# Division of Plant Sciences

## University of Dundee

**John W. S. Brown**

*In its first year, the Division of Plant Sciences has already established a strong identity within the College of Life Sciences (CLS) and SCRI, and internationally. The Division researches the mechanisms by which plants grow and develop in response to their environment, and explores opportunities to translate this basic research into crop improvement, biofuel development, biotechnology and the assessment of biodiversity.*

The Division of Plant Sciences currently has seven Principal Investigators with their research groups supported by Morven Pearson, the Divisional Secretary, and Sandie Gray, the Laboratory Manager. Plant Sciences has its own seminar series, hosts seminars within the SCRI seminar programme and has instigated joint seminars with other research Divisions in the College of Life Sciences on the main University campus. The productive interactions that have been established over the last 5–6 years with SCRI scientists are reflected in the success of joint initiatives and funding applications. The new Division will continue to build on the partnership between SCRI and CLS and exploit opportunities for interaction to benefit both organisations.

A major highlight of the past year was the international symposium on Algae, Photosynthesis and Global Change organised by Plant Sciences to honour Professor John Raven FRS who retired in September. Fourteen invited speakers, either scientists who had previously been in Professor Raven's laboratory or current collaborators, gave a range of scintillating talks interspersed with entertaining anecdotes from John's career in science. A second outstanding achievement is the success in external funding acquisition by

Left to right: Stephen Maberly, Kevin Flynn, Howard Griffiths, Richard Geider, John Beardall, Bruce Osborne, John Raven, Kath Richardson, Dianne Edwards, Mario Giordano, Charles Cockell, Paul Falkowski, Mitchell Andrews

Professor Claire Halpin who has attracted ca. £4M of funding in the areas of lignin modification, underpinning biofuel research, and in recombination. Some of this funding directly involves input from SCRI scientists and has attracted supporting funding from RERAD. Other highlights and achievements from the Division's research groups in 2008 are described below.

Plant pathogen effector delivery (Paul Birch) Plants face a constant barrage of invading microorganisms, including bacteria, fungi and oomycetes. They are able to detect these invasions and respond with rapid activation of a range of defences which are effective in preventing disease in the majority of cases. Successful pathogens secrete proteins called effectors that act either outside or inside host plant cells to manipulate key defence components and promote susceptibility to infection. The oomycete *Phytophthora infestans* causes the devastating disease late blight that remains the greatest constraint, globally, to potato production. It secretes effectors containing a motif, RXLR, which we have shown is required for these proteins to enter host cells. We have demonstrated that, although these proteins presumably suppress host defences, some of them are detected by co-evolving resistance proteins in the cytoplasm of some plant genotypes. Such molecular recognition results in host cell suicide, preventing the pathogen from spreading further in the plant. There are potentially >400 such effectors produced by *P. infestans*, suggesting that molecular interactions with the host are highly complex to evade detection and establish a successful infection. In the coming years we will explore the function, localisation and delivery of the RXLR effectors in detail.

Paul Birch and Emma Douglas

John Brown and Morven Pearson

The nucleolus and pre-mRNA processing (John Brown) When genes are expressed, they are copied into precursor messenger RNA (pre-mRNA) and introns are removed by splicing. Errors in transcription or splicing generate inaccurately spliced mRNAs which are detected by the cell and degraded. This process is called mRNA surveillance or mRNA quality control. The finding that proteins which are normally associated with mRNAs were present in the major sub-compartment of the nucleus – the nucleolus – suggested that mRNAs might also be present here. The nucleolus is now known to be multifunctional and involved in many aspects of RNA processing but is not generally thought to be involved in mRNA processing. We have now shown that the nucleolus is enriched in mRNAs which are improperly processed. The nucleolar mRNAs contain unspliced introns, unusual splicing events and some known alternatively spliced events. More importantly, the majority contain signals which would be detected by the mRNA surveillance machinery and we have shown that many are indeed degraded. This unique finding suggests that the nucleolus in plants has a function in mRNA surveillance. Using mutants in *Arabidopsis* and the RT-PCR alternative splicing panel which we have developed, we will now investigate how and where aberrant mRNAs are detected and degraded.

Regulation of flowering time (Gordon Simpson) Plants carefully control the time at which they flower through integrated responses to environmental cues and an endogenous programme of development. Flowering time control is therefore underpinned by precision in gene regulation. *Arabidopsis* mutants that lack the RNA-binding protein, FPA, flower late. Our research aims to reveal the mechanism by which this RNA binding protein controls gene expression to promote flowering. We have made a breakthrough this year in discovering that FPA controls the site of mRNA 3' end formation. Cleavage and the addition of a poly (A) tail at the 3' end of pre-mRNAs is a fundamental

Sujatha Manthri

and almost universal feature of eukaryotic mRNA expression. Since the placement of the cleavage site can include or remove RNA sequences that influence mRNA stability, mRNA localisation, protein expression, or protein localisation, cleavage site choice can have profound effects on gene expression. Consistent with this, alternative polyadenylation is a widespread feature of plant and human gene expression but the mechanisms that determine this level of gene regulation are poorly understood. Our work is unique, in that we

Division of Plant Sciences laboratory

Abbey Barakate and Claire Halpin

have identified regulators of alternative polyadenylation that are not part of the basic pre-mRNA splicing or polyadenylation machinery. Working with *Arabidopsis*, we now have the opportunity to understand how alternative polyadenylation can be controlled and how this underpins major programmes of gene regulation, including those that control flowering time.

### Understanding and manipulating lignin biosynthesis

(Claire Halpin) Over the past 15 years a huge amount of research, including work from my laboratory, has gone into understanding the pathway/genes that control lignin biosynthesis in plant secondary cell walls. The lignin pathway is now probably one of the best understood plant metabolic pathways. This is fortunate, as lignin is a major target for manipulation to improve plant raw materials as feedstocks for bioenergy production. Increasing concerns about rising $CO_2$, climate change, and the finite nature of oil supplies, has renewed interest in plant biomass as an alternative energy source. Plant biomass can produce energy either directly, by burning it, or by using it as the raw material from which bacteria and yeasts can produce biofuels. Currently, bioethanol is produced from high sugar plant materials such as grain, and has led to much debate on the issue of 'food v. fuel'. However, the rational way to make biofuel without depleting food stocks is to use non food parts of plants (for example, waste straw). In many plants, more sugar substrate for biofuel production is locked up in the cell walls of vegetative tissues (stalks, leaves) than is present in the grain, but this sugar is hard to release due to the presence of lignin. This is where detailed knowledge of the biochemistry and molecular biology of lignin production, achieved by many years of basic research, can be brought to bear on this significant industrial and environmental problem. We have several projects about to start (funded by European Union (EU), Biotechnology and Biological Sciences Research Council (BBSRC) and Global Climate and Energy Project (GCEP) at Stanford University, USA) that aim to determine how lignin can be manipulated to allow efficient production of biofuel from substrates such as barley straw. This work will benefit enormously from the barley genetic resources available at SCRI and will further our collaboration with Genetics and PPFQ.

Diversity of crop plant species (Andy Flavell) Most modern crops are domesticated forms of wild plants that still live in their old habitats. Many studies have demonstrated the value of gene alleles originating from non-cultivar germplasm, showing that selective breeding has thrown away useful alleles in addition to the many useless ones. We are interested in defining the overall genetic structure within the entire species and 'mining' useful gene alleles from wild and landrace cultivated plants by applying high throughput molecular markers to crop germplasm collections. We have developed and applied a new microarray based marker technology to the analysis of the genetic diversity of field pea (*Pisum*), in collaboration with Noel Ellis and Mike Ambrose of the John Innes Centre, showing the overall genetic structure for the species, and identify subsets of germplasm to concentrate upon for allele mining (Fig. 1).

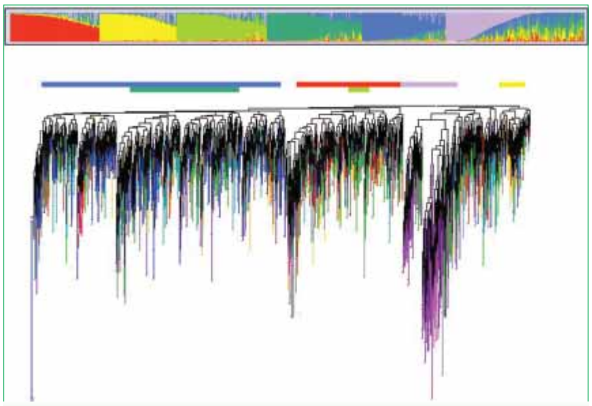


Figure 1 Genetic diversity of 3000 pea samples. Top: Species structure – each sample is represented as a vertical line comprised of a combination six colour-coded 'ancestral genotypes'. Bottom: Family tree - using the same colours as the structure chart. Wild peas are almost all in the lilac region of both graphs; the rest are landraces and cultivars.

To identify useful gene alleles we use high throughput molecular markers, including the Illumina Oligo Pool Array, which has been pioneered in barley by the SCRI Genetics programme and has already been used successfully for discovering useful marker–trait associations in barley cultivar germplasm. We are working with Genetics and the European barley community to extend these studies to landraces and wild plants to identify new alleles. Lastly, we are working with SCRI Bioinformatics staff to develop the Germinate

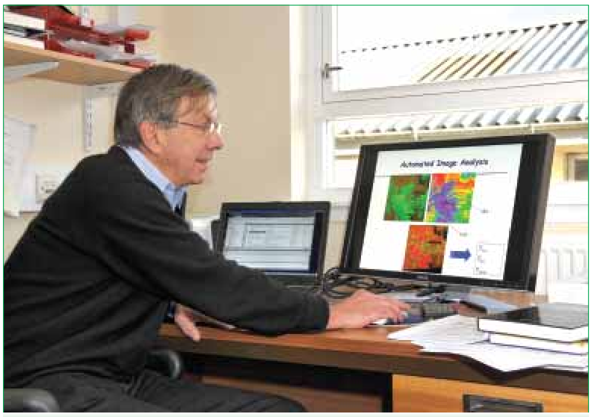
Andy Flavell

Steve Hubbard

database to store, analyse and visualise the huge amounts of data created by the above approaches.

Relationships between insect parasitoids and their hosts (Steve Hubbard) These associations are affected by the physiological health of the plant on which the host insect is feeding and on a range of micro organisms which are associated with the different elements of the system. The often complex associations between insects and microorganisms are the focus of a quickly expanding research field and range from mutualistic endosymbiosis to manipulative intracellular parasitism. Frequently, such insects are also vectors of economically important plant pathogens, but the nature of the interaction between vector microbial complement and pathogen transmission remains unclear. Vector competence depends on genetic factors that govern physiological and molecular interactions between the insect and pathogen, and on insect behavioural factors that influence interactions with the host plant, natural enemies and the physical environment.

Most aphid species possess an obligate primary bacterial endosymbiont, *Buchnera aphidicola*, and one–to–several types of facultative bacterial endosymbionts (secondary symbionts) that are members of the γ–proteobacterial family, the Enterobacteriaceae. *Buchnera* synthesises essential amino acids, thus providing aphids with nutrients that are poorly represented in plant phloem sap, and also encodes a chaperonin protein that facilitates transmission of circulative plant viruses by a number of aphid species. The role of secondary symbionts is less well characterised, particularly with respect to aphid vector competence, and has largely been investigated in the pea aphid (*Acyrthosiphon pisum*) where they have conditionally beneficial or deleterious effects on aphid performance and aphid–natural enemy interactions. Our current research aims to investigate the roles of plant, parasitoids and symbiotic microorganisms on the capacity of aphids to vector plant viruses.



Lyn Jones

Plant ecophysiology and adaptation to environmental stress (Lyn Jones) Our research continues to emphasise the development of remote sensing tools for the diagnosis of plant stresses and their use for improving crop management practices such as irrigation. One area of this work has been the development of temperature-based sensing of canopy temperature to schedule irrigation of a range of crop plants. We have now published a definitive analysis of the use of leaf temperature measurements for the estimation of leaf stomatal conductance. The equations derived in this work are now being applied in both field and glasshouse situations around the world. The work has also involved the development and testing of both image-based and Vegetation Index-based techniques for discriminating leaves from soil in mixed images using ratios between red and infrared reflectance. The resulting technology is being applied in a Defra LINK programme aimed at improving irrigation management of nursery stock plants where an automated system is being developed in collaboration with industrial partners. Field scale development of the approach has continued to involve collaboration with Commonwealth Scientific

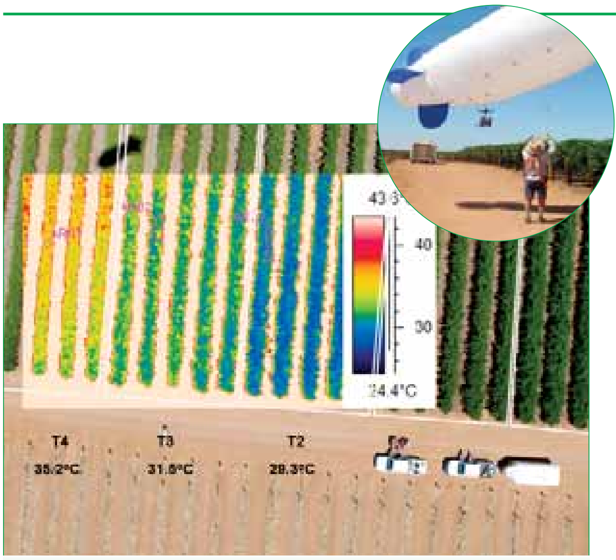



Figure 2 Oxford Landing vineyard (Australia) from a helium balloon (inset) - overlaid thermogram showing substantial increases in canopy temperature as the amount of irrigation decreases (original pictures from Ashley Wheaton).

and Industrial Research Organisation (CSIRO) and the Australian Grape and Wine Research and Development Corporation (GWRDC). These developments have been successfully tested in a field campaign using balloon-borne cameras in a vineyard at Oxford Landing, South Australia (Fig. 2). Allied work on the relative effectiveness of different ways of applying water in irrigation systems has largely been completed and generalised recommendations are being prepared.

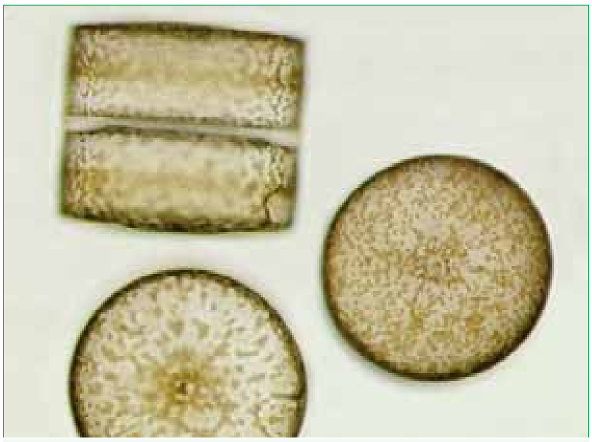
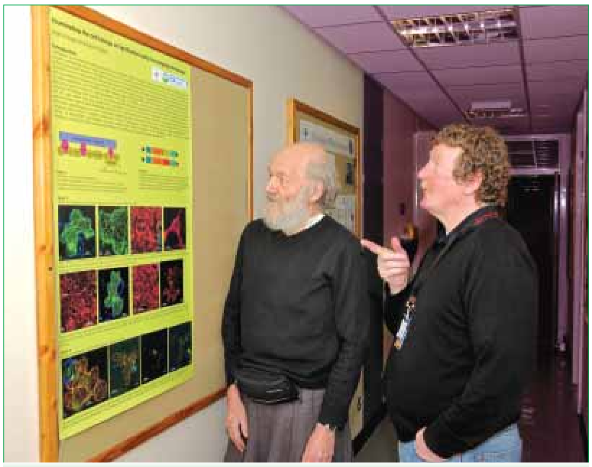


Figure 3 Cylindrical cells of *Coscinodiscus wailesii* (end view) and a cell division (side view) with cells about to separate. Cell diameter 0.4 mm; cell height 0.2 mm.

Novel aspects of the functioning and evolution of photosynthesis (John Raven) Work with Stefanie Kühn on single large cells of the diatom *Coscinodiscus wailesii*



John Raven and John Brown

show that some cells exhibit parallel oscillations, with a period of about 2.5 min. in the rates of carbon dioxide assimilation and oxygen production (Fig. 3). Previously this phenomenon was only known from vascular plants, and the diatom results show that the phenomenon occurs at the single cell level rather than necessarily involving cell–cell interaction as had been suggested for multicellular plants. A second paper, with Charles Cockell and Christine de la Rocha, examined the effects on present day cyanobacteria of the environment after oxygenic photosynthesis had evolved in cyanobacteria but before oxygen had accumulated sufficiently in the atmosphere to give an effective stratospheric ozone shield decreasing the ultraviolet (UV) flux at the Earth's surface. Such conditions allowed local accumulation of oxygen within and immediately around cyanobacteria, and hence the production of oxygen free radicals by oxidation–reduction metabolism, and a high incident UV flux because the cells had to be close to the water surface if they were to absorb enough photosynthetically active radiation to photosynthesise. Experiments mimicking these conditions showed that the high UV flux plus the presence of oxygen in and around the cells led to the production of ozone, adding to the range of active oxygen species that could have caused damage to the cells. Today the production of tropospheric ozone is also by photochemistry, but is not directly associated with photosynthetic organisms.