

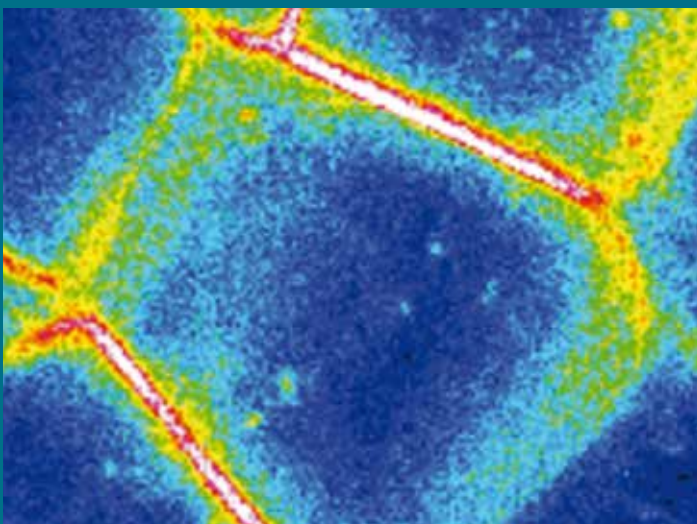
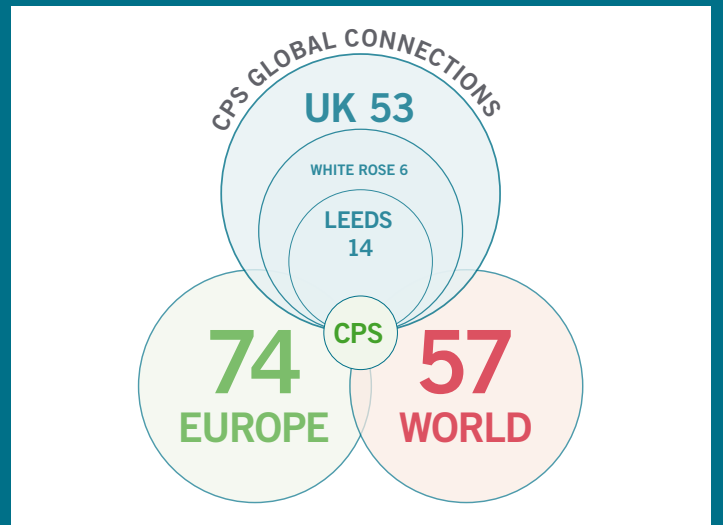
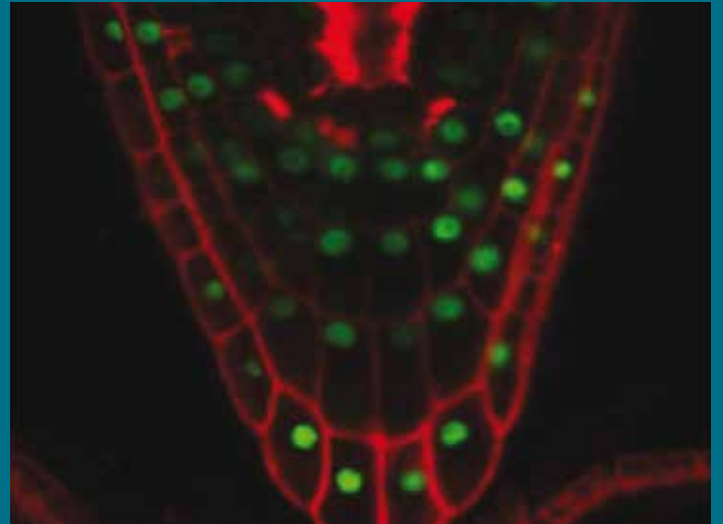


UNIVERSITY OF LEEDS

Centre for Plant Sciences

A centre of excellence in cellular and molecular
plant sciences at the University of Leeds

Report 2016



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Overview

The Centre for Plant Sciences (CPS) is a peak of research excellence at the University of Leeds. It is one of the major research groups of the Faculty of Biological Sciences at Leeds in terms of research income and publication outputs and is a major plant science research unit in the UK.

New staff: Twelve academic staff head research groups in cell & molecular plant sciences and currently CPS has over 30 postgraduates, 20 post-doctoral researchers and 9 research technicians. We are in an expansive phase welcoming, through the University of Leeds Great Minds scheme, the arrival in 2015 of Dr Katie Field working on plant-mycorrhizal symbioses and, in October 2016, Dr Thomas Bennett studying root growth – both as University Academic Fellows (UAFs). We also welcomed to our team in 2016 an in-house senior bioinformatician Dr Michael Wilson who is providing valuable input into our projects.

Major CPS research areas of international and global significance include developing resistance to the nematode pests of crops, plant genetic structures & regulation, developmental biology, plant stress biology and plant glycobiology/cell walls.

We pursue our mission of excellence and the highest standards in plant science through interdisciplinary interactions with colleagues in the Faculty of Biological Sciences, the Astbury Centre for Structural Molecular Biology, Schools of Food Science, Chemistry, Environment and Physics and use the resources of the University of Leeds farm.

CPS staff are partners in a range of current EU consortia and programmes including Crop Life, EcoSeed, Epigenome NOE and Sysflo.

Our fundamental plant science and strategic science makes us ideally placed to develop partnerships and collaborative research addressing global challenges and current agenda concerning crops and food security.

The following pages provide snapshots of the current activities of our groups, our research activities, grant funding and publications.

Full details at www.plants.leeds.ac.uk

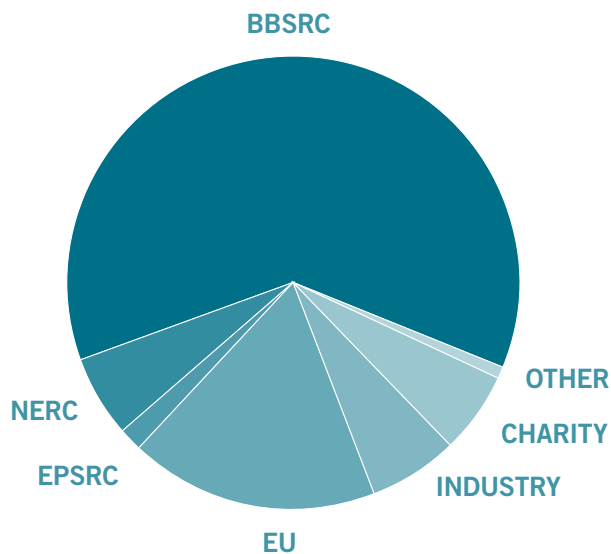
Contact: plants@leeds.ac.uk

Follow us on twitter [@plantscileeds](https://twitter.com/plantscileeds)

Summary of achievements

Research Funding

Since 2011 our CPS research funding portfolio has achieved an income of over £11 million and the breakdown of this is shown schematically here. Most funding is currently being obtained from the UK Biotechnology & Biosciences Research Council (BBSRC) with some in-roads into other research council funding from the Natural Environment Research Council (NERC) and the Engineering and Physical Sciences Research Council (EPSRC). Funding from EU programmes including Marie Curie initiatives remain as a significant component. Individual grant awards are detailed later in the report.

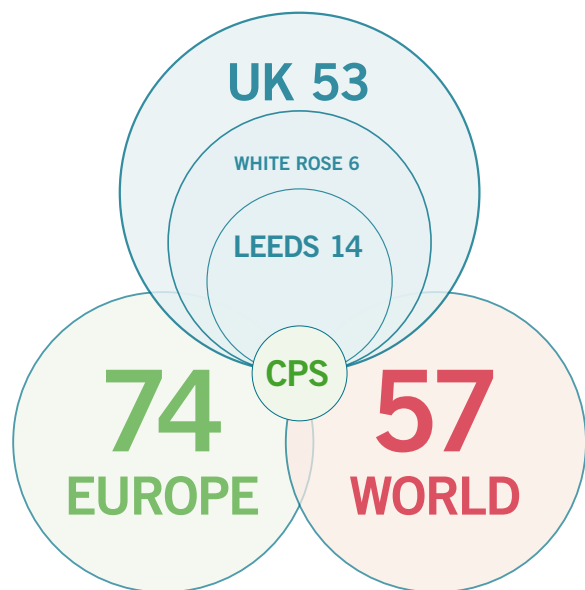


Publication and citations metrics

CPS research groups maintain and extend a high level of outputs in terms of publications. CPS researchers have averaged over 39 publications/year since 2011. In this period our publications have received over 4,900 citations thus averaging ~20 citations/article. We also congratulate Professor Christine Foyer for passing the h-index of 100 milestone on Google Citations in April 2016.

CPS global connections

In this report we highlight the internationality of our research activities and the graphic here indicates the number of publications in the last 5-year period with collaborators in Leeds, the White Rose consortium of Yorkshire universities, the rest of the UK, Europe and the rest of the World.



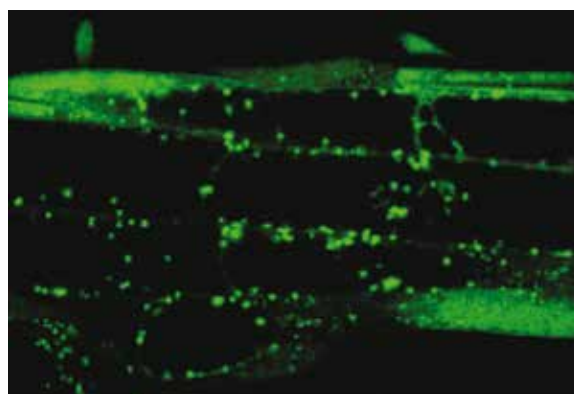
Recent publication highlights are included in the research group reports that follow and all our publications since 2011 are listed at the end of the report.

Research group reports 2016

Prof. Alison Baker

Membrane transport & organelles | Peroxisomes | Protein trafficking
Chemical Biology | Phosphate transport | ABC D subfamily transporters

My group is interested in membrane protein transport processes in plants. Much of our work has focused on peroxisomes, essential cellular organelles that are involved in an extraordinarily wide range of processes from primary metabolism, signalling and defence responses. We have used a range of biochemical, cell biological, genomic and chemical biology approaches to address the mechanism of transport of both proteins and metabolites across the peroxisome membrane. In the latter case we have identified and characterized a peroxisomal ABC transporter which acts as the primary transport route for fatty acids and pro-hormones into peroxisomes and shown that it possesses a novel thioesterase activity that cleaves acyl CoA substrates upon transport. We have recently initiated a new area of research studying the families of membrane proteins involved in uptake and transport of phosphate with emphasis on structure-function relationships, to help understand whether these proteins play a role in phosphorus use efficiency.



A small molecule that inhibits protein import into peroxisomes

Links

http://www.plants.leeds.ac.uk/people/groups_bak.php

Recent publications

Bhogal MS, Lanyon-Hogg T, Johnston KA, Warriner SL, Baker A (2016) Covalent label transfer between peroxisomal importomer components reveals export-driven import interactions. *Journal of Biological Chemistry* 291 2460-2468.

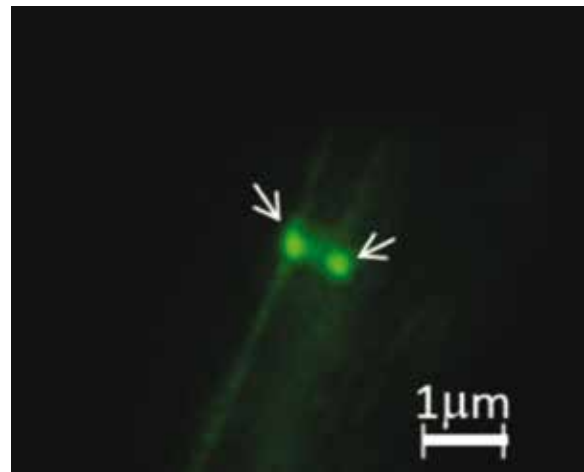
Qi W, Baldwin SA, Muench SP, Baker A (2016) Pi sensing and signalling: from prokaryotic to eukaryotic cells. *Biochem Soc Trans* 44 766-773.

Kamisugi Y, Mitsuya S, El-Shami M, Knight CD, Cuming AC, Baker A (2016) Giant peroxisomes in a moss (*Physcomitrella patens*) peroxisomal biogenesis factor 11 mutant. *New Phytologist* 209 576-589.

Dr. Yoselin Benitez-Alfonso

Plasmodesmata | Cell-to-cell communication | Root architecture | Callose metabolism | Organ development | Composite materials

Plasmodesmata are intercellular channels that transport proteins, metabolites and RNAs between cells regulating plant responses to developmental and environmental cues. Our research focuses on the mechanisms that control plasmodesmata form and function. We use cell biology, genetics and cell wall biophysics to determine the factors that regulate plasmodesmata transport and their influence on the initiation and development of root organs. We study the metabolism, structure and molecular interactions of callose, a cell wall glycan that plays a major role in plasmodesmata regulation. We are also interested in characterizing the molecular pathways that regulate plasmodesmata transport in roots in response to soil nutrition and nitrogen-fixing bacteria. Results from our research demonstrate the importance of callose in cell wall regulation during the initiation of lateral root organs. It also highlights the potential of using this biopolymer in the design of novel cellulose-based composite materials.



Plasmodesmata localisation of callose-degrading enzyme fused to GFP

Links

<https://benitezalfonso.wordpress.com/>

Recent publications

Otero S, Helariutta Y, Benitez-Alfonso Y (2016) Symplastic communication in organ formation and tissue patterning *Current Opinion in Plant Biology* 29 21-28.

Grison MS, Brocard L, Fouillen L, Nicolas W, Wewer V, Dörmann P, Nacir H, Benitez-Alfonso Y, Claverol S, Germain V, Boutté Y, Mongrand S, Bayer EM (2015) Specific membrane lipid composition is important for plasmodesmata function in *Arabidopsis*. *Plant Cell* 27 1228-1250.

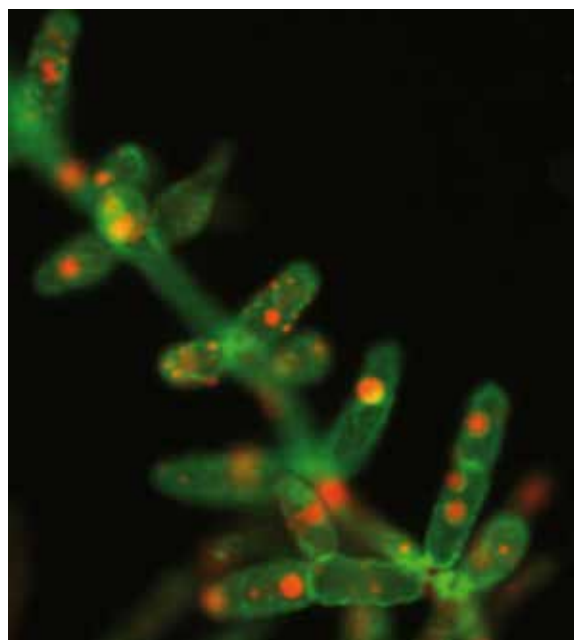
Benitez-Alfonso Y, Faulkner C, Pendle A, Miyashima S, Helariutta Y, Maule A (2013) Symplastic intercellular connectivity regulates lateral root patterning. *Developmental Cell* 26, 136-147.

Dr. Andrew Cuming

Gene targeting | *Physcomitrella patens* | DNA repair and transgene integration
| Dehydration tolerance | Abscisic acid | Comparative functional genomics

The model bryophyte *Physcomitrella patens* represents one of the earliest diverging lineages following the transition of plants from an aquatic to a terrestrial environment. We use the remarkable ability of *P. patens* to integrate transgenes at predetermined loci by “gene targeting” to probe the functions of conserved and bryophyte-specific genes. We focus on two features: (i) the way in which genes responsible for the repair of DNA-double-strand breaks participate in targeted transgene insertion, and (ii) the abscisic acid (ABA) and dehydration-stress-response pathway. We are using both “forward” and “reverse genetic” approaches to identify conserved and novel bryophyte-specific functions inherent to these processes, and recently reported the discovery of a novel regulator of ABA responses in the “lower” plants, but absent from vascular plants. We also collaborate with the wider research community, using comparative genomic approaches to explore the evolution of plant gene function. The image illustrates the accumulation of giant peroxisomes following targeted knockout of the *PEX11* peroxisome biogenesis gene, in a collaboration with Alison Baker.

Recently, we launched a contract moss transformation service (Contact ACC for details!) to enable researchers to access our skills via grant funding.



Peroxisomes and ER visualised in moss protonemata by RFP- and GFP- fusions

Links

www.plants.leeds.ac.uk/people/groups_cum.php

Recent publications

Stevenson SR, Kamisugi Y, Trinh CH, Schmutz J, Jenkins JW, Grimwood J, Muchero W, Tuskan GA, Rensing SA, Lang D, Reski R, Melkonian M, Rothfels CJ, Li F-W, Larsson A, Wong GK-S, Edwards TA, Cuming AC (2016) Genetic analysis of *Physcomitrella patens* identifies *ABSCISIC ACID NON-RESPONSIVE (ANR)*: a regulator of ABA responses unique to basal land plants, required for desiccation tolerance. *Plant Cell* 28, 1310-1327.

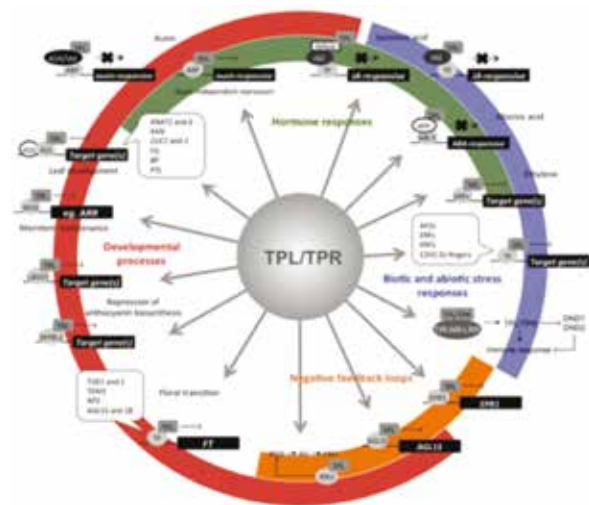
Kamisugi Y, Mitsuya S, El-Shami M, Knight CD, Cuming AC, Baker A (2016). Giant peroxisomes in a moss (*Physcomitrella patens*) peroxisome biogenesis factor 11 mutant. *New Phytologist* 209, 576-589.

Szövényi P, Perroud P-F, Rensing SA, Stevenson S, Symeonidi A, Quatrano RS, Cuming AC, McDaniel SF (2015). *De novo* assembly and comparative analysis of the *Ceratodon purpureus* transcriptome. *Molec. Ecol. Resources* 15, 203-215.

Prof. Brendan Davies

Plant development | Flower development & flowering | Transcription factors |
Transcriptional repression | Nonsense-mediated mRNA decay | Splicing

We are interested in how plants develop and how plant development is modified by the environment. There are three broad areas of research, all linked by a common theme of regulating gene expression to influence how plants grow and develop. We study flowering and flower development, the processes that provide our food. Projects in this area include understanding the robustness of flowering in a variable environment and how temperature is sensed by plants. We also study how two alternative types of gene regulatory mechanisms link to development. In one case we have identified novel regulatory elements that selectively alter the stability of specific mRNAs, allowing plants to alter gene expression rapidly in response to environmental changes. In another project we are using both mechanistic and evolutionary approaches to study how a common 'hub' of repression has been independently co-opted multiple times by a wide range of transcription factors to regulate numerous plant processes.



Links

www.plants.leeds.ac.uk/people/groups_dav.php

Recent publications

Airoldi CA, McKay M, Davies B. (2015) MAF2 Is Regulated by Temperature-Dependent Splicing and Represses Flowering at Low Temperatures in Parallel with FLM. *PLoS one* 10:e0126516.

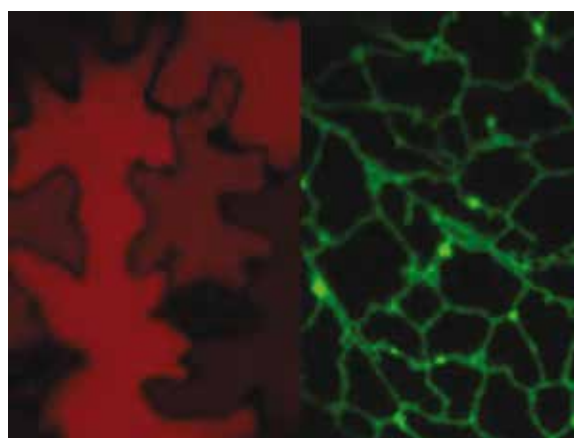
Lloyd JPB, Davies B (2013) SMG1 is an ancient nonsense-mediated mRNA decay effector. *Plant Journal* 76, 800-810.

Causier B, Ashworth M, Guo W, Davies B (2012) The TOPLESS interactome: a framework for gene repression in *Arabidopsis*. *Plant Physiology* 158, 423-438.

Prof. Jurgen Denecke

Plant Cell Biology & Biotechnology | Secretory pathway | Endoplasmic reticulum | Golgi apparatus | Organelle biogenesis | Protein targeting | Sustainable food and energy | Fermentation | Distillation | Starch saccharification

We study the secretory pathway, a group of membrane bound organelles that play key functions in virtually every process of eukaryotic life. Our research is mainly curiosity- and hypothesis-driven, and we use biochemical transport assays, cellular engineering, and in vivo imaging techniques to capture the exciting microcosmos of plant cells. We aim to understand complete transport processes so that each step can be explained via bio-molecular interactions, conformational changes, molecular switches and the principle of recycling. More recently, we have become interested in harnessing the plant secretory pathway for the renewable production of food, energy and materials from plants.



Links

www.plants.leeds.ac.uk/jd/
www.facebook.com/DeneckeLab

Recent publications

Gershlick DC, Lousa, CD, Foresti O, Lee AJ, Pereira EA, DaSilva LL, Bottanelli F, Denecke J (2014) Golgi-dependent transport of vacuolar sorting receptors is regulated by COPII, AP1, and AP4 protein complexes in tobacco. *Plant Cell* 26, 1308-1329.

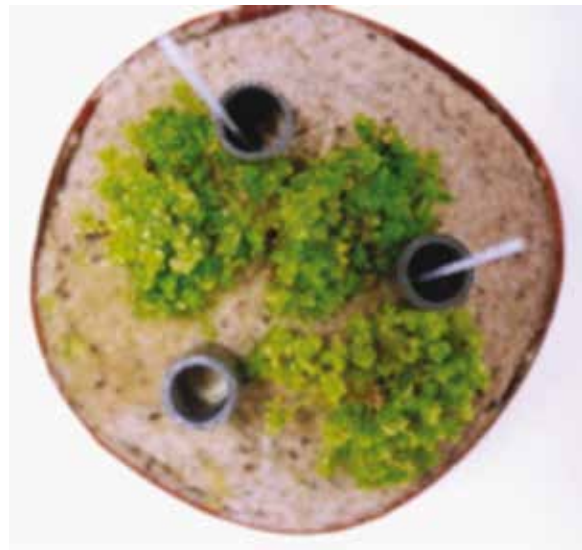
Bottanelli F, Gershlick DC, Denecke J (2012). Evidence for sequential action of Rab5 and Rab7 GTPases in prevacuolar organelle partitioning. *Traffic* 13, 338-354.

Lousa CDM, Gershlick DC, Denecke J (2012) Mechanisms and concepts paving the way towards a complete transport cycle of plant vacuolar sorting receptors. *Plant Cell* 24 1714-1732.

Dr Katie Field

Mycorrhizal symbiosis | Plant-soil processes | Plant evolution and ecophysiology
| Sustainable agriculture | Environmental metabolomics | CO₂

The nutritional symbioses formed between the vast majority of land plants and soil fungi dates back to when plants first colonized Earth's land masses, more than 475 million years ago. These associations are known as 'mycorrhizas' or 'mycorrhiza-like' in plants without roots. We work with a range of land plant lineages and their fungal partners, investigating how the efficiency by which plant-fixed carbon is exchanged for fungal-acquired nutrients is affected by environmental perturbation, such as changes in atmospheric CO₂. Using a variety of physiological tools including isotope tracing and environmental metabolomics, our research aims to shed new light on the role fungal symbionts may have played in the development of Earth's ecosystems and to expand our understanding of crop-mycorrhiza-environment interactions in sustainable agricultural systems.



Links

www.plants.leeds.ac.uk/people/groups_fie.php

Recent publications

Field KJ, Rimington WR, Bidartondo MI, Allinson KE, Beerling DJ, Cameron DD, Duckett JG, Leake JR, Pressel S. (2016) Functional analysis of liverworts in dual symbiosis with Glomeromycota and Mucoromycotina fungi under a simulated Palaeozoic CO₂ decline. *ISME Journal* 10, 1514–1526.

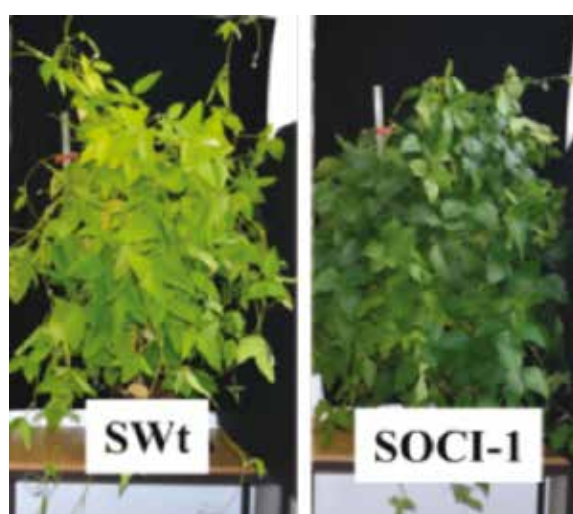
Field KJ, Pressel S, Duckett JG, Rimington WR, Bidartondo MI. (2015) Symbiotic options for the conquest of land. *Trends in Ecology and Evolution* 30, 477-486.

Field KJ, Rimington WR, Bidartondo MI, Allinson KE, Beerling DJ, Cameron DD, Duckett JG, Leake JR, Pressel S. (2015) First evidence of mutualism between ancient plant lineages (Haplomitriopsida liverworts) and Mucoromycotina fungi and its response to simulated Palaeozoic changes in atmospheric CO₂. *New Phytologist* 205, 743-756.

Prof. Christine Foyer

Stress Tolerance | Redox signalling and antioxidants | Photosynthesis | Plant growth & development | Cystatin technology | Low temperature | Drought | High light | Aphid resistance

Our research concerns how primary processes (photosynthesis, respiration) alter the reduction/oxidation (redox) status of the cell and how redox signals interact with phytohormone-mediated pathways to regulate growth and defence responses. We study responses to aphid infestation, drought, chilling and high light stress, as well as combined biotic and abiotic stress conditions. We use multidisciplinary approaches to study the relationships between primary metabolism, gene expression and growth under optimal and stress conditions. My lab tackles fundamental research problems of intrinsic scientific interest but is always mindful of the needs of agriculture and food security. In addition to undertaking fundamental studies on model plant species such as *Arabidopsis thaliana*, research in my lab is undertaken to enhance stress tolerance in a range of crop species particularly soybean, faba bean, barley and wheat.



Links

www.plants.leeds.ac.uk/people/groups_foy.php

Recent publications

Comadira G, Rasool B, Karpinska B, Márquez García B, Morris J, Verrall SR, Bayer M, Hedley PE, Hancock RD, & Foyer CH (2015) WHIRLY1 functions in the control of responses to N-deficiency but not aphid infestation in barley (*Hordeum vulgare*). *Plant Physiology* 168, 1140-1151.

Diaz-Vivancos P, de Simone A, Kiddle G & Foyer CH (2015) Glutathione –linking cell proliferation to oxidative stress. *Free Radical Biology and Medicine* 89, 1154–1164.

Schippers JHM, Foyer CH & van Dongen J T (2016) Redox regulation in shoot growth, SAM maintenance and flowering. *Current Opinion in Plant Biology*. 29, 121-128.

Dr. Stefan Kepinski

Auxin signalling & auxin-regulated development | Auxin perception & signalling
| Novel auxinic chemistry | Gravitropism | Gravitropic setpoint angle control |
Epidermal patterning

We are interested in understanding how the plant hormone auxin controls such a remarkable range of developmental events. Auxin regulates both patterning and growth and our projects reflect this broad division. For patterning we are investigating how the spatial control of auxin responsiveness in the root epidermis contributes to the formation of hair and non-hair dells. For growth we are studying how root and shoot branch angles are set and maintained with respect to gravity (so called gravitropic setpoint angles). We have discovered a novel role for auxin in the maintenance of non-vertical branch GSAs which are an important determinant of the plant's ability to capture resources above and below ground. These projects are based on genetic and molecular genetic analysis integrated with computational approaches.

We also have projects focused on the earliest events of auxin perception where we are using biophysical, thermodynamic and structural techniques to characterise the docking and binding of auxin and Aux/IAA proteins to the TIR1/AFB auxin co-receptors.

Links

www.plants.leeds.ac.uk/people/groups_kep.php

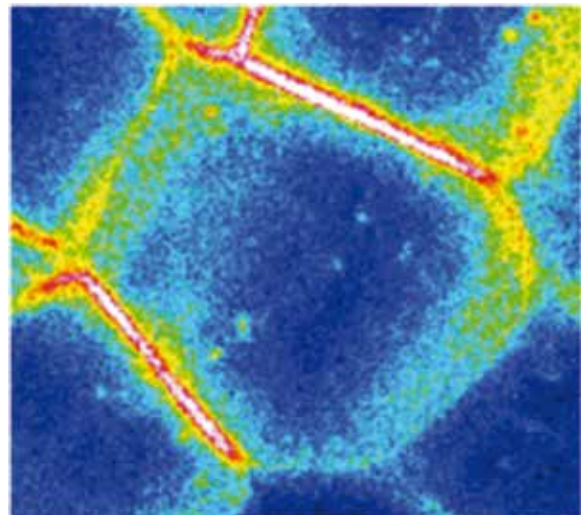
Recent publications

Roychoudhry S, Kepinski S (2015) Shoot and root branch growth angle control-the wonderfulness of lateralness. *Current Opinion in Plant Biology* 23:124-131.

Roychoudhry S, Del Bianco M, Kieffer M, Kepinski S (2013) Auxin controls gravitropic setpoint angle in higher plant lateral branches. *Current Biology* 23, 1497-504.

Calderon Villalobos L, Lee S, Armitage L, Parry G, Mao H, De Oliveira C, Ivetac A, Brandt W, McCammonn A, Zheng N, Napier R, Kepinski S, Estelle M (2012) TIR1/AFBs and Aux/IAAs constitute a combinatorial co-receptor system to perceive auxin with differential sensitivities. *Nature Chemical Biology* 8, 477-485.

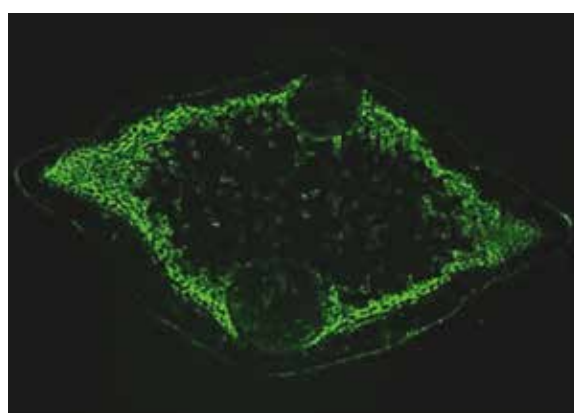
This work is providing a platform for the development of next-generation auxinic agrochemicals.



Prof. Paul Knox

Plant & algal cell walls | Plant glycobiology | Polysaccharides | Microscale analytical platforms | Growth & development | Bioenergy crops & Cell wall deconstruction | Brown algae polysaccharides

Our interests focus on the structure-function relations of the matrix glycans of plant & algal cell walls and extend from model systems to fruit, vegetable, fibre & bioenergy crops. Our strategy involves the development of monoclonal antibody probes for defined oligosaccharides and to use these to understand cell wall matrix polymer developmental dynamics. Our probes are used for *in situ* fluorescence imaging & in novel microscale chromatographic separations that can identify sub-populations and inter-polysaccharide links. Recent highlights have included the isolation of new sets of monoclonal antibodies to brown algae polysaccharides of the sulphated fucan/fuoidan class – an important set of bioactive polymers. Our antibodies are available through PlantProbes.



Fluorescent tagged fucans in *Fucus vesiculosus*

Links

www.plantcellwalls.net

www.plantprobes.net

t: @plantprobes

Recent publications

Torode TA, Marcus SE, Jam M, Tonon T, Blackburn RS, Hervé C, Knox JP (2015) Monoclonal antibodies directed to fucoidan preparations from brown algae. *PLoS ONE* 10, e0118366.

Cornuault V, Buffetto F, Rydahl MG, Marcus SE, Torode TA, Xue J, Crépeau M-J, Faria-Blanc N, Willats WGT, Dupree P, Ralet M-C, Knox JP (2015) Monoclonal antibodies indicate low-abundance links between heteroxylan and other glycans of plant cell walls. *Planta* 242, 1321-1334.

Cornuault V, Manfield IW, Ralet M-C, Knox JP (2014) Epitope Detection Chromatography (EDC): a method to dissect the structural heterogeneity and interconnections of plant cell wall matrix glycans. *Plant Journal* 78, 715-722.

Prof. Peter Meyer

Plant epigenetics | DNA methylation | Abiotic stress | Gene expression | Adaptation

We are interested in the role that DNA methylation plays in regulating plant gene expression, development and adaptation to abiotic stress. We especially focus on dense methylation patterns that are controlled by DNA methyltransferase MET1. In recent years, we have extended the functional analysis of MET1 and its target genes from *Arabidopsis* into crop species. We have used the mammalian DNA demethylase TET3 to induce heritable DNA methylation changes, producing novel epigenetic variants. Epigenetic variants are investigated for correlation between individual phenotypes and the ectopic expression of individual genes that have become hypomethylated.



Examples of epigenetic tomato lines with heritable phenotypes induced by DNA demethylation: Left: Lines with delayed or inhibited shoot apical meristem development. Right: A line displaying a terminal flower phenotype

Links

www.personal.leeds.ac.uk/~genpme/

Recent publications

Meyer, P. (2015) Epigenetic variation and environmental change. *J. Exp.Bot.* 66 (12): 3541-3548.

Watson, M., Meyer P. (2014) Transmission of epi-alleles with MET1-dependent dense methylation in *Arabidopsis thaliana*. *PLoS ONE* 9(8):e105338.

Zubko E., Gentry M, Kunova A, Meyer P (2012) De novo DNA methylation activity of METHYLTRANSFERASE 1 (MET1) partially restores body methylation in *Arabidopsis thaliana*. *Plant Journal* 71:1029-1037

Prof. P.E. Urwin

Plant nematology | Crops | Plant pathology | Nematology | Comparative genomics

Plant parasitic nematodes (PPNs) cause >\$100 billion annual losses to world agriculture of which cyst and root-knot nematodes contribute over 80%. Their management involves crop rotation and host resistance, which provide incomplete control, and chemical nematicides, which are the most toxicological and environmentally damaging pesticides in widespread use posing considerable risk to aquatic ecosystems and drinking water supplies. The approaches taken by the group to overcome this challenge include developing biofumigation to replace the withdrawn nematicides and utilising well established anti-feedant technology as well as newly developed behavioural repellents and RNAi to provide plant based resistance to nematodes in several crops. We are also undertaking fundamental research using the model species *C. elegans* and utilising the data we have generated by the sequencing the *Globodera pallida* genome and multiple transcriptomes, to identify novel strategies and targets for engineering nematode resistance.



The potato cyst nematode, *G. pallida*, infecting a root

Links

www.fbs.leeds.ac.uk/nem/

Recent publications

Jones, L.M., Flemming, A.J. & Urwin, P.E. (2015) NHR-176 regulates cyp-35d1 to control hydroxylation-dependent metabolism of thiabendazole in *Caenorhabditis elegans*. *Biochemical Journal* 466, 37-44.

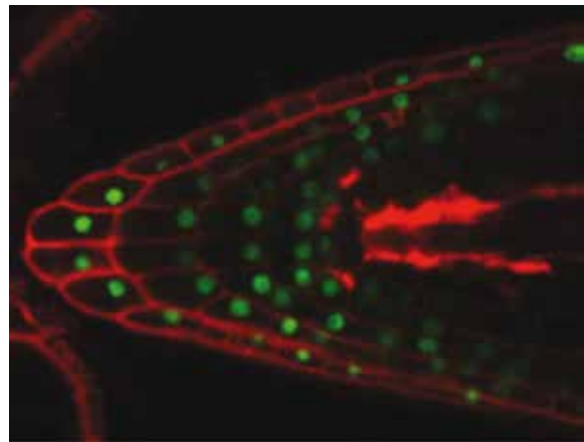
Thorpe, P., Mantelin, S., Cock, P.J.A., Blok, V.C., Coke, M.C., Cotton, J.A., Eves van den Akker, S., Guzeeva, E., Lilley, C.J., Reid, A.J., Wright, K.M., Urwin, P.E & Jones, J.T. (2014) Characterisation of the full effector complement of the potato cyst nematode *Globodera pallida*. *BMC Genomics* 15, 923.

Eves-van den Akker, S., Lilley, C.J. Jones J.T. and P. E. Urwin. (2014) Identification and characterisation of a hyper-variable apoplastic effector gene family of the potato cyst nematodes. *PLoS Pathogens* 10, e1004391.

Dr. Chris West

DNA repair and recombination | DNA damage | Plant growth & development |
Abiotic stress responses | DNA damage signalling | Seed viability and vigour

We are interested in the elucidating roles of DNA repair and recombination in plant growth and development and their potential to improve crop productivity and increase stress resistance. Our research focuses on understanding DNA repair mechanisms in plants using model species such as *Arabidopsis*, barley and brassica. In particular, we have characterised the recombination pathways that repair chromosomal breaks, one of the most cytotoxic forms of DNA damage. Our interests also include characterisation of DNA damage responses, integrating genetic, biochemical and omic approaches to understand the transcriptional and post-translational signalling pathways that regulate DNA repair, cell death and growth under stress. Recent progress has identified important roles for recombination in the seed stages of the plant life cycle, with genome repair critical to rapid germination and successful seedling establishment. Our continued research is revealing the relationship between genome repair and seed vigour. We are investigating approaches to improve seed longevity and germination performance, and are evaluating novel molecular markers for seed quality.



Links

www.plants.leeds.ac.uk/groups_wes.html

Recent publications

Waterworth, W.M., Drury, G.E., Blundell-Hunter, G., and West, C.E. (2015). *Arabidopsis* TAF1 is an MRE11-interacting protein required for resistance to genotoxic stress and viability of the male gametophyte. *Plant Journal* 84, 545-557.

Waterworth, W.M., Bray, C.M., and West, C.E. (2015). The importance of safeguarding genome integrity in germination and seed longevity. *J Exp Bot* 66, 3549-3558.

Park, S.Y., Vaghchhipawala, Z., Vasudevan, B., Lee, L.Y., Shen, Y., Singer, K., Waterworth, W.M., Zhang, Z.J., West, C.E., Mysore, K.S., and Gelvin, S.B. (2015). *Agrobacterium* T-DNA integration into the plant genome can occur without the activity of key non-homologous end-joining proteins. *Plant Journal* 81, 934-946.

Grant Funding/Publications

BBSRC CASE / Industrial CASE partnership programmes in progress

Carbogen Ltd. (2013-2017) Alison Baker

Optimising Phosphate recovery from waste water using photosynthetic aquatic organisms

ENZA ZADEN UK Ltd. (2013-2017) Peter Meyer

Generating epigenetic diversity in plants

ENZA ZADEN UK Ltd. (2013-2017) Peter Meyer

DNA demethylation strategies and targets in crops

British Sugar/British Beet Research Organisation/Rothamsted (2013-2017) Paul Knox

Genetic determinants of cell wall composition in sugar beet storage roots.

CPS Research Grants 2012 – 2016

2016

BBSRC – £2,208,389

Alison Baker, Regulation of Poly phosphate metabolism in *Chlamydomonas*, 1/7/16-30/6/2019, £451,124

Katie Field, Interactions between crops, arbuscular mycorrhizal fungi and atmospheric CO₂, 1/1/2016-31/12/2020, £830,381

Stefan Kepinski, The molecular basis of gravitropic setpoint angle control in higher plants, 1/4/2016-31/3/2019, £454,505

Paul Knox, Isolation/Characterisation/Activity screening of a high value bioactive complex of proteogalactans (glycans) from a high exopolysaccharide (EPS) forming strain of microalgae, 1/1/2016-31/12/2016, £40,000

Peter Urwin, GS effectors, 2/10/16-1/10/19, £432,379

Other – £559,732

Katie Field, NERC Standard Grant - New Investigator, Shifting symbiotic scenarios at the dawn of land plant-fungus associations, 1/4/2016-31/3/2019, £541,939

Stefan Kepinski, Newton Fund: PhD Placement Grant, 1/4/02016-30/9/2016, £17,793

2015

BBSRC – £761,427

Christine Foyer, Functions of the Whirly 1 protein in chloroplast-nucleus crosstalk in barley leaves, 1/5/2015-30/4/2018, £397,732

Christine Foyer, FACCE-JPI Knowledge Hub: A detailed climate change risk assessment for European agriculture and food security, in collaboration with international projects, 1/11/2015-31/10/2017, £160,401

Peter Urwin and Howard Atkinson, BBSRC HAPI Potato proposal, 1/10/2015-30/9/2020, £203,294

Charity – £26,700

Katie Field, Royal Society, Functiol and metabolism in ancient plant-fungal symbioses, 30/12/2015-29/12/2016, £14,700

Christine Foyer, Royal Society, Effects of abiotic stress on plant responses to aphid infestation, 1/10/2015-30/9/2017, £12,000

Other – £93,672

Yoselin Benitez-Alfonso, EPSRC, Mechano-physical properties of the biopolymer callose: a cell wall matrix or just a sealant? 3/8/2015-2/8/2016, £93,672

2014

BBSRC – £2,392,227

Alison Baker, Exploring the role of acyl CoA cleavage by COMATOSE a plant ABC transporter in regulating entry of substrates into beta oxidation, 3/2/2014 – 2/2/2017, £403,439

Brendan Davies, FLOWPLAST, 1/3/2014 – 28/2/2017, £451,829

Brendan Davies, A New Conditional Gene Regulation System in Plants, 1/1/2014 – 31/12/2016, £410,053

Stefan Kepinski, Next generation auxins and anti-auxins: principles for binding and design, 1/1/2014 – 31/12/2016, £358,506

Paul Knox, Pectic RG-I and the generation of plant cell wall properties, 1/1/2014 – 31/12/2016, £411,948

Peter Urwin and Howard Atkinson, Establishing biofumigation as a sustainable replacement to pesticides for control of soil-borne pests and pathogens of potato and horticultural crops, 1/3/2014 – 28/2/2018, £356,452

EU – £167,229

Paul Knox, Functional analysis of pectic RG-1 in tomato and strawberry fruit, 1/10/2014-30/9/2016, £167,229

Industry – £129,953

Brendan Davies, Bayer Crop Science, A New Conditional Gene Regulation System in Plants, 1/1/2014 – 31/12/2016, £60,000

Peter Urwin and Howard Atkinson, British Potato Council, Establishing biofumigation as a sustainable replacement to pesticides for control of soil-borne pests and pathogens of potato and horticultural crops, 1/3/2014 – 28/2/2018, £69,953

Charity – £181,241

Chris West, Leverhulme Trust, Understanding the molecular links between transcription and recombination, 1/6/2014 – 31/5/2017, £181,241

Christine Foyer, Roles for heme oxygenase and abscisic acid insensitive-4 in drought tolerance, 1/5/2014-30/11/2016, £24,000

Other – £13,990

Peter Urwin and Howard Atkinson, Agriculture & Horticulture Development Board, Establishing biofumigation as a sustainable replacement to pesticides for control of soil-borne pests and pathogens of potato and horticultural crops, 1/3/2014 – 28/2/2018, £13,990

2013**BBSRC – £1,033,621**

Jurgen Denecke, Functional analysis of ER and Golgi subdomains, 30/9/2013 – 29/9/2016, £382,093

Stefan Kepinski, Sparking Impact, 1/4/2013 – 31/3/2014, £74,727

Stefan Kepinski, Commercialisation of ARF-CA technology, 1/2/2013 – 31/7/2014, £155,619

Peter Urwin and Howard Atkinson, LWEC, 1/3/2013 – 31/08/2016, £421,182

EU – £777,708

Andy Cuming, Identification and Characterisation of the sex locus in the Dioecious Moss *Ceratodon purpureus*, 2/9/2013 – 1/9/2015, £237,626

Christine Foyer and Chris West, Impacts of Environmental Conditions on Seed Quality, 1/1/2013 – 31/12/2016, £311,798

Peter Meyer, Comparative analysis and mammalian DNA methylase functions in epigenetic *Arabidopsis* mutants, 1/9/2013 – 31/08/2015, £228,284

Charity – £101,765

Peter Meyer, Leverhulme Trust, Dissecting an ancient but hitherto cryptic function of DNA methyltransferases, 28/2/2013 – 27/02/2015, £101,765

2012**BBSRC – £230,582**

Christine Foyer, FACCE MACSUR Knowledge Hub Crop Modelling, 13/9/2012 – 12/9/2015, £53,820

Peter Urwin, Collaboration with Southampton, 1/6/2012 – 31/5/2015, £176,762

EU – £411,651

Alison Baker, Improved Millets for Phosphate Acquisition and Transport, 9/5/2012 – 8/5/2014, £175,304

Christine Foyer, Extending Soybean Lifespan, 1/6/2012 – 31/5/2014, £236,347

Charity – £613,106

Alison Baker and Andy Cuming, Leverhulme Trust, Synthetic organelles: manipulating peroxisome protein import to create designer compartments, 1/10/2012 – 30/9/2015, £221,906

Alison Baker, Gatsby Foundation, Gatsby Summer School, 1/4/2012 – 28/2/2014, £375,000

Christine Foyer, Royal Society, Understanding stress tolerance traits in grapevine, 21/2/2012 – 20/2/2012, £11,200

Paul Knox, Yorkshire Agricultural Society, Molecular characterization of the interaction of nitrogen-fixing cyanobacteria with wheat roots, 1/4/2012 – 31/3/2013, £5,000

Industry – £500,000

Peter Urwin and Howard Atkinson, Sinochem Corporation, Leeds Research Collaboration, 1/9/2012 – 31/8/2015, £500,000

Other – £8,000

Peter Urwin and Howard Atkinson, EPSRC, India Sciences Bridges extension, 1/1/2012 – 31/12/2013, £8,000

2011

BBSRC – £230,829

Andy Cuming, Understanding the mechanism of homologous recombination mediated gene targeting in *Physcomitrella patens*, 9/4/2011 – 8/4/2014, £230,829

EU – £559,223

Christine Foyer, Systemic signalling in plant – aphid interactions, 1/6/2011 – 31/5/2013, £224,824

Christine Foyer, Redox Regulation of Nuclear Proteins, 1/5/2011 – 30/4/2013, £153,787

Paul Knox, Plant Cell Wall Training Consortium, 1/6/2011 – 31/5/2013, £180,612

Other - £55,000

Howard Atkinson, US Agency for International Development, USAID, 31/8/2011 – 30/8/2013, £55,000

CPS publications 2011 – 2016

2016

Baker A, Lanyon Hogg T, Warriner SL (2016) Peroxisome protein import: A complex journey. *Biochemical Society Transactions* 44 783-789 doi:10.1042/bst20160036

Bhogal MS, Lanyon-Hogg T, Johnston KA, Warriner SL, Baker A (2016) Covalent Label Transfer Between Peroxisomal Importomer Components Reveals Export-Driven Import Interactions. *Journal of Biological Chemistry* 291, 2460-2468. doi: 10.1074/jbc.M115.686501

Cheng F, Yin LL, Zhou J, Xia X-J, Shi K, Yu J-Q, Zhou Y-H, Foyer CH (2016) Interactions between 2-Cys peroxiredoxins and ascorbate in autophagosome formation during the heat stress response in *Solanum lycopersicum*. *Journal of Experimental Botany* DOI:10.1093/jxb/erw013

Cross L, Ebeed HT, Baker A (2016) Peroxisome biogenesis, protein targeting mechanisms and PEX gene functions in plants. *BBA - Molecular Cell Research* 1863, 850-862. DOI:10.1016/j.bbamcr.2015.09.010

Dolzblasz A, Nardmann J, Clerici E, Causier B, van der Graaff E, Chen J, Davies B, Werr W, Laux T (2016) Stem cell regulation by Arabidopsis WOX genes. *Molecular Plant* 9, 1028-1039 DOI: 10.1016/j.molp.2016.04.007

Eves van den Akker S, Lilley CJ, Yusup HB, Jones JT, Urwin PE (2016) Functional C-terminally encoded plant peptide (CEP) hormone domains evolved de novo in the plant parasite *Rotylenchulus reniformis*. *Molecular Plant Pathology* (in press) doi: 10.1111/mpp.12402

Field KJ, Rimington WR, Bidartondo MI, Allinson KE, Beerling DJ, Cameron DD, Duckett JG, Leake JR, Pressel S (2016) Functional analysis of liverworts in dual symbiosis with Glomeromycota and Mucoromycotina fungi under a simulated Palaeozoic CO₂ decline. *ISME Journal* 10, 1514-1526 DOI:10.1038/ismej.2015.204

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Foyer CH, Rasool B, Davey J, Hancock RD (2016) Cross Tolerance to Biotic and Abiotic Stresses in Plants: A Focus on Resistance to Aphid Infestation. *Journal of Experimental Botany* 67, 2023-2024 DOI:10.1093/jxb/erw110

Hollwey E, Watson M, Meyer P (2016) Expression of the C-terminal domain of mammalian Tet3 DNA dioxygenase in *Arabidopsis thaliana* induces heritable methylation changes at rDNA loci. *Advances in Bioscience and Biotechnology* 7, 243-250 DOI: 10.4236/abb.2016.75023

Kamisugi Y, Mitsuya S, El-Shami M, Knight C, Cuming A, Baker A (2016) Giant peroxisomes in a moss (*Physcomitrella patens*) pex11 mutant. *New Phytologist* 209 576-589 doi.org/10.1016/bs.abr.2016.02.003

Knox P (2016) Delving in the deep for the origin of plant cell surface proteoglycans. *New Phytologist* 209, 1341-1343.

McDaniel SF, Perroud PF, Cuming AC, Szövényi P (2016) The *Ceratodon purpureus* transcriptome ushers in the era of moss comparative genomics. *Advances in Botanical Research* 78, 141-166. doi:10.1016/bs.abr.2016.02.003

- Meyer P, Adamo A, Pinney JW, Kunova A, Westhead DR (2016) Heat stress enhances the accumulation of polyadenylated mitochondrial transcripts in *Arabidopsis thaliana* Plos ONE in press <http://dx.doi.org/10.1371/journal.pone.0002889>
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2015

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