

Annual Report 2010



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Introduction

Peter J. Gregory

Things rarely stand still for long at SCRI and 2010 was no exception, with major changes to research direction and funding, plus a new institute structure to occupy the thoughts of many staff. Following the decisions of the Boards of the Macaulay Institute and SCRI in September 2009 to merge from April 2011, the first two months of 2010 were spent discussing and planning the new scientific opportunities that could result from the two institutions working together. This was an exciting period, with numerous ideas for projects that could

span from gene to globe and take the combined institute to the forefront of crop and land research internationally. The personal contacts that were forged in this process built trust and confidence among the scientists involved, which was exploited in the subsequent preparation of research proposals to contribute to the

scientific research programmes for 2011–16 of the Rural and Environment Research and Analysis Directorate (RERAD) of the Scottish Government. RERAD called for tenders for its new programmes in March; these were

designed to require the Scottish Research Institutes and the Scottish Agricultural College to work together and meant that a lot of time was spent building viable partnerships and writing proposals. Fortunately, SCRI's proposals generally found favour with the reviewers, meaning that only a small amount of re-writing was required in the autumn to complete the final proposals. The success of these tenders should deliver about 85% of the RERAD budget for the next five-year programme. The remaining 15% of the RERAD funding is part of

another tendering process involving a set of centres of expertise and strategic partnerships, but the outcome of these proposals has yet to be determined.

While looking forward to the new, we also had to deliver the final year of the existing RERAD programme and to continue the

process of diversification of research income so that SCRI could be less reliant on RERAD. During 2006–11, SCRI had a particular responsibility for RERAD's research programme on Sustainable Agriculture (Crops),



Peter Gregory

and we were especially grateful to Professor Janet Bainbridge who chaired the advisory committee along with external members Professor John Porter and Douglas Morrison. The programme delivered many novel outcomes and most of the required outputs and these are described in the final report that was submitted to RERAD at the end of the year. Simultaneously we have had a very good year for winning grants and contracts from non-RERAD sources, thereby meeting our target for external income and providing some long-term research projects. A particular success was our participation in the new programme of the Technology Strategy Board on developing pest and pathogen resistant crops and means of controlling diseases and pests. We were successful in all five applications for these business-led projects, with MyInfield Research Services Ltd playing a key role in the mediation of business contacts and project management. These projects last up to five years so will provide a source of research for several years to come. Success with research council funding has been slightly more elusive this year, although our links with the Division of Plant Sciences of the University of Dundee continue to provide areas of success and there is a good supply of innovative proposals on the drawing board.



A presentation case of SCRI variety jams for Her Royal Highness.

At the end of June we had a particularly good day when HRH The Princess Royal visited us to open the new glasshouse suite and National Seed Store. We now have a modern seed storage facility which can adequately conserve the seed of the Commonwealth Potato Collection and of the many collections and mapping populations of barley that we have acquired over the years. No longer will they be dependent on the vagaries of the weather and the mouse population in the storage sheds! From her visits elsewhere, HRH was clearly very knowledgeable about the sort of research that we do and contributed vigorously to the discussion about the various exhibits. She also visited our new Centre for Sustainable Cropping at Balruddery Farm in Angus and heard about the long term experiment that is being established there to investigate how research leading to the development of new crop cultivars and sound agro-ecological practices can improve the profitability and sustainability of cropping. HRH saw the second year of uniform planting with maize, but since the autumn the site has started to be developed with plantings of winter wheat, and sowings of barley, pea and potato crops in the spring of 2011 will follow across the whole experimental site. A management group for the experiment has been established and we are in the process of appointing a new research agronomist to the Environment Plant Interactions programme who will play a major role in developing novel crop husbandry practices and in linking the genetics and ecological research inputs.

Throughout all of these activities, the science of SCRI has continued to make advances. The reorganisation of our work on the barley pathogen, *Rhynchosporium secalis*, a few years ago is now starting to deliver benefits across both the Plant Pathology and Genetics Programmes. The *R. secalis* genome has been sequenced using 454 XLR and Illumina GA2 next generation sequencing technologies to reveal a genome assembly of 54Mb consisting of 2,734 scaffolds. In addition an interaction transcriptome of epidermal peels from barley leaves infected with *R. secalis* strain L2A has also been sequenced. Annotation of the genome is in progress with collaborators in Germany, and the transcriptome data have allowed identification of



potential pathogenicity factors such as structural cell wall proteins, plant cell wall degrading enzymes and putative effectors all present at the start of colonisation of the host tissue. This knowledge will be used to identify the effectors that *R. secalis* deploys to suppress host defences and then to identify and deploy novel resistance and control methods. Also in Plant Pathology, research on late blight has shown for the first time what the pathogen's effectors are manipulating and why, when the pathogen enters the host plant cell. Research on potato in the Genetics Programme has contributed to the release of the first draft of the potato genome sequence by an international consortium in which SCRI played a significant role. It is expected that the finished sequence will transform the way scientists and breeders approach improvements to yield, quality, nutritional values and disease resistance in new potato varieties. As with the *R. secalis* work, the important process of annotating the sequence is under way prior to general release of the sequence, currently scheduled for 2011.

SCRI is continuing to invest in new appointments in the area of bioinformatics, and has developed an international reputation for its work for visualising deep and complex data. Examples of this are the work in Genetics that has led to the release of 'Flapjack' software for visualising dense genotypic data in lines and populations and 'Tablet' software for analysing second generation sequence data. This has already led to over 6,000 different registered users worldwide using either or both applications in their research programmes.



More good news from SCRI.

Plant Products and Food Quality (PPFQ) was the last of our research programmes to be externally reviewed and gained numerous plaudits for the quality of its work. The review team were particularly impressed by the establishment of metabolomics as a key platform within the group and by the evidence for effective team working. In 2010 the Programme found that a key underpinning factor in potato texture was identified as pectin methyl esterase (PME). Higher PME activity was directly related to desirable tuber texture properties and provides a route to marker development for this important trait in breeding programmes. Members of the Environment Plant Interactions (EPI) programme are also working on ways to improve the nutritional quality of crops via the development of agronomic methods to biofortify potatoes, leafy vegetables and bread wheat with essential mineral elements often lacking in human diets, such as selenium, zinc, iron, calcium and iodine. In addition, recent field trials performed by the EPI and Genetics programmes have identified chromosomal loci that influence the accumulation of these elements in brassicas and potatoes. Other studies have similarly identified chromosomal loci affecting N, P and K fertiliser use efficiencies in barley, brassicas and potatoes. Identification of these loci has improved our understanding of how these mineral elements are acquired and utilised by crops and will be used to develop molecular markers to accelerate breeding for improved fertiliser use efficiency and nutritional quality.

As I write this report, concerns about food security are again in the news because grain and cotton commodity prices are back to 2008 levels, and in the UK the Government Office of the Chief Scientist is about to release its Foresight Report on Global Food and Farming Futures. This is not an issue that is going to disappear any time soon, and the merger of SCRI with the Macaulay Institute to form The James Hutton Institute from 1 April 2011 provides a real opportunity for Scotland to contribute significantly to developing innovative products and policies that can assist with alleviating these difficulties, as well as the challenges posed by global environmental changes. I shall look on with interest to see the contributions and advances that will, undoubtedly, be made.

After six years I shall be leaving SCRI. I have enjoyed my role enormously, not least because of the enthusiasm of the staff and the positive messages about their work that they have always conveyed to our many visitors. I am delighted that Gaynor McKenzie was awarded the Director's Award for 2010 in recognition of her enthusiastic communication of her work on potatoes

and especially the Commonwealth Potato Collection. Finally I should particularly like to thank my colleagues in the Executive Team, Howard Davies, Neil Hattersley and David Hopkins, and my Personal Assistant, Anne Pack, for their unfailing support during the good times and the bad over these last few years; it has been a pleasure to work with such a professional team.

SCRI Worldwide

Phil Taylor

SCRI continued to reinforce and expand its overseas links and partnerships during the course of 2010. Of the many pleasing opportunities to react with organisations around the world, one of the most notable for us was the cooperation agreement made with Zhejiang Academy of Agricultural Sciences (ZAAS) in China.

A formal signing ceremony was held at SCRI in the Autumn. The Memorandum of Understanding anticipated that the two partners would identify and develop collaborative research programmes of mutual interest. It was also hoped that the two centres would be able to exchange staff and graduate students.

The main areas of common interest between ZAAS and SCRI are plant pathology, sustainable methods of controlling pests and diseases and crop and environmental molecular biology and biotechnology.

Dr Lesley Torrance, Head of the Plant Pathology programme at SCRI said: "This is a very exciting opportunity to develop a collaboration with Chinese scientists in the important area of sustainable pest and disease control."

It was particularly appropriate that Dr Jianping Chen was able to sign the agreement for the Chinese side; he gained his PhD in Plant Virology at SCRI. He was an honoured guest at Invergowrie this time in his capacity as president of ZAAS. Director of Science Planning, Professor David Hopkins, signed on behalf of SCRI.

SCRI was also able to announce further involvement in the African continent during the year. A project to

assist farmers in Malawi was backed by the Scottish Government with an award of nearly £400,000 from the International Development Fund.

SCRI is working with farmers, national potato researchers and CIP (International Potato Center, Lima, Peru) potato specialists based in Malawi to help combat constraints on the potato crop within the Malawian agricultural system. The ultimate goal is to improve potato crop yields to reduce poverty and increase food security.

SCRI specialists are finding ways to develop sustainable potato production through the development of disease-free potato seed tuber production systems and marketing for improved productivity and trade.

Scotland's External Affairs Minister, Fiona Hyslop, said: "Scottish Government funds go directly to Scottish organisations who have demonstrated that they have the relevant skills, capacity and expertise to deliver services on the ground to the people of Malawi. Rigorous monitoring shows our funding is having a positive impact on the lives of Malawians and I was fortunate to witness this at first hand during a visit to the country."

All of the projects receiving funds target the priority areas set out in the Co-operation Agreement between the Scottish Government and the Government of Malawi. These are health, education, civil society and governance and sustainable economic development.

SCRI is also leading similar work to support potato production in Kenya as part of a project backed by The Monsanto Fund.



Dr Jianping Chen and Professor David Hopkins signing the Memorandum of Understanding.

Closer to home, 2010 saw researchers from SCRI joining their counterparts in 12 other EU countries in a consortium seeking better ways to use legume crops. The Legume Futures programme was launched in Edinburgh.

The three-year long €4 million programme is being coordinated by the Scottish Agricultural College which, along with SCRI, will fulfil the UK commitment to the project funded under the EU framework.

Dr Pietro Iannetta of the Environment Plant Interactions programme at SCRI is leading a work package on data management and novel system design, including a website www.legumefutures.eu and an online database for the exchange of information between scientists.

The aim of the research is to identify the best way to use legumes in each of Europe's climatic zones, identify the most suitable crop and design a cropping system that reduces farming's environmental impact.



Environmental Change

Lesley Torrance

Environmental change is one of the most serious threats facing our society and its effects will have major impacts on many sectors of the economy. The Scottish Government has set the challenging target of reducing greenhouse gas (GHG) emissions by 80% by 2050 and it is estimated that the land-use sector contributes about 20% of the total GHG emissions. At SCRI, research to improve fertiliser management, conserve organic matter in soils and the soil's ability to store carbon is aimed towards reducing GHG emissions. Work to increase knowledge of the effect of changing climate on the geographic range and abundance of pests and pathogens will better prepare us to counter new or emerging threats to crops.

Similarly, increased knowledge of the effect of abiotic stresses such as heat, cold and drought on the plant's ability to mount disease defence responses, and their impact on crop quality, will help us to develop the tools and technologies to mitigate, adapt and manage the effects of such changes in Scottish agricultural systems. Here we present four articles that provide a snapshot of some of our work. The articles illustrate

the wide ranging nature of the work and include using plants to stabilise slopes thereby preventing landslips or soil erosion and investigating what makes grass plants drought tolerant. We also report on research to understand the environmental influences on pathogenicity and the effect of abiotic stress on mRNA processing by alternative splicing leading to variation in the proteins produced.



Green engineering for sustainable environmental solutions

A. Glyn Bengough¹, Paul D. Hallett, Ken Loades, Blair M. McKenzie & Ron Wheatley

Increasing recognition of the ecosystem services provided by the environment to both urban and rural populations is particularly relevant to the interface between the plant-environmental sciences, and civil engineering. The needs of society for access to fresh water and food and to a healthy, biologically diverse, and aesthetically pleasing environment are highlighted in recent policy documents that also require greatly reduced disposal to landfill and transition to a low-carbon economy. These policy drivers are in addition to, and a consequence of, natural drivers associated with global environmental change.

The interface between plants and engineering is the subject of considerable interaction between SCRI and the University of Dundee, including a joint senior appointment with the Division of Civil Engineering in 2010 to further develop this area, and complement existing links between SCRI, the College of Life Sciences, and the Centre for Environmental Change and Human Resilience (CECHR). The majority of research has concentrated on quantifying biophysical interactions between roots and the soil, including the stabilising effects of plant root systems on soil slopes, to decrease the likelihood of shallow landslips. (Fig. 1) The



Figure 1 Model of rooted slope following testing in the centrifuge at 15 x gravity. Yellow line indicates failure plane.

increase in soil strength due to the direct mechanical reinforcement of soil by roots has been measured for both woody and thin fibrous root systems, and mathematical models have been tested that relate root reinforcement to root number and diameter distributions. Predicted increases in the frequency of intense rainfall events may render more slopes vulnerable to erosion and landslips, and a climate chamber has been constructed at the University of Dundee to enable this area of research on scaled models of soil slopes. (Fig. 2) The quality of output of this collaboration has been recognised (e.g. 'Outstanding Paper Award', European Society of Agricultural Engineers 2008; nomination for Institution of Civil Engineer's Award in Engineering Sustainability, 2010), has led to invited reviews, and created links with research institutions and companies throughout Europe.

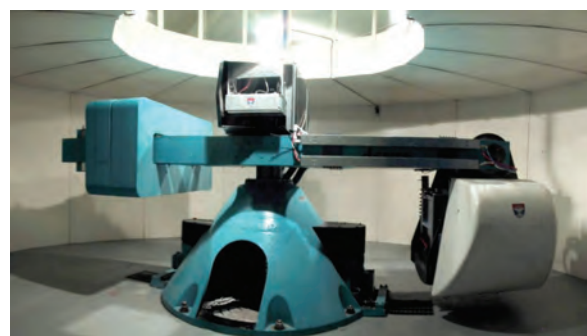


Figure 2 University of Dundee geotechnical centrifuge used to test scaled models of slopes at up to 100 x gravity.

Research encompasses both applied practical solutions, and more fundamental research. For example, the role of bulky organic waste in aiding plant establishment on embankments has been highlighted in a recent study with WRAP, that aimed to use processed waste materials for environmental benefit along our transport corridors. This work, in association with Dundee City Council, showed that grass establishment was enhanced, and surface runoff and soil erosion decreased on plots that were amended with quality green compost. Surface application of the compost was the most beneficial. (Fig. 3)

At a much smaller scale, the mechanics of soil deformations around roots is being studied both

¹ Joint with Division of Civil Engineering, University of Dundee



Figure 3 WRAP slope at Riverside, showing amendment with quality green compost enhancing grass establishment.

theoretically and experimentally. This work is showing us how plant roots deform the soil as they grow, how root hairs may help to anchor the growing root tip, and how organisms such as earthworms penetrate the soil. Our future aim is to build on this work at both fundamental and applied ends of the spectrum, to deliver both increased understanding of basic mechanisms, and practical solutions to real problems.

The impact of climate change on grasses: ryegrass and drought tolerance

Alexandre Foito, Stephen L. Byrne¹, Tom Shepherd, Susanne Barth & Derek Stewart

Climate change predictions for the north and west regions of Europe suggest a slow increase of basal temperature with an increase in extreme weather events, such as floods and droughts, consequently increasing stress experienced by crop plants. Considering that one of the major environmental factors which limits the growth and productivity of plants in the world is water-limitation, it is important to improve the ability of plants to cope with such stresses in order to at least maintain, if not increase, their current productivity.

The majority of agricultural land in the UK is devoted to grasslands, with *Lolium perenne* (perennial ryegrass) being the major grassland species present. This species

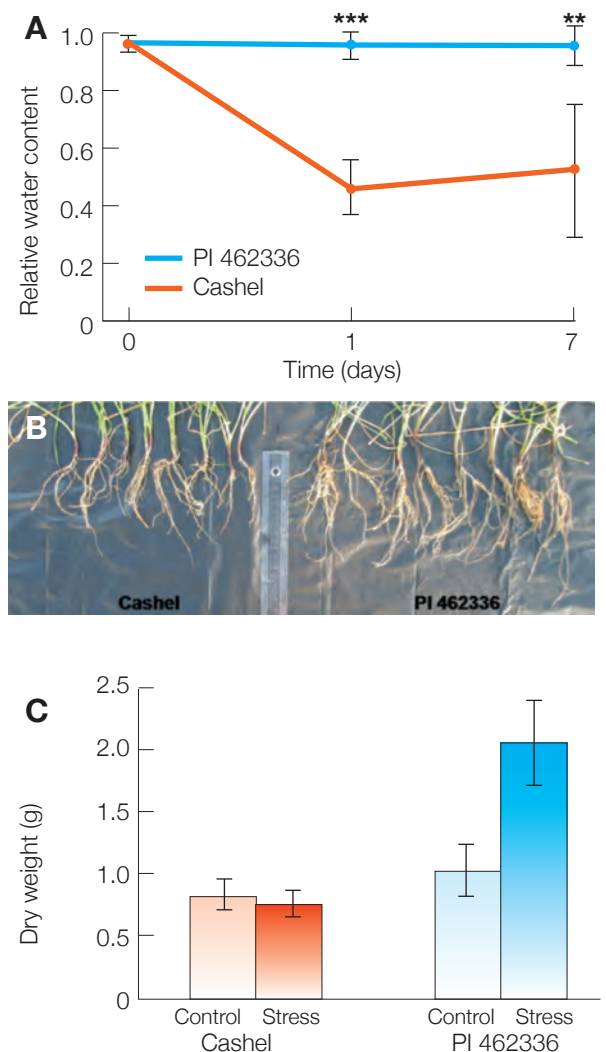


Figure 4 Physiological response of perennial ryegrass to water deficit. (a) Relative water content (RWC) levels of the leaf tissue after 1 week of stress (** $P < 0.01$. *** $P < 0.001$ $n=6$). (b) Root biomass of PI 462336 in comparison to Cashel under polyethylene glycol (PEG) induced drought stress after 2 weeks of water-limitation. (c) Root dry weight of Cashel and PI 462336 genotypes under control conditions and PEG induced drought stress after 2 weeks.

possesses high yields and digestibility compared to other grass species, hence it is an economically important forage for animal nutrition. However, perennial ryegrass is susceptible to abiotic stress conditions.

Water deficit in particular was the focus of a collaborative project with The Irish Agriculture and Food Development Authority (TEAGASC), which aimed to investigate the molecular and biochemical mechanisms which are responsible for increased tolerance to water limitation. Two genotypes, with contrasting drought response, were

¹ Teagasc, Crops Biosciences Centre, Oak Park, Co. Carlow, Ireland



exposed to one week of water limitation which resulted in the decrease of the water content in the leaf tissues of the non-tolerant genotype (Cashel) whereas in the tolerant (PI 462336) variety water content appeared to be unaffected by the water deficit treatment (Fig. 4).

A comprehensive metabolomic analysis was carried out for root and leaf tissues and major differences were observed. These included an overall reduction of metabolite levels (particularly fatty acids) in both tissues of Cashel upon exposure to stress, which suggested that water limitation was constraining source activity in the plant – possibly by affecting the photosynthetic machinery. In contrast, PI 462336 accumulated sugars and compatible solutes such as trehalose, glucose, fructose, maltose and raffinose in response to water deficit. Raffinose in particular exhibited the highest increase in both leaf and root tissues where it is thought to act as an osmolyte and potentially aid in scavenging radical oxygen species. Therefore, it appears that raffinose levels play an important role in improving tolerance to water limitation in *L. perenne* and may eventually become a target for the selection of superior drought tolerance in other crop species.

In addition to the metabolomic approach a complementary transcriptomic approach was used for the tolerant variety and revealed a number of relevant genes regulated by water deficit. These included a dehydration responsive element binding (DREB) transcription factor, an aquaporin (involved in water transport across membranes) and a gene encoding a fructan:fructan 6-G fructosyl transferase (6G-FFT), all of which have well documented roles in drought tolerance.

The results of expression of 6G-FFT prompted further experimentation in order to determine whether fructans (polymers of fructose) may be responsible for the difference in tolerance between varieties. Comparison between genotypes revealed that the tolerant genotype had 1000-fold higher expression levels in the leaves, suggesting an important role of fructans in drought tolerance. Fructan contents and polydispersity were characterised and subtle differences were observed between genotypes which were attributed to the presence of higher molecular weight fructans in the

tolerant genotype. However, the contribution of this biochemical change towards improved water limitation tolerance is not well understood.

Overall, this work highlights some of the mechanisms which may affect tolerance to water deficit periods and hence may provide target traits for the selection of enhanced tolerance to drought.

Asymptomatic infection – the Trojan horse of crop production

Adrian C. Newton, Anna Avrova, Amar Thirugnanasambandam & Mark Looseley

As plant pathologists we tend to focus on diseases and their causal agents. In barley the two we concentrate on at SCRI are 'rhynchosporium' or 'leaf scald' caused by *Rhynchosporium secalis* and 'ramularia leaf spot' caused by *Ramularia collo-cygni*. Molecular detection methods such as quantitative PCR have shown us that both of these fungi are present on many barley crops most of the time, but as macroscopically-symptomless infections. Transformation of these two pathogens with green fluorescent protein allowed live infections to be viewed microscopically. It has shown how extensive such infections are, enabling spores to be formed and the whole lifecycle completed without triggering disease symptoms (Fig. 5).

The importance of such observations is that they probably reflect the norm: the environment is packed with numerous viral, bacterial and fungal microorganisms not causing disease symptoms. However, given certain triggers when on suitable hosts, many of these organisms can lead to symptom development. We do not yet understand most of these triggers, but many are likely to be environmental stress factors. Whichever way climate change affects our environment, it will result in different abiotic stress factors or changed timing of stresses such as heat, cold snap, flood or drought. While our focus has often been on new invasive pests and pathogens, equally important will be maintaining and improving the ability of plants to defend themselves against existing pathogens and potential pathogens in the environment.

A corollary to the observation of extensive non-symptomatic infection is that plant breeding is normally against expression of disease symptoms and not against pathogen infection. That infection and symptom expression are highly correlated is both to be expected and fortuitous, as such selection is relatively straightforward and effective. However, symptomless infection may itself a) be reducing yield, as it must take some resources and could be inducing some defence reactions, b) mean that infection can become symptomatic if triggered, thereby increasing risk, and c) maintain a pool of pathogen variability and transmit inoculum to new environments. Furthermore, resistance against infection rather than symptom expression may use different mechanisms and be under separate genetic control and therefore offer unique (and potentially more effective) lines of defence. There must be some

correlation in all cases as the pathogen must be present to form symptoms. Nevertheless, we investigated whether resistance to symptoms and infection by *R. secalis* mapped to separate genetic loci. We found that while some loci controlled both types of resistance, one locus was more effective against symptomless infection. This has given us a new target for breeding that we are actively pursuing with commercial breeders.

The 'other side of the coin' is what changes in the pathogen when it progresses from non-symptomatic growth to full pathogenic development, producing visual symptoms? Recent sequencing of the *R. secalis* genome and genes transcribed by the pathogen at the start of infection allowed identification of potential pathogenicity factors, including effectors, affecting disease symptoms development. It was followed by expression profiling of potential pathogenicity factors throughout the infection. Further functional genomics will allow identification of genes essential for pathogenicity. They will also help with understanding pathogens' interaction with different host resistance genes. This information can lead to targeting resistance against essential processes and gene products in the pathogen that it is unable to avoid producing.

The presence of asymptomatic infection and potential genetic differences between cultivars also has implications for crop protection strategies. With some cultivars it may be more cost-effective to spray fungicide earlier than normal to reduce risk of symptom development later by knocking-out asymptomatic infections. In other cultivars the asymptomatic growth may have minimal risk of becoming symptomatic and therefore enables the decision not to spray as the risk of disease is low.

Understanding the mechanisms triggering symptom expression, whether host- or pathogen-mediated, along with the yield cost of symptomless infection, is important for devising multi-component, diverse and durable resistance breeding and deployment strategies. These are essential for responding to environmental change as we cannot necessarily identify what pathogens will threaten our crops in future.

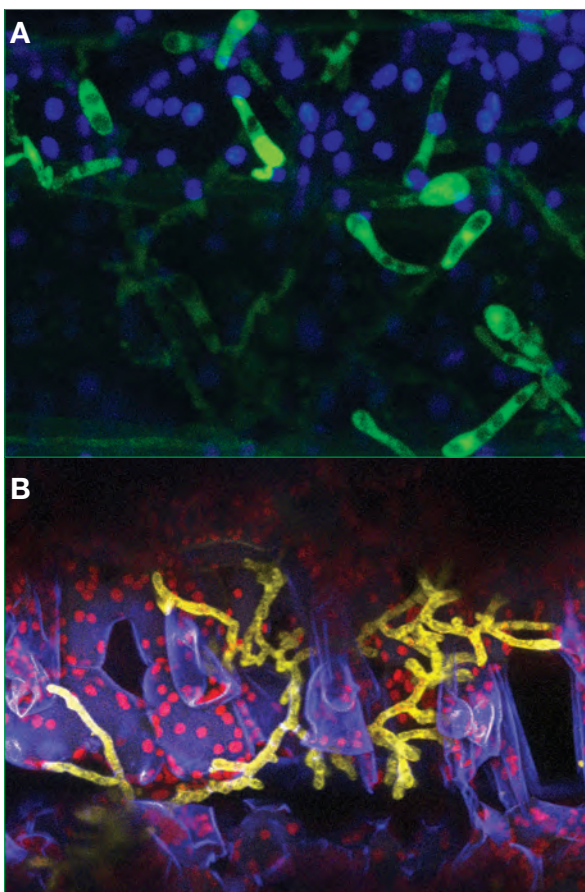


Figure 5 Confocal images of green-fluorescence protein-transformed *R. secalis* and *Ramularia collo-cygni*. A: Sporulation of *R. secalis* during asymptomatic infection. B: *R. collo-cygni* growing asymptotically inside a barley leaf stained with calcofluor.



Alternative splicing in response to abiotic stress

Craig G. Simpson, John Fuller, Dominika Lewandowska, Diane Davidson & John W.S. Brown

Gene expression involves extensive post-transcriptional processing of RNA messages before they are translated to functional proteins and ultimately influence phenotypic traits and responses. Plant messenger RNAs (mRNAs) are interrupted by non-coding sequences called introns that must be accurately and efficiently removed from the mRNA. The remaining protein coding regions, called exons, are spliced together to form the message that is translated to the functional protein. Alternative splicing (AS) occurs through alternative selection of splice sites on mRNAs derived from the same gene leading to the formation of different functional proteins (Fig. 6). The abundance of the protein variants produced by AS can differ in different plant tissues, stages of development and conditions, modulating and fine-tuning expression in developmental, signalling and metabolic pathways. In particular, AS in plants has been shown to respond to biotic and abiotic stress. In plants, the explosion in global genomic and transcriptomic sequence analysis is leading to a vast expansion of available gene sequence

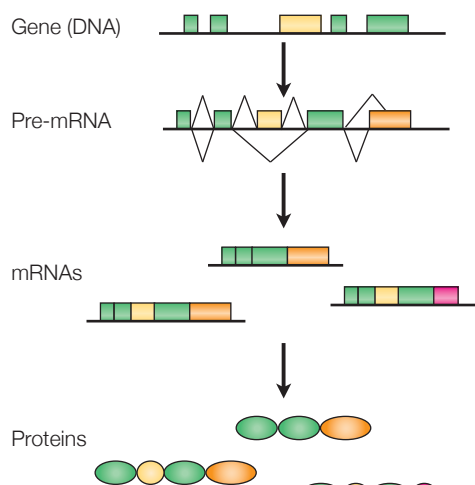


Figure 6 Schematic drawing showing the formation of alternatively spliced mRNAs and alternative proteins. Plant genes are interrupted by intron sequences that separate protein coding exons. Precursor transcripts are alternatively spliced (diagonal lines) to join different combinations of exons or parts of exons (rectangles) to give different mRNAs which are translated into different proteins.

information and is showing that AS in plants occurs extensively. Current estimates suggest that AS occurs in at least 60% of plant genes. AS in plants is, therefore, far more important than previously thought and will have a major impact on plant gene expression.

How plants respond to and tolerate external stresses is a key question in plant physiology which impacts crop productivity. Stress responses are regulated at both the transcriptional and post-transcriptional levels. Genetic screens to identify genes involved in abiotic stress acclimation or tolerance have recovered a number of proteins known to interact with RNA. This link between environmental cues, such as abiotic stresses, and RNA metabolism is likely to reflect processes underpinning RNA production, export and stability, including AS.

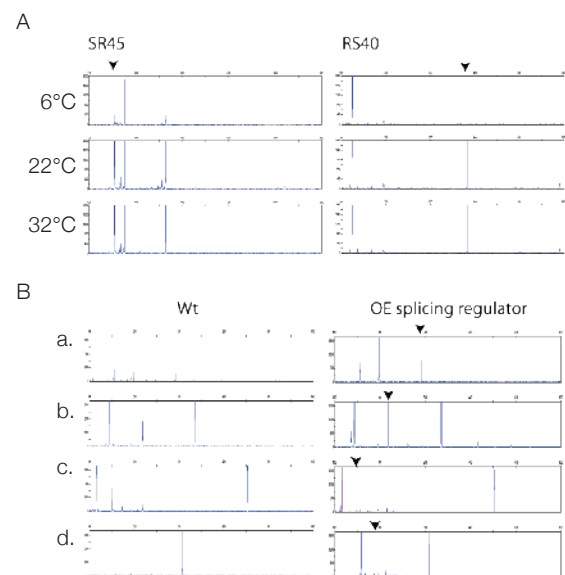


Figure 7 A high-resolution AS panel monitors changes in plant alternative splicing. Each peak in the boxes represents a different alternatively spliced transcript. Arrow heads indicate alternatively spliced transcripts that change in response to the different treatments. A. Plants grown at 22°C were given a treatment of cold (6°C) or hot (32°C) for 6 hours before isolating RNA and performing RT-PCR. Two examples of known alternative splicing regulators (SR45 and RS40) from the panel of alternative splicing events show changes in alternative splicing patterns in response to the change in temperature. B. Over-expression of the splicing regulator RS31 leads to changes in alternative splicing in stress related genes. a. Squamosa promoter binding protein-like 16 (SPL16); COLD. b. DNAJ N-terminal domain-containing protein; HEAT SHOCK. c. drought-induced-19-like; DROUGHT. d. SNF1-like protein kinase (AKin11); HYPOXIA.

AS is over-represented among genes which are up- and down-regulated under stress conditions and is thought to be one of the key points at which rapid changes in expression of proteins in response to external stimuli occurs.

The RNA processing group at SCRI has developed a high resolution reverse transcription-polymerase chain reaction (RT-PCR) system that allows us to measure dynamic changes in AS in around 300 plant genes (>900 AS transcripts). These genes represent important regulatory genes and genes with roles in responses to abiotic stresses. We are studying how AS events in these genes are regulated in response to environmental changes and to determine whether such molecular mechanisms are conserved in different crop plant species. To do this, we measure the levels of alternatively spliced variants in response to variable abiotic stresses such as, for example, temperature. We have identified genes which are transcriptionally regulated by temperature, but also have considerably altered AS patterns. Significantly, genes that regulate

AS of other genes were shown to respond directly to temperature, particularly in the cold (Fig. 7A). The effect of such factors on the AS of downstream genes can also be investigated using plants that either over-express or reduce expression of these proteins. Altered expression of these regulators has a significant effect on the AS of a number of different genes including those that are important stress response genes (Fig. 7B). This system allows us to identify whether plant splicing factors promote or inhibit selection of alternative splice sites and identify their gene targets.

It is now clear that AS has a key role in regulating processes such as abiotic stress responses and will impact crop development and productivity. There is, therefore, a need to capture AS information in crop systems and as plant scientists, we have major challenges ahead to appreciate fully the importance of AS in regulating plant growth and development, its response to environmental conditions and to incorporate AS into our thinking.



Biodiversity

Robbie Waugh

Investigating natural and induced biological diversity and biological complexity underpins plant and environmental sciences and impacts upon a wide range of issues that we face today. For example, the spectrum of biological diversity in broad acre crops such as potatoes and barley is intentionally manipulated, and frequently minimised by plant breeders during the process of developing and releasing new and better crop varieties. This is necessary to meet the current demands of regulators, growers and end users throughout the production and processing chain. In contrast, assessing and managing diversity is frequently the objective when attempting to maintain the viability and vitality of natural and managed environments. There, a diversity and balance of life forms is considered key to effective long-term function, including the ability to recover from a variety of anticipated or unanticipated events.

In the following short articles it will become clear just how central the issue of biodiversity is to the research we conduct in each of the science programmes at SCRI. They cover topics that range from the impact of genetic manipulation on the 'metabolome' of specific potato varieties, to a broad appraisal of the diversity of the vegetation currently present in Scotland's arable-grass ecosystems. It will also become apparent that the

type of data upon which the articles are based reflect a similar diversity of both approach and resolution, highlighting the impact that technological and analytical advances are having in furthering our understanding of biodiversity and consequently in generating knowledge. Importantly, each short story has practical outcomes that will benefit specific end users either in government, commerce or society.



Metabolome biodiversity in crop plant species – when, where, how much and so what?

Louise V.T. Shepherd, Gary Dobson & Howard V. Davies

Plant breeding drives the production of the new varieties required to compete successfully in the complex global agricultural marketplace, with increasing emphasis on the use of early landrace varieties and wild species to introduce the new genes and alleles required to improve yield, pest and disease resistance, quality and nutritional value. Targeted analysis of key compounds has provided the cornerstone for assessing the quality, nutritional value and safety of cultivated crop species and a benchmark against which new generations of crops and advances in production systems can be evaluated.

Profiling approaches which use 'omics' technologies (transcriptomics, proteomics and metabolomics) provide a coverage of gene and protein expression and metabolite composition that is unsurpassed compared to traditional targeted approaches. Metabolomics in particular is being used to identify significant sources of variation in the composition of crop and model plants caused by genetic background, breeding method, growing environment (site, season), genotype ×

environment interactions and crop cultural practices, to name but a few. While breeders have long been aware of such variation from tried and tested targeted analytical approaches, the broad-scale, so-called 'unbiased' analyses provided by profiling technologies offer a major upside to our understanding of the true extent of variation in compounds relevant to breeding targets.

We have used Gas Chromatography–Mass Spectrometry (GC–MS) to assess compositional variation in a range of potato cultivars (both new and old), Chilean landraces and two diploid potato cultivars developed from *Solanum tuberosum* var. Phureja. As an example, Fig. 1 shows a principal components analysis (PCA) of GC–MS data from a collection of potato genotypes where the abundance of c. 100 metabolites is used to distinguish most of the landraces from both old and new cultivars, and indeed some of the modern

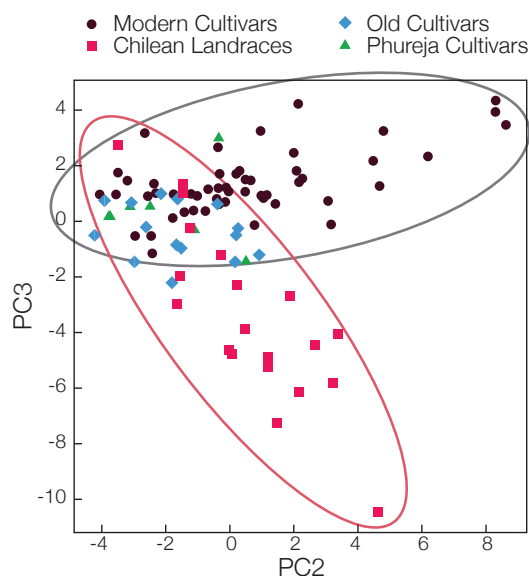


Figure 1 Statistical separation of *S. tuberosum* (old and modern cultivars), *S. phureja* and Chilean landraces, using data from the analysis of tuber composition by GC–MS.

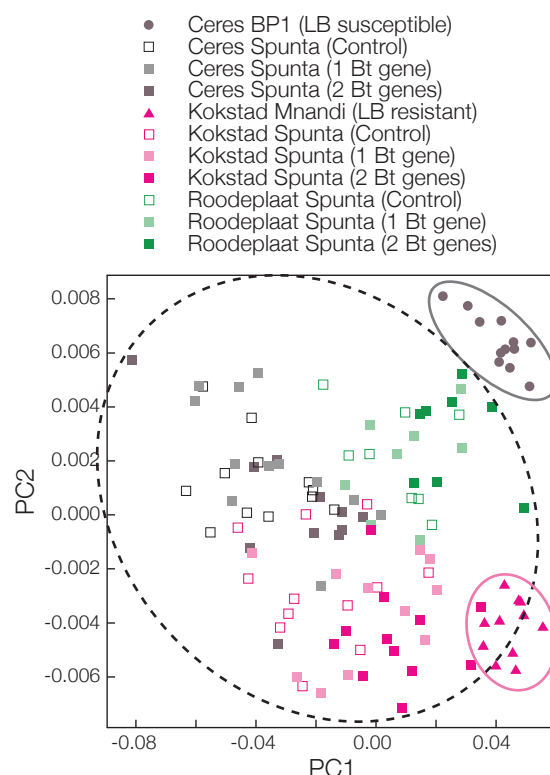


Figure 2 Statistical separation of three potato genotypes grown at three locations in South Africa, using data from the analysis of tuber composition by DI–MS. For one variety (Spunta), grown at all three locations, data is provided for both genetically modified tubers and their appropriate control.

cultivars from older material and *S. phureja* lines. This type of information can help target the selection of wild species to deploy (or potentially avoid) in potato breeding programmes.

In a study funded by the EU, and in collaboration with Dr Eugenia Barros at CSIR (Council for Scientific and Industrial Research), Pretoria, South Africa, we have used metabolomic analysis (in this example Direct Injection Mass Spectrometry [DI-MS]) to assess potential safety issues related to potential compositional differences between a specific genetically modified (GM) potato developed to express a protein conferring resistance to specific insect pests and its non-GM counterpart (the cv. Spunta). Fig. 2 shows a PCA that clearly distinguishes the three potato varieties (cvs Spunta, Mnandi and BP1; circled) included in the field trials, and between crops of the same variety grown at three different locations (Ceres, Kokstad and Roodeplaat) in South Africa. However, it was not possible to distinguish between the GM and non-GM Spunta grown in any of the locations. Thus, the DI-MS profiling approach showed that both genetic background and growing location were major drivers of compositional variation, but that the GM event did not

result in any detectable compositional changes. This is valuable information, which can be used to support the risk assessment process.

Temporal and spatial variation in gene and protein expression and metabolite composition between cultivated varieties of the same crop species is an indisputable reality. Indeed such variation underpins variety development and product differentiation and the knowledge derived from 'omics' can be harnessed to support more effective breeding. Arguably, data on the sources, drivers and extents of natural variation in raw and processed materials can help to define the boundaries of foods with a 'history of safe use', a concept often used in risk assessment but poorly defined experimentally.

Scotland's wild arable plants

Geoffrey R. Squire, Graham S. Begg, Cathy Hawes, Pietro P.M. Iannetta, Euan James, Alison J. Karley & Mark W. Young

A long-term study of the vegetation in Scotland's arable-grass ecosystems will soon be complete. The aim of the study is to design systems that exploit the synergy between crops and wild plants, such as in-field



Wood vetch (*Vicia sylvatica*) on mountain ledges in Corrie Fee, within the Cairngorms National Park



weeds. Weeds can be both a burden through reducing yield and a benefit through supporting ecological processes not provided by the crop alone. They are also a largely untapped source of new economic products. Here we report on three facets of the study that were published in 2010.

The arable flora is buffered by the seedbank – a reserve of seeds buried in the soil. The rate and degree to which the composition of the seedbank may be shaped by proactive field management, as opposed to soil and other local conditions, was, however, previously uncertain. Therefore data were collected on seedbanks from a survey of 110 fields covering a range of management preferences (organic, integrated, and general commercial practice) and environments in the east of Scotland. The results showed that while the environment had an influence, the type of management applied to fields had the greatest effect on the composition of the seedbank. The seedbank was also shown to be a more discriminating indicator of the weed flora in a field or region than the emerged

weed communities. Our overarching finding was that the seedbank can *in principle* be managed to achieve a composition in which the beneficial groups of plants are well represented. Effort is now directed towards several of the plant groups that will bring both ecological and economic benefit.

One such group is the wild legumes (Family *Fabaceae*). High inputs of mineral nitrogen (N) fertiliser have reduced the wild legumes in agricultural land, but they are still thought to fix N in semi-natural systems. Consequently, they could yet provide a major source of N to future crop systems since alternatives to mineral N are needed to offset its high cost and adverse environmental impact. However, not all members of the *Fabaceae* form the root nodules – the outcome of a ‘symbiosis’ between the plant and bacteria called ‘rhizobia’ that enables them to fix atmospheric nitrogen. To assess their potential, samples were obtained of many of the wild legumes from within and around agricultural land and tested for their ability to form symbioses. The initial results are promising in that many of the species do in fact nodulate (Fig. 3). The evolutionary relationships between the ‘rhizobia’ in different legume species are currently being examined to assess the diversity and ecological function within the group. The practical development of this work was boosted in 2010 by the EU ‘Legume Futures’ project, which will design legume-based rotations throughout Europe, and a SPARK award to examine the amino acid composition of current crop-legume varieties.

We have also made progress this year with one of the main analytical problems in this topic, which is to quantify the links between time-series in different parts of the biota. Time-series are important since something that happens early in an individual's life cycle or trajectory can affect its later performance. With machine learning experts at the Josef Stefan Institute in Slovenia, we have applied the methods of dynamic time warping (DTW) to compare a large number of paired trajectories of crop and weed cover. DTW is an approach used in voice recognition, where a reference sample of a person's speech is compared with a test sample. When our trajectories for crop and weed cover were quantified by DTW, and then further probed

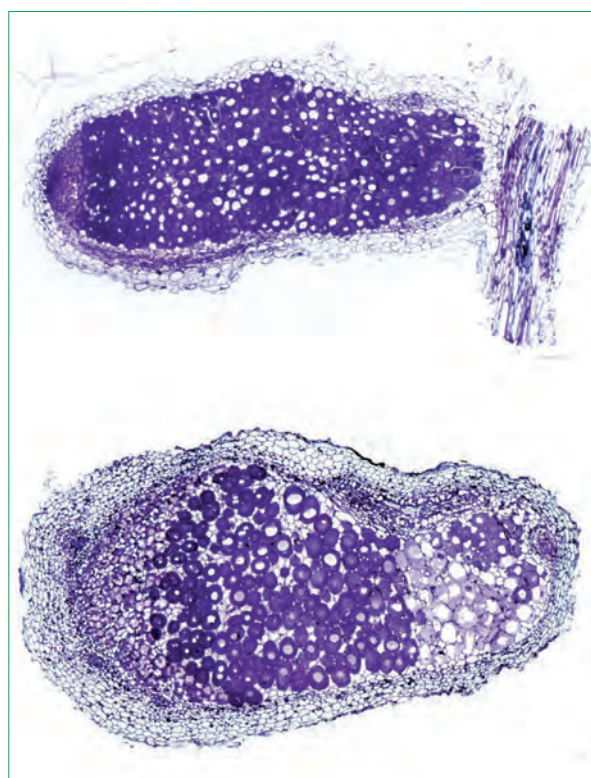


Figure 3 Micrographs of the nitrogen fixing root nodules of two wild legume species (top) *Trifolium campestre* and (bottom) *Astragalus danicus*, showing the symbiotic bacteria stained blue. The nodules are 2 mm in length.

using machine learning methods, it was apparent that the main factor driving the combination was the crop, rather than features of weed management. It appears from this first analysis that DTW may have further uses in analysing the trajectories of the entities (e.g. plants, insects, fields) that occur in managed ecosystems. The practical management of seedbanks and weed flora at field and regional scales will be facilitated as part of an EU project (called PURE) awarded in 2010.

Genetic diversity in modern barley varieties

Luke Ramsay, William T.B. Thomas, Jordi Comadran, Dave F. Marshall, Paul Shaw & Robbie Waugh

The genetic diversity of the barley varieties that are grown widely in Scotland and elsewhere in the UK has been shaped by past selection for yield and quality of the crop in the UK environment and for the demands of associated end-user industries. However, although it forms only a subset of the variation present in the species as a whole, the diversity that exists in elite UK material has been sufficient to power significant breeding progress over the last 20 years. In order to study this genetic diversity and to investigate its relationship with variation in agronomic and economic traits, we led a large coordinated project on the

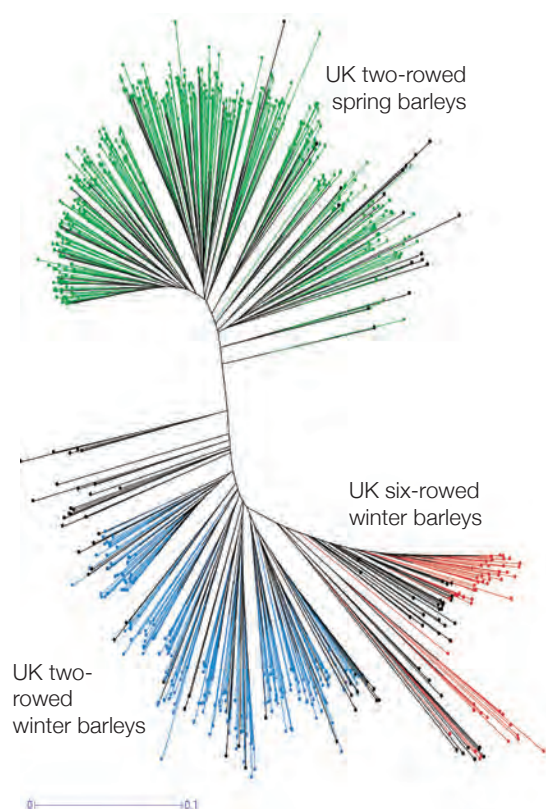
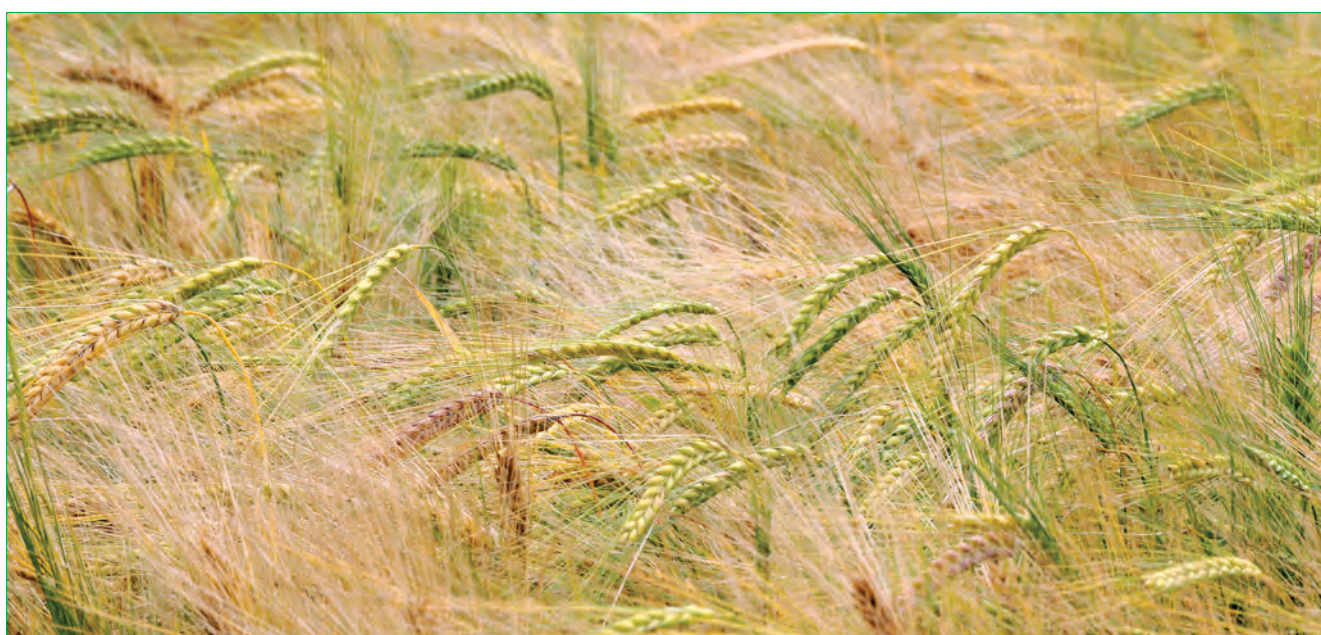


Figure 4 Phylogenetic tree using SNP marker data showing the divisions between crop types in modern UK barley varieties

'Association genetics of UK elite barley' (AGOUEB) funded by BBSRC and RERAD and supported through the Defra SA LINK programme. The project



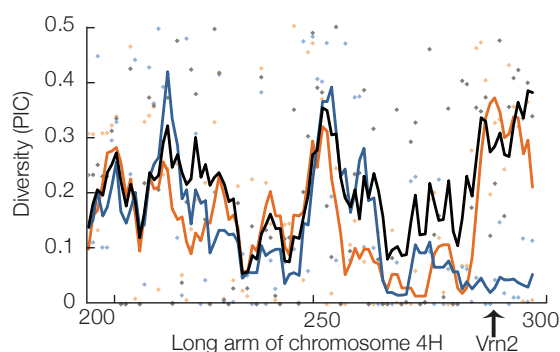


Figure 5 Diversity scan of the long arm of chromosome 4H of barley using a sliding window of 10 adjacent loci with a step of one plotted against the cumulative marker number.

Key: Two-rowed spring = orange; two-rowed winter = blue; (adjusted full data set = black); Position of vernalisation gene = Vrn2

also involved two academic collaborators (NIAB and the University of Birmingham) as well as industrial collaborators and sponsors from all sections of the industry: growers, maltsters, brewers and distillers. Importantly, the project involved all commercial UK-based barley breeding programmes.

The project used genomics resources to monitor variants of genes involving individual base changes (or single nucleotide polymorphisms, SNPs) in barley genes as markers to determine the genetic diversity in elite barley varieties. Over 3000 such SNP markers were assessed on over 1000 barley lines to determine patterns of diversity. These data have provided an unparalleled insight into the genetic variation in modern barley varieties. Overall, the data showed clear groupings that related to known divisions between spring and winter-sown bio-types and between two-rowed and six-rowed varieties within the winter material (Fig. 4). Moreover, as the markers used are variants of genes that have been accurately positioned in linear order along the barley genome, the results allowed much more detailed interrogation of how diversity changes along the chromosomes both within and between these crop bio-types. For example, the comparisons highlighted reduced variation in winter barleys at the end of chromosome 4H that corresponds to the position of one of the vernalisation genes that delays flowering until spring in winter-sown barleys (Fig. 5). This correlation between allelic forms at

specific markers and differences in a particular trait can be extended to a genome wide analysis in order to find associations between other genomic regions and many different agronomic and economic traits. In AGOUEB such associations have been found using yield and quality from historical data derived from official trials results together with data from new trials undertaken specifically for the project. Some of the other traits studied include disease resistance and specific morphological characters used in the Distinct, Uniform and Stable tests (DUS) as part of the official variety registration. This has highlighted the importance of tightly defined genomic regions in the control of certain traits and in some cases has even allowed the identification of variants of the actual gene that causes the measured differences in the targeted trait. Such results highlight the possibilities that this type of study can offer and gives breeders the tools to screen and utilise variants of genes from more diverse barley germplasm (landraces, wild barley) in future breeding programmes.

The AGOUEB project has characterised the variation that barley breeders have been utilising over the last 20 years within the UK and North-Western Europe to produce improved varieties. This characterisation is now allowing other follow-on projects to study the genetic control of resistance to fungal diseases and of nitrogen use efficiency in barley in more detail, and has also developed the tools and understanding to aid breeding companies to produce future varieties using the genetic diversity within the current adapted elite gene pool.

The impact of invasive plant pathogenic *Phytophthora* species on biodiversity

David E.L. Cooke

The influence of plant pathogens on biodiversity is not always immediately obvious and, as a consequence, has tended to be overlooked. The aptly named *Phytophthora* (from the Greek – plant destroyer) is, however, one pathogen that is changing this view. The best known of the 100 or so species, *Phytophthora infestans*, was inadvertently introduced to Europe from Central or South America in the 19th century and caused the devastating

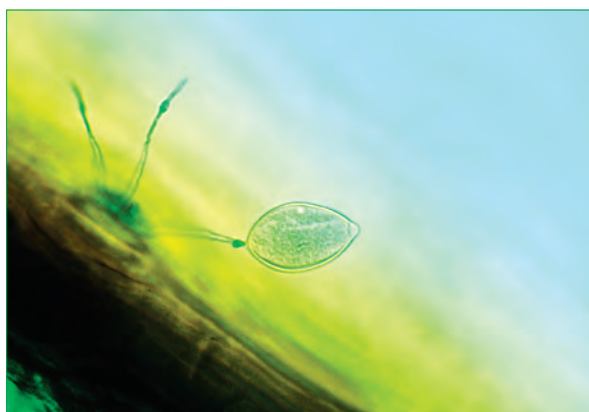


Figure 6 Sporangia of *P. kernoviae* emerging from the stomata of an infected host plant, in this case bilberry.

potato late blight disease. Although *P. infestans* does not directly impact UK biodiversity it is, unfortunately, one of a succession of invasive species that are having more serious consequences. *Phytophthora ramorum* and *Phytophthora kernoviae* were first recorded in the UK in 2002 and 2003 respectively, and between them have caused hundreds of economically damaging outbreaks across the UK horticultural industry. Plant health legislation has been enforced by teams across the UK who are working hard to prevent the spread of both pathogens. Nonetheless, movement into managed gardens and subsequently, natural ecosystems has occurred, primarily through infection of an invasive plant species, *Rhododendron ponticum*. This highly susceptible host has been shown to disseminate spores that cause disease (Fig. 6) on nearby native hosts. Severe epidemics in Japanese Larch plantations have also been observed in 2009 and 2010 affecting 1,900 hectares of forestry across South West England, South Wales, Northern Ireland and a recent case in Western Scotland. This progression to a landscape-scale disease in some areas of the UK is a serious concern, particularly in light of infections of heather and bilberry (or blaeberry) at some sites. These plant species alone are of great value to Scotland's biodiversity (Fig. 7), supporting a wide range of insect and bird species; the capercaillie, for example. At SCRI we are leading a collaborative project (with SASA, Fera, CEH and the University of St Andrews) to examine the threat of *P. ramorum* and *P. kernoviae* to the biodiversity of Scottish heathlands. We are currently investigating the susceptibility of key heathland plant species to these pathogens, using high-



Figure 7 Bilberry is a key component of many Scottish ecosystems but is under threat from invasive *Phytophthora* species.

throughput sequencing to develop molecular markers to track *P. kernoviae* inoculum and using existing DNA markers to understand the diversity and spread of *P. ramorum*.

The above studies focus on invasive *Phytophthora* species. However, it is important to remember that all pathogens originate from natural ecosystems in which they have co-evolved with their native plant hosts. In recent years extensive surveying, enhanced by molecular detection tools, has revealed many new *Phytophthora* species. Some are destructive foliar pathogens but others, in particular root infecting species, may have a more subtle and perhaps even beneficial impact on ecosystem function. A recent study in the rainforests of Central America, for example, suggests a strong influence of native below ground microbial pathogens on tree species abundance. Tools are required to characterise rapidly the pathogens involved which has led us to develop a molecular method for studying *Phytophthora* diversity by amplifying diagnostic DNA sequence signatures (or DNA-barcodes) from water and soil. The system has been validated on Scottish natural and semi-natural habitats and has revealed considerable *Phytophthora* biodiversity and sequence signatures of several new species. This test has great potential in future studies using next generation sequencing to probe soil and water for this important group of damaging plant pathogens.



Wealthier & Healthier

Derek Stewart

Food security is defined by the World Health Organisation as “when all people at all times have access to sufficient, safe, nutritious food to maintain a healthy and active life”. However, the past year has been one of uncertainty within the global financial systems, leading to restricted economic development with consequential effects on food security. The financial crises have highlighted that, more than ever before, food is a global commodity and that changes in quantity, availability, quality and nutritive value will impact from global through to personal levels on economy, health and quality of life.

Our research at SCRI continues to deliver on the high aims of food security whilst ensuring that this is done within an economically sustainable framework. The following research snapshots highlight only some of the ways in which we do this. Soft fruit is increasingly accruing a portfolio of health benefits and to ensure its continued availability, disease free stocks for breeding and propagation are vital and this is highlighted for blackcurrant. The potential for the diversification of UK soft fruit crops is also showcased by the assessment of multiple blueberry varieties for UK fresh and processing markets.

Potato continues to be a key crop with respect to both the Scottish and global economies, and human nutrition *per se*. The important issue of mineral malnutrition may, in part, be soluble via the identification and exploitation of the genetic basis for mineral accumulation in potato. Furthermore, the underpinning mechanisms defining potato texture, a key quality determinant of cooked potato and continued customer preference have been elucidated. Both the mineral and textural studies have identified genes which can be exploited in breeding programmes and ultimately, in the form of new products.



Validation of an improved diagnostic test to accelerate the certification of blackcurrant (*Ribes nigrum* L.) plants for breeding and propagation

Alison Dolan, Stuart A. MacFarlane, Yvonne Pitkin and Wendy J. McGavin

Soft fruit production and processing represent a valuable sector within the Scottish and UK economy with, for example, the UK blackcurrant processing crop valued at >£200 million in 2009. This is underpinned by a regulated certification scheme to ensure the provision of high-health planting material sold in the UK to the industry.

To support these regulations, SCRI has a key role in maintaining the UK's sole nuclear stock collection of pest and pathogen-tested blackcurrant plants. We maintain and test a wide range of cultivars, both old and new, and supply high-health certified material to propagators, for subsequent release to growers, and to breeders and researchers worldwide. The pest and pathogen testing regimes follow RERAD, Defra and European and Mediterranean Plant Protection Organisation (EPPO) guidelines.

In addition, SCRI has a lead role in the provision of robust and validated detection methods to support the certification scheme. Reversion is one of the most serious diseases of blackcurrant, and is caused by a mite-transmitted virus, *Blackcurrant reversion virus*, BRV. The disease occurs in most areas where *Ribes* plants are found, except North America and Australia,



Figure 1 Malformation of blackcurrant flowers associated with the R form of BRV resulting in a proliferation of the sepals from the usual five to ten.

and exists in two forms, the European (E) and the Russian forms (R), which have been recognised based on the severity of the symptoms displayed by the affected plant, with the latter (Fig. 1) being markedly more severe than the former.

In the most seriously affected plants, the disease causes sterility with a consequent complete loss of the crop, making BRV a serious impediment to profitable blackcurrant production. The current recommended test for detection of BRV in blackcurrants relies on grafting (Fig. 2).



Figure 2 Bottle with scion from plant under test grafted on to recipient plant.

For this, a shoot (scion) from the plant under test is grafted on to a recipient plant of a cultivar that is known to react to BRV by the formation of visual symptoms on its leaves, flowers and buds. The graft recipient is observed over a two-year period, highlighting this testing regime as costly and laborious. In addition, BRV accumulates only at low levels and has an erratic distribution in infected plants, raising concerns about the reliability of this testing method.

Diagnostic tests using reverse transcription-polymerase chain reaction (RT-PCR) methodologies have many benefits; notably that they are highly specific, and are relatively high-throughput at relatively low cost. However, if they are to replace the conventional tests that are currently recommended in certification guidelines, then they must be assessed carefully to show that they perform at least as well as, if not better than, the tests that they might replace. To this end we have developed and validated a robust RT-PCR diagnostic test for BRV in blackcurrant certification (Fig. 3).

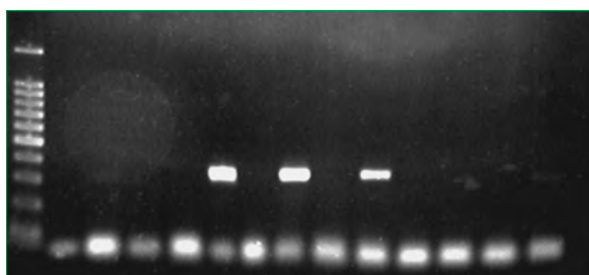


Figure 3 RT-PCR products resolved by electrophoresis through a 1.5 % agarose gel, and visualised by ethidium bromide staining and UV illumination.

From 17 initial sets of PCR primers, spanning the complete BRV genome, two were selected that gave the strongest, most reproducible amplification of BRV sequences from infected blackcurrant plants. Three sets of BRV-susceptible recipient plants (of cv. Baldwin, Ben Lomond and Ben Tirran) were grafted with scions from known infected donor plants, and the recipients were examined by RT-PCR and visually for reversion symptoms in leaves and buds over a four-year period.

Leaf symptoms alone were found to be an unreliable method for detection of BRV. The R form of the virus was detected in the buds both visually and by RT-PCR more readily than the E form. RT-PCR detection was determined to be as effective as post-grafting visual inspection in detecting BRV, with one of the primer sets detecting infection earlier in Ben Tirran than when using the conventional visual test. This primer set also detected BRV within two years after infection and for both forms of the virus in the three cultivars. The results support its use as an optimised, reliable, effective and, most importantly, validated PCR test for

BRV. This testing method is now being considered as an alternative to the existing graft method currently used within the UK certification scheme and EPPO guidelines.

Developing molecular tools for the British blueberry industry

Susan McCallum, Mary Woodhead, Rex M. Brennan & Julie Graham

Fruit consumption in the UK, particularly of berry fruits, is expanding rapidly. In 2009, sales of soft fruit increased by 17.2% in the UK with a combined retail sales value for strawberries, raspberries, blueberries and blackberries close to £700 million. Consumer demand for blueberries (*Vaccinium* spp.) is at record levels, partly due to their perceived health benefits but also their convenience and enjoyable flavour. Blueberries account for 17% of fruit sales but it is estimated that only 3% of the blueberries purchased in the UK are grown here. Imports, primarily from Argentina, Chile, Spain and Poland, supply the significant shortfall. However, this is beginning to change, with growers across the whole of the UK from the south of England to the north of Scotland beginning to produce blueberries. It is anticipated that the combination of this geographic spread, together with the temperate climate, will allow marketing of UK-grown blueberries from early July through to late October.

Blueberries are a challenging crop to grow, being shallow rooted and requiring well drained, acidic soil (pH 4.5-5.5) with high organic matter content. Although it can take up to five years before plants reach full production, a well maintained plantation can be productive for at least 20 years and beyond. UK growers are currently planting mixtures of existing varieties, mainly from the USA, but the long-term performance, fruit quality and consumer acceptance of these varieties in the UK is largely unknown. It is known that environmental cues significantly affect the performance of different blueberry varieties and informed variety selection is a key component for success. To address this, a project funded by



Figure 4 Variations in blueberry fruit juice obtained from a range of samples

Horticulture LINK has begun to look at the establishment, seasonality and machine harvestability of 40 different varieties across five locations in the UK. Fruit composition (sugars, acids, antioxidants) and other measures of quality (fruit size, colour, juice content and sensory characteristics) are being examined so that cultivars with the most appropriate qualities can be identified for the UK fresh and processing markets (Fig. 4).



Figure 5 A subset of blueberry cultivars under analysis; Liberty, Duke, Chandler and Rubel.

The project has focused on the identification and collection of diverse germplasm (Fig. 5) enriched in sensory and health promoting compounds for future breeding programmes while allowing the determination of year to year variation and hierarchy maintenance of health-promoting compounds in different genetic backgrounds.

A genetic framework for future crop improvement is required to develop a thriving and sustainable industry. The genetic component of this project builds on the statistical developments derived from the BioSS software programme, TetraploidMap, to identify fruit quality, health and agronomic related quantitative trait loci (QTL) in tetraploid blueberry for marker assisted breeding. A mapping population developed from two key US blueberry cultivars segregating for a number of important phenotypic traits (for example time to fruiting, plant habit, and fruit quality) and a selection of molecular markers have been used. Data from 100 markers have been analysed and found to show segregation patterns consistent with the simplest model for meiosis, random chromosomal segregation, allowing the production of a draft tetraploid blueberry linkage map. For a genetic map to be useful for marker assisted selection it is necessary to generate a good coverage of molecular markers (Fig. 6). As blueberry has many chromosomes (12 chromosomes with 4 alleles = 48), approximately 350–500 markers will be required.

Knowledge of cultivars and establishment will allow the UK industry to be based on the best germplasm for the growing conditions and requirements. This

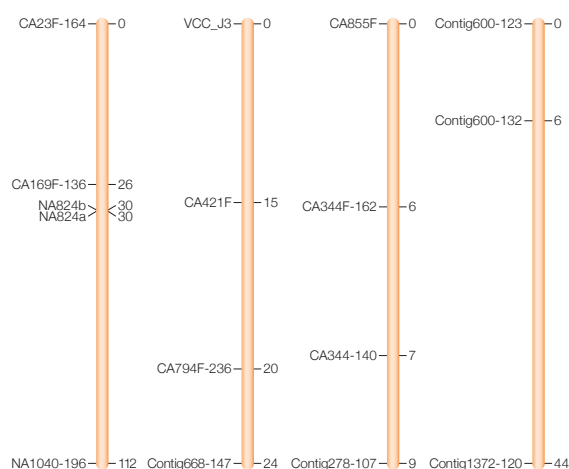


Figure 6 Chromosome map for blueberry.

project represents the first systematic study of the combined impact of genetics and environment on fruit phytochemistry in relation to the sensory and potential health properties of blueberry fruit. By linking the phenotype to genotype, a genetic framework for future crop improvement using marker assisted breeding will be established and this should greatly increase the speed and precision of blueberry breeding.

Breeding potatoes to address mineral malnutrition

Nithya K. Subramanian, Glenn J. Bryan, Christine A. Hackett, Gavin Ramsay & Philip J. White

Mineral malnutrition is one of the most serious challenges to human health, and it is estimated that up to two-thirds of the world's population might be at risk of deficiency in one or more essential mineral element. The mineral elements most commonly lacking in human diets are iron, zinc, calcium, iodine and selenium. Concentrations of these elements can be increased in plant produce through the judicious application of mineral fertilisers, and the selection of crop genotypes that acquire mineral elements more effectively from the soil and distribute them to edible portions. In collaboration with Martin Bradley and John Hammond at the University of Nottingham, we are identifying genetic factors affecting the concentrations of mineral

elements essential for human nutrition in potato tubers that will allow breeders to select genotypes for improved nutritional quality.

Potato is one of world's most important food crops. It is of increasing importance in developing countries because of its high yield potential and its nutritional qualities. Its price is relatively buffered from the vagaries of world commodity markets and it is ideal for local consumption. Potatoes are an important source of mineral elements in human diets. For example, a single, medium-sized potato weighing 200 g can provide about 18% of the US Dietary Reference Intake (DRI) of iron and about 6% of the DRI for zinc. However, it will provide only 2% of the DRI for calcium. Potatoes can also be a significant source of iodine and selenium if mineral fertilisers containing these elements are applied to the crop. In addition, the bioavailability of iron and zinc is high in potato tubers, because they have relatively high concentrations of organic compounds that stimulate the absorption of these elements in the gut and low concentrations of phytate and oxalate that inhibit their absorption.

Although tubers develop underground, they are surrounded by periderm tissue which is impregnated with hydrophobic material that prevents the indiscriminate entry of mineral elements from the soil solution to the flesh. Indeed, most mineral elements are delivered to tubers through the phloem from the shoot. The inability of mineral elements to enter the maturing tuber from the soil solution, together with differences in the mobility of mineral elements in the phloem, results in distinct spatial distributions of mineral elements within the tuber (Fig. 7). It is commonly observed that calcium, which is immobile in the phloem, is concentrated in the skin and peripheral layers of the flesh, whereas elements like potassium, which are mobile in the phloem, are distributed throughout the tuber. Both iron and zinc are present at higher concentrations in the skin than in the flesh of potato tubers. These distributions affect the nutritional significance of culinary decisions, such as whether to consume potato skins.

There is significant, heritable variation in tuber mineral concentrations. This is apparent both between

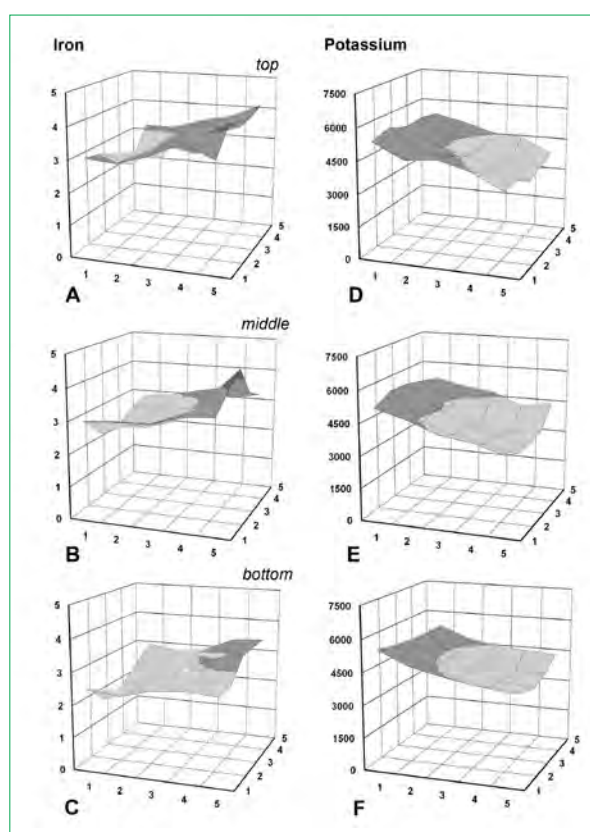


Figure 7 Distributions of iron (a, b, c) and potassium (d, e, f), from the bud (left) to stem (right) end, in the top, middle and bottom slices of recently-harvested, peeled tubers of the table variety Stirling.

commercial varieties and among the genotypes of genetic mapping populations. This variation can be used to identify chromosomal quantitative trait loci (QTL) that affect tuber mineral concentrations. Using a genetic mapping population derived from a cross between the processing clone 12601ab1 and the table cultivar Stirling, we have identified robust QTL affecting tuber iron, zinc and calcium concentrations. Several of these QTL are associated with chromosomal loci known to determine the time taken for the crop to reach maturity, which determines their market and agronomic characteristics. Other QTL are not associated with maturity classification, and can be used to select for genotypes with greater concentrations of mineral elements essential for human nutrition within the same maturity class. The latter QTL contain genes encoding ferric reductases, cation transport proteins, nicotianamine synthases and metal-chelate transporters, which are responsible for the uptake and movement of iron and zinc within the plant. This genetic

information will allow breeders to select for genotypes to address mineral malnutrition.

The role of pectin methyl esterase in determining potato tuber textural quality

Heather A. Ross, Wayne L. Morris, Laurence J.M. Ducreux, Robert D. Hancock, Susan R. Verrall, Jenny A. Morris, Derek Stewart, Peter E. Hedley, Gordon J. McDougall & Mark A. Taylor

Potato tuber texture is a key quality determinant of cooked potato and a major trait that influences consumer preference. Tuber texture is also a key issue in potato processing and is known to be affected by pre-processing procedures such as blanching, peeling and storage. Although it is possible that a number of factors may be responsible for cooked potato texture, the relative importance of these is not yet clear. Several studies have described potato germplasm that produces tubers with markedly different textural properties. In particular, members of *Solanum tuberosum* group Phureja have been identified which exhibit a boiled tuber texture described as extremely floury or crumbly. The cooking (by steaming) time of Phureja tubers is generally in the order of half that taken for typical *Solanum tuberosum* group Tuberousum tubers at the same developmental stage.

In order to identify the factors that account for textural differences between the Phureja and Tuberousum types, we compared gene expression in tubers using a potato microarray. The Potato Oligo Chip Initiative (POCI) consortium recently developed the microarray, which contains gene probes based on 42,034 potato unigene sequences, and uses the custom Agilent platform. Using this microarray we were able to identify consistent differences in gene expression profiles between Phureja and Tuberousum cultivars, including genes likely to impact on texture. In particular there was a ten-fold higher expression level of a gene encoding pectin methyl esterase (PME). Pectin is a major component of the cell wall and its structure is likely to be an important factor in texture in potato tubers. PME demethylates pectin components which are then free to strengthen



the cell wall structure by cross-linking through interaction with calcium ions, liberated during the cooking process. Thus low PME activity may account for a softer cooked texture in Phureja tubers.

We set out to test this theory using a number of different approaches. Measurements of PME activity demonstrated that the differences in gene expression levels were also seen in the activity of the PME enzyme. Biochemical analysis of tuber cell walls also showed a reduced degree of pectin methylation in the Tuberosum samples compared with those from Phureja. Conclusive evidence in support of our hypothesis came from transgenic studies, in which we increased the expression level of the PME gene. Over-expression resulted in significant changes in textural properties (a firmer texture was measured in cooked tuber samples

from transgenic lines with higher PME expression), associated with a significant increase in PME activity and reduced cell wall pectin methylation. Thus there is a clear link between PME activity, pectin methylation and processed tuber textural properties.

Our conclusion was that we had discovered a gene with an important role in determining cooked tuber texture. In current work we are aiming to identify the reasons why the Phureja version of the PME gene is expressed at much lower levels than in Tuberosum. This is done by comparing sequences that may control the degree to which the genes are switched on. Ultimately breeder-friendly markers may be developed to enable the conventional breeding of potatoes which produce tubers with specific textural properties.



Sustainability

Philip J. White

In the SCRI Annual Report 2009 we defined agricultural sustainability as the ability of a system to maintain stable levels of food production and quality in the long term, without compromising economic profitability or the environment. We described how SCRI scientists are developing agronomic practices and crop varieties that preserve soil fertility and reduce agrochemical inputs. Here, we consider the important role of soil monitoring in maintaining soil quality and report on several research projects promising novel strategies to minimise crop losses to pests and diseases.

The abundance and diversity of nematodes provides an excellent biological indicator of soil quality. Nematodes occupy key positions in soil food webs, and their populations respond rapidly to environmental perturbation. However, traditional methods for the characterisation of nematode populations are labour intensive and require trained taxonomists. To address this, Roy Neilson and colleagues have developed a simple, high-throughput, molecular method for characterising nematode assemblages that will allow the routine monitoring of nematode populations in soils. In addition to providing insight to soil quality, and the need for soil amelioration, this assay delivers information on nematode biodiversity, pest issues and bio-control opportunities.

About one third of potential food production is lost to pests and diseases. Historically, these losses were minimised by application of agrochemicals, but concerns over human and ecological wellbeing have restricted the use of these compounds. It is now imperative that crop varieties resistant to pest and pathogens are developed.

A common problem in developing crops resistant to pests and pathogens is the continued evolution of these organisms to circumvent the plant's defences. To develop durable resistance to the oomycete *Phytophthora infestans*, the organism that causes late blight in potato, Ingo Hein and colleagues are adopting a variety of approaches to identify, or create, plant defence systems that are initiated by molecules



Taking our science to a wider audience.

essential to the pathogen that are conserved during its evolution. Thus, a resistant plant will always recognise and respond to the pathogen. The genes underpinning this resistance might be used in marker-assisted breeding or deployed using GM technology.

Pavel Kerchev and colleagues are investigating the changes in plant gene expression that occur in response to the peach-potato aphid *Myzus persicae*, which is a major vector for *Potato leaf roll virus* in Scotland. They believe that an understanding of a plant's local and systemic responses to aphid infestation will provide useful information to develop technologies to disrupt aphid feeding or virus transmission, thereby reducing our reliance on synthetic insecticides.

The nucleolus of plant cells is intimately linked with the infection cycle of many viruses. Specifically, interactions with the nucleolus appear to be necessary for the

movement of viruses to upper leaves. Michael Taliany and colleagues seek to exploit their knowledge of how and why particular viruses target the nucleolus to develop novel, host-based strategies to control plant viral infections. One potential target is *Potato mop-top virus*, which has been responsible for reducing marketable yields of UK potatoes since 1966, and for which there is no known genetic source of resistance.

These examples of basic research providing intelligent, durable solutions to crop protection from plant pests and diseases reflect the necessity to avoid yield losses whilst reducing agrochemical inputs. Combined with innovative agronomic practices that preserve soil quality, and the development of crop varieties that make the best use of water and fertilisers, innate plant protection will enable the reality of sustainable agricultural production.

Molecular methods for monitoring soil nematodes and their potential use as biological indicators of soil health

Roy Neilson, Suzanne Donn², Xiaoyun Chen¹, Bryan S. Griffiths¹, Vincent O’Flaherty³, & Tim J. Daniell

“A nation who destroys its soil, destroys itself” – Franklin Roosevelt, 1937 in a Letter to all State Governors on a Uniform Soil Conservation Law.

The Millennium Ecosystem Assessment considered soil as one of the world’s most precious natural resources. Immediate threats to soils include erosion, compaction, change in biodiversity, contamination and loss of organic matter. Many of these threats can occur as a result of agronomic intensification to provide food for a burgeoning global population. Unsurprisingly, therefore, numerous recent Scottish and UK policy reports have recommended the maintenance and protection of soil. Monitoring is key to preserving soil quality, although tools for this are currently underdeveloped. At present, the

lack of suitable indicators of soil quality makes it difficult to monitor the efficacy of processes employed to protect soil. Recently a Defra study assessed 183 candidate biological indicators of soil quality, of which 21 were ranked as having potential for deployment. Of those, the characterisation of nematode assemblages was viewed favourably, although limitations of throughput were identified as being a barrier to deployment.

This view is supported by the position of nematodes at key nodes in soil food webs (Fig. 1), their contributions to soil functioning, high diversity and rapid response to changes in environmental conditions. There is good evidence that nematode phenotype (“biodiversity”) is linked to function, with mouth parts commonly being used to identify feeding groups. Knowledge of species and assemblage structure can provide useful information on soil nutrient status and biodiversity as well as pest issues and bio-control opportunities, which are particularly important in ensuring sustainable food production. However, the time taken to identify a representative number of individuals from a soil sample presents a problem in the characterisation of nematode assemblages. This issue is compounded by the constantly declining number of skilled taxonomists.

Molecular tools provide an opportunity to address this problem. Using BBSRC funding at SCRI, we have designed a Directed Terminal Restriction Fragment Length Polymorphism (DT-RFLP) method that provides a high-throughput semi-quantitative characterisation of nematode assemblages. The DT-RFLP method is based on amplification of DNA with fluorescent primers followed by a diagnostic digestion with restriction enzymes to produce labelled Terminal–Restriction Fragments (T-RFs) linked to target taxa (Fig. 2). A software package, DRAT, has been developed in collaboration with the University of Dundee to identify appropriate restriction enzyme(s) to cut nematode DNA to yield diagnostic fragments. We have demonstrated that this method aligns well with classical taxonomic analysis when adjusted for nematode size (Fig. 3) and that it is applicable to soils from a range of habitats. A recent review of molecular tools for nematode monitoring concluded that DT-RFLP has advantages of high-throughput, ease of comparison between samples, and rapid data analysis. Furthermore,

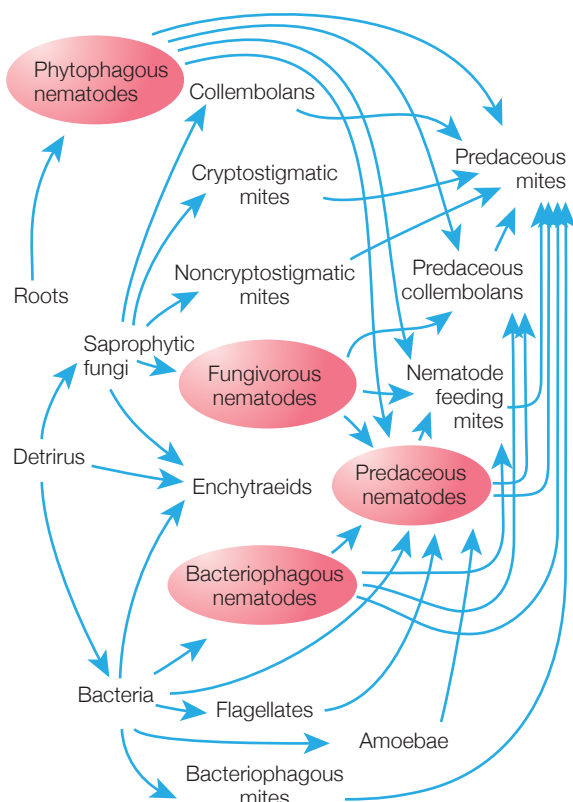


Figure 1 A schematic food web demonstrating the key positions of components of the soil nematode assemblages (after de Ruiter *et al.* 1993, *Journal of Applied Ecology* **30**, 95–106).

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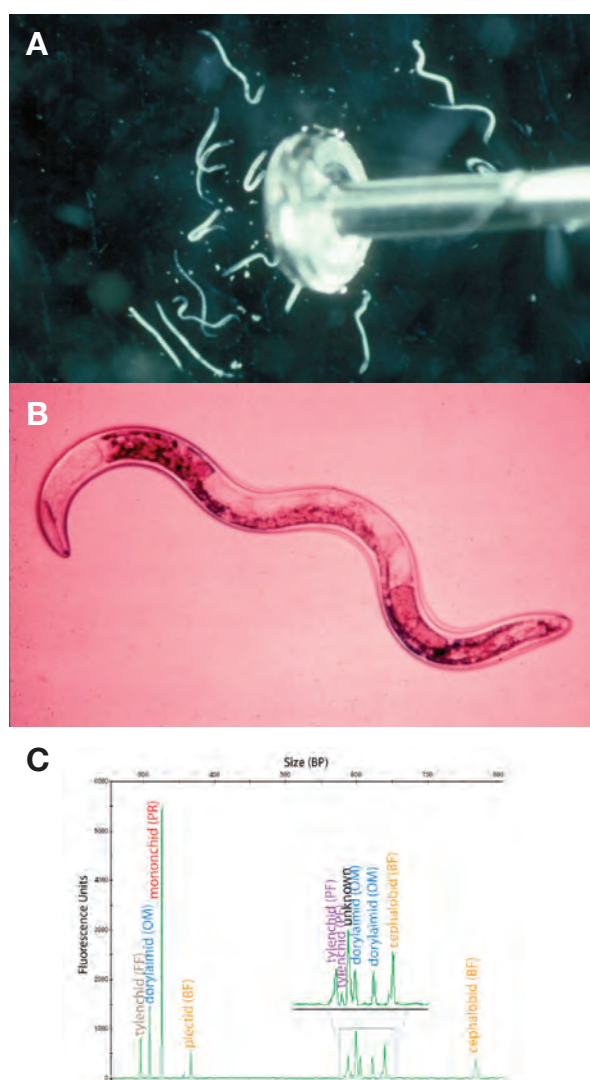


Figure 2 (a). A typical nematode assemblage isolated from arable soil illustrating the size and apparent uniformity under low magnification. (b) An individual *Trichodorus primitivus*, a free living nematode traditionally identified by high magnification by light microscopy, a requirement that restricts sample throughput. (c) An electropherogram of a DT-RFLP output illustrating discrimination of nematode assemblages below the taxonomic level of order allowing the identification of feeding groups (BF bacterial feeder, FF fungal feeder, OM omnivore, PF plant feeder and PR predator).

this technique allows comparison of samples from disparate geographic sites by converting the T-RF data into a univariate index similar to indices derived from classical morphological data.

To ensure applicability across the range of UK and other ecosystems, extensive trialling is required to develop a robust statistical protocol for analysing nematode

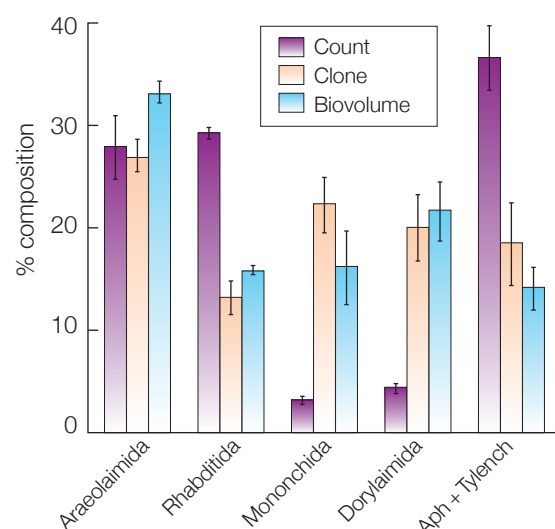


Figure 3 Characterisation of a single nematode assemblage at a taxonomic order level by cloning and sequencing (clone), morphological identification (count) and an assessment of biomass derived from counts (biovolume) (Aph – Aphelenchida, Tylench – Tylenchida); error bars represent standard error.

T-RF data. Furthermore, since nematodes are eutelic organisms (i.e. an individual of a species has a fixed number of cells, excluding epidermis and gametes), we are testing whether there is a correlation between group biomass and molecular signal in a joint project between SCRI, Teagasc and the National University of Ireland.

Pathogen effector driven search for more durable potato late blight resistance

Ingo Hein, Paul R.J. Birch, Sean N. Chapman & Glenn J. Bryan

Potato is the third most important food crop worldwide and makes a significant contribution to the UK bio-economy. The most significant threat to potato production is late blight disease, caused by the oomycete pathogen *Phytophthora infestans* that was responsible for the Irish famine in 1845–1846. Resistances to late blight have been introgressed from wild potato species but, despite intensive efforts, truly durable control mechanisms have remained elusive. The main challenge is to identify resistances that remain effective in response to changing pathogen populations.



Inducible plant resistances are based on pathogen recognition. All microbes trigger immune responses in plants via host receptor-mediated recognition of conserved pathogen-associated molecular patterns. However, successful pathogens suppress or otherwise manipulate this recognition via secretion of virulence factors called effectors. Effectors provide the plant with additional targets for recognition. In a second layer of inducible defence, resistance (*R*) genes, the products of which typically encode Receptor-Nucleotide

Binding–Leucine-Rich Repeat (NB-LRR) proteins, detect effectors which are then termed avirulence proteins (AVRs). The key towards more durable resistance is to tailor resistances that target essential and conserved pathogen molecules that are more difficult to modify without loss of virulence. Such molecules present an ‘Achilles heel’ in the pathogen armoury.

A number of *P. infestans* *Avr* genes have been identified. Although each corresponding AVR protein is distinct at the primary sequence level, they all share a signal peptide for secretion, followed by the motif RXLR which is required for translocation. More than 500 such candidate genes have been identified within the genome of *P. infestans*. The large numbers of RXLR genes raise the likelihood of functional redundancy in the effector complement. The implication of this is that, in addition to evolving critical amino acid mutations to evade recognition, effectors may also simply be shed if their function is provided by another effector.

In a ‘paradigm-shift’ from conventional disease resistance breeding we are exploiting our knowledge of recent dramatic changes in the pathogen population to unravel the underlying variation in pathogen effectors,

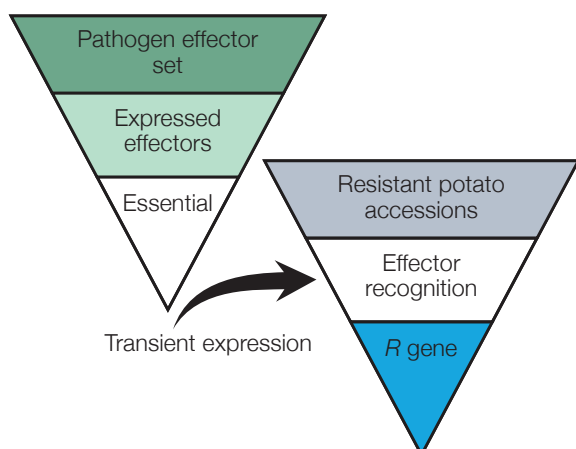


Figure 4 Pathogen effector studies are key to the identification of potentially more durable host resistance genes.



using this to drive the search for durable resistance. We seek essential and conserved *P. infestans* effectors as targets for cognate *Resistance to P. infestans (Rpi)* genes. In a two-pronged approach we seek *Rpi* genes that target all known allelic variants from these essential effectors.

The first approach (Fig. 4) utilises the diversity of *Rpi* genes within the Commonwealth Potato Collection (CPC) which contains more than 1800 potato accessions. Potato accessions that are resistant to diverse *P. infestans* isolates have been identified and are tested for their ability to recognise essential effectors. Genetic crosses are set up to demonstrate unequivocally the correlation between effector recognition and resistance. Furthermore, these segregating populations are used to characterise the resistance genetically and to isolate the underlying *Rpi* genes. A sequence analysis of the potato genome has predicted approximately 400 NB-LRR containing genes across all 12 chromosomes. We have successfully devised a strategy to enrich resistant and susceptible plants from segregating populations for *Rpi* genes and are using state-of-the-art next generation sequencing technology to identify more rapidly candidate *Rpi* genes and associated genetic markers. Effective *Rpi* genes can be deployed by marker assisted breeding or, more rapidly, via the use of GM technology.

The second approach utilises gene shuffling to alter the recognition specificity of cloned *Rpi* genes *in vitro*. Promising results have been obtained for the *Rpi* gene *R3a* that specifically recognises one form of *Avr3a* (KI) but fails to detect a virulent allele that differs from the recognised form in only two amino acids.

Using pathogen effectors as a driver to identify more durable resistance is a novel and generic approach that is amenable to every host–pathogen system. What is needed is knowledge of 1) the key effectors that are required for virulence, and 2) their diversity within pathogen populations. Resistances targeted to such effectors may be predicted to be more durable than those previously deployed and, by their nature, are intended to meet the challenge of future pathogen population changes.

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Understanding local and systemic responses to aphid infestation as a tool towards breeding aphid resistant crops

Pavel I. Kerchev, Vandana Saraswat¹, Peter E. Hedley, Jenny Morris, Brian Fenton, Christine H. Foyer² & Robert D. Hancock

Plant feeding insects represent a significant problem in global agriculture, causing yield reductions and significant control costs. Worldwide, approximately 10,000 different insect species cause annual production losses amounting to £250 billion. One of the major groups of crop pests is the phloem-feeding aphids that can inflict serious damage through the removal of photoassimilates and by acting as vectors for plant viruses. For example, the peach–potato aphid (*Myzus persicae*) can colonise over 50 families of plant species, including a wide range of important crop plants, and can vector over 100 different plant viruses. In Scotland *M. persicae* is the major vector for *Potato leafroll virus*, a significant problem within the seed potato sector.



Figure 5 Confinement of aphids to a single *Arabidopsis* leaf within a clip cage.

At present aphid numbers are controlled primarily through chemical means and while pesticide application has boosted crop production in the short term, the energy inputs required to manufacture and apply pesticides, alongside their unintended negative impacts on beneficial insects, raise questions regarding the long term sustainability of pesticide use. Within this context, understanding plant defences against aphid infestation could lead to the development of novel technologies



that disrupt aphid feeding and/or virus transmission. The mounting of defence responses against insects can be highly energetically and metabolically demanding for the host plant. Plants have therefore developed mechanisms to recognise insect infestation and only mount defence responses when necessary. These responses can be categorised into local, within the specific tissue being attacked, and systemic, that prepare the uninfested parts of the plant for subsequent attack. As aphids can feed from a single site for extended periods, systemic responses represent a significant, yet poorly studied, source of resistance.

As a first step to understanding systemic responses to aphid infestation, we examined global changes in gene expression in local and systemic tissues of the model plant *Arabidopsis thaliana* following infestation by *M. persicae*. Aphids were confined to a single leaf with clip cages (Fig. 5) and, following 6, 24 or 48 h exposure, infested and uninfested leaves from the same plant were harvested and their global gene expression compared with that of leaves from uninfested plants. Patterns of gene expression in local and systemic tissues were found to be highly divergent, suggesting very different strategies for defence in infested and uninfested systemic tissues. Further experiments showed that

the changes in gene expression in systemic tissues were effective in reducing aphid survival. Plants were 'primed' by caging aphids onto a single leaf for 24 h. Subsequently, the aphids were removed and then one day old aphid nymphs were either caged onto the previously infested leaf or caged on to a separate uninfested leaf of a previously infested plant. Three days later, aphid survival was recorded (Fig. 6), indicating

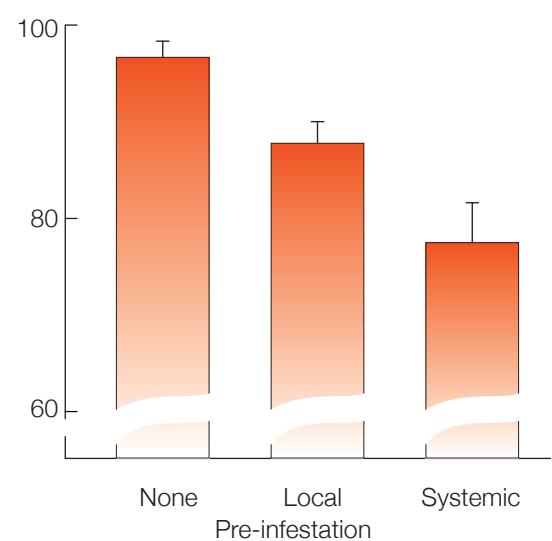
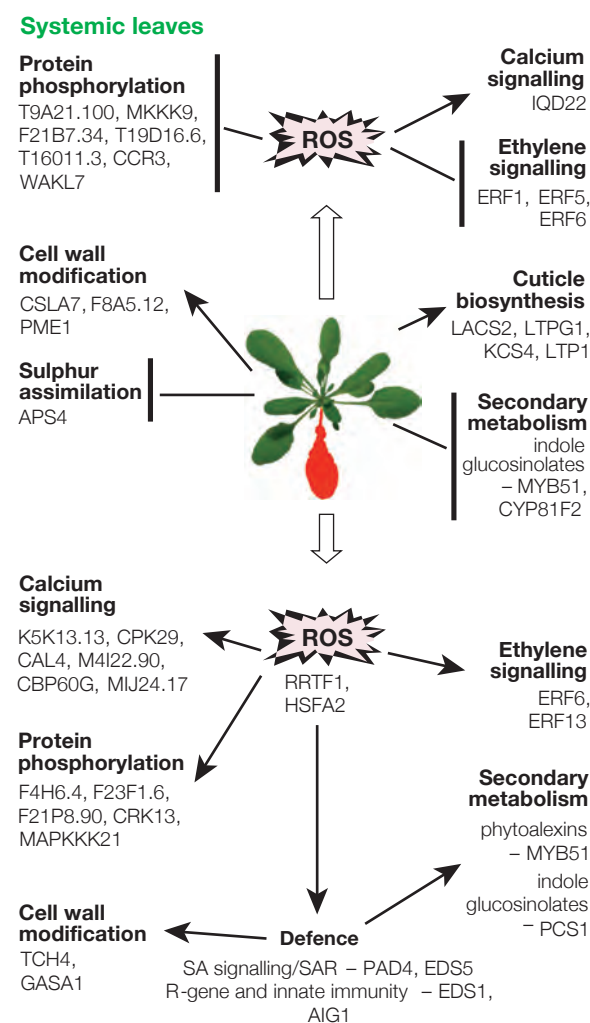


Figure 6 Impact of preinfestation on subsequent aphid survival on local and systemic leaves.



significant reduction in survival of those aphids caged onto previously infested leaves compared to those on control plants. Interestingly, survival on uninfested systemic leaves from previously infested plants was even lower, suggesting that the observed changes in gene expression result in an effective defence response.



Infested Leaf

Figure 7 Overview of local and systemic signalling and defence following aphid infestation
The figure outlines signalling and defence cascades inferred from gene expression changes in local and systemic tissues following 6 h of aphid infestation on a single leaf. Signalling and defence cascades are represented in bold type. Upregulated processes are represented by arrows while downregulated processes are represented by blunt ends. Proteins encoded by differentially expressed genes are listed underneath the appropriate process. ROS – reactive oxygen species.

Analysis of gene expression changes occurring in local and systemic leaves allowed modelling of signalling mechanisms involved in recognition of aphid infestation and the pathways of defence (Fig. 7). This suggests a key role for the generation of reactive oxygen species in the local response, as has been proposed for microbial plant pathogens. Downstream signalling cascades include protein phosphorylation and dephosphorylation, via kinases and phosphatases, calcium signalling, and a role for the phytohormone ethylene. Defence appears to be mediated via cell wall modification, enhancing the physical barrier to aphid feeding, and through biosynthesis of toxic secondary metabolites. In systemic leaves, there was also evidence of heightened physical defence, through cell wall modification and enhanced cuticle biosynthesis. In addition, sulphur assimilation was reduced and the expression of a number of transporters was down-regulated, suggesting that plants may alter phloem composition to reduce nutritional value to aphids.

The work presented here provides novel insights into plant defence against aphid infestation. It is intended that this will drive novel genetic targets for breeding aphid resistant crops, thereby reducing reliance on synthetic insecticides and increasing agricultural sustainability.

Role of the nucleolus in plant virus pathogenicity

Michael E. Taliansky, Jane Shaw & Lesley Torrance

The nucleolus is a dynamic sub-nuclear body with roles in ribosome subunit biogenesis, mediation of cell stress responses, and regulation of cell growth. The nucleolus has also been shown to play a crucial role in the infection cycle of various viruses, and the nucleolar localisation of viral proteins has recently been described as a pan-virus phenomenon. In this regard, plant viruses are not different from other eukaryotic viruses. The past few years have brought remarkable progress in our understanding of how and why some plant viruses (in particular, umbraviruses and potyviruses) target the nucleolus and the functional role of the interaction between viral and nucleolar proteins in the

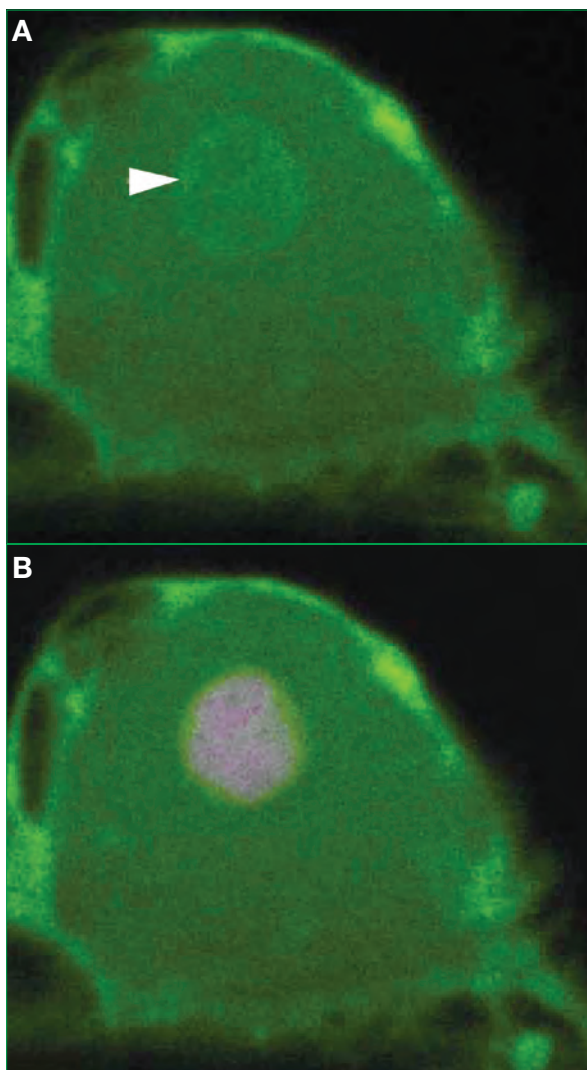


Figure 8 (a) Confocal microscope images of a nucleus showing the accumulation of PMTV TGB1 fused to green fluorescent protein in the nucleoplasm and nucleolus (arrowed). (b) The nucleolus is distinguished by the accumulation of fibrillarin labelled with red fluorescent protein (Wright *et al.* 2010, *Molecular Plant–Microbe Interactions* 23,1486–1497)

plant virus infection cycle. For example, interaction with the nucleolar protein fibrillarin is required for the systemic infection of plants by umbraviruses. Another example is *Potato mop-top virus* (PMTV) which affects potato tuber quality causing severe internal and external blemishes and yield loss in sensitive cultivars. We have recently shown that one of the PMTV movement proteins (TGB1) associates with the nucleolus and this association may be required for viral movement to upper leaves (Fig. 8). Current experiments are focused on identifying the interacting components to understand fully their role in the virus infection cycle.

There are now several examples in which the plant viruses target other sub-nuclear bodies, associated with the nucleolus, such as Cajal bodies (CBs). In particular, for umbraviruses the role of CBs in nucleolar trafficking of the viral ORF3 protein has been established. The potential role of sub-nuclear structures in other plant virus infections is currently being addressed (Fig. 9).

The study of viral interactions with the nucleolus also provides unique and valuable tools to gain new insights into novel nucleolar functions and processes. For example, as previously discussed, the major nucleolar protein fibrillarin is involved in the formation and long-distance movement of umbraviral ribonucleoprotein particles, suggesting new unexpected functions for fibrillarin. We anticipate that more information will emerge about the mechanisms involved in regulating nucleolar function and structure in response to plant virus infections and hijacking the nucleolar functions for needs of the virus infection cycle.



Figure 9 Symptoms of *Turnip vein clearing virus* are strongly attenuated in *Nicotiana benthamiana* plants deficient in Cajal bodies (bottom row) compared with wild type plants (top row).

This fundamental work can be translated into practical use since, by identifying and understanding the components of the interactions (proteins and nucleic acids), both the plant cell and viral biology of the nucleolus can be exploited to design novel host factor-derived resistance strategies to control plant virus infections. This could provide a valuable alternative to control viruses such as PMTV for which there is no identified source of resistance in germplasm collections.



Communications – Review of the Year

Phil Taylor

As the staff left for their Christmas and New Year holidays in the dusk of December 2009, it was clear we were all in for an ‘old fashioned’ winter. The fields and trial plots were frozen hard beneath a mantle of frost, topped with the first snows. Well wrapped walkers on the lane down to our home village of Invergowrie left vapour trails of breath as they trudged through the gloaming. And from a few of the glasshouses, where experiments were basking in artificial sunshine, long fingers of golden light probed upwards into the foggy night-time air.

Yet for many of us, busy planning the year ahead, we could already imagine the rumble of SCRI tractors and



machinery as the field and glasshouse staff got the growing season underway. We could hear children's laughter on open days and Staff Association barbecues, anticipate the eager questions being asked in The Living Field and glimpse the glasshouses green with seedlings or straw-filled with wheat and barley.



2010 was always going to be a pivotal year for SCRI: a year of life-changing decisions on the future of a famous and venerable institute. In the early hours of Ne'ers Day, one could imagine the faces of our previous Directors, peering out from the portraits opposite the SCRI boardroom in the hushed and deserted corridor. Their



only company were the abandoned Christmas garlands and cards on office walls. What would they be thinking – Messrs Swarbrick, Cadman, Taylor and Hillman – as SCRI's final year got underway with swirling snow and shivering gales?

Looking back, it might be a year told through the eyes of two very different visitors to SCRI. One a figure who is known to all...and who is particularly popular and appreciated in Scotland; the other, a youngster, just starting out in life and with hardly an idea of the work done at SCRI. That youngster, even now, is a bit of a mystery to us. More of both of them as we go!

The shivering months of December and January did at least allow SCRI to mark some new record breaking performances. At the Meteorological Station on the SCRI estate, the average minimum air temperature for December 2009 was -3.4 degrees Celsius, the lowest since records began in the days of the Scottish Horticultural Research Institute in 1954. January was also colder than usual, with another remarkable reading on 8 January when the 'low' was recorded at -9.4, the coldest for 26 years. Little did we expect how the year would end with eleven days of snowfall in November.

It may have seemed a long, slow haul away from the ice and snow that saw in the New Year, but it wasn't long before SCRI's annual cycle of events was underway. The institute has been a staunch supporter of the John Hope Gateway at the Royal Botanic Garden in Edinburgh. The Gateway was chosen for the launch in Scotland of the UN International Year of Biodiversity in the middle of January. The ceremony was hosted by the Scottish Government Environment Minister, Roseanna Cunningham MSP. SCRI coordinated the Scottish research institutes in preparation of a leaflet celebrating their joint contribution to the protection of the natural environment.

By Easter, SCRI was hosting another event at the John Hope Gateway: 'Potatoes Galore'. Over the Easter weekend, scientists and communications staff from Invergowrie gave hands-on advice about potato cultivation, told the story of the Commonwealth Potato Collection, gave informal presentations and also let a lot of children have a lot of fun with a large collection of Mr Potato Head toys!



Children were at the forefront again in early June, when LEAF (Linking Environment and Farming) Open Farm Sunday was hosted at SCRI. Among the highlights were



Heather the tractor driver!

the ever-resourceful team at The Living Field, open-access to the Meteorological site, an extremely popular display of farm machinery and several presentations on climate change given by the guest of honour for the day, Heather Reid OBE. Heather is a meteorologist and science communicator who first became well-known as the BBC Scotland TV presenter, 'Heather the Weather'. Her climate change presentations played to full houses.

There was a new departure for SCRI at the 2010 Royal Highland Show. With the pace quickening towards the creation of a new research institute, merging SCRI and the Macaulay Land Use Research Institute in Aberdeen, it was decided to share a stand at the show with our colleagues from the North. A common theme was chosen: the breadth of commercial services operated



Cereals in Practice, Balruddery Farm.

by the two research providers and the conversion of research knowledge into innovation and economic benefits. In the Royal Highland Education Trust building, where the focus, as ever, was on families and children, the SCRI team celebrated the UN Year of Biodiversity. The transition to the new institute was also promoted during SCRI's annual outing at the Dundee Flower and Food Festival. We also took the opportunity to promote the work now underway on blueberry cultivation.



Royal Highland Show 2010.

Our regular, summer events soon followed in sequence with Cereals in Practice, boosted by our friends and colleagues from SAC, Fruit for the Future and Potatoes in Practice.

Once again Potatoes in Practice, sponsored by the Potato Council, attracted more than 700 people who were able to visit field plots and demonstrations from SCRI, SAC, CSC Potato Care and others in the potato industry. Allan Stevenson, Chairman of Potato Council Ltd, used the opportunity to remind the visitors of the growing importance of the Chinese agricultural and food sector to the UK potato industry. He urged those involved in the industry to seize the opportunities that China had to offer. Mr Stevenson also paid tribute to Dr Stuart Wale of the Scottish Agricultural College. Stuart, who was one of the founding supporters of Potatoes in Practice, retired this year.



Potatoes in Practice.



The Royal visit, June.

2010 was always going to be a special year for SCRI as the transition to the new institute began to gather pace. But it became a memorable year on 7 June when SCRI, Mylnefield Research Services, BioSS and the Division of Plant Science, University of Dundee were honoured by a visit from Her Royal Highness, The Princess Royal, who is the patron of many, well-known Scottish organisations.

The visit had been eight months in the planning. The Lord Lieutenant of Perth and Kinross, Brigadier Melville Jameson, had been hugely supportive from the outset and paid a visit to our Invergowrie headquarters some time before the Royal visit. With Mel's help, obstacles were overcome and Buckingham Palace approved not only a visit to SCRI, including the brand new, multi-million pound AP Block glasshouse...but also a visit to

the Centre for Sustainable Cropping at Balruddery Farm in neighbouring Angus.

Her Royal Highness formally opened the new, glasshouse building, unveiling a plaque, and then enjoyed a private lunch in the SCRI boardroom. The buffet meal was prepared by SCRI's in-house catering team, operated by Sodexo, and included fruit and vegetable varieties bred at the Institute. Then, after the short journey to Fowls, Her Royal Highness inaugurated the Balruddery Farm centre, chatting to the staff and also meeting Fife dry stane dyker Robert Thomson, who had been commissioned to build a commemorative stone feature adjacent to Balruddery's old mill pond.

HRH The Princess Royal had not been scheduled to speak during the visit, but to the delight of the Chairman, Mr Peter Berry CMG and the Director, Professor Peter Gregory, she turned to the gathered staff and said: "Thank you for your invitation. This is a fascinating place and slightly too hidden a jewel, I think.

"It deserves more recognition and more understanding. But it's nice to see the investment here and I hope that will continue – that it won't just be 2010 you can be celebrating but many more years. Enjoy your new building!" After the Royal guest had departed, the staff and friends of SCRI were treated to a celebratory afternoon tea in the staff restaurant.





Visit by Roseanna Cunningham MSP.

We soon enjoyed the company of more VIP guests. During the Holyrood parliament's recess in August, we entertained the Environment Minister, Roseanna Cunningham MSP and later the Cabinet Secretary for Finance and Sustainable Growth, John Swinney MSP. Both represent neighbouring Perthshire constituencies and spent several hours meeting staff and looking at the potato and soft fruit collections and discussing the work of the Institute.

SCRI's commitment to education and the promotion of science to young people continued throughout 2010. Once again the Advanced Higher Days for young students were held during November. And the Institute, together with MRS Ltd again sponsored the Biodiversity and Environment category in the Dundee schools 'Focus on Achievement' awards. The winners this year were Craigie High School whose pupils maintain and develop the school grounds, including planting bulbs



Advanced Higher Day.



John Swinney MSP at SCRI.

and fruit trees and growing potatoes for local residents in sheltered housing.

It is right that in these pages we also celebrate our own, illustrious members of staff. Among them this year was a 36-year-old Hungarian scientist at SCRI who was awarded the Peter Massalski Prize for meritorious research. Dr Csaba Hornyik began working at SCRI in 2005. His career has seen many honours. He won a Marie Curie long term fellowship to support his research. His current research work focuses on the regulation of flowering time in the model plant *Arabidopsis thaliana*.

During the summer, the Director, Professor Peter Gregory, was elected to the council of the Royal Horticultural Society. The news was announced at the Society's annual meeting held in Harrogate. Immediately afterwards, Professor Gregory said: "I am honoured and delighted to be elected to the council



Dr Csaba Hornyik.



Ronnie Ogg (left) and Peter Gill.

of the Royal Horticultural Society. I hope I can play a part in maintaining the Society as one of the world's leading horticultural organisations and the UK's leading gardening charity." The RHS also honoured Field and Glasshouse 40 year veteran, Ronnie Ogg. Ronnie was presented with the RHS Long Service medal.

PhD student Susan Breen was the runner up in the annual Scottish research institutes student competition held at the Rowett Institute of Health and Nutrition in Aberdeen. Susan, a second year student working with the Plant Pathology programme gave a presentation called: 'Avr2, An RXLR Effector from *Phytophthora infestans*'. Susan, and her fellow SCRI competitor Jane Shaw, had been winners of the Mylnefield Research Services and Mylnefield Trust prizes at the in-house student competition earlier in the year.

There were long service awards (25 years) made during the year to Genetics Administrator Sheena Forsyth, Environment Plant Interactions Nick Birch and to Adrian Newton of Plant Pathology. The 2010 Director's Award, for an outstanding contribution by an individual to the life and reputation of the Institute, was won by Gaynor McKenzie.

John Bradshaw's extraordinary contribution to plant breeding was recognised by the award of the prestigious 2010 British Potato Industry Award. The trophy was presented to John at the Potato Council's Seed Industry

event at Crieff, Perthshire by Chairman, Allan Stevenson. John retired from SCRI in 2009 and has joined the ranks of the Honorary Research Fellows.

The institute bade farewell to several dedicated staff and associates during 2010. Field and Glasshouse Manager, Peter Gill, announced his retirement in February. A party and presentation was held in his honour a few weeks later. Also saying 'goodbye' to SCRI were Naomi Williams after a 32 year career that started in the former Mycology and Bacteriology department...and Jean Wilkie, who gave 22 years' service in first the chemistry department and latterly Plant Products and Food Quality.

SCRI's scientific successes through the year are detailed elsewhere in this annual report. But many of them also attracted headlines in the newspapers and coverage on TV, radio and the web.

In July, we learned that SCRI scientists had won no less than five grants from the Technology Strategy Board to fund research and development projects. The funding totalled more than £1.8 million and is earmarked for the development of sustainable crops and new, more resistant varieties of soft fruit, potato and barley. Director, Professor Peter Gregory was quoted in The Scotsman saying: "Our success at securing this funding underlines our position at the cutting edge of innovative research in the UK. These new projects will complement existing research at SCRI and allow us to come up with novel ideas and solutions to improve agricultural sustainability."

Other major funding awards included involvement in the £4.9 million QUOATS study aimed at developing new varieties of oats. It is funded by the Scottish Government, the Biotechnology and Biological Sciences Research Council (BBSRC), Defra and the Welsh Assembly Government.

SCRI scientists joined the North European ClimaFruit consortium, with a budget of six million Euros (£5.2 million) and with the goal of securing the long term future of the soft fruit industry. The Institute also joined counterparts in 12 other EU countries in a consortium seeking better ways to use legume crops. The Legume Futures programme, lasting for three years and costing four million Euros (£3.4 million), is being coordinated by SAC.



Hannah North.

The work of improving crops and joining overseas partners extends well beyond Europe. SCRI was awarded nearly £400,000 to help farmers in Malawi improve their potato crop. The Head of SCRI's Plant Pathology programme, Lesley Torrance, said: "Our work is having a real and positive impact. We will be able to help farmers increase yields and develop sustainable potato production and hopefully, in the longer term, improve food security and reduce poverty."

Finally to our visitors once again. The TV cameras were on hand in July when the granddaughter of the late Christopher North paid a visit to SCRI to see some of the North lily collection that has been traced and restored to health at the Institute where they were bred. Ms Hannah North spent some time looking at the lilies and commented: "It was something my grandfather was extremely passionate about and proud of. I remember seeing some of them in his garden when I was very young. It was only when I was older that I realised what an amazing thing he'd done!"

Lastly in this final annual review of the work of SCRI, we return to LEAF Open Farm Sunday. One of the new features for 2010 was an impressive display of farm equipment including tractors and a combine harvester. A



LEAF Open Farm Sunday.

few days after the event, a five year-old boy called Adam arrived at SCRI's reception with his grandmother bearing an impressive cake adorned with images of tractors. It was a gift for the farm staff in appreciation of the fun time Adam had enjoyed sitting playing on the tractors and combine. "A fascinating place" was the verdict of HRH The Princess Royal...and also, it would seem, the judgement of a five year-old boy who had the time of his life at an SCRI open day.

As we come together with the Macaulay Land Use Research Institute – to form The James Hutton Institute – it is perhaps a fitting end to this phase of our story. 2010 is not the *end* of the story by any means. Just as the Scottish Plant Breeding Station and the Scottish Horticultural Research Institute have lived on within SCRI...so our organisation will form part of the warp and weft of the new institute in the years to come. Our ambition must be to go on enthusing all those who visit us...whatever their station in life.



Biomathematics & Statistics Scotland

David A. Elston

Biomathematics & Statistics Scotland (BioSS, www.bioss.ac.uk) delivers research, consultancy and training in statistics, mathematical modelling and bioinformatics. BioSS plays a distinctive role in the Scottish research community, bridging the gap between the development of mathematical methods and their application in addressing important scientific problems. Our staff work in four broad application areas: plant science; animal health and welfare; ecology & environmental science; and human health & nutrition, and we collaborate widely with scientists from many organisations in Scotland and overseas. BioSS's programme of applied strategic research addresses generic issues encountered in these application areas and is managed in three broad themes: statistical bioinformatics; process & systems modelling; and statistical methodology.

BioSS was formed as the Scottish Agricultural Statistics Service in April 1987. This new organisation combined the staff of the AFRC Unit of Statistics in Edinburgh with statistical staff working in agricultural research institutes throughout Scotland. The critical mass of this new structure allowed individuals to specialise in emerging methodologies and application areas. A strong corporate identity was quickly established by the Director, Rob Kempton, leading to a willing sharing of expertise and a mutual desire to improve scientific research through cutting-edge quantitative techniques.

Although BioSS interacts equally with all of the Scottish Government's Main Research Providers, it has always been considered too small to be free-standing and so was established as a distinct unit within SCRI. This arrangement, overseen by a Strategic Planning Group whose membership represents all of BioSS's key stakeholders, has withstood the test of time: we look back proudly on our achievements as part of SCRI and look forward optimistically to our future as part of The James Hutton Institute.



Phylogenetic trees and molecular evolution

Frank Wright

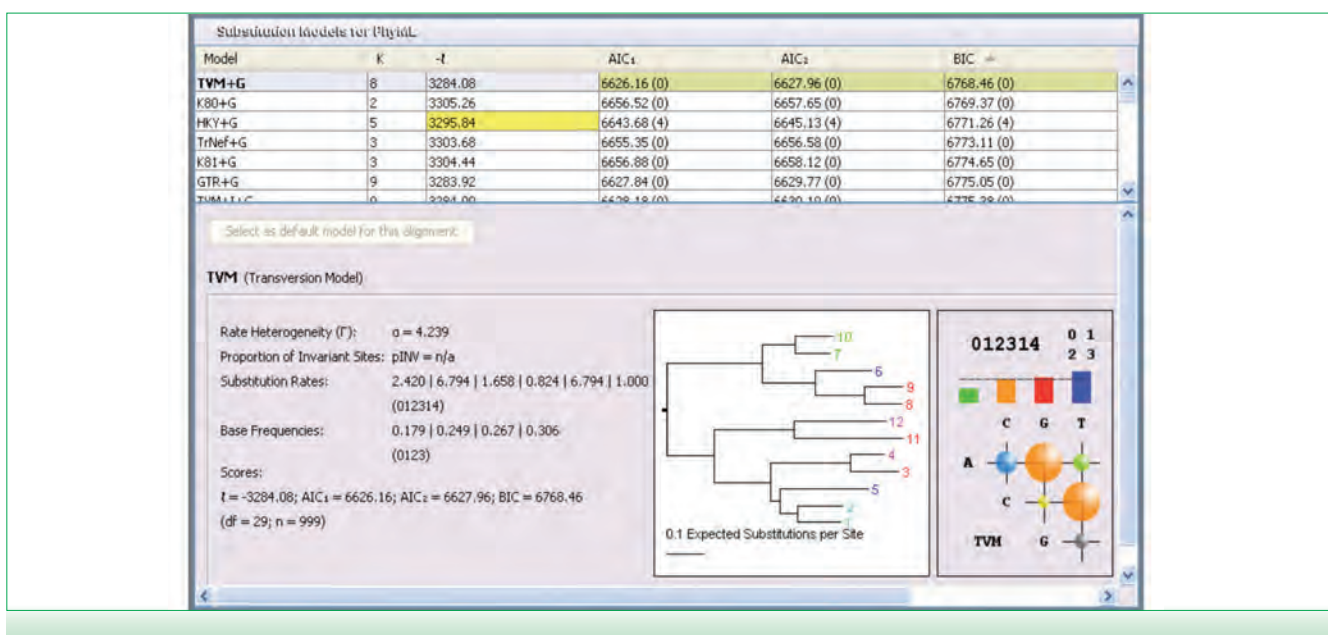
In 1993 the SCRI annual report contained an article by F. Wright and R.A. Kempton entitled 'Phylogenetic trees and molecular evolution'. This marked the beginning of the collaboration of BioSS with SCRI in analysing molecular sequence data to infer relationships among species and aspects of the evolutionary process. The BioSS involvement widened from providing consultancy, to developing statistical methods to analyse multiple alignment data and then to developing software to make the use of these sophisticated methods easier for biologists.

Over this period, the methods to infer phylogenetic trees have increased markedly in statistical sophistication. In the early 1990s Maximum Parsimony and methods based on genetic distance matrices (for example, Neighbour Joining) were common. In those days, the slowness of modern statistical approaches was a major issue. However, in the last five years we have seen a dramatic increase in the use of fast Maximum Likelihood methods and in the use of Bayesian methods which can also make use of computer cluster technology. The availability of increased computing power has also allowed the analyses of large numbers (e.g. thousands) of gene sequences.

To simplify the use of modern statistical and evolutionary phylogenetic methods and to make use of computing power, we developed the TOPALi package for the analysis of nucleotide and protein sequence multiple alignment data. TOPALi 2.0, released in 2009, includes access to methods for model selection (an important step prior to phylogenetic analysis) and phylogenetic tree estimation including the well-known PhyML and MrBayes programs. TOPALi has a rich graphical interface. The figure below is the output from a TOPALi model selection analysis applied to a DNA dataset showing the optimum model of nucleotide substitution.

More recently BioSS has also provided consultancy in specialised phylogenetic analysis methods for RNA sequence data which take into account known RNA secondary structure (i.e. position of stem and loop regions) and also in evolutionary analysis methods to detect evidence of natural selection.

With the availability of genomic sequence data, we are now in the era of Comparative Genomics, and the emphasis is moving from Phylogenetics to Phylogenomics. The analysis of thousands of loci has created new challenges for the design of phylogenetic analysis protocols. Meeting these challenges will involve close collaboration between statisticians and bioinformatics programmers to automate the analyses and to visualise the output.



Mylnefield Research Services Ltd

Nigel W. Kerby & Jonathan B. Snape

Mylnefield Research Services (MRS) Ltd was established in 1989 as a wholly-owned subsidiary of SCRI and began trading in 1992. It was established to generate commercial income from the exploitation of intellectual property developed at SCRI while protecting its charitable status. A significant proportion of the profits made by MRS, determined by the Board of Directors, is transferred to SCRI and the Mylnefield Trust through gift aid. MRS has made a profit in every year of operation and carries out its activities without subsidy.

The mission of MRS is to assist SCRI in achieving its vision, namely "To deliver innovative products, knowledge and services that enrich the life of the community and address the public goods of sustainability and high quality and health food."

A new Business Plan for the period 2010–2013 was formally approved. Under this plan, turnover will continue to grow steadily to reach £2.89 million by 2012/2013 with profitability (before tax and gift aid) to remain above 12.5%. A significant part of this increase will be achieved through growth in the contract research business, with a greater focus on winning new contracts in the area of sustainable crop production.

MRS uses a diverse range of routes to commercialise SCRI expertise and IP, including:

- Spin out companies, for example EnPrint Ltd.
- Joint Ventures, for example Danasia Berry (Beijing) Corporation
- Collaborative Research Projects, for example long-term breeding contracts with GlaxoSmithKline and Greenvale AP Ltd.
- Licensing, for example we have granted 473 licences to plant varieties bred at SCRI

- Sale of products, for example barley molecular markers, plant virus antibodies
- Analytical services, for example stable isotope analysis, lipid analysis
- Field and glasshouse services, for example supply of high-health plants, trialling new agrochemicals
- Consultancy, for example statistical services from BioSS.

Finances

The turnover of MRS was £2.4 million in 2009/2010, which represents an increase of over 35% on the previous financial year.

MRS transferred £1.08 million to the SCRI Group (SCRI plus the Mylnefield Trust), including £165k of gift aid. As in previous years, contract research (53.5%) was the biggest contributor to income, followed by royalties (20.9%) and analytical services (20.2%). In addition, MRS retained £174k (after tax) to increase significantly company reserves for future investments.

Analytical services

The turnover from Mylnefield Lipid Analysis grew by more than 20% to reach £353k in 2009/2010. As a direct result of our investment in obtaining further accreditation, we were able to secure a major new contract with a North American pharmaceutical company. In 2010, we were audited by several of our major customers who now require all our services to be fully accredited. With the assistance of Marilyn Emery Consulting (MEC) Ltd, Claire Traynor and her team have successfully implemented robust quality management systems and are currently working towards obtaining Good Manufacturing Practice (GMP) accreditation.

Under the leadership of Wolfram Meier-Augenstein, the stable isotope analysis business grew by 70% to



Dr Nigel Kerby, Managing Director MRS Ltd, is presented to HRH The Princess Royal.

reach £124k in 2009/2010. As a result of this growth it was necessary to invest in new equipment in order to increase throughput and meet market demand. A Genecom-funded project to develop a method to detect counterfeit Scotch whisky was undertaken in 2010 and generated significant interest from the major distillers in Scotland.

Associated businesses

EnPrint Ltd was established in April 2009 with a £150k investment from the Genomia Seed Fund with a follow-on investment of £75k in 2010. EnPrint are developing laboratory-based analytical services for analysing complex populations of microorganisms based on methods pioneered by Tim Daniell. These techniques have attracted considerable interest from environment agencies and water companies in the UK and elsewhere in Europe. In 2010, EnPrint secured a grant from Genecom to develop further a test for the identification of *Cryptosporidium*, a major problem for water companies throughout the world.

Plant breeding

MRS's commitment to plant breeding was strengthened by the appointment of Dorota Jarret as a soft fruit PhD plant breeder to join Vanessa Young (potatoes) and Hazel Bull (cereals). This investment will ensure that MRS has access to plant breeders with the skills required fully to exploit recently-developed molecular

breeding tools and continue to develop products that meet industry and consumer needs.

Technology Strategy Board

In 2010, the Technology Strategy Board announced major new funding in the area of crop protection. SCRI scientists applied for five projects and were successful in all five, a truly remarkable performance that secured 15% of the total funds available. MRS will be managing three of these projects, one developing physical markers for soft fruit (Julie Graham), one on controlling *Rhynchosporium* in barley (Adrian Newton) and one on Free Living Nematodes and potatoes (Roy Neilson and Finlay Dale).

Licensing and royalties

Royalty income (£492K) in 2009/2010 was maintained at similar levels to 2008/2009. Income from soft fruit accounted for almost 82% of all royalties with raspberries accounting for 48%, followed by blackberries 13%, blackcurrants 12% and strawberries 9%. Income from the strawberry variety Symphony continued to decline, a trend that we expect to continue as a direct result of increased competition. Income from brassicas exceeded £59k, an increase of 48% on the previous year, driven by strong sales of Caledonian kale and greater than expected sales of Caledonian swede in New Zealand. Income from potato varieties was £48k, an increase of 120% on 2008/2009 driven by the strong

performance of Vales Sovereign and the organic variety Lady Balfour.

In 2010, three potato varieties (Trixie, Chaski and Paru) were placed on the National List and two other potato varieties were entered into National List trials. One raspberry variety (Glen Fyne) and one blackcurrant variety (Ben Vane) were granted EU Plant Variety Rights.

Contract research

Despite the recession, income from contract research managed to grow by 47%. This strong performance was made possible by several new contracts starting in 2010 including new LINK projects on blueberries and fruit softening, several Potato Council projects and a number of contracts with BioSS. Following

the liquidation of a customer in 2009, their potato breeding programme was sold to an existing customer in 2010. We were successfully audited by the Chemicals Regulation Directorate to maintain our status as 'Officially Recognised' for efficacy testing of agrochemicals and several contracts in this area were secured.

Acknowledgements

MRS gratefully acknowledges the support of all SCRI staff, for their significant contribution to the success of the company. Also, MRS would like to thank its customers and sponsors for their continued support. Finally, we would like to thank the non-executive Directors of MRS who contribute their valuable time without recompense.



Division of Plant Sciences University of Dundee

John W. S. Brown

Over the three short years of its existence, the Division of Plant Sciences has doubled in size to around 50 people. This growth reflects great success in external grant acquisition by all of the Principal Investigators (PIs). Many of these grants involve collaborations with SCRI scientists, supporting continued and developing interactions. The international profile of the Division of Plant Sciences has been enhanced by PI's collaborations with top research groups around the world, organisation of national and international scientific meetings, and presentation of our research at such meetings. Finally, we have been particularly active in public engagement at a local level this year, taking part in the University of Dundee Botanic Garden Fun Day and the College of Life Sciences Doors Open Day where children and the general public discovered that even plants have DNA (they extracted it from raspberries) and learned about current ideas and activity in biofuels and bioenergy.

The MRes course 'Crops for the Future' had its first intake of four students in September 2009. This joint venture between the Division of Plant Sciences and SCRI exploits our unique combination of expertise in

cutting-edge plant and crop science. The course was very positively reviewed by our external examiner and the second intake of students arrived this September. In 2010 we were awarded a BBSRC Masters Training



Botanic Garden Fun Day – making raspberry DNA.

Grant of £334k to fund UK/EU student participation on this course. This was the biggest such award given out in the UK and will enhance the development of the course and its wider recognition.

We were very pleased to welcome Edgar Huitema, a Royal Society of Edinburgh Fellow, who joined the Division last October. He has quickly established his research group which seeks to exploit the model organism *Phytophthora capsici* and study basic processes that underpin disease establishment and virulence in plants. Edgar made two successful grant



Nuffield Bursary student – Marie Abraham.



Nuffield Bursary student – Ewan Barrack.

applications (Royal Society and BBSRC) to support his research and has recruited two PhD students and hosted three interns. In the summer, the lab supervised Ewan Barrack, a 5th year pupil from Arbroath High School, who completed a five-week training period funded by a Nuffield Bursary.

Paul Birch's lab has won a major collaborative grant worth £1.7M to find resistance genes from wild potato species which will provide effective (durable) disease control against *Phytophthora infestans*. *Phytophthora* causes late blight, the number one disease of the world's third largest food crop, potato. It causes an estimated £5 billion a year in chemical control costs and crop losses. The collaboration involves scientists from SCRI and the Sainsbury lab in Norwich. A major breakthrough was the identification of the first host defence protein target of an effector protein from a filamentous plant pathogen and the mode-of-action for the effector. The work reveals that eukaryotic plant pathogens can manipulate the host ubiquitination machinery (as bacterial pathogens are known to do) in order to switch off key defence processes. Among other collaborators, the main author of this work, Jorunn Bos, has recently joined SCRI as a Royal Society of Edinburgh Fellow.

Gordon Simpson's lab discovered that FPA, one of the regulators of flowering, controls the site of cleavage and polyadenylation of mRNA. Unusually, FPA appears to affect alternative processing of long non-coding antisense RNAs embedded at the locus encoding the floral repressor, FLC. This work was published in *Developmental Cell*. A preview article (James Manley,



Claire Halpin and Abdellah Barakate – planning molecular constructs.

Columbia University, New York) said the work “has the potential to provide a significant new mechanism of gene control, not only in signalling when a plant will flower, but also more generally in animals as well as plants”. Gordon’s lab has built on this discovery to ask how widespread alternative sites of RNA 3’ end formation are in plants using genome-wide RNA sequencing in a collaboration with Geoff Barton’s bioinformatics group.

In John Brown’s lab, the major focus is on alternative splicing (AS) and its role in gene expression. The lab has shown that alternative splicing is far more prevalent in plants than previously thought and that it significantly affects gene expression in many plant processes. AS therefore needs to be taken into account in plant and crop research on processes such as growth and development, responses to environmental stress, and pests and pathogens. For example, circadian rhythms allow organisms to anticipate daily changes in environmental conditions and optimise timing of metabolic processes in the day–night cycle. The alternative splicing expertise and systems in the Dundee lab have been key in the discovery, by collaborators in Argentina, of a link between the circadian clock and alternative splicing (published in *Nature* in November 2010). John’s lab also hosted a Nuffield Bursary student, Marie Abraham, for a summer molecular biology project.

Over the last two years, Claire Halpin’s research group has expanded to 18 researchers and her major projects on bioenergy and meiosis are making good progress. One highlight of 2010 has been the harvesting and phenotyping of a large polytunnel experiment of 640 spring barley genotypes which will enable her team to identify quantitative trait loci for straw biofuel production potential using association genetics. Both the biofuel project and Claire’s LOLA project on barley recombination have made extensive use of the SCRI barley transformation facility and her group are currently characterising many novel and potentially useful transgenic lines.

Andy Flavell’s lab has been using association genetics to isolate genes responsible for grain size in spring barley. This requires a combination of field trials, high throughput SNP marker analysis and ‘next generation sequencing’ of presumptive gene candidates in a collection of around 400 barley cultivars. Andy has developed a new approach for this. His lab has published key papers describing the properties of the SNP marker diversity parameters within the barley germplasm and the genetic diversity of field pea (*Pisum*) and its relationship to the geographic distribution of the genus.

Our Emeritus and Associate members have been very active in the last year, producing many publications and giving presentations at meetings around the world. Janet Sprent was awarded an Honorary Doctorate by the Swedish Agricultural University, Uppsala. John Raven spent a productive March in the School of Plant Biology in the University of Western Australia as part of his five year appointment as an Honorary Professor at UWA. Lyn Jones is involved in the collaborative development of methods (thermal and RGB imaging and high resolution reflectance spectroscopy) for the rapid field phenotyping of cereals for stress tolerance in the field with the Australian High Resolution Plant Phenomics Centre in Canberra.

The Scottish Society for Crop Research

Bill Macfarlane Smith

The Society provides a link between the Scottish Crop Research Institute and farmers, processors and other interested bodies:

- by organising field walks in the summer and meetings during the winter for the exchange of information
- by financing science-based publications for the benefit of the membership
- through the formation of crop-based sub-committees which maintain contact with members on specialised topics
- by funding research at SCRI which is either 'pump-priming' to initiate new research, or work for minority interests that the large funding bodies would not support.

The Society also has a role in raising awareness of items of interest and concern to the agriculture,

horticulture and forestry industries. At the moment, this is achieved by funding the Annual SSCR Lecture immediately following the Annual General Meeting. This year's AGM was held on Wednesday 26 May and the Annual Lecture was given by Professor Martin Tangney, Professor of the Biofuels Research Centre at Edinburgh Napier University. The title of the Lecture was 'Biofuels'.

The Society currently supports research on a range of topics, with funding being made available on an



Cereals in Practice.



Fruit for the Future.



Potatoes in Practice.

annual basis for work selected by the three Crop Sub-Committees. Short notes on the outcome of research funded in the past by SSCR are on the Society's web pages which can be accessed directly or via links from SCRI's website. Funding continues to be provided on a biennial basis for a keynote speaker at the Crop Protection Northern Britain Conference.

All meetings organised by the Society were again well supported, with similar or greater numbers attracted than in previous years. 'Cereals in Practice' was held on 8 July 2010, again at the Institute's Balruddery Farm. This event combined the research and practical demonstrations of the work of SCRI and SAC scientists and again included demonstrations of machinery.

The 'Fruit for the Future' event was held on 15 July 2010, and attracted breeders, growers, end-users and processors. The provision of additional facilities for visitors to meet, and for the presentations on research, was greatly appreciated. New selections of raspberries, strawberries, blackcurrants, and gooseberries were displayed, with the opportunity provided for the tasting and evaluation of prospective new varieties of raspberry.

'Potatoes in Practice' was held on 12 August, at Balruddery Farm. This was attended by well over 700 growers, breeders, scientists and advisers who had come to see new research, new cultivars and methods of crop husbandry. It may well be difficult to better this attendance in future years. Support was again provided by the Potato Council, the Scottish Agricultural College, CSC Crop Protection Ltd., SCRI and the Society. Plot demonstrations, including those of potato crop handling machinery and other equipment, were of particular interest, in spite of the generally inclement weather on the day.

The Potato and Soft Fruit Crop Sub-Committees held other half day meetings during the year to provide information on current research and to permit interaction between end users, growers, processors and scientists. The Cereal and Combinable Crop Sub-Committee has planned a winter event at Battleby on 24 February 2011.

The Society continues to review its remit, to ensure that it both is fit for the 21st century and continues to meet the objectives and aspirations of its members. Members were invited by the Chairman, Dr Wale, in his AGM address when he demitted office, to contribute views on the future objectives and structure of the Society.

Postgraduate studies at SCRI

Craig G. Simpson & Tracy A. Valentine

SCRI this year hosted over 70 postgraduate students, working on a wide range of problems in plant science, agriculture and the environment. We encourage an open interactive environment, which allows access to all the skills and facilities available at the Institute. The University of Dundee Plant Science Division is housed on site and this further enhances interaction with our postgraduate students and University students. This opens opportunities for the development of interdisciplinary research essential for modern biological research.

Students are monitored throughout their study time at SCRI to encourage and maintain progress. Through this process, students are not only supported by their direct supervisors but benefit from a postgraduate team that gives positive critical scientific assessment and pastoral support as required, under the auspices of the Institute's University Interactions Committee. Ultimately, the aim of the studentship is to train and produce postdoctoral workers with positive enquiring minds and the intellectual and technical tools to develop their own interests and science programmes.

In addition to their research training, SCRI encourages further training to expand generic knowledge and understanding of important skills required for success in their chosen field. In the past, we have supported meetings that allow students to gain information and advice from senior experienced Institute staff. In the coming year, this will be formalised with the development of a Postgraduate School on Academic Skills with topics and skills directly relevant to completion of a PhD and future postdoctoral positions. All students have further access to Dundee University Generic Skills training that expands their existing activities and will be useful in a variety of employment destinations after their studentship is completed.

Jane Shaw describing the role of Cajal bodies and the nucleolus in plant virus infection and Susan Breen

describing Avr2, an RXLR effector from *Phytophthora infestans* won our annual postgraduate student competition. Both went on to represent the Institute at the annual Scottish Research Institutes Postgraduate Student competition at the Rowett Institute at Aberdeen University. Susan came home with the runner-up place at this competition and further won the University of Dundee, College of Life Sciences annual poster competition, which represents a tremendous achievement.

We hosted the SCRI/Dundee University Master of Research (MRes) course titled 'Crops for the Future' for the first time over the past year. This course provides advanced study in practical and theoretical aspects of crop bioscience through lectures and practical, technically demanding projects.

Successful PhD Submissions

Brown, E. (nee Coates) 2010. Anti-cancer effects of soft fruit phytochemicals. *University of Ulster*, PhD Thesis.

Campbell, R. 2010. Determining the genetic and molecular control of carotenoids in potato tubers. *University of Dundee*, PhD Thesis.

Clark, E.L. 2010. Molecular characterisation of the bacterial communities in cabbage aphid (*Brevicoryne brassicae*) and their associated fitness effects. *University of Dundee*, PhD Thesis.

Clark, K. 2010. Does mother know best? Is host plant selection by above ground insects influenced by below ground herbivores. *University of Sussex*, PhD Thesis.

Foito, A. 2010. A metabolomics-based approach to study abiotic stress in *Lolium perenne*. *University of Dundee*, PhD Thesis.

Hochshartner, G. 2010. Revealing the past: The potential of a novel small nucleolar RNA (snoRNA) marker system for studying plant evolution. *University of St Andrews*, PhD Thesis.

Loades, K.W. 2010. Quantifying the role of fibrous roots on soil reinforcement. *University of Dundee*, PhD Thesis.

Thorsen, M.K. 2010. Biological mechanisms involved in stabilizing sandy soils of the Machair. *University of Aberdeen*, PhD Thesis.

Wojciechowski, T. 2010. Root development in semi dwarfing lines of wheat and barley. *University of Reading*, PhD Thesis.

Xiao, H. 2010. Mechanisms by which natural polyphenols regulate expression of cytoprotective genes. *University of Dundee*, PhD Thesis.

Publications

Publications listed between 1 October 2008 and 31 September 2009 are classified in the following manner:

- J Papers describing original research in refereed journals.
- R Books, book chapters and reviews in books – provided each has been edited externally
- P Published proceedings of contributions to conferences or learned societies (including published abstracts)
- O Popular articles and unrefereed publications

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Meteorological Records

Marion Grassie

The main features of 2010 were the November / December snowfall and prolonged very low temperatures, breaking SCRI's previous records for December, set in 2009. Most significant were the 13 days from 24 November until 6 December, when 11 days of snow were recorded. The total precipitation for this period totalled 60 mm, the greatest amount falling during the 24 hour period from 0900 on 27 November, with 26.5 mm. Continuous low temperatures prevented melting and snow depth reached 25 cm on 2 December. Considerable national disruption occurred, including closure of SCRI.

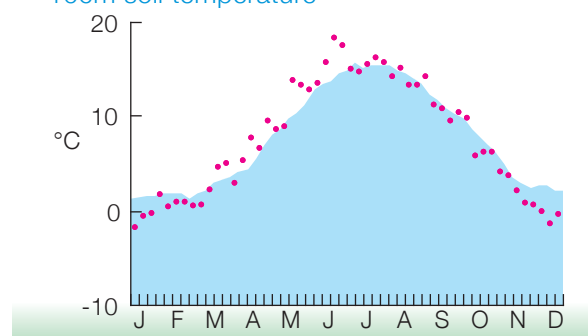
In contrast, higher than normal air and soil temperatures occurred for 8 months of the year, the warmest single day being 24 May, the sunniest month, with an air maximum of 26°C. Other features include greater than average sunshine and greater than average rainfall, with widespread flooding during July.

Temperature All months from March to October boasted mean maximum air temperatures higher than the Long Term Average (LTA), most significant being June with 19.3°C (LTA 16.8°C). Highest air temperatures recorded during months May to September were 26.0°C, 23.7°C, 22.4°C, 23.7°C and 21.4°C respectively. Average maximum figures for January, February, November and

December were all lower than expected, in particular December, at 1.7°C (LTA 6.7°C), the lowest on our records.

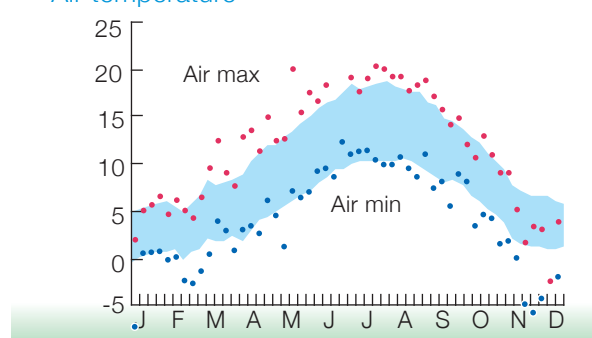
Mean minimum air temperatures were all lower than the LTA with the exceptions of June, July and October, which were all slightly higher, most noteworthy being December with -5.7°C, the lowest on our records, considerably lower than the LTA of 1.2°C, and beating the -3.4°C recorded in 2009.

10cm soil temperature

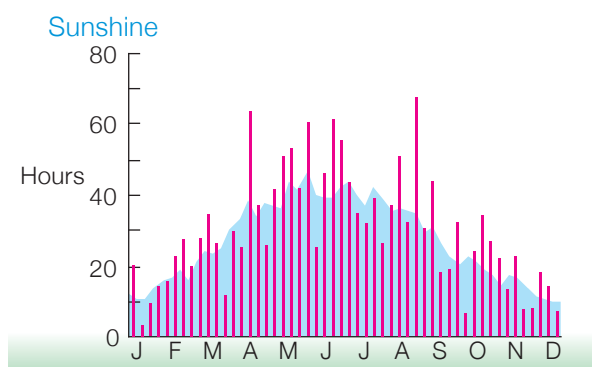


The lowest air temperatures recorded throughout the year were, with the exception of June and July, all lower than the LTA. In particular, January, February, March and December displayed temperatures down to -9.4°C, -7.5°C, -5.2°C and -13.8°C respectively (-5.5°C, -4.7°C, -2.8°C and -5.3°C LTA). December's figure is again the lowest on our records and January, the second lowest. The total number of days for 2010 with air temperature <0°C came to 90, double that of the LTA of 47. January to March, May, November and December all had higher figures than the LTA, particularly December, with 28 days against the expected 10, the highest number on our records, surpassing the record 25 days registered in 2009. All other months had equal to, and April less than, the LTA.

Air temperature



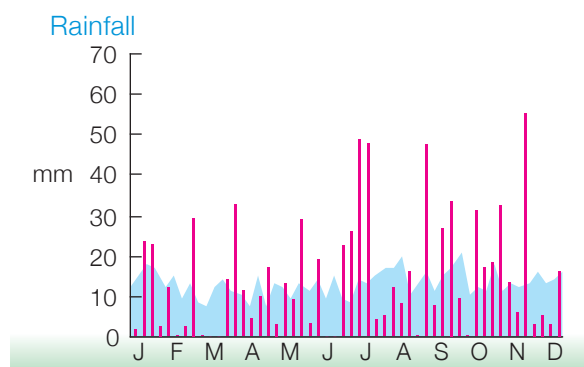
Blue areas on figures indicate long term average 1961–1990
Statistics are measured against the monthly Long Term Average (LTA) for 1971 to 2000.



Minimum grass temperatures showed mixed results with January, June, July and November all displaying higher than expected figures, particularly July with 6.1°C (LTA 1.2°C). The rest were equal to or lower than the LTA. Of particular note was December with -13.8°C against the LTA figure of -9.2°C. The total number of days with grass temperature <0°C (frost) was 140, 6 days more than the LTA of 134. Although only June, July and August escaped frost, most months had fewer nights of frost than expected, with the exceptions of February with 22 (LTA 20), May with 11 (LTA 7), November with 20 (LTA 18) and notably December, which had 31 nights of frost for the second year running – the only occasions on our records (LTA 21).

Mean soil temperatures for 10, 20 and 30 cm were at or close to the LTA for most months. However the general trend showed April to October to be above the LTA with January to March, November and December all slightly lower than normal.

Sunshine and solar radiation With the exception of March and July which were slightly lower than normal, sunshine figures were all higher than expected with a total of 1563.4 hours of bright sunshine, compared to the LTA of 1411.6 hours. In particular April, May, June and August had 177.3, 209.3, 206.7 and 183.4 sunshine hours respectively (143.3, 188.1, 170.6 and 164.9 hours LTA).



Solar radiation values were again higher than normal with the exception of August and October.

Rainfall For the seventh year in a row, rainfall levels were higher than the LTA, the annual total reaching 773.5 mm as compared to the expected 664.5 mm. May, July and September to November all had higher rainfall levels, significant months being July, with 144.3 mm – three times the LTA of 52.7, September, with 104.3 mm (LTA 64.4) and November, which produced 120.2 mm, more than double the LTA 52.1 mm. 2010 produced 49 days with >5.0 mm rain against the expected 37. Particular days of note are 14 and 20 July which had 41.1 mm and 37 mm rainfall respectively. Of the seven months with less than normal rainfall, most noteworthy is June, with 23.2 mm (LTA 51.7 mm) and December with 32.8 (LTA 66.4 mm), both with less than half the rainfall expected. No rainfall at all was recorded during the first three weeks of March, nor for two full weeks in June.

Thunder was reported four times during the year, during January, July, September and most notably on 28 November when it constituted a thunder snowstorm.

Snow or sleet was recorded on 28 days, notably January with 8 days of snow, November and December both with 7. Hail was recorded on 5 days.

Wind Generally, wind speeds were unremarkable with only 3 recorded days of gale (mean wind speeds of 34 knots+) compared with the 20 in 2008.

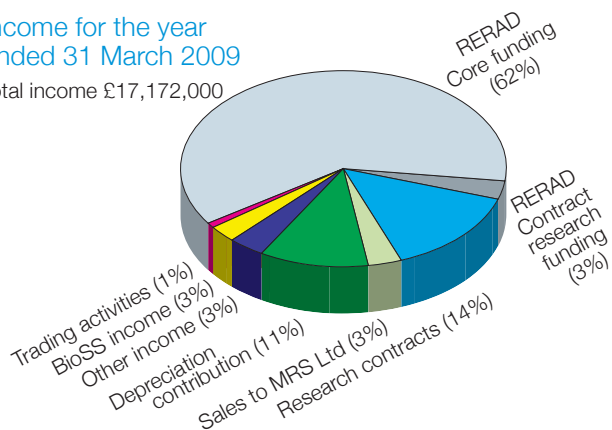
SCRI's weather data is available on our website. You can find a general overview, a data page and a current weather page that displays the present day's data from SCRI's Automatic Weather Station, updated in 15 minute intervals.

Every month, our weather data is featured in the Courier and Dundee Evening Telegraph.

Accounts

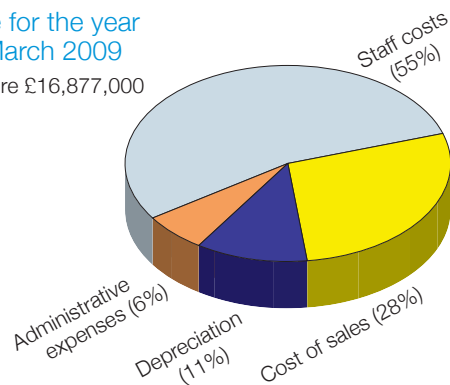
Income for the year ended 31 March 2009

Total income £17,172,000



Expenditure for the year ended 31 March 2009

Total expenditure £16,877,000



Balance sheet at 31 March 2009

Total value £33,655,000

Assets

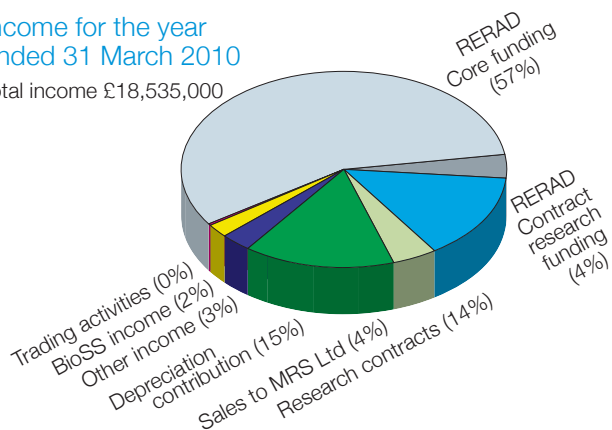
Fixed assets	93 %
Stocks	0 %
Debtors	7 %

Liabilities

Capital reserve	81 %
Income & expenditure account	8 %
Current liabilities	11 %

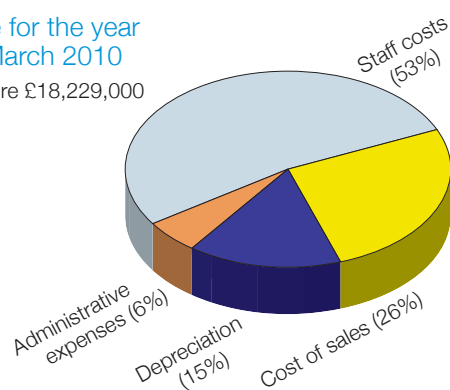
Income for the year ended 31 March 2010

Total income £18,535,000



Expenditure for the year ended 31 March 2010

Total expenditure £18,229,000



Balance sheet at 31 March 2010

Total value £31,982,000

Assets

Fixed assets	91 %
Stocks	0 %
Debtors	8 %

Liabilities

Capital reserve	77 %
Income & expenditure account	10 %
Current liabilities	13 %

Copies of the statutory accounts can be obtained from the Director of Finance & Corporate Services, SCRI

Staff List

as at 1 October 2010

Chief Executive and Institute Director
Director of Science Co-ordination
Director of Science Planning
Director of Finance and Corporate Services

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J Graham BSc PhD
B Harrower HND BSc MSc
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I Hein MSc PhD
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L Jorgensen HND

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¹³ Honorary Professor, University of Dundee
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¹⁸ Special Professor, University of Nottingham
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D W Hopkins BSc PhD CBiol FBS
P P M Iannetta BSc PGCE(S) PhD
S N Johnson BSc DPhil
A J Karley BA DPhil
M Krol MSc
K Loades BSc PhD
M MacAskill
B M McKenzie BSc PhD

C Mitchell BSc
S M Mitchell BSc
B Mulholland BSc PhD
P Neave NC
R Neilson HNC MSc PhD
D M Roberts HND BSc PhD
G R Squire BA PhD
J A Thompson BSc
T Valentine BSc PhD
L Wiesel BSc
G M Wright HNC
M Young HND MSc PG Dip IT
[Mylnefield Research Services](#)
R E Wheatley BSc PhD



University of Dundee, Division of Plant Sciences

J W S Brown BSc PhD^{3,4,13} (Head of Division)
M Armstrong BSc PhD
A Barakate BSc PhD
P R J Birch BSc PhD (Principal Investigator)
T Bukharova
C Duc
A J Flavell BSc PhD (Principal Investigator)
A Ghatak
K Graham
S Gray BSc
D Grussu

C Halpin BSc MSc HDip PhD (Principal Investigator)
T Ho
S F Hubbard PhD (Principal Investigator)
E Huitema
H G Jones MA PhD FIHort (Principal Investigator)
J Kam
S Y Kim PhD
C McClellan
H McLellan
J Marshall BSc DPhil
M Pearson
K Rataj

J A Raven BA PhD HonPhD(Umea) CBiol FBS FRS FRSE
(Principal Investigator)
R Shafiei
G G Simpson BSc PhD (Principal Investigator)
M Spensley
N H Syed BSc PhD
S Vivera BSc MSc
N Walker
P Walsh
A Wier
Y Wilson BSc
Y Xiao
X Xu



Communication and Information Services

P Taylor MCIPR (Head of CIS)
P Cassidy
S Charman
S E Collier BSc MA MCLIP

U M McKean MA DipLib
C V Morton BA
S J Neilson DipBiolSci DipPollCon BSc

I R Pitkethly HND
A Thomas
L Wakefield MA



Information Technology

S Clark HNC MSc (Head of IT)
L H Davidson BA
I Grant HNC

P J R Grimmond BA
R McCreary BSc
L A McGregor BSc

V Pandey BSc
P Smith BSc



Finance and Corporate Services

N G Hattersley BSc PhD ACMA
(Director of Finance and Corporate Services)

S Bell

A J Cartwright BA DMS FCIPD

M Dalziel MA PgDPM MCIPD

R G Davidson

P Duncan

S Forsyth

K L Grant BA

B V Gunn

S Inglis

J Keith

C F Kydd FCCA

L Logie HNC MinstAM(AdvDip)

A Pack BA

W Patterson HND

K Robb

A Ross HNC CPP

F I F Rowe MA DipNEBOSH Grad IOSH EnvDipNEBOSH
(Safety Quality Environment Manager)

A Sandilands

S Sinclair

M Soutar

E L Stewart

L Young



Engineering and Maintenance

S Petrie BSc (Head of Engineering and Maintenance)

J Anderson

D Byrne

C Conejo

L A Crichton

G J E Ewart

A G Fox

D Gray HNC

K A Henry

R D McLean

I C McNaughton HNC

D J Redford

G C Roberts

J Rowe

W Scott

B Semple



Glasshouse and Field Services

J Abernethy

P Baird

J R K Bennett

J T Bennett

E Caldwell

M Cook

A G Dobson HNC HND

I Fleming

J M Ford

A C Fuller

M A Grassie HNC BEd

P Heffell ONC

R Keith

M Lipska MSc

J Mason

T A Mason NEBSM

D I Matthew BSc

A D Munro HND

R Ogg

G R Pitkin HND

A M Thain HNC

J K Wilde

D Young



Mylnefield Research Services

N W Kerby BSc PhD CBiol FBS (Managing Director)

L Beaton HNC DMS MBA

R Gregson

J Kelly

R Longhurst

A McNally

J B Snape MA MSc PhD CBiol MIBiol MBA



Biomathematics and Statistics Scotland

D A Elston BA MSc PhD (Director of BioSS)

King's Buildings, University of Edinburgh

C A Glasbey MA DipMathStats PhD DSc MISI

(Head of Group)^{7,8,9}

A Butler BSc PhD

S Catterall BA MSc PhD

D Glancy

S L Hirstwood

D Husmeier BSc PhD

G T Innocent

H R Kettle BSc MSc PhD

M A M Kirkwood DA

A D Mann BSc

G R Marion BSc MSc PhD

I J McKendrick BSc PhD

M Nath BSc MSc PhD

I M Nevison MA

D Nutter BSc

J Palarea-Albaladejo BSc PhD

A M I Roberts BSc MSc

Y Song BSc MSc PhD

L Spezia BSc PhD

A Vogogias HND BSc MSc PhD

West of Scotland Unit, SAC Auchincruive

S Brocklehurst BSc PhD

Environmental Modelling Unit, Macaulay

D A Elston BA MSc PhD (Head of Group)

M J Brewer BSc PhD

E I Duff BSc

J M Potts BSc MSc PhD

Aberdeen Unit, Rowett

G W Horgan BA MSc PhD (Head of Group)

G Holtrop MSc PhD

C D Mayer MSc PhD

Dundee Unit, SCRI

F G Wright BSc MSc PhD (Acting Head of Group)

C Alexander BSc PhD

C A Hackett BA DipMathStats PhD

K M MacKenzie BSc MSc PhD



Visiting workers

Name	Country of origin	Programme	Month/yr of arrival	Length of stay	Name	Country of origin	Programme	Month/yr of arrival	Length of stay
K Abbott	UK	PPFQ	Sep-10	7 mth	R MacLeod	UK	EPI	Sep-10	6 mth
R Adams	UK	UoD	Sep-10	1 yr	R Marsden	UK	UoD	Sep-10	7 mth
F Angles	France	GEN	Jul-10	2 mth	A McRae	UK	EPI	Sep-10	7 mth
T Aslam	UK	EPI	Sep-10	8 mth	E Mellado	Spain	PPFQ	May-10	15 mth
V Berrie	UK	UoD	Sep-10	8 mth	A Nwankwo	Nigeria	PPFQ	Apr-10	5 mth
H Bhanot	India	PPFQ	Apr-10	5 mth	I P Pasare	Romania	MRS	Dec-09	1 yr
L Birse	UK	PP	Sep-10	4 mth	I P Pasare	Romania	UoD	Sep-10	1 yr
D Borowska	Poland	EPI	Jan-10	9 mth	N Patel	India	PPFQ	Apr-10	5 mth
D Borowska	Poland	UoD	Sep-10	1 yr	C Plissonneau	France	PP	Aug-10	5 mth
J Bos	Netherlands	PP	Sep-10	1 mth	M Pope	UK	PP	Jul-10	2 mth
X Chen	China	EPI	Apr-09	2 yr	P Pourmohamadi	Iran	EPI	Aug-10	8 mth
W Deasy	UK	EPI	Jun-10	3 yr	K Putta	UoD	Sep-10	1 yr	
J Dolata	Poland	GEN	Sep-10	2 wks	S Rahman	India	EPI	Apr-10	5 mth
M Ehwaeti	Libya	PP	Oct-10	6 mth	B Rigney	UK	UoD	Sep-10	1 yr
S Engelhardt	Germany	PP	Feb-09	2 yr	J E P Rius	Spain	PP	Aug-10	2 yr
E Fambely	UK	UoD	Sep-10	8 mth	A Roberts	UK	PPFQ	Sep-10	5 mth
A Frew	UK	PP	Sep-10	10 mth	A S Samuel	India	UoD	Sep-09	1 yr
R Grabowski	France	EPI	Apr-10	5 mth	R Saraswat	India	PP	Apr-10	5 mth
S Hackett	UK	UoD	Jun-10	10 mth	V Saraswat	India	PPFQ	Apr-10	5 mth
A Haegmann	Belgium	PP	Sep-10	1 mth	J E Scherwinski-Pereira	Brazil	GEN	Jul-10	6 mth
K Hamilton	UK	PP	Sep-10	10 mth	H Shanks	UK	EPI	Sep-10	7 mth
V Helbig	Germany	EPI	Aug-10	2 mth	O Siang	Malaysia	GEN	Jul-10	3 mth
C Hennayake	Sri Lanka	GEN	Jun-10	6 mth	D Souter	UK	PP	Sep-10	10 mth
A Hernandez	USA	UoD	Mar-10	11 mth	B Steffenson	USA	GEN	May-10	10 mth
M Hooper	UK	UoD	Sep-10	1 yr	A A Sumi	India	PPFQ	Apr-10	5 mth
T Ilany	USA	EPI	Sep-10	1 yr	Z Syed	Pakistan	GEN	Aug-10	3 mth
E James	UK	EPI	Jan-09	2 yr	Z Syed	Pakistan	UoD	Aug-10	3 mth
C Jorna	UK	EPI	Aug-10	1 mth	A Tahir	Pakistan	UoD	Sep-09	1 yr
M Kaczmarek	Poland	UoD	Sep-09	1 yr	M Thorsen	Denmark	EPI	Aug-10	7 mth
M Kalak	Poland	GEN	Sep-10	2 wks	N Ti Mmayagari	India	PPFQ	May-10	5 mth
J Keron	UK	EPI	Aug-10	7 mth	V Tillemans	Belgium	UoD	May-10	6 mth
S Kurian	India	PP	May-10	6 mth	D Turnbull	UK	PP	Jun-10	2 mth
D Laird	UK	PP	Sep-10	9 mth	A Verley	France	EPI	Jun-10	3 mth
F Lamkadmy	France	PPFQ	Jul-10	3 mth	N Vij	India	PPFQ	Apr-10	5 mth
J Lamont	UK	UoD	Sep-09	1 yr	D Wang	China	EPI	Mar-10	8 mth
H Leeper	UK	EPI	Sep-10	7 mth	L Wiesel	Germany	EPI	Feb-10	11 mth
J Liyu	India	PPFQ	Apr-10	5 mth	X Yan	China	PP	Aug-10	1 mth
N Lukhovitskaya	Russia	PP	Aug-10	4 mth	S Yli-Seppanen	Finland	UoD	Sep-10	6 mth
V Lund	UK	PPFQ	Aug-10	1 mth					



Postgraduate students

Name	Programme	Project Title
Aqueel Al-Abedy	PP	Studies on <i>Potyvirus</i> resistance in <i>Solanum phureja</i>
Anathi Anandandesan	UoD/EPI	Mathematical modelling of the spatio-temporal dynamics of aphid-parasitoid-plant-virus interactions
Anka Asandei	EPI	Global warming: Impacts on soil temperatures and C mineralisation rates
Sandra Bacon	PPFQ	Potential of the action of novel nutrient regulators of the longevity factor FOXO1a by the trace metal zinc
Natasha Bahri-Esfahani	EPI	Metal and mineral transformations by microorganisms
Gillian Banks	EPI	Dynamics for feral oilseed rape populations and the impacts on associated insect communities
Natalie Bernaert	PPFQ	Metabolite profiles of leek as a function of genetic variation, breeding and processing techniques
Rachel Berry	PPFQ	The real uncertainty of stable isotope data for provenancing humans and drugs
Susan Breen	PP	Translocation of effector proteins into host plants
Hazel Bull	GEN	Development and characterisation of a meta-population of <i>Hordeum spontaneum</i> introgression lines into cultivated barley
Cristiane Calixto	UoD/GEN	Regulation of gene expression by novel plant specific small nucleolar RNAs (snoRNAs)
Natasa Cerekovic	GEN	Plasticity of blackcurrants in a changing climate: Focus on water efficiency
Allison Chapman	PP	The changing <i>Phytophthora infestans</i> population: Implications for late blight epidemics and control
Xiaoyun Chen	EPI	Biodiversity and soil food web activity in different managed grasslands
Canford Chiroro	EPI	Adapting to climate change: An evaluation of social and physical determinants of resilience in agricultural systems faced with increased drought risk in Malawi
Hannah Clarke	UoD/EPI	The role of bacterial secondary symbionts of <i>Macrosiphum euphorbiae</i> in the dynamics of multitrophic interactions
Nicky Cook	UoD/EPI	Population genetics of fernland sawflies
Marion Cubitt	PP	A systems approach to virulence regulation in <i>Pectobacterium</i>
Paul Daly	UoD	Manipulation of lignin biosynthesis in barley
Jayne Davis	EPI	Molecular interactions of potassium deficiency and pathogen resistance in barley
William Deasy	EPI	Novel approaches for the management of cabbage root fly (<i>Delia radicum</i>)
Wenni Deng	EPI	Engineering novel geotextiles from an understanding of the dynamic properties of seed coat mucus
Ralf Dietrich	UoD/EPI	Root soil dynamics: New ways of studying roots in a changing climate
Helen Downie	EPI	3D Imaging of root particle interactions using optical projection tomography and x-ray microtomography
Natasha Duckett	EPI	Soil reinforcement using plant roots: A sustainable alternative to traditional slope stabilisation
Daniel Dzdzienny	GEN	Manipulation of self-incompatibility in diploid potato species
Fiona Fraser	EPI	Temperature responses of soil nitrogen transformations
Joanna Fyans	PP	The role of protein transport in the pathogenicity of <i>Streptomyces</i> spp.
Claire Ghee	EPI	Plant-soil C-dynamics under contrasting farming systems
Madeline Giles	EPI	Where does denitrification occur in the rhizosphere?
Varun Gopalakrishnan	PP	Acquisition and transmission of <i>Potato mop-top virus</i> by <i>Spongopora subterranea</i>
Katarzyna Goszcz	PPFQ	The impact of soft fruit on degenerative diseases: Metabolomic fate and mechanisms of action
Tek Prasad Gotame	GEN	Impact of climate on productivity and quality of raspberry
Clement Gravouil	PP	Multiple disease interactions on cereals and interactions with other crop environment organisms
Severine Grouffaud	PP	Translocation of <i>Phytophthora</i> effectors and their manipulation of host plant disease resistance
Will Hently	EPI	[Agrifood] Trophic cascades in a changing climate – effects of elevated CO ₂ on breakdown of crop defences
Miriam Hérold	EPI	Plant roots as drivers of denitrification
Lydia Hunter	PP	Role of potato RNA-dependent RNA Polymerase 1 in virus resistance
Ning Jiang	GEN	Linkage disequilibrium based mapping of complex traits in crops
Florian Jupe	GEN	Utilising next generation sequencing to clone and characterise durable potato resistance genes
Julietta Jupe	UoD	The role of conserved <i>Phytophthora</i> effectors in virulence
Agata Kaczmarek	PP	Research to support further development of the PCL PCN model
Kabindra Prasad Kandel	PP	Temporal and spatial mapping of <i>Phytophthora infestans</i> infection
Pavel Kerchev	PPFQ	Influence of ascorbic acid on plant aphid interactions
Adnan Lahuf	PP	Role of phloem transport in infection transmission in resistance for <i>Potato mop-top virus</i>
Timothy Lewis	EPI	Linking erosional processes with seedbank dynamics to inform sustainable cropping
David Lloyd	GEN	Mapping genes and QTLs linked to flavour and texture in potatoes
Marta Maluk	UoD	Improving barley for biofuel production – investigating the roles of CCR and 4CL in lignin biosynthesis
Ashleigh McKenzie	PP	The role of <i>Rhynchosporium secalis</i> cell wall proteins in cell wall integrity and pathogenicity
Scott Wesley McKenzie	EPI	Effects of elevated CO ₂ on plant mediated interactions between aboveground and belowground herbivores
Lindsay McMenemy	EPI	Cooperation between plant enemies – do raspberry viruses attract more aphid vectors?
Yuan Yuan Mei	PP	Functional analysis of <i>Globodera pallida</i> SPRYSEC proteins
Giovanni Melandri	EPI	Biological nitrogen fixation by <i>Rhizobium leguminosarum</i> by Viciae
Christine Messner	PPFQ	Impact of genetics and environment on quality and sensory traits of blueberry
Claire Mitchell	PP	Optical transfection and transformation technologies in plant cells and tissues
Adriana Stefania Pasare	PPFQ	The regulation of isoprenoid metabolism in <i>Solanaceae</i> crop plants
Namrata Reeto	UoD/GEN	Controlling <i>Arabidopsis</i> RNA binding proteins with phosphorylation
Ghulam Sahi	PP	Molecular studies of the movement of <i>Tobacco rattle virus</i>
Sonja Schmidt	EPI	Microtomography in soil root interactions
Zulkifli Ahmad Bin Seman	GEN	Functional and evolutionary characterisation of host genes targeted by <i>Phytophthora infestans</i> effectors and defence associated candidate genes
Jane Shaw	PP	The role of Cajal bodies in the nucleolus in plant virus infection
Marcin Skiba	EPI	Biological nitrification inhibition in the rhizosphere of temperate arable plants
Remco Stam	PP	Identification and functional characterisation of the <i>P. capsici</i> crinkler effector repertoire
Rachel Storrs	EPI	Machair vulnerability and landscape resilience in South Uist and Benbecula, Outer Hebrides, Scotland
Nithya Subramanian	GEN	Increasing mineral delivery through potatoes
Hui Tan	PP	Dissection of the <i>Pectobacterium</i> virulence quorum sensing regulation
Amar Thirugnansambandam	PP	Role of seed-borne infection in <i>Rhynchosporium</i> and <i>Ramularia</i> epidemics in barley
Peter Thorpe	MRS	Bioinformatic and functional analysis of the <i>Globodera pallida</i> genome
Sebastian Eves-Van Den Akker	PP	Characterisation of the feeding tubes of plant parasitic nematodes
David Oscar Yawson	EPI	Virtual water and climate change: Implications for food security in the UK
Vanessa Young	MRS	Genetic analysis in a commercially relevant cross and application of markers in a tetraploid breeding programme
Dzeti Zait	GEN	Sensory and compositional analysis of flavour in red raspberry
Monica Zwirek	UoD	Improving barley for biofuel production – efficient transformation for lignin manipulation



Honorary Research Fellows

Professor Richard Abbott BSc PhD
Dr Pamela Anderson PhD
Dr Hugh Barker BSc PhD
Professor Geoffrey J Barton BSc PhD
Professor Jill J.F. Belch MD(Hons) FRCP FAcadMedSci
Professor Jim Beynon BSc PhD
Professor Stephen Blackmore BSc PhD FLS CBiol FBiol FRSE
Professor Mike Blatt BSc PhD FRSE
Dr John E Bradshaw MA MSc PhD
Dr Meredith Bonierbale PhD
Dr Fraser Bransby BA MA PhD
Dr William W Christie MBE BSc PhD DSc FRSE
Professor Sir Philip Cohen FRS FRSE
Professor Pete Downes OBE FRSE MIBiol PhD
Dr Jim M Duncan MBE BSc PhD
Dr Andy Flavell BSc PhD
Professor Geoff Gadd BSc PhD DSc FBS FLS
Professor Mary Gibby BSc PhD FRSE FRSA
Professor Frank Gunstone BSc PhD DSc FRSC FRSE
Professor Claire Halpin BSc MSc H Dip PhD
Professor Bryan Harrison CBE BSc PhD DAgFor FRS FRSE
Dr John Hayes BSc PhD
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Dr Steve Hubbard MSc DIC(London) DPhil (Oxon)

Professor Lindsey Innes OBE BSc PhD DSc FRSE
Professor Hamlyn Jones MA PhD FIHort
Professor Ken Killham FRSE FAAM
Professor Peter Langridge BSc PhD
Dr William H Macfarlane Smith BSc PhD CBiol MIBiol FIMgt
Professor Gordon Machray BSc PhD
Mr George R Mackay MBE BSc MSc CBiol FBS
Dr Donald K L MacKerron MBE BSc PhD
Professor Tom Meagher BA PhD
Professor Andrew J Millar BA PhD
Professor Hugh Nimmo MA PhD FRSA
Professor Karl Oparka BSc PhD
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Professor Wayne Powell BSc MSc PhD DSc
Professor John Raven BA PhD HonPhD(Umea) CBiol FBS FRS FRSE
Dr David J Robinson MA PhD
Professor David J Robinson BSc PhD
Professor Janet Sprent OBE BSc DSc PhD ARCS FRSE
Dr Alyson Tobin BSc PhD
Dr David L Trudgill BSc PhD FIBiol MBE
Dr Pieter van West MSc PhD
Professor Roberto Viola DipAgrSci PhD
Dr Brian Williamson BSc MSc PhD DSc

SCRI Research Programme

ongoing as at 1 October 2010

The research programme is commissioned by RERAD (Scottish Government: Rural and Environment Research and Analysis Directorate) and a variety of other funders. The list contains the body that awarded the grant and the title of the project and, in the case of RERAD, the commissioning number.

RERAD Core – Programme 1

Workpackage 1.1	Barley Genetics
Workpackage 1.2	Potato Genetics
Workpackage 1.3	Soft Fruit Genetics & Pathology
Workpackage 1.4	Barley Pathology
Workpackage 1.5	Potato Pathology
Workpackage 1.7	Sustainable Crop Systems

RERAD Contract Research Funding

SCR/850/10	Support for additional knowledge exchange activities: Phase 2.
SCR/918/07	Genomics-assisted dissection of barley morphology and development.
SCR/919/07	<i>Dickeya dianthicola</i> – a threat to Scottish seed potatoes.
SCR/921/09	Cell wall lignin programme: Manipulating lignin to improve biofuel conversion of plant biomass.
SCR/925/09	Study the epidemiology of <i>Phytophthora ramorum</i> and <i>Phytophthora kernoviae</i> in managed gardens and heathland in Scotland.
SCR/926/09	Functional characterisation of novel pathogenicity genes of the parasitic nematode <i>Globodera pallida</i> .
BSS/038/10	Integrating the use of climate impact projections in the MRPs.
BSS/845/06	Epidemiology, population, health and infectious disease control.
BSS/850/10	Support for additional knowledge exchange activities: Phase 2.

External research contracts

Aviagen Ltd	Development of software package for the semi-automatic tracing of longitudinal cross-sections of poultry breast images.
BASF plc	Impact of fungicidal treatments on quality blackcurrant fruit and identification of active ingredients.
Bayer Crop Science	Comparison of fungicide treatments and spray programmes for crop safety and disease control in raspberries 2010.
Biotechnology and Biological Sciences Research Council (CSI)	Exploiting the <i>Phytophthora infestans</i> genome to identify gene targets for sustainable potato protection.
BBSRC (via University of Dundee)	LoLa: What are the roles of oomycete RXLR effectors in the establishment of plant disease?
BBSRC (via University of Birmingham)	LoLa: Meiosis in barley: Manipulating crossover frequency and distribution.



Bioforsk	Plant metabolites for healthy plants and healthy people.
British Council	British–Italian Partnership Programme 2009–10: Identifying quality–structure relationships for lipase inhibition amongst the natural variation of ellagitannins from <i>Rubus</i> species.
British Ecological Society	Climate change in the underworld: how elevated CO ₂ affects root–herbivore interactions.
Carnegie Trust	Trophic cascades in a changing climate: The impact of elevated CO ₂ on above- and below-ground interactions.
Commercial	Brassica breeding.
Commercial	Soft fruit analysis.
Commercial	Potato breeding.
Commercial	Blackcurrant breeding.
Commercial	Lipid analysis.
Commercial	Barley analysis.
Department for Environment Food and Rural Affairs (Defra)	Development of appropriate variety testing methodology for assessing nitrogen requirements of new varieties in trials undertaken for national listing.
Defra (via Duchy College)	Micropropagation for the conservation of rare species under threat of infection by <i>Phytophthora ramorum</i> and <i>P. kernoviae</i> in the UK.
Defra (via Greenwich University)	Reducing energy usage and wastage by improving ethylene control of potato sprouting.
Defra (via SAC)	Sustainable and effective control of potato blight: Matching fungicide inputs to cultivar resistance level.
Defra (via SAC)	Welfare costs and benefits of existing and novel on-farm culling methods of poultry.
Defra LINK (via ADAS)	TRAMLINES: Practical cost-effective techniques to reduce pollution from tramlines in combinable crops: A field and catchment scale evaluation.
Defra LINK (via East Malling Research)	Developing biocontrol methods and their integration in sustainable pest and disease management in blackcurrant production.
Defra LINK (via SAC)	CORACLE: Control of <i>Ramularia</i> leaf spot in a changing climate.
Defra/RERAD	Integrated pest and disease management for high quality protected raspberry production.
Defra/RERAD LINK	QUOATS: Harnessing new technologies for sustainable oat production and utilisation. (SCR/928/09)
European Union (EU)	EURASNET: European alternative splicing network.
EU	EU-SOL: High quality solanaceous crops for consumers, processors and producers by exploration of natural biodiversity
EU	BIOEXPLOIT: Exploitation of natural plant biodiversity for the pesticide-free production of food.
EU	GENBERRY: European small berries.
EU	SPICY: Smart tools for prediction and improvement of crop yield.
EU	<i>Triticeae</i> Genome: Genomics for <i>Triticeae</i> improvement.
EU	PLAPROVA: Plant production of vaccines.
EU	BrainHealthFood: Bioactive compounds from blackcurrant processing waste for brain health.
EU	Meiosys: Systematic analysis of factors controlling meiotic recombination in higher plants.
EU	NUECrops: Improving nutrient efficiency in major European food, feed and biofuel crops to reduce the negative environmental impact of crop production.

EU	METAPRO: The development of tools and effective strategies for the optimisation of useful secondary metabolite production in plants.
EU	TiMet: Linking the circadian clock to metabolism.
EU	Legume Futures: Legume supported cropping systems for Europe.
EU Interreg IVB	Climafruit: Future proofing the North Sea berry fruit industry in times of climate change.
European Science Foundation	Exploiting genomics to understand plant–nematode interactions.
Home-Grown Cereals Authority (HGCA)	Fungicide performance information for barley growers.
Horticultural Development Council (HDC)	Assessment of plant elicitors to induce resistance against head rot in broccoli.
International Atomic Energy Agency	SCRI barley mutation grids.
Just the Berries Ltd	Blackcurrant spinal blood testing for Parkinson's disease.
Ministerio de Educacion y Ciencia (CICYT) in Spain	Study of the effect of the treatment with methyl jasmonate on the bioformation of chiral volatile compounds in vegetal foods.
Natural Environmental Research Council (via University of Stirling)	Microbial diversity in Antarctic soils.
Norwegian Research Council	Metabolic profiling of <i>Rubus</i> (cloudberry and raspberry): Effect of inheritance and environment on phytochemicals beneficial to human health and the identification of viable targets for nutritional enhancement.
Potato Council Ltd	Independent variety trials.
Potato Council Ltd	GB late blight populations: Monitoring and implications of population changes.
Potato Council Ltd	Informing management of potato diseases through epidemiology and diagnostics.
Potato Council Ltd	Aphids and virus transmission in seed potato crops.
Potato Council Ltd	Review of umami in potato.
Potato Council Ltd	Research to support further development of the PCN model: Understanding interactions in mixed populations and the potential for a second generation of PCN.
RERAD/Agriculture and Horticulture Development Board (AHDB)	A raspberry (<i>Rubus idaeus</i>) breeding consortium for the UK. (MRS/008/09)
RERAD/Defra/Potato Council Ltd	Sequencing the 'gene space' of potato chromosome IV, comparative analysis with tomato and development of a gene-based mapping platform. (SCR/920/08)
RERAD/Defra LINK (via John Innes Centre)	INSPYR: Integrated strategy to prevent mycotoxin risks.
RERAD/GSK (HortLink)	Development of high profile germplasm for UK production of blueberries. (MRS/007/09)
RERAD/HDC (HortLink)	Developing breeding and selection tools to reduce spoilage of soft fruits and wastage in the supply chain. (SCR/924/09)
RERAD/Rothamsted International LINK	Producing low acrylamide risk potatoes. (SCR/923/09)
RERAD (via SAC)	Research towards an integrated measurement of meat eating quality.
Royal Society	A novel caspase-like protease for plant programmed cell death (PCD).

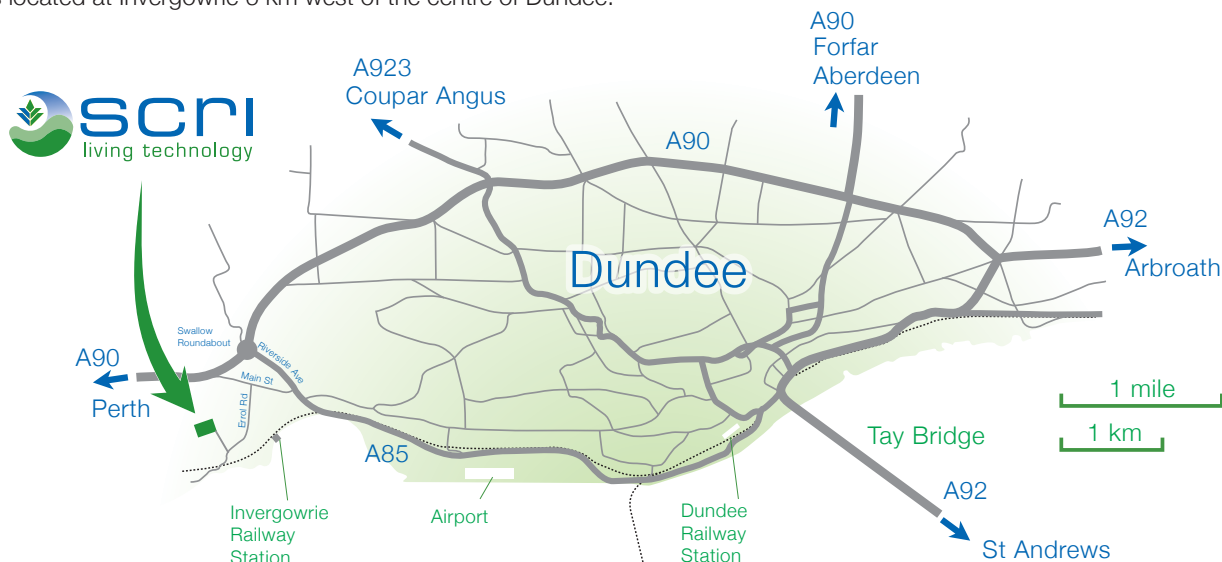


Royal Society of Edinburgh/ Scottish Government/Marie Curie Actions 2010	Personal Research Fellowship – Dr Jorunn Bos.
Scottish Agricultural College (SAC)	Study to assess the subjective experience, including pain, of broiler chickens with different gait scores.
Scottish Agricultural College	Strategies for the eradication of bovine tuberculosis.
Scottish Agricultural College	Early environment effects on welfare, health and productivity.
Scottish Agricultural College	Novel approaches for the management of cabbage root fly.
Scottish Agricultural College	WildTech: Novel technologies for surveillance of emerging and re-emerging infections of wildlife.
Scottish Government	Malawi Development Fund: Strengthening potato development.
Scottish Funding Council	Scottish Bioinformatics Research Network (SBRN) maximising bioinformatics infrastructure for Scottish health, agriculture and industry.
Technology Strategy Board	Breeding for physical resistance traits – protecting soft fruit crops from pests and pathogens.
Technology Strategy Board	MIDRIB: Molecular improvement of disease resistance in barley.
Technology Strategy Board	SIBLINGS: Symptomless infection of barley–resistance breeding and integrated crop protection strategies.
Tio Ltd & Innovation Portal	Shelf life extension in carrots.
Universidade de Evora, Portugal	Genomic analysis of bacteria associated with pinewood nematode infection.
University of Aarhus, Denmark	Ultrastructural analysis of rhizobial endocytosis in the model legume <i>Medicago truncatula</i> .
University of Ghent, Belgium	EUMAINE: European Master of Science in Nematology.

Directions to SCRI

SCRI is on the east coast of Scotland, midway between Edinburgh and Aberdeen.

It is located at Invergowrie 6 km west of the centre of Dundee.



By road

From Dundee: Leave the city in a westerly direction along Riverside Drive and Riverside Avenue, towards Perth (A85). Take the left hand turn into Invergowrie, continue past the shops and the Post Office then turn left into Errol Road, which is signposted for SCRI. Follow the road round a sharp right hand bend. The entrance to SCRI is marked with a sign at the foot of the drive on your right.

From Aberdeen: Take the A90 south to Dundee, following the Kingsway around the city in the direction of Perth to the Swallow/Landmark Hotel roundabout. Turn left into Riverside Avenue (signposted for the city centre A85) and take the next on the right signposted for Invergowrie. Follow Main Street past the shops and the Post Office taking the next left into Errol Road, signposted for SCRI. Follow the road round a sharp right hand bend. The entrance to SCRI is marked with a sign at the foot of the drive on your right.

From Perth: Take the A90 in an easterly direction to Dundee to the roundabout at the junction with the A85. Turn right into Riverside Avenue (signposted for the city centre A85) and take the next on the right signposted for Invergowrie. Follow Main Street past the shops and the Post Office taking the next left into Errol Road,

signposted for SCRI. Follow the road round a sharp right hand bend. The entrance to SCRI is marked with a sign at the foot of the drive on your right.

By bus

Invergowrie is served by the 16 and 77 bus routes. There are bus stops on Main Street, Station Road and Errol Road and there is a footpath to SCRI between the houses on Errol Road. For information on travelling in Dundee visit the Dundee Travel Information website. For bus timetables and information see the Stagecoach Bus website.

www.dundee-travelinfo.com
www.stagecoachbus.com

By train

Regular trains from Glasgow, Edinburgh, London and other UK cities run to Dundee. Infrequent trains stop at Invergowrie

www.nationalrail.co.uk

By air

Air France runs regular flights between London City and Dundee airports as part of its CityJet service. Flybe flies to Belfast City and Birmingham International airports from Dundee.

www.airfrance.co.uk
www.flybe.com

