alexander Kel, Edgar Wingender

Chloroplast proteome analysis: New insights into intracellular trafficking **P453**
Sylvain Bischof, Thomas Wildhaber, Trösch Raphael, Felix Kessler, Wilhelm Gruissem, Sacha Baginsky

Global control of rhythmic gene expression by the transcription factor LHY **P454**
Sally Adams, Siren Veflingstad, David Rand, Bärbel Finkenstädt, Sashca Ott, Isabelle Carré

Hot Topics

Genetic mechanisms of hybrid incompatibility in *Arabidopsis thaliana* **P455**
Roosa Laitinen, Kirsten Bomblies, Helena Boldt, Marco Todesco, Detlef Weigel

Inhibition of SNF1-related protein kinase1 activity and regulation of metabolic pathways by trehalose 6-phosphate **P456**
Lucia F Primavesi, Cátia Nunes, Anabela Bernardes da Silva, Pedro M Fevereiro, P John Andralojc, Alfred J Keys, Astrid Wingler, Mitul Patel, Ram S Misra, Ben G Davis, Matthew J Paul

Design and analysis of ChIP-Seq experiments in plants: a systematic comparison of ChIP-Seq and ChIP-chip for APETALA2 (AP2), FD, and SCHLAFMÜTZE (SMZ) **P457**
Levi Yant, Felix Ott, Heike Keller, Detlef Weigel, Markus Schmid

New Tools and Resources

Transcriptome profiling of RNA-processing mutants – Uncovering the hidden layer of the Arabidopsis transcriptome **P480**
Sascha Laubinger, Georg Zeller, Stefan R Henz, Timo Sachsenberg, Gunnar Rãtsch, Detlef Weigel

Molecular tools for studying the Arabidopsis transcription factor ORFeome **P481**
Christoph Weiste, Tim Iven, Nora Glaser, Stefan Dröge, Andrea Hermann, Luis Oñate-Sánchez, Wolfgang Dröge-Laser

Resources for Gateway recombinational cloning in plant cells **P482**
Mansour Karimi, Rebecca De Clercq, Björn De Meyer, Rudy Vanderhaegen, Wilson Ardilez, Pierre Hilson

AraCyc and PlantCyc: Metabolic pathway databases for plant research **P483**
K Dreher, S Singh, M Ahn, A Chi, K He, E Huala, A S Karthikeyan, V Kirkup, C Lee, R Leitao, T Meyer, R Muller, L Ploetz, S Rhee, S Singh, C Wilks and P Zhang

Imaging of individual leaf expansion in three dimensions: the analysis of cell volume of epidermal and sub-epidermal tissues **P484**
Nathalie Wuyts, Genevieve Conejero, Jean-Luc Verdeil, Catherine Massonnet, Jean-Luc Regnard, Evelyne Costes, Christine Granier

Fluorescence activated cell sorting (FACS) of embryonic cells by use of the *DRN::erGFP marker* **P485**
Melanie Cole, Wolfgang Werr

New data, new challenges – Improving Arabidopsis annotation **P486**
David Swarbreck, Philippe Lamesch, Cynthia Lee, Robert Muller, Rajkumar Sasidharan, Chris Wilks, Eva Huala

The CPIB Root Atlas: A tool for viewing integrative root systems biology data **P487**
Michael Wilson, Tara Holman, Andrew French, Mike Stout, Darren Wells, Kim Kenobi, Malcolm Bennett, Mike Holdsworth, Tony Pridmore, Charlie Hodgman

SUBA: The Arabidopsis protein subcellular database **P488**
Sandra K Tanz, Joshua L Heazlewood, Julian Tonti-Filippini, A Harvey Millar, Ian Small

Alternative splicing and NMD in Arabidopsis **P489**
Craig Simpson, Maria Kalyna, Dominika Lewandowska, Branislav Kusenda, John Fuller, Linda Milne, Jim McNicoll, Gillian Clark, Andrea Barta, John Brown

Mining small RNA sequencing data: A new approach to identify small nucleolar RNAs in Arabidopsis **P490**
Ho-Ming Chen, Shu-Hsing Wu

The classical genetic map of *Arabidopsis thaliana* **P491**
David Meinke

Characterization of fluorescent carbohydrate binding dyes for analysis of the cell wall **P492**
Andrew Carroll, Charlie Anderson, Laila Akhmetova, Chris Somerville

RARGE: A web database of Arabidopsis resources **P493**
Kenji Akiyama, Fumiyoshi Myouga, Takashi Kuromori, Kazuo Shinozaki, Tetsuya Sakurai

No bridge too far: A simple method for multi-protein interaction analysis **P494**
Christopher Grefen, Annegret Honsbein, Klaus Harter, Mike Blatt

Summary of resource projects in RIKEN BRC **P495**
Shiori Ota, Hiroshi Abe, Satoshi Iuchi, Toshihiro Kobayashi, Masatomo Kobayashi

Expression analysis of short open reading frames (sORFs) in Arabidopsis by custom microarray **P496**
Mieko Higuchi, Kousuke Hanada, Youichi Kondou, Tatsuya Sakai, Yoko Horii, Mika Kawashima, Minami Matsui

Where to fasten – transcription factors and their DNA-motif companions **P497**
Luise H Brand, Sabine Hummel, Achim Hahn, Klaus Harter, Dierk Wanke

Optical contrast enhancement by decay shape analysis of fluorescence intensity decay curves **P498**
Frank Schleifenbaum, Kirstin Elgass, Marcus Sackro, Katharina Caesar, Kenneth Berendzen, Klaus Harter, Alfred J Meixner

The Arabidopsis Biological Resource Center – Stock donation and distribution **P499**
Randy Scholl, Luz Rivero, Emma Knee, Deborah Crist, Christopher Calhoun, Natalie Case, Juan Castro, James Mann, Julie Miller, Bhuma Muthuvel, Garret Posey, Ridhima Shah, Pamela Vivian, Damitha Wickramasinghe, Hehua Yan, Zhen Zhang

Subcellular compartmentation of primary metabolism in *Arabidopsis thaliana* leaves – new insights from non-aqueous fractionation **P500**
Daniel Vosloh, Stéphanie Arrivault, Regina Feil, John Lunn, Mark Stitt

Streamlined sub-protocols for floral-dip transformation and selection of transformants **P501**
Amanda M Davis, Anthony Hall, Andrew Millar, Chiarina Darrah, Seth J Davis

Characterising the mechanical properties of elongating root cells **P502**
Darren M Wells, Rosemary J Dyson, Ming Qian, Malcolm Bennett, T Charlie Hodgman, Oliver E Jensen, Nicola M Everitt

PosMed-plus: An information system making the utmost use of Arabidopsis knowledge to assist molecular breeding of crops **P503**
Yuko Makita, Norio Kobayashi, Kei Iida, Satomi Asano, Yuko Yoshida, Naohiko Heida, Mrinalini Deshpande, Rinki Bhatia, Akihiro Matsushima, Manabu Ishii, Yoshiki Mochizuki, Kousuke Hanada, Shuji Kawaguchi, Takashi Kuromori, Motoaki Seki, Kazuo Shinozaki, Tetsuro Toyoda

Rice Fox Database: A database of rice full length cDNA overexpressed Arabidopsis mutants **P504**
Tetsuya Sakurai, Youichi Kondou, Atsushi Kurotani, Kenji Akiyama, Hitoshi Sakakibara, Miyako Kusano, Takeshi Yoshizumi, Mieko Higuchi, Shinya Takahashi, Takanari Ichikawa, Hirofumi Kuroda, Hideki Takahashi, Masaki Mori, Hiroshi Takatsuji, Kenji Oda, Hirohiko Hirochika, Minami Matsui

GABI-Kat: Keeping the standard high in an intensively used T-DNA insertion line collection **P505**
Gunnar Huep, Nils Kleinboelting, Andreas Klassen, Prisca Viehoever, Heinz Saedler, Bernd Weisshaar

Transport of auxins in Arabidopsis cell suspension **P506**
Daniela Seifertova, Jan Petrasek, Eva Zazimalova

Improvement of the generation of stable knockdown lines using primary synthetic microRNAs (pri-smiRNAs) in Arabidopsis **P507**
Sandra Niemeier, Thomas Merkle

Comprehensive prediction of novel microRNA targets in *Arabidopsis thaliana* **P508**
Leonardo Alves-Junior, Sandra Niemeier, Arne Hauenschild, Marc Rehmsmeier, Thomas Merkle

Specific labelling of cell types, structures and developmental stages in *Arabidopsis thaliana* **P509**
J Grønlund, S Kumar, S Dhondt, G Beemster, P Hilson, J Beynon, V Buchanan-Wollaston

AGRONOMICS1 – A new resource for Arabidopsis transcriptome profiling **P510**
Hubert Rehrauer, Catherine Fournier, Naira Naouar, Andrea Patrignani, Stephane Rombauts, Sascha Laubinger, Georg Zeller, Stefan Henz, Yves Van de Peer, Marnik Vuylsteke, Detlef Weigel, Pierre Hilson, Wilhelm Gruissem, Lars Hennig

A quantitative approach to monitor amiRNA-mediated RNA interference in Arabidopsis protoplasts **P511**
Claude Becker, Alexander Dovzhenko, Dominik Lenz, Klaus Palme

The Arabidopsis Biological Resource Center – 2009 activities and stock holdings **P512**
Randy Scholl, Emma Knee, Deborah Crist, Luz Rivero, Christopher Calhoun, Natalie Case, Juan Castro, James Mann, Julie Miller, Bhuma Muthuvel, Garret Posey, Ridhima Shah, Pamela Vivian, Damitha Wickramasinghe, Hehua Yan, Zhen Zhang

The NASC Affymetrix service **P513**
Daisy Belfield, Marcos Castelallanos, Zoe Emmerson, Graeme Gill, Neil Graham, Nick James, Lubomira Kacinova, Nicola Leftley, Bob Parkinson, Rebecca Roberts, Beatrice Schildknecht, Sean May

Rapid and efficient analysis of protein subcellular localization and interactions using transient transformation of Arabidopsis seedlings **P514**
Jessica Marion, Mehdi Khafif, Yannick Bellec, Lien Bach, Lionel Gissot, Jean-Denis Faure, Christian Meyer

High complexity, random-primed domain libraries for yeast two-hybrid analysis of the *A. thaliana* interactome **P515**
Hélène Kiefer, Petra Tafelmeyer, Maryline Masson, Emilie Vinolo, Jean-Christophe Rain, Nam-Hai Chua, Heribert Hirt, Jens D Schwenn, Martin F Yanofsky, Laurent Daviet, Etienne Formstecher

NASC germplasm resources and annotation **P516**
Daisy Belfield, Marcos Castellanos, Zoe Emmerson, Graeme Gill, Neil Graham, Nick James, Lubomira Kacinova, Nicola Leftley, Bob Parkinson, Rebecca Roberts, Beatrice Schildnecht, Sean May

Transcriptomic responses of Arabidopsis to post-emergence herbicides targeting diverse cellular processes **P517**
Scott Baerson, Zhiqiang Pan, Julie Blessitt, Ameeta Agarwal, Stephen Duke

The *Arabidopsis lyrata* genome – what can we learn from the close relative of *Arabidopsis thaliana* **P518**
Ya-Long Gu, Jan-Fang Chen, Tina T Hu, Georg Haberer, Jesse Hollister, Pedro Pattyn, Richard M Clark, Stephan Ossowski, Korbinian Schneeberger, Sang-Tae Kim, Jun Cao, Christa Lanz, Robert P Otillar, Joy M Bergelson, Justin O Borevitz, Anne E Hall, Charles H Langley, Barbara Neuffer, June B Nasrallah, Outi Savolainen, Stephen I Wright, Igor V Grigoriev, Klaus F X Mayer, Jeremy Schmutz, Yves Van de Peer, Brandon S Gaut, Magnus Nordborg, Dan Rokshar and Detlef Weigel

AtEnsembl. **P519**
Daisy Belfield, Marcos Castellanos, Zoe Emmerson, Graeme Gill, Neil Graham, Nick James, Lubomira Kacinova, Nicola Leftley, Bob Parkinson, Rebecca Roberts, Beatrice Schildnecht, Sean May

Plant Growth Regulators

A subunit of the Anaphase-Promoting Complex (APC) affects auxin-regulated development in Arabidopsis **P520**
Donna Lindsay, Peta Bonham-Smith, Gordon Gray, Troy Harkness

Arabidopsis ATP-binding cassette transporters promote efflux of the auxin precursor indole-3-butyric acid **P521**
Lucia Strader, Bonnie Bartel

Effects of gibberellin on the growth and gene expression in the Arabidopsis root **P522**
Haniyeh Bidadi, Masashi Asahina, Shinjiro Yamaguchi, Shinobu Satoh

Cytosolic activity of SPINDLY implies the existence of a DELLA-independent gibberellin-response pathway to suppress cytokinin responses **P523**
Inbar Maymon, Yaarit Greenboim-Wainberg, Sivan Sagiv, David Weiss

ABA regulation of nodulation in *Medicago truncatula* **P524**
Yiliang Ding, Jeanne Harris, Giles Oldroyd

Nitric oxide biosynthesis and genome-wide analysis of its regulatory functions in *Arabidopsis thaliana* **P525**
Jorge Lozano-Juste, Laura Yeves, Jose Leon

Far-red light inhibits germination through DELLA-dependent stimulation of ABA synthesis and ABI3 activity **P526**
Urszula Piskurewicz, Eric Lacombe, Luis Lopez-Molina

A J-domain containing protein, JRF1, regulates the floral transition in Arabidopsis **P527**
Lisha Shen, Hao Yu

The bHLH transcription factor SPT and DELLA proteins act together to regulate cell size of Arabidopsis cotyledons in a GA-dependant manner **P528**
Eve-Marie Josse, Yinbo Gan, Kelly Stewart, Alison Gilday, Ian Graham, Karen Halliday

Local action of GOLVEN secretory peptides stabilizes an auxin efflux carrier during plant gravitropic responses **P529**
Ryan Whitford, Ana Fernandez, Amparo Cuellar, Jurgen Kleine-Vehn, Ruth De Groodt, Steffen Vanneste, Tom Beeckman, Jiri Friml, Pierre Hilson

A transcriptional cascade mediates the Arabidopsis cytokinin response **P530**
Kristine Hill, Dennis E Mathews, G Eric Schaller

High-throughput functional genomics of cell wall dynamics during root growth and development **P531**
Tara Holman, Michael Wilson, Darren Wells, Iben Sorrensen, William Willats, Paul Knox, Michael Holdsworth, Malcolm Bennett

Regulation of cell morphology by auxin **P532**
Angharad Jones, Eric Kramer, Kirsten Knox, Ranjan Swarup, Colin Lazarus, Ottoline Leyser, Claire Grierson, Malcolm Bennett

Gibberellin signaling controls cell proliferation rate in Arabidopsis **P533**
Patrick Achard, Andi Gusti, Soizic Cheminant, Malek Alioua, Stijn Dhondt, Frederik Coppens, Gerrit Beemster, Pascal Genschik

Modelling auxin response **P534**
Martin Kieffer, Gary Mirams, Sarah Lee, Lynne Armitage, Alistair Middleton, Sara Peterson, Karin Ljung, Richard Napier, John King and Stefan Kepinski
Please note this abstract is associated with the Quantitative Modelling of Signalling Systems workshop and will not be presented as a poster

SERKs family of co-receptors functions in multiple pathways **P535**
Catherine Albrecht, Eugenia Russinova, Birgit Kemmerling, Wilma van Esse, Rumyana Karlova, Na Li, Sacco de Vries

The role of salicylic acid in Arabidopsis root growth **P536**
Mary Wildermuth, Alexander Jones

ROP localisation by auxin in Arabidopsis root hair cells **P537**
Robert Payne, Claire Grierson

Calmodulin binding transcription activator (CAMTA) 1 serves as a link between growth signals and stress responses **P538**
Yael Galon-Wolfenson, Roni Aloni, Dikla Nachmias, Orly Snir, Ester Feldmeser, Sarah Scrase-Field, Joy M Boyce, Nicolas Bouche, Mark R Knight, Hillel Fromm

Nucleus-focused proteomic analysis of Arabidopsis suspension cells treated by Brassinolide and/or Brz **P539**
Tomoaki Matsuo, Tomoaki Shigeta, Daisuke Yasuda, Yuya Yoshimitsu, Takafumi Mori

A dwarf mutant of *Arabidopsis thaliana* impaired in carbohydrate and gibberellin metabolism **P540**
Eleonora Paparelli, Silvia Gonzali, Giacomo Novi, Sandro Parlanti, Elena Loreti, Lorenzo Mariotti, Elena Degl'Innocenti, Lucia Guidi, Pierdomenico Perata

ASK3, a novel regulator of brassinosteroid signalling **P541**
Juliane Mayerhofer, Wilfried Rozhon, Elena Petutschnig, Shozo Fujioka, Claudia Jonak

Arabidopsis RPT2a, a subunit of 19S proteasome that negatively regulates endoreduplication and confers leaf size control **P542**
Kaori Sako, Yutaka Sonoda, Yuko Maki, Hiroko Yamamoto, Junji Yamaguchi

Isolation of a novel RING-type ubiquitin ligase SSV1 that regulates carbon/nitrogen response at early post-germinative growth stage in *Arabidopsis thaliana* **P543**
Takeo Sato, Shugo Maekawa, Yutaka Sonoda, Junji Yamaguchi

Molecular characterization of EIN2, a central element in plant hormone signalling **P544**
Silke Allekotte, Jan Voet van Vormizeele, Nicole Voet van Vormizeele, Georg Groth

Arabidopsis RACK1 proteins are negative regulators of ABA signalling in seed germination and early seedling development **P545**
Jianjun Guo, Junbi Wang, Wei-Dong Huang, Jiansheng Liang, Jin-Gui Chen

The role of the *Gibberellin 20-Oxidase* gene family in Arabidopsis development **P546**
Andrew Plackett, Nieves Fernandez-Garcia, Steven Thomas, Peter Hedden, Andy Phillips, Zoe Wilson

Indole-3-acetaldoxime dependent auxin biosynthesis in Arabidopsis **P547**
Satoko Sugawara, Yuji Kamiya, Yusuke Jikumaru, Atsushi Hanada, Shojiro Hishiyama, Takeshi Nishimura, Yunde Zhao, Tomokazu Koshiba, Hiroyuki Kasahara

A role for *KLU* in seed size control **P548**
Nikolai M Adamski, Elena Anastasiou, Sven Eriksson, Carmel O'Neill, Michael Lenhard

An intracellular ABA receptor regulates ABA signaling through direct inhibition of clade A PP2Cs **P549**
Julia Santiago, Americo Rodrigues, Angela Saez, Silvia Rubio, Regina Antoni, Lesia Rodriguez, Sang-Youl Park, Florine Dupeux, Jose Marquez, Sean Cutler, Pedro Rodriguez

A novel point mutation in a Poly (A) polymerase inversely affects the size of leaves and flowers in *Arabidopsis thaliana* **P550**
Son Lang Vi, Nicola Stacey, Michael Lenhard

The extracellular EXO protein mediates cell expansion in Arabidopsis **P551**
Florian Schröder, Janina Lisso, Carsten Müssig

Gibberellin biosynthesis and action in Arabidopsis roots **P552**
Richard Barker, Stephen Thomas, Peter Hedden, Malcolm Bennett

Putative phosphorylation sites of PIN3 are critical for its auxin efflux activity in Arabidopsis root hairs **P553**
Anindya Ganguly, Sang Ho Lee, Hyung-Taeg Cho

AtDOF6, an Arabidopsis DOF transcription factor putatively involved in the regulation of seed germination **P554**
Paloma Rueda, Cristina Barrero, Pilar Carbonero, Luis Oñate-Sánchez

The molecular mechanism of growth repression by BIG BROTHER **P555**
Lena Stransfeld, Michael Lenhard

Active CLV3 is an arabinosylated glycopeptide **P556**
Kentaro Ohyama, Hidefumi Shinohara, Mari Ogawa-Ohnishi, Yoshikatsu Matsubayashi

CES, a novel basic helix-loop-helix transcription factor regulating brassinosteroid responses and homeostasis **P557**
Wilfried Rozhon, Mamoona Khan, Sigrid Husar, Shozo Fujioka, Gerhard Adam, Christian Luschnig, Tobias Sieberer, Brigitte Poppenberger

Methyl jasmonate affects adventitious rooting in *Arabidopsis thaliana* plants and thin cell layers **P558**
Laura Fattorini, Giuseppina Falasca, Federica Della Rovere, Catherine Bellini, Maria Maddalena Altamura

Fruit growth in Arabidopsis occurs via DELLA-dependent and DELLA-independent GA responses **P559**
Sara Fuentes, Liz Alvey, Karin Ljung, Karim Sorefan, Nicholas P Harberd, Lars Østergaard

Differential expression of *Arabidopsis thaliana* sucrose phosphate synthase and sucrose phosphate phosphatase encoding genes **P560**
Cristóbal Girón, Beatriz Castrillo, Federico Valverde, Mª Teresa Ruiz, José Mª Romero

DELLA-mediated transcriptional control of GA-responsive growth and development in Arabidopsis **P561**
Anne Grønlund, Jane Griffiths, Aakriti Wanchoo, Michael Wilson, Tara Holman, Malcolm Bennett, Andy Phillips, Peter Hedden, Stephen Thomas

Flavonol 3-O-glycosylation is required for flavonol biosynthesis in Arabidopsis **P562**
Yin Ruohe, Messner Burkhard, Schaffner Anton R

Regulation of ABA signalling and lipid catabolism by the N-end rule pathway of targeted protein degradation **P563**
Tara Holman, Peter D Jones, Laurel Russell, Anne Medhurst, Susanna Úbeda-Tomás, Prabhavathi Talloji, Steven Footitt, Andreas Bachmair, Frederica Theodoulou, Michael Holdsworth

Identifying downstream regulators of cytokinin signalling during cambial development in Arabidopsis **P564**
Annakaisa Elo, Kaisa Nieminen, Juha Immanen, Ji-Young Lee, Ykä Helariutta

Bioenergy

Peroxisome

21st International Conference on Arabidopsis Research

Pacifico Yokohama, Japan
June 6-10, 2010

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Development
Cell Biology
Environmental Responses
Epigenomics and RNA Regulation
Crop Genomics
Systems Biology and Metabolism
Evolution and Natural Variations
Plant Hormone Regulation

Confirmed Invited Speakers

Motoyuki Ashikari
Kathryn Barton
David Baulcombe
Philip Benfey
Michael Bevan
Joseph Ecker
Ikuko Hara-Nishimura
Inhwan Hwang
Koh Iba
Dirk Inze
Tetsuji Kakutani
Steve Kay
Maarten Koornneef
Cris Kuhlemeier
Chentao Lin
Olivier Loudet
Makoto Matsuoka
Peter McCourt
Elliot Meyerowitz
Seung Yon Rhee
Kazuki Saito
Satoshi Tabata
Keiko Torii
Detlef Weigel
Shinjiro Yamaguchi
Qifa Zhang

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Takashi Araki, Masatomo Kobayashi, Yoshibumi Komeda, Minami Matsui, Akira Nagatani, Satoshi Naito, Yasukazu Nakamura, Masaru Ohme-Takagi, Kazuki Saito, Motoaki Seki and Hirokazu Tsukaya

http://arabidopsis2010.psc.riken.jp

Workshops

Tuesday 30th June 2009

16:00 - 17:30

1 Plant proteomics *Tinto*
Main Organiser - Harvey Millar

2 Programmed Cell Death *Moorfoot*
Main Organisers – Patrick Gallois and Paul McCabe

3 Quantitative modelling of signalling systems *Kilsyth*
Main Organisers – Stefan Kepinski and Alex Webb
This workshop starts at 15:45

Thursday 2nd July

16:30 - 18:00

1 Stomata - the ins and outs *Tinto*
Main Organisers – Julie Gray and Dominique Bergmann

2 Putting TAIR to work for you *Moorfoot*
Main Organisers – Eva Huala and Kate Dreher

3 Root system architecture *Kilsyth*
Main Organiser – Anna Amtmann

Saturday 4th July

16:30 - 18:00

1 Anther/pollen development *Tinto*
Main Organisers – Zoe Wilson and Hong Ma

2 Ambient temperature *Moorfoot*
Main Organiser – Seth Davis

Descriptions and Programmes

Tuesday 30th June

16:00 - 17:30

1 Plant proteomics *Tinto*

Breakthroughs in studying intra-cellular dynamics and environmental response in the Arabidopsis proteome

Workshop Organisers - Harvey Millar, Wolfram Weckwerth, Joshua Heazlewood, Alex Jones

The MASC Proteomics Subcommittee has run a workshop at each ICAR meeting since Berlin 2004. Proteomics is a rapidly growing field that is being widely adopted by Arabidopsis researchers. This workshop aims to provide updates to the community on proteomic tools and resources available in Arabidopsis, presented by members of this MASC committee. It also showcases the work of selected researchers from submitted abstracts that have used proteomics to address interesting biological questions in diverse fields. This year has a focus on quantification of proteomes and post-translation modification of proteins. This workshop has benefit for researchers with a general interested in proteomics and its uses, to those interested to meet and interact with potential collaborators, to those with specific interest in the biological results presented.

Programme

16:00 - 16:05	Introduction from Harvey Millar (UWA)
	Short talks on new resources/approaches since 2008 from MASCP
16:05 - 16:15	**Wolfram Weckwerth** (MSB, Vienna) Integrating metabolomics and proteomics: a how-to guide
16:15 - 16.25	**Josh Heazlewood** (JBEI/LBL) Mining online Arabidopsis proteomic resources
16:25 - 16.35	**Alex Jones** (Sainbury Lab, Norwich) Recent advances to aid phospho-peptide analysis
	Talk selected from Abstracts
16:35 - 16:50	**Waltraud Schulze** (MPIMP, Golm) **P431** ^{15}N metabolic labeling as a tool to study stress-induced dynamic changes in plasma membrane protein composition in Arabidopsis
16:50 - 17:05	**Alexander van der Krol** (Wageningen University) **P474** Mapping of the Arabidopsis ER and post-ER glycoproteome
17:05 - 17:20	**Georgia Drakakaki** (University of California, Riverside) **P436** Towards dissecting the trans golgi network using proteomics and chemical genomics
17:20 - 17:30	Guided discussion with attendees on topics of interest, new resources etc

2 Assaying for Hall Mark Features of Programmed Cell Death *Moorfoot*

Workshop Organisers – Patrick Gallois and Dr Paul McCabe

Programmed cell death (PCD) in plants is a vital process that is essential to correct development, defence and stress responses. However, there has been a lack of uniformity in the literature in identifying programmed cell death and identifying the various types of death. Cell death modes include apoptotic-like PCD, autophagic cell death and necrosis. The workshop will consist of short talks to discuss techniques for identifying, assaying and quantifying death in Arabidopsis. The workshop will illustrate the hallmark features of PCD including morphologies, release of mitochondrial proteins, activation of caspase-like molecules and degradation of DNA. There will be a discussion slot at the end of the workshop during which aspects not covered in talks could be brought up.

Programme

16:00 - 16:15	**Paul McCabe** (University College Dublin) Integrating metabolomics and proteomics: a how-to guide
16:15 - 16.30	**Morten Petersen** (Copenhagen University) Autophagy and cell death
16:30 - 16:45	**Hannele Tuominen** (Umea Plant Science Centre) **P029** Morphology of PCD in xylem elements
16:45 - 17:00	**G E Yuan** (University of Manchester) **P170** Caspase-like assays
17:00 - 17:15	**Bennett Young** (University of Manchester) Intracellular pH as a marker of PCD
17:15 - 17:30	Discussions

3 Quantitative modeling of signalling systems *Kilsyth*

Workshop Organisers – Stephan Kepinski and Alex Webb

Many areas of plant research have reached a point where quantitative modelling has become an extremely useful, if not essential tool for gaining deeper understanding of the mechanisms and systems underlying development. Befitting the diversity of questions in biology, there are a variety of mathematical modelling approaches, which are suited to different problems and types of data. As a starting point for discussion this workshop includes a range of talks, focused on questions in auxin and circadian biology, in which mathematical modelling is specifically being used to gain new insight by generating hypotheses and concepts to inform further work. The workshop will be an informal event with ample time for discussion.

Programme

15:45 - 15:50	Welcome and Introduction
15:50 - 16:10	**Ottoline Leyser** (University of York) Auxin, the motion picture
16:10 - 16:30	**Stefan Kepinski** (University of Leeds) **P534** Modelling auxin response
16:30 - 16:50	**Claire Grierson** (University of Bristol) **P537** ROP localisation by auxin in Arabidopsis root hair cells
16:50 - 17:10	**Alex Webb** (University of Cambridge) **P430** Simple models of circadian oscillations identify signalling network architecture
17:10 - 17:30	Discussions

Thursday 2nd July

16:30 - 18:00

1 Stomata - the ins and outs *Tinto*

Workshop Organisers – Julie Gray and Dominique Bergmann

Stomata are crucial for the regulated exchange of gases between the plant and atmosphere. As stomata are gated by guard cells, a specialised cell type that is particularly responsive to environmental signals, they provide a convenient system for the study of both plant cell differentiation and the transduction of environmental signals. Stomatal biology is now at a critical juncture where there is interest from researchers in a variety of disciplines and the basic elements of stomatal development and signalling have been laid out. What has yet to be fully realized is how an integrated picture of stomata (from molecules to cells to leaves to ecosystems) might be built from combining recent technical and intellectual advances generated from different subdisciplines. Our aim in this workshop is to highlight recent progress, to identify areas for future research and to discuss tools that may be broadly applicable across fields of stomatal research. Short presentations from both new and established investigators in the stomatal development and signalling fields will be followed by equal time for discussion. Additional workshop participants will be encouraged to present tools or reagents generated in their studies and to help identify areas in which such tools are needed.

Programme

16:30 - 17:20	**Maik Bohmer** (UC San Diego) **P289** Proteomic analyses of protein modifications
	Alex Webb (University of Cambridge) Enhancer trap screens
	Keiko Torii (University of Washington) **P095** Microarray studies
	Lee Hunt (University of Sheffield) **P114** Signalling peptides
	Discussion about resources and tools
17:20 - 17:50	**Derek White** (Agresearch New Zealand) **P022** Challenges of integrating development and environment
	Sally Assmann (Pennsylvania State University) Systems biology
	Sarah Robinson (John Innes Centre) Modelling development
17:50 - 18:00	Discussion about challenges and future directions

2 Putting TAIR to work for you: hands-on workshop for beginning and advanced users *Moorfoot*

Workshop Organisers – Eva Huala and Kate Dreher

Stomata are crucial for the regulated exchange of gases between the plant and this two-part workshop will teach effective search strategies and highlight important data sets available at TAIR. Both beginning and experienced users will learn new ways to get the information they need and discover new tools and data that can enhance their own research efforts.

In the first part curators will demonstrate how to get detailed information (e.g. sequence and map information, phenotype data, functional annotations, AraCyc metabolic pathway information, etc.) about specific genes and will show users several ways to retrieve bulk data for groups of genes. In the second part of the workshop audience members will have the chance to practice the skills they have learned using a set of prepared exercises or to ask curators for one-on-one help with particular tasks. Participants should bring a laptop computer if possible. For those without computers a couple of extras will be provided and people will be asked to share if needed. In addition, all attendees will get hand-outs and

links to online documents covering all of the information presented. All ICAR attendees are invited to ask follow-up questions, submit data or get help with specific tasks at the TAIR curation booth. Materials for the workshop will be available at: www.arabidopsis/portals/education/presentations/2009/ICAR/ICAR_workshop_2009.jsp

Programme

16:30 - 16:50	**Eva Huala** (TAIR) The Arabidopsis Information Resource (TAIR)
16:50 - 17:10	**Dave Swarbreck** (TAIR) Structural Annotation
17:10 - 17:30	**Kate Dreher** (TAIR) TAIR and the Plant Metabolic Network
17:30 - 18:00	Skills Practice and Discussion

3 Root systems architecture *Kilsyth*

Workshop Organisers – Anna Amtmann, Brian Forde, Peter Doerner, Lionel Dupuy and Malcolm Bennett

Root system architecture (RSA) is the spatial arrangement of the plant root system. RSA is both output and input for plant development, and its plasticity clearly reflects the interplay between plant development and the environment. As different parts of the root system are exposed to micro-conditions within the soil, RSA also fulfils a sensory function using a multitude of environmental cues to gather information about the root's surroundings. This enables the plant to optimally exploit the physical and chemical properties of the soil. RSA is therefore a model system for fundamental research into plant development and an important trait for agricultural productivity.

To understand the signalling pathways underlying RSA development and its responsiveness to the environment, researchers have to measure RSA in controlled environmental conditions and diverse genetic backgrounds. The complex geometry and underground location of the root make this a difficult task, yet comprehensive quantification of RSA is paramount for integrating this important phenotype with genetic and molecular parameters (e.g. mutations, QTLs, transcript and metabolite profiles).

Several labs have recently developed methods and resources to facilitate the study of RSA. In this workshop we will present different approaches including live imaging, dynamic modelling and functional genomics. The general discussion will focus on how these techniques can be put to best usage within the plant science community.

Programme

16:30 - 16:45	**Philip Benfey** (Duke University) Automated phenotyping and classification of plant root systems
16:45 - 17:00	**Nick Chapman** (Rothamsted Research and Durham) Investigating root development within a multi-stress system
17:00 - 17:15	**Lionel Dupuy** (SCRI Dundee) New approaches for the modelling of root architecture
17:15 - 17:30	**Malcolm Bennett** (University of Nottingham) Future roots for UK research
17:30 - 17:45	General Discussion
17:45 - 18:00	Software demonstration

In conjunction with this workshop we will demonstrate new software in the poster hall:

EZ Rhizo (Glasgow)
Root Trace (Nottingham)
Balloon (SCRI)

Saturday 4th July
16:30 - 18:00

1 Anther/pollen development *Tinto*

Workshop Organisers – Zoe Wilson and Hong Ma

Male reproduction is important for both basic science and agricultural applications. This is an area of very active research and has seen rapid progress in recent years. The workshop will cover presentations linked to pollen and anther development that will involve the characterization of new mutants, discussion of techniques for the analysis of pollen development and the development of resources required for such analyses. It is envisaged that this will principally focus on Arabidopsis research, however it will also extend into the analysis of crop species and the potential translatability of the research area.

Programme

16:30 - 16:45	**Hong Ma** (Fudan University/Pennsylvania State University) Regulation of anther gene expression by the DYT1 transcription factor
16:45 - 17:00	**Zoe A Wilson** (University of Nottingham) **P022** Establishing regulatory models for anther endothecium development and the regulation of dehiscence
17:00 - 17:15	**Maura Cardarelli** (Universita La Sapienza, Roma) The role of auxin in Arabidopsis late stamen development
17:15 - 17:30	**Reidunn B Aalen** (University of Oslo) **P098** The ASH1 HOMOLOG 2 (ASHH2) histone H3 methyltransferase is required for ovule and anther development in Arabidopsis
17:30 - 17:45	**Trudie Allen** (University of Leicester) **P375** Functional analysis of fused-kinase signalling in gametophytic cytokinesis
17:45 - 18:00	**Gael Le Trionnaire** (University of Oxford) **P154** MicroRNA profiling of *Arabidopsis thaliana* mature pollen

2 Ambient temperature *Moorfoot*

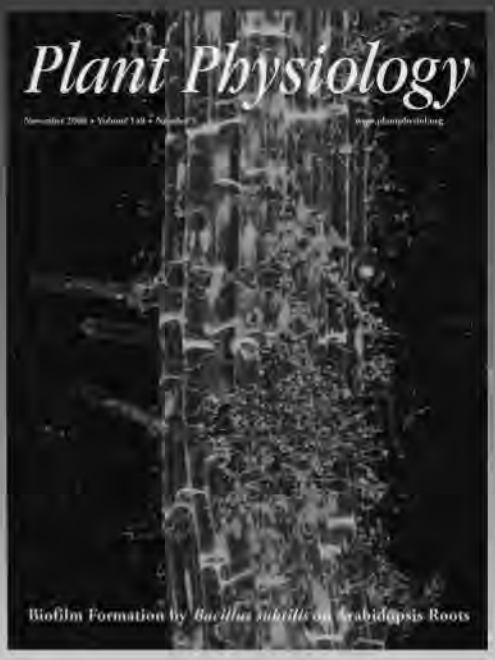
Workshop Organiser – Seth Davis

Small changes in growth temperature can have dramatic effects on plant development. This workshop will highlight recent efforts to understand the responses and mechanisms that *Arabidopsis thaliana* uses in the detection of non-stress temperatures. Discussions will be led that highlight rhythmic reactions to daily thermal changes, responses to climate effects, the role of temperature in allele-by-allele interactions, and the role of RNAs as potential "thermometers." It is hoped that this workshop serves as a primer to promote the study of plant responses to the ambient-temperature environment.

Programme

16:30 - 16:45	**Seth Davis** (MPI Cologne) Temperature entrainment of the circadian oscillator: memory of the past
16:45 - 17:00	**Joanna Schmitt** (Brown University) Photothermal time and response to temperature variation in dynamic real-world environments
17:00 - 17:15	**Ji Hoon Ahn** (Korea University) Regulation of temperature response by small RNA: toward an understanding of the ambient temperature sensing
17:15 - 17:30	**Anthony Hall** (University of Liverpool) A systems biology approach to understand the regulation of signalling pathways by temperature
17:30 - 17:45	**Kirsten Bomblies** (MPI Tubingen) Temperature sensitivity of plant autoimmunity
17:45 - 18:00	Discussion

Plant Physiology® Among 100 Most Influential Journals of the Century!



Plant Physiology has been named one of the 100 most influential journals in biology or medicine of the past 100 years! To celebrate the 100th anniversary of the Special Libraries Association, SLA's BioMedical & Life Sciences Division conducted a poll of its membership to identify which journals have been the most influential. *Plant Physiology* is one of only three journals from the "Experimental Botany, Plant Physiology & Related Molecular/Cellular Plant Biology" category to make the list. Other journals listed in the top 100 include such prestigious titles as *Science, Nature,* and the *Proceedings of the National Academy of Sciences.* The American Society of Plant Biologists and *Plant Physiology* are proud to have received this honor. A full list of the top 100 journals can be found at http://units.sla.org/division/dbio/publications/resources/dbio100.html.

DBIO
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www.plantphysiol.org

Exhibition

The ICAR 2009 Exhibition will be held in the Cromdale Hall on Level -2 of the Edinburgh International Conference Centre from Tuesday 30th June until Saturday 4th July. The exhibition will comprise of a host of displays designed to showcase current products, publications, research and applications in Arabidopsis. Admittance is restricted to registered delegates and badges must be worn.

Exhibition Opening Hours

Tuesday 30th June	14:00 - 21:00
Wednesday 1st July	09:00 - 20:00
Thursday 2nd July	09:00 - 20:00
Friday 3rd July	09:00 - 14:00 and 18:00 - 20:00
Saturday 4th July	09:00 - 14:00

Exhibitors

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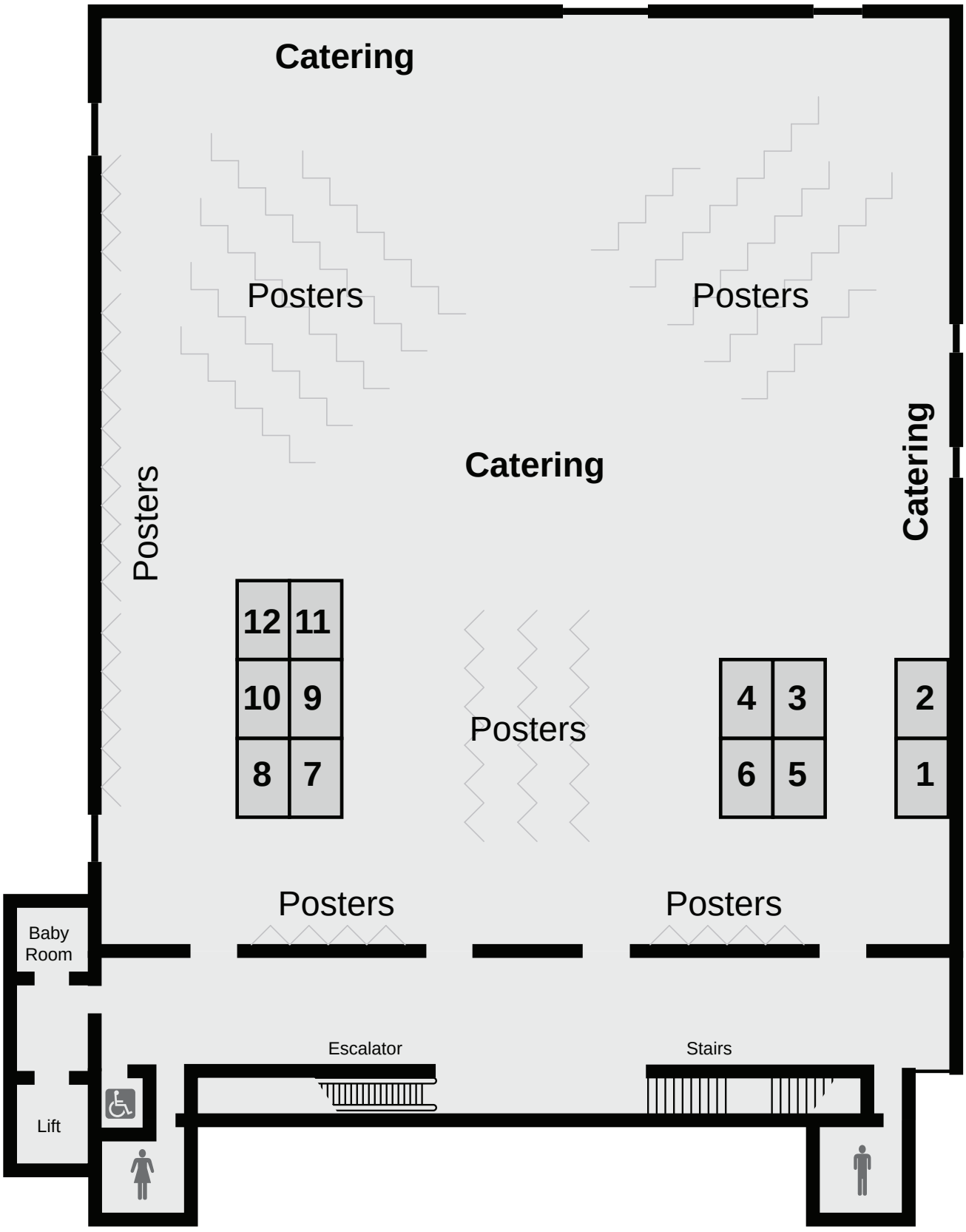
Exhibition Floor Plan



Stand 1

Journal of Experimental Botany

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Stand 8

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Stand 12

Bioinformatics And Systems Engineering Division

RIKEN BASE (Bioinformatics And Systems Engineering, directed by Dr Tetsuro Toyoda) is the database division of the life science research centers and institutes of RIKEN, Japan.

We contribute to the plant-science communities together with RIKEN PSC (Plant Science Center, directed by Dr Kazuo Shinozaki). We are providing a plant integrated database based on the semantic-web standard (http://database.riken.jp).
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